CORONAVIRUS VACCINE

This disclosure relates to the field of RNA to prevent or treat coronavirus infection. In particular, the present disclosure relates to methods and agents for vaccination against coronavirus infection and inducing effective coronavirus antigen-specific immune responses such as antibody and/or T cell responses. These methods and agents are, in particular, useful for the prevention or treatment of coronavirus infection. Administration of RNA disclosed herein to a subject can protect the subject against coronavirus infection. Specifically, in one embodiment, the present disclosure relates to methods comprising administering to a subject RNA encoding a peptide or protein comprising an epitope of SARS-CoV-2 spike protein (S protein) for inducing an immune response against coronavirus S protein, in particular S protein of SARS-CoV-2, in the subject, i.e., vaccine RNA encoding vaccine antigen. Administering to the subject RNA encoding vaccine antigen may provide (following expression of the RNA by appropriate target cells) vaccine antigen for inducing an immune response against vaccine antigen (and disease-associated antigen) in the subject.

The present disclosure further relates to the fields of packaging, transportation, and storage of temperature-sensitive materials, such as biological and/or pharmaceutical products. Various aspects of such packaging, transportation, and storage are provided herein for ultra-low temperature materials useful for the treatment and/or prevention of disease. The present disclosure also provides packaging materials, methods of transportation, and methods of storage for maintaining biological and/or pharmaceutical materials at ultra-low temperatures in order to maintain the integrity of the materials.

In December 2019, a pneumonia outbreak of unknown cause occurred in Wuhan, China and it became clear that a novel coronavirus (severe acute respiratory syndrome coronavirus 2;

SARS-CoV-2) was the underlying cause. The genetic sequence of SARS-CoV-2 became available to the WHO and public (MN908947.3) and the virus was categorized into the betacoronavirus subfamily. By sequence analysis, the phylogenetic tree revealed a closer relationship to severe acute respiratory syndrome (SARS) virus isolates than to another coronavirus infecting humans, namely the Middle East respiratory syndrome (MERS) virus. On February 2nd, a total of 14'557 cases were globally confirmed in 24 countries including Germany and a subsequent self-sustaining, human-to-human virus spread resulted in that SARS-CoV-2 became a global epidemic.

Coronaviruses are positive-sense, single-stranded RNA ((+)ssRNA) enveloped viruses that encode for a total of four structural proteins, spike protein (S), envelope protein (E), membrane protein (M) and nucleocapsid protein (N). The spike protein (S protein) is responsible for receptor-recognition, attachment to the cell, infection via the endosomal pathway, and the genomic release driven by fusion of viral and endosomal membranes. Though sequences between the different family members vary, there are conserved regions and motifs within the S protein making it possible to divide the S protein into two subdomains: S1 and S2. While the S2, with its transmembrane domain, is responsible for membrane fusion, the S1 domain recognizes the virus-specific receptor and binds to the target host cell. Within several coronavirus isolates, the receptor binding domain (RBD) was identified and a general structure of the S protein defined (Figure 1).

Vaccine approaches and therapeutics against SARS-CoV-2 are currently not available, but urgently needed.

Due to the importance of the S protein in host cell recognition and entry, as well as in the induction of virus neutralising antibodies by the host immune system, we decided to target the viral S protein of SARS-CoV-2 and subdomains of the S protein such as S1 or RBD for vaccine development. Mutations within the regions important for conformation might be beneficial for inducing a stronger protective immune response. Therefore, we envision testing

several constructs (Figure 2). As the naïve S protein is a trimer and this trimeric structure has most likely an effect on the stability of the protein and the antigenicity, we included a strategy based on a stabilized construct introducing the T4 bacteriophage fibritin domain which is also in use in HIV for generating stable gp140 trimers and functional for SARS RBD-constructs.

Summary

The present invention generally embraces the immunotherapeutic treatment of a subject comprising the administration of RNA, i.e., vaccine RNA, encoding an amino acid sequence, i.e., a vaccine antigen, comprising SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof, i.e., an antigenic peptide or protein. Thus, the vaccine antigen comprises an epitope of SARS-CoV-2 S protein for inducing an immune response against coronavirus S protein, in particular SARS-CoV-2 S protein, in the subject. RNA encoding vaccine antigen is administered to provide (following expression of the polynucleotide by appropriate target cells) antigen for induction, i.e., stimulation, priming and/or expansion, of an immune response, e.g., antibodies and/or immune effector cells, which is targeted to target antigen (coronavirus S protein, in particular SARS-CoV-2 S protein) or a procession product thereof. In one embodiment, the immune response which is to be induced according to the present disclosure is a B cell-mediated immune response, i.e., an antibody-mediated immune response. Additionally or alternatively, in one embodiment, the immune response which is to be induced according to the present disclosure is a T cell-mediated immune response. In one embodiment, the immune response is an anti-coronavirus, in particular anti-SARS-CoV-2 immune response.

The vaccine described herein comprises as the active principle single-stranded RNA that may be translated into the respective protein upon entering cells of a recipient. In addition to wildtype or codon-optimized sequences encoding the antigen sequence, the RNA may contain one or more structural elements optimized for maximal efficacy of the RNA with respect to

stability and translational efficiency (5' cap, 5' UTR, 3' UTR, poly(A)-tail). In one embodiment, the RNA contains all of these elements. In one embodiment, beta-S-ARCA(D1) ($m_2^{7,2'-O}$GppSpG) or $m_2^{7,3'-O}$Gppp($m_1^{2'-O}$)ApG may be utilized as specific capping structure at the 5'-end of the RNA drug substances. As 5'-UTR sequence, the 5'-UTR sequence of the human alpha-globin mRNA, optionally with an optimized 'Kozak sequence' to increase translational efficiency may be used. As 3'-UTR sequence, a combination of two sequence elements (FI element) derived from the "amino terminal enhancer of split" (AES) mRNA (called F) and the mitochondrial encoded 12S ribosomal RNA (called I) placed between the coding sequence and the poly(A)-tail to assure higher maximum protein levels and prolonged persistence of the mRNA may be used. These were identified by an *ex vivo* selection process for sequences that confer RNA stability and augment total protein expression (see WO 2017/060314, herein incorporated by reference). Alternatively, the 3'-UTR may be two re-iterated 3'-UTRs of the human beta-globin mRNA. Furthermore, a poly(A)-tail measuring 110 nucleotides in length, consisting of a stretch of 30 adenosine residues, followed by a 10 nucleotide linker sequence (of random nucleotides) and another 70 adenosine residues may be used. This poly(A)-tail sequence was designed to enhance RNA stability and translational efficiency.

Furthermore, a secretory signal peptide (sec) may be fused to the antigen-encoding regions preferably in a way that the sec is translated as N terminal tag. In one embodiment, sec corresponds to the secreotory signal peptide of the S protein. Sequences coding for short linker peptides predominantly consisting of the amino acids glycine (G) and serine (S), as commonly used for fusion proteins may be used as GS/Linkers.

The vaccine RNA described herein may be complexed with proteins and/or lipids, preferably lipids, to generate RNA-particles for administration. If a combination of different RNAs is used, the RNAs may be complexed together or complexed separately with proteins and/or lipids to generate RNA-particles for administration.

In one aspect, the invention relates to a composition or medical preparation comprising RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof.

In one embodiment, an immunogenic fragment of the SARS-CoV-2 S protein comprises the S1 subunit of the SARS-CoV-2 S protein, or the receptor binding domain (RBD) of the S1 subunit of the SARS-CoV-2 S protein.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is able to form a multimeric complex, in particular a trimeric complex. To this end, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof may comprise a domain allowing the formation of a multimeric complex, in particular a trimeric complex of the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof. In one embodiment, the domain allowing the formation of a multimeric complex comprises a trimerization domain, for example, a trimerization domain as described herein.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is encoded by a coding sequence which is codon-optimized and/or the G/C content of which is increased compared to wild type coding sequence, wherein the codon-optimization and/or the increase in the G/C content preferably does not change the sequence of the encoded amino acid sequence.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a secretory signal peptide.

In one embodiment, the secretory signal peptide is fused, preferably N-terminally, to a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof.

In one embodiment,

(i) the RNA encoding the secretory signal peptide comprises the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9; and/or

(ii) the secretory signal peptide comprises the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of SEQ ID NO: 6, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6, or a fragment of the nucleotide sequence of SEQ ID NO: 6, or the nucleotide sequence

having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of SEQ ID NO: 5, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 5, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5.

In one embodiment, the RNA is a modified RNA, in particular a stabilized mRNA. In one embodiment, the RNA comprises a modified nucleoside in place of at least one uridine. In one embodiment, the RNA comprises a modified nucleoside in place of each uridine. In one embodiment, the modified nucleoside is independently selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U).

In one embodiment, the RNA comprises a modified nucleoside in place of uridine.

In one embodiment, the modified nucleoside is selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U).

In one embodiment, the RNA comprises a 5' cap.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a 5' UTR comprising the nucleotide sequence of SEQ ID NO: 12, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 12.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a 3' UTR comprising the nucleotide

sequence of SEQ ID NO: 13, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 13.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a poly-A sequence.

In one embodiment, the poly-A sequence comprises at least 100 nucleotides.

In one embodiment, the poly-A sequence comprises or consists of the nucleotide sequence of SEQ ID NO: 14.

In one embodiment, the RNA is formulated or is to be formulated as a liquid, a solid, or a combination thereof.

In one embodiment, the RNA is formulated or is to be formulated for injection.

In one embodiment, the RNA is formulated or is to be formulated for intramuscular administration.

In one embodiment, the RNA is formulated or is to be formulated as particles.

In one embodiment, the particles are lipid nanoparticles (LNP) or lipoplex (LPX) particles.

In one embodiment, the LNP particles comprise ((4-hydroxybutyl)azanediyl)bis(hexane-6,1-diyl)bis(2-hexyldecanoate), 2-[(polyethylene glycol)-2000]-N,N-ditetradecylacetamide, 1,2-Distearoyl-sn-glycero-3-phosphocholine, and cholesterol.

In one embodiment, the RNA lipoplex particles are obtainable by mixing the RNA with liposomes. In one embodiment, the RNA lipoplex particles are obtainable by mixing the RNA with lipids.

In one embodiment, the RNA is formulated or is to be formulated as colloid. In one embodiment, the RNA is formulated or is to be formulated as particles, forming the dispersed phase of a colloid. In one embodiment, 50% or more, 75% or more, or 85% or more of the RNA are present in the dispersed phase. In one embodiment, the RNA is formulated or is to be formulated as particles comprising RNA and lipids. In one embodiment, the particles are

formed by exposing RNA, dissolved in an aqueous phase, with lipids, dissolved in an organic phase. In one embodiment, the organic phase comprises ethanol. In one embodiment, the particles are formed by exposing RNA, dissolved in an aqueous phase, with lipids, dispersed in an aqueous phase. In one embodiment, the lipids dispersed in an aqueous phase form liposomes.

In one embodiment, the RNA is mRNA or saRNA.

In one embodiment, the composition or medical preparation is a pharmaceutical composition.

In one embodiment, the composition or medical preparation is a vaccine.

In one embodiment, the pharmaceutical composition further comprises one or more pharmaceutically acceptable carriers, diluents and/or excipients.

In one embodiment, the composition or medical preparation is a kit.

In one embodiment, the RNA and optionally the particle forming components are in separate vials.

In one embodiment, the kit further comprises instructions for use of the composition or medical preparation for inducing an immune response against coronavirus in a subject.

In one aspect, the invention relates to the composition or medical preparation described herein for pharmaceutical use.

In one embodiment, the pharmaceutical use comprises inducing an immune response against coronavirus in a subject.

In one embodiment, the pharmaceutical use comprises a therapeutic or prophylactic treatment of a coronavirus infection.

In one embodiment, the composition or medical preparation described herein is for administration to a human.

In one embodiment, the coronavirus is a betacoronavirus.

In one embodiment, the coronavirus is a sarbecovirus.

In one embodiment, the coronavirus is SARS-CoV-2.

In one aspect, the invention relates to a method of inducing an immune response against coronavirus in a subject comprising administering to the subject a composition comprising RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof.

In one embodiment, an immunogenic fragment of the SARS-CoV-2 S protein comprises the S1 subunit of the SARS-CoV-2 S protein, or the receptor binding domain (RBD) of the S1 subunit of the SARS-CoV-2 S protein.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is able to form a multimeric complex, in particular a trimeric complex. To this end, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof may comprise a domain allowing the formation of a multimeric complex, in particular a trimeric complex of the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof. In one embodiment, the domain allowing the formation of a multimeric complex comprises a trimerization domain, for example, a trimerization domain as described herein.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is encoded by a coding sequence which is codon-optimized and/or the G/C content of which is increased compared to wild type coding sequence, wherein the codon-optimization and/or the increase in the G/C content preferably does not change the sequence of the encoded amino acid sequence.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7.

In one embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a secretory signal peptide.

In one embodiment, the secretory signal peptide is fused, preferably N-terminally, to a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof.

In one embodiment,

(i) the RNA encoding the secretory signal peptide comprises the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9; and/or

(ii) the secretory signal peptide comprises the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1.

In one embodiment,

(i) the RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the nucleotide sequence of SEQ ID NO: 6, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6, or a fragment of the nucleotide sequence of SEQ ID NO: 6, or the nucleotide sequence

having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6; and/or

(ii) a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises the amino acid sequence of SEQ ID NO: 5, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 5, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5.

In one embodiment, the RNA is a modified RNA, in particular a stabilized mRNA. In one embodiment, the RNA comprises a modified nucleoside in place of at least one uridine. In one embodiment, the RNA comprises a modified nucleoside in place of each uridine. In one embodiment, the modified nucleoside is independently selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U).

In one embodiment, the RNA comprises a modified nucleoside in place of uridine.

In one embodiment, the modified nucleoside is selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U).

In one embodiment, the RNA comprises a cap.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a 5' UTR comprising the nucleotide sequence of SEQ ID NO: 12, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 12.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a 3' UTR comprising the nucleotide

sequence of SEQ ID NO: 13, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 13.

In one embodiment, the RNA encoding an amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprises a poly-A sequence.

In one embodiment, the poly-A sequence comprises at least 100 nucleotides.

In one embodiment, the poly-A sequence comprises or consists of the nucleotide sequence of SEQ ID NO: 14.

In one embodiment, the RNA is formulated as a liquid, a solid, or a combination thereof.

In one embodiment, the RNA is administered by injection.

In one embodiment, the RNA is administered by intramuscular administration.

In one embodiment, the RNA is formulated as particles.

In one embodiment, the particles are lipid nanoparticles (LNP) or lipoplex (LPX) particles.

In one embodiment, the LNP particles comprise ((4-hydroxybutyl)azanediyl)bis(hexane-6,1-diyl)bis(2-hexyldecanoate), 2-[(polyethylene glycol)-2000]-N,N-ditetradecylacetamide, 1,2-Distearoyl-sn-glycero-3-phosphocholine, and cholesterol.

In one embodiment, the RNA lipoplex particles are obtainable by mixing the RNA with liposomes. In one embodiment, the RNA lipoplex particles are obtainable by mixing the RNA with lipids.

In one embodiment, the RNA is formulated as colloid. In one embodiment, the RNA is formulated as particles, forming the dispersed phase of a colloid. In one embodiment, 50% or more, 75% or more, or 85% or more of the RNA are present in the dispersed phase. In one embodiment, the RNA is formulated as particles comprising RNA and lipids. In one embodiment, the particles are formed by exposing RNA, dissolved in an aqueous phase, with lipids, dissolved in an organic phase. In one embodiment, the organic phase comprises ethanol. In one embodiment, the particles are formed by exposing RNA, dissolved in an

aqueous phase, with lipids, dispersed in an aqueous phase. In one embodiment, the lipids dispersed in an aqueous phase form liposomes.

In one embodiment, the RNA is mRNA or saRNA.

In one embodiment, the method is a method for vaccination against coronavirus.

In one embodiment, the method is a method for therapeutic or prophylactic treatment of a coronavirus infection.

In one embodiment, the subject is a human.

In one embodiment, the coronavirus is a betacoronavirus.

In one embodiment, the coronavirus is a sarbecovirus.

In one embodiment, the coronavirus is SARS-CoV-2.

In one embodiment of the method described herein, the composition is a composition described herein.

In one aspect, the invention relates to a composition or medical preparation described herein for use in a method described herein.

Among other things, the present disclosure demonstrates that a composition comprising a lipid nanoparticle encapsulated mRNA encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein) can achieve detectable antibody titer against the epitope in serum within 7 days after administration to a population of adult human subjects according to a regimen that includes administration of at least one dose of the vaccine composition. Moreover, the present disclosure demonstrates persistence of such antibody titer. In some embodiments, the present disclosure demonstrates increased such antibody titer when a modified mRNA is used, as compared with that achieved with a corresponding unmodified mRNA.

In some embodiments, a provided regimen includes at least one dose. In some embodiments, a provided regimen includes a first dose and at least one subsequent dose. In some embodiments, the first dose is the same amount as at least one subsequent dose. In some embodiments, the first dose is the same amount as all subsequent doses. In some embodiments, the first dose is a different amount as at least one subsequent dose. In some embodiments, the first dose is a different amount than all subsequent doses. In some embodiments, a provided regimen comprises two doses. In some embodiments, a provided regimen consists of two doses.

In particular embodiments, the immunogenic composition is formulated as a single-dose in a container, e.g., a vial. In some embodiments, the immunogenic composition is formulated as a multi-dose formulation in a vial. In some embodiments, the multi-dose formulation includes at least 2 doses per vial. In some embodiments, the multi-dose formulation includes a total of 2-20 doses per vial, such as, for example, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, or 12 doses per vial. In some embodiments, each dose in the vial is equal in volume. In some embodiments, a first dose is a different volume than a subsequent dose.

A "stable" multi-dose formulation exhibits no unacceptable levels of microbial growth, and substantially no or no breakdown or degradation of the active biological molecule component(s). As used herein, a "stable" immunogenic composition includes a formulation that remains capable of eliciting a desired immunologic response when administered to a subject.

In some embodiments, the multi-dose formulation remains stable for a specified time with multiple or repeated inoculations/insertions into the multi-dose container. For example, in some embodiments the multi-dose formulation may be stable for at least three days with up to ten usages, when contained within a multi-dose container. In some embodiments, the multi-dose formulations remain stable with 2-20 inoculations/insertions.

In some embodiments, administration of a composition comprising a lipid nanoparticle encapsulated mRNA encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein), e.g., according to a regimen as described herein, may result in lymphopenia in some subjects (e.g., in all subjects, in most subjects, in about 50% or fewer, in about 40% or fewer, in about 40% or fewer, in about 25% or fewer, in about 20% or fewer, in about 15% or fewer, in about 10% or fewer, in about 5% or fewer, etc). Among other things, the present disclosure demonstrates that such lymphopenia can resolve over time. For example, in some embodiments, lymphopenia resolves within about 14, about 10, about 9, about 8, about 7 days or less. In some embodiments, lymphopenia is Grade 3, Grade 2, or less.

Thus, among other things, the present disclosure provides compositions comprising a lipid nanoparticle encapsulated mRNA encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein) that are characterized, when administered to a relevant population of adults, to display certain characteristics (e.g., achieve certain effects) as described herein. In some embodiments, provided compositions may have been prepared, stored, transported, characterized, and/or used under conditions where temperature does not exceed a particular threshold. Alternatively or additionally, in some embodiments, provided compositions may have been protected from light (e.g., from certain wavelengths) during some or all of their preparation, storage, transport, characterization, and/or use. In some embodiments, one or more features of provided compositions (e.g., mRNA stability, as may be assessed, for example, by one or more of size, presence of particular moiety or modification, etc; lipid nanoparticle stability or aggregation, pH, etc) may be or have been assessed at one or more points during preparation, storage, transport, and/or use prior to administration.

Among other things, the present disclosure documents that certain provided compositions in which nucleotides within an mRNA are not modified (e.g., are naturally-occurring A, U, C, G),

and/or provided methods relating to such compositions, are characterized (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population), by an intrinsic adjuvant effect. In some embodiments, such composition and/or method can induce an antibody and/or a T cell response. In some embodiments, such a composition and/or method can induce a higher T cell response, as compared to conventional vaccines (e.g., non-mRNA vaccines such as protein vaccines).

Alternatively or additionally, the present disclosure documents that provided compositions (e.g., compositions comprising a lipid nanoparticle encapsulated mRNA encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein)) in which nucleotides within an mRNA are modified, and/or provided methods relating to such compositions, are characterized (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population), by absence of an intrinsic adjuvant effect, or by a reduced intrinsic adjuvant effect as compared with an otherwise comparable composition (or method) with unmodified results. Alternatively or additionally, in some embodiments, such compositions (or methods) are characterized in that they (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population) induce an antibody response and/or a CD4+ T cell response. Still further alternatively or additionally, in some embodiments, such compositions (or methods) are characterized in that they (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population) induce a higher CD4+ T cell response than that observed with an alternative vaccine format (e.g., a peptide vaccine). In some embodiments involving modified nucleotides, such modified nucleotides may be present, for example, in a 3' UTR sequence, an antigen-encoding sequence, and/or a 5'UTR sequence. In some embodiments, modified nucleotides are or include one or more modified uracil residues and/or one or more modified cytosine residues.

Among other things, the present disclosure documents that provided (e.g., compositions comprising a lipid nanoparticle encapsulated mRNA encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein)) and/or methods are characterized by (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population) sustained expression of an encoded polypeptide (e.g., of a SARS-CoV-2-encoded protein [such as an S protein] or portion thereof, which portion, in some embodiments, may be or comprise an epitope thereof). For example, in some embodiments, such compositions and/or methods are characterized in that, when administered to a human, they achieve detectable polypeptide expression in a biological sample (e.g., serum) from such human and, in some embodiments, such expression persists for a period of time that is at least at least 36 hours or longer, including, e.g., at least 48 hours, at least 60 hours, at least 72 hours, at least 96 hours, at least 120 hours, at least 148 hours, or longer.

Those skilled in the art, reading the present disclosure, will appreciate that it describes various mRNA constructs encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein)). Such person of ordinary skill, reading the present disclosure, will particularly appreciate that it describes various mRNA constructs encoding at least a portion of a SARS-CoV-2 S protein, for example at least an RBD portion of a SARS-CoV-2 S protein. Still further, such a person of ordinary skill, reading the present disclosure, will appreciate that it describes particular characteristics and/or advantages of mRNA constructs encoding at least a portion (e.g., that is or comprises an epitope) of a SARS-CoV-2-encoded polypeptide (e.g., of a SARS-CoV-2-encoded S protein). Among other things, the present disclosure particularly documents surprising and useful characteristics and/or advantages of certain mRNA constructs encoding a SARS-CoV-2 RBD portion and, in some embodiments, not encoding a full length SARS-CoV-2 S protein. Without wishing to be bound by any particular theory, the present disclosure suggests that provided

mRNA constructs that encode less than a full-length SARS-CoV-2 S protein, and particularly those that encode at least an RBD portion of such SARS-CoV-2 S protein may be particularly useful and/or effective for use as or in an immunogenic composition (e.g., a vaccine), and/or for achieving immunological effects as described herein (e.g., generation of SARS-CoV-2 neutralizing antibodies, and/or T cell responses (e.g., CD4+ and/or CD8+ T cell responses)).

In some embodiments, the present disclosure provides an RNA (e.g., mRNA) comprising an open reading frame encoding a polypeptide that comprises a receptor-binding portion of a SARS-CoV-2 S protein, which RNA is suitable for intracellular expression of the polypeptide. In some embodiments, such an encoded polypeptide does not comprise the complete S protein. In some embodiments, the encoded polypeptide comprises the receptor binding domain (RBD), for example, as shown in SEQ ID NO: 5. In some embodiments, the encoded polypeptide comprises the peptide according to SEQ ID NO: 29 or 31. In some embodiments, such an RNA (e.g., mRNA) may be complexed by a (poly)cationic polymer, polyplex(es), protein(s) or peptide(s). In some embodiments, such an RNA may be formulated in a lipid nanoparticle (e.g., ones described herein). In some embodiments, such an RNA (e.g., mRNA) may be particularly useful and/or effective for use as or in an immunogenic composition (e.g., a vaccine), and/or for achieving immunological effects as described herein (e.g., generation of SARS-CoV-2 neutralizing antibodies, and/or T cell responses (e.g., CD4+ and/or CD8+ T cell responses)). In some embodiments, such an RNA (e.g., mRNA) may be useful for vaccinating humans (including, e.g., humans known to have been exposed and/or infected by SARS-CoV-2, and/or humans not known to have been exposed to SARS-CoV-2).

Those skilled in the art, reading the present disclosure, will further appreciate that it describes various mRNA constructs comprising a nucleic acid sequence that encodes a full-length SARS-CoV-2 Spike protein (e.g., including embodiments in which such encoded SARS-CoV-2 Spike protein may comprise at least one or more amino acid substitutions, e.g., proline substitutions as described herein, and/or embodiments in which the mRNA sequence is codon-optimized

e.g., for mammalian, e.g., human, subjects). In some embodiments, such a full-length SARS-CoV-2 Spike protein may have an amino acid sequence that is or comprises that set forth in SEQ ID NO: 7. Still further, such a person of ordinary skill, reading the present disclosure, will appreciate, among other things, that it describes particular characteristics and/or advantages of certain mRNA constructs comprising a nucleic acid sequence that encodes a full-length SARS-CoV-2 Spike protein. Without wishing to be bound by any particular theory, the present disclosure suggests that provided mRNA constructs that encode a full-length SARS-CoV-2 S protein may be particularly useful and/or effective for use as or in an immunogenic composition (e.g., a vaccine) in particular subject population (e.g., particular age populations). For example, in some embodiments, such an mRNA composition may be particularly useful in younger (e.g., less than 25 years old, 20 years old, 18 years old, 15 years, 10 years old, or lower) subjects; alternatively or additionally, in some embodiments, such an mRNA composition may be particularly useful in elderly subjects (e.g., over 55 years old, 60 years old, 65 years old, 70 years old, 75 years old, 80 years old, 85 years old, or higher). In particular embodiments, an immunogenic composition comprising such an mRNA construct provided herein exhibits a minimal to modest increase (e.g., no more than 30% increase, no more than 20% increase, or no more than 10% increase, or lower) in dose level and/or dose number-dependent systemic reactogenicity (e.g., fever, fatigue, headache, chills, diarrhea, muscle pain, and/or joint pain, etc.) and/or local tolerability (e.g., pain, redness, and/or swelling, etc.), at least in some subjects (e.g., in some subject age groups); in some embodiments, such reactogenicity and/or local tolerability is observed particularly, in in younger age group (e.g., less than 25 years old, 20 years old, 18 years years old or lower) subjects, and/or in older (e.g., elderly) age group (e.g., 65-85 years old). In some embodiments, provided mRNA constructs that encode a full-length SARS-CoV-2 S protein may be particularly useful and/or effective for use as or in an immunogenic composition (e.g., a vaccine) for inducing SARS-CoV-2 neutralizing antibody response level in a population of subjects that are at high risk for severe dieases

associated with SARS-CoV-2 infection (e.g., an elderly population, for example, 65-85 year-old group). In some embodiments, a person of ordinary skill, reading the present disclosure, will appreciate, among other things, that provided mRNA constructs that encode a full-length SARS-CoV-2 S protein, which exhibit a favorable reactogenicity profile (e.g., as described herein) in younger and elderly age populations, may be particularly useful and/or effective for use as or in an immunogenic composition (e.g., a vaccine) for achieving immunological effects as described herein (e.g., generation of SARS-CoV-2 neutralizing antibodies, and/or T cell responses (e.g., CD4+ and/or CD8+ T cell responses)). In some embodiments, the present disclosure also suggests that provided mRNA constructs that encode a full-lenth SARS-CoV-2 S protein may be particularly effective to protect against SARS-CoV-2 infection, as characterized by earlier clearance of SARS-CoV-2 viral RNA in non-human mammalian subjects (e.g., rhesus macaques) that were immunized with immunogenic compositions comprising such mRNA constructs and subsequently challenged by SARS-CoV-2 strain. In some embodiments, such earlier clearance of SARS-CoV-2 viral RNA may be observed in the nose of non-human mammalian subjects (e.g., rhesus macaques) that were immunized with immunogenic compositions comprising such mRNA constructs and subsequently challenged by SARS-CoV-2 strain.

In some embodiments, the present disclosure provides an RNA (e.g., mRNA) comprising an open reading frame encoding a full-length SARS-CoV-2 S protein (e.g., a full-length SARS-CoV-2 S protein with one or more amino acid substitutions), which RNA is suitable for intracellular expression of the polypeptide. In some embodiments, the encoded polypeptide comprises the amino acid sequence of SEQ ID NO:_7. In some embodiments, such an RNA (e.g., mRNA) may be complexed by a (poly)cationic polymer, polyplex(es), protein(s) or peptide(s). In some embodiments, such an RNA may be formulated in a lipid nanoparticle (e.g., ones described herein).

In some embodiments, an immunogenic composition provided herein may comprise a plurality of (e.g., at least two or more, including, e.g., at least three, at least four, at least five, at least six, at least seven, at least eight, at least nine, at least ten, etc.) immunoreactive epitopes of a SARS-CoV-2 polypeptide or variants thereof. In some such embodiments, such a plurality of immunoreactive epitopes may be encoded by a plurality of RNAs (e.g., mRNAs). In some such embodiments, such a plurality of immunoreactive epitopes may be encoded by a single RNA (e.g., mRNA). In some embodiments, nucleic acid sequences encoding a plurality of immunoreactive epitopes may be separated from each other in a single RNA (e.g., mRNA) by a linker (e.g., a peptide linker in some embodiments). Without wishing to be bound by any particular theory, in some embodiments, provided polyepitope immunogenic compositions (including, e.g., those that encode a full-length SARS-CoV-2 spike protein) may be particularly useful, when considering the genetic diversity of SARS-CoV-2 variants, to provide protection against numerous viral variants and/or may offer a greater opportunity for development of a diverse and/or otherwise robust (e.g., persistent, e.g., detectable about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60 or more days after administration of one or more doses) neutralizing antibody and/or T cell response, and in particular a particularly robust T_H1-type T cell (e.g., CD4+ and/or CD8+ T cell) response.

In some embodiments, the present disclosure documents that provided compositions and/or methods are characterized by (e.g., when administered to a relevant population, which may in some embodiments be or comprise an adult population) in that they achieve one or more particular therapeutic outcomes (e.g., effective immune responses as described herein and/or detectable expression of encoded SARS-CoV-2 S protein or an immunogenic fragment thereof) with a single administration; in some such embodiments, an outcome may be assessed, for example, as compared to that observed in absence of mRNA vaccines described herein. In some embodiments, a particular outcome may be achieved at a lower dose than required for one or more alternative strategies.

In some embodiments, the present disclosure provides an immunogenic composition comprising an isolated messenger ribonucleic acid (mRNA) polynucleotide, wherein the isolated mRNA polynucleotide comprises an open reading frame encoding a polypeptide that comprises a receptor-binding portion of a SARs-CoV-2 S protein, and wherein the isolated mRNA polynucleotide is formulated in at least one lipid nanoparticle. For example, in some embodiments, such a lipid nanoparticle may comprise a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid (e.g., neutral lipid), 25-55% sterol or steroid, and 0.5-15% polymer-conjugated lipid (e.g., PEG-modified lipid). In some embodiments, a sterol or steroid included in a lipid nanoparticle may be or comprise cholesterol. In some embodiments, a neutral lipid may be or comprise 1,2-distearoyl-sn-glycero-3-phosphocholine (DSPC). In some embodiments, a polymer-conjugated lipid may be or comprise PEG2000 DMG. In some embodiments, such an immunogenic composition may comprise a total lipid content of about 1 mg to 10 mg, or 3 mg to 8 mg, or 4 mg to 6 mg. In some embodiments, such an immunogenic composition may comprise a total lipid content of about 5 mg/mL -15 mg/mL or 7.5 mg/mL-12.5 mg/mL or 9-11 mg/mL. In some embodiments, such an isolated mRNA polynucleotide is provided in an effective amount to induce an immune response in a subject administered at least one dose of the immunogenic composition. In some embodiments, a polypeptide encoded by a provided isolated mRNA polynucleotide does not comprise the complete S protein. In some embodiments, such an isolated mRNA polynucleotide provided in an immunogenic composition is not self-replicating RNA.

In some embodiments, an immune response may comprise generation of a binding antibody titer against SARS-CoV-2 protein (including, e.g., a stabilized prefusion spike trimer in some embodiments) or a fragment thereof. In some embodiments, an immune response may comprise generation of a binding antibody titer against the receptor binding domain (RBD) of the SARS-CoV-2 spike protein. In some embodiments, a provided immunogenic composition has been established to achieve a detectable binding antibody titer after administration of a

first dose, with seroconversion in at least 70% (including, e.g., at least 80%, at least 90%, at least 95% and up to 100%) of a population of subjects receiving such a provided immunogenic composition, for example, by about 2 weeks.

In some embodiments, an immune response may comprise generation of a neutralizing antibody titer against SARS-CoV-2 protein (including, e.g., a stabilized prefusion spike trimer in some embodiments) or a fragment thereof. In some embodiments, an immune response may comprise generation of a neutralizing antibody titer against the receptor binding domain (RBD) of the SARS-CoV-2 spike protein. In some embodiments, a provided immunogenic composition has been established to achieve a neutralizing antibody titer in an appropriate system (e.g., in a human infected with SARS-CoV-2 and/or a population thereof, and/or in a model system therefor). For example, in some embodiments, such neutralizing antibody titer may have been demonstrated in one or more of a population of humans, a non-human primate model (e.g., rhesus macaques), and/or a mouse model.

In some embodiments, a neutralizing antibody titer is a titer that is (e.g., that has been established to be) sufficient to reduce viral infection of B cells relative to that observed for an appropriate control (e.g., an unvaccinated control subject, or a subject vaccinated with a live attenuated viral vaccine, an inactivated viral vaccine, or a protein subunit viral vaccine, or a combination thereof). In some such embodiments, such reduction is of at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more.

In some embodiments, a neutralizing antibody titer is a titer that is (e.g., that has been established to be) sufficient to reduce the rate of asymptomatic viral infection relative to that observed for an appropriate control (e.g., an unvaccinated control subject, or a subject vaccinated with a live attenuated viral vaccine, an inactivated viral vaccine, or a protein subunit viral vaccine, or a combination thereof). In some such embodiments, such reduction is of at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more. In some embodiments, such reduction can be characterized by assessment of SARS-

CoV-2 N protein serology. Significant protection against asymptomatic infection was also confirmed by real life observations (see also: Dagan N. et al., N Engl J Med. 2021, doi: 10.1056/NEJMoa2101765. Epub ahead of print. PMID: 33626250)

In some embodiments, a neutralizing antibody titer is a titer that is (e.g., that has been established to be) sufficient to reduce or block fusion of virus with epithelial cells and/or B cells of a vaccinated subject relative to that observed for an appropriate control (e.g., an unvaccinated control subject, or a subject vaccinated with a live attenuated viral vaccine, an inactivated viral vaccine, or a protein subunit viral vaccine, or a combination thereof). In some such embodiments, such reduction is of at least 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or more.

In some embodiments, induction of a neutralizing antibody titer may be characterized by an elevation in the number of B cells, which in some embodiments may include plasma cells, class-switched IgG1- and IgG2-positive B cells, and/or germinal center B cells. In some embodiments, a provided immunogenic composition has been established to achieve such an elevation in the number of B cells in an appropriate system (e.g., in a human infected with SARS-CoV-2 and/or a population thereof, and/or in a model system therefor). For example, in some embodiments, such an elevation in the number of B cells may have been demonstrated in one or more of a population of humans, a non-human primate model (e.g., rhesus macaques), and/or a mouse model. In some embodiments, such an elevation in the number of B cells may have been demonstrated in draining lymph nodes and/or spleen of a mouse model after (e.g., at least 7 days, at least 8 days, at least 9 days, at least 10 days, at least 11 days, at least 12 days, at least 13 days, at least 14 days, after) immunization of such a mouse model with a provided immunogenic composition.

In some embodiments, induction of a neutralizing antibody titer may be characterized by a reduction in the number of circulating B cells in blood. In some embodiments, a provided immunogenic composition has been established to achieve such a reduction in the number of

circulating B cells in blood of an appropriate system (e.g., in a human infected with SARS-CoV-2 and/or a population thereof, and/or in a model system therefor). For example, in some embodiments, such a reduction in the number of circulating B cells in blood may have been demonstrated in one or more of a population of humans, a non-human primate model (e.g., rhesus macaques), and/or a mouse model. In some embodiments, such a reduction in the number of circulating B cells in blood may have been demonstrated in a mouse model after (e.g., at least 4 days, at least 5 days, at least 6 days, at least 7 days, at least 8 days, at least 9 days, at least 10 days, after) immunization of such a mouse model with a provided immunogenic composition. Without wishing to be bound by theory, a reduction in circulating B cells in blood may be due to B cell homing to lymphoid compartments.

In some embodiments, an immune response induced by a provided immunogenic composition may comprise an elevation in the number of T cells. In some embodiments, such an elevation in the number of T cells may include an elevation in the number of T follicular helper (T_{FH}) cells, which in some embodiments may comprise one or more subsets with ICOS upregulation. One of skilled in the art wil understand that proliferation of T_{FH} in germinal centres is integral for generation of an adaptive B-cell response, and also that in humans, T_{FH} occurring in the circulation after vaccination is typically correlated with a high frequency of antigen-specific antibodies. In some embodiments, a provided immunogenic composition has been established to achieve such an elevation in the number of T cells (e.g., T_{FH} cells) in an appropriate system (e.g., in a human infected with SARS-CoV-2 and/or a population thereof, and/or in a model system therefor). For example, in some embodiments, such an elevation in the number of T cells (e.g., T_{FH} cells) may have been demonstrated in one or more of a population of humans, a non-human primate model (e.g., rhesus macaques), and/or a mouse model. In some embodiments, such an elevation in the number of T cells (e.g., e.g., T_{FH} cells) may have been demonstrated in draining lymph nodes, spleen, and/or blood of a mouse model after (e.g., at least 4 days, at least 5 days, at least 6 days, at least 7 days, at least 8 days,

at least 9 days, at least 10 days, at least 11 days, at least 12 days, at least 13 days, at least 14 days, after) immunization of such a mouse model with a provided immunogenic composition. In some embodiments, a protective response against SARS-CoV-2 induced by a provided immunogenic composition has been established in an appropriate model system for SARS-CoV-2. For example, in some embodiments, such a protective response may have been demonstrated in an animal model, e.g., a non-human primate model (e.g., rhesus macaques) and/or a mouse model. In some embodiments, a non-human primate (e.g., rhesus macaque) or a polulation thereof that has/have received at least one immunization with a provided immunogenic composition is/are challenged with SARS-CoV-2, e.g., through intranasal and/or intratracheal route. In some embodiments, such a challenge may be performed several weeks (e.g., 5-10 weeks) after at least one immunization (including, e.g., at least two immunizations) with a provided immunogenic composition. In some embodiments, such a challenge may be performed when a detectable level of a SARS-CoV-2 neutralizing titer (e.g., antibody response to SARS-CoV-2 spike protein and/or a fragment thereof, including, e.g., but not limited to a stabilized prefusion spike trimer, S-2P, and/or antibody response to receptor-binding portion of SARS-CoV-2) is achieved in non-human primate(s) (e.g., rhesus macaque(s)) that has received at least one immunization (including, e.g., at least two immunizations) with a provided immunogenic composition. In some embodiments, a protective response is characterized by absence of or reduction in detectable viral RNA in bronchoalveolar lavage (BAL) and/or nasal swabs of challenged non-human primate(s) (e.g., rhesus macaque(s)). In some embodiments, immunogenic compositions described herein may have been characterized in that a larger percent of challenged animals, for example, non-human primates in a population (e.g., rhesus macaques), that have received at least one immunization (including, e.g., at least two immunizations) with a provided immunogenic composition display absence of detectable RNA in their BAL and/or nasal swab, as compared to a population of non-immunized animals, for example, non-human primates (e.g., rhesus

macaques). In some embodiments, immunogenic compositions described herein may have been characterized in that challenged animals, for example, non-human in a population (e.g., rhesus macaques), that have received at least one immunization (including, e.g., at least two immunizations) with a provided immunogenic composition may show clearance of viral RNA in nasal swab no later than 10 days, including, e.g., no later than 8 days, no later than 6 days, no later than 4 days, etc., as compared to a population of non-immunized animals, for example, non-human primates (e.g., rhesus macaques).

In some embodiments, immunogenic compositions described herein when administered tosubjects in need thereof do not substantially increase the risk of vaccine-associated enhanced respiratory disease. In some embodiments, such vaccine-associated enhanced respiratory disease may be associated with antibody-dependent enhancement of replication and/or with vaccine antigens that induced antibodies with poor neutralizing activity and Th2-biased responses. In some embodiments, immunogenic compositions described herein when administered to subjects in need thereof do not substantially increase the risk of antibody-dependent enhancement of replication.

In some embodiments, a single dose of an mRNA composition (e.g., formulated in lipid nanoparticles) can induce a therapeutic antibody response in less than 10 days of vaccination. In some embodiments, such a therapeutic antibody response may be characterized in that when such an mRNA vaccine can induce production of about 10-100 ug/mL IgG measured at 10 days after vaccination at a dose of 0.1 to 10 ug or 0.2- 5 ug in an animal model. In some embodiments, such a therapeutic antibody response may be characterized in that such an mRNA vaccine induces about 100-1000 ug/mL IgG measured at 20 days of vaccination at a dose of 0.1 to 10 ug or 0.2- 5 ug in an animal model. In some embodiments, a single dose may induce a pseudovirus-neutralization titer, as measured in an animal model, of 10-200 pVN50 titer 15 days after vaccination. In some embodiments, a single dose may induce a pseudovirus-

neutralization titer, as measured in an animal model, of 50-500 pVN50 titer 15 days after vaccination.

In some embodiments, a single dose of an mRNA composition can expand antigen-specific CD8 and/or CD4 T cell response by at least at 50% or more (including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or more), as compared to that observed in absence of such an mRNA construct encoding a SARS-COV2 immunogenic protein or fragment thereof (e.g., spike protein and/or receptor binding domain). In some embodiments, a single dose of an mRNA composition can expand antigen-specific CD8 and/or CD4 T cell response by at least at 1.5-fold or more (including, e.g., at least 2-fold, at least 3-fold, at least 5-fold, at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1000-fold, or more), as compared to that observed in absence of such an mRNA construct encoding a SARS-COV2 immunogenic protein or fragment thereof (e.g., spike protein and/or receptor binding domain).

In some embodiments, a regimen (e.g., a single dose of an mRNA composition) can expand T cells that exhibit a Th1 phenotype (e.g., as characterized by expression of IFN-gamma, IL-2, IL-4, and/or IL-5) by at least at 50% or more (including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or more), as compared to that observed in absence of such an mRNA construct encoding a SARS-COV2 immunogenic protein or fragment thereof (e.g., spike protein and/or receptor binding domain). In some embodiments, a regimen (e.g., a single dose of an mRNA composition) can expand T cells that exhibit a Th1 phenotype (e.g., as characterized by expression of IFN-gamma, IL-2, IL-4, and/or IL-5), for example by at least at 1.5-fold or more (including, e.g., at least 2-fold, at least 3-fold, at least 5-fold, at least 10-fold, at least 50-fold, at least 100-fold, at least 500-fold, at least 1000-fold, or more), as compared to that observed in absence of such an mRNA construct encoding a SARS-COV2 immunogenic protein or fragment thereof (e.g., spike protein and/or receptor binding domain). In some embodiments, a T-cell phenotype may be or comprise a Th1-dominant cytokine profile (e.g.,

as characterized by INF-gamma positive and/or IL-2 positive), and/or no by or biologically insignificant IL-4 secretion.

In some embodiments, a regimen as described herein (e.g., one or more doses of an mRNA composition) induces and/or achieves production of RBD-specific CD4+ T cells. Among other things, the present disclosure documents that mRNA compositions encoding an RBD-containing portion of a SARS-CoV-2 spike protein (e.g., and not encoding a full-length SARS-CoV-2 spike protein) may be particularly useful and/or effective in such induction and/or production of RBD-specific CD4+ T cells. In some embodiments, RBD-specific CD4+ T-cells induced by an mRNA composition described herein (e.g., by an mRNA composition that encodings an RBD-containing-portion of a SARS-CoV-2 spike protein and, in some embodiments not encoding a full-length SARS-CoV-2 spike protein) demonstrate a Th1-dominant cytokine profile (e.g., as characterized by INF-gamma positive and/or IL-2 positive), and/or by no or biologically insignificant IL-4 secretion.

In some embodiments, characterization of CD4+ and/or CD8+ T cell responses (e.g., described herein) in subjects receiving mRNA compositions (e.g., as described herein) may be performed using ex vivo assays using PBMCs collected from the subjects, e.g., assays as described in the Examples.

In some embodiments, immunogenicity of mRNA compositions described herein may be assessed by one of or more of the following serological immunongenicity assays: detection of IgG, IgM, and/or IgA to SARS-CoV-2 S protein present in blood samples of a subject receiving a provided mRNA composition, and/or neutralization assays using SARS-CoV-2 pseudovirus and/or a wild-type SARS-CoV-2 virus.

In some embodiments, an mRNA composition (e.g., as described herein) provide a relatively low adverse effect (e.g., Grade 1-Grade 2 pain, redness and/or swelling) within 7 days after vaccinations at a dose of 10 ug – 100 ug or 1 ug-50 ug. In some embodiments, mRNA compositions (e.g., as described herein) provide a relatively low observation of systemic

events (e.g., Grade 1-Grade 2 fever, fatigue, headache, chills, vomiting, diarrhea, muscle pain, joint pain, medication, and combinations thereof) within 7 days after vaccinations at a dose of 10 ug – 100 ug.

In some embodiments, mRNA compositions are characterized in that when administered to subjects at 10-100 ug dose or 1 ug-50 ug, IgG directed to a SARS-CoV2 immunogenic protein or fragment thereof (e.g., spike protein and/or receptor binding domain) may be produced at a level of 100-100,000 U/mL or 500-50,000 U/mL 21 days after vaccination.

In some embodiments, an mRNA encodes a natively-folded trimeric receptor binding protein of SARS-CoV-2. In some embodiments, an mRNA encodes a variant of such receptor binding protein such that the encoded variant binds to ACE2 at a Kd of 10 pM or lower, including, e.g., at a Kd of 9 pM, 8 pM, 7 pM, 6 pM, 5 pM, 4 pM, or lower. In some embodiments, an mRNA encodes a variant of such receptor binding protein such that the encoded variant binds to ACE2 at a Kd of 5 pM. In some embodiments, an mRNA encodes a trimeric receptor binding portion of SARS-CoV-2 that comprises an ACE2 receptor binding site. In some embodiments, an mRNA comprises a coding sequence for a receptor-binding portion of SARS-CoV-2 and a trimerization domain (e.g., a natural trimerization domain (foldon) of T4 fibritin) such that the coding sequence directs expression of a trimeric protein that has an ACE2 receptor binding site and binds ACE2. In some embodiments, an mRNA encodes a trimeric receptor binding portion of SARS-CoV-2 or a variant thereof such that its Kd is smaller than that for a monomeric receptor-binding domain (RBD) of SARS-CoV-2. For example, in some embodiments, an mRNA encodes a trimeric receptor binding portion of SARS-CoV-2 or a variant thereof such that its Kd is at least 10-fold (including, e.g., at least 50-fold, at least 100-fold, at least 500-fold, at least 1000-fold, etc.) smaller than that for a RBD of SARS-CoV-2.

In some embodiments, a trimer receptor binding portion of SARS-CoV-2 encoded by an mRNA (e.g., as described herein) may be determined to have a size of about 3-4 angstroms when it is complexed with ACE2 and B^0AT1 neutral amino acid acid transporter in a closed

conformation, as characterized by electron cryomicroscopy (cryoEM). In some embodiments, geometric mean SARS-CoV-2 neutralizing titer that characterizes and/or is achieved by an mRNA composition or method as described herein can reach at least 1.5-fold, including, at least 2-fold, at least 2.5-fold, at least 3-fold, or higher, that of a COVID-19 convalescent human panel (e.g., a panel of sera from COVID-19 convalescing humans obtained 20-40 days after the onset of symptoms and at least 14 days after the start of asymptomatic convalescence.

In some embodiments, mRNA compositions as provided herein may be characterized in that subjects who have been treated with such compositions (e.g., with at least one dose, at least two doses, etc) may show reduced and/or more transient presence of viral RNA in relevant site(s) (e.g., nose and/or lungs, etc, and/or any other tissue susceptible to infection) as compared with an appropriate control (e.g., an established expected level for a comparable subject or population not having been so treated and having been exposed to virus under reasonably comparable exposure conditions)

In some embodiments, the RBD antigen expressed by an mRNA construct (e.g., as described herein) can be modified by addition of a T4-fibritin-derived "foldon" trimerization domain, for example, to increase its immunogenicity.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that certain local reactions (e.g., pain, redness, and/or swelling, etc.) and/or systemic events (e.g., fever, fatigue, headache, etc.) may appear and/or peak at Day 2 after vaccination. In some embodiments, mRNA compositions described herein are characterized in that certain local reactions (e.g., pain, redness, and/or swelling, etc.) and/or systemic events (e.g., fever, fatigue, headache, etc.) may resolve by Day 7 after vaccination.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that no Grade 1 or greater change in routine clinical laboratory values or laboratory abnormalities are observed in subjects receiving mRNA compositions (e.g., as

described herein). Examples of such clinical laboratory assays may include lymphocyte count, hematological changes, etc.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that by 21 days after a first dose (e.g., 10-100 ug inclusive or 1 ug-50 ug inclusive), geometric mean concentrations (GMCs) of IgG directed to a SARS-CoV-2 S polypeptide or an immunogenic fragment thereof (e.g., RBD) may reach 200-3000 units/mL or 500-3000 units/mL or 500-2000 units/mL, compared to 602 units/mL for a panel of COVID-19 convalescent human sera. In some embodiments, mRNA compositions described herein are characterized in that by 7 days after a second dose (e.g., 10-30 ug inclusive; or 1 ug-50 ug inclusive), geometric mean concentrations (GMCs) of IgG directed to a SARS-CoV-2 spike polypeptide or an immunogenic fragment thereof (e.g., RBD) may increase by at least 8-fold or higher, including, e.g., at least 9-fold, at least 10-fold, at least 15-fold, at least 20-fold, at least 25-fold, at least 30-fold, at least 35-fold, at least 40-fold, or higher. In some embodiments, mRNA compositions described herein are characterized in that by 7 days after a second dose (e.g., 10-30 ug inclusive; or 1 ug-50 ug inclusive), geometric mean concentrations (GMCs) of IgG directed to a SARS-CoV-2 S polypeptide or an immunogenic fragment thereof (e.g., RBD) may increase to 1500 units/mL to 40,000 units/mL or 4000 units/mL to 40,000 units/mL. In some embodiments, antibody concentrations described herein can persist to at least 20 days or longer, including, e.g., at least 25 days, at least 30 days, at least 35 days, at least 40 days, at least 45 days, at least 50 days, after a first dose, or at least 10 days or longer, including, e.g., at least 15 days, at least 20 days, at least 25 days, or longer, after a second dose. In some embodiments, antibody concentrations can persist to 35 days after a first dose, or at least 14 days after a second dose.

In some embodiments, mRNA compositions described herein are characterized in that when measured at 7 days after a second dose (e.g., 1-50 ug inclusive), GMC of IgG directed to a SARS-CoV-2 S polypeptide or an immunogenic fragment thereof (e.g., RBD) is at least 30%

higher (including, e.g., at least 40% higher, at least 50% higher, at least 60%, higher, at least 70% higher, at least 80% higher, at least 90% higher, at least 95 % higher, as compared to antibody concentrations observed in a panel of COVID-19 convalescent human serum. In many embodiments, geometric mean concentration (GMC) of IgG described herein is GMCs of RBD-binding IgG.

In some embodiments, mRNA compositions described herein are characterized in that when measured at 7 days after a second dose (e.g., 10-50 ug inclusive), GMC of IgG directed to a SARS-CoV-2 S polypeptide or an immunogenic fragment thereof (e.g., RBD) is at least 1.1-fold higher (including, e.g., at least 1.5-fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold higher, at least 7-fold higher, at least 8-fold higher, at least 9-fold higher, at least 10-fold higher, at least 15-fold higher, at least 20-fold higher, at least 25-fold higher, at least 30-fold higher), as compared to antibody concentrations observed in a panel of COVID-19 convalescent human serum, In many embodiments, geometric mean concentration (GMC) of IgG described herein is GMCs of RBD-binding IgG.

In some embodiments, mRNA compositions described herein are characterized in that when measured at 21 days after a second dose, GMC of IgG directed to a SARS-CoV-2 S polypeptide or an immunogenic fragment thereof (e.g., RBD) is at least 5-fold higher (including, e.g., at least 6-fold higher, at least 7-fold higher, at least 8-fold higher, at least 9-fold higher, at least 10-fold higher, at least 15-fold higher, at least 20-fold higher, at least 25-fold higher, at least 30-fold higher), as compared to antibody concentrations observed in a panel of COVID-19 convalescent human serum, In many embodiments, geometric mean concentration (GMC) of IgG described herein is GMCs of RBD-binding IgG.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that an increase (e.g., at least 30%, at least 40%, at least 50%, or more) in SARS-CoV-2 neutralizing geometric mean titers (GMTs) is observed 21 days after a first dose.

In some embodiments, mRNA compositions described herein are characterized in that a

substantially greater serum neutralizing GMTs are achieved 7 days after subjects receive a second dose (e.g., 10 μg-30 μg inclusive), reaching 150-300, compared to 94 for a COVID-19 convalescent serum panel.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that 7 days after administration of the second dose, the protective efficacy is at least 60%, e.g., at least 70%, at least 80%, at least 90, or at least 95%. In one embodiment, mRNA compositions and/or methods described herein are characterized in that 7 days after administration of the second dose, the protective efficacy is at least 70%. In one embodiment, mRNA compositions and/or methods described herein are characterized in that 7 days after administration of the second dose, the protective efficacy is at least 80%. In one embodiment, mRNA compositions and/or methods described herein are characterized in that 7 days after administration of the second dose, the protective efficacy is at least 90%. In one embodiment, mRNA compositions and/or methods described herein are characterized in that 7 days after administration of the second dose, the protective efficacy is at least 95%.

In some embodiments, an RNA composition provided herein is characterized in that it induces an immune response against SARS-CoV-2 after at least 7 days after a dose (e.g., after a second dose). In some embodiments, an RNA composition provided herein is characterized in that it induces an immune response against SARS-CoV-2 in less than 14 days after a dose (e.g., after a second dose). In some embodiments, an RNA composition provided herein is characterized in that it induces an immune response against SARS-CoV-2 after at least 7 days after a vaccination regimen. In some embodiments, a vaccination regimen comprises a first dose and a second dose. In some embodiments, a first dose and a second dose are administered by at least 21 days apart. In some such embodiments, an immune response against SARS-CoV-2 is induced at least after 28 days after a first dose.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that geometric mean concentration (GMCs) of antibodies directed to a SARS-

CoV-2 spike polypeptide or an immunogenic fragment thereof (e.g., RBD), as measured in serum from subjects receiving mRNA compositions of the present disclosure (e.g., at a dose of 10-30 ug inclusive), is substantially higher than in a convalescent serum panel (e.g., as described herein). In some embodiments where a subject may receive a second dose (e.g., 21 days after 1 first dose), geometric mean concentration (GMCs) of antibodies directed to a SARS-CoV-2 spike polypeptide or an immunogenic fragment thereof (e.g., RBD), as measured in serum from the subject, may be 8.0-fold to 50-fold higher than a convalescent serum panel GMC. In some embodiments where a subject may receive a second dose (e.g., 21 days after 1 first dose), geometric mean concentration (GMCs) of antibodies directed to a SARS-CoV-2 spike polypeptide or an immunogenic fragment thereof (e.g., RBD), as measured in serum from the subject, may be at least 8.0-fold or higher, including, e.g., at least 10-fold, at least 20-fold, at least 30-fold, at least 40-fold, at least 50-fold, at least 60-fold or higher, as compared to a convalescent serum panel GMC.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that the SARS-CoV-2 neutralizing geometric mean titer, as measured at 28 days after a first dose or 7 days after a second dose, may be at least 1.5-fold or higher (including, e.g., at least 2-fold, at least 2.5-fold, at least 3-fold, at least 3.5-fold or higher), as compared to a neutralizing GMT of a convalescent serum panel.

In some embodiments, a regimen administered to a subject may be or comprise a single dose. In some embodiments, a regimen administered to a subject may comprise a plurality of doses (e.g., at least two doses, at least three doses, or more). In some embodiments, a regimen administered to a subject may comprise a first dose and a second dose, which are given at least 2 weeks apart, at least 3 weeks apart, at least 4 weeks apart, or more. In some embodiments, such doses may be at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months, at least 10 months, at least 11 months, at least 12 months, or more apart. In

some embodiments, doses may be administered days apart, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 ,10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60 or more days apart. In some embodiments, doses may be administered about 1 to about 3 weeks apart, or about 1 to about 4 weeks apart, or about 1 to about 5 weeks apart, or about 1 to about 6 weeks apart, or about 1 to more than 6 weeks apart. In some embodiments, doses may be separated by a period of about 7 to about 60 days, such as for example about 14 to about 48 days, etc. In some embodiments, a minimum number of days between doses may be about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 or more. In some embodiments, a maximum number of days between doses may be about 60, 59, 58, 57, 56, 55, 54, 53, 52, 51, 50, 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, or fewer. In some embodiments, doses may be about 21 to about 28 days apart. In some embodiments, doses may be about 19 to about 42 days apart. In some embodiments, doses may be about 7 to about 28 days apart. In some embodiments, doses may be about 14 to about 24 days. In some embodiments, doses may be about 21 to about 42 days.

In some embodiments, particularly for compositions established to achieve elevated antibody and/or T-cell titres for a period of time longer than about 3 weeks – e.g., in some embodiments, a provided composition is established to achieve elevated antibody and/or T-cell titres (e.g., specific for a relevant portion of a SARS-CoV-2 spike protein) for a period of time longer than about 3 weeks; in some such embodiments, a dosing regimen may involve only a single dose, or may involve two or more doses, which may, in some embodiments, be separated from one another by a period of time that is longer than about 21 days or three weeks. For example, in some such embodiments, such period of time may be about 4 weeks, 5 weeks, 6 weeks 7 weeks, 8 weeks, 9 weeks, 10 weeks, 11 weeks, 12 weeks, 13 weeks, 14 weeks, 15 wees, 16 weeks, 17 weeks, 18 weeks, 19 weeks, 20 weeks or more, or about 1

month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10, months, 11 months, 12 months or more, or in some embodiments about a year or more. In some embodiments, a first dose and a second dose (and/or other subsequent dose) may be administered by intramuscular injection. In some embodiments, a first dose and a second dose may be administered in the deltoid muscle. In some embodiments, a first dose and a second dose may be administered in the same arm. In some embodiments, an mRNA composition described herein is administered (e.g., by intramuscular injection) as a series of two doses (e.g., 0.3 mL each) 21 days part. In some embodiments, each dose is about 30 ug. In some embodiments, each dose may be higher than 30 ug, e.g., about 40 ug, about 50 ug, about 60 ug. In some embodiments, each dose may be lower than 30 ug, e.g., about 20 ug, about 10 ug, about 5 ug, etc. In some embodiments, each dose is about 3 ug or lower, e.g., about 1 ug. In some such embodiments, an mRNA composition described herein is administered to subjects of age 16 or older (including, e.g., 16-85 years). In some such embodiments, an mRNA composition described herein is administered to subjects of age 18-55. In some such embodiments, an mRNA composition escribed herein is administered to subjects of age 56-85. In some embodiments, an mRNA composition described herein is administered (e.g., by intramuscular injection) as a single dose.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that RBD-specific IgG (e.g., polyclonal response) induced by such mRNA compositions and/or methods exhibit a higher binding affinity to RBD, as compared to a reference human monoclonal antibody with SARS-CoV-2 RBD-binding affinity (e.g., CR3022 as described in J. ter Meulen et al., PLOS Med. 3, e237 (2006).)

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity across a panel (e.g., at least 10, at least 15, or more) of SARs-CoV-2 spike variants. In some embodiments, such SARs-CoV-2 spike variants include mutations in RBD (e.g., but not limited to Q321L,

V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P, etc., as compared to SEQ ID NO: 1), and/or mutations in spike protein (e.g., but not limited to D614G, etc., as compared to SEQ ID NO: 1). Those skilled in the art are aware of various spike variants, and/or resources that document them (e.g., the Table of mutating sites in Spike maintained by the COVID-19 Viral Genome Analysis Pipeline and found at https://cov.lanl.gov/components/sequence/COV/int_sites_tbls.comp) (last accessed 24 Aug 2020), and, reading the present specification, will appreciate that mRNA compositions and/or methods described herein can be characterized for there ability to induce sera in vaccinated subject that display neutralizing activity with respect to any or all of such variants and/or combinations thereof.

In particular embodiments, mRNA compositions encoding RBD of a SARS-CoV-2 spike protein are characterized in that sera of vaccinated subjects display neutralizing activity across a panel (e.g., at least 10, at least 15, or more) of SARs-CoV-2 spike variants including RBD variants (e.g., but not limited to Q321L, V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P, etc., as compared to SEQ ID NO: 1) and spike protein variants (e.g., but not limited to D614G, as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions encoding a SARS-CoV-2 spike protein variant that includes two consecutive proline substitutions at amino acid positions 986 and 987, at the top of the central helix in the S2 subunit, are characterized in that sera of vaccinated subjects display neutralizing activity across a panel (e.g., at least 10, at least 15, or more) of SARs-CoV-2 spike variants including RBD variants (e.g., but not limited to Q321L, V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P, etc., as compared to SEQ ID NO: 1) and spike protein variants (e.g., but not limited to D614G, as compared to SEQ ID NO: 1). For example, in some embodiments, the mRNA composition encoding SEQ ID NO: 7 (S P2) elicits an immune response against any one of a SARs-CoV-2 spike variant including RBD variants (e.g., but not limited to Q321L, V341I,

A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P, etc., as compared to SEQ ID NO: 1) and spike protein variants (e.g., but not limited to D614G, as compared to SEQ ID NO: 1).

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at position 501 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a N501Y mutation in spike protein as compared to SEQ ID NO: 1.

Said one or more SARs-CoV-2 spike variants including a mutation at position 501 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a N501Y mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, K417N, L242/A243/L244 deletion etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "Variant of Concern 202012/01" (VOC-202012/01; also known as lineage B.1.1.7). The variant had previously been named the first Variant Under Investigation in December 2020 (VUI – 202012/01) by Public Health England, but was reclassified to a Variant of Concern (VOC-202012/01). VOC-202012/01 is a variant of SARS-CoV-2 which was first detected in October 2020 during the COVID-19 pandemic in the United Kingdom from a sample taken the previous month, and it quickly began to spread by mid-December. It is correlated with a significant increase in the rate of COVID-19 infection in United Kingdom; this increase is thought to be at least partly because of change N501Y inside the spike

glycoprotein's receptor-binding domain, which is needed for binding to ACE2 in human cells. The VOC-202012/01 variant is defined by 23 mutations: 13 non-synonymous mutations, 4 deletions, and 6 synonymous mutations (i.e., there are 17 mutations that change proteins and six that do not). The spike protein changes in VOC 202012/01 include deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H. One of the most important changes in VOC-202012/01 seems to be N501Y, a change from asparagine (N) to tyrosine (Y) at amino-acid site 501. This mutation alone or in combination with the deletion at positions 69/70 in the N terminal domain (NTD) may enhance the transmissibility of the virus.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2". This variant was first observed in samples from October 2020, and since then more than 300 cases with the 501.V2 variant have been confirmed by whole genome sequencing (WGS) in South Africa, where in December 2020 it was the dominant form of the virus. Preliminary results indicate that this variant may have an increased transmissibility. The 501.V2 variant is defined by multiple spike protein changes including: D80A, D215G, E484K, N501Y and A701V, and more recently collected viruses have additional changes: L18F, R246I, K417N, and deletion 242-244.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y and A701V as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as

compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a H69/V70 deletion in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a H69/V70 deletion in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to Y144 deletion, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I etc., as compared to SEQ ID NO: 1),

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "Variant of Concern 202012/01" (VOC-202012/01; also known as lineage B.1.1.7).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "Cluster 5", also referred to as ΔFVI-spike by the Danish State Serum Institute (SSI). It was discovered in North Jutland, Denmark, and is believed to have been spread from minks to humans via mink farms. In cluster 5, several different mutations in the spike protein of the virus have been confirmed. The specific mutations include 69–70deltaHV (a deletion of

the histidine and valine residues at the 69th and 70th position in the protein), Y453F (a change from tyrosine to phenylalanine at position 453), I692V (isoleucine to valine at position 692), M1229I (methionine to isoleucine at position 1229), and optionally S1147L (serine to leucine at position 1147).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: deletion 69-70, Y453F, I692V, M1229I, and optionally S1147L, as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at position 614 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a D614G mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at position 614 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a D614G mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, N501Y, A570D, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-

2 spike variant "Variant of Concern 202012/01" (VOC-202012/01; also known as lineage B.1.1.7).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V, and D614G as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at positions 501 and 614 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a N501Y mutation and a D614G mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at positions 501 and 614 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a N501Y mutation and a D614G mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, A570D, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "Variant of Concern 202012/01" (VOC-202012/01; also known as lineage B.1.1.7).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V, and D614G as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at position 484 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a E484K mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at position 484 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a E484K mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G,

A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, K417T, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, and A701V, as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

Lineage B.1.1.248, known as the Brazil(ian) variant, is one of the variants of SARS-CoV-2 which has been named P.1 lineage and has 17 unique amino acid changes, 10 of which in its spike protein, including N501Y and E484K. B.1.1.248 originated from B.1.1.28. E484K is present in both B.1.1.28 and B.1.1.248. B.1.1.248 has a number of S-protein polymorphisms [L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, V1176F] and is similar in certain key RBD positions (K417, E484, N501) to variant described from South Africa.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "B.1.1.28".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "B.1.1.248".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-

2 spike variant including the following mutations: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at positions 501 and 484 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a N501Y mutation and a E484K mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at positions 501 and 484 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a N501Y mutation and a E484K mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, K417T, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y and A701V as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "B.1.1.248".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at positions 501, 484 and 614 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a N501Y mutation, a E484K mutation and a D614G mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at positions 501, 484 and 614 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a N501Y mutation, a E484K mutation and a D614G mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, A570D, P681H, T716I, S982A, D1118H, D80A, D215G, A701V, L18F, R246I, K417N, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, K417T, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V, and

D614G as compared to SEQ ID NO: 1, and optionally: L18F, R246I, K417N, and deletion 242-244 as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a L242/A243/L244 deletion in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a L242/A243/L244 deletion in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, K417N, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, K417T, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V and deletion 242-244 as compared to SEQ ID NO: 1, and optionally: L18F, R246I, and K417N, as compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at position 417 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing

activity against one or more SARs-CoV-2 spike variants including a K417N or K417T mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at position 417 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a K417N or K417T mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, N501Y, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, E484K, A701V, L18F, R246I, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V and K417N,, as compared to SEQ ID NO: 1, and optionally: L18F, R246I, and deletion 242-244 as compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "B.1.1.248".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a mutation at positions 417 and 484 and/or 501 in spike protein as compared to SEQ ID NO: 1. In some embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against one or more SARs-CoV-2 spike variants including a K417N or K417T mutation and a E484K and/or N501Y mutation in spike protein as compared to SEQ ID NO: 1.

In some embodiments, one or more SARs-CoV-2 spike variants including a mutation at positions 417 and 484 and/or 501 in spike protein as compared to SEQ ID NO: 1 or said one or more SARs-CoV-2 spike variants including a K417N or K417T mutation and a E484K and/or N501Y mutation in spike protein as compared to SEQ ID NO: 1 may include one or more further mutations as compared to SEQ ID NO: 1 (e.g., but not limited to H69/V70 deletion, Y144 deletion, A570D, D614G, P681H, T716I, S982A, D1118H, D80A, D215G, A701V, L18F, R246I, L242/A243/L244 deletion, Y453F, I692V, S1147L, M1229I, T20N, P26S, D138Y, R190S, H655Y, T1027I, V1176F etc., as compared to SEQ ID NO: 1).

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "501.V2".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: D80A, D215G, E484K, N501Y, A701V and K417N, as compared to SEQ ID NO: 1, and optionally: L18F, R246I, and deletion 242-244 as compared to SEQ ID NO: 1. Said SARs-CoV-2 spike variant may also include a D614G mutation as compared to SEQ ID NO: 1.

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant "B.1.1.248".

In particular embodiments, mRNA compositions and/or methods described herein are characterized in that sera of vaccinated subjects display neutralizing activity against SARs-CoV-2 spike variant including the following mutations: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F as compared to SEQ ID NO: 1.

The SARs-CoV-2 spike variants described herein may or may not include a D614G mutation as compared to SEQ ID NO: 1.

In some embodiments, mRNA compositions and/or methods described herein can provide protection against SARS-CoV-2 and/or decrease severity of SARS-CoV-2 infection in at least 50% of subjects receiving such mRNA compositions and/or methods.

In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 18-55. In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 56-85. In some embodiments, populations to be treated with mRNA compositions described herein include older subjects (e.g., over age 60, 65, 70, 75, 80, 85, etc, for example subjects of age 65-85). In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 18-85. In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 18 or younger. In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 12 or younger. In some embodiments, populations to be treated with mRNA compositions described herein include subjects of age 10 or younger. In some embodiments, populations to be treated with mRNA compositions described herein may include adolescent populations (e.g., individuals approximately 12 to approximately 17 years of age). In some embodiments, populations to be treated with mRNA compositions described herein include infants (e.g., less

than 1 year old). In some embodiments, populations to be treated with mRNA compositions described herein do not include infants (e.g., less than 1 year) whose mothers have received such mRNA compositions described herein during pregnancy. Without wishing to be bound by any particular theory, a rat study as shown in Example 31 has suggested that a SARS-CoV-2 neutralizing antibody response induced in female rats given such mRNA compositions during pregnancy can pass onto fetuses. In some embodiments, populations to be treated with mRNA compositions described herein include infants (e.g., less than 1 year) whose mothers did not receive such mRNA compositions described herein during pregnancy. In some embodiments, populations to be treated with mRNA compositions described herein may include pregnant women; in some embodiments, infants whose mothers were vaccinated during pregnancy (e.g., who received at least one dose, or alternatively only who received both doses), are not vaccinated during the first weeks, months, or even years (e.g., 1, 2, 3, 4, 5, 6, 7, 8 weeks or more, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 moths or more, or 1, 2, 3, 4, 5 years or more) post-birth. Alternatively or additionally, in some embodiments, infants whose whose mothers were vaccinated during pregnancy (e.g., who received at least one dose, or alternatively only who received both doses), receive reduced vaccination (e.g., lower doses and/or smaller numbers of administrations – e.g., boosters – and/or lower total exposure over a given period of time) after birth, for example during the first weeks, months, or even years (e.g., 1, 2, 3, 4, 5, 6, 7, 8 weeks or more, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 months or more, or 1, 2, 3, 4, 5 years or more) post-birthor may need reduced vaccination (e.g., lower doses and/or smaller numbers of administrations – e.g., boosters – over a given period of time), In some embodiments, compositions as provided herein are administered to populations that do not include pregnant women.

In some particular embodiments, compositions as provided herein are administered to pregnant women according to a regimen that includes a first dose administered after about

24 weeks of gestation (e.g., after about 22, 23, 24, 25, 26, 27, 28 or more weeks of gestation); in some embodiments, compositions as provided herein are administered to pregnant women according to a regimen that includes a first dose administered before about 34 weeks of gestation (e.g., before about 30, 31, 32, 33, 34, 35, 36, 37, 38 weeks of gestation). In some embodiments, compositions as provided herein are administered to pregnant women according to a regimen that includes a first dose administered after about 24 weeks (e.g., after about 27 weeks of gestation, e.g., between about 24 weeks and 34 weeks, or between about 27 weeks and 34 weeks) of gestation and a second dose administered about 21 days later; in some embodiments both doses are administered prior to delivery. Without wishing to be bound by any particular theory, it is proposed that such a regimen (e.g., involving administration of a first dose after about 24 weeks, or 27 weeks of gestation and optionally before about 34 weeks of gestation), and optionally a second dose within about 21 days, ideally before delivery, may have certain advantages in terms of safety (e.g., reduced risk of premature delivery or of fetal morbidity or mortality) and/or efficacy (e.g., carryover vaccination imparted to the infant) relative to alternative dosing regimens (e.g., dosing at any time during pregnancy, refraining from dosing during pregnancy, and/or dosing later in pregnancy for example so that only one dose is administered during gestation. In some embodiments, as noted herein (see also Example 34), infants born of mothers vaccinated during pregnancy, e.g, according to a particular regimen as described herein, may not need further vaccination, or may need reduced vaccination (e.g., lower doses and/or smaller numbers of administrations – e.g., boosters –, and/or lower overall exposure over a given period of time), for a period of time (e.g., as noted herein) after birth.

In some embodiments, compositions as provided herein are administered to populations in which women are advised against becoming pregnant for a period of time after receipt of the vaccine (e.g., after receipt of a first dose of the vaccine, after receipt of a final dose of the vaccine, etc.); in some such embodiments, the period of time may be at least 1 week, at least

2 weeks, at least 3 weeks, at least 4 weeks, at least 5 weeks, at least 6 weeks, at least 7 weeks, at least 8 weeks, at least 9 weeks, at least 10 weeks or more, or may be at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, or more.

In some embodiments, populations to be treated with mRNA compositions described herein may include one or more populations with one or more particularly high risk conditions or history, e.g., as noted herein. For example, in some embodiments, populations to be treated with mRNA compositions described herein may include subjects whose profession and/or environmental exposure may dramatically increase their risk of getting SARS-CoV-2 infection (including, e.g., but not limited to mass transportation, prisoners, grocery store workers, residents in long-term care facilities, butchers or other meat processing workers, healthcare workers, and/or first responders, e.g., emergency responders). In particular embodiments, populations to be treated with mRNA compositions described herein may include healthcare workers and/or first responders, e.g., emergency responders. In some embodiments, populations to be treated with mRNA compositions described herein may include those with a history of smoking or vaping (e.g., within 6 months, 12 months or more, including a history of chronic smoking or vaping). In some embodiments, populations to be treated with mRNA compositions described herein may include certain ethnic groups that have been determined to be more susceptible to SARS-CoV-2 infection.

In some embodiments, populations to be treated with mRNA compositions described herein may include certain populations with a blood type that may have been determined to more susceptible to SARS-CoV-2 infection. In some embodiments, populations to be treated with mRNA compositions described herein may include immunocompromised subjects (e.g., those with HIV/AIDS; cancer and transplant patients who are taking certain immunosuppressive drugs; autoimmune diseases or other physiological conditions expected to warrant immunosuppressive therapy (e.g., within 3 months, within 6 months, or more); and those with

inherited diseases that affect the immune system (e.g., congenital agammaglobulinemia, congenital IgA deficiency)). In some embodiments, populations to be treated with mRNA compositions described herein may include those with an infectious disease. For example, in some embodiments, populations to be treated with mRNA compositions described herein may include those infected with human immunodeficiency virus (HIV) and/or a hepatitis virus (e.g., HBV, HCV). In some embodiments, populations to be treated with mRNA compositions described herein may include those with underlying medical conditions. Examples of such underlying medical conditions may include, but are not limited to hypertension, cardiovascular disease, diabetes, chronic respiratory disease, e.g., chronic pulmonary disease, asthma, etc., cancer, and other chronic diseases such as, e.g., lupus, rheumatoid arthritis, chonic liver diseases, chronic kidney diseases (e.g., Stage 3 or worse such as in some embodiments as characterized by a glomerular filtration rate (GFR) of less than 60 mL/min/1.73m^2). In some embodiments, populations to be treated with mRNA compositions described herein may include overweight or obese subjects, e.g., specifically including those with a body mass index (BMI) above about 30 kg/m^2. In some embodiments, populations to be treated with mRNA compositions described herein may include subjects who have prior diagnosis of COVID-19 or evidence of current or prior SARS-CoV-2 infection, e.g., based on serology or nasal swab. In some embodiments, populations to be treated include white and/or non-Hispanic/non-Latino.

In some embodiments, certain mRNA compositions described herein (e.g., BNT162b1) may be selected for administration to Asian populations (*e.g.*, Chinese populations), or in particular embodiments to older Asian populations (*e.g*, 60 years old or over, e.g., 60-85 or 65-85 years old).

In some embodiments, an mRNA composition as provided herein is administered to and/or assessed in subject(s) who have been determined not to show evidence of prior infection, and/or of present infection, before administration; in some embodiments, evidence of prior

infection and/or of present infection, may be or include evidence of intact virus, or any viral nucleic acid, protein, lipid etc. present in the subject (e.g., in a biological sample thereof, such as blood, cells, mucus, and/or tissue), and/or evidence of a subject's immune response to the same. In some embodiments, an mRNA composition as provided herein is administered to and/or assessed in subject(s) who have been determined to show evidence of prior infection, and/or of present infection, before administration; in some embodiments, evidence of prior infection and/or of present infection, may be or include evidence of intact virus, or any viral nucleic acid, protein, lipid etc. present in the subject (e.g., in a biological sample thereof, such as blood, cells, mucus, and/or tissue), and/or evidence of a subject's immune response to the same. In some embodiments, a subject is considered to have a prior infection based on having a positive N-binding antibody test result or positive nucleic acid amplification test (NAAT) result on the day of Dose 1.

In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject who has been informed of a risk of side effects that may include one or more of, for example: chills, fever, headache, injection site pain, muscle pain, tiredness; in some embodiments, an RNA (e.g., mRNA) composition is administered to a subject who has been invited to notify a healthcare provider if one or more such side effects occurs, is experienced as more than mild or moderate, persists for a period of more than a day or a few days, or if any serious or unexpected event is experienced that the subject reasonably considers may be associated with receipt of the composition. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject who has been invited to notify a healthcare provider of particular medical conditions which may include, for example, one or more of allergies, bleeding disorder or taking a blood thinner medication, breastfeeding, fever, immunocompromised state or taking medication that affects the immune system, pregnancy or plan to become pregnant, etc. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject who has been invited to notify a healthcare

provider of having received another COVID-19 vaccine. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject not having one of the following medical conditions: experiencing febrile illness, receiving immunosuppressant therapy, receiving anticoagulant therapy, suffering from a bleeding disorder (e.g., one that would contraindicate intramuscular injection), or pregnancy and/or breatfeeding/lactation. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject not having received another COVID-19 vaccine. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject who has not had an allergic reaction to any component of the RNA (e.g., mRNA) composition. Examples of such allergic reaction may include, but are not limited to difficulty breathing, swelling of fact and/or throat, fast hearbeat, rash, dizziness and/or weakness. In some embodiments, an RNA (e.g., mRNA) composition as provided herein is administered to a subject who received a first dose and did not have an allergic reaction (e.g., as described herein) to the first dose. In some embodiments where allergic reaction occurs in subject(s) after receiving a dose of an RNA (e.g., mRNA) composition as provided herein, such subject(s) may be administered one or more interventions such as treatment to manage and/or reduce symptom(s) of such allergic reactions, for example, fever-reducing and/or anti-inflammatory agents.

In some embodiments, a subject who has received at least one dose of an RNA (e.g., mRNA) composition as provided herein is informed of avoiding being exposed to a coronavirus (e.g., SARS-CoV-2) unless and until several days (e.g., at least 7 days, at least 8 days, 9 days, at least 10 days, at least 11 days, at least 12 days, at least 13 days, at least 14 days, etc.) have passed since administration of a second dose. For example, a subject who has received at at least one dose of an RNA (e.g., mRNA) composition as provided herein is informed of taking precautionary measures against SARS-CoV-2 infection (e.g., remaining socially distant, wearing masks, frequent hand-washing, etc.) unless and until several days (e.g., at least 7 days, at least 8 days, 9 days, at least 10 days, at least 11 days, at least 12 days, at least 13 days, at

least 14 days, etc.) have passed since administration of a second dose. Accordingly, in some embodiments, methods of administering an RNA (e.g., mRNA) composition as provided herein comprise administering a second dose of such an RNA (e.g., mRNA) composition as provided herein to a subject who received a first dose and took precautionary measures to avoid being exposed to a coronavirus (e.g., SARS-CoV-2).

In some embodiments, mRNA compositions described herein may be delivered to a draining lymph node of a subject in need thereof, for example, for vaccine priming. In some embodiments, such delivery may be performed by intramuscular administration of a provided mRNA composition.

In some embodiments, different particular mRNA compositions may be administered to different subject population(s); alternatively or additionally, in some embodiments, different dosing regimens may be administered to different subject populations. For example, in some embodiments, mRNA compositions administered to particular subject population(s) may be characterized by one or more particular effects (e.g., incidence and/or degree of effect) in those subject populations. In some embodiments, such effect(s) may be or comprise, for example titer and/or persistence of neutralizing antibodies and/or T cells (e.g., T_H1-type T cells such as $CD4^+$ and/or $CD8^+$ T cells), protection against challenge (e.g., via injection and/or nasal exposure, etc), incidence, severity, and/or persistence of side effects (e.g., reactogenicity), etc.

In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to reduce COVID-19 incidence per 1000 person-years, e.g., based on a laboratory test such as nucleic acid amplification test (NAAT).

In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to reduce COVID-19 incidence per 1000 person-years based on a laboratory test such as nucleic acid amplification test (NAAT) in subjects receiving at least one dose of a provided mRNA composition with no serological or

virological evidence (e.g., up to 7 days after receipt of the last dose) of past SARS-CoV-2 infection. In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to reduce confirmed severe COVID-19 incidence per 1000 person-years. In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to reduce confirmed severe COVID-19 incidence per 1000 person-years in subjects receiving at least one dose of a provided mRNA composition with no serological or virological evidence of past SARS-CoV-2 infection.

In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to produce neutralizing antibodies directed to a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD) as measured in serum from a subject that achieves or exceeds a reference level (e.g., a reference level determined based on human SARS-CoV-2 infection/COVID-19 convalescent sera) for a period of time and/or induction of cell-mediated immune response (e.g., a T cell response against SARS-CoV-2), including, e.g., in some embodiments induction of T cells that recognize at least one or more MHC-restricted (e.g., MHC class I-restricted) eptiopes within a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD) for a period of time. In some such embodiments, the period of time may be at least 2 months, 3 months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months, at least 10 months, at least 11 months, at least 12 months or longer. In some embodiments, one or more epitopes recognized by vaccine-induced T cells (e.g., CD8+ T cells) may be presented on a MHC class I allele that is present in at least 50% of subjects in a population, including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, or more; in some such embodiments, the MHC class I allele may be HLA-B*0702, HLA-A*2402, HLA-B*3501, HLA-B*4401, or HLA-A*0201. In some embodiments, an epitope may comprise HLA-A*0201 YLQPRTFLL; HLA-A*0201 RLQSLQTYV; HLA-A*2402 QYIKWPWYI; HLA-A*2402

NYNYLYRLF; HLA-A*2402 KWPWYIWLGF; HLA-B*3501 QPTESIVRF; HLA-B*3501 IPFAMQMAY; or HLA-B*3501 LPFNDGVYF.

In some embodiments, efficacy is assessed as COVID-19 incidence per 1000 person-years in individuals without serological or virological ecidence of past SARS-CoV-2 infection before and during vaccination regimen; alternatively or additionally, in some embodiments, efficacy is assessed as COVID-19 incidence per 1000 person-years in subjects with and without evidence of past SARS-CoV-2 infection before and during vaccination regimen. In some such embodiments, such incidence is of COVID-19 cases confirmed within a specific time period after the final vaccination dose (e.g., a first dose in a single-dose regimen; a second dose in a two-dose regimen, etc); in some embodiments, such time period may be within (i.e., up to and including 7 days) a particular number of days (e.g., 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 days or more). In some embodiments, such time period may be within 7 days or within 14 days or within 21 days or within 28 days. In some embodiments, such time period may be within 7 days. In some embodiments, such time period may be within 14 days.

In some embodiments (e.g., in some embodiments of assessing efficacy), a subject is determined to have experienced COVID-19 infection if one or more of the following is established: detection of SARS-CoV-2 nucleic acid in a sample from the subject, detection of antibodies that specifically recognize SARS-CoV-2 (e.g., a SARS-Co-V-2 spike protein), one or more symptoms of COVID-19 infection, and combinations thereof. In some such embodiments, detection of SARS-CoV-2 nucleic acid may involve, for example, NAAT testing on a mid-turbinatae swap sample. In some such embodiments, detection of relevant antibodies may involve serological testing of a blood sample or portion thereof. In some such embodiments, symptoms of COVID-19 infection may be or include: fever, new or increased cough, new or increased shortness of breath, chills, new or increased muscle pain, new loss of taste or smell, sore throat, diarrhea, vomiting and combinations thereof. In some such

embodiments, symptoms of COVID-19 infection may be or include: fever, new or increased cough, new or increased shortness of breath, chills, new or increased muscle pain, new loss of taste or smell, sore throat, diarrhea, vomiting, fatigue, headache, nasal congestion or runny nose, nausea, and combinations thereof. In some such embodiments, a subject is determined to have experienced COVID-19 infection if such subject both has experienced one such symptom and also has received a positive test for SARS-CoV-2 nucleic acid or antibodies, or both. In some such embodiments, a subject is determined to have experienced COVID-19 infection if such subject both has experienced one such symptom and also has received a positive test for SARS-CoV-2 nucleic acid. In some such embodiments, a subject is determined to have experienced COVID-19 infection if such subject both has experienced one such symptom and also has received a positive test for SARS-CoV-2 antibodies.

In some embodiments (e.g., in some embodiments of assessing efficacy), a subject is determined to have experienced severe COVID-19 infection if such subject has experienced one or more of: clinical signs at rest indicative or severe systemic illness (e.g., one or more of respiratory rate at greater than or equal to 30 breaths per minute, heart rate at or above 125 beats per minute, SpO_2 less than or equal to 93% on room air at sea level or a PaO_2/FiO_2 below 300 m Hg), respiratory failure (e.g., one or more of needing high-flow oxygen, noninvasive ventilation, mechanical ventilation, ECMO), evidence of shock (systolic blood pressure below 90 mm Hg, diastolic blood pressure below 60mm Hg, requiring vasopressors), significant acute renal, hepatic, or neurologic dystfunction, admission ot an intensive care unit, death, and combinations thereof.

In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to reduce the percentage of subjects reporting at least one of the following: (i) one or more local reactions (e.g., as described herein) for up to 7 days following each dose; (ii) one or more systemic events for up to 7 days

following each dose; (iii) adverse events (e.g., as described herein) from a first dose to 1 month after the last dose; and/or (iv) serious adverse events (e.g., as described herein) from a first dose to 6 months after the last dose.

In some embodiments, one or more subjects who have received an RNA (e.g., mRNA) composition as described herein may be monitored (e.g., for a period of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 days or more, including, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 weeks or more, including for example 1, 2, 3, 4, 5, 6, 7, 8, 9 ,10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 months or more, including for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 years or more) to assess, for example, presence of an immune response to component(s) of the administered composition, evidence of exposure to and/or immune response to SARS-CoV-2 or another coronavirus, evidence of any adverse event, etc. In some embodiments, monitoring may be via tele-visit. Alternatively or additionally, in some embodiments, monitoring may be in-person.

In some embodiments, a treatment effect conferred by one or more mRNA compositions described herein may be characterized by (i) a SARS-CoV-2 anti-S1 binding antibody level above a pre-determined threshold; (ii) a SARS-CoV-2 anti-RBD binding antibody level above a pre-determined threshold; and/or (iii) a SARS-CoV-2 serum neutralizing titer above a threshold level, e.g., at baseline, 1 month, 3 months, 6 months, 9 months, 12 months, 18 months, and/or 24 months after completion of vaccination. In some embodiments, anti-S1 binding antibody and/or anti-RBD binding antibody levels and/or serum neutralizing titers may be characterized by geometric mean concentration (GMC), geometric mean titer (GMT), or geometric mean fold-rise (GMFR).

In some embodiments, a treatment effect conferred by one or more mRNA compositions described herein may be characterized in that percentage of treated subjects showing a SARS-CoV-2 serum neutralizing titer above a pre-determined threshold, e.g., at baseline, 1 month, 3 months, 6 months, 9 months, 12 months, 18 months, and/or 24 months after completion of

vaccination, is higher than the percentage of non-treated subjects showing a SARS-CoV-2 serum neutralizing titer above such a pre-determined threshold (e.g., as described herein). In some embodiments, a serum neutralizing titer may be characterized by geometric mean concentration (GMC), geometric mean titer (GMT), or geometric mean fold-rise (GMFR).

In some embodiments, a treatment effect conferred by one or more mRNA compositions described herein may be characterized by detection of SARS-CoV-2 NVA-specific binding antibody.

In some embodiments, a treatment effect conferred by one or more mRNA compositions described herein may be characterized by SARS-CoV-2 detection by nucleic acid amplification test.

In some embodiments, a treatment effect conferred by one or more mRNA compositions described herein may be characterized by induction of cell-mediated immune response (e.g., a T cell response against SARS-CoV-2), including, e.g., in some embodiments induction of T cells that recognize at least one or more MHC-restricted (e.g., MHC class I-restricted) eptiopes within a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD). In some embodiments, one or more epitopes recognized by vaccine-induced T cells (e.g., CD8+ T cells) may be presented on a MHC class I allele that is present in at least 50% of subjects in a population, including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, or more; in some such embodiments, the MHC class I allele may be HLA-B*0702, HLA-A*2402, HLA-B*3501, HLA-B*4401, or HLA-A*0201. In some embodiments, an epitope may comprise HLA-A*0201 YLQPRTFLL; HLA-A*0201 RLQSLQTYV; HLA-A*2402 QYIKWPWYI; HLA-A*2402 NYNYLYRLF; HLA-A*2402 KWPWYIWLGF; HLA-B*3501 QPTESIVRF; HLA-B*3501 IPFAMQMAY; or HLA-B*3501 LPFNDGVYF.

In some embodiments, primary vaccine efficacy (VE) of one or more mRNA compositions described herein may be established when there is sufficient evidence (posterior probability) that either primary VE1 or both primary VE1 and primary VE2 are >30% or higher (including,

e.g., greater than 40%, greater than 50%, greater than 60%, greater than 70%, greater than 80%, greater than 90%, greater than 95%, greater than 96%, greater than 97%, greater than 98%, or higher), wherein primary VE is defined as primary VE = 100 × (1 – IRR); and IRR is calculated as the ratio of COVID-19 illness rate in the vaccine group to the corresponding illness rate in the placebo group. Primary VE1 represents VE for prophylactic mRNA compositions described herein against confirmed COVID-19 in participants without evidence of infection before vaccination, and primary VE2 represents VE for prophylactic mRNA compositions described herein against confirmed COVID-19 in all participants after vaccination. In some embodiments, primary VE1 and VE2 can be evaluated sequentially to control the overall type I error of 2.5% (hierarchical testing). In some embodiments where one or more RNA (e.g., mRNA) compositions described herein are demonstrated to achieve primary VE endponts as discussed above, secondary VE endpoints (e.g., confirmed severe COVID-19 in participants without evidence of infection before vaccination and confirmed severe COVID-19 in all participants) can be evaluated sequentially, e.g., by the same method used for the primary VE endpoint evaluation (hierarchical testing) as discussed above. In some embodiments, evaluation of primary and/or secondary VE endpoints may be based on at least 20,000 or more subjects (e.g., at least 25,000 or more subjects) randomized in a 1:1 ratio to the vaccine or placebo group, e.g., based on the following assumptions: (i) 1.0% illness rate per year in the placebo group, and (ii) 20% of the participants being non-evaluable or having serological evidence of prior infection with SARS-CoV-2, potentially making them immune to further infection.

In some embodiments, one or more mRNA compositions described herein may be administered according to a regimen established to achieve maintenance and/or continued enhancement of an immune response. For example, in some embodiments, an administration regimen may include a first dose optionally followed by one or more subsequent doses; in some embodiments, need for, timing of, and/or magnitude of any such subsequent dose(s)

may be selected to maintain, enhance, and/or modify one or more immune responses or features thereof. In some embodiments, number, timing, and/or amount(s) of dose(s) have been established to be effective when administered to a relevant population. In some embodiments, number, timing and/or amount(s) of dose(s) may be adjusted for an individual subject; for example, in some embodiments, one or more features of an immune response in an individual subject may be assessed at least once (and optionally more than once, for example multiple times, typically spaced apart, often at pre-selected intervals) after receipt of a first dose. For example, presence of antibodies, B cells, and/or T cells (e.g., $CD4^+$ and/or $CD8^+$ T cells), and/or of cytokines secreted thereby and/or identity of and/or extent of responses to particular antigen(s) and/or epitope(s) may be assessed. In some embodiments, need for, timing of, and/or amount of a subsequent dose may be determined in light of such assessments.

As noted hereinabove, in some embodiments, one or more subjects who have received an RNA (e.g., mRNA) composition as described herein may be monitored (e.g., for a period of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 days or more, including, for example, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 weeks or more, including for example 1, 2, 3, 4, 5, 6, 7, 8, 9 ,10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 months or more, including for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 years or more) from receipt of any particular dose to assess, for example, presence of an immune response to component(s) of the administered composition, evidence of exposure to and/or immune response to SARS-CoV-2 or another coronavirus, evidence of any adverse event, etc, including to perform assessment of one or more of presence of antibodies, B cells, and/or T cells (e.g., $CD4^+$ and/or $CD8^+$ T cells), and/or of cytokines secreted thereby and/or identity of and/or extent of responses to particular antigen(s) and/or epitope(s) may be assessed. Administration of a composition as described herein may be in accordance with a regimen that includes one or more such monitoring steps.

For example, in some embodiments, need for, timing of, and/or amount of a second dose relative to a first dose (and/or of a subsequent dose relative to a prior dose) is assessed, determined, and/or selected such that administration of such second (or subsequent) dose achieves amplification or modification of an immune response (e.g., as described herein) observed after the first (or other prior) dose. In some embodiments, such amplification of an immune response (e.g., ones described herein) may be at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or higher, as compared to the level of an immune response observed after the first dose. In some embodiments, such amplification of an immune response may be at least 1.5 fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 6-fold, at least 7-fold, at least 8-fold, at least 9-fold, at least 10-fold, at least 20-fold, at least 30-fold, or higher, as compared to the level of an immune response observed after the first dose.

In some embodiments, need for, timing of, and/or amount of a second (or subsequent) dose relative to a first (or other prior) dose is assessed, determined, and/or selected such that administration of the later dose extends the durability of an immune response (e.g., as described herein) observed after the earlier dose; in some such embodiments, the durability may be extended by at least 1 week, at least 2 weeks, at least 3 weeks, at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, at least 7 months, at least 8 months, at least 9 months, or longer. In some embodiments, an immune response observed after the first dose may be characterized by production of neutralizing antibodies directed to a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD) as measured in serum from a subject and/or induction of cell-mediated immune response (e.g., a T cell response against SARS-CoV-2), including, e.g., in some embodiments induction of T cells that recognize at least one or more MHC-restricted (e.g., MHC class I-restricted) eptiopes within a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD). In some embodiments, one or more epitopes

recognized by vaccine-induced T cells (e.g., CD8+ T cells) may be presented on a MHC class I allele that is present in at least 50% of subjects in a population, including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, or more; in some such embodiments, the MHC class I allele may be HLA-B*0702, HLA-A*2402, HLA-B*3501, HLA-B*4401, or HLA-A*0201. In some embodiments, an epitope may comprise HLA-A*0201 YLQPRTFLL; HLA-A*0201 RLQSLQTYV; HLA-A*2402 QYIKWPWYI; HLA-A*2402 NYNYLYRLF; HLA-A*2402 KWPWYIWLGF; HLA-B*3501 QPTESIVRF; HLA-B*3501 IPFAMQMAY; or HLA-B*3501 LPFNDGVYF.

In some embodiments, need for, timing of, and/or amount of a second dose relative to a first dose (or other subsequent dose relative to a prior dose) is assessed, determined and/or selected such that administration of such second (or subsequent) dose maintains or exceeds a reference level of an immune response; in some such embodiments, the reference level is determined based on human SARS-CoV-2 infection/COVID-19 convalescent sera and/ro PBMC samples drawn from subjects (e.g., at least a period of time such as at least 14 days or longer, including, e.g., 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 25 days, 30 days, 35 days, 40 days, 45 days, 50 days, 55 days, 60 days, or longer, after PCR-confirmed diagnosis when the subjects were asymptomatic. In some embodiments, an immune response may be characterized by production of neutralizing antibodies directed to a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD) as measured in serum from a subject and/or induction of cell-mediated immune response (e.g., a T cell response against SARS-CoV-2), including, e.g., in some embodiments induction of T cells that recognize at least one or more MHC-restricted (e.g., MHC class I-restricted) eptiopes within a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD). In some embodiments, one or more epitopes recognized by vaccine-induced T cells (e.g., CD8+ T cells) may be presented on a MHC class I allele that is present in at least 50% of subjects in a population, including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, or more; in some such embodiments, the MHC class I allele may be HLA-B*0702, HLA-A*2402, HLA-B*3501, HLA-B*4401, or HLA-

A*0201. In some embodiments, an epitope may comprise HLA-A*0201 YLQPRTFLL; HLA-A*0201 RLQSLQTYV; HLA-A*2402 QYIKWPWYI; HLA-A*2402 NYNYLYRLF; HLA-A*2402 KWPWYIWLGF; HLA-B*3501 QPTESIVRF; HLA-B*3501 IPFAMQMAY; or HLA-B*3501 LPFNDGVYF.

In some embodiments, determination of need for, timing of, and/or amount of a second (or subsequent) dose may include one or more steps of assessing, after (e.g., 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 days or longer after) a first (or other prior) dose, presence and/or expression levels of neutralizing antibodies directed to a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD) as measured in serum from a subject and/or induction of cell-mediated immune response (e.g., a T cell response against SARS-CoV-2), including, e.g., in some embodiments induction of T cells that recognize at least one or more MHC-restricted (e.g., MHC class I-restricted) eptiopes within a SARS-CoV-2 spike polypeptide and/or an immunogenic fragment thereof (e.g., RBD). In some embodiments, one or more epitopes recognized by vaccine-induced T cells (e.g., CD8+ T cells) may be presented on a MHC class I allele that is present in at least 50% of subjects in a population, including, e.g., at least 60%, at least 70%, at least 80%, at least 90%, or more; in some such embodiments, the MHC class I allele may be HLA-B*0702, HLA-A*2402, HLA-B*3501, HLA-B*4401, or HLA-A*0201. In some embodiments, an epitope may comprise HLA-A*0201 YLQPRTFLL; HLA-A*0201 RLQSLQTYV; HLA-A*2402 QYIKWPWYI; HLA-A*2402 NYNYLYRLF; HLA-A*2402 KWPWYIWLGF; HLA-B*3501 QPTESIVRF; HLA-B*3501 IPFAMQMAY; or HLA-B*3501 LPFNDGVYF.

In some embodiments, a kit as provided herein may comprise a real-time monitoring logging device, which, for example in some embodiments, is capable of providing shipment temperatures, shipment time and/or location.

In some embodiments, an RNA (e.g., mRNA) composition as described herein may be shipped, stored, and/or utilized, in a container (such as a vial or syringe), e.g., a glass container (such

as a glass vial or syringe), which, in some embodiments, may be a single-dose container or a multi-dose container (e.g., may be arranged and constructed to hold, and/or in some embodiments may hold, a single dose, or multiple doses of a product for administration). In some embodiments, a multi-dose container (such as a multi-dose vial or syringe) may be arranged and constructed to hold, and/or may hold 2, 3, 4, 5, 6, 7, 8, 9, 10 or more doses; in some particular embodiments, it may be designed to hold and/or may hold 5 doses. In some embodiments, a single-dose or multi-dose container (such as a single-dose or multi-dose vial or syringe) may be arranged and constructed to hold and/or may hold a volume or amount greater than the indicated number of doses, e.g., in order to permit some loss in transfer and/or administration. In some embodiments, an RNA (e.g., mRNA) composition as described herein may be shipped, stored, and/or utilized, in a preservative-free glass container (e.g., a preservative-free glass vial or syringe, e.g., a single-dose or multi-dose preservative-free glass vial or syringe). In some embodiments, an RNA (e.g., mRNA) composition as described herein may be shipped, stored, and/or utilized, in a preservative-free glass container (e.g., a preservative-free glass vial or syringe, e.g., a single-dose or multi-dose preservative-free glass vial or syringe) that contains 0.45 ml of frozen liquid (e.g., including 5 doses). In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a vial or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature below room temperature, at or below 4 °C, at or below 0 °C, at or below -20 °C, at or below -60 °C, at or below -70 °C, at or below -80 °C , at or below -90 °C, etc. In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature between -80°C and -60°C and in some embodiments protected from light. In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature below about 25°C, and in some embodiments protected

from light. In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature below about 5°C (e.g., below about 4°C), and in some embodiments protected from light. In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature below about -20°C, and in some embodiments protected from light. In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature above about -60°C (e.g., in some embodiments at or above about -20°C, and in some embodiments at or above about 4-5°C, in either case optionally below about 25°C), and in some embodiments protected from light, or otherwise without affirmative steps (e.g., cooling measures) taken to achieve a storage temperature materially below about -20°C.

In some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a vial or syringe) in which it is disposed is shipped, stored, and/or utilized together with and/or in the context of a thermally protective material or container and/or of a temperature adjusting material. For example, in some embodiments, an RNA (e.g., mRNA) composition as described herein and/or a container (e.g., a vial or syringe) in which it is disposed is shipped, stored, and/or utilized together with ice and/or dry ice and/or with an insulating material. In some particular embodiments, a container (e.g., a vial or syringe) in which an RNA (e.g., mRNA) composition is disposed is positioned in a tray or other retaining device and is further contacted with (or otherwise in the presence of) temperature adjusting (e.g., ice and/or dry ice) material and/or insulating material. In some embodiments, multiple containers (e.g., multiple vials or syringes such as single use or multi-use vials or syringes as described herein) in which a provided RNA (e.g., mRNA) composition is disposed are co-localized (e.g., in a common tray, rack, box, etc.) and packaged with (or otherwise in the

presence of) temperature adjusting (e.g., ice and/or dry ice) material and/or insulating material. To give but one example, in some embodiments, multiple containers (e.g., multiple vials or syringes such as single use or multi-use vials or syringes as described herein) in which an RNA (e.g., mRNA) composition is disposed are positioned in a common tray or rack, and multiple such trays or racks are stacked in a carton that is surrounded by a temperature adjusting material (e.g., dry ice) in a thermal (e.g., insulated) shipper. In some embodiments, temperature adjusting material is replenished periodically (e.g., within 24 hours of arrival at a site, and/or every 2 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, etc.). Preferably, re-entry into a thermal shipper should be infrequent, and desirably should not occur more than twice a day. In some embodiments, a thermal shipper is re-closed within 5, 4, 3, 2, or 1 minute, or less, of having been opened. In some embodiments, a provided RNA (e.g., mRNA) composition that has been stored within a thermal shipper for a period of time, optionally within a particular temperature range remains useful. For example, in some embodiments, if a thermal shipper as described herein containing a provided RNA (e.g., mRNA) composition is or has been maintained (e.g., stored) at a temperature within a range of about 15 °C to about 25 °C, the RNA (e.g., mRNA) composition may be used for up to 10 days; that is, in some embodiments, a provided RNA (e.g., mRNA) composition that has been maintained within a thermal shipper, which thermal shipper is at a temperature within a range of about 15 °C to about 25 °C, for a period of not more than 10 days is administered to a subject. Alternatively or additionally, in some embodiments, if a provided RNA (e.g., mRNA) composition is or has been maintained (e.g., stored) within a thermal shipper, which thermal shipper has been maintained (e.g., stored) at a temperature within a range of about 15 °C to about 25 °C, it may be used for up to 10 days; that is, in some embodiments, a provided RNA (e.g., mRNA) composition that has been maintained within a thermal shipper, which thermal shipper has been maintained at a

temperature within a range of about 15 °C to about 25 °C for a period of not more than 10 days is administered to a subject.

In some embodiments, a provided RNA (e.g., mRNA) composition is shipped and/or stored in a frozen state. In some embodiments, a provided RNA (e.g., mRNA composition is shipped and/or stored as a frozen suspension, which in some embodiments does not contain preservative. In some embodiments, a frozen RNA (e.g., mRNA) composition is thawed. In some embodiments, a thawed RNA (e.g., mRNA) composition (e.g., a suspension) may contain white to off-white opaque amorphous particles. In some embodiments, a thawed RNA (e.g., mRNA) composition may be used for up to a small number (e.g., 1, 2, 3, 4, 5, or 6) of days after thawing if maintained (e.g., stored) at a temperature at or below room temperature (e.g., below about 30 °C, 25 °C, 20 °C, 15 °C, 10 °C, 8 °C, 4 °C, etc). In some embodiments, a thawed RNA (e.g., mRNA) composition may be used after being stored (e.g., for such small number of days) at a temperature between about 2 °C and about 8 °C; alternatively or additionally, a thawed RNA (e.g., mRNA) composition may be used within a small number (e.g., 1, 2, 3, 4, 5, 6) of hours after thawing at room temperature. Thus, in some embodiments, a provided RNA (e.g., mRNA) composition that has been thawed and maintained at a temperature at or below room temperature, and in some embodiments between about 2 °C and about 8 °C, for not more than 6, 5, 4, 3, 2, or 1 days is administered to a subject. Alternatively or additionally, in some embodiments, a provided RNA (e.g., mRNA) composition that has been thawed and maintained at room temperature for not more than 6, 5, 4, 3, 2, or 1 hours is administered to a subject. In some embodiments, a provided RNA (e.g., mRNA) composition is shipped and/or stored in a concentrated state. In some embodiments, such a concentrated composition is diluted prior to administration. In some embodiments, a diluted composition is administered within a period of about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 hour(s) post-dilution; in some embodiments, such administration is within 6 hours post-dilution. Thus, in some embodiments, diluted preparation of a provided RNA (e.g., mRNA) composition is

administered to a subject within 6 hours post-dilution (e.g., as described herein after having been maintained at an appropriate temperature, e.g., at a temperature below room temperature, at or below 4 °C, at or below 0 °C, at or below -20 °C, at or below -60 °C, at or below -70 °C, at or below - 80 °C, etc, and typically at or above about 2 °C, for example between about 2 °C and about 8 °C or between about 2 °C and about 25 °C). In some embodiments, unusued composition is discarded within several hours (e.g., about 10, about 9, about 8, about 7, about 6, about 5 or fewer hours) after dilution; in some embodiments, unused composition is discarded within 6 hours of dilution.

In some embodiments, an RNA (e.g., mRNA) composition that is stored, shipped or utilized (e.g., a frozen composition, a liquid concentrated composition, a diluted liquid composition, etc.) may have been maintained at a temperature materially above -60°C for a period of time of at least 1, 2, 3, 4, 5, 6, 7 days or more, or at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 weeks or more, or at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 months or more; in some such embodiments, such composition may have been maintained at a temperature at or above about -20°C for such period of time, and/or at a temperature up to or about 4-5°C for such period of time, and/or may have been maintained at a temperature above about 4-5°C, and optionally about 25°C for a period of time up that is less than two (2) months and/or optionally up to about one (1) month. In some embodiments, such composition may not have been stored, shipped or utilized (or otherwise exposed to) a temperature materially above about 4-5°C, and in particular not at or near a temperature of about 25°C for a period of time as long as about 2 weeks, or in some embodiments 1 week. In some embodiments, such composition may not have been stored, shipped or utilized (or otherwise exposed to) a temperature materially above about -20°C, and in particular not at or near a temperature of about 4-5°C for a period of time as long as about 12 months, 11 months, 10 months, 9 months, 8 months, 7 months, 6 months, 5 months, 4 months, 3 months, 2 months, or, in some embodiments, for a period of

time as long as about 8 weeks or 6 weeks or materially more than about 2 months or, in some embodiments, 3 months or, in some embodiments 4 months.

In some embodiments, an RNA (e.g., mRNA) composition that is stored, shipped or utilized (e.g., a frozen composition, a liquid concentrated composition, a diluted liquid composition, etc.) may be protected from light. In some embodiments, one or more steps may be taken to reduce or minimize exposure to light for such compositions (e.g., which may be disposed within a container such as a vial or a syringe). In some embodiments, exposure to direct sunlight and/or to ultraviolent light is avoided. In some embodiments, a diluted solution may be handled and/or utilized under normal room light conditions (e.g., without particular steps taken to minimize or reduce exposure to room light). It should be understood that strict adherence to aseptic techniques is desirable during handling (e.g., diluting and/or administration) of an RNA (e.g., mRNA) composition as described herein. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered (e.g., is not injected) intravenously. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered (e.g., is not injected) intradermally. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered (e.g., is not injected) subcutaneously. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered (e.g., is not injected) any of intravenously, intradermally, or subcutaneously. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered to a subject with a known hypersensitivity to any ingredient thereof. In some embodiments, a subject to whom an RNA (e.g., mRNA) composition has been administered is monitored for one or more signs of anaphylaxis. In some embodiments, a subject to whom an RNA (e.g., mRNA) composition is administered had previously received at least one dose of a different vaccine for SARS-CoV-2; in some embodiments, a subject to whom an RNA (e.g., mRNA) composition is administered had not previously received a different vaccine for SARS-CoV-2. In some embodiments, a subject's temperature is taken

promptly prior to administration of an RNA (e.g., mRNA) composition (e.g., shortly before or after thawing, dilution, and/or administration of such composition); in some embodiments, if such subject is determined to be febrile, administration is delayed or canceled. In some embodiments, an RNA (e.g., mRNA) composition as described herein is not administered to a subject who is receiving anticoagulant therapy or is suffering from or susceptible to a bleeding disorder or condition that would contraindicate intramuscular injection. In some embodiments, an RNA (e.g., mRNA) composition as described herein is administered by a healthcare professional who has communicated with the subject receiving the composition information relating to side effects and risks. In some embodiments, an RNA (e.g., mRNA) composition as described herein is administered by a healthcare professional who has agreed to submit an adverse event report for any serious adverse events, which may include for example one or more of death, development of a disability or congenital anomaly/birth defect (e.g., in a child of the subject), in-patient hospitalization (including prolongation of an existing hospitalization), a life-threatening event, a medical or surgical intervention to prevent death, a persistent or significant or substantial disruption of the ability to conduct normal life functions; or another important medical event that may jeopardize the individual and may require medical or surgical intervention (treatment) to prevent one of the other outcomes.

In some embodiments, provided RNA compositions are administered to a population of individuals under 18 years of age, or under 17 years of age, or under 16 years of age, or under 15 years of age, or under 14 years of age, or under 13 years of age, for example according to a regimen established to have a rate of incidence for one or more of the local reaction events indicated below that does not exceed the rate of incidence indicated below:

- pain at the injection site (75% after a first dose and/or a second dose, and/or a lower incidence after a second dose, e.g., 65% after a second dose);
- redness at the injection site (less than 5% after a first dose and/or a second dose); and/or

- swelling at the injection site (less than 5% after a first dose and/or a second dose).

In some embodiments, provided RNA compositions are administered to a population of individuals under 18 years of age, or under 17 years of age, or under 16 years of age, or under 15 years of age, or under 14 years of age, or under 13 years of age, for example according to a regimen established to have a rate of incidence for one or more of the systemic reaction events indicated below that does not exceed the rate of incidence indicated below:

- fatigue (55% after a first dose and/or a second dose);
- headache (50% after a first dose and/or a second dose);
- muscle pain (40% after a first dose and/or a second dose);
- chills (40% after a first dose and/or a second dose);
- joint pain (20% after a first dose and/or a second dose);
- fever (25% after a first dose and/or a second dose);
- vomiting (10% after a first dose and/or a second dose); and/or
- diarrhea (10% after a first dose and/or a second dose).

In some embodiments, medication that alleviates one or more symptoms of one or more local reaction and/or systemic reaction events (e.g., described herein) are administered to individuals under 18 years of age, or under 17 years of age, or under 16 years of age, or under 15 years of age, or under 14 years of age, or under 13 years of age who have been administered with provided RNA compositions and have experienced one or more of the local and/or systemic reaction events (e.g., described herein). In some embodiments, antipyretic and/or pain medication can be administered to such individuals.

In some embodiments, the present disclosure provides a kit and/or container system comprising: a) a primary container; b) a payload container; c) at least one tray for placement within the payload container, wherein the at least one tray contains a temperature-sensitive material; and d) a dry ice container; wherein the at least one tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to

about 46 mm. For example, the A dimension can be about 228 mm, 229 mm, 230 mm, 231 mm, 232 mm, or about 233 mm; the B dimension can be about 228 mm, 229 mm, 230 mm, 231 mm, 232 mm, or about 233 mm; and the H dimension can be about 38 mm, 39 mm, 40 mm, 41 mm, 42 mm, 43 mm, 44 mm, 45 mm, or about 46 mm. Further, for example, the payload container in such a kit can have dimensions such as 229 ± 10 mm x 229 ± 10 mm x 229 ± 10 mm.

Further, for example, the primary container (or thermal shipper) can have internal dimensions of about 200mm to about 300mm X about 200mm to about 300mm X about 200mm to about 300mm; and external dimensions of about 300 mm to about 500 mm X about 300mm to about 500mm X about 350mm to about 700mm. For example, the primary container can have internal dimensions of A x B x C, wherein A and B are each independently about 200mm, 220mm, 230mm, 240mm, 245 mm, 255mm, 260mm, 265mm, 270mm, 280mm, 290mm, or about 300mm; and wherein C is independently about 200mm, 220mm, 230mm, 235 mm, 237mm, 238 mm, 239 mm, 240mm, 241mm, 242mm, 243 mm, 244mm, 245 mm, 255mm, 260mm, 265mm, 270mm, 280mm, 290mm, or about 300mm. Further, for example, the primary container can have external dimensions of A x B x C, wherein A and B are each independently about 300mm, 320mm, 340mm, 360mm, 380mm, 390mm, 395mm, 400mm, 405mm, 410mm, 420mm, 440mm, 460mm, 480mm or about 500mm; and wherein C is independently about 350mm, 370mm, 390mm, 410mm, 430mm, 450mm, 470mm, 490mm, 510mm, 520mm, 530mm, 540mm, 550mm, 555mm, 560mm, 565mm, 570mm, 575mm, 580mm, 600mm, 620mm, 640mm, 660mm, 680mm, or about 700 mm.

Further, for example, the kits and/or container systems disclosed herein are capable of maintaining the temperature of the material within the tray, and/or the interior of the payload container, at −10°C or lower, −20°C or lower, −30°C or lower, −40°C or lower, −50°C or lower, −60°C or lower, −70°C or lower, −80°C or lower, or −90°C or lower for at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 days. In a further example, the kits and/or container systems can

further comprise a temperature monitoring system. For example, the temperature monitoring system can comprise a temperature sensor and a display, wherein the temperature monitoring system displays or warns when the temperature of the material, or the temperature of a specific region within the container system attains a temperature greater than a specific threshold temperature. For example, such threshold temperature can be about −10°C, −20°C, −30°C, −40°C, −50°C, −60°C, −70°C, −80°C, or about −90°C.

Further, for example, the kits and/or container systems disclosed herein can have the payload container placed at the bottom of the primary container, and further wherein the dry ice container is placed on top (or on bottom) of the payload container.

Further, for example, the kits and/or container systems disclosed herein can have the at least one tray placed inside the payload container. For example, there can be 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, or more trays within the payload container.

Further, for example, the temperature-sensitive material can be contained within at least one glass vial, wherein the at least one glass vial is placed within the tray. The temperature-sensitive material can also be contained within a specimen tube, a bag, or a syringe. Such vials, syringes, tubes, and/or bags can be single-dose, or multi-dose.

Further, for example, the trays described herein can each contain any number of vials, such as 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 185, 195, 200 or more.

Further disclosed herein is a method of transporting a temperature-sensitive material comprising the steps of: a) placing the material in a kit or container system according as disclosed herein; and b) transporting the kit or container system to an intended destination. In some examples, the temperature inside the payload container and/or its location is continuously monitored throughout the duration of the transportation. In some examples, the transportation is carried out on land, air, and/or water. In some examples, the transportation is carried out via land vehicle (such as delivery truck or van), airplane (or other modes of air transportation such as drone or helicopter), and/or boat. In further examples,

the temperature inside the payload container is maintained at −10°C or lower, −20°C or lower, −30°C or lower, −40°C or lower, −50°C or lower, −60°C or lower, −70°C or lower, −80°C or lower, or −90°C or lower throughout the duration of the transportation. In further examples, there are at least 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 125, 150, 175, 185, 195, 200 or more vials in each tray through the transportation. In further examples, there are at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 trays within the payload container throughout the transportation. In further examples, the location of the kit or container system is periodically or continuously monitored through use of a global positioning system (GPS).

Further disclosed herein is a payload container having dimensions A x B x C, wherein each of the A, B, and C dimensions can independently be about 225 mm, 226 mm, 227 mm, 228 mm, 229 mm, 230 mm, 231 mm or about 232 mm. Further, for example, at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 trays are placed within the payload container, wherein each tray contains at least 50, 75, 100, 125, 150, 160, 170, 180, 185, 190, 195, or at least 200 vials of temperature-sensitive material.

Further disclosed herein is a tray for carrying temperature-sensitive material, wherein the tray has dimensions A x B x H, wherein: A is about 227 mm, 228 mm, 229 mm, 230 mm, 231 mm, 232 mm, or about 233 mm; B is about 227 mm, 228 mm, 229 mm, 230 mm, 231 mm, 232 mm, or about 233 mm; and H is about 38 mm, 39 mm, 40 mm, 41 mm, 42 mm, 43 mm, 44 mm, 45 mm, or about 46 mm. Further, for example, a tray contains at least 50, 75, 100, 125, 150, 160, 170, 180, 185, 190, 195, or at least 200 vials of temperature-sensitive material. In some embodiments, the tray is made of polypropylene (e.g. Akylux®, Biplex®, or equivalent thereof).

In a further example, the kit and/or container system of the present disclosure can be used to store a temperature-sensitive material for up to 10 days if stored at 15°C to 25°C without opening. For example, the temperature-sensitive material can be stored for 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 days under such conditions. In a further example, after the primary container

is opened, it can be replenished with dry ice within 24 hours. For example, replenishment can occur within 1 hour, within 2 hours, within 4 hours, within 8 hours, within 12 hours, within 16 hours, within 20 hours, or within 24 hours of being opened following transportation. Further for example, the amount of dry ice used to replenish the kit or container system can be up to 1 kg, 5kg, 10kg, 15 kg, 20 kg, 21kg, 22 kg, 22 kg, 23 kg, 24 kg, 25 kg or up to 30 kg. Dry ice that can be used includes various sizes, such as 1mm pellets up to 20 mm pellets. The kit or container system can be re-iced, for example, every 1 day, every 2 days, every 3 days, every 4 days, every 5 days, every 6 days, every 7 days, every 8 days, every 9 days, or every 10 days. In a further example, the kit or container system is opened not more than once per day, or not more than twice per day. In a further example, the kit or container system can be closed within 1 minute (or less), within 2 minutes (or less), within 3 minutes (or less), within 4 minutes (or less), or within 5 minutes (or less) after opening. In some examples, the temperature-sensitive material can be stored at about 2°C to about 8°C up to 2 days or at room temperature for no more than 1 hours, or no more than 2 hours after thawing.

Brief description of the drawings

Figure 1: Schematic overview of the S protein organization of the SARS-CoV-2 S protein.
The sequence within the S1 subunit consists of the signal sequence (SS) and the receptor binding domain (RBD) which is the key subunit within the S protein which is relevant for binding to the human cellular receptor ACE2. The S2 subunit contains the S2 protease cleavage site (S2') followed by a fusion peptide (FP) for membrane fusion, heptad repeats (HR1 and HR2) with a central helix (CH) domain, the transmembrane domain (TM) and a cytoplasmic tail (CT).

Figure 2: Anticipated constructs for the development of a SARS-CoV-2 vaccine.
Based on the full and wildtype S protein, we have designed different construct encoding the (1) full protein with mutations in close distance to the first heptad repeat (HRP1) that include stabilizing mutations preserving neutralisation sensitive sites, the (2) S1 domain or the (3) RB domain (RBD) only. Furthermore, to stabilize the protein fragments a fibritin domain (F) was fused to the C-terminus. All constructs start with the signal peptide (SP) to ensure Golgi transport to the cell membrane.

Figure 3: Antibody immune response against Influenza HA using the LNP-formulated modRNA.
BALB/c mice were immunized twice with 1 µg of the vaccine candidate. Total amount of viral antigen specific immunoglobulin G (IgG) was measured via ELISA. The functionality of the antibodies was assessed via VNT.

Figure 4: T cell response against Influenza HA using the LNP-formulated modRNA platform.

BALB/c mice were immunized IM with 1 µg of the vaccine candidate, twice. The T cell response was analyzed using antigen specific peptides for T cell stimulation recovered from the spleen. IFNγ release was measured after peptide stimulation using an ELISpot assay.

Figure 5: Anti-S protein IgG response 7, 14, 21 and 28 d after immunization with BNT162a1.
BALB/c mice were immunized IM once with 1, 5 or 10 µg of LNP-formulated RBL063.3. On day 7, 14, 21 and 28 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7, day 14, day 21 and day 28, values for a serum dilution of 1:100 were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 6: Anti-S protein IgG response 7, 14, 21 and 28 d after immunization with BNT162b1.
BALB/c mice were immunized IM once with 0.2, 1 or 5µg of LNP-formulated RBP020.3. On day 7, 14. 21 and 28 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7 (1:100), day 14 (1:300), day21 (1:900), and day 28 (1:2700) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 7: Neutralization of SARS-CoV-2 pseudovirus 14, 21 and 28 d after immunization with BNT162b1.
BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulated RBP020.3. On 14, 21 and 28 d after immunization, animals were bled, and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious

events, compared to positive controls without serum). One point in the graphs stands for one mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 8: Anti-S protein IgG response 7, 14 and 21 d after immunization with BNT162c1.

BALB/c mice were immunized IM once with 0.2, 1 or 5µg of LNP-formulated RBS004.3. On day 7, 14 and 21 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7 (1:100), day 14 (1:300), and day 21 (1:900) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 9: Neutralization of SARS-CoV-2 pseudovirus 14 and 21 d after immunization with BNT162c1.

BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulated RBS004.3. On 14 and 21 d after immunization, animals were bled and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious events, compared to positive controls without serum). One point in the graphs stands for one mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 10: Anti-S protein IgG response 7, 14, 21 and 28 d after immunization with LNP-formulated RBL063.1.

BALB/c mice were immunized IM once with 1, 5 or 10 µg of LNP-formulated RBL063.1. On day 7, 14, 21 and 28 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7 (1:100), day 14 (1:100), day 21 (1:300) and day 28 (1:900) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 11: Neutralization of SARS-CoV-2 pseudovirus 14, 21 and 28 d after immunization with LNP-formulated RBL063.1.

BALB/c mice were immunized IM once with 1, 5 or 10 µg of LNP-formulated RBL063.1. On 14, 21, and 28 d after immunization, animals were bled and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious events, compared to positive controls without serum). One point in the graphs stands for one mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 12: Anti-S protein IgG response 7, 14 and 21 d after immunization with BNT162b2 (LNP-formulated RBP020.1).

BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulatedRBP020.1. On day 7, 14, and 21 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7 (1:100), day 14 (1:300), and day 21 (1:1100) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 13: Neutralization of SARS-CoV-2 pseudovirus 14 and 21 after immunization with BNT162b2 (LNP-formulated RBP020.1).

BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulated RBP020.1. On day 14 and 21 after immunization, animals were bled and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious events, compared to positive controls without serum). One point in the graphs stands for one mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 14: Anti-S protein IgG response 7, 14 and 21 d after immunization with LNP-formulated RBS004.2.

BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulated RBS004.2. On day 7, 14 and 21 after immunization, animals were bled and the serum samples were analyzed for total amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 7 (1:100), day 14 (1:300), and day 21 (1:900) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 15: Neutralization of SARS-CoV-2 pseudovirus 14 and 21 after immunization with LNP-formulated RBS004.2.

BALB/c mice were immunized IM once with 0.2, 1 or 5 µg of LNP-formulated RBS004.2. On 14, and 21 d after immunization, animals were bled, and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious events, compared to positive controls without serum). One point in the graphs stands for one

mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 16: ALC-0315 activity in the screening process.

Figure 17: Luciferase expression was monitored on the right (site of injection), dorsal (site of injection) and ventral (drainage to the liver) sides of the animal after intramuscular administration in wild-type (WT) or ApoE knockout C57Bl/6 mice in the presence or absence of ApoE3. Luciferase expression was detected using Xenolight D-Luciferin Rediject at 4, 24, 72 and 96 hours post administration.

Figure 18: Luciferase activity after intravenous (IV) and intramuscular (IM) administration in wild-type (WT) or ApoE knockout C57Bl/6 mice in the presence (KO+) or absence (KO) of ApoE3. Luciferase expression was detected using Xenolight D-Luciferin Rediject at 4 hours post administration.

Figure 19: General structure of the RNA.

Schematic illustration of the general structure of the RNA vaccines with 5'-cap, 5'- and 3'-untranslated regions, coding sequences with intrinsic secretory signal peptide as well as GS-linker, and poly(A)-tail. Please note that the individual elements are not drawn exactly true to scale compared to their respective sequence lengths.

UTR = Untranslated region; sec = Secretory signal peptide; RBD = Receptor Binding Domain; GS = Glycine-serine linker.

Figure 20: General structure of the RNA.

Schematic illustration of the general structure of the RNA drug substances with 5'-cap, 5'- and 3'-untranslated regions, coding sequences with intrinsic secretory signal peptide as well as GS-linker, and poly(A)-tail. Please note that the individual elements are not drawn exactly true to scale compared to their respective sequence lengths.
GS = Glycine-serine linker; UTR = Untranslated region; Sec = Secretory signal peptide; RBD = Receptor Binding Domain.

Figure 21: General structure of the RNA.

Schematic illustration of the general structure of the RNA vaccines with 5'-cap, 5'- and 3'-untranslated regions, coding sequences of the Venezuelan equine encephalitis virus (VEEV) RNA-dependent RNA polymerase replicase and the SARS-CoV-2 antigen with intrinsic secretory signal peptide as well as GS-linker, and poly(A)-tail. Please note that the individual elements are not drawn exactly true to scale compared to their respective sequence lengths.
UTR = Untranslated region; Sec = Secretory signal peptide; RBD = Receptor Binding Domain; GS = Glycine-serine linker.

Figure 22: ELISpot analysis 28 d after immunization with BNT162b1.

BALB/c mice were immunized IM once with 1µg of LNP-formulated RBP020.3. On day 28 after immunization, mice were euthanized and splenocytes were prepared. ELISpot assay was performed using MACS-sorted CD4+ and CD8+ T cells. T cells were stimulated with an S protein- or RBD-specific overlapping peptide pool and IFN-γ secretion was measured to assess T-cell responses. One point in the graph stands for the individual spot count of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 23: Cytokine concentrations in supernatants of re-stimulated splenocytes 12 d after immunization with BNT162b1.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBP020.3. On day 12 after immunization, mice were euthanized. Splenocytes were prepared and were stimulated with an S protein-specific overlapping peptide pool. After 48 h of stimulation, supernatant was collected and cytokine concentrations were determined. One point in the graph stands for the individual cytokine concentration of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 24: T cell immunophenotyping in PBMCs 7 days after immunization with BNT162b1.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBP020.3. On day 7 after immunization, mice were bled. Flow cytometry analysis of PBMCs was performed of T cells. T cells were defined as viable $CD3^+CD4^+$ and $CD3^+CD8^+$ T cells. Additional phenotyping markers are included in the figures. Tfh cells were gated from $CD4^+$ T cells and defined as $CD4^+$T-bet^- $GATA3^-CD44^+CD62L^-PD\text{-}1^+CXCR5^+$ cells. One point in the graph stands for the individual cell fraction of one mouse (group size n=8; mean is included for the groups).

Figure 25: B cell immunophenotyping in draining lymph nodes 12 days after immunization with BNT162b1.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBP020.3. On day 12 after immunization, mice were euthanized. Flow cytometry analysis of lymphocytes was performed of B cells. Activated B cells were gated within single, viable lymphocytes and defined as IgD-Dump (CD4, CD8, F4/80, GR-1)$^-$ cells. Plasma cells were defined as $CD138^+B220^{low/-}$ cells. Switched B cells were gated from non-plasma cells and defined as $CD19^+CD138^-IgM^-$. Germinal center (GC) B cells were gated from switched B cells and defined as $CD19^+IgM^-CD38^-CD95^+$

cells and gated for IgG1 and IgG2a. One point in the graph stands for the individual cell fraction of one mouse (group size n=8; mean is included for the groups).

Figure 26: ELISpot analysis 28 d after immunization with LNP-formulated modRNA RBP020.1.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBP020.1. On day 28 after immunization, mice were euthanized and splenocytes were prepared. ELISpot assay was performed using MACS-sorted CD4+ and CD8+ T cells. T cells were stimulated with an S protein-specific overlapping peptide pool and IFN-γ secretion was measured to assess T-cell responses. One point in the graph stands for the individual spot count of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 27: Cytokine concentrations in supernatants of re-stimulated splenocytes 28 d after immunization with LNP-formulated modRNA RBP020.1.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBP020.1. On day 28 after immunization, mice were euthanized. Splenocytes were prepared and were stimulated with an S protein-specific overlapping peptide pool. After 48 h of stimulation, supernatant was collected and cytokine concentrations were determined. One point in the graph stands for the individual cytokine concentration of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 28: ELISpot analysis 28 d after immunization with LNP-formulated saRNA RBS004.2.

BALB/c mice were immunized IM once with 5µg of LNP-formulated RBS004.2. On day 28 after immunization, mice were euthanized and splenocytes were prepared. ELISpot assay was performed using MACS-sorted CD4+ and CD8+ T cells. T cells were stimulated with an S protein-specific overlapping peptide pool and IFN-γ secretion was measured to assess T-cell

responses. One point in the graph stands for the individual spot count of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 29: Cytokine concentrations in supernatants of re-stimulated splenocytes 28 d after immunization with LNP-formulated saRNA RBS004.2.

BALB/c mice were immunized IM once with 1µg of LNP-formulated RBS004.2. On day 28 after immunization, mice were euthanized. Splenocytes were prepared and were stimulated with an S protein-specific overlapping peptide pool. After 48 h of stimulation, supernatant was collected and cytokine concentrations were determined. One point in the graph stands for the individual cytokine concentration of one mouse, every mouse sample was measured in duplicates (group size n=8; mean is included for the groups).

Figure 30: Schematic overview of the S protein organization of the SARS-CoV-2 S protein and novel constructs for the development of a SARS-CoV-2 vaccine.

Based on the wildtype S protein, we have designed two different transmembrane-anchored RBD-based vaccine constructs encoding the RBD fragment fused to the T4 fibritin trimerization domain (F) and the autochthonus transmembrane domain (TM). Construct (1) starts with the SARS-CoV-2-S signal peptide (SP; AA 1-19 of the S protein) whereas construct (2) starts with the human Ig heavy chain signal peptide (huSec) to ensure Golgi transport to the cell membrane.

Figure 31: Anti-S protein IgG response 6, 14 and 21 d after immunization with LNP-C12 formulated modRNA coding for transmembrane-anchored RBD-based vaccine constructs.

BALB/c mice were immunized IM once with 4 µg of LNP-C12-formulated transmembrane-anchored RBD-based vaccine constructs (surrogate to BNT162b3c/BNT162b3d). On day 6, 14 and 21 after immunization, animals were bled and the serum samples were analyzed for total

amount of anti-S1 (left) and anti-RBD (right) antigen specific immunoglobulin G (IgG) measured via ELISA. For day 6 (1:50), day 14 (1:300) and day 21 (1:900) different serum dilution were included in the graph. One point in the graph stands for one mouse, every mouse sample was measured in duplicates (group size n=8; mean + SEM is included for the groups).

Figure 32: Neutralization of SARS-CoV-2 pseudovirus 6, 14 and 21 d after immunization with LNP-C12 formulated modRNA coding for transmembrane-anchored RBD-based vaccine constructs.

BALB/c mice were immunized IM once with 4 µg of LNP-C12-formulated transmembrane-anchored RBD-based vaccine constructs (surrogate to BNT162b3c/BNT162b3d). On day 6, 14 and 21 after immunization, animals were bled and the sera were tested for SARS CoV-2 pseudovirus neutralization. Graphs depict pVN50 serum dilutions (50% reduction of infectious events, compared to positive controls without serum). One point in the graphs stands for one mouse. Every mouse sample was measured in duplicate. Group size n=8. Mean + SEM is shown by horizontal bars with whiskers for each group. LLOQ, lower limit of quantification. ULOQ, upper limit of quantification.

Figure 33: Immunogenicity of BNT162b1 in rhesus macaques and comparison to human convalescent sera.

Rhesus macaques were immunized IM on days 0 and 21 with 30 µg or 100 µg of BNT162b1 or with placebo (0.9% NaCl). Sera were obtained before immunization and 14, 21, 28, and 35 days after immunization; PBMCs were obtained before and 14 and 42 days after immunization. Sera from COVID-19 patients were obtained 20-40 days after the onset of symptoms and after at least 14 days of asymptomatic convalescence. **a,** Geometric mean concentrations of IgG binding to a recombinant S1 protease fragment of SARS-CoV-2 S, in rhesus macaque sera drawn at the indicated times after immunization (n=6 per group, all

measurement time points of the placebo group depicted under 'Control') and in human convalescent sera (n=62). **b,** SARS-CoV-2 geometric mean 50% neutralization titers of the rhesus macaque sera (n=6 per group, all measurement time points of the placebo group depicted under 'Control') and human convalescent sera (n=38). P values were determined by a two-tailed one-way ANOVA and Dunnett's multiple comparisons test. **c,** Flow cytometry analysis of $CD4^+$ T cells producing IFN γ , IL-2, TNF (T_H1), IL-21 or IL-4 (T_H2) cytokines in the rhesus macaque PBMCs on day 42. P values were determined by a two-tailed Kruskal-Wallis test followed by Dunn's multiple comparisons test. Each data point corresponds to an individual animal.

Figure 34: Overview of study population

Figure 35: Local Reactions Reported within 7 Days of Vaccination all Dose Levels

Solicited injection-site (local) reactions were: pain at injection site (mild = does not interfere with activity; moderate = interferes with activity; severe = prevents daily activity; Grade 4 = emergency room visit or hospitalization) and redness and swelling (mild = 2.5 to 5.0 cm in diameter; moderate = 5.5 to 10.0 cm in diameter; severe = >10.0 cm in diameter; Grade 4 = necrosis or exfoliative dermatitis for redness, and necrosis for swelling). Data were collected with the use of electronic diaries for 14 days after each vaccination.

Figure 36: a: Systemic Events Reported within 7 days after Vaccination 1: All Dose Levels; b: Systemic Events Reported within 7 days after Vaccination 2: 10 µg & 30 µg Dose Levels

Solicited systemic events were: nausea/vomiting (mild = no interference with activity or 1 to 2 times in 24 hours; moderate = some interference with activity or >2 times in 24 hours; severe = prevents daily activity or requires intravenous hydration; Grade 4 = emergency room visit or hospitalization for hypotensive shock), diarrhea (mild, 2 to 3 loose stools in 24 hours;

moderate, 4 to 5 loose stools in 24 hours; severe, ≥6 loose stools in 24 hours; Grade 4 = emergency room visit or hospitalization), headache (mild = no interference with activity; moderate = repeated use of non-narcotic pain reliever >24 hours or some interference with activity; severe = significant, any use of narcotic pain reliever or prevents daily activity; Grade 4 = emergency room visit or hospitalization), fatigue/tiredness (mild = no interference with activity; moderate = some interference with activity; severe = significant; prevents daily activity; Grade 4 = emergency room visit or hospitalization), muscle pain (pain that is occurring in areas other than the injection site; mild = no interference with activity; moderate = some interference with activity; severe = significant; prevents daily activity; Grade 4 = emergency room visit or hospitalization), joint pain (mild = no interference with activity; moderate = some interference with activity; severe = significant; prevents daily activity; Grade 4 = emergency room visit or hospitalization), and fever (mild = 100.4°F to 101.1°F [38.0°C to 38.4°C]; moderate = 101.2°F to 102.0°F [38.5°C to 38.9°C]; severe = 102.1°F to 104.0°F [39.0°C to 40.0°C]; Grade 4 = >104.0°F [>40.0°C]).

Figure 37: Immunogenicity of BNT162b1 - RBD-Binding IgG GMCs and SARS CoV2 50% Neutralizing Titers after 1 or 2 doses

Subjects in groups of 15 were immunized with the indicated dose levels of BNT162b1 (n=12) or with placebo (P, n=3) on days 1 (all dose levels and placebo) and 21 (10 µg and 30 µg dose levels and placebo). Sera were obtained before immunization (Day 1) and 7, 21, and 28 days after the first immunization. Human COVID-19 convalescent sera (HCS) (n=38) were obtained 20-40 days after the onset of symptoms and after at least 14 days of asymptomatic convalescence. **a**, GMCs of recombinant RBD-binding IgG. Lower limit of quantitation (LLOQ) 1.15 (dotted line). **b**, 50% SARS-CoV-2 neutralizing GMTs. Each data point represents a serum sample, and each vertical bar represents a geometric mean with 95% confidence interval.

Figure 38: BNT162b1 induces strong CD4 and CD8 T cell response in humans

BNT162 induced T cells: INFγ ELISpot *ex vivo*; T cell responses in 8 of 8 tested subjects. Here: subject vaccinated prime / boost with 10 µg BNT162b1; CEF: CMV, EBV, Influenza CD8 T cell epitope mix, CEFT: CMV, EBV, Influenza, Tetanus CD4 T cell epitope mix.

Figure 39: BNT162b1-induced IgG concentrations

Subjects were immunised with BNT162b1 on days 1 (all dose levels) and 22 (all dose levels except 60 µg) (*n*=12 per group, from day 22 on *n*=11 for the 10 µg and 50 µg cohort). Sera were obtained on day 1 (Pre prime) and on day 8, 22 (pre boost), 29 and 43. Pre-dose responses across all dose levels were combined. Human COVID-19 convalescent sera (HCS, *n*=38) were obtained at least 14 days after PCR-confirmed diagnosis and at a time when the donors were no longer symptomatic. For RBD-binding IgG concentrations below the lower limit of quantification (LLOQ = 1.15), LLOQ/2 values were plotted. Arrowheads indicate vaccination. Chequered bars indicate that no boost immunisation was performed. Values above bars are geometric means with 95% confidence intervals. At the time of submission, day 43 data were pending for five subjects of the 50 µg cohort and all subjects of the 60 µg cohort.

Figure 40: BNT162b1-induced virus neutralisation titers

The vaccination schedule and serum sampling are the same as in Figure 39. **a,** SARS-CoV-2 50% neutralisation titers (VNT_{50}) in immunized subjects and COVID-19 convalescent patients (HCS). For values below the lower limit of quantification (LLOQ) = 20, LLOQ/2 values were plotted. Arrowheads indicate days of immunisation. Chequered bars indicate that no boost immunisation was performed. Geometric mean (values above bars) with 95% confidence interval. At the time of submission, day 43 data were not yet available for five subjects of the 50 µg cohort and all subjects of the 60 µg cohort, **b,** Correlation of RBD-binding IgG geometric

mean concentrations (GMC) (as in Figure 39) with VNT_{50} on day 29 (all evaluable subject sera). Nonparametric Spearman correlation. **c,** Pseudovirus 50% neutralisation titers ($pVNT_{50}$) across a pseudovirus panel displaying 17 SARS-CoV-2 spike protein variants including 16 RBD mutants and the dominant spike protein variant D614G (dose level 10, 30 and 50 µg, *n*=1-2 each; day 29). Lower limit of quantification (LLOQ) = 40. Geometric mean.

Figure 41: Frequency and magnitude of BNT162b1-induced $CD4^+$ and $CD8^+$ T-cell responses

The vaccination schedule is as in Figure 39. PBMCs obtained on day 1 (Pre) and on day 29 (Post, 7 days after boost) (1 and 50 µg, *n*=8 each; 10 and 30 µg, *n*=10 each) were enriched for $CD4^+$ or $CD8^+$ T cell effectors and separately stimulated over night with an overlapping peptide pool representing the vaccine-encoded RBD for assessment in direct *ex vivo* IFNγ ELISpot. Common pathogen T-cell epitope pools CEF (CMV, EBV, influenza virus HLA class I epitopes) and CEFT (CMV, EBV, influenza virus, tetanus toxoid HLA class II epitopes) served to assess general T-cell reactivity, medium served as negative control. Each dot represents the normalized mean spot count from duplicate wells for one study subject, after subtraction of the medium-only control. **a,** Ratios above post-vaccination data points are the number of subjects with detectable $CD4^+$ or $CD8^+$ T cell response within the total number of tested subjects per dose cohort. **b,** Exemplary $CD4^+$ and $CD8^+$ ELISpot of a 10-µg cohort subject. **c,** RBD-specific $CD4^+$ and $CD8^+$ T cell responses in all prime/boost vaccinated subjects and their baseline CEFT- and CEF-specific T-cell responses. **d,** Correlation of VNT_{50} (as in Figure 40a) with $CD4^+$ T-cell responses (as in Figure 41) of dose cohorts 10 to 50 µg (1 and 50 µg, *n*=8 each; 10 and 30 µg, *n*=10 each). Nonparametric Spearman correlation.

Figure 42: Cytokine polarisation of BNT162b1-induced T cells

The vaccination schedule and PBMC sampling are as in Figure 41. PBMCs of vaccinees and COVID-19 recovered donors (HCS *n*=6; in (c)) were stimulated over night with an overlapping

peptide pool representing the vaccine-encoded RBD and analysed by flow cytometry (a-c) and bead-based immunoassay (d). **a**, Exemplary pseudocolor flow cytometry plots of cytokine-producing $CD4^+$ and $CD8^+$ T cells of a 10-µg cohort subject. **b**, RBD-specific $CD4^+$ T cells producing the indicated cytokine as fraction of total cytokine-producing RBD-specific $CD4^+$ T cells, and **c**, RBD-specific $CD8^+$ (left) or $CD4^+$ (right) T cells producing the indicated cytokine as fraction of total circulating T cells of the same subset. One CD4 non-responder (<0.02%total cytokine producing T cells) and one CD8 non-responder (<0.01%total cytokine producing T cells) from the 30-µg cohort were excluded in (b). Values above data points are the mean fractions across all dose cohorts. **d**, PBMCs from the 50-µg cohort. Each dot represents the mean from duplicate wells subtracted by the DMSO control for one study subject. Lower limits of quantification (LLOQ) were 6.3 pg/mL for TNF, 2.5 pg/mL for IL-1β, and 7.6 pg/mL for IL-12p70. Mean (b).

Figure 43: Schedule of vaccination and assessment

Figure 44: Solicited adverse events

Subjects were immunized with the indicated dose levels of BNT162b1 on days 1 (all dose levels) and 22 (all dose levels except 60 µg) (*n*=12 per group, *n*=11 for 10 µg and 50 µg cohort from day 22 on). **a, b,** Number of subjects with local (**a**) or systemic reactions (**b**) by day (day 1-9, 22-30) and cohort. Grading of adverse events was performed according to FDA recommendations (U.S. Department of Health and Human Services, Administration, F. and D. & Research, C. for B. E. and. Toxicity grading scale for healthy adult and adolescent volunteers enrolled in preventive vaccine clinical trials. (2007). Available at: https://www.fda.gov/regulatory-information/search-fda-guidance-documents/toxicity-grading-scale-healthy-adult-and-adolescent-volunteers-enrolled-preventive-vaccine-clinical.).

Figure 45: Pharmacodynamic markers

Subjects were immunised with the indicated dose levels of BNT162b1 on days 1 (all dose levels) and 22 (all dose levels except 60 µg). **a,** Kinetics of C-reactive protein (CRP) level and **b,** Kinetics of lymphocyte counts. Dotted lines indicate upper and lower limit of reference range. For values below the lower limit of quantification (LLOQ = 0.3), LLOQ/2 values were plotted (a).

Figure 46: Correlation of antibody and T-cell responses

Subjects were immunised with the indicated dose levels of BNT162b1 on days 1 (all dose levels) and 22 (all dose levels except 60 µg). **a**, Correlation of RBD-specific IgG responses (from Figure 39a) with $CD4^+$ T-cell responses on day 29 (1 and 50 µg, *n*=8 each; 10 and 30 µg, *n*=10 each). Nonparametric Spearman correlation. **b**, Correlation of $CD4^+$ with $CD8^+$ T-cell responses (as in Figure 41) from day 29 of dose cohorts 10 to 50 µg (1 and 50 µg, *n*=8 each; 10 and 30 µg, *n*=10 each). Parametric Pearson correlation. **c**, Correlation of RBD-specific IgG responses (from Figure 39a) with $CD8^+$ T-cell responses on day 29 (1 and 50 µg, *n*=8 each; 10 and 30 µg, *n*=10 each). Nonparametric Spearman correlation.

Figure 47: Gating strategy for flow cytometry analysis of data shown in Figure 42

Flow cytometry gating strategy for identification of IFNγ, IL-2 and IL-4 secreting T cells in study subject PBMC samples. **a,** $CD4^+$ and $CD8^+$ T cells were gated within single, viable lymphocytes. **b, c,** Gating of IFNγ, IL-2 and IL-4 in $CD4^+$ T cells (b), and IFNγ and IL-2 in $CD8^+$ T cells (c).

Figure 48: BNT162b1 18-55 years of age: Local Reactions After Each Dose

Figure 49: BNT162b1 18-55 years of age: Systemic Events After Each Dose

Figure 50: BNT162b1 65-85 years of age: RBD-Binding IgG GMCs

Figure 51: BNT162b1 65-85 years of age: 50% SARS-CoV-2 Neutralizing GMTs

Figure 52: BNT162b2 18-55 years of age: Local Reactions After Each Dose

Figure 53: BNT162b2 18-55 years of age: Systemic Events After Each Dose

Figure 54: BNT162b2 65-85 years of age: Local Reactions After Each Dose

Figure 55: BNT162b2 65-85 years of age: Systemic Events After Each Dose

Figure 56: BNT162b2 18-55 years of age: S1-Binding IgG GMCs

Figure 57: BNT162b2 18-55 years of age: 50% SARS-CoV-2 Neutralizing GMTs

Figure 58: BNT162b2 65-85 years of age: S1-Binding IgG GMCs

Figure 59: BNT162b2 65-85 years of age: 50% SARS-CoV-2 Neutralizing GMTs

Figure 60: BNT162b2-elicited T cell responses in mice

Splenocytes of BALB/c mice immunized IM with BNT162b2 or buffer were *ex vivo* restimulated with full-length S peptide mix or negative controls (irrelevant peptide in a, right); no peptide in (a, left) and in (c)). P-values were determined by a two-tailed paired t-test. (a) IFNγ ELISpot of splenocytes collected 12 days after immunization of mice (n=8 per group) with 5 µg

BNT162b2 (left). IFNγ ELISpot of isolated splenic CD4+ T cells or CD8+ T cells 28 days after immunization of mice (n=8 mice per group) with 1 µg BNT162b2 (middle and right). (b) CD8+ T-cell specific cytokine release by splenocytes of mice (n=8 per group) immunized with 5 µg BNT162b2 or buffer (control), determined by flow cytometry. S-peptide specific responses are corrected for background (no peptide). (c) Cytokine production by splenocytes obtained 28 days after immunization of mice (n=8 per group, n=7 for IL-4, IL-5, and IL-13, as one outlier was removed via routs test [Q=1%] for the S peptide stimulated samples) with 1 µg BNT162b2, determined by bead-based multiplex analysis.

Figure 61: IFNγ ELISpot data for 5 subjects vaccinated with 10 µg BNT162b2

Background-subtracted spot counts from duplicates prior to vaccination (Pre) and on day 29 (Post - 7 days post boost) per 10^6 cells. T cell response analysis was performed in a GCLP-compliant manner using a validated *ex-vivo* IFNγ ELISpot assay. All tests were performed in duplicate and included negative and positive controls (medium only and anti-CD3). In addition, peptide epitopes derived from cytomegalovirus (CMV), Epstein Barr virus (EBV), and influenza virus were used as positive controls. CD4- or CD8-depleted PBMCs were stimulated for 16-20 h in pre-coated ELISpot plates (Mabtech) with overlapping peptides covering the N-terminal portion and C-terminal portion of the spike glycoprotein. For analysis of *ex vivo* T-cell responses, bound IFNγ was visualized by an alkaline phosphatase-conjugated secondary antibody. Plates were scanned using a Robot ELISPOT Reader and analysed by ImmunoCapture V6.3 or AID ELISPOT 7.0 software. Spot counts were summarized as mean values for each duplicate. T cell counts were calculated as the sum of spot counts detected after stimulation with S pool 1 and S pool 2. T-cell responses stimulated by peptides were compared to effectors incubated with medium only as negative control using an ELISpot data analysis Tool (EDA), based on two statistical tests (distribution free resampling) according to Moodie et al. (Moodie Z. et al., J Immunol Methods 315, 2006,121-32; Moodie Z. et al., Cancer Immunol Immunother

59, 2010, 1489-501) thus providing sensitivity while maintaining control over false positive rate. No significant changes were observed between the pre- and day 29 T cell responses against the positive control peptides from CMV, EBV, and influenza virus (not shown).

Figure 62: Example of CD4+ and CD8+ IFNγ ELISpot data

IFNγ ELISpot was performed as in Fig. 61 using PBMCs obtained from a subject prior to immunization and on day 29 after dose 1 of 10 µg BNT162b2 (7 days post dose 2). HLA class I and class II peptide pools CEF (cytomegalovirus [CMV], Epstein Barr virus [EBV] (7 days post dose 2), and influenza virus, HLA class I epitope mix) and CEFT (CMV, EBV, influenza virus, and tetanus toxoid HLA class II cell epitope mix) were used as benchmarking controls to assess CD8+ and CD4+ T cell reactivity.

Figure 63: Comparison of BNT162b2-elicited and benchmark INFγ ELISpot responses

IFNγ spot counts from day 29 (7 day post dose 2) PBMC samples obtained from 5 subjects who were immunized with 10 µg of BNT162b2 on days 1 and 22. CEF (CMV, EBV, and influenza virus HLA class I epitope mix), and CEFT (CMV, EBV, influenza virus, and tetanus toxoid HLA class II cell epitope mix) were used as benchmarking controls to assess CD8+ and CD4+ T cell reactivity. Horizontal lines indicate median values.

Figure 64: Design and characterisation of the immunogen

a, Structure of BNT162b1. Linear diagram of RNA (left), and cartoon of LNP (right). UTR, untranslated region; SP, signal peptide. **b**, Representative 2D class averages from electron microscopy of negatively stained RBD-foldon trimers. Box edge: 37 nm. **c**, Density map of the ACE2/B^0AT1/RBD-foldon trimer complex at 3.24 Å after focused refinement of the ACE2 extracellular domain bound to an RBD monomer. Surface color-coding by subunit. A ribbon

model refined to the density shows the RBD-ACE2 binding interface, with residues potentially mediating polar interactions labeled.

Figure 65: Mouse immunogenicity

a-c, BALB/c mice (n=8 per group) were immunised intramuscularly (IM) with 0.2, 1 or 5 µg of BNT162b1 or buffer. Geometric mean of each group ± 95% CI, P-values compare day 28 to non-immunised (0 µg; n=8) baseline sera (multiple comparison of mixed-effect analysis using Dunnett's multiple comparisons test) (a, c). **a**, RBD-binding IgG responses in sera obtained 7, 14, 21 and 28 days after immunisation, determined by ELISA. For day 0, a pre-screening of randomised animals was performed (n=4). **b**, Representative surface plasmon resonance sensorgram of the binding kinetics of His-tagged RBD to immobilised mouse IgG from serum 28 days after immunisation with 5 µg BNT162b1 (n=8). Actual binding (green) and the best fit of the data to a 1:1 binding model (black). **c**, VSV-SARS-CoV-2 pseudovirus 50% serum neutralising titers ($pVNT_{50}$). **d-f**, Splenocytes of BALB/c mice immunised IM with BNT162b1 or buffer (control) were *ex vivo* re-stimulated with full-length S peptide mix or negative controls (no peptide in (d, left) and in (e, f); irrelevant peptide in (d, right)). P-values were determined by a two-tailed paired t-test. **d**, IFNγ ELISpot of splenocytes collected 12 days after immunisation of mice (n=8 per group) with 5 µg BNT162b1 (left). IFNγ ELISpot of isolated splenic $CD4^+$ T cells (n=7, one outlier removed by Grubbs test, α=0.05) or $CD8^+$ T cells (n=8) 28 days after immunisation with 1 µg BNT162b1 (middle and right). **e**, T-cell specific cytokine release by splenocytes of mice (n=8 per group) immunised with 5 µg BNT162b1, determined by flow cytometry. S-peptide specific responses are corrected for background (no peptide). **f**, Cytokine production by splenocytes obtained 28 days after immunisation of mice (n=8 per group) with 0.2 µg BNT162b1, determined by bead-based multiplex analysis.

Figure 66: Immunogenicity of BNT162b1 in rhesus macaques and comparison to human convalescent sera

a, b, Male rhesus macaques 2-4 years of age (n=6 per group) were immunised IM on Days 0 and 21 with 30 µg or 100 µg of BNT162b1 or with buffer, and serum was obtained before and 14, 21, 28, 35 and 42 days after immunisation. Human convalescent sera (HCS) were obtained from SARS-CoV-2-infected patients at least 14 days after PCR-confirmed diagnosis and at a time when acute COVID-19 symptoms had resolved (n=38). Values above bars give the geometric means. **a**, Geometric mean concentrations (GMCs) of IgG binding a recombinant SARS-CoV-2 RBD. Dashed line indicates geometric mean of sera from all time points for the placebo group (1.72 U/mL). Group IgG titers for every time point were analysed for statistical significance against HCS samples using one-way ANOVA with Dunnett's multiple comparison correction, and statistical significance was confirmed in the 30 µg dose-level group (Day 28, $p<0.0001$; Day 35, $p=0.0016$), and in the 100 µg dose-level group (Day 28, 35 and 42, all $p<0.0001$). **b**, SARS-CoV-2 50% neutralisation titers (VNT_{50}). Dashed line indicates geometric mean of sera from all time points for the placebo group (10.31 U/mL). Group VNT_{50} for every time point were analysed for statistical significance against HCS samples using one-way ANOVA with Dunnett's multiple comparison correction, and statistical significance was confirmed in the 30 µg dose-level group (Day 28, $p<0.0001$), and in the 100 µg dose-level group (Day 28 and 35, both $p<0.0001$; Day 42, $p=0.007$).

Figure 67: Viral RNA in non-immunised and immunised rhesus macaques after SARS-CoV-2 challenge

Rhesus macaques (n=6 per group) were immunised on Days 0 and 21 with 100 µg BNT162b1 or buffer (Control) as described in Figure 66. Forty-one to 48 days after the second immunisation, the animals were challenged with 1×10^6 total pfu of SARS-CoV-2 split equally between the IN and IT routes. Three non-immunised age-matched male rhesus macaques

were challenged with cell culture medium (Sentinel). Viral RNA levels were detected by RT-qPCR. Ratios above data points are the number of viral RNA positive animals within all animals per group. **a**, Viral RNA in bronchoalveolar lavage (BAL) fluid obtained before, and on Days 3 and 6 after challenge. At day 6, the viral load between the control and BNT162b1-immunized animals was statistically significant (p=0.0131). **b**, Viral RNA in nasal swabs obtained before challenge and on day 1, 3, and 6 after challenge. At day 3, the viral load between the control and BNT162b1-immunized animals was statistically significant (p=0.0229). Dotted lines indicate the lower limits of detection (LLOD). Negative specimens were set to ½ the LLOD. P-values were determined by categorical analysis for binomial response (undetectable viral load after challenge as success, measurable viral load after challenge as failure).

Figure 68: BNT162b1 and b2 V8 immunization reduces viral RNA in rhesus macaques after challenge with SARS-CoV-2; b2 shows earlier clearance in nose

Figure 69: Exemplary pandemic supply product packaging overview

Figure 70: Exemplary vaccine storage & handling at the point of vaccination

Figure 71: Exemplary multi-dose preparation

Figure 72. Geometric Mean Titers and 95% CI: SARS-CoV-2 Neutralization Assay - NT50 – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b1 – Evaluable Immunogenicity Population

Figure 73. Geometric Mean Titers and 95% CI: SARS-CoV-2 Neutralization Assay - NT50 – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b1 – Evaluable Immunogenicity Population

Figure 74. Geometric Mean Titers and 95% CI: SARS-CoV-2 Neutralization Assay - NT50 – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 75. Geometric Mean Titers and 95% CI: SARS-CoV-2 Neutralization Assay - NT50 – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 76. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 RBD-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b1 – Evaluable Immunogenicity Population

Figure 77. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 RBD-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age, BNT162b1 – Evaluable Immunogenicity Population

Figure 78. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 S1-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b1 – Evaluable Immunogenicity Population

Figure 79. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 S1-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b1 – Evaluable Immunogenicity Population

Figure 80. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 S1-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 81. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 S1-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 82. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 RBD-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 83. Geometric Mean Concentrations and 95% CI: SARS-CoV-2 RBD-binding IgG Level Assay – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b2 – Evaluable Immunogenicity Population

Figure 84. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b1 – Safety Population

Figure 85. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b1 – Safety Population

Figure 86. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b2 – Safety Population

Figure 87. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b2 – Safety Population

Figure 88. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b1 – Safety Population

Figure 89. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b1 – Safety Population

Figure 90. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 18-55 Years of Age – BNT162b2 – Safety Population

Figure 91. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose – Phase 1, 2 Doses, 21 Days Apart – 65-85 Years of Age – BNT162b2 – Safety Population

Figure 92. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose, Age Group 18 55 Years – Phase 2 – Safety Population

Figure 93. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose, Age Group 56 85 Years – Phase 2 – Safety Population

Figure 94. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose, Age Group 18 55 Years – Phase 2 – Safety Population

Figure 95. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose, Age Group 56 85 Years – Phase 2 – Safety Population

Figure 96. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose, Age Group 18 55 Years – ~6000 Subjects for Phase 2/3 – Safety Population

Figure 97. Subjects Reporting Local Reactions, by Maximum Severity, Within 7 Days After Each Dose, Age Group 56 85 Years – ~6000 Subjects for Phase 2/3 – Safety Population

Figure 98. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose, Age Group 18-55 Years – ~6000 Subjects for Phase 2/3 – Safety Population

Figure 99. Subjects Reporting Systemic Events, by Maximum Severity, Within 7 Days After Each Dose, Age Group 56-85 Years – ~6000 Subjects for Phase 2/3 – Safety Population

Figure 100. Cumulative Incidence Curves for the First COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population

Figure 101. BNT162b2- Exemplary functional 50% SARS-CoV-2 neutralising antibody titers (VN_{50}). Younger adults (aged 18 to 55 years) and older adults (aged 56 to 85 years) were immunized with BNT162b2 on day 1 and day 22 (n=12 per group). Sera were obtained from younger adults on day 1 (baseline) and on day 8, 22 (pre boost), 29, 43, 50 and 85. Sera were obtained from older adults on day 1 (baseline) and on day 8, 22, and 29. Human COVID-19 convalescent sera (HSC, n=38) were obtained at least 14 days after a confirmed diagnosis and at a time when the donors were no longer symptomatic. SARS-CoV-2 50% neutralization titers (VN_{50} titers) with 95% confidence intervals are shown for younger adults immunized with 1, 3, 10, 20, or 30 µg BNT162b2, and older adults immunized with 20 µg BNT162b2. Values smaller than the limit of detection (LOD) are plotted as 0.5*LOD. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). The dotted horizontal line represents the LOD. VN_{50} = 50% SARS-CoV-2 neutralizing antibody titers; HCS = human COVID-19 convalescent serum.

Figure 102. BNT162b1- Exemplary fold increase from baseline in functional 50% SARS-CoV-2 neutralizing antibody titers (VN_{50}).

The vaccination schedule and serum sampling are the same as in Figure 39 (n=12 per group). Geometric means fold increase (GMFI) from baseline in VN_{50} titer with 95% confidence intervals are shown for younger participants (aged 18 to 55 yrs) immunized with 1, 10, 30, 50, or 60 µg BNT162b1. Arrowheads indicate baseline (pre-dose 1, Day 1) and dose 2

(Day 22). Dose 2 was not performed in the 60 µg dose group. The dotted horizontal line represents the threshold for seroconversion (fold increase ≥4). VN_{50} = 50% SARS-CoV-2 neutralizing antibody titers.

Figure 103. BNT162b2 – Exemplary fold increase from baseline in functional 50% SARS-CoV-2 neutralizing antibody titers (VN_{50}).

The vaccination schedule and serum sampling are the same as in Figure 101. Geometric means fold increase (GMFI) from baseline in VN_{50} titer with 95% confidence intervals are shown for (**A**) younger participants (aged 18 to 55 yrs) immunized with 1, 3, 10, 20, or 30 µg BNT162b2, and (**B**) older participants (aged 56 to 85 yrs) immunized with 20 µg BNT162b2. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). The dotted horizontal line represents the threshold for seroconversion (fold increase ≥4). VN_{50} = 50% SARS-CoV-2 neutralizing antibody titers.

Figure 104. Exemplary frequencies of participants with SARS-CoV-2 GMT seroconversion after immuniziation with BNT162b1.

The vaccination schedule and serum sampling are the same as in Figure 39 (n=12 per group). Seroconversion with regard to 50% SARS-CoV-2 neutralizing antibody titers (VN_{50}) is shown for younger participants (aged 18 to 55 yrs) immunized with 1, 10, 30, 50, or 60 µg BNT162b1. Seroconversion is defined as a minimum of a 4-fold increase of functional antibody response as compared to baseline. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). Dose 2 was not performed in the 60 µg dose group. GMT = geometric mean titer.

Figure 105. Exemplary frequencies of participants with SARS-CoV-2 GMT seroconversion after immuniziation with BNT162b2.

The vaccination schedule and serum sampling are the same as in Figure 101. Seroconversion with regard to 50% SARS-CoV-2 neutralizing antibody titers (VN_{50}) is shown for (**A**) younger participants (aged 18 to 55 yrs) dosed with 1, 3, 10, 20, or 30 µg BNT162b2, and (**B**) older participants (aged 56 to 85 yrs) dosed with 20 µg BNT162b2. Seroconversion is defined as a minimum of 4-fold increase of functional antibody response as compared to baseline. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). GMT = geometric mean titer.

Figure 106. Exemplary fold increase from baseline in S1-binding antibody concentrations after immunization with BNT162b1.

The vaccination schedule and serum sampling are the same as in Figure 39 (n=12 per group). Geometric means fold increase (GMFI) from baseline in S1-binding antibody concentrations with 95% confidence intervals are shown for younger participants (aged 18 to 55 yrs) immunized with 1, 10, 30, 50, or 60 µg BNT162b1. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). Dose 2 was not performed in the 60 µg dose group. The dotted horizontal line represents the threshold for seroconversion (fold increase ≥4).

Figure 107. Exemplary fold increase from baseline in S1-binding antibody concentration after immunization with BNT162b2.

The vaccination schedule and serum sampling are the same as in Figure 101. Geometric means fold increase (GMFI) from baseline in S1-binding antibody concentrations with 95% confidence intervals are shown for (**A**) younger participants (aged 18 to 55 yrs) immunized with 1, 3, 10, 20, or 30 µg BNT162b2, and (**B**) older participants (aged 56 to 85 yrs) immunized with 20 µg BNT162b2. Arrowheads indicate baseline (pre-Dose 1, Day 1) and

Dose 2 (Day 22). The dotted horizontal line represents the threshold for seroconversion (fold increase ≥4).

Figure 108. Exemplary frequencies of participants with S1-binding IgG GMC seroconversion after immunization with BNT162b1.

The vaccination schedule and serum sampling are the same as in Figure 39 (n=12 per group). Seroconversion with regard to S1-binding antibody GMC is shown for younger participants (aged 18 to 55 yrs) immunized with 1, 10, 30, 50, or 60 µg BNT162b1. Seroconversion is defined as at least a 4-fold increase of S1-binding IgG GMC response as compared to baseline. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). Dose 2 was not performed in the 60 µg dose group. GMC = geometric mean concentration.

Figure 109. Exemplary frequencies of participants with S1-binding IgG GMC seroconversion after immunization with BNT162b2.

The vaccination schedule and serum sampling are the same as in Figure 101. Seroconversion with regard to S1-binding antibody GMC is shown for (**A**) younger participants (aged 18 to 55 yrs) immunized with 1, 3, 10, 20, or 30 µg BNT162b2, and (**B**) older participants (aged 56 to 85 yrs) dosed with 20 µg BNT162b2. Seroconversion is defined as at least a 4-fold increase of S1-binding IgG GMC response as compared to baseline. Arrowheads indicate baseline (pre-Dose 1, Day 1) and Dose 2 (Day 22). GMC = geometric mean concentration

Figure 110. Exemplary results of cytokine production produced from S-specific $CD4^+$ T cells from younger participants immunized with BNT162b2.

Peripheral blood mononuclear cell (PBMC) cell fractions isolated from blood of participants treated with varying doses of BNT162b2 were collected at baseline (pre-Dose one) and 29 days (±3 days) after Dose one and analyzed. Participants included younger participants (age

18-55 years) dosed at 1 µg (n =8), 3 µg (n=9), 10 µg (n=10), 20 µg (n=9), or 30 µg (n=10). Bar charts show arithmetic means with 95% confidence interval. Cytokine production was calculated by summing up the fractions of all $CD4^+$ T cells positive for either IFNγ, IL-2, or IL-4, setting this sum to 100% and calculating the fraction of each specific cytokine-producing subset thereof. Two participants from the 1 µg cohort, 1 participant from the 3 µg cohort, and 1 participant from the 10 µg cohort were excluded from this analysis (frequency of total cytokine-producing $CD4^+$ T cells <0.03%). IFN = interferon; IL = interleukin; younger participants = participants aged 18 to 55 yrs; S protein = SARS-CoV-2 spike protein.

Figure 111. Exemplary results of cytokine production produced from S-specific $CD4^+$ T cells from older participants immunized with BNT162b2.

Peripheral blood mononuclear cell (PBMC) cell fractions isolated from blood of participants treated with varying doses of BNT162b2 were collected at baseline (pre-Dose one) and 29 days (±3 days) after Dose one and analyzed. Participants included older participants (age 56-85 years) dosed at 10 µg (n=11), 20 µg (n=8), or 30 µg (n=9). Bar charts show arithmetic means with 95% CI. Cytokine production was calculated by summing up the fractions of all $CD4^+$ T cells positive for either IFNγ, IL-2, or IL-4, setting this sum to 100%, and calculating the fraction of each specific cytokine-producing subset thereof. Six participants from the 10 µg cohort and 1 participant from the 20 µg cohort were excluded from this analysis (frequency of total cytokine-producing $CD4^+$ T cells <0.03%). IFN = interferon; IL = interleukin; older participants = participants aged 56 to 85 yrs; S protein = SARS-CoV-2 spike protein.

Figure 112. Incidence and magnitude of BNT162b2-induced T-cell responses.

PBMCs obtained on day 1 (pre-prime) and day 29 (7 days post-boost) (dose cohorts 1, 10 and 20 µg, *n*=9 each; 30 µg, *n*=10) were enriched for $CD4^+$ or $CD8^+$ T cell effectors and separately stimulated over night with three overlapping peptide pools representing different portions of

the wild-type sequence of SARS-CoV-2 S (N-terminal pools S pool 1 and RBD, and the C-terminal S pool 2), for assessment in direct ex vivo IFNγ ELISpot. Common pathogen T-cell epitope pools CEF (immune dominant HLA class I epitopes of CMV, EBV, influenza virus) and CEFT (immune dominant HLA class II epitopes CMV, EBV, influenza virus, tetanus toxoid) were used as controls. Cell culture medium served as negative control. Each dot represents the normalised mean spot count from duplicate wells for one study participant, after subtraction of the medium-only control (**a, c**). **a,** Antigen-specific $CD4^+$ and $CD8^+$ T-cell responses for each dose cohort. The number of participants with a detectable T-cell response on day 29 over the total number of tested participants per dose cohort is provided. Spot count data from two participants from the 20 μg dose cohort could not be normalised and are not plotted. **b,** Example of $CD4^+$ and $CD8^+$ ELISpot for a 30 μg dose cohort participant. **c**, S-specific T-cell responses in all participants who recognised either S peptide pool and their baseline CEFT- and CEF-specific T-cell responses. Horizontal bars indicate median values.

Figure 113. BNT162b2-induced S-specific $CD8^+$ and $CD4^+$ T cells.

$CD4^+$ or $CD8^+$ T cell effector-enriched fractions of immunised participants derived from PBMCs obtained on day 1 (pre-prime) and day 29 (7 days post-boost) (1, 10 and 20 μg dose cohorts, *n*=9 each; 30 μg dose cohort, *n*=10) were stimulated overnight with two overlapping peptide pools covering the wild-type SARS-CoV-2 S (S pool 1 and S pool 2) for assessment in direct ex vivo IFNγ ELISpot (**a-c**). Each dot represents the normalised mean spot count from duplicate wells for one study participant, after subtraction of the medium-only control. T-cell responses against S pool 1 and S pool 2 per participant were combined. Spot count data from two participants from the 20 μg dose cohort could not be normalised and are not plotted. PBMCs from vaccinated participants on day 29 (7 days post-boost) (dose cohorts 1 μg, *n*=7; 10 and 30 μg, *n*=10; 20 μg, *n*=9) were stimulated as described above and analysed by flow cytometry (**d,e**). **a,** S-specific $CD4^+$ and $CD8^+$ T-cell responses for each dose cohort. Number of

participants with detectable T-cell response on day 29 over the total number of tested participants per dose cohort is provided. **b,** Mapping of vaccine-induced responses of participants with evaluable baseline data (*n*=34 for $CD4^+$ and *n*=37 for $CD8^+$ T cell responses) to different portions of S. De novo induced or amplified responses are classified as BNT162b2-induced response; no responses or pre-existing responses that were not amplified by the vaccinations are classified as no vaccine response (none). **c,** Response strength to S pool 1 in individuals with or without a pre-existing response to S pool 2. Data from the 1 µg dose cohort are excluded, as no baseline response to S pool 2 was present in this dose cohort. Horizontal bars represent median of each group. **d,** Examples of pseudocolor flow cytometry plots of cytokine-producing $CD4^+$ and $CD8^+$ T cells from a participant prime/boost vaccinated with 30 µg BNT162b2. **e**, Frequency of vaccine-induced, S-specific $IFN\gamma^+$ $CD4^+$ T cells vs. $IL4^+$ $CD4^+$ T cells. ICS stimulation was performed using a peptide mixture of S pool 1 and S pool 2. Each data point represents one study participant (1 µg dose cohort, n=8; 20 µg dose cohort, n=8; 10 and 30 µg, n=10 each). One participant from the 20 µg dose cohort with a strong pre-existing $CD4^+$ T cell response to S pool 2 was excluded. **f,** Antigen-specific $CD8^+$ T cell frequencies determined by pMHC class I multimer staining (% $multimer^+$ of $CD8^+$), ICS and ELISpot (% $IFN\gamma^+$ of $CD8^+$) for the three participants analysed in **Figure 116**. Signals for S pool 1 and S pool 2 were merged.

Figure 114. Correlation of antibody and T-cell responses.

Data are plotted for all prime/boost vaccinated participants (dose cohorts 1, 10, 20 and 30 µg) from day 29, with data points for participants with no detectable T cell response (open circles; **b,c**) excluded from correlation analysis. **a**, Correlation of S1-specific IgG responses with S-

specific $CD4^+$ T-cell responses. **b**, Correlation of S-specific $CD4^+$ with $CD8^+$ T-cell responses. **c**, Correlation of S1-specific IgG responses with S-specific $CD8^+$ T-cell responses.

Figure 115. Cytokine polarisation of BNT162b2-induced T cells.

PBMCs obtained on day 1 (pre-prime) and day 29 (7 days post-boost) (dose cohorts 1 µg, *n*=8; 10 and 30 µg, *n*=10 each; 20 µg, *n*=9) and COVID-19 recovered donors (HCS, *n*=18; **c,d**) were stimulated over night with three overlapping peptide pools representing different portions of the wild-type sequence of SARS-CoV-2 S (N-terminal pools S pool 1 [aa 1-643] and RBD [aa1-16 fused to aa 327-528 of S], and the C-terminal S pool 2 [aa 633-1273]), and analysed by flow cytometry. **a**, Example of pseudocolor flow cytometry plots of cytokine-producing $CD4^+$ and $CD8^+$ T cells from a 30 µg dose cohort participant in response to S pool 1. **b**, S-specific $CD4^+$ T cells producing the indicated cytokine as a fraction of total cytokine-producing S-specific $CD4^+$ T cells in response to S pool 1 and S pool 2. CD4 non-responders (<0.03% total cytokine producing T cells: 1 µg, *n*=2 [S pool 1] and *n*=1 [S pool 2]; 10 µg, *n*=1) were excluded. Arithmetic mean with 95% confidence interval. **c,** S-specific $CD4^+$ (S pool 1, S pool 2 and RBD) and **d**, $CD8^+$ T cells (S pool 1, S pool 2 and RBD) producing the indicated cytokine as a fraction of total circulating T cells of the same subset. Values above data points indicate mean fractions per dose cohort. Participant PBMCs were tested as single instance (**b-d**).

Figure 116. Characterization of BNT162b2-induced T cells on the single epitope level.

PBMCs obtained on day 1 (pre-prime) and day 29 (7 days post-boost) of three vaccinated participants (dose cohorts 10 µg, *n*=1; 30 µg, *n*=2) were stained with individual pMHC class I multimer cocktails and analysed for T cell epitope specificity **(a)** and phenotype (**b**; example from participant 3; YLQPRTFLL) by flow cytometry. Peptide sequences above dot plots indicate pMHC class I multimer epitope specificity, numbers above dot plots indicate the amino acids

corresponding to the epitope within S. **c**, Localization of identified MHC class I-restricted epitopes within S.

Figure 117. ELISA screening analysis of exemplary cohort sera to detect antibody responses directed against the recombinant SARS-CoV-2 spike protein S1 domain.

ELISA was performed using serum samples collected on day 10 after two immunisations (prime/boost on days 1 and 8) with BNT162c1, or on day 17 after three administrations (prime/boost on days 1/8/15) of BNT162a1, BNT162b1, or BNT162b2 to analyse elicited antibody responses. The serum samples were tested against the S1 protein. Group mean ΔOD values of n=20 mice/group are shown by dots across serum dilutions ranging from 1:100 to 1:24,300.

Figure 118. ELISA screening analysis of exemplary cohort sera to detect antibody responses directed against the recombinant SARS-CoV-2 spike protein RBD domain.

ELISA was performed using serum samples collected on day 10 after two immunisations (prime/boost on days 1 and 8) with BNT162c1, or on day 17 after three administrations (prime/boost on days 1/8/15) of BNT162a1, BNT162b1, or BNT162b2 to analyse elicited antibody responses. The serum samples were tested against the RBD domain. Group mean ΔOD values of n=20 mice/group are shown by dots across serum dilutions ranging from 1:100 to 1:24,300.

Figure 119. Pseudovirus neturalisation activity of exemplary cohort sera plotted as pVN_{50} titre.

Serum samples were collected on day 10 (BNT162c1, saRNA) or day 17 (all other cohorts) after first immunisation of the animals and titres of virus-neutralising antibodies were determined by pseudovirus-based neutralisation test (pVNT). Individual VNT titres resulting in 50%

pseudovirus neutralisation (pVN_{50}) are shown by dots; group mean values are indicated by horizontal bars (±SEM, standard error of the mean).

Figure 120. The virus-neutralising antibodies and specific binding antibody responses to RBD and S1 in participants.

RBD=receptor binding domain. GMT=geometric mean titer. Serum samples were obtained before vaccination (day 1) and day 8, 22, 29, and 43 after the prime vaccination in younger adult group, and they were obtained before vaccination (day 1) and day 22, 29, and 43 days after the prime vaccination in older adult group. A panel of human COVID-19 convalescent serum (n=24) were obtained at least 14 days after PCR-confirmed diagnosis in COVID-19 patients. (A) GMTs of SARS-CoV-2 neutralizing antibodies. (B) GMTs of binding antibodies to RBD measured by ELISA. (C) GMTs of ELISA antibodies to S1. Each point represents a serum sample, and each vertical bar represents a geometric mean with 95% CI.

Figure 121. T-cell response in participants before and after vaccination measured by IFN-γ ELISpot.

IFN=interferon. PBMC=peripheral blood mononuclear cells. The S1 peptide pool covers the N-terminal half of SARS-CoV-2 spike, including RBD. S2 peptide pool covers the C-terminal of SARS-CoV-2 spike, not including RBD. CEF peptide pool consists of 32 MHC class I restricted viral peptides from human cytomegalovirus, Epstein-Barr virus and influenza virus. Panel A shows the number of specific T cell with secretion of IFN-γ at day 1, 29, and 43 in the younger participants aged 18-55 years. Panel B shows the number of specific T cell with secretion of IFN-γ at day 1, 29, and 43 in the older participants aged 65-85 years.

Figure 122. 50% pseudovirus neutralization titers of 16 sera from BNT162b2 vaccine recipients against VSV-SARS-CoV-2-S pseudovirus bearing the Wuhan or lineage B.1.1.7 spike protein. *N*=8 representative sera each from younger adults (aged 18 to 55 yrs; indicated

by triangles) and older adults (aged 56 to 85 yrs; indicated by circles) drawn at day 43 (21 days after dose 2) were tested.

Figure 123. Schematic illustration of the production of VSV pseudoviruses bearing SARS-CoV-2 S protein. (1) Transfection of SARS-CoV-2-S expression plasmid into HEK293/T17 cells. (2) Infection of SARS-CoV-2 S expressing cells with VSV-G complemented input virus lacking the VSV-G in its genome (VSVΔG) and encoding for reporter genes. (3) Neutralization of residual VSV-G complemented input virus by addition of anti-VSV-G antibody yields SARS-CoV-2 S pseudotyped VSVΔG as a surrogate for live SARS-CoV-2.

Figure 124. Titration of SARS-CoV-2 Wuhan reference strain and lineage B.1.1.7 spike-pseudotyped VSV on Vero 76 cells using GFP-infected cells as read-out.

Figure 125. Scheme of the BNT162b2 vaccination and serum sampling.

Figure 126. Plot of the ratio of $pVNT_{50}$ between SARS-CoV-2 lineage B.1.1.7 and Wuhan reference strain spike-pseudotyped VSV. Triangles represent sera from younger adults (aged 18 to 55 yrs), and circles represent sera from older adults (aged 56 to 85 yrs). The sea were drawn on day 43 (21 days after dose 2).

Fig. 127. 50% pseudovirus neutralization titers (pVNT50) of 12 sera from BNT162b2 vaccine recipients against VSV-SARS-CoV-2-S pseudovirus bearing the Wuhan Hu-1 reference, lineage B.1.1.298 or lineage B.1.351 spike protein. N=12 sera from younger adults immunized with 30 µg BNT162b2 drawn at either day 29 or day 43 (7 or 21 days after dose 2) were tested. Geometric mean titers are indicated. Statistical significance of the difference between the neutralization of the Wuhan Hu-1 reference pseudovirus and either the lineage B.1.1.298 or

the lineage B.1.351 pseudovirus was calculated by a Wilcoxon matched-pairs signed rank test. Two-tailed p-values are reported. ns, not significant;***, $P<0.001$; LLOQ, lower limit of quantification.

Figure 128. 50% plaque reduction neutralization titers of 20 sera from BNT162b2 vaccine recipients against N501 and Y501 SARS-CoV-2. Seven sera (indicated by triangles) were drawn 2 weeks after the second dose of vaccine; 13 sera (indicated by circles) were drawn 4 weeks after the second dose.

Figure 129. Diagram of the N501Y substitution. L – leader sequence; ORF – open reading frame; RBD – receptor binding domain; S – spike glycoprotein; S1 – N-terminal furin cleavage fragment of S; S2 – C-terminal furin cleavage fragment of S; E – envelope protein; M – membrane protein; N – nucleoprotein; UTR – untranslated region.

Figure 130. Plaque morphologies of N501 and Y501 SARS-CoV-2 on Vero E6 cells.

Figure 131. Scheme of the BNT162 vaccination and serum sampling.

Figure 132. Plot of the ratio of $PRNT_{50}$ between Y501 and N501 viruses. Triangles represent sera drawn two weeks after the second dose; circles represent sera drawn four weeks after the second dose.

Figure 133. Engineered mutations. Nucleotide and amino acid positions are indicated. Deletions are depicted by dotted lines. Mutant nucleotides are in red. L, leader sequence; ORF, open reading frame; RBD, receptor binding domain; S, spike glycoprotein; S1, N-terminal furin

cleavage fragment of S; S2, C-terminal furin cleavage fragment of S; E, envelope protein; M, membrane protein; N, nucleoprotein; UTR, untranslated region.

Figure 134. Plaque morphologies of WT (USA-WA1/2020), mutant N501Y, Δ69/70+N501Y+D614G, and E484K+N501Y+D614G SARS-CoV-2s on Vero E6 cells.

Figure 135. Scheme of the BNT162 vaccination and serum sampling.

Figure 136. $PRNT_{50}$s of twenty BNT162b2-vaccinated human sera against wild-type (WT) and mutant SARS-CoV-2. (a) WT (USA-WA1/2020) and mutant N501Y. **(b)** WT and Δ69/70+N501Y+D614G. **(c)** WT and E484K+N501Y+D614G. Seven (triangles) and thirteen (circles) sera were drawn 2 and 4 weeks after the second dose of vaccination, respectively. Sera with different $PRNT_{50}$s against WT and mutant viruses are connected by lines. Results in (**a**) were from one experiment; results in (**b**) and (**c**) were from another set of experiments. Each data point is the average of duplicate assay results.

Figure 137. Ratios of neutralization GMTs against mutant viruses to GMTs against WT virus. Triangles represent sera drawn two weeks after the second dose of vaccination; circles represent sera drawn four weeks after the second dose of vaccination.

Figure 138. Diagram of engineered spike substitutions and deletions. The genome and sequence of clinical isolate USA-WA1/2020 are used as the wild-type virus in this study. Mutations from the United Kingdom B.1.1.7, Brazilian P.1, and South African B.1.351 lineages are presented. Deletions are indicated by dotted lines. Mutated nucleotides are in red. Nucleotide and amino acid positions are indicated. L – leader sequence; ORF – open reading frame; RBD – receptor binding domain; S – spike glycoprotein; S1 – N-terminal furin cleavage

fragment of S; S2 – C-terminal furin cleavage fragment of S; E – envelope protein; M – membrane protein; N – nucleoprotein; UTR – untranslated region.

Figure 139. Plaque morphologies of USA-WA1/2020 and mutant SARS-CoV-2's. The plaque assays were performed on Vero E6 cells in 6-well plates.

Figure 140. Scheme of BNT162 immunization and serum collection.

Figure 141. Serum Neutralization of Variant Strains of SARS-CoV-2 after the Second Dose of BNT162b2 Vaccine. Shown are the results of 50% plaque reduction neutralization testing ($PRNT_{50}$) with the use of 20 samples obtained from 15 trial participants 2 weeks (circles) or 4 weeks (triangles) after the administration of the second dose of the BNT162b2 vaccine. The mutant viruses were obtained by engineering the full set of mutations in the B.1.1.7, P.1., or B.1.351 lineages or subsets of the S gene mutations in the B.1.351 lineage (B.1.351-Δ242-244+D614G and B.1.351-RBD-D614G) into USA-WA1/2020. Each data point represents the geometric mean $PRNT_{50}$ obtained with a serum sample against the indicated virus, including data from repeat experiments, as detailed in Table 31. The data for USA-WA1/2020 are from three experiments; for B.1.1.7-spike, B.1.351-Δ242-244+D614G, and B.1.351-RBD-D614G viruses from one experiment each; and for P.1-spike and B.1.351-spike viruses from two experiments each. In each experiment, the neutralization titer was determined in duplicate assays, and the geometric mean was taken. LOD: limit of detection.

Figure 142. Durability of BNT162b2-induced T cell responses.

PBMCs obtained on Day 1 (pre-prime), Day 29, Day 85, and Day 184 (7 days, 9 and 23 weeks post-boost, respectively), were analyzed in *ex vivo* IFNγ ELISpot (for details see GA-RB-022-01A). Common pathogen T-cell epitope pools CEF (CMV, EBV, and influenza virus HLA class I

epitopes) and CEFT (CMV, EBV, influenza virus, and tetanus toxoid HLA class II epitopes) served to assess general T-cell reactivity, cell culture medium served as negative control. Each dot represents the sum of normalized mean spot count from duplicate wells stimulated with two peptide pools corresponding to the full-length wt S protein for one study subject, after subtraction of the medium-only control. Ratios above post-vaccination data points are the number of subjects with detectable $CD4^+$ or $CD8^+$ T-cell responses within the total number of tested subjects per dose cohort and time-point.

Figure 143. A specific vaccine mRNA signal (red) is detected in the LN 6h post injection using modV9 probe in dual IHC-ISH assay. Vaccine is mostly localized to subcapsular sinus (LN in 9 and 5 positions) and B cell follicles (LN in 12 and 1 positions). Dendritic cells are visualized by CD11c staining (turquoise, upper images) and only some of them uptake the vaccine. Majority of CD169+ macrophages (subcapsular sinus macrophages, turquoise, middle images) are positive for the vaccine. B cells (CD19+, turquoise, lower images) are the second major population showing vaccine signal.

Figure 144. A specific vaccine mRNA signal (red) is detected in the spleen 6h post injection using modV9 probe in dual IHC-ISH assay. Majority of the vaccine signal is detected in the white pulp. Dendritic cells are visualized by CD11c staining (turquoise, upper images) and only some of them uptake the vaccine. A small portion of F4/80+ macrophages (turquoise, middle images) uptake the vaccine. B cells (CD19+, turquoise, lower images) are the major population showing the vaccine signal.

Figure 145. Exemplary Stability Data. Exemplary data from certain stability studies (see, for example, Example 42, are shown for a BNT162b2 LNP preparation at indicated concentrations and temperature conditions, as assessed by ELISA characterizing antibodies reactive to S1

spike protein.

Figure 146 provides an exemplary pandemic supply product packaging overview.

Figure 147 provides an exemplary vaccine storage & handling at the point of vaccination overview.

Figure 148 provides a diagram of example vial trays according to FEFCO 0201 and FEFCO 0204.

Figure 149 provides a diagram of an example vial tray according to FEFCO 0426.

Figure 150 provides a diagram of an example vial tray (Tray 7 according to Table 33 in Example 45).

Figure 151 provides a picture of one type of thermal shipper that can be used, with the following descriptions: A) Dry ice pod – holds the top layer of dry ice; B) Vial trays – the vial trays look like small pizza boxes. Each vial try contains multiple dose vials. Each thermal shipping container can have up to 5 vial trays inside. C) Box that holds the vial trays – box within the thermal shipping container that includes the vial trays. This box has handles and can be fully removed from the thermal shipping container. D) Foam lid – top foam lid that includes an embedded temperature-monitor device and remains connected to the box; E) Thermal shipping container – outer box of the thermal shipping container.

Figure 152 provides a picture of one type of thermal shipper that can be used, with the following descriptions: A) Dry ice pod – holds the top layer of dry ice; B) Vial tray – the vial trays look like small pizza boxes. Each vial try contains multiple dose vials. C) Box that holds the vial trays – box within the thermal shipping container that includes the vial tray. This box can be fully removed from the thermal shipping container. D) Foam lid – top foam lid that can be removed from the thermal shipping container. The temperature-monitor device is located in a foam packet on the top of the lid. E) Thermal shipping container – outer box of the thermal shipping container.

Figure 153 provides the positions of the edge and center vials in the stack of vial trays.

Figure 154 provides the dynamic thawing profile during a 5 minute walk.

Figure 155 provides the dynamic thawing profile during a 10 minute walk.

Figure 156 provides the dynamic thawing profile during a 15 minute walk.

Figure 157 provides a depiction of Configuration A as described in Table 35. Figure 157 i) shows how the vials are placed in the tray; Figure 157 ii) shows how the trays are stacked in the payload box; Figure 157 iii) shows the dimensions of a single tray; and Figure 157 iv) shows a top view of how the trays are stacked in the payload box.

Figure 158 provides a depiction of Configuration B as described in Table 35. Figure 158 i) shows how the vials are placed in the tray; Figure 158 ii) shows how the trays are stacked in the payload box; Figure 158 iii) shows the dimensions of a single tray; and Figure 158 iv) shows a top view of how the trays are stacked in the payload box.

Figure 159 provides a depiction of Configurations C and D as described in Table 35. Figure 159 i) shows how the vials are placed in the tray; Figure 159 ii) shows how the trays are stacked in the payload box; Figure 159 iii) shows the dimensions of a single tray; and Figure 159 iv) shows a top view of how the trays are stacked in the payload box.

Figure 160 provides a depiction of Configuration E as described in Table 35. Figure 160 i) shows how the vials are placed in the tray; Figure 160 ii) shows how the trays are stacked in the payload box; Figure 160 iii) shows the dimensions of a single tray; and Figure 160 iv) shows a top view of how the trays are stacked in the payload box.

Figure 161 provides a depiction of Configuration F as described in Table 35. Figure 161 i) shows how the vials are placed in the tray; Figure 161 ii) shows how the trays are stacked in the payload box; Figure 161 iii) shows the dimensions of a single tray; and Figure 161 iv) shows a top view of how the trays are stacked in the payload box.

Figure 162 provides a depiction of Configuration G as described in Table 35. Figure 162 i) shows how the vials are placed in the tray; Figure 162 ii) shows how the trays are stacked in

the payload box; Figure 162 iii) shows the dimensions of a single tray; and Figure 162 iv) shows a top view of how the trays are stacked in the payload box.

Figure 163 provides a depiction of Configuration H as described in Table 35. Figure 163 i) and ii) show how the vials are placed in the tray; Figure 163 iii) shows the dimensions of a single tray; and Figure 163 iv) shows how the trays are stacked in the payload box.

Figure 164 provides a depiction of Configuration I as described in Table 35. Figure 164 i) shows how the vials are placed in the tray; Figure 164 ii) shows the dimensions of a single tray; and Figure 164 iii) shows how the trays are stacked in the payload box.

Figure 165 provides a depiction of Configuration J as described in Table 35. Figure 165 i) shows how the vials are placed in the tray; Figure 165 ii) shows the dimensions of a single tray; and Figure 165 iii) shows how the trays are stacked in the payload box.

Figure 166 provides a depiction of Configuration K as described in Table 35. Figure 166 shows how the vials are placed in the tray and the dimensions of the length and base of the tray.

Figure 167 provides a depiction of Configuration L as described in Table 35. Figure 167 shows how the vials are placed in the tray and the dimensions of the length and base of the tray.

Description of the sequences

The following table provides a listing of certain sequences referenced herein.

TABLE 1: DESCRIPTION OF THE SEQUENCES		
SEQ ID NO:	Description	SEQUENCE
Antigenic S protein sequences		
1	S protein (amino acid)	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEK SNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFV FKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCAL DPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF TNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNC YFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEIL DITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSP RRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQE VFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAG TITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS VLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQE KNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDI SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKG VKLHYT

2	S protein (CDS)	augauugugauuucuugugcugcugccucuugugucuucucagugugugaauuugacaacaagaacacagcugccaccaguuauaacaaauucuuuuaccagaggagug uauuaucccugauaaaguguuuagaucuucugugcugcacagcacacaggaccaccuguuucugccauuuuuuagcaauggugacaauggguuucaugcaauucaugugucugg aacaaauggaacaaaaagauuugaauaaucccugugcugccuuuuaaugauggaguauuuuugcuucaacagaaaagucaaauauuauuagaggauggaauuuuugga acaacacuggaauucuaaaacacagucucugcugauugugaauauaaugcaacaaauggugugaauuucaguuuuguaaugauccuuuucugggagu guauuaucacaaaaauaaauaaauucuggaauggaaucugaagagaauuugaguguuuccucugcaaauaaauuguacauuugaauaugugucucagccuuuucugauggau cuggaaggaaaacagggcaauuuuaaaaaaucugagagaauuugguguuuaaaaauauugauggauauuuuaaaauuuauucuaaacacacaccaauuaauuuuaguga gagaucugccucagggauuuucugcucuggaacccucuggugggaucugccaauuggcauuaauauuacaagauuucagacacugcuggcucugcucacagaucuuauccugac accuggagauucuucuucuggauggacagccggagcugcagcuauuauguggggcuauucugcagccaagaacacauuucugcugaaauauaaaugaaaauggaacaauuac agaugcuggaauugugcucuggaauccucugucugaaacaaaauguacauuuaaaauucuuuuacagugggaaaaaggcauuuuaucagacaucuaauuuuuagagugcagc caacagaaucuauuugugagauuuccaaauauuacaaauucugucuguccauuuggagaagugguuuaaaugcaacaagauuugcaucugugauagcauggaauagaaaaaga auuucuaaauugugugguggcugauuauucugugcugcuuuuuuccacauuuaaaauguuauaugguggagugucuccaacaaaauuaaaugauuuauguuuuu acaaaugugauaugcugauuucuuuuugugaucagaggugaagugagaagugcccccggacagacaggaaaaauugcugauuacaaauacaaacugccugaugau uuuacaggaugugugauugcuuggaauucuaaauauuuagauucuaaagugggaggaaauuacaauuaucuguacagacuguuuagaaaaucaaauccugaaaccuu uugaaagagauauuucacagaaauuuaucaggcuggaucaacaccuguaaugggagugggaaggauuuaaauguuauuuuccaauacagagcuauggauuucagcca accauggugugggauaucagccauauagagugguggugcuucuuugaacugcugcaccugcaacaguguggaccuaaaaaaaucuacaaauuuagugaaa aauaaaugugugaauuuaauuuuaaugguauuaacaggaacaggagugcugacagaaucuaauaaaaaauuucugccuuuucagcaguuuggcagagauauugcag auaccacagaugcagugagagauccucagacauuagaaauucuggauauucaccuguuucuuuuuggggugugucugugauuacaccuggaacaaauacaucuaauc agguggcugugcuguaucaggauguagaauuguacagaaaguccaguggccaauucaugcagaucagcugacaccaacaugagagugguauuucuacaggaucuaauguu uucagacaagagagcaggauucugauuggagcagaacaugugaauaauucuuaugaauggauauuccaauuggagcaggcauuuugugcaucuuaucagacacagacaa auucccaaggagagcaagaucuguggcaucucagucuauuauugcauacaccaugucucuggggcagaaaauucugugguacaccauguacaauucuaauugcuauuc caacaaauuuuaccaauuucugugacaacagaaauuuuaaccgugucuaugacaaaaacaucugugguauguaccauguacauuuuguggagauucuacagaauguucu aaucugcugcugcaguauggaucuuuuuguuacacagcugaauagagcuuuaacaggaauugcugugguaacaggaaauaaaaacacaggaaguguuuugcucaggugaaa cagauuuacaaaaacaccaccaauuaaagauuuuuggaggauuuaauuuuuagcccagauucugccuguccuaaaaccuucuaaaagaucuuuuauuugaagaucugcu guuuaauaaagugacacuggcagauguagcaggauuuuaauuaaacagauggagauuugccuggggugauauuugugcucagaaaauuuaauggac ugacagugcugccucccucugcugacagaugaaaugauugccagucacacaucugccuuuacuggccuggaacaauuacaagcggauggacagcuuggagcugcugccucu gcagauuccuuuugcaaugcagauggcuuacagauuuaauggaauuggagugacacagaaaugugauauaugaaaaucagaaaucaguuuaauuucug caauuggcaaaauucaggauucucugucuucuacagccuucugcucuggggaaacugcaggaugugguugaaucagaaugcacaggcacugaauccucuggugaaacagcu gucuagcaauuuuuggggcaauuucucugugcugaugauauucucugucuagacugguuaagaagcugaagugcagauugauagacugaucacaggaagacugca gucucugcagacuuauguguacacagcagcugaauuagagcugcugaauuagagcuucugcuaauucuggcugcuacaaaauguccugaauguggugcugggacagucaaa

		aagaguggauuuuuguggaaaaggauaucaucugaugucuuuuccacagucugcuccacauggagugguguuuuuacaugugacauaugugccagcacaggaaaagaauuuuaccacagcaccagcaauuugucaugauggaaaagcacauuuuccaagagaaggaguguuugugucuaauggaacacauugguuugugacacagagaaauuuuuaugaaccucagauuauuacaacagauaaauacauuugugucaggaaauugugaugguggugauuggaauugugaauaauacaguguaugauccacugcagccagaacuggauucuuuuaaagaagaacuggauaaaauauuuuaaaaaucacacaucuccugaugguggauuuaggagauauuucuggaaucaaugcaucuguggugaaauauucagaaagaaauugauagacugaaugaaguggccaaaaaucugaaugaaucucugauugaucugcaggaacuuggaaaauaugaacaguacauuaaaauggccuugguacauuuggcuuggauuuauugcaggauuaauugcaauugugauggugacaauuauguuauguuguuguaugacaucauguuguucuuguuuaaaaggauguuguucuugugagagcuguuguaaaauuugaugaagaugauucugaaccuguguuaaaaggagugaaauugcauuacaca
3	S protein RBD (amino acid)(V05)	MFVFLVLLPLVSSQCVVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPK
4	S protein RBD (CDS) (V05)	auguuuguguuucuugugcugcugccucuugugucuucucagugugguggugagauuuccaaauauuacaaaucuguguccauuuggagaaguguuuaaugcaacaagauuugcaucuguguaugcauggaauagaaaaagaauuucuaauugugugguggcugauuauucugugcuguauaauagugcuucuuuuuccacauuuaaauguuauggagugucuccaacaaaauuaaaugauuuauguuuuacaaauguguaugcugauucuuuugugaucagaggugaugaagugagacagauugccccggacagacaggaaaaauugcugauuacaauuacaaacugccugaugauuuuacaggaugugugauugcuuggaauucuaauaauuuagauucuaaaguggggaggaaauuacaauuaucuguacagacuguuuagaaaaucaaaucugaaaccuuuugaaagagauauuucaacagaaauuuaucaggcuggaucaacaccuuguaauggaguggaaggauuuaaauguuauauuuccauuacagagcuauggauuucagccaaccaauggugugggauaucagccauauagagugguggugcugucuuuugaacugcugcaugcaccugcaacaguguguggaccuaaa
5	S protein RBD / Fibritin (amino acid) (V05)	MFVFLVLLPLVSSQCVVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCFTNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNCYFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKGSPGSGSGSGYIPEAPRDGQAYVRKDGEWVLLSTFLGRSLEVLFQGPG
6	S protein RBD / Fibritin (CDS) (V05)	auguuuguguuucuugugcugcugccucuugugucuucucagugugguggugagauuuccaaauauuacaaaucuguguccauuuggagaaguguuuaaugcaacaagauuugcaucuguguaugcauggaauagaaaaagaauuucuaauugugugguggcugauuauucugugcuguauaauagugcuucuuuuuccacauuuaaauguuauggagugucuccaacaaaauuaaaugauuuauguuuuacaaauguguaugcugauucuuuugugaucagaggugaugaagugagacagauugccccggacagacaggaaaaauugcugauuacaauuacaaacugccugaugauuuuacaggaugugugauugcuuggaauucuaauaauuuagauucuaaaguggggaggaaauuacaauuaucuguacagacuguuuagaaaaucaaaucugaaaccuuuugaaagagauauuucaacagaaauuuaucaggcuggaucaacaccuuguaauggaguggaaggauuuaaauguuauauuuccauuacagagcuauggauuucagccaaccaauggugugggauaucagccauauagagugguggugcugucuuuugaacugcugcaugcaccugcaacaguguguggaccuaaaggcucccccggcuccggcuccggaucugguuauauuccugaagcuccaagagaugggcaagcuuacguucguaaagauggcgaaugggguauuacuucuaccuuuuuaggccggucccuggaggugcuguuccagggccccggc

7	S protein PP (amino acid) (V08/V09)	MFVFLVLLPLVSSQCVNLTTRTQLPPAYTNSFTRGVYYPDKVFRSSVLHSTQDLFLPFFSNVTWFHAIHVSGTNGTKRFDNPVLPFNDGVYFASTEK SNIIRGWIFGTTLDSKTQSLLIVNNATNVVIKVCEFQFCNDPFLGVYYHKNNKSWMESEFRVYSSANNCTFEYVSQPFLMDLEGKQGNFKNLREFV FKNIDGYFKIYSKHTPINLVRDLPQGFSALEPLVDLPIGINITRFQTLLALHRSYLTPGDSSSGWTAGAAAYYVGYLQPRTFLLKYNENGTITDAVDCAL DPLSETKCTLKSFTVEKGIYQTSNFRVQPTESIVRFPNITNLCPFGEVFNATRFASVYAWNRKRISNCVADYSVLYNSASFSTFKCYGVSPTKLNDLCF TNVYADSFVIRGDEVRQIAPGQTGKIADYNYKLPDDFTGCVIAWNSNNLDSKVGGNYNYLYRLFRKSNLKPFERDISTEIYQAGSTPCNGVEGFNC YFPLQSYGFQPTNGVGYQPYRVVVLSFELLHAPATVCGPKKSTNLVKNKCVNFNFNGLTGTGVLTESNKKFLPFQQFGRDIADTTDAVRDPQTLEIL DITPCSFGGVSVITPGTNTSNQVAVLYQDVNCTEVPVAIHADQLTPTWRVYSTGSNVFQTRAGCLIGAEHVNNSYECDIPIGAGICASYQTQTNSP RRARSVASQSIIAYTMSLGAENSVAYSNNSIAIPTNFTISVTTEILPVSMTKTSVDCTMYICGDSTECSNLLLQYGSFCTQLNRALTGIAVEQDKNTQE VFAQVKQIYKTPPIKDFGGFNFSQILPDPSKPSKRSFIEDLLFNKVTLADAGFIKQYGDCLGDIAARDLICAQKFNGLTVLPPLLTDEMIAQYTSALLAG TITSGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKLIANQFNSAIGKIQDSLSSTASALGKLQDVVNQNAQALNTLVKQLSSNFGAISS VLNDILSRLDPPEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQSAPHGVVFLHVTYVPAQE KNFTTAPAICHDGKAHFPREGVFVSNGTHWFVTQRNFYEPQIITTDNTFVSGNCDVVIGIVNNTVYDPLQPELDSFKEELDKYFKNHTSPDVDLGDI SGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKYEQYIKWPWYIWLGFIAGLIAIVMVTIMLCCMTSCCSCLKGCCSCGSCCKFDEDDSEPVLKG VKLHYT

8	S protein (CDS) (V08) PP	auguuugugguuucuuugugcugcugccucuuguguucuucacagugugugaauuuugacaacaagaacacagcugccaccagcugccuauacaaauucuuuuaccagaggagug uauuaucccugauaaaguguuuagaucuucugugcugcacagcacacaggaccugguuucugccauuuuuuagcaaugacaugaccguucaauucaugcaauucaugucucugg aacaaauggaacaaaaagauuugauaauccuugugcugccuuuuuaauguggagugauauuuuugcuucacagaaaagucaaauauuauuagaggauggauuuuuuggga acaacacuggaauucuaaaacacaguucucugcugauuugugaauaaugcaacaaauggugguugauaaagugugugaauuucaguuuuguaaugaucccuuuucuggggagu guauuaucacaaaauaauaaauaaucuuggaauggaaucugaauuuagagugauauuccucugcaaauaauugugaauauguguucucagcccuuuucugaugguau cuggaaggaaaacagggcaauuuuaaaaauuugugauuuuaaaaauuauggauauuuuaaauuuuauucuaaacacacaccaauuaauuuuagauga gagaucugccucagggauuuuucugcucuggaaccucuggugggauucugccaauuaauauuacaagauuucagacacugcugccucugcacagaucuuauucugac accuggagauucuucuucuuggaggacagccggagcugcagcuauuauugugggcuaucugcagccaagaacauuucugcugaaauauaaugaaaauggaacaauuac agaugcuguggauuguggcuccuggauccucuguucugaaacaaauguacauuaaaauucuuuuacagugggaaaaaggcauuuaucagacaucuaauuuuuagaggugcagc caacagaauccuauuugugagauuuccaaauauuacaaauccugugucccauuuggagaaguguuuaaugcaacaagauuugcaucuguguauugcauggaauagaaaaaga auuucuaauugugugguggcugauauuucugugcuguauaaauagugcuucuuuuucccacauuuaaauguuauggagugugucucccaacaaauuaaaugauuuuauguuuu acaaaugguaugucugauuucuuuuugugaucagaggugaugaagagacagauugccccggacagacaggaaaaauugcugauuacaaauacaaacugccugaugau uuuuacaggaugugugauugcuuggaauucuaauauuuagauucuaaagugggaggaaauuacaauuaucuguacagacuguuuagaaaaucaaaucugaaaccuu uugaaagagauauuucaacagaaauuuaucaggcuggaucaacaccuuguauauggagugggaaggauuuauguuauuuuccauuacagagcuauggauuucagcca accaauggugugggauaucagccauuagagugguggugcugcuuuuugaacugcugcaugcaccugcaacagugugguggaccuaaaaaaaucuacaaaauuuagugaaa aauaaaaugugugaauuuuaauuuuaaugguaauacaggagugcugacagaauuauaaaaaauuucugccuuuucagcaguuuggcagagauauugcag auaccacagaugcagugagagauccucagacauuagaaauucuggauauuacaccuuguuucuuuuggggguguucugugauuacaccuggaacaaauacaucuaaauc aggugcugugcuguaucaggaugugaauuguacagaagugccaguggcaauucaugcagaucagcugacacccaacaugagaguguauucuacaggaucuaaaugugu uucagacaagagcaggaugucugauuggagcagaacauguggaauaauucuuuaugaaugugauauuccaauuggagcaggcauuugugcaucuuaucagacacagacaa auucccaaggagagcaagaucuguggcaucucaguucuauauugcauacaccaugucucuggggagcagaaaauucuguggcauauucuaaauaauucuauugcuauuc caacaaauuuuaccauuucugugacaacagaaauuuuaccugugucuauugacaaaaacaucugugguauguacaauuugguggagauucuacagaauguucu aaucugcugcugcaguauggaucuuuuuguacacagcugaauagagcuuuaacaggaauugcugugaacaggauaaaaaacacaggaagugguuugcucaggugaaa cagauuuacaaaacaccaccaauuaaagauuuuggagguuuauuuuuuagccagauucugccuguaucuucuaaaagauucuuuuauugaagaucugcu guuuauaaaagugacacuggcagaugcaggauuuauuauuaaacagugauggagauuugccuggggugauauugcugcagaagaucugauuuugugcugccuucu ugacagugcugccuccucugcugacagaugaaaugauugcucagucacacaucugcuuuuacuggccuggaacaauuacaagcggauggagcuggagcugcucu gcagauucuuuugcaaugcagaugggcuuacagauuuaaugggaguugacacagaauguguauauggaaaucagaaaugcagcacuggaaucacugguuaaacagcu caauuggcaaaauucaggauucucugucuucuacagcuucugcucuggggaaacugcaggauguggguucagaaugcacaggcacugaauacucuggugaaacagcu gucuagcaauuuuggggcaauuucuucugugcugaaugauauucugucuagacuggaagcugaaugugauagaucagaggaagacuguca gucucugcagacuuaugugacacagcagcugauuagagcugcugaaauuagagcuucugcuaauccuggcugcuacaaaaaugucugaauguguguggcugcacagucaaa

	aagaguggauuuuuuguggaaaaggaauaucaucugauguucuuuuuccacaguucugcucccacauggaguggugguguuuuuuacauugugacauuauguccagcacaggaaaaagaa uuuuaccacagcaccagcaauuugucaugauggaaaaagcacauuuuccaagaagggaguguuuguguucuaauggaacacauuggguuuugugacacagagaaauuuuuu augaaccucagauuauuuacaacagauaaauacauuuugugucaggaaaauugugaugauuggaauugugaauuuaggagauauuucuggaaucaaugcaucugugguugaauuucaga gauucuuuuuaaagaagaacuggauaaauauuuuuaaaaaucacacaucuccugauguggauuuuaggagauauuucuggaaucaaugcaucugugguugaauuucaga aagaaauugauagacugaauggaaggcccaaaaaauucugaauugaaucucugauuugaucugcaggaacuuggaaaauagaacaguacauuaaaauggccuuggguacaauu uggcuuggauuuauuugcaggauuuaauugcaauugugauggugacaauuuauguuauguguacaucauguuguucuuguuuuaaaaggaauguuguucuuguggga agcuguuguaaaauuugaugaagaugauucugaaccuguguuuaaaaggagugaaauugcauuacaca

9	S protein (CDS) (V09)	PP	auguucguguucuggugcugcuccuggugucccagcagguguugaaaccugaccacagaacacagcugccuccagccuacaccaacagcuuuaccagaaggcguguac uaccccgacaagguguucagauccagcgugcugcacuuacccaggaccuguuccugcuuuucuucagcaacgugaccugguuccacgccauccacgugucccggcaccaaug gcaccaagagauucgacaaccccgugcugcccuucaacgacgggguguacuuugccagcaccgagaaguccaacaucaucagaggcuggauucuucggcaccacacugacag caagacccagagccugcugaucgugaacaacgccaccaacgugguccaaguucugcaucaagacccccuucuccgggcgucuacuaccacaagaacaac aagagcuggaugaggaaagcgaguucgggguacagcagccgccaacaacugccaguucaccgaguacguguucccagcuuuccgaugaaggcaagcaggcaacuuc aagaaccugcgcgaguucguguuuaagaacaucgacggcuacuucaagaucuacagcaagcacaccccuaucaaccugcgggauucugccccagggcuucucugcucug gaaccccuggugaucugcccaucggcgcaucaacaccacccgguuucagacacugucggcccugcacagaagcuaccugacacuccggcgauagcagcacgcggauggacagcug gugccgccgcuuacuauguggggcuaccugcagccuagaacuccuucgugaaguacaacgagaacggcaccaucaccgacgccguggauuugugcucuggauccucgagcg agacaaaugugcacccugaaguccuucaccgugaaaagggcaucuaccagacccagcaacuccgggugcagcccaccgaauccaucgugcgguucccaauaucaccaaucu gugccccuucggcgagguguucaaugccaccagauucgccuguguacgccuggaaccggaaagcggaucagcaauugcguggccgacuacuccgugcuguacaacucccgcc agcuucagcaccuucaagugcuacggcgugucccccuaccaagcugaacgaccugugcuucacaaacguguacgccgacagcuucgugaucccggggagaugaagugcggcag auugccccuggacagacaggcaagaucgccgacuacaacuacaagcugcccgacgacuucaccggcugugugauugccuggaacagcaacaaccuggacucccaaagucggcg gcaacuacaauuaccuguaccggcuguuccgaaguccaaucugaagcccuucgagcgggacaucuccaccgagaucuaucaggccggcagcacccccuguaacggcgugg aaggcuucaacugcuacuucccccacugcaguccuacggcuuucagcccacaaaugggcgugggcuauccagcccuacagaguggugguugcugaacuucgaacugcugcaugccc cugccacagugugcggcccuaagaaaagcaccaauucucgugaagacaaaaugcguguucaacuucaacgccugaccggccaccggcgcugcugacagagagcaacaaga aguuccugccauuccagcaguuuggccgggauaucgccgauaccacagacgccguuagagauccccagacacuggaaauccuggacaucaccccuugcagcuucggcggag ugucugugaucaccccuggcaccaacaccagcaaucaggugcaguguguaccaggacgugaacuguaccgaagugccccguggccauucacgccgaucagcugacaccuac auggcggguguacuccaccggcagcaauguguuucagaccagagccggcuguucgaucgugaacgagcacgugaacaauuagcuacgaguucgacaucccccauccggcgcugg aaucugcgccagcuaccagacacaaacagcccuccggagaagccguggccagccagaagcaucauuggccucuacacaauguccucuggggccgccgagaacacagcgugggcc uacuccaacaacuacuaucgcuauccccaccaacuucaccaucagcgugaccacagaggauccugccuguguccaugaccaagacgugguccaccauguacaucugcg gcgauuccaccgagugcuccaaccugcugcuucagcuacggcagcuucugcacccagcugaauagagcccgugacagggauccgcguggaacacccaagaggu guucgcccaagugaagcagauucuacaagaccccuucuaucaaggacuucggcgccuucaauuucagcccgauccugcccgacaagcggagcuucau cgaggaccucguguucaacaaagugacacugcgccgacgccggcuucaucaagcaguauggcgauugucuggggcgacauugccgccgagggaucugauuuggcgcccagaaguu uaacggacucgacaguugcugccuccucugugaccgaugagaugaucgcccaguacacacaucugccccugcuggccggcacaaucacaagcggcuggacauuuuggagcaggcgcc gcucugcagaucccccuuugcuaugcagauggccuaccggguucaacggcagugacccagaauguugcuguacgagaaccagaucgaucgccaaccagguucaagc gccaucggcaagauccaggacagccugagcacacagcagccccuggggaaagcugcaggacgugguucaaccagaaugcccaggcacugacagacgugucgaagcgu ccuccaacuucggccgccaucagcucugugcugaacgauauccuugagcagacuucccuccugaggccgaggugcagaucgacagacugaucacaggcagacugccagacgu ccagacauacgugaccgagcagcugaucagagccgccgagauuaagagccucugcuccaaucuggccgccaccaagaugucugagugugugcugggccagcagaagaguggga cuuuugcggcaaggguaccaccuugaugagcuucccccucagucuggccccucacggcgugguguuucugcacgugacauaugugcccgcucaagagaagaauuucaccaccgc

		uccagccaucugccacgacggcaaagcccacuuuccuagagaaggcguguucguguccaacggcacccauugguucgugacacagcggaacuucuacgagccccagaucauc accaccgacaacaccuucgugucuggcaacugcgacgucgugaucggcauugugaacaauaccguguacgacccucugcagcccgagcuggacagcuucaaagaggaacug gacaaguacuuuaagaaccacacaagccccgacguggaccugggcgauaucagcggaaucaaugccagcgucgugaacauccagaaagagaucgaccggcugaacgaggug gccaagaaucugaacgagagccugaucgaccugcaagaacuggggaaguacgagcaguacaucaaguggcccugguacaucuggcugggcuuuaucgccggacugauugc caucgugauggucacaaucaugcuguguugcaugaccagcugcuguagcugccugaagggcuguuguagcuguggcagcugcugcaaguucgacgaggacgauucugag cccgugcugaagggcgugaaacugcacuacaca
Foldon		
10	Foldon (amino acid)	GSGYIPEAPRDGQAYVRKDGEWVLLSTFLGRSLEVLFQGPG
11	Foldon (CDS)	ggaucugguuauauuccugaagcuccaagagaugggcaagcuuacguucguaaagauggcgaaugguauuacuuucuaccuuuuuaggccggucccuggaggugcug uuccagggccccggc
5'-UTR (hAg-Kozak)		
12	5'-UTR	AACUAGUAUUCUUCUGGUCCCCACAGACUCAGAGAGAACCCGCCACC
3'-UTR (FI element)		
13	3'-UTR	CUGGUACUGCAUGCACGCAAUGCUAGCUGCCCCUUUCCCGUCCUGGGUACCCCGAGUCUCCCCCGACCUCGGGUCCCAGGUAUGCUCCC ACCUCCACCUGCCCCACUCACCACCUCUGCUAGUUCCAGACACCUCCCAAGCACGCAGCAAUGCAGCUCAAAACGCUUAGCCUAGCCACA CCCCCACGGGAAACAGCAGUGAUUAACCUUUAGCAAUAAACGAAAGUUUAACUAAGCUAUACUAACCCCAGGGUUGGUCAAUUUCGU GCCAGCCACACC
A30L70		
14	A30L70	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGCAUAUGACUAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA AAAAAAAAAAAAAAAAAAAAAA

Detailed description

Although the present disclosure is described in detail below, it is to be understood that this disclosure is not limited to the particular methodologies, protocols and reagents described herein as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present disclosure which will be limited only by the appended claims. Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art.

Preferably, the terms used herein are defined as described in "A multilingual glossary of biotechnological terms: (IUPAC Recommendations)", H.G.W. Leuenberger, B. Nagel, and H. Kölbl, Eds., Helvetica Chimica Acta, CH-4010 Basel, Switzerland, (1995).

The practice of the present disclosure will employ, unless otherwise indicated, conventional methods of chemistry, biochemistry, cell biology, immunology, and recombinant DNA techniques which are explained in the literature in the field (cf., e.g., Molecular Cloning: A Laboratory Manual, 2nd Edition, J. Sambrook et al. eds., Cold Spring Harbor Laboratory Press, Cold Spring Harbor 1989).

In the following, the elements of the present disclosure will be described. These elements are listed with specific embodiments, however, it should be understood that they may be combined in any manner and in any number to create additional embodiments. The variously described examples and embodiments should not be construed to limit the present disclosure to only the explicitly described embodiments. This description should be understood to disclose and encompass embodiments which combine the explicitly described embodiments with any number of the disclosed elements. Furthermore, any permutations and combinations of all described elements should be considered disclosed by this description unless the context indicates otherwise.

The term "about" means approximately or nearly, and in the context of a numerical value or range set forth herein in one embodiment means ± 20%, ± 10%, ± 5%, or ± 3% of the numerical value or range recited or claimed.

The terms "a" and "an" and "the" and similar reference used in the context of describing the disclosure (especially in the context of the claims) are to be construed to cover both the singular and the plural, unless otherwise indicated herein or clearly contradicted by context. Recitation of ranges of values herein is merely intended to serve as a shorthand method of referring individually to each separate value falling within the range. Unless otherwise indicated herein, each individual value is incorporated into the specification as if it was individually recited herein. All methods described herein can be performed in any suitable order unless otherwise indicated herein or otherwise clearly contradicted by context. The use of any and all examples, or exemplary language (e.g., "such as"), provided herein is intended merely to better illustrate the disclosure and does not pose a limitation on the scope of the claims. No language in the specification should be construed as indicating any non-claimed element essential to the practice of the disclosure.

Unless expressly specified otherwise, the term "comprising" is used in the context of the present document to indicate that further members may optionally be present in addition to the members of the list introduced by "comprising". It is, however, contemplated as a specific embodiment of the present disclosure that the term "comprising" encompasses the possibility of no further members being present, i.e., for the purpose of this embodiment "comprising" is to be understood as having the meaning of "consisting of" or "consisting essentially of".

Several documents are cited throughout the text of this specification. Each of the documents cited herein (including all patents, patent applications, scientific publications, manufacturer's specifications, instructions, etc.), whether supra or infra, are hereby incorporated by reference in their entirety. Nothing herein is to be construed as an admission that the present disclosure was not entitled to antedate such disclosure.

Definitions

In the following, definitions will be provided which apply to all aspects of the present disclosure. The following terms have the following meanings unless otherwise indicated. Any undefined terms have their art recognized meanings.

Terms such as "reduce", "decrease", "inhibit" or "impair" as used herein relate to an overall reduction or the ability to cause an overall reduction, preferably of at least 5%, at least 10%, at least 20%, at least 50%, at least 75% or even more, in the level. These terms include a complete or essentially complete inhibition, i.e., a reduction to zero or essentially to zero.

Terms such as "increase", "enhance" or "exceed" preferably relate to an increase or enhancement by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 80%, at least 100%, at least 200%, at least 500%, or even more.

According to the disclosure, the term "peptide" comprises oligo- and polypeptides and refers to substances which comprise about two or more, about 3 or more, about 4 or more, about 6 or more, about 8 or more, about 10 or more, about 13 or more, about 16 or more, about 20 or more, and up to about 50, about 100 or about 150, consecutive amino acids linked to one another via peptide bonds. The term "protein" or "polypeptide" refers to large peptides, in particular peptides having at least about 150 amino acids, but the terms "peptide", "protein" and "polypeptide" are used herein usually as synonyms.

A "therapeutic protein" has a positive or advantageous effect on a condition or disease state of a subject when provided to the subject in a therapeutically effective amount. In one embodiment, a therapeutic protein has curative or palliative properties and may be administered to ameliorate, relieve, alleviate, reverse, delay onset of or lessen the severity of one or more symptoms of a disease or disorder. A therapeutic protein may have prophylactic properties and may be used to delay the onset of a disease or to lessen the severity of such disease or pathological condition. The term "therapeutic protein" includes entire proteins or peptides, and can also refer to therapeutically active fragments thereof. It can also include therapeutically active variants of a protein. Examples of therapeutically active proteins

include, but are not limited to, antigens for vaccination and immunostimulants such as cytokines.

"Fragment", with reference to an amino acid sequence (peptide or protein), relates to a part of an amino acid sequence, i.e. a sequence which represents the amino acid sequence shortened at the N-terminus and/or C-terminus. A fragment shortened at the C-terminus (N-terminal fragment) is obtainable e.g. by translation of a truncated open reading frame that lacks the 3'-end of the open reading frame. A fragment shortened at the N-terminus (C-terminal fragment) is obtainable e.g. by translation of a truncated open reading frame that lacks the 5'-end of the open reading frame, as long as the truncated open reading frame comprises a start codon that serves to initiate translation. A fragment of an amino acid sequence comprises e.g. at least 50 %, at least 60 %, at least 70 %, at least 80%, at least 90% of the amino acid residues from an amino acid sequence. A fragment of an amino acid sequence preferably comprises at least 6, in particular at least 8, at least 12, at least 15, at least 20, at least 30, at least 50, or at least 100 consecutive amino acids from an amino acid sequence.

By "variant" herein is meant an amino acid sequence that differs from a parent amino acid sequence by virtue of at least one amino acid modification. The parent amino acid sequence may be a naturally occurring or wild type (WT) amino acid sequence, or may be a modified version of a wild type amino acid sequence. Preferably, the variant amino acid sequence has at least one amino acid modification compared to the parent amino acid sequence, e.g., from 1 to about 20 amino acid modifications, and preferably from 1 to about 10 or from 1 to about 5 amino acid modifications compared to the parent.

By "wild type" or "WT" or "native" herein is meant an amino acid sequence that is found in nature, including allelic variations. A wild type amino acid sequence, peptide or protein has an amino acid sequence that has not been intentionally modified.

For the purposes of the present disclosure, "variants" of an amino acid sequence (peptide, protein or polypeptide) comprise amino acid insertion variants, amino acid addition variants,

amino acid deletion variants and/or amino acid substitution variants. The term "variant" includes all mutants, splice variants, posttranslationally modified variants, conformations, isoforms, allelic variants, species variants, and species homologs, in particular those which are naturally occurring. The term "variant" includes, in particular, fragments of an amino acid sequence.

Amino acid insertion variants comprise insertions of single or two or more amino acids in a particular amino acid sequence. In the case of amino acid sequence variants having an insertion, one or more amino acid residues are inserted into a particular site in an amino acid sequence, although random insertion with appropriate screening of the resulting product is also possible. Amino acid addition variants comprise amino- and/or carboxy-terminal fusions of one or more amino acids, such as 1, 2, 3, 5, 10, 20, 30, 50, or more amino acids. Amino acid deletion variants are characterized by the removal of one or more amino acids from the sequence, such as by removal of 1, 2, 3, 5, 10, 20, 30, 50, or more amino acids. The deletions may be in any position of the protein. Amino acid deletion variants that comprise the deletion at the N-terminal and/or C-terminal end of the protein are also called N-terminal and/or C-terminal truncation variants. Amino acid substitution variants are characterized by at least one residue in the sequence being removed and another residue being inserted in its place. Preference is given to the modifications being in positions in the amino acid sequence which are not conserved between homologous proteins or peptides and/or to replacing amino acids with other ones having similar properties. Preferably, amino acid changes in peptide and protein variants are conservative amino acid changes, i.e., substitutions of similarly charged or uncharged amino acids. A conservative amino acid change involves substitution of one of a family of amino acids which are related in their side chains. Naturally occurring amino acids are generally divided into four families: acidic (aspartate, glutamate), basic (lysine, arginine, histidine), non-polar (alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), and uncharged polar (glycine, asparagine, glutamine, cysteine, serine, threonine, tyrosine) amino acids. Phenylalanine, tryptophan, and tyrosine are sometimes classified

jointly as aromatic amino acids. In one embodiment, conservative amino acid substitutions include substitutions within the following groups:

glycine, alanine;

valine, isoleucine, leucine;

aspartic acid, glutamic acid;

asparagine, glutamine;

serine, threonine;

lysine, arginine; and

phenylalanine, tyrosine.

Preferably the degree of similarity, preferably identity between a given amino acid sequence and an amino acid sequence which is a variant of said given amino acid sequence will be at least about 60%, 70%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99%. The degree of similarity or identity is given preferably for an amino acid region which is at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or about 100% of the entire length of the reference amino acid sequence. For example, if the reference amino acid sequence consists of 200 amino acids, the degree of similarity or identity is given preferably for at least about 20, at least about 40, at least about 60, at least about 80, at least about 100, at least about 120, at least about 140, at least about 160, at least about 180, or about 200 amino acids, in some embodiments continuous amino acids. In some embodiments, the degree of similarity or identity is given for the entire length of the reference amino acid sequence. The alignment for determining sequence similarity, preferably sequence identity can be done with art known tools, preferably using the best sequence alignment, for example, using Align, using standard settings, preferably EMBOSS::needle, Matrix: Blosum62, Gap Open 10.0, Gap Extend 0.5.

"Sequence similarity" indicates the percentage of amino acids that either are identical or that represent conservative amino acid substitutions. "Sequence identity" between two amino

acid sequences indicates the percentage of amino acids that are identical between the sequences. "Sequence identity" between two nucleic acid sequences indicates the percentage of nucleotides that are identical between the sequences.

The terms "% identical", "% identity" or similar terms are intended to refer, in particular, to the percentage of nucleotides or amino acids which are identical in an optimal alignment between the sequences to be compared. Said percentage is purely statistical, and the differences between the two sequences may be but are not necessarily randomly distributed over the entire length of the sequences to be compared. Comparisons of two sequences are usually carried out by comparing the sequences, after optimal alignment, with respect to a segment or "window of comparison", in order to identify local regions of corresponding sequences. The optimal alignment for a comparison may be carried out manually or with the aid of the local homology algorithm by Smith and Waterman, 1981, Ads App. Math. 2, 482, with the aid of the local homology algorithm by Neddleman and Wunsch, 1970, J. Mol. Biol. 48, 443, with the aid of the similarity search algorithm by Pearson and Lipman, 1988, Proc. Natl Acad. Sci. USA 88, 2444, or with the aid of computer programs using said algorithms (GAP, BESTFIT, FASTA, BLAST P, BLAST N and TFASTA in Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Drive, Madison, Wis.). In some embodiments, percent identity of two sequences is determined using the BLASTN or BLASTP algorithm, as available on the United States National Center for Biotechnology Information (NCBI) website (e.g., at blast.ncbi.nlm.nih.gov/Blast.cgi?PAGE_TYPE=BlastSearch&BLAST_SPEC=blast2seq&LINK_LOC=align2seq). In some embodiments, the algorithm parameters used for BLASTN algorithm on the NCBI website include: (i) Expect Threshold set to 10; (ii) Word Size set to 28; (iii) Max matches in a query range set to 0; (iv) Match/Mismatch Scores set to 1, -2; (v) Gap Costs set to Linear; and (vi) the filter for low complexity regions being used. In some embodiments, the algorithm parameters used for BLASTP algorithm on the NCBI website include: (i) Expect Threshold set to 10; (ii) Word Size set to 3; (iii) Max matches in a query range set to 0; (iv)

Matrix set to BLOSUM62; (v) Gap Costs set to Existence: 11 Extension: 1; and (vi) conditional compositional score matrix adjustment.

Percentage identity is obtained by determining the number of identical positions at which the sequences to be compared correspond, dividing this number by the number of positions compared (e.g., the number of positions in the reference sequence) and multiplying this result by 100.

In some embodiments, the degree of similarity or identity is given for a region which is at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90% or about 100% of the entire length of the reference sequence. For example, if the reference nucleic acid sequence consists of 200 nucleotides, the degree of identity is given for at least about 100, at least about 120, at least about 140, at least about 160, at least about 180, or about 200 nucleotides, in some embodiments continuous nucleotides. In some embodiments, the degree of similarity or identity is given for the entire length of the reference sequence.

Homologous amino acid sequences exhibit according to the disclosure at least 40%, in particular at least 50%, at least 60%, at least 70%, at least 80%, at least 90% and preferably at least 95%, at least 98 or at least 99% identity of the amino acid residues.

The amino acid sequence variants described herein may readily be prepared by the skilled person, for example, by recombinant DNA manipulation. The manipulation of DNA sequences for preparing peptides or proteins having substitutions, additions, insertions or deletions, is described in detail in Sambrook et al. (1989), for example. Furthermore, the peptides and amino acid variants described herein may be readily prepared with the aid of known peptide synthesis techniques such as, for example, by solid phase synthesis and similar methods.

In one embodiment, a fragment or variant of an amino acid sequence (peptide or protein) is preferably a "functional fragment" or "functional variant". The term "functional fragment" or "functional variant" of an amino acid sequence relates to any fragment or variant exhibiting one or more functional properties identical or similar to those of the amino acid sequence from which it is derived, i.e., it is functionally equivalent. With respect to antigens or antigenic

sequences, one particular function is one or more immunogenic activities displayed by the amino acid sequence from which the fragment or variant is derived. The term "functional fragment" or "functional variant", as used herein, in particular refers to a variant molecule or sequence that comprises an amino acid sequence that is altered by one or more amino acids compared to the amino acid sequence of the parent molecule or sequence and that is still capable of fulfilling one or more of the functions of the parent molecule or sequence, e.g., inducing an immune response. In one embodiment, the modifications in the amino acid sequence of the parent molecule or sequence do not significantly affect or alter the characteristics of the molecule or sequence. In different embodiments, the function of the functional fragment or functional variant may be reduced but still significantly present, e.g., immunogenicity of the functional variant may be at least 50%, at least 60%, at least 70%, at least 80%, or at least 90% of the parent molecule or sequence. However, in other embodiments, immunogenicity of the functional fragment or functional variant may be enhanced compared to the parent molecule or sequence.

An amino acid sequence (peptide, protein or polypeptide) "derived from" a designated amino acid sequence (peptide, protein or polypeptide) refers to the origin of the first amino acid sequence. Preferably, the amino acid sequence which is derived from a particular amino acid sequence has an amino acid sequence that is identical, essentially identical or homologous to that particular sequence or a fragment thereof. Amino acid sequences derived from a particular amino acid sequence may be variants of that particular sequence or a fragment thereof. For example, it will be understood by one of ordinary skill in the art that the antigens suitable for use herein may be altered such that they vary in sequence from the naturally occurring or native sequences from which they were derived, while retaining the desirable activity of the native sequences.

As used herein, an "instructional material" or "instructions" includes a publication, a recording, a diagram, or any other medium of expression which can be used to communicate the usefulness of the compositions and methods of the invention. The instructional material

of the kit of the invention may, for example, be affixed to a container which contains the compositions of the invention or be shipped together with a container which contains the compositions. Alternatively, the instructional material may be shipped separately from the container with the intention that the instructional material and the compositions be used cooperatively by the recipient.

"Isolated" means altered or removed from the natural state. For example, a nucleic acid or a peptide naturally present in a living animal is not "isolated", but the same nucleic acid or peptide partially or completely separated from the coexisting materials of its natural state is "isolated". An isolated nucleic acid or protein can exist in substantially purified form, or can exist in a non-native environment such as, for example, a host cell.

The term "recombinant" in the context of the present invention means "made through genetic engineering". Preferably, a "recombinant object" such as a recombinant nucleic acid in the context of the present invention is not occurring naturally.

The term "naturally occurring" as used herein refers to the fact that an object can be found in nature. For example, a peptide or nucleic acid that is present in an organism (including viruses) and can be isolated from a source in nature and which has not been intentionally modified by man in the laboratory is naturally occurring.

"Physiological pH" as used herein refers to a pH of about 7.5.

The term “genetic modification” or simply “modification” includes the transfection of cells with nucleic acid. The term "transfection" relates to the introduction of nucleic acids, in particular RNA, into a cell. For purposes of the present invention, the term "transfection" also includes the introduction of a nucleic acid into a cell or the uptake of a nucleic acid by such cell, wherein the cell may be present in a subject, e.g., a patient. Thus, according to the present invention, a cell for transfection of a nucleic acid described herein can be present *in vitro* or *in vivo*, e.g. the cell can form part of an organ, a tissue and/or an organism of a patient. According to the invention, transfection can be transient or stable. For some applications of transfection, it is sufficient if the transfected genetic material is only transiently expressed. RNA can be

transfected into cells to transiently express its coded protein. Since the nucleic acid introduced in the transfection process is usually not integrated into the nuclear genome, the foreign nucleic acid will be diluted through mitosis or degraded. Cells allowing episomal amplification of nucleic acids greatly reduce the rate of dilution. If it is desired that the transfected nucleic acid actually remains in the genome of the cell and its daughter cells, a stable transfection must occur. Such stable transfection can be achieved by using virus-based systems or transposon-based systems for transfection. Generally, nucleic acid encoding antigen is transiently transfected into cells. RNA can be transfected into cells to transiently express its coded protein.

The term "seroconversion" includes a ≥4-fold rise from before vaccination to 1-month post Dose 2.

As used herein a "primary container" refers to an outer container of a system or kit, wherein other containers (such as a payload container and/or a dry ice container) can be placed inside.

As used herein, a "payload container" refers to a container that can hold the "payload" – or the temperature-sensitive material – that desirably is kept at a low temperature.

As used herein, a "tray" refers to a container intended to house the payload – or the temperature-sensitive material – and wherein the tray is intended to be placed within the payload container.

As used herein, a "temperature-sensitive material" refers to a biological and/or pharmaceutical composition, wherein the chemical, physical, and/or medicinal properties are impacted by elevated temperatures (e.g. temperatures above 0°C).

As used herein, a "dry ice container" refers to a container that can adequately hold dry ice to be used within the kits and/or container systems described herein.

Coronavirus

Coronaviruses are enveloped, positive-sense, single-stranded RNA ((+) ssRNA) viruses. They have the largest genomes (26–32 kb) among known RNA viruses and are phylogenetically divided into four genera (α, β, γ, and δ), with betacoronaviruses further subdivided into four lineages (A, B, C, and D). Coronaviruses infect a wide range of avian and mammalian species, including humans. Some human coronaviruses generally cause mild respiratory diseases, although severity can be greater in infants, the elderly, and the immunocompromised. Middle East respiratory syndrome coronavirus (MERS-CoV) and severe acute respiratory syndrome coronavirus (SARS-CoV), belonging to betacoronavirus lineages C and B, respectively, are highly pathogenic. Both viruses emerged into the human population from animal reservoirs within the last 15 years and caused outbreaks with high case-fatality rates. The outbreak of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) that causes atypical pneumonia (coronavirus disease 2019; COVID-19) has raged in China since mid-December 2019, and has developed to be a public health emergency of international concern. SARS-CoV-2 (MN908947.3) belongs to betacoronavirus lineage B. It has at least 70% sequence similarity to SARS-CoV.

In general, coronaviruses have four structural proteins, namely, envelope (E), membrane (M), nucleocapsid (N), and spike (S). The E and M proteins have important functions in the viral assembly, and the N protein is necessary for viral RNA synthesis. The critical glycoprotein S is responsible for virus binding and entry into target cells. The S protein is synthesized as a single-chain inactive precursor that is cleaved by furin-like host proteases in the producing cell into two noncovalently associated subunits, S1 and S2. The S1 subunit contains the receptor-binding domain (RBD), which recognizes the host-cell receptor. The S2 subunit contains the fusion peptide, two heptad repeats, and a transmembrane domain, all of which are required to mediate fusion of the viral and host-cell membranes by undergoing a large conformational rearrangement. The S1 and S2 subunits trimerize to form a large prefusion spike.

The S precursor protein of SARS-CoV-2 can be proteolytically cleaved into S1 (685 aa) and S2 (588 aa) subunits. The S1 subunit consists of the receptor-binding domain (RBD), which mediates virus entry into sensitive cells through the host angiotensin-converting enzyme 2 (ACE2) receptor.

Antigen

The present invention comprises the use of RNA encoding an amino acid sequence comprising SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof. Thus, the RNA encodes a peptide or protein comprising at least an epitope SARS-CoV-2 S protein or an immunogenic variant thereof for inducing an immune response against coronavirus S protein, in particular SARS-CoV-2 S protein in a subject. The amino acid sequence comprising SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof (i.e., the antigenic peptide or protein) is also designated herein as "vaccine antigen", "peptide and protein antigen", "antigen molecule" or simply "antigen". The SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is also designated herein as "antigenic peptide or protein" or "antigenic sequence".

SARS-CoV-2 coronavirus full length spike (S) protein consist of 1273 amino acids (see SEQ ID NO: 1). In specific embodiments, full length spike (S) protein according to SEQ ID NO: 1 is modified in such a way that the prototypical prefusion conformation is stabilized. Stabilization of the prefusion conformation may be obtained by introducing two consecutive proline substitutions at AS residues 986 and 987 in the full length spike protein. Specifically, spike (S) protein stabilized protein variants are obtained in a way that the amino acid residue at position 986 is exchanged to proline and the amino acid residue at position 987 is also exchanged to proline. In one embodiment, a SARS-CoV-2 S protein variant comprises the amino acid sequence shown in SEQ ID NO: 7.

In one embodiment, the vaccine antigen described herein comprises, consists essentially of or consists of a spike protein (S) of SARS-CoV-2, a variant thereof, or a fragment thereof.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 3819 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 1273 of SEQ ID NO: 1 or 7.

In one embodiment, the vaccine antigen comprises, consists essentially of or consists of SARS-CoV-2 spike S1 fragment (S1) (the S1 subunit of a spike protein (S) of SARS-CoV-2), a variant thereof, or a fragment thereof.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 2049 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2049 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 2049 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2049 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 2049 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 683 of SEQ ID NO: 1.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 49 to 2055 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 17 to 685 of SEQ ID NO: 1.

In one embodiment, the vaccine antigen comprises, consists essentially of or consists of the receptor binding domain (RBD) of the S1 subunit of a spike protein (S) of SARS-CoV-2, a variant thereof, or a fragment thereof. The amino acid sequence of amino acids 327 to 528 of SEQ ID

NO: 1, a variant thereof, or a fragment thereof is also referred to herein as "RBD" or "RBD domain".

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 979 to 1584 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1.

According to certain embodiments, a signal peptide is fused, either directly or through a linker, to a SARS-CoV-2 S protein, a variant thereof, or a fragment thereof, i.e., the antigenic peptide or protein. Accordingly, in one embodiment, a signal peptide is fused to the above described amino acid sequences derived from SARS-CoV-2 S protein or immunogenic fragments thereof (antigenic peptides or proteins) comprised by the vaccine antigens described above.

Such signal peptides are sequences, which typically exhibit a length of about 15 to 30 amino acids and are preferably located at the N-terminus of the antigenic peptide or protein, without being limited thereto. Signal peptides as defined herein preferably allow the transport of the antigenic peptide or protein as encoded by the RNA into a defined cellular compartment, preferably the cell surface, the endoplasmic reticulum (ER) or the endosomal-lysosomal compartment. In one embodiment, the signal peptide sequence as defined herein includes, without being limited thereto, the signal peptide sequence of SARS-CoV-2 S protein, in particular a sequence comprising the amino acid sequence of amino acids 1 to 16 or 1 to 19 of SEQ ID NO: 1 or a functional variant thereof.

In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1. In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1.

In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or

9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1. In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 1 to 48 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 16 of SEQ ID NO: 1.

In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1. In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1.

In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 1 to 57 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 57 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 57 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 57 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or

80% identity to the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1. In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 1 to 57 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 19 of SEQ ID NO: 1.

The signal peptide sequence as defined herein further includes, without being limited thereto, the signal peptide sequence of an immunoglobulin, e.g., the signal peptide sequence of an immunoglobulin heavy chain variable region, wherein the immunoglobulin may be human immunoglobulin. In particular, the signal peptide sequence as defined herein includes a sequence comprising the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31 or a functional variant thereof.

In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, or a functional fragment of the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31. In one embodiment, a signal sequence comprises the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31.

In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 54 to 119 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 119 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 54 to 119 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 119 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 22 of SEQ ID

NO: 31, or a functional fragment of the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31. In one embodiment, RNA encoding a signal sequence (i) comprises the nucleotide sequence of nucleotides 54 to 119 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31.

Such signal peptides are preferably used in order to promote secretion of the encoded antigenic peptide or protein. More preferably, a signal peptide as defined herein is fused to an encoded antigenic peptide or protein as defined herein.

Accordingly, in particularly preferred embodiments, the RNA described herein comprises at least one coding region encoding an antigenic peptide or protein and a signal peptide, said signal peptide preferably being fused to the antigenic peptide or protein, more preferably to the N-terminus of the antigenic peptide or protein as described herein.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 1 or 7. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 1 or 7.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 1 or 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%,

85%, or 80% identity to the amino acid sequence of SEQ ID NO: 1 or 7, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 1 or 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 1 or 7. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 1 or 7.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 7.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 15, 16, 19, 20, 24, or 25, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 15, 16, 19, 20, 24, or 25, or a fragment of the nucleotide sequence of SEQ ID NO: 15, 16, 19, 20, 24, or 25, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 15, 16, 19, 20, 24, or 25; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 7, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 15, 16, 19, 20, 24, or 25; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 1 to 2049 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 2049 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 2049 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 2049 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 1 to 2049 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 683 of SEQ ID NO: 1.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 685 of SEQ ID NO:

1, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 1 to 2055 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 2055 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 1 to 2055 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 1 to 2055 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 1 to 2055 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 685 of SEQ ID NO: 1.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 3, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 3, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 3, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 3. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 3.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 4, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 4, or a fragment of the nucleotide sequence of SEQ ID NO: 4, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 4; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 3, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 3, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 3, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 3. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 4; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 3.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 716 of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 716 of SEQ ID NO: 30, or a fragment of the nucleotide sequence of nucleotides 54 to 716 of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 716 of SEQ ID NO: 30;

and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 716 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 221 of SEQ ID NO: 29.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 725 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 725 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 54 to 725 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 725 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 224 of

SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 725 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 224 of SEQ ID NO: 31.

According to certain embodiments, a trimerization domain is fused, either directly or through a linker, e.g., a glycine/serine linker, to a SARS-CoV-2 S protein, a variant thereof, or a fragment thereof, i.e., the antigenic peptide or protein. Accordingly, in one embodiment, a trimerization domain is fused to the above described amino acid sequences derived from SARS-CoV-2 S protein or immunogenic fragments thereof (antigenic peptides or proteins) comprised by the vaccine antigens described above (which may optionally be fused to a signal peptide as described above).

Such trimerization domains are preferably located at the C-terminus of the antigenic peptide or protein, without being limited thereto. Trimerization domains as defined herein preferably allow the trimerization of the antigenic peptide or protein as encoded by the RNA. Examples of trimerization domains as defined herein include, without being limited thereto, foldon, the natural trimerization domain of T4 fibritin. The C-terminal domain of T4 fibritin (foldon) is obligatory for the formation of the fibritin trimer structure and can be used as an artificial trimerization domain. In one embodiment, the trimerization domain as defined herein includes, without being limited thereto, a sequence comprising the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10 or a functional variant thereof. In one embodiment, the trimerization domain as defined herein includes, without being limited thereto, a sequence comprising the amino acid sequence of SEQ ID NO: 10 or a functional variant thereof.

In one embodiment, a trimerization domain comprises the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10, or a functional fragment of the amino acid sequence of amino acids 3 to 29 of SEQ ID

NO: 10, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10. In one embodiment, a trimerization domain comprises the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10.

In one embodiment, RNA encoding a trimerization domain (i) comprises the nucleotide sequence of nucleotides 7 to 87 of SEQ ID NO: 11, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 7 to 87 of SEQ ID NO: 11, or a fragment of the nucleotide sequence of nucleotides 7 to 87 of SEQ ID NO: 11, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 7 to 87 of SEQ ID NO: 11; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10, or a functional fragment of the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10. In one embodiment, RNA encoding a trimerization domain (i) comprises the nucleotide sequence of nucleotides 7 to 87 of SEQ ID NO: 11; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10.

In one embodiment, a trimerization domain comprises the amino acid sequence SEQ ID NO: 10, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 10, or a functional fragment of the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 10. In one embodiment, a trimerization domain comprises the amino acid sequence of SEQ ID NO: 10.

In one embodiment, RNA encoding a trimerization domain (i) comprises the nucleotide sequence of SEQ ID NO: 11, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%,

90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 11, or a fragment of the nucleotide sequence of SEQ ID NO: 11, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 11; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 10, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 10, or a functional fragment of the amino acid sequence of SEQ ID NO: 10, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 10. In one embodiment, RNA encoding a trimerization domain (i) comprises the nucleotide sequence of SEQ ID NO: 11; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 10.

Such trimerization domains are preferably used in order to promote trimerization of the encoded antigenic peptide or protein. More preferably, a trimerization domain as defined herein is fused to an antigenic peptide or protein as defined herein.

Accordingly, in particularly preferred embodiments, the RNA described herein comprises at least one coding region encoding an antigenic peptide or protein and a trimerization domain as defined herein, said trimerization domain preferably being fused to the antigenic peptide or protein, more preferably to the C-terminus of the antigenic peptide or protein.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 5, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 5, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 5.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 6, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6, or a fragment of the nucleotide

sequence of SEQ ID NO: 6, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 6; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 5, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 6; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 17, 21, or 26, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 17, 21, or 26, or a fragment of the nucleotide sequence of SEQ ID NO: 17, 21, or 26, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 17, 21, or 26; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 5, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 17, 21, or 26; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 18, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 18, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 18, or the amino acid sequence having at least 99%, 98%, 97%, 96%,

95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 18. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 18.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 824 of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 824 of SEQ ID NO: 30, or a fragment of the nucleotide sequence of nucleotides 54 to 824 of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 824 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 824 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 257 of SEQ ID NO: 29.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%,

90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 833 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 833 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 54 to 833 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 833 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 833 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 260 of SEQ ID NO: 31.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29. In one

embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 111 to 824 of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 111 to 824 of SEQ ID NO: 30, or a fragment of the nucleotide sequence of nucleotides 111 to 824 of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 111 to 824 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 111 to 824 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 20 to 257 of SEQ ID NO: 29.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 120 to 833 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%,

97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 120 to 833 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 120 to 833 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 120 to 833 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 120 to 833 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 23 to 260 of SEQ ID NO: 31.

According to certain embodiments, a transmembrane domain domain is fused, either directly or through a linker, e.g., a glycine/serine linker, to a SARS-CoV-2 S protein, a variant thereof, or a fragment thereof, i.e., the antigenic peptide or protein. Accordingly, in one embodiment, a transmembrane domain is fused to the above described amino acid sequences derived from SARS-CoV-2 S protein or immunogenic fragments thereof (antigenic peptides or proteins) comprised by the vaccine antigens described above (which may optionally be fused to a signal peptide and/or trimerization domain as described above).

Such transmembrane domains are preferably located at the C-terminus of the antigenic peptide or protein, without being limited thereto. Preferably, such transmembrane domains are located at the C-terminus of the trimerization domain, if present, without being limited thereto. In one embodiment, a trimerization domain is present between the SARS-CoV-2 S protein, a variant thereof, or a fragment thereof, i.e., the antigenic peptide or protein, and the transmembrane domain.

Transmembrane domains as defined herein preferably allow the anchoring into a cellular membrane of the antigenic peptide or protein as encoded by the RNA.

In one embodiment, the transmembrane domain sequence as defined herein includes, without being limited thereto, the transmembrane domain sequence of SARS-CoV-2 S protein, in particular a sequence comprising the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1 or a functional variant thereof.

In one embodiment, a transmembrane domain sequence comprises the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1. In one embodiment, a transmembrane domain sequence comprises the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1.

In one embodiment, RNA encoding a transmembrane domain sequence (i) comprises the nucleotide sequence of nucleotides 3619 to 3762 of SEQ ID NO: 2, 8 or 9, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 3619 to 3762 of SEQ ID NO: 2, 8 or 9, or a fragment of the nucleotide sequence of nucleotides 3619 to 3762 of SEQ ID NO: 2, 8 or 9, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 3619 to 3762 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, or a functional fragment of the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1. In one

embodiment, RNA encoding a transmembrane domain sequence (i) comprises the nucleotide sequence of nucleotides 3619 to 3762 of SEQ ID NO: 2, 8 or 9; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 986 of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 986 of SEQ ID NO: 30, or a fragment of the nucleotide sequence of nucleotides 54 to 986 of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 986 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 986 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 311 of SEQ ID NO: 29.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 995 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 995 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 54 to 995 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 54 to 995 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 54 to 995 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 1 to 314 of SEQ ID NO: 31.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 20 to 311 of SEQ

ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 111 to 986 of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 111 to 986 of SEQ ID NO: 30, or a fragment of the nucleotide sequence of nucleotides 111 to 986 of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 111 to 986 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 111 to 986 of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 20 to 311 of SEQ ID NO: 29.

In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31. In one embodiment, a vaccine antigen comprises the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 120 to 995 of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 120 to 995 of SEQ ID NO: 32, or a fragment of the nucleotide sequence of nucleotides 120 to 995 of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of nucleotides 120 to 995 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of nucleotides 120 to 995 of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of amino acids 23 to 314 of SEQ ID NO: 31.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 30, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 30, or a fragment of the nucleotide sequence of SEQ ID NO: 30, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 29, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 29, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 29, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 29. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ

ID NO: 30; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 29.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 32, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 32, or a fragment of the nucleotide sequence of SEQ ID NO: 32, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 31, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 31, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 31, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 31. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 32; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 31.

In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 28, an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 28, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 28, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 28. In one embodiment, a vaccine antigen comprises the amino acid sequence of SEQ ID NO: 28.

In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 27, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 27, or a fragment of the nucleotide sequence of SEQ ID NO: 27, or the nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 27; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 28, an

amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 28, or an immunogenic fragment of the amino acid sequence of SEQ ID NO: 28, or the amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 28. In one embodiment, RNA encoding a vaccine antigen (i) comprises the nucleotide sequence of SEQ ID NO: 27; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 28.

In one embodiment, the vaccine antigens described above comprise a contiguous sequence of SARS-CoV-2 coronavirus spike (S) protein that consists of or essentially consists of the above described amino acid sequences derived from SARS-CoV-2 S protein or immunogenic fragments thereof (antigenic peptides or proteins) comprised by the vaccine antigens described above. In one embodiment, the vaccine antigens described above comprise a contiguous sequence of SARS-CoV-2 coronavirus spike (S) protein of no more than 220 amino acids, 215 amino acids, 210 amino acids, or 205 amino acids.

In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) described herein as BNT162b1 (RBP020.3), BNT162b2 (RBP020.1 or RBP020.2). In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) described herein as RBP020.2.

In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 21, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 21, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5. In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 21; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5.

In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 19, or 20, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 19, or 20, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 19, or 20; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7.

In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 20, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 20, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, RNA encoding a vaccine antigen is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 20; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7.

As used herein, the term "vaccine" refers to a composition that induces an immune response upon inoculation into a subject. In some embodiments, the induced immune response provides protective immunity.

In one embodiment, the RNA encoding the antigen molecule is expressed in cells of the subject to provide the antigen molecule. In one embodiment, expression of the antigen molecule is at the cell surface or into the extracellular space. In one embodiment, the antigen molecule is presented in the context of MHC. In one embodiment, the RNA encoding the antigen molecule is transiently expressed in cells of the subject. In one embodiment, after administration of the

RNA encoding the antigen molecule, in particular after intramuscular administration of the RNA encoding the antigen molecule, expression of the RNA encoding the antigen molecule in muscle occurs. In one embodiment, after administration of the RNA encoding the antigen molecule, expression of the RNA encoding the antigen molecule in spleen occurs. In one embodiment, after administration of the RNA encoding the antigen molecule, expression of the RNA encoding the antigen molecule in antigen presenting cells, preferably professional antigen presenting cells occurs. In one embodiment, the antigen presenting cells are selected from the group consisting of dendritic cells, macrophages and B cells. In one embodiment, after administration of the RNA encoding the antigen molecule, no or essentially no expression of the RNA encoding the antigen molecule in lung and/or liver occurs. In one embodiment, after administration of the RNA encoding the antigen molecule, expression of the RNA encoding the antigen molecule in spleen is at least 5-fold the amount of expression in lung.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration, in particular following intramuscular administration, to a subject result in delivery of the RNA encoding a vaccine antigen to lymph nodes and/or spleen. In some embodiments, RNA encoding a vaccine antigen is detectable in lymph nodes and/or spleen 6 hours or later following administration and preferably up to 6 days or longer.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration, in particular following intramuscular administration, to a subject result in delivery of the RNA encoding a vaccine antigen to B cell follicles, subcapsular sinus, and/or T cell zone, in particular B cell follicles and/or subcapsular sinus of lymph nodes.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration, in particular following intramuscular administration, to a subject result in delivery of the RNA encoding a vaccine antigen to B cells (CD19+), subcapsular sinus macrophages (CD169+) and/or dendritic cells (CD11c+) in the T cell zone and intermediary

sinus of lymph nodes, in particular to B cells (CD19+) and/or subcapsular sinus macrophages (CD169+) of lymph nodes.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration, in particular following intramuscular administration, to a subject result in delivery of the RNA encoding a vaccine antigen to white pulp of spleen.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration, in particular following intramuscular administration, to a subject result in delivery of the RNA encoding a vaccine antigen to B cells, DCs (CD11c+), in particular those surrounding the B cells, and/or mcrophages of spleen, in particular to B cells and/or DCs (CD11c+).

In one embodiment, the vaccine antigen is expressed in lymph node and/or spleen, in particular in the cells of lymph node and/or spleen described above.

The peptide and protein antigens suitable for use according to the disclosure typically include a peptide or protein comprising an epitope of SARS-CoV-2 S protein or a functional variant thereof for inducing an immune response. The peptide or protein or epitope may be derived from a target antigen, i.e. the antigen against which an immune response is to be elicited. For example, the peptide or protein antigen or the epitope contained within the peptide or protein antigen may be a target antigen or a fragment or variant of a target antigen. The target antigen may be a coronavirus S protein, in particular SARS-CoV-2 S protein.

The antigen molecule or a procession product thereof, e.g., a fragment thereof, may bind to an antigen receptor such as a BCR or TCR carried by immune effector cells, or to antibodies.

A peptide and protein antigen which is provided to a subject according to the invention by administering RNA encoding the peptide and protein antigen, i.e., a vaccine antigen, preferably results in the induction of an immune response, e.g., a humoral and/or cellular immune response in the subject being provided the peptide or protein antigen. Said immune response is preferably directed against a target antigen, in particular coronavirus S protein, in particular SARS-CoV-2 S protein. Thus, a vaccine antigen may comprise the target antigen, a

variant thereof, or a fragment thereof. In one embodiment, such fragment or variant is immunologically equivalent to the target antigen. In the context of the present disclosure, the term "fragment of an antigen" or "variant of an antigen" means an agent which results in the induction of an immune response which immune response targets the antigen, i.e. a target antigen. Thus, the vaccine antigen may correspond to or may comprise the target antigen, may correspond to or may comprise a fragment of the target antigen or may correspond to or may comprise an antigen which is homologous to the target antigen or a fragment thereof. Thus, according to the disclosure, a vaccine antigen may comprise an immunogenic fragment of a target antigen or an amino acid sequence being homologous to an immunogenic fragment of a target antigen. An "immunogenic fragment of an antigen" according to the disclosure preferably relates to a fragment of an antigen which is capable of inducing an immune response against the target antigen. The vaccine antigen may be a recombinant antigen.

The term "immunologically equivalent" means that the immunologically equivalent molecule such as the immunologically equivalent amino acid sequence exhibits the same or essentially the same immunological properties and/or exerts the same or essentially the same immunological effects, e.g., with respect to the type of the immunological effect. In the context of the present disclosure, the term "immunologically equivalent" is preferably used with respect to the immunological effects or properties of antigens or antigen variants used for immunization. For example, an amino acid sequence is immunologically equivalent to a reference amino acid sequence if said amino acid sequence when exposed to the immune system of a subject induces an immune reaction having a specificity of reacting with the reference amino acid sequence.

"Activation" or "stimulation", as used herein, refers to the state of an immune effector cell such as T cell that has been sufficiently stimulated to induce detectable cellular proliferation. Activation can also be associated with initiation of signaling pathways, induced cytokine production, and detectable effector functions. The term "activated immune effector cells" refers to, among other things, immune effector cells that are undergoing cell division.

The term "priming" refers to a process wherein an immune effector cell such as a T cell has its first contact with its specific antigen and causes differentiation into effector cells such as effector T cells.

The term "clonal expansion" or "expansion" refers to a process wherein a specific entity is multiplied. In the context of the present disclosure, the term is preferably used in the context of an immunological response in which immune effector cells are stimulated by an antigen, proliferate, and the specific immune effector cell recognizing said antigen is amplified. Preferably, clonal expansion leads to differentiation of the immune effector cells.

The term "antigen" relates to an agent comprising an epitope against which an immune response can be generated. The term "antigen" includes, in particular, proteins and peptides. In one embodiment, an antigen is presented by cells of the immune system such as antigen presenting cells like dendritic cells or macrophages. An antigen or a procession product thereof such as a T-cell epitope is in one embodiment bound by a T- or B-cell receptor, or by an immunoglobulin molecule such as an antibody. Accordingly, an antigen or a procession product thereof may react specifically with antibodies or T lymphocytes (T cells). In one embodiment, an antigen is a viral antigen, such as a coronavirus S protein, e.g., SARS-CoV-2 S protein, and an epitope is derived from such antigen.

The term "viral antigen" refers to any viral component having antigenic properties, i.e. being able to provoke an immune response in an individual. The viral antigen may be coronavirus S protein, e.g., SARS-CoV-2 S protein.

The term "expressed on the cell surface" or "associated with the cell surface" means that a molecule such as an antigen is associated with and located at the plasma membrane of a cell, wherein at least a part of the molecule faces the extracellular space of said cell and is accessible from the outside of said cell, e.g., by antibodies located outside the cell. In this context, a part is preferably at least 4, preferably at least 8, preferably at least 12, more preferably at least 20 amino acids. The association may be direct or indirect. For example, the association may be by one or more transmembrane domains, one or more lipid anchors, or by

the interaction with any other protein, lipid, saccharide, or other structure that can be found on the outer leaflet of the plasma membrane of a cell. For example, a molecule associated with the surface of a cell may be a transmembrane protein having an extracellular portion or may be a protein associated with the surface of a cell by interacting with another protein that is a transmembrane protein.

"Cell surface" or "surface of a cell" is used in accordance with its normal meaning in the art, and thus includes the outside of the cell which is accessible to binding by proteins and other molecules. An antigen is expressed on the surface of cells if it is located at the surface of said cells and is accessible to binding by e.g. antigen-specific antibodies added to the cells.

The term "extracellular portion" or "exodomain" in the context of the present invention refers to a part of a molecule such as a protein that is facing the extracellular space of a cell and preferably is accessible from the outside of said cell, e.g., by binding molecules such as antibodies located outside the cell. Preferably, the term refers to one or more extracellular loops or domains or a fragment thereof.

The term "epitope" refers to a part or fragment of a molecule such as an antigen that is recognized by the immune system. For example, the epitope may be recognized by T cells, B cells or antibodies. An epitope of an antigen may include a continuous or discontinuous portion of the antigen and may be between about 5 and about 100, such as between about 5 and about 50, more preferably between about 8 and about 30, most preferably between about 8 and about 25 amino acids in length, for example, the epitope may be preferably 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids in length. In one embodiment, an epitope is between about 10 and about 25 amino acids in length. The term "epitope" includes T cell epitopes.

The term "T cell epitope" refers to a part or fragment of a protein that is recognized by a T cell when presented in the context of MHC molecules. The term "major histocompatibility complex" and the abbreviation "MHC" includes MHC class I and MHC class II molecules and relates to a complex of genes which is present in all vertebrates. MHC proteins or molecules

are important for signaling between lymphocytes and antigen presenting cells or diseased cells in immune reactions, wherein the MHC proteins or molecules bind peptide epitopes and present them for recognition by T cell receptors on T cells. The proteins encoded by the MHC are expressed on the surface of cells, and display both self-antigens (peptide fragments from the cell itself) and non-self-antigens (e.g., fragments of invading microorganisms) to a T cell. In the case of class I MHC/peptide complexes, the binding peptides are typically about 8 to about 10 amino acids long although longer or shorter peptides may be effective. In the case of class II MHC/peptide complexes, the binding peptides are typically about 10 to about 25 amino acids long and are in particular about 13 to about 18 amino acids long, whereas longer and shorter peptides may be effective.

The peptide and protein antigen can be 2-100 amino acids, including for example, 5 amino acids, 10 amino acids, 15 amino acids, 20 amino acids, 25 amino acids, 30 amino acids, 35 amino acids, 40 amino acids, 45 amino acids, or 50 amino acids in length. In some embodiments, a peptide can be greater than 50 amino acids. In some embodiments, the peptide can be greater than 100 amino acids.

The peptide or protein antigen can be any peptide or protein that can induce or increase the ability of the immune system to develop antibodies and T cell responses to the peptide or protein.

In one embodiment, vaccine antigen is recognized by an immune effector cell. Preferably, the vaccine antigen if recognized by an immune effector cell is able to induce in the presence of appropriate co-stimulatory signals, stimulation, priming and/or expansion of the immune effector cell carrying an antigen receptor recognizing the vaccine antigen. In the context of the embodiments of the present invention, the vaccine antigen is preferably presented or present on the surface of a cell, preferably an antigen presenting cell. In one embodiment, an antigen is presented by a diseased cell such as a virus-infected cell. In one embodiment, an antigen receptor is a TCR which binds to an epitope of an antigen presented in the context of MHC. In one embodiment, binding of a TCR when expressed by T cells and/or present on T

cells to an antigen presented by cells such as antigen presenting cells results in stimulation, priming and/or expansion of said T cells. In one embodiment, binding of a TCR when expressed by T cells and/or present on T cells to an antigen presented on diseased cells results in cytolysis and/or apoptosis of the diseased cells, wherein said T cells preferably release cytotoxic factors, e.g. perforins and granzymes.

In one embodiment, an antigen receptor is an antibody or B cell receptor which binds to an epitope in an antigen. In one embodiment, an antibody or B cell receptor binds to native epitopes of an antigen.

Nucleic acids

The term "polynucleotide" or "nucleic acid", as used herein, is intended to include DNA and RNA such as genomic DNA, cDNA, mRNA, recombinantly produced and chemically synthesized molecules. A nucleic acid may be single-stranded or double-stranded. RNA includes *in vitro* transcribed RNA (IVT RNA) or synthetic RNA. According to the invention, a polynucleotide is preferably isolated.

Nucleic acids may be comprised in a vector. The term "vector" as used herein includes any vectors known to the skilled person including plasmid vectors, cosmid vectors, phage vectors such as lambda phage, viral vectors such as retroviral, adenoviral or baculoviral vectors, or artificial chromosome vectors such as bacterial artificial chromosomes (BAC), yeast artificial chromosomes (YAC), or P1 artificial chromosomes (PAC). Said vectors include expression as well as cloning vectors. Expression vectors comprise plasmids as well as viral vectors and generally contain a desired coding sequence and appropriate DNA sequences necessary for the expression of the operably linked coding sequence in a particular host organism (e.g., bacteria, yeast, plant, insect, or mammal) or in *in vitro* expression systems. Cloning vectors are generally used to engineer and amplify a certain desired DNA fragment and may lack functional sequences needed for expression of the desired DNA fragments.

In one embodiment of all aspects of the invention, the RNA encoding the vaccine antigen is expressed in cells such as antigen presenting cells of the subject treated to provide the vaccine antigen.

The nucleic acids described herein may be recombinant and/or isolated molecules.

In the present disclosure, the term "RNA" relates to a nucleic acid molecule which includes ribonucleotide residues. In preferred embodiments, the RNA contains all or a majority of ribonucleotide residues. As used herein, "ribonucleotide" refers to a nucleotide with a hydroxyl group at the 2'-position of a β-D-ribofuranosyl group. RNA encompasses without limitation, double stranded RNA, single stranded RNA, isolated RNA such as partially purified RNA, essentially pure RNA, synthetic RNA, recombinantly produced RNA, as well as modified RNA that differs from naturally occurring RNA by the addition, deletion, substitution and/or alteration of one or more nucleotides. Such alterations may refer to addition of non-nucleotide material to internal RNA nucleotides or to the end(s) of RNA. It is also contemplated herein that nucleotides in RNA may be non-standard nucleotides, such as chemically synthesized nucleotides or deoxynucleotides. For the present disclosure, these altered RNAs are considered analogs of naturally-occurring RNA.

In certain embodiments of the present disclosure, the RNA is messenger RNA (mRNA) that relates to a RNA transcript which encodes a peptide or protein. As established in the art, mRNA generally contains a 5' untranslated region (5'-UTR), a peptide coding region and a 3' untranslated region (3'-UTR). In some embodiments, the RNA is produced by *in vitro* transcription or chemical synthesis. In one embodiment, the mRNA is produced by *in vitro* transcription using a DNA template where DNA refers to a nucleic acid that contains deoxyribonucleotides.

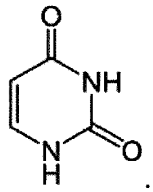
In one embodiment, RNA is *in vitro* transcribed RNA (IVT-RNA) and may be obtained by *in vitro* transcription of an appropriate DNA template. The promoter for controlling transcription can be any promoter for any RNA polymerase. A DNA template for *in vitro* transcription may be obtained by cloning of a nucleic acid, in particular cDNA, and introducing it into an appropriate

vector for *in vitro* transcription. The cDNA may be obtained by reverse transcription of RNA. In certain embodiments of the present disclosure, the RNA is "replicon RNA" or simply a "replicon", in particular "self-replicating RNA" or "self-amplifying RNA". In one particularly preferred embodiment, the replicon or self-replicating RNA is derived from or comprises elements derived from a ssRNA virus, in particular a positive-stranded ssRNA virus such as an alphavirus. Alphaviruses are typical representatives of positive-stranded RNA viruses. Alphaviruses replicate in the cytoplasm of infected cells (for review of the alphaviral life cycle see José et al., Future Microbiol., 2009, vol. 4, pp. 837–856). The total genome length of many alphaviruses typically ranges between 11,000 and 12,000 nucleotides, and the genomic RNA typically has a 5'-cap, and a 3' poly(A) tail. The genome of alphaviruses encodes non-structural proteins (involved in transcription, modification and replication of viral RNA and in protein modification) and structural proteins (forming the virus particle). There are typically two open reading frames (ORFs) in the genome. The four non-structural proteins (nsP1–nsP4) are typically encoded together by a first ORF beginning near the 5' terminus of the genome, while alphavirus structural proteins are encoded together by a second ORF which is found downstream of the first ORF and extends near the 3' terminus of the genome. Typically, the first ORF is larger than the second ORF, the ratio being roughly 2:1. In cells infected by an alphavirus, only the nucleic acid sequence encoding non-structural proteins is translated from the genomic RNA, while the genetic information encoding structural proteins is translatable from a subgenomic transcript, which is an RNA molecule that resembles eukaryotic messenger RNA (mRNA; Gould et al., 2010, Antiviral Res., vol. 87 pp. 111–124). Following infection, i.e. at early stages of the viral life cycle, the (+) stranded genomic RNA directly acts like a messenger RNA for the translation of the open reading frame encoding the non-structural poly-protein (nsP1234). Alphavirus-derived vectors have been proposed for delivery of foreign genetic information into target cells or target organisms. In simple approaches, the open reading frame encoding alphaviral structural proteins is replaced by an open reading frame encoding a protein of interest. Alphavirus-based trans-replication systems rely on alphavirus nucleotide

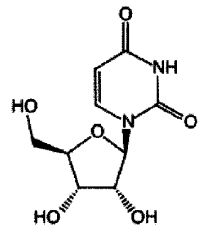
sequence elements on two separate nucleic acid molecules: one nucleic acid molecule encodes a viral replicase, and the other nucleic acid molecule is capable of being replicated by said replicase in trans (hence the designation trans-replication system). Trans-replication requires the presence of both these nucleic acid molecules in a given host cell. The nucleic acid molecule capable of being replicated by the replicase in trans must comprise certain alphaviral sequence elements to allow recognition and RNA synthesis by the alphaviral replicase.

In one embodiment, the RNA described herein may have modified nucleosides. In some embodiments, the RNA comprises a modified nucleoside in place of at least one (e.g., every) uridine.

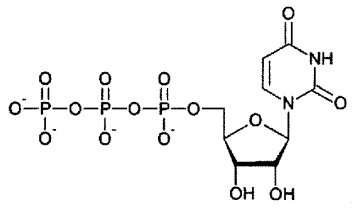
The term "uracil," as used herein, describes one of the nucleobases that can occur in the nucleic acid of RNA. The structure of uracil is:



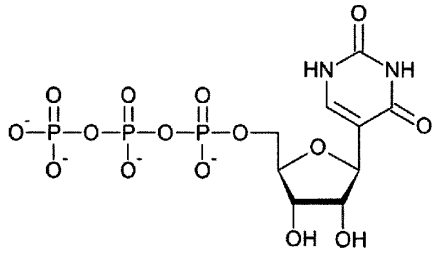
The term "uridine," as used herein, describes one of the nucleosides that can occur in RNA. The structure of uridine is:



UTP (uridine 5'-triphosphate) has the following structure:

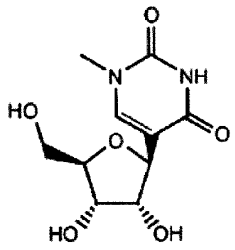


Pseudo-UTP (pseudouridine 5'-triphosphate) has the following structure:

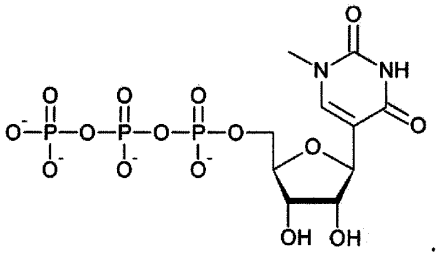


"Pseudouridine" is one example of a modified nucleoside that is an isomer of uridine, where the uracil is attached to the pentose ring via a carbon-carbon bond instead of a nitrogen-carbon glycosidic bond.

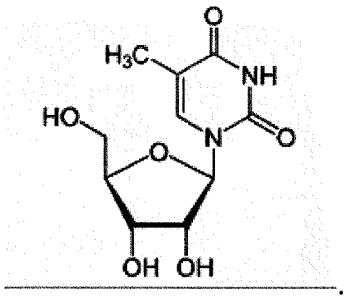
Another exemplary modified nucleoside is N1-methyl-pseudouridine (m1Ψ), which has the structure:



N1-methyl-pseudo-UTP has the following structure:



Another exemplary modified nucleoside is 5-methyl-uridine (m5U), which has the structure:



In some embodiments, one or more uridine in the RNA described herein is replaced by a modified nucleoside. In some embodiments, the modified nucleoside is a modified uridine. In some embodiments, RNA comprises a modified nucleoside in place of at least one uridine. In some embodiments, RNA comprises a modified nucleoside in place of each uridine.

In some embodiments, the modified nucleoside is independently selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U). In some embodiments, the modified nucleoside comprises pseudouridine (ψ). In some embodiments, the modified nucleoside comprises N1-methyl-pseudouridine (m1ψ). In some embodiments, the modified nucleoside comprises 5-methyl-uridine (m5U). In some embodiments, RNA may comprise more than one type of modified nucleoside, and the modified nucleosides are independently selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U). In some embodiments, the modified nucleosides comprise pseudouridine (ψ) and N1-methyl-pseudouridine (m1ψ). In some embodiments, the modified nucleosides comprise pseudouridine (ψ) and 5-methyl-uridine (m5U). In some embodiments, the modified nucleosides comprise N1-methyl-pseudouridine (m1ψ) and 5-methyl-uridine (m5U). In some

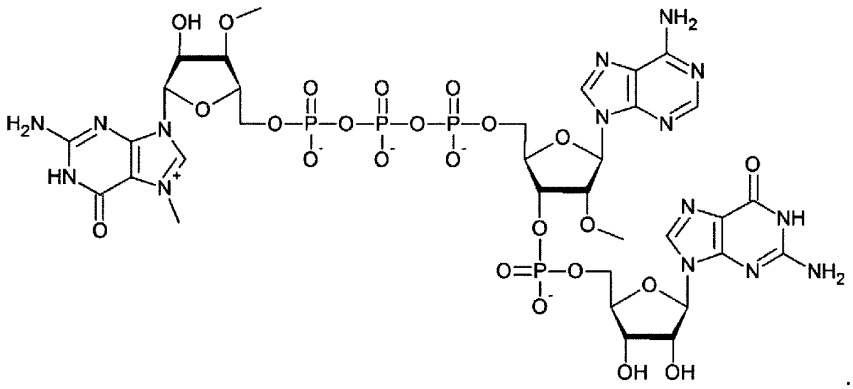
embodiments, the modified nucleosides comprise pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U).

In some embodiments, the modified nucleoside replacing one or more, e.g., all, uridine in the RNA may be any one or more of 3-methyl-uridine (m^3U), 5-methoxy-uridine (mo^5U), 5-aza-uridine, 6-aza-uridine, 2-thio-5-aza-uridine, 2-thio-uridine (s^2U), 4-thio-uridine (s^4U), 4-thio-pseudouridine, 2-thio-pseudouridine, 5-hydroxy-uridine (ho^5U), 5-aminoallyl-uridine, 5-halo-uridine (e.g., 5-iodo-uridine or 5-bromo-uridine), uridine 5-oxyacetic acid (cmo^5U), uridine 5-oxyacetic acid methyl ester ($mcmo^5U$), 5-carboxymethyl-uridine (cm^5U), 1-carboxymethyl-pseudouridine, 5-carboxyhydroxymethyl-uridine (chm^5U), 5-carboxyhydroxymethyl-uridine methyl ester ($mchm^5U$), 5-methoxycarbonylmethyl-uridine (mcm^5U), 5-methoxycarbonylmethyl-2-thio-uridine (mcm^5s^2U), 5-aminomethyl-2-thio-uridine (nm^5s^2U), 5-methylaminomethyl-uridine (mnm^5U), 1-ethyl-pseudouridine, 5-methylaminomethyl-2-thio-uridine (mnm^5s^2U), 5-methylaminomethyl-2-seleno-uridine (mnm^5se^2U), 5-carbamoylmethyl-uridine (ncm^5U), 5-carboxymethylaminomethyl-uridine ($cmnm^5U$), 5-carboxymethylaminomethyl-2-thio-uridine ($cmnm^5s^2U$), 5-propynyl-uridine, 1-propynyl-pseudouridine, 5-taurinomethyl-uridine (τm^5U), 1-taurinomethyl-pseudouridine, 5-taurinomethyl-2-thio-uridine($\tau m5s2U$), 1-taurinomethyl-4-thio-pseudouridine), 5-methyl-2-thio-uridine (m^5s^2U), 1-methyl-4-thio-pseudouridine ($m^1s^4\psi$), 4-thio-1-methyl-pseudouridine, 3-methyl-pseudouridine ($m^3\psi$), 2-thio-1-methyl-pseudouridine, 1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-1-deaza-pseudouridine, dihydrouridine (D), dihydropseudouridine, 5,6-dihydrouridine, 5-methyl-dihydrouridine (m^5D), 2-thio-dihydrouridine, 2-thio-dihydropseudouridine, 2-methoxy-uridine, 2-methoxy-4-thio-uridine, 4-methoxy-pseudouridine, 4-methoxy-2-thio-pseudouridine, N1-methyl-pseudouridine, 3-(3-amino-3-carboxypropyl)uridine (acp^3U), 1-methyl-3-(3-amino-3-carboxypropyl)pseudouridine ($acp^3\ \psi$), 5-(isopentenylaminomethyl)uridine (inm^5U), 5-(isopentenylaminomethyl)-2-thio-uridine (inm^5s^2U), α-thio-uridine, 2'-O-methyl-uridine (Um), 5,2'-O-dimethyl-uridine (m^5Um), 2'-O-methyl-pseudouridine (ψm), 2-thio-2'-O-methyl-

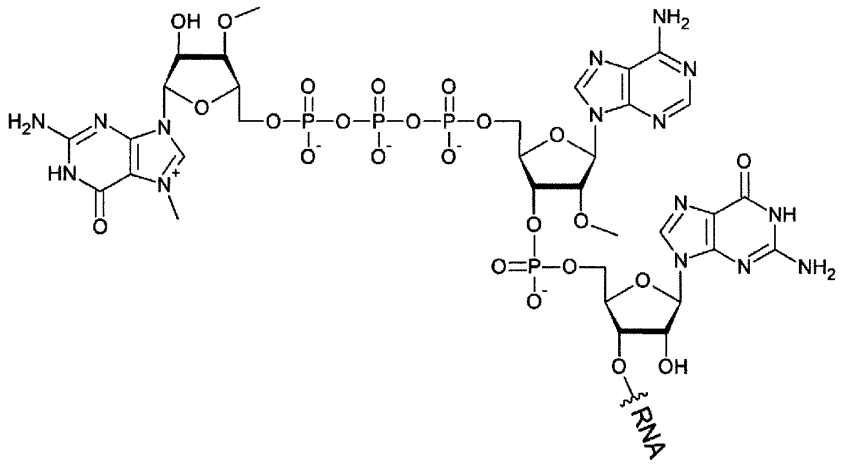
uridine (s^2Um), 5-methoxycarbonylmethyl-2'-O-methyl-uridine (mcm^5Um), 5-carbamoylmethyl-2'-O-methyl-uridine (ncm^5Um), 5-carboxymethylaminomethyl-2'-O-methyl-uridine ($cmnm^5Um$), 3,2'-O-dimethyl-uridine (m^3Um), 5-(isopentenylaminomethyl)-2'-O-methyl-uridine (inm^5Um), 1-thio-uridine, deoxythymidine, 2'-F-ara-uridine, 2'-F-uridine, 2'-OH-ara-uridine, 5-(2-carbomethoxyvinyl) uridine, 5-[3-(1-E-propenylamino)uridine, or any other modified uridine known in the art.

In one embodiment, the RNA comprises other modified nucleosides or comprises further modified nucleosides, e.g., modified cytidine. For example, in one embodiment, in the RNA 5-methylcytidine is substituted partially or completely, preferably completely, for cytidine. In one embodiment, the RNA comprises 5-methylcytidine and one or more selected from pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ), and 5-methyl-uridine (m5U). In one embodiment, the RNA comprises 5-methylcytidine and N1-methyl-pseudouridine (m1ψ). In some embodiments, the RNA comprises 5-methylcytidine in place of each cytidine and N1-methyl-pseudouridine (m1ψ) in place of each uridine.

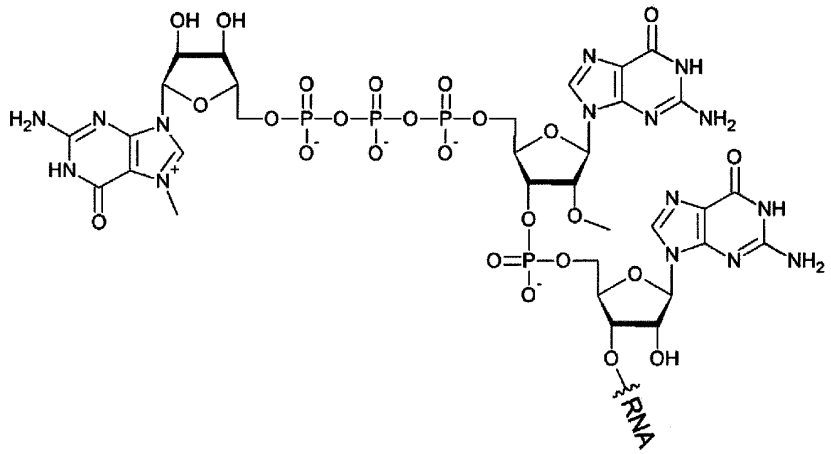
In some embodiments, the RNA according to the present disclosure comprises a 5'-cap. In one embodiment, the RNA of the present disclosure does not have uncapped 5'-triphosphates. In one embodiment, the RNA may be modified by a 5'- cap analog. The term "5'-cap" refers to a structure found on the 5'-end of an mRNA molecule and generally consists of a guanosine nucleotide connected to the mRNA via a 5'- to 5'-triphosphate linkage. In one embodiment, this guanosine is methylated at the 7-position. Providing an RNA with a 5'-cap or 5'-cap analog may be achieved by *in vitro* transcription, in which the 5'-cap is co-transcriptionally expressed into the RNA strand, or may be attached to RNA post-transcriptionally using capping enzymes. In some embodiments, the building block cap for RNA is $m_2^{7,3'-O}Gppp(m_1^{2'-O})ApG$ (also sometimes referred to as $m_2^{7,3'O}G(5')ppp(5')m^{2'-O}ApG$), which has the following structure:



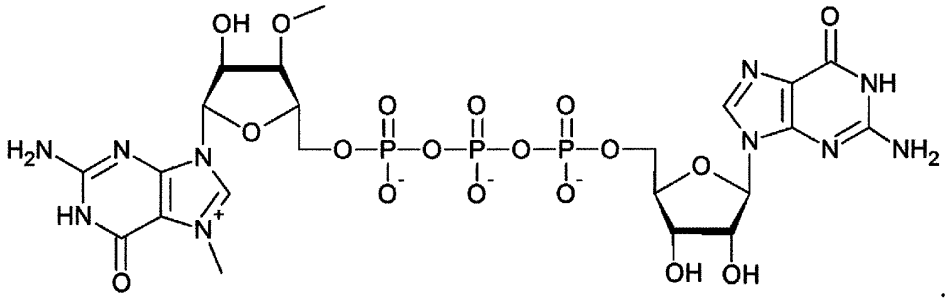
Below is an exemplary Cap1 RNA, which comprises RNA and $m_2^{7,3'-O}G(5')ppp(5')m^{2'-O}ApG$:



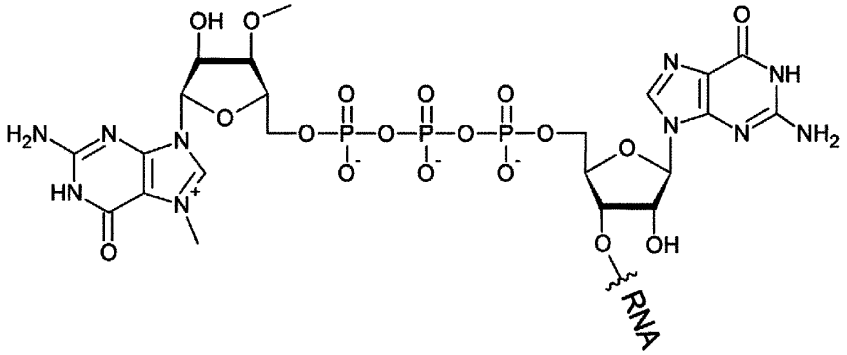
Below is another exemplary Cap1 RNA (no cap analog):



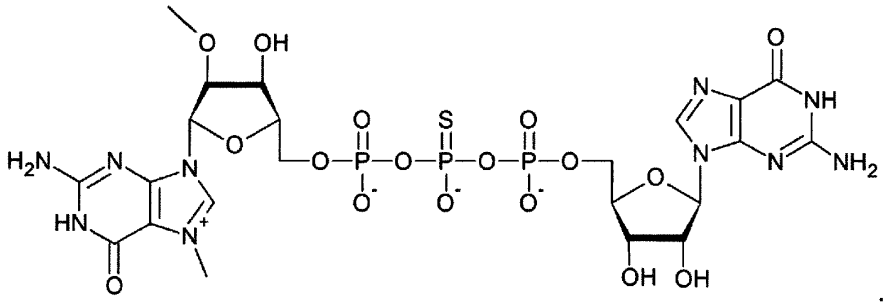
In some embodiments, the RNA is modified with "Cap0" structures using, in one embodiment, the cap analog anti-reverse cap (ARCA Cap ($m_2^{7,3'O}$G(5')ppp(5')G)) with the structure:



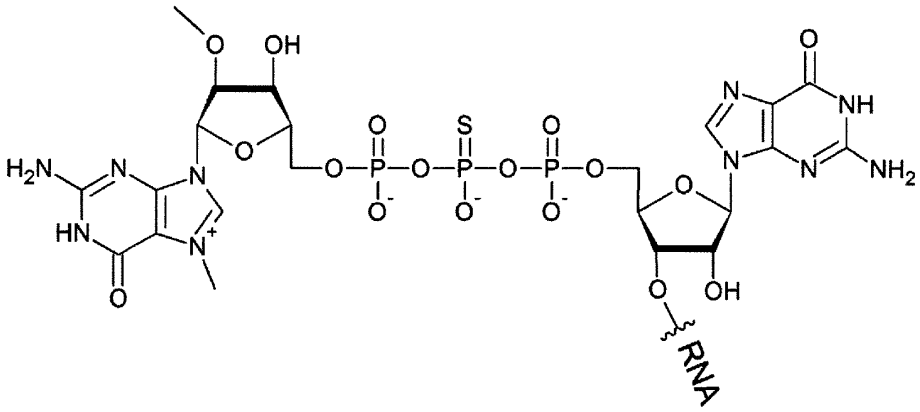
Below is an exemplary Cap0 RNA comprising RNA and $m_2^{7,3'O}$G(5')ppp(5')G:



In some embodiments, the "Cap0" structures are generated using the cap analog Beta-S-ARCA ($m_2^{7,2'O}$G(5')ppSp(5')G) with the structure:



Below is an exemplary Cap0 RNA comprising Beta-S-ARCA ($m_2^{7,2'O}$G(5')ppSp(5')G) and RNA:



The "D1" diastereomer of beta-S-ARCA or "beta-S-ARCA(D1)" is the diastereomer of beta-S-ARCA which elutes first on an HPLC column compared to the D2 diastereomer of beta-S-ARCA (beta-S-ARCA(D2)) and thus exhibits a shorter retention time (cf., WO 2011/015347, herein incorporated by reference).

A particularly preferred cap is beta-S-ARCA(D1) ($m_2^{7,2'-O}$GppSpG) or $m_2^{7,3'-O}$Gppp($m_1^{2'-O}$)ApG.

In some embodiments, RNA according to the present disclosure comprises a 5'-UTR and/or a 3'-UTR. The term "untranslated region" or "UTR" relates to a region in a DNA molecule which is transcribed but is not translated into an amino acid sequence, or to the corresponding region in an RNA molecule, such as an mRNA molecule. An untranslated region (UTR) can be present 5' (upstream) of an open reading frame (5'-UTR) and/or 3' (downstream) of an open

reading frame (3'-UTR). A 5'-UTR, if present, is located at the 5' end, upstream of the start codon of a protein-encoding region. A 5'-UTR is downstream of the 5'-cap (if present), e.g. directly adjacent to the 5'-cap. A 3'-UTR, if present, is located at the 3' end, downstream of the termination codon of a protein-encoding region, but the term "3'-UTR" does preferably not include the poly(A) sequence. Thus, the 3'-UTR is upstream of the poly(A) sequence (if present), e.g. directly adjacent to the poly(A) sequence.

In some embodiments, RNA comprises a 5'-UTR comprising the nucleotide sequence of SEQ ID NO: 12, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 12.

In some embodiments, RNA comprises a 3'-UTR comprising the nucleotide sequence of SEQ ID NO: 13, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 13.

A particularly preferred 5'-UTR comprises the nucleotide sequence of SEQ ID NO: 12. A particularly preferred 3'-UTR comprises the nucleotide sequence of SEQ ID NO: 13.

In some embodiments, the RNA according to the present disclosure comprises a 3'-poly(A) sequence.

As used herein, the term "poly(A) sequence" or "poly-A tail" refers to an uninterrupted or interrupted sequence of adenylate residues which is typically located at the 3'-end of an RNA molecule. Poly(A) sequences are known to those of skill in the art and may follow the 3'-UTR in the RNAs described herein. An uninterrupted poly(A) sequence is characterized by consecutive adenylate residues. In nature, an uninterrupted poly(A) sequence is typical. RNAs disclosed herein can have a poly(A) sequence attached to the free 3'-end of the RNA by a template-independent RNA polymerase after transcription or a poly(A) sequence encoded by DNA and transcribed by a template-dependent RNA polymerase.

It has been demonstrated that a poly(A) sequence of about 120 A nucleotides has a beneficial influence on the levels of RNA in transfected eukaryotic cells, as well as on the levels of protein

that is translated from an open reading frame that is present upstream (5') of the poly(A) sequence (*Holtkamp et al.*, 2006, Blood, vol. 108, pp. 4009-4017).

The poly(A) sequence may be of any length. In some embodiments, a poly(A) sequence comprises, essentially consists of, or consists of at least 20, at least 30, at least 40, at least 80, or at least 100 and up to 500, up to 400, up to 300, up to 200, or up to 150 A nucleotides, and, in particular, about 120 A nucleotides. In this context, "essentially consists of" means that most nucleotides in the poly(A) sequence, typically at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99% by number of nucleotides in the poly(A) sequence are A nucleotides, but permits that remaining nucleotides are nucleotides other than A nucleotides, such as U nucleotides (uridylate), G nucleotides (guanylate), or C nucleotides (cytidylate). In this context, "consists of" means that all nucleotides in the poly(A) sequence, i.e., 100% by number of nucleotides in the poly(A) sequence, are A nucleotides. The term "A nucleotide" or "A" refers to adenylate.

In some embodiments, a poly(A) sequence is attached during RNA transcription, e.g., during preparation of *in vitro* transcribed RNA, based on a DNA template comprising repeated dT nucleotides (deoxythymidylate) in the strand complementary to the coding strand. The DNA sequence encoding a poly(A) sequence (coding strand) is referred to as poly(A) cassette.

In some embodiments, the poly(A) cassette present in the coding strand of DNA essentially consists of dA nucleotides, but is interrupted by a random sequence of the four nucleotides (dA, dC, dG, and dT). Such random sequence may be 5 to 50, 10 to 30, or 10 to 20 nucleotides in length. Such a cassette is disclosed in WO 2016/005324 A1, hereby incorporated by reference. Any poly(A) cassette disclosed in WO 2016/005324 A1 may be used in the present invention. A poly(A) cassette that essentially consists of dA nucleotides, but is interrupted by a random sequence having an equal distribution of the four nucleotides (dA, dC, dG, dT) and having a length of e.g., 5 to 50 nucleotides shows, on DNA level, constant propagation of plasmid DNA in *E. coli* and is still associated, on RNA level, with the beneficial properties with respect to supporting RNA stability and translational efficiency is encompassed. Consequently,

in some embodiments, the poly(A) sequence contained in an RNA molecule described herein essentially consists of A nucleotides, but is interrupted by a random sequence of the four nucleotides (A, C, G, U). Such random sequence may be 5 to 50, 10 to 30, or 10 to 20 nucleotides in length.

In some embodiments, no nucleotides other than A nucleotides flank a poly(A) sequence at its 3'-end, i.e., the poly(A) sequence is not masked or followed at its 3'-end by a nucleotide other than A.

In some embodiments, the poly(A) sequence may comprise at least 20, at least 30, at least 40, at least 80, or at least 100 and up to 500, up to 400, up to 300, up to 200, or up to 150 nucleotides. In some embodiments, the poly(A) sequence may essentially consist of at least 20, at least 30, at least 40, at least 80, or at least 100 and up to 500, up to 400, up to 300, up to 200, or up to 150 nucleotides. In some embodiments, the poly(A) sequence may consist of at least 20, at least 30, at least 40, at least 80, or at least 100 and up to 500, up to 400, up to 300, up to 200, or up to 150 nucleotides. In some embodiments, the poly(A) sequence comprises at least 100 nucleotides. In some embodiments, the poly(A) sequence comprises about 150 nucleotides. In some embodiments, the poly(A) sequence comprises about 120 nucleotides.

In some embodiments, RNA comprises a poly(A) sequence comprising the nucleotide sequence of SEQ ID NO: 14, or a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 14.

A particularly preferred poly(A) sequence comprises comprises the nucleotide sequence of SEQ ID NO: 14.

According to the disclosure, vaccine antigen is preferably administered as single-stranded, 5'-capped mRNA that is translated into the respective protein upon entering cells of a subject being administered the RNA. Preferably, the RNA contains structural elements optimized for maximal efficacy of the RNA with respect to stability and translational efficiency (5'-cap, 5'-UTR, 3'-UTR, poly(A) sequence).

In one embodiment, beta-S-ARCA(D1) is utilized as specific capping structure at the 5'-end of the RNA. In one embodiment, $m_2^{7,3'-O}Gppp(m_1^{2'-O})ApG$ is utilized as specific capping structure at the 5'-end of the RNA. In one embodiment, the 5'-UTR sequence is derived from the human alpha-globin mRNA and optionally has an optimized 'Kozak sequence' to increase translational efficiency. In one embodiment, a combination of two sequence elements (FI element) derived from the "amino terminal enhancer of split" (AES) mRNA (called F) and the mitochondrial encoded 12S ribosomal RNA (called I) are placed between the coding sequence and the poly(A) sequence to assure higher maximum protein levels and prolonged persistence of the mRNA. In one embodiment, two re-iterated 3'-UTRs derived from the human beta-globin mRNA are placed between the coding sequence and the poly(A) sequence to assure higher maximum protein levels and prolonged persistence of the mRNA. In one embodiment, a poly(A) sequence measuring 110 nucleotides in length, consisting of a stretch of 30 adenosine residues, followed by a 10 nucleotide linker sequence and another 70 adenosine residues is used. This poly(A) sequence was designed to enhance RNA stability and translational efficiency.

In one embodiment of all aspects of the invention, RNA encoding a vaccine antigen is expressed in cells of the subject treated to provide the vaccine antigen. In one embodiment of all aspects of the invention, the RNA is transiently expressed in cells of the subject. In one embodiment of all aspects of the invention, the RNA is *in vitro* transcribed RNA. In one embodiment of all aspects of the invention, expression of the vaccine antigen is at the cell surface. In one embodiment of all aspects of the invention, the vaccine antigen is expressed and presented in the context of MHC. In one embodiment of all aspects of the invention, expression of the vaccine antigen is into the extracellular space, i.e., the vaccine antigen is secreted.

In the context of the present disclosure, the term "transcription" relates to a process, wherein the genetic code in a DNA sequence is transcribed into RNA. Subsequently, the RNA may be translated into peptide or protein.

According to the present invention, the term "transcription" comprises "*in vitro* transcription", wherein the term "*in vitro* transcription" relates to a process wherein RNA, in particular mRNA, is *in vitro* synthesized in a cell-free system, preferably using appropriate cell extracts. Preferably, cloning vectors are applied for the generation of transcripts. These cloning vectors are generally designated as transcription vectors and are according to the present invention encompassed by the term "vector". According to the present invention, the RNA used in the present invention preferably is *in vitro* transcribed RNA (IVT-RNA) and may be obtained by *in vitro* transcription of an appropriate DNA template. The promoter for controlling transcription can be any promoter for any RNA polymerase. Particular examples of RNA polymerases are the T7, T3, and SP6 RNA polymerases. Preferably, the *in vitro* transcription according to the invention is controlled by a T7 or SP6 promoter. A DNA template for *in vitro* transcription may be obtained by cloning of a nucleic acid, in particular cDNA, and introducing it into an appropriate vector for *in vitro* transcription. The cDNA may be obtained by reverse transcription of RNA.

With respect to RNA, the term "expression" or "translation" relates to the process in the ribosomes of a cell by which a strand of mRNA directs the assembly of a sequence of amino acids to make a peptide or protein.

In one embodiment, after administration of the RNA described herein, e.g., formulated as RNA lipid particles, at least a portion of the RNA is delivered to a target cell. In one embodiment, at least a portion of the RNA is delivered to the cytosol of the target cell. In one embodiment, the RNA is translated by the target cell to produce the peptide or protein it enodes. In one embodiment, the target cell is a spleen cell. In one embodiment, the target cell is an antigen presenting cell such as a professional antigen presenting cell in the spleen. In one embodiment, the target cell is a dendritic cell or macrophage. RNA particles such as RNA lipid particles described herein may be used for delivering RNA to such target cell. Accordingly, the present disclosure also relates to a method for delivering RNA to a target cell in a subject comprising the administration of the RNA particles described herein to the subject. In one

embodiment, the RNA is delivered to the cytosol of the target cell. In one embodiment, the RNA is translated by the target cell to produce the peptide or protein encoded by the RNA.

"Encoding" refers to the inherent property of specific sequences of nucleotides in a polynucleotide, such as a gene, a cDNA, or an mRNA, to serve as templates for synthesis of other polymers and macromolecules in biological processes having either a defined sequence of nucleotides (i.e., rRNA, tRNA and mRNA) or a defined sequence of amino acids and the biological properties resulting therefrom. Thus, a gene encodes a protein if transcription and translation of mRNA corresponding to that gene produces the protein in a cell or other biological system. Both the coding strand, the nucleotide sequence of which is identical to the mRNA sequence and is usually provided in sequence listings, and the non-coding strand, used as the template for transcription of a gene or cDNA, can be referred to as encoding the protein or other product of that gene or cDNA.

In one embodiment, the RNA encoding vaccine antigen to be administered according to the invention is non-immunogenic. RNA encoding immunostimulant may be administered according to the invention to provide an adjuvant effect. The RNA encoding immunostimulant may be standard RNA or non-immunogenic RNA.

The term "non-immunogenic RNA" as used herein refers to RNA that does not induce a response by the immune system upon administration, e.g., to a mammal, or induces a weaker response than would have been induced by the same RNA that differs only in that it has not been subjected to the modifications and treatments that render the non-immunogenic RNA non-immunogenic, i.e., than would have been induced by standard RNA (stdRNA). In one preferred embodiment, non-immunogenic RNA, which is also termed modified RNA (modRNA) herein, is rendered non-immunogenic by incorporating modified nucleosides suppressing RNA-mediated activation of innate immune receptors into the RNA and removing double-stranded RNA (dsRNA).

For rendering the non-immunogenic RNA non-immunogenic by the incorporation of modified nucleosides, any modified nucleoside may be used as long as it lowers or suppresses

immunogenicity of the RNA. Particularly preferred are modified nucleosides that suppress RNA-mediated activation of innate immune receptors. In one embodiment, the modified nucleosides comprises a replacement of one or more uridines with a nucleoside comprising a modified nucleobase. In one embodiment, the modified nucleobase is a modified uracil. In one embodiment, the nucleoside comprising a modified nucleobase is selected from the group consisting of 3-methyl-uridine (m^3U), 5-methoxy-uridine (mo^5U), 5-aza-uridine, 6-aza-uridine, 2-thio-5-aza-uridine, 2-thio-uridine (s^2U), 4-thio-uridine (s^4U), 4-thio-pseudouridine, 2-thio-pseudouridine, 5-hydroxy-uridine (ho^5U), 5-aminoallyl-uridine, 5-halo-uridine (e.g., 5-iodo-uridine or 5-bromo-uridine), uridine 5-oxyacetic acid (cmo^5U), uridine 5-oxyacetic acid methyl ester ($mcmo^5U$), 5-carboxymethyl-uridine (cm^5U), 1-carboxymethyl-pseudouridine, 5-carboxyhydroxymethyl-uridine (chm^5U), 5-carboxyhydroxymethyl-uridine methyl ester ($mchm^5U$), 5-methoxycarbonylmethyl-uridine (mcm^5U), 5-methoxycarbonylmethyl-2-thio-uridine (mcm^5s^2U), 5-aminomethyl-2-thio-uridine (nm^5s^2U), 5-methylaminomethyl-uridine (mnm^5U), 1-ethyl-pseudouridine, 5-methylaminomethyl-2-thio-uridine (mnm^5s^2U), 5-methylaminomethyl-2-seleno-uridine (mnm^5se^2U), 5-carbamoylmethyl-uridine (ncm^5U), 5-carboxymethylaminomethyl-uridine ($cmnm^5U$), 5-carboxymethylaminomethyl-2-thio-uridine ($cmnm^5s^2U$), 5-propynyl-uridine, 1-propynyl-pseudouridine, 5-taurinomethyl-uridine (τm^5U), 1-taurinomethyl-pseudouridine, 5-taurinomethyl-2-thio-uridine($\tau m5s2U$), 1-taurinomethyl-4-thio-pseudouridine), 5-methyl-2-thio-uridine (m^5s^2U), 1-methyl-4-thio-pseudouridine ($m^1s^4\psi$), 4-thio-1-methyl-pseudouridine, 3-methyl-pseudouridine ($m^3\psi$), 2-thio-1-methyl-pseudouridine, 1-methyl-1-deaza-pseudouridine, 2-thio-1-methyl-1-deaza-pseudouridine, dihydrouridine (D), dihydropseudouridine, 5,6-dihydrouridine, 5-methyl-dihydrouridine (m^5D), 2-thio-dihydrouridine, 2-thio-dihydropseudouridine, 2-methoxy-uridine, 2-methoxy-4-thio-uridine, 4-methoxy-pseudouridine, 4-methoxy-2-thio-pseudouridine, N1-methyl-pseudouridine, 3-(3-amino-3-carboxypropyl)uridine (acp^3U), 1-methyl-3-(3-amino-3-carboxypropyl)pseudouridine ($acp^3\ \psi$), 5-(isopentenylaminomethyl)uridine (inm^5U), 5-(isopentenylaminomethyl)-2-thio-uridine (inm^5s^2U), α-thio-uridine, 2'-O-methyl-uridine (Um),

5,2'-O-dimethyl-uridine (m^5Um), 2'-O-methyl-pseudouridine (ψm), 2-thio-2'-O-methyl-uridine (s^2Um), 5-methoxycarbonylmethyl-2'-O-methyl-uridine (mcm^5Um), 5-carbamoylmethyl-2'-O-methyl-uridine (ncm^5Um), 5-carboxymethylaminomethyl-2'-O-methyl-uridine ($cmnm^5Um$), 3,2'-O-dimethyl-uridine (m^3Um), 5-(isopentenylaminomethyl)-2'-O-methyl-uridine (inm^5Um), 1-thio-uridine, deoxythymidine, 2'-F-ara-uridine, 2'-F-uridine, 2'-OH-ara-uridine, 5-(2-carbomethoxyvinyl) uridine, and 5-[3-(1-E-propenylamino)uridine. In one particularly preferred embodiment, the nucleoside comprising a modified nucleobase is pseudouridine (ψ), N1-methyl-pseudouridine (m1ψ) or 5-methyl-uridine (m5U), in particular N1-methyl-pseudouridine.

In one embodiment, the replacement of one or more uridines with a nucleoside comprising a modified nucleobase comprises a replacement of at least 1%, at least 2%, at least 3%, at least 4%, at least 5%, at least 10%, at least 25%, at least 50%, at least 75%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% of the uridines.

During synthesis of mRNA by *in vitro* transcription (IVT) using T7 RNA polymerase significant amounts of aberrant products, including double-stranded RNA (dsRNA) are produced due to unconventional activity of the enzyme. dsRNA induces inflammatory cytokines and activates effector enzymes leading to protein synthesis inhibition. dsRNA can be removed from RNA such as IVT RNA, for example, by ion-pair reversed phase HPLC using a non-porous or porous C-18 polystyrene-divinylbenzene (PS-DVB) matrix. Alternatively, an enzymatic based method using E. coli RNaseIII that specifically hydrolyzes dsRNA but not ssRNA, thereby eliminating dsRNA contaminants from IVT RNA preparations can be used. Furthermore, dsRNA can be separated from ssRNA by using a cellulose material. In one embodiment, an RNA preparation is contacted with a cellulose material and the ssRNA is separated from the cellulose material under conditions which allow binding of dsRNA to the cellulose material and do not allow binding of ssRNA to the cellulose material.

As the term is used herein, "remove" or "removal" refers to the characteristic of a population of first substances, such as non-immunogenic RNA, being separated from the proximity of a

population of second substances, such as dsRNA, wherein the population of first substances is not necessarily devoid of the second substance, and the population of second substances is not necessarily devoid of the first substance. However, a population of first substances characterized by the removal of a population of second substances has a measurably lower content of second substances as compared to the non-separated mixture of first and second substances.

In one embodiment, the removal of dsRNA from non-immunogenic RNA comprises a removal of dsRNA such that less than 10%, less than 5%, less than 4%, less than 3%, less than 2%, less than 1%, less than 0.5%, less than 0.3%, or less than 0.1% of the RNA in the non-immunogenic RNA composition is dsRNA. In one embodiment, the non-immunogenic RNA is free or essentially free of dsRNA. In some embodiments, the non-immunogenic RNA composition comprises a purified preparation of single-stranded nucleoside modified RNA. For example, in some embodiments, the purified preparation of single-stranded nucleoside modified RNA is substantially free of double stranded RNA (dsRNA). In some embodiments, the purified preparation is at least 90%, at least 91%, at least 92%, at least 93 %, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, at least 99.5%, or at least 99.9% single stranded nucleoside modified RNA, relative to all other nucleic acid molecules (DNA, dsRNA, etc.).

In one embodiment, the non-immunogenic RNA is translated in a cell more efficiently than standard RNA with the same sequence. In one embodiment, translation is enhanced by a factor of 2-fold relative to its unmodified counterpart. In one embodiment, translation is enhanced by a 3-fold factor. In one embodiment, translation is enhanced by a 4-fold factor. In one embodiment, translation is enhanced by a 5-fold factor. In one embodiment, translation is enhanced by a 6-fold factor. In one embodiment, translation is enhanced by a 7-fold factor. In one embodiment, translation is enhanced by an 8-fold factor. In one embodiment, translation is enhanced by a 9-fold factor. In one embodiment, translation is enhanced by a 10-fold factor. In one embodiment, translation is enhanced by a 15-fold factor. In one

embodiment, translation is enhanced by a 20-fold factor. In one embodiment, translation is enhanced by a 50-fold factor. In one embodiment, translation is enhanced by a 100-fold factor. In one embodiment, translation is enhanced by a 200-fold factor. In one embodiment, translation is enhanced by a 500-fold factor. In one embodiment, translation is enhanced by a 1000-fold factor. In one embodiment, translation is enhanced by a 2000-fold factor. In one embodiment, the factor is 10-1000-fold. In one embodiment, the factor is 10-100-fold. In one embodiment, the factor is 10-200-fold. In one embodiment, the factor is 10-300-fold. In one embodiment, the factor is 10-500-fold. In one embodiment, the factor is 20-1000-fold. In one embodiment, the factor is 30-1000-fold. In one embodiment, the factor is 50-1000-fold. In one embodiment, the factor is 100-1000-fold. In one embodiment, the factor is 200-1000-fold. In one embodiment, translation is enhanced by any other significant amount or range of amounts.

In one embodiment, the non-immunogenic RNA exhibits significantly less innate immunogenicity than standard RNA with the same sequence. In one embodiment, the non-immunogenic RNA exhibits an innate immune response that is 2-fold less than its unmodified counterpart. In one embodiment, innate immunogenicity is reduced by a 3-fold factor. In one embodiment, innate immunogenicity is reduced by a 4-fold factor. In one embodiment, innate immunogenicity is reduced by a 5-fold factor. In one embodiment, innate immunogenicity is reduced by a 6-fold factor. In one embodiment, innate immunogenicity is reduced by a 7-fold factor. In one embodiment, innate immunogenicity is reduced by a 8-fold factor. In one embodiment, innate immunogenicity is reduced by a 9-fold factor. In one embodiment, innate immunogenicity is reduced by a 10-fold factor. In one embodiment, innate immunogenicity is reduced by a 15-fold factor. In one embodiment, innate immunogenicity is reduced by a 20-fold factor. In one embodiment, innate immunogenicity is reduced by a 50-fold factor. In one embodiment, innate immunogenicity is reduced by a 100-fold factor. In one embodiment, innate immunogenicity is reduced by a 200-fold factor. In one embodiment, innate immunogenicity is reduced by a 500-fold factor. In one embodiment, innate immunogenicity

is reduced by a 1000-fold factor. In one embodiment, innate immunogenicity is reduced by a 2000-fold factor.

The term "exhibits significantly less innate immunogenicity" refers to a detectable decrease in innate immunogenicity. In one embodiment, the term refers to a decrease such that an effective amount of the non-immunogenic RNA can be administered without triggering a detectable innate immune response. In one embodiment, the term refers to a decrease such that the non-immunogenic RNA can be repeatedly administered without eliciting an innate immune response sufficient to detectably reduce production of the protein encoded by the non-immunogenic RNA. In one embodiment, the decrease is such that the non-immunogenic RNA can be repeatedly administered without eliciting an innate immune response sufficient to eliminate detectable production of the protein encoded by the non-immunogenic RNA.

"Immunogenicity" is the ability of a foreign substance, such as RNA, to provoke an immune response in the body of a human or other animal. The innate immune system is the component of the immune system that is relatively unspecific and immediate. It is one of two main components of the vertebrate immune system, along with the adaptive immune system.

As used herein "endogenous" refers to any material from or produced inside an organism, cell, tissue or system.

As used herein, the term "exogenous" refers to any material introduced from or produced outside an organism, cell, tissue or system.

The term "expression" as used herein is defined as the transcription and/or translation of a particular nucleotide sequence.

As used herein, the terms "linked," "fused", or "fusion" are used interchangeably. These terms refer to the joining together of two or more elements or components or domains.

Codon-optimization / Increase in G/C content

In some embodiment, the amino acid sequence comprising a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof described herein is encoded by a coding sequence which is codon-optimized and/or the G/C content of which is increased compared to wild type coding sequence. This also includes embodiments, wherein one or more sequence regions of the coding sequence are codon-optimized and/or increased in the G/C content compared to the corresponding sequence regions of the wild type coding sequence. In one embodiment, the codon-optimization and/or the increase in the G/C content preferably does not change the sequence of the encoded amino acid sequence.

The term "codon-optimized" refers to the alteration of codons in the coding region of a nucleic acid molecule to reflect the typical codon usage of a host organism without preferably altering the amino acid sequence encoded by the nucleic acid molecule. Within the context of the present invention, coding regions are preferably codon-optimized for optimal expression in a subject to be treated using the RNA molecules described herein. Codon-optimization is based on the finding that the translation efficiency is also determined by a different frequency in the occurrence of tRNAs in cells. Thus, the sequence of RNA may be modified such that codons for which frequently occurring tRNAs are available are inserted in place of "rare codons".

In some embodiments of the invention, the guanosine/cytosine (G/C) content of the coding region of the RNA described herein is increased compared to the G/C content of the corresponding coding sequence of the wild type RNA, wherein the amino acid sequence encoded by the RNA is preferably not modified compared to the amino acid sequence encoded by the wild type RNA. This modification of the RNA sequence is based on the fact that the sequence of any RNA region to be translated is important for efficient translation of that mRNA. Sequences having an increased G (guanosine)/C (cytosine) content are more stable than sequences having an increased A (adenosine)/U (uracil) content. In respect to the fact that several codons code for one and the same amino acid (so-called degeneration of the genetic code), the most favourable codons for the stability can be determined (so-called

alternative codon usage). Depending on the amino acid to be encoded by the RNA, there are various possibilities for modification of the RNA sequence, compared to its wild type sequence. In particular, codons which contain A and/or U nucleotides can be modified by substituting these codons by other codons, which code for the same amino acids but contain no A and/or U or contain a lower content of A and/or U nucleotides.

In various embodiments, the G/C content of the coding region of the RNA described herein is increased by at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 55%, or even more compared to the G/C content of the coding region of the wild type RNA.

Embodiments of administered RNAs

In some embodiments, compositions or medical preparations described herein comprise RNA encoding an amino acid sequence comprising SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof. Likewise, methods described herein comprise administration of such RNA.

The active platform for use herein is based on an antigen-coding RNA vaccine to induce robust neutralising antibodies and accompanying/concomitant T cell response to achieve protective immunization with preferably minimal vaccine doses. The RNA administered is preferably *in-vitro* transcribed RNA.

Three different RNA platforms are particularly preferred, namely non-modified uridine containing mRNA (uRNA), nucleoside modified mRNA (modRNA) and self-amplifying RNA (saRNA). In one particularly preferred embodiment, the RNA is in vitro transcribed RNA.

As described herein, embodiments of each of these platforms are assessed herein (see, for example Example 2), representing a novel and powerful approach to and system for rapid vaccine development. This described approach and system achieved remarkable and efficient success, enabling development of an effective clinical candidate within several months of provision of antigen (e.g., SARS-CoV-2 S1 protein and/or RBD thereof) sequence (as described herein, relevant sequence information (e.g., GenBank: MN908947.3) became available in Jan

2020). Insights and advantages embodied in this described approach and system include, for example, ability to directly compare one or more features of different strategies to achieve rapid, efficient, and effective development. Among other things, the present disclosure encompasses insights that identify the source of a problem with more typical strategies for vaccine development. Moreover, findings included herein establish a variety of advantages and benefits, particularly in rapid vaccine development and notably of special benefit in a pandemic.

As described herein, in some embodiments, vaccine candidates are assessed for titer of antibodies induced in a model organism (e.g., mouse; see e.g., Example 2) directed to an encoded antigen (e.g., S1 protein) or portion thereof (e.g., RBD). In some embodiments, vaccine candidates are assessed for pseudoviral neutralization (see e.g., Example 2) activity of induced antibodies. In some embodiments, vaccine candidates are characterized for nature of T cell response induced (e.g., T_H1 vs T_H2 character; see, e.g., Example 4). In some embodiments, vaccine candidates are assessed in more than one model organism (see. E.g., Examples 2, Example 4, etc)

In the following, embodiments of these three different RNA platforms are described, wherein certain terms used when describing elements thereof have the following meanings:

S1S2 protein/S1S2 RBD: Sequences encoding the respective antigen of SARS-CoV-2.

nsP1, nsP2, nsP3, and nsP4: Wildtype sequences encoding the Venezuelan equine encephalitis virus (VEEV) RNA-dependent RNA polymerase replicase and a subgenomic promotor plus conserved sequence elements supporting replication and translation.

virUTR: Viral untranslated region encoding parts of the subgenomic promotor as well as replication and translation supporting sequence elements.

hAg-Kozak: 5'-UTR sequence of the human alpha-globin mRNA with an optimized 'Kozak sequence' to increase translational efficiency.

Sec: Sec corresponds to the intrinsic S1S2 protein secretory signal peptide (sec), which guides translocation of the nascent polypeptide chain into the endoplasmatic reticulum.

Glycine-serine linker (GS): Sequences coding for short linker peptides predominantly consisting of the amino acids glycine (G) and serine (S), as commonly used for fusion proteins.

Fibritin: Partial sequence of T4 fibritin (foldon), used as artificial trimerization domain.

TM: TM sequence corresponds to the transmembrane part of the S1S2 protein.

FI element: The 3'-UTR is a combination of two sequence elements derived from the "amino terminal enhancer of split" (AES) mRNA (called F) and the mitochondrial encoded 12S ribosomal RNA (called I). These were identified by an *ex vivo* selection process for sequences that confer RNA stability and augment total protein expression.

A30L70: A poly(A)-tail measuring 110 nucleotides in length, consisting of a stretch of 30 adenosine residues, followed by a 10 nucleotide linker sequence and another 70 adenosine residues designed to enhance RNA stability and translational efficiency in dendritic cells.

In general, vaccine RNA described herein may comprise, from 5' to 3', one of the following structures:

Cap-5'-UTR-Vaccine Antigen-Encoding Sequence-3'-UTR-Poly(A)

or

beta-S-ARCA(D1)-hAg-Kozak-Vaccine Antigen-Encoding Sequence-FI-A30L70.

In general, a vaccine antigen described herein may comprise, from N-terminus to C-terminus, one of the following structures:

Signal Sequence-RBD-Trimerization Domain

or

Signal Sequence-RBD-Trimerization Domain-Transmembrane Domain.

RBD and Trimerization Domain may be separated by a linker, in particular a GS linker such as a linker having the amino acid sequence GSPGSGSGS. Trimerization Domain and Transmembrane Domain may be separated by a linker, in particular a GS linker such as a linker having the amino acid sequence GSGSGS.

Signal Sequence may be a signal sequence as described herein. RBD may be a RBD domain as described herein. Trimerization Domain may be a trimerization domain as described herein. Transmembrane Domain may be a transmembrane domain as described herein.

In one embodiment,

Signal sequence comprises the amino acid sequence of amino acids 1 to 16 or 1 to 19 of SEQ ID NO: 1 or the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to this amino acid sequence,

RBD comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to this amino acid sequence,

Trimerization Domain comprises the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to this amino acid sequence; and

Transmembrane Domain comprises the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to this amino acid sequence.

In one embodiment,

Signal sequence comprises the amino acid sequence of amino acids 1 to 16 or 1 to 19 of SEQ ID NO: 1 or the amino acid sequence of amino acids 1 to 22 of SEQ ID NO: 31,

RBD comprises the amino acid sequence of amino acids 327 to 528 of SEQ ID NO: 1,

Trimerization Domain comprises the amino acid sequence of amino acids 3 to 29 of SEQ ID NO: 10 or the amino acid sequence of SEQ ID NO: 10; and

Transmembrane Domain comprises the amino acid sequence of amino acids 1207 to 1254 of SEQ ID NO: 1.

The above described RNA or RNA encoding the above described vaccine antigen may be non-modified uridine containing mRNA (uRNA), nucleoside modified mRNA (modRNA) or self-amplifying RNA (saRNA). In one embodiment, the above described RNA or RNA encoding the above described vaccine antigen is nucleoside modified mRNA (modRNA).

Non-modified uridine messenger RNA (uRNA)

The active principle of the non-modified messenger RNA (uRNA) drug substance is a single-stranded mRNA that is translated upon entering a cell. In addition to the sequence encoding the coronavirus vaccine antigen (i.e. open reading frame), each uRNA preferably contains common structural elements optimized for maximal efficacy of the RNA with respect to stability and translational efficiency (5'-cap, 5'-UTR, 3'-UTR, poly(A)-tail). The preferred 5' cap structure is beta-S-ARCA(D1) ($m_2^{7,2'-O}$GppSpG). The preferred 5'-UTR and 3'-UTR comprise the nucleotide sequence of SEQ ID NO: 12 and the nucleotide sequence of SEQ ID NO: 13, respectively. The preferred poly(A)-tail comprises the sequence of SEQ ID NO: 14.

Different embodiment of this platform are as follows:

RBL063.1 (SEQ ID NO: 15; SEQ ID NO: 7)

Structure	beta-S-ARCA(D1)-hAg-Kozak-S1S2-PP-FI-A30L70
Encoded antigen	Viral spike protein (S1S2 protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

RBL063.2 (SEQ ID NO: 16; SEQ ID NO: 7)

Structure	beta-S-ARCA(D1)-hAg-Kozak-S1S2-PP-FI-A30L70
Encoded antigen	Viral spike protein (S1S2 protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

BNT162a1; RBL063.3 (SEQ ID NO: 17; SEQ ID NO: 5)

Structure	beta-S-ARCA(D1)-hAg-Kozak-RBD-GS-Fibritin-FI-A30L70
Encoded antigen	Viral spike protein (S protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein)

Figure 19 schematizes the general structure of the antigen-encoding RNAs.

Nucleotide Sequence of RBL063.1

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
         10         20         30         40         50  52
GGGCGAACUA GUAUUCUUCU GGUCCCCACA GACUCAGAGA GAACCCGCCA CC
```

hAg-Kozak

```
        62         72         82         92        102        112
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGAA UUUGACAACA
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   N  L  T  T
```

S protein

```
       122        132        142        152        162        172
AGAACACAGC UGCCACCAGC UUAUACAAAU UCUUUUACCA GAGGAGUGUA UUAUCCUGAU
  R  T  Q   L  P  P   A  Y  T  N   S  F  T   R  G  V   Y  Y  P  D
```

S protein

```
       182        192        202        212        222        232
AAAGUGUUUA GAUCUUCUGU GCUGCACAGC ACACAGGACC UGUUUCUGCC AUUUUUUAGC
  K  V  F   R  S  S   V  L  H  S   T  Q  D   L  F  L   P  F  F  S
```

S protein

```
       242        252        262        272        282        292
AAUGUGACAU GGUUUCAUGC AAUUCAUGUG UCUGGAACAA AUGGAACAAA AAGAUUUGAU
  N  V  T   W  F  H   A  I  H  V   S  G  T   N  G  T   K  R  F  D
```

S protein

```
       302        312        322        332        342        352
AAUCCUGUGC UGCCUUUUAA UGAUGGAGUG UAUUUUGCUU CAACAGAAAA GUCAAAUAUU
  N  P  V   L  P  F   N  D  G  V   Y  F  A   S  T  E   K  S  N  I
```

S protein

```
       362        372        382        392        402        412
AUUAGAGGAU GGAUUUUUGG AACAACACUG GAUUCUAAAA CACAGUCUCU GCUGAUUGUG
  I  R  G   W  I  F   G  T  T  L   D  S  K   T  Q  S   L  L  I  V
```

S protein

```
       422        432        442        452        462        472
AAUAAUGCAA CAAAUGUGGU GAUUAAAGUG UGUGAAUUUC AGUUUUGUAA UGAUCCUUUU
```

N N A T N V V I K V C E F Q F C N D P F

S protein

482 492 502 512 522 532

CUGGGAGUGU AUUAUCACAA AAAUAAUAAA UCUUGGAUGG AAUCUGAAUU UAGAGUGUAU

L G V Y Y H K N N K S W M E S E F R V Y

S protein

542 552 562 572 582 592

UCCUCUGCAA AUAAUUGUAC AUUUGAAUAU GUGUCUCAGC CUUUUCUGAU GGAUCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

602 612 622 632 642 652

GGAAAACAGG GCAAUUUUAA AAAUCUGAGA GAAUUUGUGU UUAAAAAUAU UGAUGGAUAU

G K Q G N F K N L R E F V F K N I D G Y

S protein

662 672 682 692 702 712

UUUAAAAUUU AUUCUAAACA CACACCAAUU AAUUUAGUGA GAGAUCUGCC UCAGGGAUUU

F K I Y S K H T P I N L V R D L P Q G F

S protein

722 732 742 752 762 772

UCUGCUCUGG AACCUCUGGU GGAUCUGCCA AUUGGCAUUA AUAUUACAAG AUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

782 792 802 812 822 832

CUGCUGGCUC UGCACAGAUC UUAUCUGACA CCUGGAGAUU CUUCUUCUGG AUGGACAGCC

L L A L H R S Y L T P G D S S S G W T A

S protein

842 852 862 872 882 892

GGAGCUGCAG CUUAUUAUGU GGGCUAUCUG CAGCCAAGAA CAUUUCUGCU GAAAUAUAAU

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

902 912 922 932 942 952

GAAAAUGGAA CAAUUACAGA UGCUGUGGAU UGUGCUCUGG AUCCUCUGUC UGAAACAAAA

E N G T I T D A V D C A L D P L S E T K

S protein

962 972 982 992 1002 1012

UGUACAUUAA AAUCUUUUAC AGUGGAAAAA GGCAUUUAUC AGACAUCUAA UUUUAGAGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

1022 1032 1042 1052 1062 1072

CAGCCAACAG AAUCUAUUGU GAGAUUUCCA AAUAUUACAA AUCUGUGUCC AUUUGGAGAA

Q P T E S I V R F P N I T N L C P F G E

S protein

1082 1092 1102 1112 1122 1132

GUGUUUAAUG CAACAAGAUU UGCAUCUGUG UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU

V F N A T R F A S V Y A W N R K R I S N

S protein

1142 1152 1162 1172 1182 1192

UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU AGUGCUUCUU UUUCCACAUU UAAAUGUUAU

C V A D Y S V L Y N S A S F S T F K C Y

S protein

1202 1212 1222 1232 1242 1252

GGAGUGUCUC CAACAAAAUU AAAUGAUUUA UGUUUUACAA AUGUGUAUGC UGAUUCUUUU

G V S P T K L N D L C F T N V Y A D S F

S protein

1262 1272 1282 1292 1302 1312

GUGAUCAGAG GUGAUGAAGU GAGACAGAUU GCCCCCGGAC AGACAGGAAA AAUUGCUGAU

V I R G D E V R Q I A P G Q T G K I A D

S protein

1322 1332 1342 1352 1362 1372

UACAAUUACA AACUGCCUGA UGAUUUUACA GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU

Y N Y K L P D D F T G C V I A W N S N N

S protein

1382 1392 1402 1412 1422 1432

UUAGAUUCUA AAGUGGGAGG AAAUUACAAU UAUCUGUACA GACUGUUUAG AAAAUCAAAU

L D S K V G G N Y N Y L Y R L F R K S N

S protein

1442 1452 1462 1472 1482 1492

CUGAAACCUU UUGAAAGAGA UAUUUCAACA GAAAUUUAUC AGGCUGGAUC AACACCUUGU

L K P F E R D I S T E I Y Q A G S T P C

S protein

1502 1512 1522 1532 1542 1552

AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU CCAUUACAGA GCUAUGGAUU UCAGCCAACC

N G V E G F N C Y F P L Q S Y G F Q P T

S protein

1562 1572 1582 1592 1602 1612

AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG GUGGUGCUGU CUUUUGAACU GCUGCAUGCA

N G V G Y Q P Y R V V V L S F E L L H A

S protein

1622 1632 1642 1652 1662 1672

CCUGCAACAG UGUGUGGACC UAAAAAAUCU ACAAAUUUAG UGAAAAAUAA AUGUGUGAAU

P A T V C G P K K S T N L V K N K C V N

S protein

1682 1692 1702 1712 1722 1732

UUUAAUUUUA AUGGAUUAAC AGGAACAGGA GUGCUGACAG AAUCUAAUAA AAAAUUUCUG

F N F N G L T G T G V L T E S N K K F L

S protein

1742 1752 1762 1772 1782 1792

CCUUUUCAGC AGUUUGGCAG AGAUAUUGCA GAUACCACAG AUGCAGUGAG AGAUCCUCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

1802 1812 1822 1832 1842 1852

ACAUUAGAAA UUCUGGAUAU UACACCUUGU UCUUUUGGGG GUGUGUCUGU GAUUACACCU

T L E I L D I T P C S F G G V S V I T P

S protein

1862 1872 1882 1892 1902 1912

GGAACAAAUA CAUCUAAUCA GGUGGCUGUG CUGUAUCAGG AUGUGAAUUG UACAGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

1922 1932 1942 1952 1962 1972

CCAGUGGCAA UUCAUGCAGA UCAGCUGACA CCAACAUGGA GAGUGUAUUC UACAGGAUCU

P V A I H A D Q L T P T W R V Y S T G S

S protein

1982 1992 2002 2012 2022 2032

AAUGUGUUUC AGACAAGAGC AGGAUGUCUG AUUGGAGCAG AACAUGUGAA UAAUUCUUAU

N V F Q T R A G C L I G A E H V N N S Y

S protein

2042 2052 2062 2072 2082 2092

GAAUGUGAUA UUCCAAUUGG AGCAGGCAUU UGUGCAUCUU AUCAGACACA GACAAAUUCC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

2102 2112 2122 2132 2142 2152

CCAAGGAGAG CAAGAUCUGU GGCAUCUCAG UCUAUUAUUG CAUACACCAU GUCUCUGGGA

P R R A R S V A S Q S I I A Y T M S L G

S protein

2162 2172 2182 2192 2202 2212

GCAGAAAAUU CUGUGGCAUA UUCUAAUAAU UCUAUUGCUA UUCCAACAAA UUUUACCAUU

A E N S V A Y S N N S I A I P T N F T I

S protein

2222 2232 2242 2252 2262 2272

UCUGUGACAA CAGAAAUUUU ACCUGUGUCU AUGACAAAAA CAUCUGUGGA UUGUACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

2282 2292 2302 2312 2322 2332

UACAUUUGUG GAGAUUCUAC AGAAUGUUCU AAUCUGCUGC UGCAGUAUGG AUCUUUUUGU

Y I C G D S T E C S N L L L Q Y G S F C

S protein

2342 2352 2362 2372 2382 2392

ACACAGCUGA AUAGAGCUUU AACAGGAAUU GCUGUGGAAC AGGAUAAAAA UACACAGGAA

T Q L N R A L T G I A V E Q D K N T Q E

S protein

2402 2412 2422 2432 2442 2452

GUGUUUGCUC AGGUGAAACA GAUUUACAAA ACACCACCAA UUAAAGAUUU UGGAGGAUUU

V F A Q V K Q I Y K T P P I K D F G G F

S protein

2462 2472 2482 2492 2502 2512

AAUUUUAGCC AGAUUCUGCC UGAUCCUUCU AAACCUUCUA AAAGAUCUUU UAUUGAAGAU

N F S Q I L P D P S K P S K R S F I E D

S protein

2522 2532 2542 2552 2562 2572

CUGCUGUUUA AUAAAGUGAC ACUGGCAGAU GCAGGAUUUA UUAAACAGUA UGGAGAUUGC

L L F N K V T L A D A G F I K Q Y G D C

S protein

2582 2592 2602 2612 2622 2632

CUGGGUGAUA UUGCUGCAAG AGAUCUGAUU UGUGCUCAGA AAUUUAAUGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

2642 2652 2662 2672 2682 2692

CUGCCUCCUC UGCUGACAGA UGAAAUGAUU GCUCAGUACA CAUCUGCUUU ACUGGCUGGA

L P P L L T D E M I A Q Y T S A L L A G

S protein

2702 2712 2722 2732 2742 2752

ACAAUUACAA GCGGAUGGAC AUUUGGAGCU GGAGCUGCUC UGCAGAUUCC UUUUGCAAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

2762 2772 2782 2792 2802 2812

CAGAUGGCUU ACAGAUUUAA UGGAAUUGGA GUGACACAGA AUGUGUUAUA UGAAAAUCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

2822 2832 2842 2852 2862 2872

AAACUGAUUG CAAAUCAGUU UAAUUCUGCA AUUGGCAAAA UUCAGGAUUC UCUGUCUUCU

K L I A N Q F N S A I G K I Q D S L S S

S protein

2882 2892 2902 2912 2922 2932

ACAGCUUCUG CUCUGGGAAA ACUGCAGGAU GUGGUGAAUC AGAAUGCACA GGCACUGAAU

T A S A L G K L Q D V V N Q N A Q A L N

S protein

2942 2952 2962 2972 2982 2992

ACUCUGGUGA AACAGCUGUC UAGCAAUUUU GGGGCAAUUU CUUCUGUGCU GAAUGAUAUU

T L V K Q L S S N F G A I S S V L N D I

S protein

3002 3012 3022 3032 3042 3052

CUGUCUAGAC UGGAUCCUCC UGAAGCUGAA GUGCAGAUUG AUAGACUGAU CACAGGAAGA

L S R L D P P E A E V Q I D R L I T G R

S protein

3062 3072 3082 3092 3102 3112

CUGCAGUCUC UGCAGACUUA UGUGACACAG CAGCUGAUUA GAGCUGCUGA AAUUAGAGCU

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

3122 3132 3142 3152 3162 3172

UCUGCUAAUC UGGCUGCUAC AAAAAUGUCU GAAUGUGUGC UGGGACAGUC AAAAAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

3182 3192 3202 3212 3222 3232

GAUUUUUGUG GAAAAGGAUA UCAUCUGAUG UCUUUUCCAC AGUCUGCUCC ACAUGGAGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

3242 3252 3262 3272 3282 3292

GUGUUUUUAC AUGUGACAUA UGUGCCAGCA CAGGAAAAGA AUUUUACCAC AGCACCAGCA

V F L H V T Y V P A Q E K N F T T A P A

S protein

3302 3312 3322 3332 3342 3352

AUUUGUCAUG AUGGAAAAGC ACAUUUUCCA AGAGAAGGAG UGUUUGUGUC UAAUGGAACA

I C H D G K A H F P R E G V F V S N G T

S protein

3362 3372 3382 3392 3402 3412

CAUUGGUUUG UGACACAGAG AAAUUUUUAU GAACCUCAGA UUAUUACAAC AGAUAAUACA

H W F V T Q R N F Y E P Q I I T T D N T

S protein

3422 3432 3442 3452 3462 3472

UUUGUGUCAG GAAAUUGUGA UGUGGUGAUU GGAAUUGUGA AUAAUACAGU GUAUGAUCCA

F V S G N C D V V I G I V N N T V Y D P

S protein

3482 3492 3502 3512 3522 3532

CUGCAGCCAG AACUGGAUUC UUUUAAAGAA GAACUGGAUA AAUAUUUUAA AAAUCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

```
      3542        3552        3562        3572        3582        3592
UCUCCUGAUG UGGAUUUAGG AGAUAUUUCU GGAAUCAAUG CAUCUGUGGU GAAUAUUCAG
  S  P  D   V  D  L   G  D  I  S   G  I  N   A  S  V   V  N  I  Q
```

S protein

```
      3602        3612        3622        3632        3642        3652
AAAGAAAUUG AUAGACUGAA UGAAGUGGCC AAAAAUCUGA AUGAAUCUCU GAUUGAUCUG
  K  E  I   D  R  L   N  E  V  A   K  N  L   N  E  S   L  I  D  L
```

S protein

```
      3662        3672        3682        3692        3702        3712
CAGGAACUUG GAAAAUAUGA ACAGUACAUU AAAUGGCCUU GGUACAUUUG GCUUGGAUUU
  Q  E  L   G  K  Y   E  Q  Y  I   K  W  P   W  Y  I   W  L  G  F
```

S protein

```
      3722        3732        3742        3752        3762        3772
AUUGCAGGAU UAAUUGCAAU UGUGAUGGUG ACAAUUAUGU UAUGUUGUAU GACAUCAUGU
  I  A  G   L  I  A   I  V  M  V   T  I  M   L  C  C   M  T  S  C
```

S protein

```
      3782        3792        3802        3812        3822        3832
UGUUCUUGUU UAAAAGGAUG UUGUUCUUGU GGAAGCUGUU GUAAAUUUGA UGAAGAUGAU
  C  S  C   L  K  G   C  C  S  C   G  S  C   C  K  F   D  E  D  D
```

S protein

```
      3842        3852        3862        3872   3877
UCUGAACCUG UGUUAAAAGG AGUGAAAUUG CAUUACACAU GAUGA
  S  E  P   V  L  K   G  V  K  L   H  Y  T   *  *
```

S protein

```
      3887        3897        3907        3917        3927        3937
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
      3947        3957        3967        3977        3987        3997
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
      4007        4017        4027        4037        4047        4057
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

4067 4077 4087 4097 4107 4117

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

4127 4137 4147 4157 4167 4172

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC

FI element

4182 4192 4202 4212 4222 4232

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

4242 4252 4262 4272 4282

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Nucleotide Sequence of RBL063.2

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
        10          20          30          40          50  52
GGGCGAACUA GUAUUCUUCU GGUCCCCACA GACUCAGAGA GAACCCGCCA CC
```

hAg-Kozak

```
        62          72          82          92         102         112
AUGUUCGUGU UCCUGGUGCU GCUGCCUCUG GUGUCCAGCC AGUGUGUGAA CCUGACCACC
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   N  L  T  T
```

S protein

```
       122         132         142         152         162         172
AGAACACAGC UGCCUCCAGC CUACACCAAC AGCUUUACCA GAGGCGUGUA CUACCCCGAC
  R  T  Q   L  P  P   A  Y  T  N   S  F  T   R  G  V   Y  Y  P  D
```

S protein

```
       182         192         202         212         222         232
AAGGUGUUCA GAUCCAGCGU GCUGCACUCU ACCCAGGACC UGUUCCUGCC UUUCUUCAGC
  K  V  F   R  S  S   V  L  H  S   T  Q  D   L  F  L   P  F  F  S
```

S protein

```
       242         252         262         272         282         292
AACGUGACCU GGUUCCACGC CAUCCACGUG UCCGGCACCA AUGGCACCAA GAGAUUCGAC
  N  V  T   W  F  H   A  I  H  V   S  G  T   N  G  T   K  R  F  D
```

S protein

```
       302         312         322         332         342         352
AACCCCGUGC UGCCCUUCAA CGACGGGGUG UACUUUGCCA GCACCGAGAA GUCCAACAUC
  N  P  V   L  P  F   N  D  G  V   Y  F  A   S  T  E   K  S  N  I
```

S protein

```
       362         372         382         392         402         412
AUCAGAGGCU GGAUCUUCGG CACCACACUG GACAGCAAGA CCCAGAGCCU GCUGAUCGUG
  I  R  G   W  I  F   G  T  T  L   D  S  K   T  Q  S   L  L  I  V
```

S protein

```
       422         432         442         452         462         472
AACAACGCCA CCAACGUGGU CAUCAAAGUG UGCGAGUUCC AGUUCUGCAA CGACCCCUUC
```

N N A T N V V I K V C E F Q F C N D P F

S protein

482 492 502 512 522 532

CUGGGCGUCU ACUACCACAA GAACAACAAG AGCUGGAUGG AAAGCGAGUU CCGGGUGUAC

L G V Y Y H K N N K S W M E S E F R V Y

S protein

542 552 562 572 582 592

AGCAGCGCCA ACAACUGCAC CUUCGAGUAC GUGUCCCAGC CUUUCCUGAU GGACCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

602 612 622 632 642 652

GGCAAGCAGG GCAACUUCAA GAACCUGCGC GAGUUCGUGU UUAAGAACAU CGACGGCUAC

G K Q G N F K N L R E F V F K N I D G Y

S protein

662 672 682 692 702 712

UUCAAGAUCU ACAGCAAGCA CACCCCUAUC AACCUCGUGC GGGAUCUGCC UCAGGGCUUC

F K I Y S K H T P I N L V R D L P Q G F

S protein

722 732 742 752 762 772

UCUGCUCUGG AACCCCUGGU GGAUCUGCCC AUCGGCAUCA ACAUCACCCG GUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

782 792 802 812 822 832

CUGCUGGCCC UGCACAGAAG CUACCUGACA CCUGGCGAUA GCAGCAGCGG AUGGACAGCU

L L A L H R S Y L T P G D S S S G W T A

S protein

842 852 862 872 882 892

GGUGCCGCCG CUUACUAUGU GGGCUACCUG CAGCCUAGAA CCUUCCUGCU GAAGUACAAC

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

902 912 922 932 942 952

GAGAACGGCA CCAUCACCGA CGCCGUGGAU UGUGCUCUGG AUCCUCUGAG CGAGACAAAG

E N G T I T D A V D C A L D P L S E T K

S protein

962 972 982 992 1002 1012

UGCACCCUGA AGUCCUUCAC CGUGGAAAAG GGCAUCUACC AGACCAGCAA CUUCCGGGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

1022 1032 1042 1052 1062 1072

CAGCCCACCG AAUCCAUCGU GCGGUUCCCC AAUAUCACCA AUCUGUGCCC CUUCGGCGAG

Q P T E S I V R F P N I T N L C P F G E

S protein

1082 1092 1102 1112 1122 1132

GUGUUCAAUG CCACCAGAUU CGCCUCUGUG UACGCCUGGA ACCGGAAGCG GAUCAGCAAU

V F N A T R F A S V Y A W N R K R I S N

S protein

1142 1152 1162 1172 1182 1192

UGCGUGGCCG ACUACUCCGU GCUGUACAAC UCCGCCAGCU UCAGCACCUU CAAGUGCUAC

C V A D Y S V L Y N S A S F S T F K C Y

S protein

1202 1212 1222 1232 1242 1252

GGCGUGUCCC CUACCAAGCU GAACGACCUG UGCUUCACAA ACGUGUACGC CGACAGCUUC

G V S P T K L N D L C F T N V Y A D S F

S protein

1262 1272 1282 1292 1302 1312

GUGAUCCGGG GAGAUGAAGU GCGGCAGAUU GCCCCUGGAC AGACAGGCAA GAUCGCCGAC

V I R G D E V R Q I A P G Q T G K I A D

S protein

1322 1332 1342 1352 1362 1372

UACAACUACA AGCUGCCCGA CGACUUCACC GGCUGUGUGA UUGCCUGGAA CAGCAACAAC

Y N Y K L P D D F T G C V I A W N S N N

S protein

1382 1392 1402 1412 1422 1432

CUGGACUCCA AAGUCGGCGG CAACUACAAU UACCUGUACC GGCUGUUCCG GAAGUCCAAU

L D S K V G G N Y N Y L Y R L F R K S N

S protein

1442 1452 1462 1472 1482 1492

CUGAAGCCCU UCGAGCGGGA CAUCUCCACC GAGAUCUAUC AGGCCGGCAG CACCCCUUGU

L K P F E R D I S T E I Y Q A G S T P C

S protein

1502 1512 1522 1532 1542 1552

AACGGCGUGG AAGGCUUCAA CUGCUACUUC CCACUGCAGU CCUACGGCUU UCAGCCCACA

N G V E G F N C Y F P L Q S Y G F Q P T

S protein

1562 1572 1582 1592 1602 1612

AAUGGCGUGG GCUAUCAGCC CUACAGAGUG GUGGUGCUGA GCUUCGAACU GCUGCAUGCC

N G V G Y Q P Y R V V V L S F E L L H A

S protein

1622 1632 1642 1652 1662 1672

CCUGCCACAG UGUGCGGCCC UAAGAAAAGC ACCAAUCUCG UGAAGAACAA AUGCGUGAAC

P A T V C G P K K S T N L V K N K C V N

S protein

1682 1692 1702 1712 1722 1732

UUCAACUUCA ACGGCCUGAC CGGCACCGGC GUGCUGACAG AGAGCAACAA GAAGUUCCUG

F N F N G L T G T G V L T E S N K K F L

S protein

1742 1752 1762 1772 1782 1792

CCAUUCCAGC AGUUUGGCCG GGAUAUCGCC GAUACCACAG ACGCCGUUAG AGAUCCCCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

1802 1812 1822 1832 1842 1852

ACACUGGAAA UCCUGGACAU CACCCCUUGC AGCUUCGGCG GAGUGUCUGU GAUCACCCCU

T L E I L D I T P C S F G G V S V I T P

S protein

1862 1872 1882 1892 1902 1912

GGCACCAACA CCAGCAAUCA GGUGGCAGUG CUGUACCAGG ACGUGAACUG UACCGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

1922 1932 1942 1952 1962 1972

CCCGUGGCCA UUCACGCCGA UCAGCUGACA CCUACAUGGC GGGUGUACUC CACCGGCAGC

P V A I H A D Q L T P T W R V Y S T G S

S protein

1982 1992 2002 2012 2022 2032

AAUGUGUUUC AGACCAGAGC CGGCUGUCUG AUCGGAGCCG AGCACGUGAA CAAUAGCUAC

N V F Q T R A G C L I G A E H V N N S Y

S protein

2042 2052 2062 2072 2082 2092

GAGUGCGACA UCCCCAUCGG CGCUGGAAUC UGCGCCAGCU ACCAGACACA GACAAACAGC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

2102 2112 2122 2132 2142 2152

CCUCGGAGAG CCAGAAGCGU GGCCAGCCAG AGCAUCAUUG CCUACACAAU GUCUCUGGGC

P R R A R S V A S Q S I I A Y T M S L G

S protein

2162 2172 2182 2192 2202 2212

GCCGAGAACA GCGUGGCCUA CUCCAACAAC UCUAUCGCUA UCCCCACCAA CUUCACCAUC

A E N S V A Y S N N S I A I P T N F T I

S protein

2222 2232 2242 2252 2262 2272

AGCGUGACCA CAGAGAUCCU GCCUGUGUCC AUGACCAAGA CCAGCGUGGA CUGCACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

2282 2292 2302 2312 2322 2332

UACAUCUGCG GCGAUUCCAC CGAGUGCUCC AACCUGCUGC UGCAGUACGG CAGCUUCUGC

Y I C G D S T E C S N L L L Q Y G S F C

S protein

2342 2352 2362 2372 2382 2392

ACCCAGCUGA AUAGAGCCCU GACAGGGAUC GCCGUGGAAC AGGACAAGAA CACCCAAGAG

T Q L N R A L T G I A V E Q D K N T Q E

S protein

2402 2412 2422 2432 2442 2452

GUGUUCGCCC AAGUGAAGCA GAUCUACAAG ACCCCUCCUA UCAAGGACUU CGGCGGCUUC

V F A Q V K Q I Y K T P P I K D F G G F

S protein

2462 2472 2482 2492 2502 2512

AAUUUCAGCC AGAUUCUGCC CGAUCCUAGC AAGCCCAGCA AGCGGAGCUU CAUCGAGGAC

N F S Q I L P D P S K P S K R S F I E D

S protein

2522 2532 2542 2552 2562 2572

CUGCUGUUCA ACAAAGUGAC ACUGGCCGAC GCCGGCUUCA UCAAGCAGUA UGGCGAUUGU

L L F N K V T L A D A G F I K Q Y G D C

S protein

2582 2592 2602 2612 2622 2632

CUGGGCGACA UUGCCGCCAG GGAUCUGAUU UGCGCCCAGA AGUUUAACGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

2642 2652 2662 2672 2682 2692

CUGCCUCCUC UGCUGACCGA UGAGAUGAUC GCCCAGUACA CAUCUGCCCU GCUGGCCGGC

L P P L L T D E M I A Q Y T S A L L A G

S protein

2702 2712 2722 2732 2742 2752

ACAAUCACAA GCGGCUGGAC AUUUGGAGCA GGCGCCGCUC UGCAGAUCCC CUUUGCUAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

2762 2772 2782 2792 2802 2812

CAGAUGGCCU ACCGGUUCAA CGGCAUCGGA GUGACCCAGA AUGUGCUGUA CGAGAACCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

2822 2832 2842 2852 2862 2872

AAGCUGAUCG CCAACCAGUU CAACAGCGCC AUCGGCAAGA UCCAGGACAG CCUGAGCAGC

K L I A N Q F N S A I G K I Q D S L S S

S protein

2882 2892 2902 2912 2922 2932

ACAGCAAGCG CCCUGGGAAA GCUGCAGGAC GUGGUCAACC AGAAUGCCCA GGCACUGAAC

T A S A L G K L Q D V V N Q N A Q A L N

S protein

2942 2952 2962 2972 2982 2992

ACCCUGGUCA AGCAGCUGUC CUCCAACUUC GGCGCCAUCA GCUCUGUGCU GAACGAUAUC

T L V K Q L S S N F G A I S S V L N D I

S protein

3002 3012 3022 3032 3042 3052

CUGAGCAGAC UGGACCCUCC UGAGGCCGAG GUGCAGAUCG ACAGACUGAU CACAGGCAGA

L S R L D P P E A E V Q I D R L I T G R

S protein

3062 3072 3082 3092 3102 3112

CUGCAGAGCC UCCAGACAUA CGUGACCCAG CAGCUGAUCA GAGCCGCCGA GAUUAGAGCC

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

3122 3132 3142 3152 3162 3172

UCUGCCAAUC UGGCCGCCAC CAAGAUGUCU GAGUGUGUGC UGGGCCAGAG CAAGAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

3182 3192 3202 3212 3222 3232

GACUUUUGCG GCAAGGGCUA CCACCUGAUG AGCUUCCCUC AGUCUGCCCC UCACGGCGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

3242 3252 3262 3272 3282 3292

GUGUUUCUGC ACGUGACAUA UGUGCCCGCU CAAGAGAAGA AUUUCACCAC CGCUCCAGCC

V F L H V T Y V P A Q E K N F T T A P A

S protein

3302 3312 3322 3332 3342 3352

AUCUGCCACG ACGGCAAAGC CCACUUUCCU AGAGAAGGCG UGUUCGUGUC CAACGGCACC

I C H D G K A H F P R E G V F V S N G T

S protein

3362 3372 3382 3392 3402 3412

CAUUGGUUCG UGACACAGCG GAACUUCUAC GAGCCCCAGA UCAUCACCAC CGACAACACC

H W F V T Q R N F Y E P Q I I T T D N T

S protein

3422 3432 3442 3452 3462 3472

UUCGUGUCUG GCAACUGCGA CGUCGUGAUC GGCAUUGUGA ACAAUACCGU GUACGACCCU

F V S G N C D V V I G I V N N T V Y D P

S protein

3482 3492 3502 3512 3522 3532

CUGCAGCCCG AGCUGGACAG CUUCAAAGAG GAACUGGACA AGUACUUUAA GAACCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

```
     3542       3552       3562       3572       3582       3592
AGCCCCGACG UGGACCUGGG CGAUAUCAGC GGAAUCAAUG CCAGCGUCGU GAACAUCCAG
  S  P  D   V  D  L   G  D  I  S   G  I  N   A  S  V   V  N  I  Q
```

S protein

```
     3602       3612       3622       3632       3642       3652
AAAGAGAUCG ACCGGCUGAA CGAGGUGGCC AAGAAUCUGA ACGAGAGCCU GAUCGACCUG
  K  E  I   D  R  L   N  E  V  A   K  N  L   N  E  S   L  I  D  L
```

S protein

```
     3662       3672       3682       3692       3702       3712
CAAGAACUGG GGAAGUACGA GCAGUACAUC AAGUGGCCCU GGUACAUCUG GCUGGGCUUU
  Q  E  L   G  K  Y   E  Q  Y  I   K  W  P   W  Y  I   W  L  G  F
```

S protein

```
     3722       3732       3742       3752       3762       3772
AUCGCCGGAC UGAUUGCCAU CGUGAUGGUC ACAAUCAUGC UGUGUUGCAU GACCAGCUGC
  I  A  G   L  I  A   I  V  M  V   T  I  M   L  C  C   M  T  S  C
```

S protein

```
     3782       3792       3802       3812       3822       3832
UGUAGCUGCC UGAAGGGCUG UUGUAGCUGU GGCAGCUGCU GCAAGUUCGA CGAGGACGAU
  C  S  C   L  K  G   C  C  S  C   G  S  C   C  K  F   D  E  D  D
```

S protein

```
     3842       3852       3862       3872  3877
UCUGAGCCCG UGCUGAAGGG CGUGAAACUG CACUACACAU GAUGA
  S  E  P   V  L  K   G  V  K  L   H  Y  T   *  *
```

S protein

```
     3887       3897       3907       3917       3927       3937
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
     3947       3957       3967       3977       3987       3997
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
     4007       4017       4027       4037       4047       4057
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

4067 4077 4087 4097 4107 4117

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

4127 4137 4147 4157 4167 4172

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC

FI element

4182 4192 4202 4212 4222 4232

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

4242 4252 4262 4272 4282

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Nucleotide Sequence of RBL063.3

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
          10         20         30         40         50 52
GGGCGAACUA GUAUUCUUCU GGUCCCCACA GACUCAGAGA GAACCCGCCA CC
                                 hAg-Kozak
        62         72         82         92        102        112
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGGU GAGAUUUCCA
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   V  R  F  P
                                 RBD (S protein)
       122        132        142        152        162        172
AAUAUUACAA AUCUGUGUCC AUUUGGAGAA GUGUUUAAUG CAACAAGAUU UGCAUCUGUG
  N  I  T   N  L  C   P  F  G  E   V  F  N   A  T  R   F  A  S  V
                                 RBD (S protein)
       182        192        202        212        222        232
UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU
  Y  A  W   N  R  K   R  I  S  N   C  V  A   D  Y  S   V  L  Y  N
                                 RBD (S protein)
       242        252        262        272        282        292
AGUGCUUCUU UUUCCACAUU UAAAUGUUAU GGAGUGUCUC CAACAAAAUU AAAUGAUUUA
  S  A  S   F  S  T   F  K  C  Y   G  V  S   P  T  K   L  N  D  L
                                 RBD (S protein)
       302        312        322        332        342        352
UGUUUUACAA AUGUGUAUGC UGAUUCUUUU GUGAUCAGAG GUGAUGAAGU GAGACAGAUU
  C  F  T   N  V  Y   A  D  S  F   V  I  R   G  D  E   V  R  Q  I
                                 RBD (S protein)
       362        372        382        392        402        412
GCCCCCGGAC AGACAGGAAA AAUUGCUGAU UACAAUUACA AACUGCCUGA UGAUUUUACA
  A  P  G   Q  T  G   K  I  A  D   Y  N  Y   K  L  P   D  D  F  T
                                 RBD (S protein)
       422        432        442        452        462        472
GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU UUAGAUUCUA AAGUGGGAGG AAAUUACAAU
  G  C  V   I  A  W   N  S  N  N   L  D  S   K  V  G   G  N  Y  N
```

RBD (S protein)

```
      482        492        502        512        522        532
UAUCUGUACA GACUGUUUAG AAAAUCAAAU CUGAAACCUU UUGAAAGAGA UAUUUCAACA
  Y  L  Y   R  L  F   R  K  S  N   L  K  P   F  E  R   D  I  S  T
```

RBD (S protein)

```
      542        552        562        572        582        592
GAAAUUUAUC AGGCUGGAUC AACACCUUGU AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU
  E  I  Y   Q  A  G   S  T  P  C   N  G  V   E  G  F   N  C  Y  F
```

RBD (S protein)

```
      602        612        622        632        642        652
CCAUUACAGA GCUAUGGAUU UCAGCCAACC AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG
  P  L  Q   S  Y  G   F  Q  P  T   N  G  V   G  Y  Q   P  Y  R  V
```

RBD (S protein)

```
      662        672        682        692        702  706
GUGGUGCUGU CUUUUGAACU GCUGCAUGCA CCUGCAACAG UGUGUGGACC UAAA
  V  V  L   S  F  E   L  L  H  A   P  A  T   V  C  G   P  K
```

RBD (S protein)

```
      716        726     733
GGCUCCCCCG GCUCCGGCUC CGGAUCU
  G  S  P   G  S  G   S  G  S
```

GS linker

```
      743        753        763        773        783        793
GGUUAUAUUC CUGAAGCUCC AAGAGAUGGG CAAGCUUACG UUCGUAAAGA UGGCGAAUGG
  G  Y  I   P  E  A   P  R  D  G   Q  A  Y   V  R  K   D  G  E  W
```

fibritin

```
      803        813        823        833        843        853
GUAUUACUUU CUACCUUUUU AGGCCGGUCC CUGGAGGUGC UGUUCCAGGG CCCCGGCUGA
  V  L  L   S  T  F   L  G  R  S   L  E  V   L  F  Q   G  P  G  *
```

fibritin

```
 856
UGA
  *
```

fibritin

866 876 886 896 906 916

CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG

FI element

926 936 946 956 966 976

AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC

FI element

986 996 1006 1016 1026 1036

UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG

FI element

1046 1056 1066 1076 1086 1096

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

1106 1116 1126 1136 1146 1151

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC

FI element

1161 1171 1181 1191 1201 1211

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

1221 1231 1241 1251 1261

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Nucleoside modified messenger RNA (modRNA)

The active principle of the nucleoside modified messenger RNA (modRNA) drug substance is as well a single-stranded mRNA that is translated upon entering a cell. In addition to the sequence encoding the coronavirus vaccine antigen (i.e. open reading frame), each modRNA contains common structural elements optimized for maximal efficacy of the RNA as the uRNA (5'-cap, 5'-UTR, 3'-UTR, poly(A)-tail). Compared to the uRNA, modRNA contains 1-methyl-pseudouridine instead of uridine. The preferred 5' cap structure is $m_2^{7,3'\text{-}O}Gppp(m_1^{2'\text{-}O})ApG$. The preferred 5'-UTR and 3'-UTR comprise the nucleotide sequence of SEQ ID NO: 12 and the nucleotide sequence of SEQ ID NO: 13, respectively. The preferred poly(A)-tail comprises the sequence of SEQ ID NO: 14. An additional purification step is applied for modRNA to reduce dsRNA contaminants generated during the in vitro transcription reaction.

Different embodiment of this platform are as follows:

BNT162b2; RBP020.1 (SEQ ID NO: 19; SEQ ID NO: 7)

Structure	$m_2^{7,3'\text{-}O}Gppp(m_1^{2'\text{-}O})ApG$)-hAg-Kozak-S1S2-PP-FI-A30L70
Encoded antigen	Viral spike protein (S1S2 protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

BNT162b2; RBP020.2 (SEQ ID NO: 20; SEQ ID NO: 7)

Structure	$m_2^{7,3'\text{-}O}Gppp(m_1^{2'\text{-}O})ApG$)-hAg-Kozak-S1S2-PP-FI-A30L70
Encoded antigen	Viral spike protein (S1S2 protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

BNT162b1; RBP020.3 (SEQ ID NO: 21; SEQ ID NO: 5)

Structure $m_2^{7,3'\text{-}O}Gppp(m_1^{2'\text{-}O})ApG$)-hAg-Kozak-RBD-GS-Fibritin-FI-A30L70

Encoded antigen Viral spike protein (S1S2 protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein fused to fibritin)

Figure 20 schematizes the general structure of the antigen-encoding RNAs.

Nucleotide Sequence of RBP020.1

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
         10         20         30         40         50  53
AGAAUAAACU AGUAUUCUUC UGGUCCCCAC AGACUCAGAG AGAACCCGCC ACC
```

hAg-Kozak

```
        63         73         83         93        103        113
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGAA UUUGACAACA
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   N  L  T  T
```

S protein

```
       123        133        143        153        163        173
AGAACACAGC UGCCACCAGC UUAUACAAAU UCUUUUACCA GAGGAGUGUA UUAUCCUGAU
  R  T  Q   L  P  P   A  Y  T  N   S  F  T   R  G  V   Y  Y  P  D
```

S protein

```
       183        193        203        213        223        233
AAAGUGUUUA GAUCUUCUGU GCUGCACAGC ACACAGGACC UGUUUCUGCC AUUUUUUAGC
  K  V  F   R  S  S   V  L  H  S   T  Q  D   L  F  L   P  F  F  S
```

S protein

```
       243        253        263        273        283        293
AAUGUGACAU GGUUUCAUGC AAUUCAUGUG UCUGGAACAA AUGGAACAAA AAGAUUUGAU
  N  V  T   W  F  H   A  I  H  V   S  G  T   N  G  T   K  R  F  D
```

S protein

```
       303        313        323        333        343        353
AAUCCUGUGC UGCCUUUUAA UGAUGGAGUG UAUUUUGCUU CAACAGAAAA GUCAAAUAUU
  N  P  V   L  P  F   N  D  G  V   Y  F  A   S  T  E   K  S  N  I
```

S protein

```
       363        373        383        393        403        413
AUUAGAGGAU GGAUUUUUGG AACAACACUG GAUUCUAAAA CACAGUCUCU GCUGAUUGUG
  I  R  G   W  I  F   G  T  T  L   D  S  K   T  Q  S   L  L  I  V
```

S protein

```
       423        433        443        453        463        473
AAUAAUGCAA CAAAUGUGGU GAUUAAAGUG UGUGAAUUUC AGUUUUGUAA UGAUCCUUUU
```

N N A T N V V I K V C E F Q F C N D P F

S protein

483 493 503 513 523 533

CUGGGAGUGU AUUAUCACAA AAAUAAUAAA UCUUGGAUGG AAUCUGAAUU UAGAGUGUAU

L G V Y Y H K N N K S W M E S E F R V Y

S protein

543 553 563 573 583 593

UCCUCUGCAA AUAAUUGUAC AUUUGAAUAU GUGUCUCAGC CUUUUCUGAU GGAUCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

603 613 622 633 643 653

GGAAAACAGG GCAAUUUUAA AAAUCUGAGA GAAUUUGUGU UUAAAAAUAU UGAUGGAUAU

G K Q G N F K N L R E F V F K N I D G Y

S protein

663 673 683 693 703 713

UUUAAAAUUU AUUCUAAACA CACACCAAUU AAUUUAGUGA GAGAUCUGCC UCAGGGAUUU

F K I Y S K H T P I N L V R D L P Q G F

S protein

723 733 743 753 763 773

UCUGCUCUGG AACCUCUGGU GGAUCUGCCA AUUGGCAUUA AUAUUACAAG AUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

783 793 803 813 823 833

CUGCUGGCUC UGCACAGAUC UUAUCUGACA CCUGGAGAUU CUUCUUCUGG AUGGACAGCC

L L A L H R S Y L T P G D S S S G W T A

S protein

843 853 863 873 883 893

GGAGCUGCAG CUUAUUAUGU GGGCUAUCUG CAGCCAAGAA CAUUUCUGCU GAAAUAUAAU

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

903 913 923 933 943 953

GAAAAUGGAA CAAUUACAGA UGCUGUGGAU UGUGCUCUGG AUCCUCUGUC UGAAACAAAA

E N G T I T D A V D C A L D P L S E T K

S protein

963 973 983 993 1003 1013

UGUACAUUAA AAUCUUUUAC AGUGGAAAAA GGCAUUUAUC AGACAUCUAA UUUUAGAGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

1023 1033 1043 1053 1063 1073

CAGCCAACAG AAUCUAUUGU GAGAUUUCCA AAUAUUACAA AUCUGUGUCC AUUUGGAGAA

Q P T E S I V R F P N I T N L C P F G E

S protein

1083 1093 1103 1113 1123 1133

GUGUUUAAUG CAACAAGAUU UGCAUCUGUG UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU

V F N A T R F A S V Y A W N R K R I S N

S protein

1143 1153 1163 1173 1183 1193

UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU AGUGCUUCUU UUUCCACAUU UAAAUGUUAU

C V A D Y S V L Y N S A S F S T F K C Y

S protein

1203 1213 1223 1233 1243 1253

GGAGUGUCUC CAACAAAAUU AAAUGAUUUA UGUUUUACAA AUGUGUAUGC UGAUUCUUUU

G V S P T K L N D L C F T N V Y A D S F

S protein

1263 1273 1283 1293 1303 1313

GUGAUCAGAG GUGAUGAAGU GAGACAGAUU GCCCCCGGAC AGACAGGAAA AAUUGCUGAU

V I R G D E V R Q I A P G Q T G K I A D

S protein

1323 1333 1343 1353 1363 1373

UACAAUUACA AACUGCCUGA UGAUUUUACA GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU

Y N Y K L P D D F T G C V I A W N S N N

S protein

1383 1393 1403 1413 1423 1433

UUAGAUUCUA AAGUGGGAGG AAAUUACAAU UAUCUGUACA GACUGUUUAG AAAAUCAAAU

L D S K V G G N Y N Y L Y R L F R K S N

S protein

1443 1453 1463 1473 1483 1493

CUGAAACCUU UUGAAAGAGA UAUUUCAACA GAAAUUUAUC AGGCUGGAUC AACACCUUGU

L K P F E R D I S T E I Y Q A G S T P C

S protein

1503 1513 1523 1533 1543 1553

AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU CCAUUACAGA GCUAUGGAUU UCAGCCAACC

N G V E G F N C Y F P L Q S Y G F Q P T

S protein

1563 1573 1583 1593 1603 1613

AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG GUGGUGCUGU CUUUUGAACU GCUGCAUGCA

N G V G Y Q P Y R V V V L S F E L L H A

S protein

1623 1633 1643 1653 1663 1673

CCUGCAACAG UGUGUGGACC UAAAAAAUCU ACAAAUUUAG UGAAAAAUAA AUGUGUGAAU

P A T V C G P K K S T N L V K N K C V N

S protein

1683 1693 1703 1713 1723 1733

UUUAAUUUUA AUGGAUUAAC AGGAACAGGA GUGCUGACAG AAUCUAAUAA AAAAUUUCUG

F N F N G L T G T G V L T E S N K K F L

S protein

1743 1753 1763 1773 1783 1793

CCUUUUCAGC AGUUUGGCAG AGAUAUUGCA GAUACCACAG AUGCAGUGAG AGAUCCUCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

1803 1813 1823 1833 1843 1853

ACAUUAGAAA UUCUGGAUAU UACACCUUGU UCUUUUGGGG GUGUGUCUGU GAUUACACCU

T L E I L D I T P C S F G G V S V I T P

S protein

1863 1873 1883 1893 1903 1913

GGAACAAAUA CAUCUAAUCA GGUGGCUGUG CUGUAUCAGG AUGUGAAUUG UACAGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

1923 1933 1943 1953 1963 1973

CCAGUGGCAA UUCAUGCAGA UCAGCUGACA CCAACAUGGA GAGUGUAUUC UACAGGAUCU

P V A I H A D Q L T P T W R V Y S T G S

S protein

1983 1993 2003 2013 2023 2033

AAUGUGUUUC AGACAAGAGC AGGAUGUCUG AUUGGAGCAG AACAUGUGAA UAAUUCUUAU

N V F Q T R A G C L I G A E H V N N S Y

S protein

2043 2053 2063 2073 2083 2093

GAAUGUGAUA UUCCAAUUGG AGCAGGCAUU UGUGCAUCUU AUCAGACACA GACAAAUUCC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

2103 2113 2123 2133 2143 2153

CCAAGGAGAG CAAGAUCUGU GGCAUCUCAG UCUAUUAUUG CAUACACCAU GUCUCUGGGA

P R R A R S V A S Q S I I A Y T M S L G

S protein

2163 2173 2183 2193 2203 2213

GCAGAAAAUU CUGUGGCAUA UUCUAAUAAU UCUAUUGCUA UUCCAACAAA UUUUACCAUU

A E N S V A Y S N N S I A I P T N F T I

S protein

2223 2233 2243 2253 2263 2273

UCUGUGACAA CAGAAAUUUU ACCUGUGUCU AUGACAAAAA CAUCUGUGGA UUGUACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

2283 2293 2303 2313 2323 2333

UACAUUUGUG GAGAUUCUAC AGAAUGUUCU AAUCUGCUGC UGCAGUAUGG AUCUUUUUGU

Y I C G D S T E C S N L L L Q Y G S F C

S protein

2343 2353 2363 2373 2383 2393

ACACAGCUGA AUAGAGCUUU AACAGGAAUU GCUGUGGAAC AGGAUAAAAA UACACAGGAA

T Q L N R A L T G I A V E Q D K N T Q E

S protein

2403 2413 2423 2433 2443 2453

GUGUUUGCUC AGGUGAAACA GAUUUACAAA ACACCACCAA UUAAAGAUUU UGGAGGAUUU

V F A Q V K Q I Y K T P P I K D F G G F

S protein

2463 2473 2483 2493 2503 2513

AAUUUUAGCC AGAUUCUGCC UGAUCCUUCU AAACCUUCUA AAAGAUCUUU UAUUGAAGAU

N F S Q I L P D P S K P S K R S F I E D

S protein

2523 2533 2543 2553 2563 2573

CUGCUGUUUA AUAAAGUGAC ACUGGCAGAU GCAGGAUUUA UUAAACAGUA UGGAGAUUGC

L L F N K V T L A D A G F I K Q Y G D C

S protein

2583 2593 2603 2613 2623 2633

CUGGGUGAUA UUGCUGCAAG AGAUCUGAUU UGUGCUCAGA AAUUUAAUGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

2643 2653 2663 2673 2683 2693

CUGCCUCCUC UGCUGACAGA UGAAAUGAUU GCUCAGUACA CAUCUGCUUU ACUGGCUGGA

L P P L L T D E M I A Q Y T S A L L A G

S protein

2703 2713 2723 2733 2743 2753

ACAAUUACAA GCGGAUGGAC AUUUGGAGCU GGAGCUGCUC UGCAGAUUCC UUUUGCAAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

2763 2773 2783 2793 2803 2813

CAGAUGGCUU ACAGAUUUAA UGGAAUUGGA GUGACACAGA AUGUGUUAUA UGAAAAUCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

2823 2833 2843 2853 2863 2873

AAACUGAUUG CAAAUCAGUU UAAUUCUGCA AUUGGCAAAA UUCAGGAUUC UCUGUCUUCU

K L I A N Q F N S A I G K I Q D S L S S

S protein

2883 2893 2903 2913 2923 2933

ACAGCUUCUG CUCUGGGAAA ACUGCAGGAU GUGGUGAAUC AGAAUGCACA GGCACUGAAU

T A S A L G K L Q D V V N Q N A Q A L N

S protein

2943 2953 2963 2973 2983 2993

ACUCUGGUGA AACAGCUGUC UAGCAAUUUU GGGGCAAUUU CUUCUGUGCU GAAUGAUAUU

T L V K Q L S S N F G A I S S V L N D I

S protein

3003 3013 3023 3033 3043 3053

CUGUCUAGAC UGGAUCCUCC UGAAGCUGAA GUGCAGAUUG AUAGACUGAU CACAGGAAGA

L S R L D P P E A E V Q I D R L I T G R

S protein

3063 3073 3083 3093 3103 3113

CUGCAGUCUC UGCAGACUUA UGUGACACAG CAGCUGAUUA GAGCUGCUGA AAUUAGAGCU

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

3123 3133 3143 3153 3163 3173

UCUGCUAAUC UGGCUGCUAC AAAAAUGUCU GAAUGUGUGC UGGGACAGUC AAAAAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

3183 3193 3203 3213 3223 3233

GAUUUUUGUG GAAAAGGAUA UCAUCUGAUG UCUUUUCCAC AGUCUGCUCC ACAUGGAGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

3243 3253 3263 3273 3283 3293

GUGUUUUUAC AUGUGACAUA UGUGCCAGCA CAGGAAAAGA AUUUUACCAC AGCACCAGCA

V F L H V T Y V P A Q E K N F T T A P A

S protein

3303 3313 3323 3333 3343 3353

AUUUGUCAUG AUGGAAAAGC ACAUUUUCCA AGAGAAGGAG UGUUUGUGUC UAAUGGAACA

I C H D G K A H F P R E G V F V S N G T

S protein

3363 3373 3383 3393 3403 3413

CAUUGGUUUG UGACACAGAG AAAUUUUUAU GAACCUCAGA UUAUUACAAC AGAUAAUACA

H W F V T Q R N F Y E P Q I I T T D N T

S protein

3423 3433 3443 3453 3463 3473

UUUGUGUCAG GAAAUUGUGA UGUGGUGAUU GGAAUUGUGA AUAAUACAGU GUAUGAUCCA

F V S G N C D V V I G I V N N T V Y D P

S protein

3483 3493 3503 3513 3523 3533

CUGCAGCCAG AACUGGAUUC UUUUAAAGAA GAACUGGAUA AAUAUUUUAA AAAUCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

```
     3543        3553        3563        3573        3583        3593
UCUCCUGAUG UGGAUUUAGG AGAUAUUUCU GGAAUCAAUG CAUCUGUGGU GAAUAUUCAG
  S  P  D   V  D  L   G  D  I  S   G  I  N   A  S  V   V  N  I  Q
```

S protein

```
     3603        3613        3623        3633        3643        3653
AAAGAAAUUG AUAGACUGAA UGAAGUGGCC AAAAAUCUGA AUGAAUCUCU GAUUGAUCUG
  K  E  I   D  R  L   N  E  V  A   K  N  L   N  E  S   L  I  D  L
```

S protein

```
     3663        3673        3683        3693        3703        3713
CAGGAACUUG GAAAAUAUGA ACAGUACAUU AAAUGGCCUU GGUACAUUUG GCUUGGAUUU
  Q  E  L   G  K  Y   E  Q  Y  I   K  W  P   W  Y  I   W  L  G  F
```

S protein

```
     3723        3733        3743        3753        3763        3773
AUUGCAGGAU UAAUUGCAAU UGUGAUGGUG ACAAUUAUGU UAUGUUGUAU GACAUCAUGU
  I  A  G   L  I  A   I  V  M  V   T  I  M   L  C  C   M  T  S  C
```

S protein

```
     3783        3793        3803        3813        3823        3833
UGUUCUUGUU UAAAAGGAUG UUGUUCUUGU GGAAGCUGUU GUAAAUUUGA UGAAGAUGAU
  C  S  C   L  K  G   C  C  S  C   G  S  C   C  K  F   D  E  D  D
```

S protein

```
     3843        3853        3863        3873   3878
UCUGAACCUG UGUUAAAAGG AGUGAAAUUG CAUUACACAU GAUGA
  S  E  P   V  L  K   G  V  K  L   H  Y  T   *  *
```

S protein

```
     3888        3898        3908        3918        3928        3938
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
     3948        3958        3968        3978        3988        3998
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
     4008        4018        4028        4038        4048        4058
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

```
     4068        4078        4088        4098        4108        4118
CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA
```

FI element

```
      4128        4138        4148        4158        4168   4173
GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC
```

FI element

```
      4183        4193        4203        4213        4223        4233
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA
```

Poly(A)

```
      4243        4253        4263        4273        4283
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

Poly(A)

Nucleotide Sequence of RBP020.2

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
        10         20         30         40         50  53
AGAAUAAACU AGUAUUCUUC UGGUCCCCAC AGACUCAGAG AGAACCCGCC ACC
```

hAg-Kozak

```
        63         73         83         93        103        113
AUGUUCGUGU UCCUGGUGCU GCUGCCUCUG GUGUCCAGCC AGUGUGUGAA CCUGACCACC
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   N  L  T  T
```

S protein

```
       123        133        143        153        163        173
AGAACACAGC UGCCUCCAGC CUACACCAAC AGCUUUACCA GAGGCGUGUA CUACCCCGAC
  R  T  Q   L  P  P   A  Y  T  N   S  F  T   R  G  V   Y  Y  P  D
```

S protein

```
       183        193        203        213        223        233
AAGGUGUUCA GAUCCAGCGU GCUGCACUCU ACCCAGGACC UGUUCCUGCC UUUCUUCAGC
  K  V  F   R  S  S   V  L  H  S   T  Q  D   L  F  L   P  F  F  S
```

S protein

```
       243        253        263        273        283        293
AACGUGACCU GGUUCCACGC CAUCCACGUG UCCGGCACCA AUGGCACCAA GAGAUUCGAC
  N  V  T   W  F  H   A  I  H  V   S  G  T   N  G  T   K  R  F  D
```

S protein

```
       303        313        323        333        343        353
AACCCCGUGC UGCCCUUCAA CGACGGGGUG UACUUUGCCA GCACCGAGAA GUCCAACAUC
  N  P  V   L  P  F   N  D  G  V   Y  F  A   S  T  E   K  S  N  I
```

S protein

```
       363        373        383        393        403        413
AUCAGAGGCU GGAUCUUCGG CACCACACUG GACAGCAAGA CCCAGAGCCU GCUGAUCGUG
  I  R  G   W  I  F   G  T  T  L   D  S  K   T  Q  S   L  L  I  V
```

S protein

```
       423        433        443        453        463        473
AACAACGCCA CCAACGUGGU CAUCAAAGUG UGCGAGUUCC AGUUCUGCAA CGACCCCUUC
```

N N A T N V V I K V C E F Q F C N D P F

S protein

483 493 503 513 523 533

CUGGGCGUCU ACUACCACAA GAACAACAAG AGCUGGAUGG AAAGCGAGUU CCGGGUGUAC

L G V Y Y H K N N K S W M E S E F R V Y

S protein

543 553 563 573 583 593

AGCAGCGCCA ACAACUGCAC CUUCGAGUAC GUGUCCCAGC CUUUCCUGAU GGACCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

603 613 623 633 643 653

GGCAAGCAGG GCAACUUCAA GAACCUGCGC GAGUUCGUGU UUAAGAACAU CGACGGCUAC

G K Q G N F K N L R E F V F K N I D G Y

S protein

663 673 683 693 703 713

UUCAAGAUCU ACAGCAAGCA CACCCCUAUC AACCUCGUGC GGGAUCUGCC UCAGGGCUUC

F K I Y S K H T P I N L V R D L P Q G F

S protein

723 733 743 753 763 773

UCUGCUCUGG AACCCCUGGU GGAUCUGCCC AUCGGCAUCA ACAUCACCCG GUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

783 793 803 813 823 833

CUGCUGGCCC UGCACAGAAG CUACCUGACA CCUGGCGAUA GCAGCAGCGG AUGGACAGCU

L L A L H R S Y L T P G D S S S G W T A

S protein

843 853 863 873 883 893

GGUGCCGCCG CUUACUAUGU GGGCUACCUG CAGCCUAGAA CCUUCCUGCU GAAGUACAAC

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

903 913 923 933 943 953

GAGAACGGCA CCAUCACCGA CGCCGUGGAU UGUGCUCUGG AUCCUCUGAG CGAGACAAAG

E N G T I T D A V D C A L D P L S E T K

S protein

963 973 983 993 1003 1013

UGCACCCUGA AGUCCUUCAC CGUGGAAAAG GGCAUCUACC AGACCAGCAA CUUCCGGGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

1023 1033 1043 1053 1063 1073

CAGCCCACCG AAUCCAUCGU GCGGUUCCCC AAUAUCACCA AUCUGUGCCC CUUCGGCGAG

Q P T E S I V R F P N I T N L C P F G E

S protein

1083 1093 1103 1113 1123 1133

GUGUUCAAUG CCACCAGAUU CGCCUCUGUG UACGCCUGGA ACCGGAAGCG GAUCAGCAAU

V F N A T R F A S V Y A W N R K R I S N

S protein

1143 1153 1163 1173 1183 1193

UGCGUGGCCG ACUACUCCGU GCUGUACAAC UCCGCCAGCU UCAGCACCUU CAAGUGCUAC

C V A D Y S V L Y N S A S F S T F K C Y

S protein

1203 1213 1223 1233 1243 1253

GGCGUGUCCC CUACCAAGCU GAACGACCUG UGCUUCACAA ACGUGUACGC CGACAGCUUC

G V S P T K L N D L C F T N V Y A D S F

S protein

1263 1273 1283 1293 1303 1313

GUGAUCCGGG GAGAUGAAGU GCGGCAGAUU GCCCCUGGAC AGACAGGCAA GAUCGCCGAC

V I R G D E V R Q I A P G Q T G K I A D

S protein

1323 1333 1343 1353 1363 1373

UACAACUACA AGCUGCCCGA CGACUUCACC GGCUGUGUGA UUGCCUGGAA CAGCAACAAC

Y N Y K L P D D F T G C V I A W N S N N

S protein

1383 1393 1403 1413 1423 1433

CUGGACUCCA AAGUCGGCGG CAACUACAAU UACCUGUACC GGCUGUUCCG GAAGUCCAAU

L D S K V G G N Y N Y L Y R L F R K S N

S protein

1443 1453 1463 1473 1483 1493

CUGAAGCCCU UCGAGCGGGA CAUCUCCACC GAGAUCUAUC AGGCCGGCAG CACCCCUUGU

L K P F E R D I S T E I Y Q A G S T P C

S protein

1503 1513 1523 1533 1543 1553

AACGGCGUGG AAGGCUUCAA CUGCUACUUC CCACUGCAGU CCUACGGCUU UCAGCCCACA

N G V E G F N C Y F P L Q S Y G F Q P T

S protein

1563 1573 1583 1593 1603 1613

AAUGGCGUGG GCUAUCAGCC CUACAGAGUG GUGGUGCUGA GCUUCGAACU GCUGCAUGCC

N G V G Y Q P Y R V V V L S F E L L H A

S protein

1623 1633 1643 1653 1663 1673

CCUGCCACAG UGUGCGGCCC UAAGAAAAGC ACCAAUCUCG UGAAGAACAA AUGCGUGAAC

P A T V C G P K K S T N L V K N K C V N

S protein

1683 1693 1703 1713 1723 1733

UUCAACUUCA ACGGCCUGAC CGGCACCGGC GUGCUGACAG AGAGCAACAA GAAGUUCCUG

F N F N G L T G T G V L T E S N K K F L

S protein

1743 1753 1763 1773 1783 1793

CCAUUCCAGC AGUUUGGCCG GGAUAUCGCC GAUACCACAG ACGCCGUUAG AGAUCCCCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

1803 1813 1823 1833 1843 1853

ACACUGGAAA UCCUGGACAU CACCCCUUGC AGCUUCGGCG GAGUGUCUGU GAUCACCCCU

T L E I L D I T P C S F G G V S V I T P

S protein

1863 1873 1883 1893 1903 1913

GGCACCAACA CCAGCAAUCA GGUGGCAGUG CUGUACCAGG ACGUGAACUG UACCGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

1923 1933 1943 1953 1963 1973

CCCGUGGCCA UUCACGCCGA UCAGCUGACA CCUACAUGGC GGGUGUACUC CACCGGCAGC

P V A I H A D Q L T P T W R V Y S T G S

S protein

1983 1993 2003 2013 2023 2033

AAUGUGUUUC AGACCAGAGC CGGCUGUCUG AUCGGAGCCG AGCACGUGAA CAAUAGCUAC

N V F Q T R A G C L I G A E H V N N S Y

S protein

2043 2053 2063 2073 2083 2093

GAGUGCGACA UCCCCAUCGG CGCUGGAAUC UGCGCCAGCU ACCAGACACA GACAAACAGC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

2103 2113 2123 2133 2143 2153

CCUCGGAGAG CCAGAAGCGU GGCCAGCCAG AGCAUCAUUG CCUACACAAU GUCUCUGGGC

P R R A R S V A S Q S I I A Y T M S L G

S protein

2163 2173 2183 2193 2203 2213

GCCGAGAACA GCGUGGCCUA CUCCAACAAC UCUAUCGCUA UCCCCACCAA CUUCACCAUC

A E N S V A Y S N N S I A I P T N F T I

S protein

2223 2233 2243 2253 2263 2273

AGCGUGACCA CAGAGAUCCU GCCUGUGUCC AUGACCAAGA CCAGCGUGGA CUGCACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

2283 2293 2303 2313 2323 2333

UACAUCUGCG GCGAUUCCAC CGAGUGCUCC AACCUGCUGC UGCAGUACGG CAGCUUCUGC

Y I C G D S T E C S N L L L Q Y G S F C

S protein

2343 2353 2363 2373 2383 2393

ACCCAGCUGA AUAGAGCCCU GACAGGGAUC GCCGUGGAAC AGGACAAGAA CACCCAAGAG

T Q L N R A L T G I A V E Q D K N T Q E

S protein

2403 2413 2423 2433 2443 2453

GUGUUCGCCC AAGUGAAGCA GAUCUACAAG ACCCCUCCUA UCAAGGACUU CGGCGGCUUC

V F A Q V K Q I Y K T P P I K D F G G F

S protein

2463 2473 2483 2493 2503 2513

AAUUUCAGCC AGAUUCUGCC CGAUCCUAGC AAGCCCAGCA AGCGGAGCUU CAUCGAGGAC

N F S Q I L P D P S K P S K R S F I E D

S protein

2523 2533 2543 2553 2563 2573

CUGCUGUUCA ACAAAGUGAC ACUGGCCGAC GCCGGCUUCA UCAAGCAGUA UGGCGAUUGU

L L F N K V T L A D A G F I K Q Y G D C

S protein

2583 2593 2603 2613 2623 2633

CUGGGCGACA UUGCCGCCAG GGAUCUGAUU UGCGCCCAGA AGUUUAACGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

2643 2653 2663 2673 2683 2693

CUGCCUCCUC UGCUGACCGA UGAGAUGAUC GCCCAGUACA CAUCUGCCCU GCUGGCCGGC

L P P L L T D E M I A Q Y T S A L L A G

S protein

2703 2713 2723 2733 2743 2753

ACAAUCACAA GCGGCUGGAC AUUUGGAGCA GGCGCCGCUC UGCAGAUCCC CUUUGCUAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

2763 2773 2783 2793 2803 2813

CAGAUGGCCU ACCGGUUCAA CGGCAUCGGA GUGACCCAGA AUGUGCUGUA CGAGAACCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

2823 2833 2843 2853 2863 2873

AAGCUGAUCG CCAACCAGUU CAACAGCGCC AUCGGCAAGA UCCAGGACAG CCUGAGCAGC

K L I A N Q F N S A I G K I Q D S L S S

S protein

2883 2893 2903 2913 2923 2933

ACAGCAAGCG CCCUGGGAAA GCUGCAGGAC GUGGUCAACC AGAAUGCCCA GGCACUGAAC

T A S A L G K L Q D V V N Q N A Q A L N

S protein

2943 2953 2963 2973 2983 2993

ACCCUGGUCA AGCAGCUGUC CUCCAACUUC GGCGCCAUCA GCUCUGUGCU GAACGAUAUC

T L V K Q L S S N F G A I S S V L N D I

S protein

3003 3013 3023 3033 3043 3053

CUGAGCAGAC UGGACCCUCC UGAGGCCGAG GUGCAGAUCG ACAGACUGAU CACAGGCAGA

L S R L D P P E A E V Q I D R L I T G R

S protein

3063 3073 3083 3093 3103 3113

CUGCAGAGCC UCCAGACAUA CGUGACCCAG CAGCUGAUCA GAGCCGCCGA GAUUAGAGCC

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

3123 3133 3143 3153 3163 3173

UCUGCCAAUC UGGCCGCCAC CAAGAUGUCU GAGUGUGUGC UGGGCCAGAG CAAGAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

3183 3193 3203 3213 3223 3233

GACUUUUGCG GCAAGGGCUA CCACCUGAUG AGCUUCCCUC AGUCUGCCCC UCACGGCGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

3243 3253 3263 3273 3283 3293

GUGUUUCUGC ACGUGACAUA UGUGCCCGCU CAAGAGAAGA AUUUCACCAC CGCUCCAGCC

V F L H V T Y V P A Q E K N F T T A P A

S protein

3303 3313 3323 3333 3343 3353

AUCUGCCACG ACGGCAAAGC CCACUUUCCU AGAGAAGGCG UGUUCGUGUC CAACGGCACC

I C H D G K A H F P R E G V F V S N G T

S protein

3363 3373 3383 3393 3403 3413

CAUUGGUUCG UGACACAGCG GAACUUCUAC GAGCCCCAGA UCAUCACCAC CGACAACACC

H W F V T Q R N F Y E P Q I I T T D N T

S protein

3423 3433 3443 3453 3463 3473

UUCGUGUCUG GCAACUGCGA CGUCGUGAUC GGCAUUGUGA ACAAUACCGU GUACGACCCU

F V S G N C D V V I G I V N N T V Y D P

S protein

3483 3493 3503 3513 3523 3533

CUGCAGCCCG AGCUGGACAG CUUCAAAGAG GAACUGGACA AGUACUUUAA GAACCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

```
     3543       3553       3563       3573       3583       3593
AGCCCCGACG UGGACCUGGG CGAUAUCAGC GGAAUCAAUG CCAGCGUCGU GAACAUCCAG
  S  P  D   V  D  L   G  D  I  S   G  I  N   A  S  V   V  N  I  Q
```

S protein

```
     3603       3613       3623       3633       3643       3653
AAAGAGAUCG ACCGGCUGAA CGAGGUGGCC AAGAAUCUGA ACGAGAGCCU GAUCGACCUG
  K  E  I   D  R  L   N  E  V  A   K  N  L   N  E  S   L  I  D  L
```

S protein

```
     3663       3673       3683       3693       3703       3713
CAAGAACUGG GGAAGUACGA GCAGUACAUC AAGUGGCCCU GGUACAUCUG GCUGGGCUUU
  Q  E  L   G  K  Y   E  Q  Y  I   K  W  P   W  Y  I   W  L  G  F
```

S protein

```
     3723       3733       3743       3753       3763       3773
AUCGCCGGAC UGAUUGCCAU CGUGAUGGUC ACAAUCAUGC UGUGUUGCAU GACCAGCUGC
  I  A  G   L  I  A   I  V  M  V   T  I  M   L  C  C   M  T  S  C
```

S protein

```
     3783       3793       3803       3813       3823       3833
UGUAGCUGCC UGAAGGGCUG UUGUAGCUGU GGCAGCUGCU GCAAGUUCGA CGAGGACGAU
  C  S  C   L  K  G   C  C  S  C   G  S  C   C  K  F   D  E  D  D
```

S protein

```
     3843       3853       3863       3873   3878
UCUGAGCCCG UGCUGAAGGG CGUGAAACUG CACUACACAU GAUGA
  S  E  P   V  L  K   G  V  K  L   H  Y  T   *  *
```

S protein

```
     3888       3898       3908       3918       3928       3938
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
     3948       3958       3968       3978       3988       3998
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
     4008       4018       4028       4038       4048       4058
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

```
      4068        4078        4088        4098        4108        4118
CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA
```

FI element

```
      4128        4138        4148        4158        4168   4173
GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC
```

FI element

```
      4183        4193        4203        4213        4223        4233
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA
```

Poly(A)

```
      4243        4253        4263        4273        4283
AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
```

Poly(A)

Nucleotide Sequence of RBP020.3

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
         10         20         30         40          50  53
AGAAUAAACU AGUAUUCUUC UGGUCCCCAC AGACUCAGAG AGAACCCGCC ACC
```

hAg-Kozak

```
        63         73         83         93         103        113
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGGU GAGAUUUCCA
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   V  R  F  P
```

RBD (S protein)

```
       123        133        143        153        163        173
AAUAUUACAA AUCUGUGUCC AUUUGGAGAA GUGUUUAAUG CAACAAGAUU UGCAUCUGUG
  N  I  T   N  L  C   P  F  G  E   V  F  N   A  T  R   F  A  S  V
```

RBD (S protein)

```
       183        193        203        213        223        233
UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU
  Y  A  W   N  R  K   R  I  S  N   C  V  A   D  Y  S   V  L  Y  N
```

RBD (S protein)

```
       243        253        263        273        283        293
AGUGCUUCUU UUUCCACAUU UAAAUGUUAU GGAGUGUCUC CAACAAAAUU AAAUGAUUUA
  S  A  S   F  S  T   F  K  C  Y   G  V  S   P  T  K   L  N  D  L
```

RBD (S protein)

```
       303        313        323        333        343        353
UGUUUUACAA AUGUGUAUGC UGAUUCUUUU GUGAUCAGAG GUGAUGAAGU GAGACAGAUU
  C  F  T   N  V  Y   A  D  S  F   V  I  R   G  D  E   V  R  Q  I
```

RBD (S protein)

```
       363        373        383        393        403        413
GCCCCCGGAC AGACAGGAAA AAUUGCUGAU UACAAUUACA AACUGCCUGA UGAUUUUACA
  A  P  G   Q  T  G   K  I  A  D   Y  N  Y   K  L  P   D  D  F  T
```

RBD (S protein)

```
       423        433        443        453        463        473
GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU UUAGAUUCUA AAGUGGGAGG AAAUUACAAU
  G  C  V   I  A  W   N  S  N  N   L  D  S   K  V  G   G  N  Y  N
```

RBD (S protein)

```
      483         493         503         513         523         533
UAUCUGUACA GACUGUUUAG AAAAUCAAAU CUGAAACCUU UUGAAAGAGA UAUUUCAACA
  Y  L  Y   R  L  F   R  K  S  N   L  K  P   F  E  R   D  I  S  T
```

RBD (S protein)

```
      543         553         563         573         583         593
GAAAUUUAUC AGGCUGGAUC AACACCUUGU AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU
  E  I  Y   Q  A  G   S  T  P  C   N  G  V   E  G  F   N  C  Y  F
```

RBD (S protein)

```
      603         613         623         633         643         653
CCAUUACAGA GCUAUGGAUU UCAGCCAACC AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG
  P  L  Q   S  Y  G   F  Q  P  T   N  G  V   G  Y  Q   P  Y  R  V
```

RBD (S protein)

```
      663         673         683         693         703  707
GUGGUGCUGU CUUUUGAACU GCUGCAUGCA CCUGCAACAG UGUGUGGACC UAAA
  V  V  L   S  F  E   L  L  H  A   P  A  T   V  C  G   P  K
```

RBD (S protein)

```
      717         727      734
GGCUCCCCCG GCUCCGGCUC CGGAUCU
  G  S  P   G  S  G   S  G  S
```

GS linker

```
      744         754         764         774         784         794
GGUUAUAUUC CUGAAGCUCC AAGAGAUGGG CAAGCUUACG UUCGUAAAGA UGGCGAAUGG
  G  Y  I   P  E  A   P  R  D  G   Q  A  Y   V  R  K   D  G  E  W
```

fibritin

```
      804         814         824         834         844         854
GUAUUACUUU CUACCUUUUU AGGCCGGUCC CUGGAGGUGC UGUUCCAGGG CCCCGGCUGA
  V  L  L   S  T  F   L  G  R  S   L  E  V   L  F  Q   G  P  G  *
```

fibritin

```
 857
UGA
  *
```

fibritin

```
      867         877         887         897         907         917
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
      927         937         947         957         967         977
```

AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC

FI element

987 997 1007 1017 1027 1037

UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG

FI element

1047 1057 1067 1077 1087 1097

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

1107 1117 1127 1137 1147 1152

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCCUGGAG CUAGC

FI element

1162 1172 1182 1192 1202 1212

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

1222 1232 1242 1252 1262

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Further embodiments of the nucleoside modified messenger RNA (modRNA) platform are as follows:

BNT162b3c (SEQ ID NO: 29; SEQ ID NO: 30)

Structure $m_2^{7,3'\text{-}O}$Gppp($m_1^{2'\text{-}O}$)ApG-hAg-Kozak-RBD-GS-Fibritin-GS-TM-FI-A30L70

Encoded antigen Viral spike protein (S1S2 protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein fused to Fibritin fused to Transmembrane Domain (TM) of S1S2 protein); intrinsic S1S2 protein secretory signal peptide (aa 1-19) at the N-terminus of the antigen sequence

```
agaauaaacu aguauucuuc uggucccCAC agacucagag agaacccgcc acc aug          56
                                                           Met
                                                           1

uuu gug uuu cuu gug cug cug ccu cuu gug ucu ucu cag ugu gug aau        104
Phe Val Phe Leu Val Leu Leu Pro Leu Val Ser Ser Gln Cys Val Asn
            5                   10                  15

uug aca gug aga uuu cca aau auu aca aau cug ugu cca uuu gga gaa        152
Leu Thr Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu
        20                  25                  30

gug uuu aau gca aca aga uuu gca ucu gug uau gca ugg aau aga aaa        200
Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp Asn Arg Lys
    35                  40                  45

aga auu ucu aau ugu gug gcu gau uau ucu gug cug uau aau agu gcu        248
Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr Asn Ser Ala
50                  55                  60                  65

ucu uuu ucc aca uuu aaa ugu uau gga gug ucu cca aca aaa uua aau        296
Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr Lys Leu Asn
                70                  75                  80

gau uua ugu uuu aca aau gug uau gcu gau ucu uuu gug auc aga ggu        344
Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val Ile Arg Gly
            85                  90                  95

gau gaa gug aga cag auu gcc ccc gga cag aca gga aaa auu gcu gau        392
Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys Ile Ala Asp
        100                 105                 110

uac aau uac aaa cug ccu gau gau uuu aca gga ugu gug auu gcu ugg        440
Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val Ile Ala Trp
```

```
    115                 120                 125

aau ucu aau aau uua gau ucu aaa gug gga gga aau uac aau uau cug        488
Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr Asn Tyr Leu
130                 135                 140                 145

uac aga cug uuu aga aaa uca aau cug aaa ccu uuu gaa aga gau auu        536
Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu Arg Asp Ile
                150                 155                 160

uca aca gaa auu uau cag gcu gga uca aca ccu ugu aau gga gug gaa        584
Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn Gly Val Glu
            165                 170                 175

gga uuu aau ugu uau uuu cca uua cag agc uau gga uuu cag cca acc        632
Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe Gln Pro Thr
        180                 185                 190

aau ggu gug gga uau cag cca uau aga gug gug gug cug ucu uuu gaa        680
Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu
    195                 200                 205

cug cug cau gca ccu gca aca gug ugu gga ccu aaa ggc ucc ccc ggc        728
Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys Gly Ser Pro Gly
210                 215                 220                 225

ucc ggc ucc gga ucu ggu uau auu ccu gaa gcu cca aga gau ggg caa        776
Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln
                230                 235                 240

gcu uac guu cgu aaa gau ggc gaa ugg gua uua cuu ucu acc uuu uua        824
Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
            245                 250                 255

gga agc ggc agc gga ucu gaa cag uac auu aaa ugg ccu ugg uac auu        872
Gly Ser Gly Ser Gly Ser Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Ile
        260                 265                 270

ugg cuu gga uuu auu gca gga uua auu gca auu gug aug gug aca auu        920
Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile
    275                 280                 285

aug uua ugu ugu aug aca uca ugu ugu ucu ugu uua aaa gga ugu ugu        968
Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Cys Cys
290                 295                 300                 305

ucu ugu gga agc ugu ugu uga ugacucgagc ugguacugca ugcacgcaau          1019
Ser Cys Gly Ser Cys Cys
                310

gcuagcugcc ccuuucccgu ccuggguacc ccgagucucc cccgaccucg ggucccaggu      1079

augcucccac cuccaccugc cccacucacc accucugcua guuccagaca ccucccaagc      1139
```

acgcagcaau gcagcucaaa acgcuuagcc uagccacacc cccacgggaa acagcaguga 1199

uuaaccuuua gcaauaaacg aaaguuuaac uaagcuauac uaaccccagg guuggucaau 1259

uucgugccag ccacacccug gagcuagcaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagc 1319

auaugacuaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1379

aaaaaaaaaa aaaaaaaa 1397

BNT162b3d (SEQ ID NO: 31; SEQ ID NO: 32)

Structure $m_2^{7,3'-O}Gppp(m_1^{2'-O})$ApG-hAg-Kozak-RBD-GS-Fibritin-GS-TM-FI-A30L70

Encoded antigen Viral spike protein (S1S2 protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein fused to Fibritin fused to Transmembrane Domain (TM) of S1S2 protein); immunoglobulin secretory signal peptide (aa 1-22) at the N-terminus of the antigen sequence

```
agaauaaacu aguauucuuc uggucccCac agacucagag agaacccgcc acc aug          56
                                                           Met
                                                           1

gau ugg auu ugg aga auc cug uuc cuc gug gga gcc gcu aca gga gcc         104
Asp Trp Ile Trp Arg Ile Leu Phe Leu Val Gly Ala Ala Thr Gly Ala
            5                   10                  15

cac ucc cag aug cag gug aga uuu cca aau auu aca aau cug ugu cca         152
His Ser Gln Met Gln Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro
        20                  25                  30

uuu gga gaa gug uuu aau gca aca aga uuu gca ucu gug uau gca ugg         200
Phe Gly Glu Val Phe Asn Ala Thr Arg Phe Ala Ser Val Tyr Ala Trp
    35                  40                  45

aau aga aaa aga auu ucu aau ugu gug gcu gau uau ucu gug cug uau         248
Asn Arg Lys Arg Ile Ser Asn Cys Val Ala Asp Tyr Ser Val Leu Tyr
50                  55                  60                  65

aau agu gcu ucu uuu ucc aca uuu aaa ugu uau gga gug ucu cca aca         296
Asn Ser Ala Ser Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Pro Thr
                70                  75                  80

aaa uua aau gau uua ugu uuu aca aau gug uau gcu gau ucu uuu gug         344
Lys Leu Asn Asp Leu Cys Phe Thr Asn Val Tyr Ala Asp Ser Phe Val
            85                  90                  95

auc aga ggu gau gaa gug aga cag auu gcc ccc gga cag aca gga aaa         392
Ile Arg Gly Asp Glu Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Lys
        100                 105                 110

auu gcu gau uac aau uac aaa cug ccu gau gau uuu aca gga ugu gug         440
Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe Thr Gly Cys Val
    115                 120                 125

auu gcu ugg aau ucu aau aau uua gau ucu aaa gug gga gga aau uac         488
Ile Ala Trp Asn Ser Asn Asn Leu Asp Ser Lys Val Gly Gly Asn Tyr
130                 135                 140                 145
```

```
aau uau cug uac aga cug uuu aga aaa uca aau cug aaa ccu uuu gaa        536
Asn Tyr Leu Tyr Arg Leu Phe Arg Lys Ser Asn Leu Lys Pro Phe Glu
                150                 155                 160

aga gau auu uca aca gaa auu uau cag gcu gga uca aca ccu ugu aau        584
Arg Asp Ile Ser Thr Glu Ile Tyr Gln Ala Gly Ser Thr Pro Cys Asn
            165                 170                 175

gga gug gaa gga uuu aau ugu uau uuu cca uua cag agc uau gga uuu        632
Gly Val Glu Gly Phe Asn Cys Tyr Phe Pro Leu Gln Ser Tyr Gly Phe
        180                 185                 190

cag cca acc aau ggu gug gga uau cag cca uau aga gug gug gug cug        680
Gln Pro Thr Asn Gly Val Gly Tyr Gln Pro Tyr Arg Val Val Val Leu
    195                 200                 205

ucu uuu gaa cug cug cau gca ccu gca aca gug ugu gga ccu aaa ggc        728
Ser Phe Glu Leu Leu His Ala Pro Ala Thr Val Cys Gly Pro Lys Gly
210                 215                 220                 225

ucc ccc ggc ucc ggc ucc gga ucu ggu uau auu ccu gaa gcu cca aga        776
Ser Pro Gly Ser Gly Ser Gly Ser Gly Tyr Ile Pro Glu Ala Pro Arg
                230                 235                 240

gau ggg caa gcu uac guu cgu aaa gau ggc gaa ugg gua uua cuu ucu        824
Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser
            245                 250                 255

acc uuu uua gga agc ggc agc gga ucu gaa cag uac auu aaa ugg ccu        872
Thr Phe Leu Gly Ser Gly Ser Gly Ser Glu Gln Tyr Ile Lys Trp Pro
        260                 265                 270

ugg uac auu ugg cuu gga uuu auu gca gga uua auu gca auu gug aug        920
Trp Tyr Ile Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val Met
    275                 280                 285

gug aca auu aug uua ugu ugu aug aca uca ugu ugu ucu ugu uua aaa        968
Val Thr Ile Met Leu Cys Cys Met Thr Ser Cys Cys Ser Cys Leu Lys
290                 295                 300                 305

gga ugu ugu ucu ugu gga agc ugu ugu uga ugacucgagc ugguacugca         1018
Gly Cys Cys Ser Cys Gly Ser Cys Cys
                310

ugcacgcaau gcuagcugcc ccuuucccgu ccuggguacc ccgagucucc cccgaccucg     1078

ggucccaggu augcucccac cuccaccugc cccacucacc accucugcua guuccagaca     1138

ccucccaagc acgcagcaau gcagcucaaa acgcuuagcc uagccacacc cccacgggaa     1198

acagcaguga uuaaccuuua gcaauaaacg aaaguuuaac uaagcuauac uaaccccagg     1258

guuggucaau uucgugccag ccacacccug gagcuagcaa aaaaaaaaaa aaaaaaaaaa     1318
```

aaaaaaaagc auaugacuaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1378

aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1406

Self-amplifying RNA (saRNA)

The active principle of the self-amplifying mRNA (saRNA) drug substance is a single-stranded RNA, which self-amplifies upon entering a cell, and the coronavirus vaccine antigen is translated thereafter. In contrast to uRNA and modRNA that preferably code for a single protein, the coding region of saRNA contains two open reading frames (ORFs). The 5'-ORF encodes the RNA-dependent RNA polymerase such as Venezuelan equine encephalitis virus (VEEV) RNA-dependent RNA polymerase (replicase). The replicase ORF is followed 3' by a subgenomic promoter and a second ORF encoding the antigen. Furthermore, saRNA UTRs contain 5' and 3' conserved sequence elements (CSEs) required for self-amplification. The saRNA contains common structural elements optimized for maximal efficacy of the RNA as the uRNA (5'-cap, 5'-UTR, 3'-UTR, poly(A)-tail). The saRNA preferably contains uridine. The preferred 5' cap structure is beta-S-ARCA(D1) ($m_2^{7,2'\text{-}O}$GppSpG).

Cytoplasmic delivery of saRNA initiates an alphavirus-like life cycle. However, the saRNA does not encode for alphaviral structural proteins that are required for genome packaging or cell entry, therefore generation of replication competent viral particles is very unlikely to not possible. Replication does not involve any intermediate steps that generate DNA. The use/uptake of saRNA therefore poses no risk of genomic integration or other permanent genetic modification within the target cell. Furthermore, the saRNA itself prevents its persistent replication by effectively activating innate immune response via recognition of dsRNA intermediates.

Different embodiment of this platform are as follows:

RBS004.1 (SEQ ID NO: 24; SEQ ID NO: 7)

Structure beta-S-ARCA(D1)-replicase-S1S2-PP-FI-A30L70

Encoded antigen Viral spike protein (S protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

RBS004.2 (SEQ ID NO: 25; SEQ ID NO: 7)

Structure beta-S-ARCA(D1)-replicase-S1S2-PP-FI-A30L70

Encoded antigen Viral spike protein (S protein) of the SARS-CoV-2 (S1S2 full-length protein, sequence variant)

BNT162c1; RBS004.3 (SEQ ID NO: 26; SEQ ID NO: 5)

Structure beta-S-ARCA(D1)-replicase-RBD-GS-Fibritin-FI-A30L70

Encoded antigen Viral spike protein (S protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein)

RBS004.4 (SEQ ID NO: 27; SEQ ID NO: 28)

Structure beta-S-ARCA(D1)-replicase-RBD-GS-Fibritin-TM-FI-A30L70

Encoded antigen Viral spike protein (S protein) of the SARS-CoV-2 (partial sequence, Receptor Binding Domain (RBD) of S1S2 protein)

Figure 21 schematizes the general structure of the antigen-encoding RNAs.

Nucleotide Sequence of RBS004.1

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
        10         20         30         40     45
GAUGGGCGGC GCAUGAGAGA AGCCCAGACC AAUUACCUAC CCAAA
                                5'UTR
        55         65         75         85         95         105
AUGGAGAAAG UUCACGUUGA CAUCGAGGAA GACAGCCCAU UCCUCAGAGC UUUGCAGCGG
  M  E  K   V  H  V   D  I  E  E   D  S  P   F  L  R   A  L  Q  R
                               nsp1
       115        125        135        145        155        165
AGCUUCCCGC AGUUUGAGGU AGAAGCCAAG CAGGUCACUG AUAAUGACCA UGCUAAUGCC
  S  F  P   Q  F  E   V  E  A  K   Q  V  T   D  N  D   H  A  N  A
                               nsp1
       175        185        195        205        215        225
AGAGCGUUUU CGCAUCUGGC UUCAAAACUG AUCGAAACGG AGGUGGACCC AUCCGACACG
  R  A  F   S  H  L   A  S  K  L   I  E  T   E  V  D   P  S  D  T
                               nsp1
       235        245        255        265        275        285
AUCCUUGACA UUGGAAGUGC GCCCGCCCGC AGAAUGUAUU CUAAGCACAA GUAUCAUUGU
  I  L  D   I  G  S   A  P  A  R   R  M  Y   S  K  H   K  Y  H  C
                               nsp1
       295        305        315        325        335        345
AUCUGUCCGA UGAGAUGUGC GGAAGAUCCG GACAGAUUGU AUAAGUAUGC AACUAAGCUG
  I  C  P   M  R  C   A  E  D  P   D  R  L   Y  K  Y   A  T  K  L
                               nsp1
       355        365        375        385        395        405
AAGAAAAACU GUAAGGAAAU AACUGAUAAG GAAUUGGACA AGAAAAUGAA GGAGCUCGCC
  K  K  N   C  K  E   I  T  D  K   E  L  D   K  K  M   K  E  L  A
                               nsp1
       415        425        435        445        455        465
GCCGUCAUGA GCGACCCUGA CCUGGAAACU GAGACUAUGU GCCUCCACGA CGACGAGUCG
```

A V M S D P D L E T E T M C L H D D E S

nsp1

475 485 495 505 515 525

UGUCGCUACG AAGGGCAAGU CGCUGUUUAC CAGGAUGUAU ACGCGGUUGA CGGACCGACA

C R Y E G Q V A V Y Q D V Y A V D G P T

nsp1

535 545 555 565 575 585

AGUCUCUAUC ACCAAGCCAA UAAGGGAGUU AGAGUCGCCU ACUGGAUAGG CUUUGACACC

S L Y H Q A N K G V R V A Y W I G F D T

nsp1

595 605 615 625 635 645

ACCCCUUUUA UGUUUAAGAA CUUGGCUGGA GCAUAUCCAU CAUACUCUAC CAACUGGGCC

T P F M F K N L A G A Y P S Y S T N W A

nsp1

655 665 675 685 695 705

GACGAAACCG UGUUAACGGC UCGUAACAUA GGCCUAUGCA GCUCUGACGU UAUGGAGCGG

D E T V L T A R N I G L C S S D V M E R

nsp1

715 725 735 745 755 765

UCACGUAGAG GGAUGUCCAU UCUUAGAAAG AAGUAUUUGA AACCAUCCAA CAAUGUUCUA

S R R G M S I L R K K Y L K P S N N V L

nsp1

775 785 795 805 815 825

UUCUCUGUUG GCUCGACCAU CUACCACGAA AAGAGGGACU UACUGAGGAG CUGGCACCUG

F S V G S T I Y H E K R D L L R S W H L

nsp1

835 845 855 865 875 885

CCGUCUGUAU UUCACUUACG UGGCAAGCAA AAUUACACAU GUCGGUGUGA GACUAUAGUU

P S V F H L R G K Q N Y T C R C E T I V

nsp1

895 905 915 925 935 945

AGUUGCGACG GGUACGUCGU UAAAAGAAUA GCUAUCAGUC CAGGCCUGUA UGGGAAGCCU

S C D G Y V V K R I A I S P G L Y G K P

nsp1

955 965 975 985 995 1005
UCAGGCUAUG CUGCUACGAU GCACCGCGAG GGAUUCUUGU GCUGCAAAGU GACAGACACA
S G Y A A T M H R E G F L C C K V T D T

nsp1

1015 1025 1035 1045 1055 1065
UUGAACGGGG AGAGGGUCUC UUUUCCCGUG UGCACGUAUG UGCCAGCUAC AUUGUGUGAC
L N G E R V S F P V C T Y V P A T L C D

nsp1

1075 1085 1095 1105 1115 1125
CAAAUGACUG GCAUACUGGC AACAGAUGUC AGUGCGGACG ACGCGCAAAA ACUGCUGGUU
Q M T G I L A T D V S A D D A Q K L L V

nsp1

1135 1145 1155 1165 1175 1185
GGGCUCAACC AGCGUAUAGU CGUCAACGGU CGCACCCAGA GAAACACCAA UACCAUGAAA
G L N Q R I V V N G R T Q R N T N T M K

nsp1

1198 1205 1215 1225 1235 1245
AAUUACCUUU UGCCCGUAGU GGCCCAGGCA UUUGCUAGGU GGGCAAAGGA AUAUAAGGAA
N Y L L P V V A Q A F A R W A K E Y K E

nsp1

1255 1265 1275 1285 1295 1305
GAUCAAGAAG AUGAAAGGCC ACUAGGACUA CGAGAUAGAC AGUUAGUCAU GGGGUGUUGU
D Q E D E R P L G L R D R Q L V M G C C

nsp1

1315 1325 1335 1345 1355 1365
UGGGCUUUUA GAAGGCACAA GAUAACAUCU AUUUAUAAGC GCCCGGAUAC CCAAACCAUC
W A F R R H K I T S I Y K R P D T Q T I

nsp1

1375 1385 1395 1405 1415 1425
AUCAAAGUGA ACAGCGAUUU CCACUCAUUC GUGCUGCCCA GGAUAGGCAG UAACACAUUG
I K V N S D F H S F V L P R I G S N T L

nsp1

1435 1445 1455 1465 1475 1485
GAGAUCGGGC UGAGAACAAG AAUCAGGAAA AUGUUAGAGG AGCACAAGGA GCCGUCACCU
E I G L R T R I R K M L E E H K E P S P

nsp1

1495 1505 1515 1525 1535 1545

CUCAUUACCG CCGAGGACGU ACAAGAAGCU AAGUGCGCAG CCGAUGAGGC UAAGGAGGUG

L I T A E D V Q E A K C A A D E A K E V

nsp1

1555 1565 1575 1585 1595 1605

CGUGAAGCCG AGGAGUUGCG CGCAGCUCUA CCACCUUUGG CAGCUGAUGU UGAGGAGCCC

R E A E E L R A A L P P L A A D V E E P

nsp1

1615 1625 1635 1645 1650

ACUCUGGAAG CCGAUGUCGA CUUGAUGUUA CAAGAGGCUG GGGCC

T L E A D V D L M L Q E A G A

nsp1

1660 1670 1680 1690 1700 1710

GGCUCAGUGG AGACACCUCG UGGCUUGAUA AAGGUUACCA GCUACGCUGG CGAGGACAAG

G S V E T P R G L I K V T S Y A G E D K

nsp2

1720 1730 1740 1750 1760 1770

AUCGGCUCUU ACGCUGUGCU UUCUCCGCAG GCUGUACUCA AGAGUGAAAA AUUAUCUUGC

I G S Y A V L S P Q A V L K S E K L S C

nsp2

1780 1790 1800 1810 1820 1830

AUCCACCCUC UCGCUGAACA AGUCAUAGUG AUAACACACU CUGGCCGAAA AGGGCGUUAU

I H P L A E Q V I V I T H S G R K G R Y

nsp2

1840 1850 1860 1870 1880 1890

GCCGUGGAAC CAUACCAUGG UAAAGUAGUG GUGCCAGAGG GACAUGCAAU ACCCGUCCAG

A V E P Y H G K V V V P E G H A I P V Q

nsp2

1900 1910 1920 1930 1940 1950

GACUUUCAAG CUCUGAGUGA AAGUGCCACC AUUGUGUACA ACGAACGUGA GUUCGUAAAC

D F Q A L S E S A T I V Y N E R E F V N

nsp2

1960 1970 1980 1990 2000 2010

AGGUACCUGC ACCAUAUUGC CACACAUGGA GGAGCGCUGA ACACUGAUGA AGAAUAUUAC

R Y L H H I A T H G G A L N T D E E Y Y

nsp2

2020 2030 2040 2050 2060 2070

AAAACUGUCA AGCCCAGCGA GCACGACGGC GAAUACCUGU ACGACAUCGA CAGGAAACAG

K T V K P S E H D G E Y L Y D I D R K Q

nsp2

2080 2090 2100 2110 2120 2130

UGCGUCAAGA AAGAGCUAGU CACUGGGCUA GGGCUCACAG GCGAGCUGGU CGAUCCUCCC

C V K K E L V T G L G L T G E L V D P P

nsp2

2140 2150 2160 2170 2180 2190

UUCCAUGAAU UCGCCUACGA GAGUCUGAGA ACACGACCAG CCGCUCCUUA CCAAGUACCA

F H E F A Y E S L R T R P A A P Y Q V P

nsp2

2200 2210 2220 2230 2240 2250

ACCAUAGGGG UGUAUGGCGU GCCAGGAUCA GGCAAGUCUG GCAUCAUUAA AAGCGCAGUC

T I G V Y G V P G S G K S G I I K S A V

nsp2

2260 2270 2280 2290 2300 2310

ACCAAAAAAG AUCUAGUGGU GAGCGCCAAG AAAGAAAACU GUGCAGAAAU UAUAAGGGAC

T K K D L V V S A K K E N C A E I I R D

nsp2

2320 2330 2340 2350 2360 2370

GUCAAGAAAA UGAAAGGGCU GGACGUCAAU GCCAGAACUG UGGACUCAGU GCUCUUGAAU

V K K M K G L D V N A R T V D S V L L N

nsp2

2380 2390 2400 2410 2420 2430

GGAUGCAAAC ACCCCGUAGA GACCCUGUAU AUUGACGAGG CUUUUGCUUG UCAUGCAGGU

G C K H P V E T L Y I D E A F A C H A G

nsp2

2440 2450 2460 2470 2480 2490

ACUCUCAGAG CGCUCAUAGC CAUUAUAAGA CCUAAAAAGG CAGUGCUCUG CGGAGAUCCC

T L R A L I A I I R P K K A V L C G D P

nsp2

2500 2510 2520 2530 2540 2550

AAACAGUGCG GUUUUUUUAA CAUGAUGUGC CUGAAAGUGC AUUUUAACCA CGAGAUUUGC

K Q C G F F N M M C L K V H F N H E I C

nsp2

2560 2570 2580 2590 2600 2610

ACACAAGUCU UCCACAAAAG CAUCUCUCGC CGUUGCACUA AAUCUGUGAC UUCGGUCGUC

T Q V F H K S I S R R C T K S V T S V V

nsp2

2620 2630 2640 2650 2660 2670

UCAACCUUGU UUUACGACAA AAAAAUGAGA ACGACGAAUC CGAAAGAGAC UAAGAUUGUG

S T L F Y D K K M R T T N P K E T K I V

nsp2

2680 2690 2700 2710 2720 2730

AUUGACACUA CCGGCAGUAC CAAACCUAAG CAGGACGAUC UCAUUCUCAC UUGUUUCAGA

I D T T G S T K P K Q D D L I L T C F R

nsp2

2740 2750 2760 2770 2780 2790

GGGUGGGUGA AGCAGUUGCA AAUAGAUUAC AAAGGCAACG AAAUAAUGAC GGCAGCUGCC

G W V K Q L Q I D Y K G N E I M T A A A

nsp2

2800 2810 2820 2830 2840 2850

UCUCAAGGGC UGACCCGUAA AGGUGUGUAU GCCGUUCGGU ACAAGGUGAA UGAAAAUCCU

S Q G L T R K G V Y A V R Y K V N E N P

nsp2

2860 2870 2880 2890 2900 2910

CUGUACGCAC CCACCUCAGA ACAUGUGAAC GUCCUACUGA CCCGCACGGA GGACCGCAUC

L Y A P T S E H V N V L L T R T E D R I

nsp2

2920 2930 2940 2950 2960 2970

GUGUGGAAAA CACUAGCCGG CGACCCAUGG AUAAAAACAC UGACUGCCAA GUACCCUGGG

V W K T L A G D P W I K T L T A K Y P G

nsp2

2980 2990 3000 3010 3020 3030

AAUUUCACUG CCACGAUAGA GGAGUGGCAA GCAGAGCAUG AUGCCAUCAU GAGGCACAUC

N F T A T I E E W Q A E H D A I M R H I

nsp2

3040 3050 3060 3070 3080 3090

UUGGAGAGAC CGGACCCUAC CGACGUCUUC CAGAAUAAGG CAAACGUGUG UUGGGCCAAG

L E R P D P T D V F Q N K A N V C W A K

nsp2

3100 3110 3120 3130 3140 3150

GCUUUAGUGC CGGUGCUGAA GACCGCUGGC AUAGACAUGA CCACUGAACA AUGGAACACU

A L V P V L K T A G I D M T T E Q W N T

nsp2

3160 3170 3180 3190 3200 3210

GUGGAUUAUU UUGAAACGGA CAAAGCUCAC UCAGCAGAGA UAGUAUUGAA CCAACUAUGC

V D Y F E T D K A H S A E I V L N Q L C

nsp2

3220 3230 3240 3250 3260 3270

GUGAGGUUCU UUGGACUCGA UCUGGACUCC GGUCUAUUUU CUGCACCCAC UGUUCCGUUA

V R F F G L D L D S G L F S A P T V P L

nsp2

3280 3290 3300 3310 3320 3330

UCCAUUAGGA AUAAUCACUG GGAUAACUCC CCGUCGCCUA ACAUGUACGG GCUGAAUAAA

S I R N N H W D N S P S P N M Y G L N K

nsp2

3340 3350 3360 3370 3380 3390

GAAGUGGUCC GUCAGCUCUC UCGCAGGUAC CCACAACUGC CUCGGGCAGU UGCCACUGGU

E V V R Q L S R R Y P Q L P R A V A T G

nsp2

3400 3410 3420 3430 3440 3450

AGAGUCUAUG ACAUGAACAC UGGUACACUG CGCAAUUAUG AUCCGCGCAU AAACCUAGUA

R V Y D M N T G T L R N Y D P R I N L V

nsp2

3460 3470 3480 3490 3500 3510

CCUGUAAACA GAAGACUGCC UCAUGCUUUA GUCCUCCACC AUAAUGAACA CCCACAGAGU

P V N R R L P H A L V L H H N E H P Q S

nsp2

3520 3530 3540 3550 3560 3570

GACUUUUCUU CAUUCGUCAG CAAAUUGAAG GGCAGAACUG UCCUGGUGGU CGGGGAAAAG

D F S S F V S K L K G R T V L V V G E K

nsp2

3580 3590 3600 3610 3620 3630

UUGUCCGUCC CAGGCAAAAU GGUUGACUGG UUGUCAGACC GGCCUGAGGC UACCUUCAGA

L S V P G K M V D W L S D R P E A T F R

nsp2

3640 3650 3660 3670 3680 3690

GCUCGGCUGG AUUUAGGCAU CCCAGGUGAU GUGCCCAAAU AUGACAUAAU AUUUGUUAAU

A R L D L G I P G D V P K Y D I I F V N

nsp2

3700 3710 3720 3730 3740 3750

GUGAGGACCC CAUAUAAAUA CCAUCACUAU CAGCAGUGUG AAGACCAUGC CAUUAAGCUA

V R T P Y K Y H H Y Q Q C E D H A I K L

nsp2

3760 3770 3780 3790 3800 3810

AGCAUGUUGA CCAAGAAAGC AUGUCUGCAU CUGAAUCCCG GCGGAACCUG UGUCAGCAUA

S M L T K K A C L H L N P G G T C V S I

nsp2

3820 3830 3840 3850 3860 3870

GGUUAUGGUU ACGCUGACAG GGCCAGCGAA AGCAUCAUUG GUGCUAUAGC GCGGCAGUUC

G Y G Y A D R A S E S I I G A I A R Q F

nsp2

3880 3890 3900 3910 3920 3930

AAGUUUUCCC GAGUAUGCAA ACCGAAAUCC UCACUUGAGG AGACGGAAGU UCUGUUUGUA

K F S R V C K P K S S L E E T E V L F V

nsp2

3940 3950 3960 3970 3980 3990

UUCAUUGGGU ACGAUCGCAA GGCCCGUACG CACAAUCCUU ACAAGCUAUC AUCAACCUUG

F I G Y D R K A R T H N P Y K L S S T L

nsp2

4000 4010 4020 4030 4032

ACCAACAUUU AUACAGGUUC CAGACUCCAC GAAGCCGGAU GU

T N I Y T G S R L H E A G C

nsp2

4042 4052 4062 4072 4082 4092

GCACCCUCAU AUCAUGUGGU GCGAGGGGAU AUUGCCACGG CCACCGAAGG AGUGAUUAUA

A P S Y H V V R G D I A T A T E G V I I

nsp3

4102 4112 4122 4132 4142 4152

AAUGCUGCUA ACAGCAAAGG ACAACCUGGC GGAGGGGUGU GCGGAGCGCU GUAUAAGAAA

N A A N S K G Q P G G G V C G A L Y K K

nsp3

4162 4172 4182 4192 4202 4212

UUCCCGGAAA GUUUCGAUUU ACAGCCGAUC GAAGUAGGAA AAGCGCGACU GGUCAAAGGU

F P E S F D L Q P I E V G K A R L V K G

nsp3

4222 4232 4242 4252 4262 4272

GCAGCUAAAC AUAUCAUUCA UGCCGUAGGA CCAAACUUCA ACAAAGUUUC GGAGGUUGAA

A A K H I I H A V G P N F N K V S E V E

nsp3

4282 4292 4302 4312 4322 4332

GGUGACAAAC AGUUGGCAGA GGCUUAUGAG UCCAUCGCUA AGAUUGUCAA CGAUAACAAU

G D K Q L A E A Y E S I A K I V N D N N

nsp3

4342 4352 4362 4372 4382 4392

UACAAGUCAG UAGCGAUUCC ACUGUUGUCC ACCGGCAUCU UUUCCGGGAA CAAAGAUCGA

Y K S V A I P L L S T G I F S G N K D R

nsp3

4402 4412 4422 4432 4442 4452

CUAACCCAAU CAUUGAACCA UUUGCUGACA GCUUUAGACA CCACUGAUGC AGAUGUAGCC

L T Q S L N H L L T A L D T T D A D V A

nsp3

4462 4472 4482 4492 4502 4512

AUAUACUGCA GGGACAAGAA AUGGGAAAUG ACUCUCAAGG AAGCAGUGGC UAGGAGAGAA

I Y C R D K K W E M T L K E A V A R R E

nsp3

4522 4532 4542 4552 4562 4572

GCAGUGGAGG AGAUAUGCAU AUCCGACGAU UCUUCAGUGA CAGAACCUGA UGCAGAGCUG

A V E E I C I S D D S S V T E P D A E L

nsp3

4582 4592 4602 4612 4622 4632

GUGAGGGUGC AUCCCAAGAG UUCUUUGGCU GGAAGGAAGG GCUACAGCAC AAGCGAUGGC

V R V H P K S S L A G R K G Y S T S D G

nsp3

4642 4652 4662 4672 4682 4692

AAAACUUUCU CAUAUUUGGA AGGGACCAAG UUUCACCAGG CGGCCAAGGA UAUAGCAGAA

K T F S Y L E G T K F H Q A A K D I A E

nsp3

4702 4712 4722 4732 4742 4752

AUUAAUGCCA UGUGGCCCGU UGCAACGGAG GCCAAUGAGC AGGUAUGCAU GUAUAUCCUC

I N A M W P V A T E A N E Q V C M Y I L

nsp3

4762 4772 4782 4792 4802 4812

GGAGAAAGCA UGAGCAGUAU UAGGUCGAAA UGCCCCGUCG AGGAGUCGGA AGCCUCCACA

G E S M S S I R S K C P V E E S E A S T

nsp3

4822 4832 4842 4852 4862 4872

CCACCUAGCA CGCUGCCUUG CUUGUGCAUC CAUGCCAUGA CUCCAGAAAG AGUACAGCGC

P P S T L P C L C I H A M T P E R V Q R

nsp3

4882 4892 4902 4912 4922 4932

CUAAAAGCCU CACGUCCAGA ACAAAUUACU GUGUGCUCAU CCUUUCCAUU GCCGAAGUAU

L K A S R P E Q I T V C S S F P L P K Y

nsp3

4942 4952 4962 4972 4982 4992

AGAAUCACUG GUGUGCAGAA GAUCCAAUGC UCCCAGCCUA UAUUGUUCUC ACCGAAAGUG

R I T G V Q K I Q C S Q P I L F S P K V

nsp3

5002 5012 5022 5032 5042 5052

CCUGCGUAUA UUCAUCCAAG GAAGUAUCUC GUGGAAACAC CACCGGUAGA CGAGACUCCG

P A Y I H P R K Y L V E T P P V D E T P

nsp3

5062 5072 5082 5092 5102 5112

GAGCCAUCGG CAGAGAACCA AUCCACAGAG GGGACACCUG AACAACCACC ACUUAUAACC

E P S A E N Q S T E G T P E Q P P L I T

nsp3

5122 5132 5142 5152 5162 5172

GAGGAUGAGA CCAGGACUAG AACGCCUGAG CCGAUCAUCA UCGAAGAAGA AGAAGAAGAU

E D E T R T R T P E P I I I E E E E E D

nsp3

5182 5192 5202 5212 5222 5232

AGCAUAAGUU UGCUGUCAGA UGGCCCGACC CACCAGGUGC UGCAAGUCGA GGCAGACAUU

S I S L L S D G P T H Q V L Q V E A D I

nsp3

5242 5252 5262 5272 5282 5292

CACGGGCCGC CCUCUGUAUC UAGCUCAUCC UGGUCCAUUC CUCAUGCAUC CGACUUUGAU

H G P P S V S S S S W S I P H A S D F D

nsp3

5302 5312 5322 5332 5342 5352

GUGGACAGUU UAUCCAUACU UGACACCCUG GAGGGAGCUA GCGUGACCAG CGGGGCAACG

V D S L S I L D T L E G A S V T S G A T

nsp3

5362 5372 5382 5392 5402 5412

UCAGCCGAGA CUAACUCUUA CUUCGCAAAG AGUAUGGAGU UUCUGGCGCG ACCGGUGCCU

S A E T N S Y F A K S M E F L A R P V P

nsp3

5422 5432 5442 5452 5462 5472

GCGCCUCGAA CAGUAUUCAG GAACCCUCCA CAUCCCGCUC CGCGCACAAG AACACCGUCA

A P R T V F R N P P H P A P R T R T P S

nsp3

5482 5492 5502 5512 5522 5532

CUUGCACCCA GCAGGGCCUG CUCCAGAACC AGCCUAGUUU CCACCCCGCC AGGCGUGAAU

L A P S R A C S R T S L V S T P P G V N

nsp3

```
     5542       5552       5562       5572       5582       5592
AGGGUGAUCA CUAGAGAGGA GCUCGAAGCG CUUACCCCGU CACGCACUCC UAGCAGGUCG
  R  V  I   T  R  E   E  L  E  A   L  T  P   S  R  T   P  S  R  S
```

nsp3

```
     5602       5612       5622       5632       5642       5652
GUCUCCAGAA CCAGCCUGGU CUCCAACCCG CCAGGCGUAA AUAGGGUGAU UACAAGAGAG
  V  S  R   T  S  L   V  S  N  P   P  G  V   N  R  V   I  T  R  E
```

nsp3

```
     5662       5672       5682       5692       5702 5703
GAGUUUGAGG CGUUCGUAGC ACAACAACAA UGACGGUUUG AUGCGGGUGC A
  E  F  E   A  F  V   A  Q  Q  Q   *  R  F   D  A  G   A
```

nsp3

```
     5713       5723       5733       5743       5753       5763
UACAUCUUUU CCUCCGACAC CGGUCAAGGG CAUUUACAAC AAAAAUCAGU AAGGCAAACG
  Y  I  F   S  S  D   T  G  Q  G   H  L  Q   Q  K  S   V  R  Q  T
```

nsp4

```
     5773       5783       5793       5803       5813       5823
GUGCUAUCCG AAGUGGUGUU GGAGAGGACC GAAUUGGAGA UUUCGUAUGC CCCGCGCCUC
  V  L  S   E  V  V   L  E  R  T   E  L  E   I  S  Y   A  P  R  L
```

nsp4

```
     5833       5843       5853       5863       5873       5883
GACCAAGAAA AAGAAGAAUU ACUACGCAAG AAAUUACAGU UAAAUCCCAC ACCUGCUAAC
  D  Q  E   K  E  E   L  L  R  K   K  L  Q   L  N  P   T  P  A  N
```

nsp4

```
     5893       5903       5913       5923       5933       5943
AGAAGCAGAU ACCAGUCCAG GAAGGUGGAG AACAUGAAAG CCAUAACAGC UAGACGUAUU
  R  S  R   Y  Q  S   R  K  V  E   N  M  K   A  I  T   A  R  R  I
```

nsp4

```
     5953       5963       5973       5983       5993       6003
CUGCAAGGCC UAGGGCAUUA UUUGAAGGCA GAAGGAAAAG UGGAGUGCUA CCGAACCCUG
  L  Q  G   L  G  H   Y  L  K  A   E  G  K   V  E  C   Y  R  T  L
```

nsp4

```
     6013       6023       6033       6043       6053       6063
```

CAUCCUGUUC CUUUGUAUUC AUCUAGUGUG AACCGUGCCU UUUCAAGCCC CAAGGUCGCA

H P V P L Y S S S V N R A F S S P K V A

nsp4

6073 6083 6093 6103 6113 6123

GUGGAAGCCU GUAACGCCAU GUUGAAAGAG AACUUUCCGA CUGUGGCUUC UUACUGUAUU

V E A C N A M L K E N F P T V A S Y C I

nsp4

6133 6143 6153 6163 6173 6183

AUUCCAGAGU ACGAUGCCUA UUUGGACAUG GUUGACGGAG CUUCAUGCUG CUUAGACACU

I P E Y D A Y L D M V D G A S C C L D T

nsp4

6193 6203 6213 6223 6233 6243

GCCAGUUUUU GCCCUGCAAA GCUGCGCAGC UUUCCAAAGA AACACUCCUA UUUGGAACCC

A S F C P A K L R S F P K K H S Y L E P

nsp4

6253 6263 6273 6283 6293 6303

ACAAUACGAU CGGCAGUGCC UUCAGCGAUC CAGAACACGC UCCAGAACGU CCUGGCAGCU

T I R S A V P S A I Q N T L Q N V L A A

nsp4

6313 6323 6333 6343 6353 6363

GCCACAAAAA GAAAUUGCAA UGUCACGCAA AUGAGAGAAU UGCCCGUAUU GGAUUCGGCG

A T K R N C N V T Q M R E L P V L D S A

nsp4

6373 6383 6393 6403 6413 6423

GCCUUUAAUG UGGAAUGCUU CAAGAAAUAU GCGUGUAAUA AUGAAUAUUG GGAAACGUUU

A F N V E C F K K Y A C N N E Y W E T F

nsp4

6433 6443 6453 6463 6473 6483

AAAGAAAACC CCAUCAGGCU UACUGAAGAA AACGUGGUAA AUUACAUUAC CAAAUUAAAA

K E N P I R L T E E N V V N Y I T K L K

nsp4

6493 6503 6513 6523 6533 6543

GGACCAAAAG CUGCUGCUCU UUUUGCGAAG ACACAUAAUU UGAAUAUGUU GCAGGACAUA

G P K A A A L F A K T H N L N M L Q D I

nsp4

6553 6563 6573 6583 6593 6603

CCAAUGGACA GGUUUGUAAU GGACUUAAAG AGAGACGUGA AAGUGACUCC AGGAACAAAA

P M D R F V M D L K R D V K V T P G T K

nsp4

6613 6623 6633 6643 6653 6663

CAUACUGAAG AACGGCCCAA GGUACAGGUG AUCCAGGCUG CCGAUCCGCU AGCAACAGCG

H T E E R P K V Q V I Q A A D P L A T A

nsp4

6673 6683 6693 6703 6713 6723

UAUCUGUGCG GAAUCCACCG AGAGCUGGUU AGGAGAUUAA AUGCGGUCCU GCUUCCGAAC

Y L C G I H R E L V R R L N A V L L P N

nsp4

6733 6743 6753 6763 6773 6783

AUUCAUACAC UGUUUGAUAU GUCGGCUGAA GACUUUGACG CUAUUAUAGC CGAGCACUUC

I H T L F D M S A E D F D A I I A E H F

nsp4

6793 6803 6813 6823 6833 6843

CAGCCUGGGG AUUGUGUUCU GGAAACUGAC AUCGCGUCGU UUGAUAAAAG UGAGGACGAC

Q P G D C V L E T D I A S F D K S E D D

nsp4

6853 6863 6873 6883 6893 6903

GCCAUGGCUC UGACCGCGUU AAUGAUUCUG GAAGACUUAG GUGUGGACGC AGAGCUGUUG

A M A L T A L M I L E D L G V D A E L L

nsp4

6913 6923 6933 6943 6953 6963

ACGCUGAUUG AGGCGGCUUU CGGCGAAAUU UCAUCAAUAC AUUUGCCCAC UAAAACUAAA

T L I E A A F G E I S S I H L P T K T K

nsp4

6973 6983 6993 7003 7013 7023

UUUAAAUUCG GAGCCAUGAU GAAAUCUGGA AUGUUCCUCA CACUGUUUGU GAACACAGUC

F K F G A M M K S G M F L T L F V N T V

nsp4

7033 7043 7053 7063 7073 7083

AUUAACAUUG UAAUCGCAAG CAGAGUGUUG AGAGAACGGC UAACCGGAUC ACCAUGUGCA

I N I V I A S R V L R E R L T G S P C A

nsp4

7093 7103 7113 7123 7133 7143

GCAUUCAUUG GAGAUGACAA UAUCGUGAAA GGAGUCAAAU CGGACAAAUU AAUGGCAGAC

A F I G D D N I V K G V K S D K L M A D

nsp4

7153 7163 7173 7183 7193 7203

AGGUGCGCCA CCUGGUUGAA UAUGGAAGUC AAGAUUAUAG AUGCUGUGGU GGGCGAGAAA

R C A T W L N M E V K I I D A V V G E K

nsp4

7213 7223 7233 7243 7253 7263

GCGCCUUAUU UCUGUGGAGG GUUUAUUUUG UGUGACUCCG UGACCGGCAC AGCGUGCCGU

A P Y F C G G F I L C D S V T G T A C R

nsp4

7273 7283 7293 7303 7313 7323

GUGGCAGACC CCCUAAAAAG GCUGUUUAAG CUAGGCAAAC CUCUGGCAGC AGACGAUGAA

V A D P L K R L F K L G K P L A A D D E

nsp4

7333 7343 7353 7363 7373 7383

CAUGAUGAUG ACAGGAGAAG GGCAUUGCAU GAGGAGUCAA CACGCUGGAA CCGAGUGGGU

H D D D R R R A L H E E S T R W N R V G

nsp4

7393 7403 7413 7423 7433 7443

AUUCUUUCAG AGCUGUGCAA GGCAGUAGAA UCAAGGUAUG AAACCGUAGG AACUUCCAUC

I L S E L C K A V E S R Y E T V G T S I

nsp4

7453 7463 7473 7483 7493 7503

AUAGUUAUGG CCAUGACUAC UCUAGCUAGC AGUGUUAAAU CAUUCAGCUA CCUGAGAGGG

I V M A M T T L A S S V K S F S Y L R G

nsp4

7513 7523 7527

GCCCCUAUAA CUCUCUACGG CUAA

*A P I T L Y G **

nsp4

```
      7537        7547        7557        7567  7568
CCUGAAUGGA CUACGACAUA GUCUAGUCCG CCAAGACUAG U
```

virUTR

```
      7578        7588        7598        7608        7618        7628
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGAA UUUGACAACA
  M   F   V   F   L   V   L   L   P   L   V   S   S   Q   C   V   N   L   T   T
```

S protein

```
      7638        7648        7658        7668        7678        7688
AGAACACAGC UGCCACCAGC UUAUACAAAU UCUUUUACCA GAGGAGUGUA UUAUCCUGAU
  R   T   Q   L   P   P   A   Y   T   N   S   F   T   R   G   V   Y   Y   P   D
```

S protein

```
      7698        7708        7718        7728        7738        7748
AAAGUGUUUA GAUCUUCUGU GCUGCACAGC ACACAGGACC UGUUUCUGCC AUUUUUUAGC
  K   V   F   R   S   S   V   L   H   S   T   Q   D   L   F   L   P   F   F   S
```

S protein

```
      7758        7768        7778        7788        7798        7808
AAUGUGACAU GGUUUCAUGC AAUUCAUGUG UCUGGAACAA AUGGAACAAA AAGAUUUGAU
  N   V   T   W   F   H   A   I   H   V   S   G   T   N   G   T   K   R   F   D
```

S protein

```
      7818        7828        7838        7848        7858        7868
AAUCCUGUGC UGCCUUUUAA UGAUGGAGUG UAUUUUGCUU CAACAGAAAA GUCAAAUAUU
  N   P   V   L   P   F   N   D   G   V   Y   F   A   S   T   E   K   S   N   I
```

S protein

```
      7878        7888        7898        7908        7918        7928
AUUAGAGGAU GGAUUUUUGG AACAACACUG GAUUCUAAAA CACAGUCUCU GCUGAUUGUG
  I   R   G   W   I   F   G   T   T   L   D   S   K   T   Q   S   L   L   I   V
```

S protein

```
      7938        7948        7958        7968        7978        7988
AAUAAUGCAA CAAAUGUGGU GAUUAAAGUG UGUGAAUUUC AGUUUUGUAA UGAUCCUUUU
  N   N   A   T   N   V   V   I   K   V   C   E   F   Q   F   C   N   D   P   F
```

S protein

```
      7998        8008        8018        8028        8038        8048
CUGGGAGUGU AUUAUCACAA AAAUAAUAAA UCUUGGAUGG AAUCUGAAUU UAGAGUGUAU
```

L G V Y Y H K N N K S W M E S E F R V Y

S protein

8058 8068 8078 8088 8098 8108

UCCUCUGCAA AUAAUUGUAC AUUUGAAUAU GUGUCUCAGC CUUUUCUGAU GGAUCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

8118 8128 8138 8148 8158 8168

GGAAAACAGG GCAAUUUUAA AAAUCUGAGA GAAUUUGUGU UUAAAAAUAU UGAUGGAUAU

G K Q G N F K N L R E F V F K N I D G Y

S protein

8178 8188 8198 8208 8218 8228

UUUAAAAUUU AUUCUAAACA CACACCAAUU AAUUUAGUGA GAGAUCUGCC UCAGGGAUUU

F K I Y S K H T P I N L V R D L P Q G F

S protein

8238 8248 8258 8268 8278 8288

UCUGCUCUGG AACCUCUGGU GGAUCUGCCA AUUGGCAUUA AUAUUACAAG AUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

8298 8308 8318 8328 8338 8348

CUGCUGGCUC UGCACAGAUC UUAUCUGACA CCUGGAGAUU CUUCUUCUGG AUGGACAGCC

L L A L H R S Y L T P G D S S S G W T A

S protein

8358 8368 8378 8388 8398 8408

GGAGCUGCAG CUUAUUAUGU GGGCUAUCUG CAGCCAAGAA CAUUUCUGCU GAAAUAUAAU

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

8418 8428 8438 8448 8458 8468

GAAAAUGGAA CAAUUACAGA UGCUGUGGAU UGUGCUCUGG AUCCUCUGUC UGAAACAAAA

E N G T I T D A V D C A L D P L S E T K

S protein

8478 8488 8498 8508 8518 8528

UGUACAUUAA AAUCUUUUAC AGUGGAAAAA GGCAUUUAUC AGACAUCUAA UUUUAGAGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

8538 8548 8558 8568 8578 8588

CAGCCAACAG AAUCUAUUGU GAGAUUUCCA AAUAUUACAA AUCUGUGUCC AUUUGGAGAA

Q P T E S I V R F P N I T N L C P F G E

S protein

8598 8608 8618 8628 8638 8648

GUGUUUAAUG CAACAAGAUU UGCAUCUGUG UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU

V F N A T R F A S V Y A W N R K R I S N

S protein

8658 8668 8678 8688 8698 8708

UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU AGUGCUUCUU UUUCCACAUU UAAAUGUUAU

C V A D Y S V L Y N S A S F S T F K C Y

S protein

8718 8728 8738 8748 8758 8768

GGAGUGUCUC CAACAAAAUU AAAUGAUUUA UGUUUUACAA AUGUGUAUGC UGAUUCUUUU

G V S P T K L N D L C F T N V Y A D S F

S protein

8778 8788 8798 8808 8818 8828

GUGAUCAGAG GUGAUGAAGU GAGACAGAUU GCCCCCGGAC AGACAGGAAA AAUUGCUGAU

V I R G D E V R Q I A P G Q T G K I A D

S protein

8838 8848 8858 8868 8878 8888

UACAAUUACA AACUGCCUGA UGAUUUUACA GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU

Y N Y K L P D D F T G C V I A W N S N N

S protein

8898 8908 8918 8928 8938 8948

UUAGAUUCUA AAGUGGGAGG AAAUUACAAU UAUCUGUACA GACUGUUUAG AAAAUCAAAU

L D S K V G G N Y N Y L Y R L F R K S N

S protein

8958 8968 8978 8988 8998 9008

CUGAAACCUU UUGAAAGAGA UAUUUCAACA GAAAUUUAUC AGGCUGGAUC AACACCUUGU

L K P F E R D I S T E I Y Q A G S T P C

S protein

9018 9028 9038 9048 9058 9068

AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU CCAUUACAGA GCUAUGGAUU UCAGCCAACC

N G V E G F N C Y F P L Q S Y G F Q P T

S protein

9078 9088 9098 9108 9118 9128

AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG GUGGUGCUGU CUUUUGAACU GCUGCAUGCA

N G V G Y Q P Y R V V V L S F E L L H A

S protein

9138 9148 9158 9168 9178 9188

CCUGCAACAG UGUGUGGACC UAAAAAAUCU ACAAAUUUAG UGAAAAAUAA AUGUGUGAAU

P A T V C G P K K S T N L V K N K C V N

S protein

9198 9208 9218 9228 9238 9248

UUUAAUUUUA AUGGAUUAAC AGGAACAGGA GUGCUGACAG AAUCUAAUAA AAAAUUUCUG

F N F N G L T G T G V L T E S N K K F L

S protein

9258 9268 9278 9288 9298 9308

CCUUUUCAGC AGUUUGGCAG AGAUAUUGCA GAUACCACAG AUGCAGUGAG AGAUCCUCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

9318 9328 9338 9348 9358 9368

ACAUUAGAAA UUCUGGAUAU UACACCUUGU UCUUUUGGGG GUGUGUCUGU GAUUACACCU

T L E I L D I T P C S F G G V S V I T P

S protein

9378 9388 9398 9408 9418 9428

GGAACAAAUA CAUCUAAUCA GGUGGCUGUG CUGUAUCAGG AUGUGAAUUG UACAGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

9438 9448 9458 9468 9478 9488

CCAGUGGCAA UUCAUGCAGA UCAGCUGACA CCAACAUGGA GAGUGUAUUC UACAGGAUCU

P V A I H A D Q L T P T W R V Y S T G S

S protein

9498 9508 9518 9528 9538 9548

AAUGUGUUUC AGACAAGAGC AGGAUGUCUG AUUGGAGCAG AACAUGUGAA UAAUUCUUAU

N V F Q T R A G C L I G A E H V N N S Y

S protein

9558 9568 9578 9588 9598 9608

GAAUGUGAUA UUCCAAUUGG AGCAGGCAUU UGUGCAUCUU AUCAGACACA GACAAAUUCC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

9618 9628 9638 9648 9658 9668

CCAAGGAGAG CAAGAUCUGU GGCAUCUCAG UCUAUUAUUG CAUACACCAU GUCUCUGGGA

P R R A R S V A S Q S I I A Y T M S L G

S protein

9678 9688 9698 9708 9718 9728

GCAGAAAAUU CUGUGGCAUA UUCUAAUAAU UCUAUUGCUA UUCCAACAAA UUUUACCAUU

A E N S V A Y S N N S I A I P T N F T I

S protein

9738 9748 9758 9768 9778 9788

UCUGUGACAA CAGAAAUUUU ACCUGUGUCU AUGACAAAAA CAUCUGUGGA UUGUACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

9798 9808 9818 9828 9838 9848

UACAUUUGUG GAGAUUCUAC AGAAUGUUCU AAUCUGCUGC UGCAGUAUGG AUCUUUUUGU

Y I C G D S T E C S N L L L Q Y G S F C

S protein

9858 9868 9878 9888 9898 9908

ACACAGCUGA AUAGAGCUUU AACAGGAAUU GCUGUGGAAC AGGAUAAAAA UACACAGGAA

T Q L N R A L T G I A V E Q D K N T Q E

S protein

9918 9928 9938 9948 9958 9968

GUGUUUGCUC AGGUGAAACA GAUUUACAAA ACACCACCAA UUAAAGAUUU UGGAGGAUUU

V F A Q V K Q I Y K T P P I K D F G G F

S protein

9978 9988 9998 10008 10018 10028

AAUUUUAGCC AGAUUCUGCC UGAUCCUUCU AAACCUUCUA AAAGAUCUUU UAUUGAAGAU

N F S Q I L P D P S K P S K R S F I E D

S protein

10038 10048 10058 10068 10078 10088

CUGCUGUUUA AUAAAGUGAC ACUGGCAGAU GCAGGAUUUA UUAAACAGUA UGGAGAUUGC

L L F N K V T L A D A G F I K Q Y G D C

S protein

10098 10108 10118 10128 10138 10148

CUGGGUGAUA UUGCUGCAAG AGAUCUGAUU UGUGCUCAGA AAUUUAAUGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

10158 10168 10178 10188 10198 10208

CUGCCUCCUC UGCUGACAGA UGAAAUGAUU GCUCAGUACA CAUCUGCUUU ACUGGCUGGA

L P P L L T D E M I A Q Y T S A L L A G

S protein

10218 10228 10238 10248 10258 10268

ACAAUUACAA GCGGAUGGAC AUUUGGAGCU GGAGCUGCUC UGCAGAUUCC UUUUGCAAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

10278 10288 10298 10308 10318 10328

CAGAUGGCUU ACAGAUUUAA UGGAAUUGGA GUGACACAGA AUGUGUUAUA UGAAAAUCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

10338 10348 10358 10368 10378 10388

AAACUGAUUG CAAAUCAGUU UAAUUCUGCA AUUGGCAAAA UUCAGGAUUC UCUGUCUUCU

K L I A N Q F N S A I G K I Q D S L S S

S protein

10398 10408 10418 10428 10438 10448

ACAGCUUCUG CUCUGGGAAA ACUGCAGGAU GUGGUGAAUC AGAAUGCACA GGCACUGAAU

T A S A L G K L Q D V V N Q N A Q A L N

S protein

10458 10468 10478 10488 10498 10508

ACUCUGGUGA AACAGCUGUC UAGCAAUUUU GGGGCAAUUU CUUCUGUGCU GAAUGAUAUU

T L V K Q L S S N F G A I S S V L N D I

S protein

10518 10528 10538 10548 10558 10568

CUGUCUAGAC UGGAUCCTCC TGAAGCUGAA GUGCAGAUUG AUAGACUGAU CACAGGAAGA

L S R L D P P E A E V Q I D R L I T G R

S protein

10578 10588 10598 10608 10618 10628

CUGCAGUCUC UGCAGACUUA UGUGACACAG CAGCUGAUUA GAGCUGCUGA AAUUAGAGCU

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

10638 10648 10658 10668 10678 10688

UCUGCUAAUC UGGCUGCUAC AAAAAUGUCU GAAUGUGUGC UGGGACAGUC AAAAAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

10698 10708 10718 10728 10738 10748

GAUUUUUGUG GAAAAGGAUA UCAUCUGAUG UCUUUUCCAC AGUCUGCUCC ACAUGGAGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

10758 10768 10778 10788 10798 10808

GUGUUUUUAC AUGUGACAUA UGUGCCAGCA CAGGAAAAGA AUUUUACCAC AGCACCAGCA

V F L H V T Y V P A Q E K N F T T A P A

S protein

10818 10828 10838 10848 10858 10868

AUUUGUCAUG AUGGAAAAGC ACAUUUUCCA AGAGAAGGAG UGUUUGUGUC UAAUGGAACA

I C H D G K A H F P R E G V F V S N G T

S protein

10878 10888 10898 10908 10918 10928

CAUUGGUUUG UGACACAGAG AAAUUUUUAU GAACCUCAGA UUAUUACAAC AGAUAAUACA

H W F V T Q R N F Y E P Q I I T T D N T

S protein

10938 10948 10958 10968 10978 10988

UUUGUGUCAG GAAAUUGUGA UGUGGUGAUU GGAAUUGUGA AUAAUACAGU GUAUGAUCCA

F V S G N C D V V I G I V N N T V Y D P

S protein

10998 11008 11018 11028 11038 11048

CUGCAGCCAG AACUGGAUUC UUUUAAAGAA GAACUGGAUA AAUAUUUUAA AAAUCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

11058 11068 11078 11088 11098 11108

UCUCCUGAUG UGGAUUUAGG AGAUAUUUCU GGAAUCAAUG CAUCUGUGGU GAAUAUUCAG

S P D V D L G D I S G I N A S V V N I Q

S protein

```
    11118       11128       11138       11148       11158       11168
AAAGAAAUUG AUAGACUGAA UGAAGUGGCC AAAAAUCUGA AUGAAUCUCU GAUUGAUCUG
  K   E   I   D   R   L   N   E   V   A   K   N   L   N   E   S   L   I   D   L
```

S protein

```
    11178       11188       11198       11208       11218       11228
CAGGAACUUG GAAAAUAUGA ACAGUACAUU AAAUGGCCUU GGUACAUUUG GCUUGGAUUU
  Q   E   L   G   K   Y   E   Q   Y   I   K   W   P   W   Y   I   W   L   G   F
```

S protein

```
    11238       11248       11258       11268       11278       11288
AUUGCAGGAU UAAUUGCAAU UGUGAUGGUG ACAAUUAUGU UAUGUUGUAU GACAUCAUGU
  I   A   G   L   I   A   I   V   M   V   T   I   M   L   C   C   M   T   S   C
```

S protein

```
    11298       11308       11318       11328       11338       11348
UGUUCUUGUU UAAAAGGAUG UUGUUCUUGU GGAAGCUGUU GUAAAUUUGA UGAAGAUGAU
  C   S   C   L   K   G   C   C   S   C   G   S   C   C   K   F   D   E   D   D
```

S protein

```
    11358       11368       11378       11388  11393
UCUGAACCUG UGUUAAAAGG AGUGAAAUUG CAUUACACAU GAUGA
  S   E   P   V   L   K   G   V   K   L   H   Y   T   *   *
```

S protein

```
    11403       11413       11423       11433       11443       11453
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
    11463       11473       11483       11493       11503       11513
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
    11523       11533       11543       11553       11563       11573
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

```
    11583       11593       11603       11613       11623       11633
CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA
```

FI element

```
    11643       11653       11663       11673       11683       11693
```

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCGCGGCC GCAUGAAUAC

FI element

11703 11713 11723 11733 11743 11753

AGCAGCAAUU GGCAAGCUGC UUACAUAGAA CUCGCGGCGA UUGGCAUGCC GCCUUAAAAU

FI element

11763 11773 11783 11793 11803 11807

UUUUAUUUUA UUUUUUCUUU UCUUUUCCGA AUCGGAUUUU GUUUUUAAUA UUUC

FI element

11817 11827 11837 11847 11857 11867

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

11877 11887 11897 11907 11917

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Nucleotide Sequence of RBS004.2

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
         10         20         30         40     45
GAUGGGCGGC GCAUGAGAGA AGCCCAGACC AAUUACCUAC CCAAA
```

5' UTR

```
        55         65         75         85         95        105
AUGGAGAAAG UUCACGUUGA CAUCGAGGAA GACAGCCCAU UCCUCAGAGC UUUGCAGCGG
  M  E  K   V  H  V   D  I  E  E   D  S  P   F  L  R   A  L  Q  R
```

nsp1

```
       115        125        135        145        155        165
AGCUUCCCGC AGUUUGAGGU AGAAGCCAAG CAGGUCACUG AUAAUGACCA UGCUAAUGCC
  S  F  P   Q  F  E   V  E  A  K   Q  V  T   D  N  D   H  A  N  A
```

nsp1

```
       175        185        195        205        215        225
AGAGCGUUUU CGCAUCUGGC UUCAAAACUG AUCGAAACGG AGGUGGACCC AUCCGACACG
  R  A  F   S  H  L   A  S  K  L   I  E  T   E  V  D   P  S  D  T
```

nsp1

```
       235        245        255        265        275        285
AUCCUUGACA UUGGAAGUGC GCCCGCCCGC AGAAUGUAUU CUAAGCACAA GUAUCAUUGU
  I  L  D   I  G  S   A  P  A  R   R  M  Y   S  K  H   K  Y  H  C
```

nsp1

```
       295        305        315        325        335        345
AUCUGUCCGA UGAGAUGUGC GGAAGAUCCG GACAGAUUGU AUAAGUAUGC AACUAAGCUG
  I  C  P   M  R  C   A  E  D  P   D  R  L   Y  K  Y   A  T  K  L
```

nsp1

```
       355        365        375        385        395        405
AAGAAAAACU GUAAGGAAAU AACUGAUAAG GAAUUGGACA AGAAAAUGAA GGAGCUCGCC
  K  K  N   C  K  E   I  T  D  K   E  L  D   K  K  M   K  E  L  A
```

nsp1

```
       415        425        435        445        455        465
GCCGUCAUGA GCGACCCUGA CCUGGAAACU GAGACUAUGU GCCUCCACGA CGACGAGUCG
```

A V M S D P D L E T E T M C L H D D E S

nsp1

475 485 495 505 515 525

UGUCGCUACG AAGGGCAAGU CGCUGUUUAC CAGGAUGUAU ACGCGGUUGA CGGACCGACA

C R Y E G Q V A V Y Q D V Y A V D G P T

nsp1

535 545 555 565 575 585

AGUCUCUAUC ACCAAGCCAA UAAGGGAGUU AGAGUCGCCU ACUGGAUAGG CUUUGACACC

S L Y H Q A N K G V R V A Y W I G F D T

nsp1

595 605 615 625 635 645

ACCCCUUUUA UGUUUAAGAA CUUGGCUGGA GCAUAUCCAU CAUACUCUAC CAACUGGGCC

T P F M F K N L A G A Y P S Y S T N W A

nsp1

655 665 675 685 695 705

GACGAAACCG UGUUAACGGC UCGUAACAUA GGCCUAUGCA GCUCUGACGU UAUGGAGCGG

D E T V L T A R N I G L C S S D V M E R

nsp1

715 725 735 745 755 765

UCACGUAGAG GGAUGUCCAU UCUUAGAAAG AAGUAUUUGA AACCAUCCAA CAAUGUUCUA

S R R G M S I L R K K Y L K P S N N V L

nsp1

775 785 795 805 815 825

UUCUCUGUUG GCUCGACCAU CUACCACGAA AAGAGGGACU UACUGAGGAG CUGGCACCUG

F S V G S T I Y H E K R D L L R S W H L

nsp1

835 845 855 865 875 885

CCGUCUGUAU UUCACUUACG UGGCAAGCAA AAUUACACAU GUCGGUGUGA GACUAUAGUU

P S V F H L R G K Q N Y T C R C E T I V

nsp1

895 905 915 925 935 945

AGUUGCGACG GGUACGUCGU UAAAAGAAUA GCUAUCAGUC CAGGCCUGUA UGGGAAGCCU

S C D G Y V V K R I A I S P G L Y G K P

nsp1

955 965 975 985 995 1005
UCAGGCUAUG CUGCUACGAU GCACCGCGAG GGAUUCUUGU GCUGCAAAGU GACAGACACA
S G Y A A T M H R E G F L C C K V T D T

nsp1

1015 1025 1035 1045 1055 1065
UUGAACGGGG AGAGGGUCUC UUUUCCCGUG UGCACGUAUG UGCCAGCUAC AUUGUGUGAC
L N G E R V S F P V C T Y V P A T L C D

nsp1

1075 1085 1095 1105 1115 1125
CAAAUGACUG GCAUACUGGC AACAGAUGUC AGUGCGGACG ACGCGCAAAA ACUGCUGGUU
Q M T G I L A T D V S A D D A Q K L L V

nsp1

1135 1145 1155 1165 1175 1185
GGGCUCAACC AGCGUAUAGU CGUCAACGGU CGCACCCAGA GAAACACCAA UACCAUGAAA
G L N Q R I V V N G R T Q R N T N T M K

nsp1

1198 1205 1215 1225 1235 1245
AAUUACCUUU UGCCCGUAGU GGCCCAGGCA UUUGCUAGGU GGGCAAAGGA AUAUAAGGAA
N Y L L P V V A Q A F A R W A K E Y K E

nsp1

1255 1265 1275 1285 1295 1305
GAUCAAGAAG AUGAAAGGCC ACUAGGACUA CGAGAUAGAC AGUUAGUCAU GGGGUGUUGU
D Q E D E R P L G L R D R Q L V M G C C

nsp1

1315 1325 1335 1345 1355 1365
UGGGCUUUUA GAAGGCACAA GAUAACAUCU AUUUAUAAGC GCCCGGAUAC CCAAACCAUC
W A F R R H K I T S I Y K R P D T Q T I

nsp1

1375 1385 1395 1405 1415 1425
AUCAAAGUGA ACAGCGAUUU CCACUCAUUC GUGCUGCCCA GGAUAGGCAG UAACACAUUG
I K V N S D F H S F V L P R I G S N T L

nsp1

1435 1445 1455 1465 1475 1485
GAGAUCGGGC UGAGAACAAG AAUCAGGAAA AUGUUAGAGG AGCACAAGGA GCCGUCACCU
E I G L R T R I R K M L E E H K E P S P

nsp1

1495 1505 1515 1525 1535 1545

CUCAUUACCG CCGAGGACGU ACAAGAAGCU AAGUGCGCAG CCGAUGAGGC UAAGGAGGUG

L I T A E D V Q E A K C A A D E A K E V

nsp1

1555 1565 1575 1585 1595 1605

CGUGAAGCCG AGGAGUUGCG CGCAGCUCUA CCACCUUUGG CAGCUGAUGU UGAGGAGCCC

R E A E E L R A A L P P L A A D V E E P

nsp1

1615 1625 1635 1645 1650

ACUCUGGAAG CCGAUGUCGA CUUGAUGUUA CAAGAGGCUG GGGCC

T L E A D V D L M L Q E A G A

nsp1

1660 1670 1680 1690 1700 1710

GGCUCAGUGG AGACACCUCG UGGCUUGAUA AAGGUUACCA GCUACGCUGG CGAGGACAAG

G S V E T P R G L I K V T S Y A G E D K

nsp2

1720 1730 1740 1750 1760 1770

AUCGGCUCUU ACGCUGUGCU UUCUCCGCAG GCUGUACUCA AGAGUGAAAA AUUAUCUUGC

I G S Y A V L S P Q A V L K S E K L S C

nsp2

1780 1790 1800 1810 1820 1830

AUCCACCCUC UCGCUGAACA AGUCAUAGUG AUAACACACU CUGGCCGAAA AGGGCGUUAU

I H P L A E Q V I V I T H S G R K G R Y

nsp2

1840 1850 1860 1870 1880 1890

GCCGUGGAAC CAUACCAUGG UAAAGUAGUG GUGCCAGAGG GACAUGCAAU ACCCGUCCAG

A V E P Y H G K V V V P E G H A I P V Q

nsp2

1900 1910 1920 1930 1940 1950

GACUUUCAAG CUCUGAGUGA AAGUGCCACC AUUGUGUACA ACGAACGUGA GUUCGUAAAC

D F Q A L S E S A T I V Y N E R E F V N

nsp2

1960 1970 1980 1990 2000 2010

AGGUACCUGC ACCAUAUUGC CACACAUGGA GGAGCGCUGA ACACUGAUGA AGAAUAUUAC

R Y L H H I A T H G G A L N T D E E Y Y

nsp2

2020 2030 2040 2050 2060 2070

AAAACUGUCA AGCCCAGCGA GCACGACGGC GAAUACCUGU ACGACAUCGA CAGGAAACAG

K T V K P S E H D G E Y L Y D I D R K Q

nsp2

2080 2090 2100 2110 2120 2130

UGCGUCAAGA AAGAGCUAGU CACUGGGCUA GGGCUCACAG GCGAGCUGGU CGAUCCUCCC

C V K K E L V T G L G L T G E L V D P P

nsp2

2140 2150 2160 2170 2180 2190

UUCCAUGAAU UCGCCUACGA GAGUCUGAGA ACACGACCAG CCGCUCCUUA CCAAGUACCA

F H E F A Y E S L R T R P A A P Y Q V P

nsp2

2200 2210 2220 2230 2240 2250

ACCAUAGGGG UGUAUGGCGU GCCAGGAUCA GGCAAGUCUG GCAUCAUUAA AAGCGCAGUC

T I G V Y G V P G S G K S G I I K S A V

nsp2

2260 2270 2280 2290 2300 2310

ACCAAAAAAG AUCUAGUGGU GAGCGCCAAG AAAGAAAACU GUGCAGAAAU UAUAAGGGAC

T K K D L V V S A K K E N C A E I I R D

nsp2

2320 2330 2340 2350 2360 2370

GUCAAGAAAA UGAAAGGGCU GGACGUCAAU GCCAGAACUG UGGACUCAGU GCUCUUGAAU

V K K M K G L D V N A R T V D S V L L N

nsp2

2380 2390 2400 2410 2420 2430

GGAUGCAAAC ACCCCGUAGA GACCCUGUAU AUUGACGAGG CUUUUGCUUG UCAUGCAGGU

G C K H P V E T L Y I D E A F A C H A G

nsp2

2440 2450 2460 2470 2480 2490

ACUCUCAGAG CGCUCAUAGC CAUUAUAAGA CCUAAAAAGG CAGUGCUCUG CGGAGAUCCC

T L R A L I A I I R P K K A V L C G D P

nsp2

2500 2510 2520 2530 2540 2550

AAACAGUGCG GUUUUUUUAA CAUGAUGUGC CUGAAAGUGC AUUUUAACCA CGAGAUUUGC

K Q C G F F N M M C L K V H F N H E I C

nsp2

2560 2570 2580 2590 2600 2610

ACACAAGUCU UCCACAAAAG CAUCUCUCGC CGUUGCACUA AAUCUGUGAC UUCGGUCGUC

T Q V F H K S I S R R C T K S V T S V V

nsp2

2620 2630 2640 2650 2660 2670

UCAACCUUGU UUUACGACAA AAAAAUGAGA ACGACGAAUC CGAAAGAGAC UAAGAUUGUG

S T L F Y D K K M R T T N P K E T K I V

nsp2

2680 2690 2700 2710 2720 2730

AUUGACACUA CCGGCAGUAC CAAACCUAAG CAGGACGAUC UCAUUCUCAC UUGUUUCAGA

I D T T G S T K P K Q D D L I L T C F R

nsp2

2740 2750 2760 2770 2780 2790

GGGUGGGUGA AGCAGUUGCA AAUAGAUUAC AAAGGCAACG AAAUAAUGAC GGCAGCUGCC

G W V K Q L Q I D Y K G N E I M T A A A

nsp2

2800 2810 2820 2830 2840 2850

UCUCAAGGGC UGACCCGUAA AGGUGUGUAU GCCGUUCGGU ACAAGGUGAA UGAAAAUCCU

S Q G L T R K G V Y A V R Y K V N E N P

nsp2

2860 2870 2880 2890 2900 2910

CUGUACGCAC CCACCUCAGA ACAUGUGAAC GUCCUACUGA CCCGCACGGA GGACCGCAUC

L Y A P T S E H V N V L L T R T E D R I

nsp2

2920 2930 2940 2950 2960 2970

GUGUGGAAAA CACUAGCCGG CGACCCAUGG AUAAAAACAC UGACUGCCAA GUACCCUGGG

V W K T L A G D P W I K T L T A K Y P G

nsp2

2980 2990 3000 3010 3020 3030

AAUUUCACUG CCACGAUAGA GGAGUGGCAA GCAGAGCAUG AUGCCAUCAU GAGGCACAUC

N F T A T I E E W Q A E H D A I M R H I

nsp2

3040 3050 3060 3070 3080 3090

UUGGAGAGAC CGGACCCUAC CGACGUCUUC CAGAAUAAGG CAAACGUGUG UUGGGCCAAG

L E R P D P T D V F Q N K A N V C W A K

nsp2

3100 3110 3120 3130 3140 3150

GCUUUAGUGC CGGUGCUGAA GACCGCUGGC AUAGACAUGA CCACUGAACA AUGGAACACU

A L V P V L K T A G I D M T T E Q W N T

nsp2

3160 3170 3180 3190 3200 3210

GUGGAUUAUU UUGAAACGGA CAAAGCUCAC UCAGCAGAGA UAGUAUUGAA CCAACUAUGC

V D Y F E T D K A H S A E I V L N Q L C

nsp2

3220 3230 3240 3250 3260 3270

GUGAGGUUCU UUGGACUCGA UCUGGACUCC GGUCUAUUUU CUGCACCCAC UGUUCCGUUA

V R F F G L D L D S G L F S A P T V P L

nsp2

3280 3290 3300 3310 3320 3330

UCCAUUAGGA AUAAUCACUG GGAUAACUCC CCGUCGCCUA ACAUGUACGG GCUGAAUAAA

S I R N N H W D N S P S P N M Y G L N K

nsp2

3340 3350 3360 3370 3380 3390

GAAGUGGUCC GUCAGCUCUC UCGCAGGUAC CCACAACUGC CUCGGGCAGU UGCCACUGGU

E V V R Q L S R R Y P Q L P R A V A T G

nsp2

3400 3410 3420 3430 3440 3450

AGAGUCUAUG ACAUGAACAC UGGUACACUG CGCAAUUAUG AUCCGCGCAU AAACCUAGUA

R V Y D M N T G T L R N Y D P R I N L V

nsp2

3460 3470 3480 3490 3500 3510

CCUGUAAACA GAAGACUGCC UCAUGCUUUA GUCCUCCACC AUAAUGAACA CCCACAGAGU

P V N R R L P H A L V L H H N E H P Q S

nsp2

3520 3530 3540 3550 3560 3570

GACUUUUCUU CAUUCGUCAG CAAAUUGAAG GGCAGAACUG UCCUGGUGGU CGGGGAAAAG

D F S S F V S K L K G R T V L V V G E K

nsp2

3580 3590 3600 3610 3620 3630

UUGUCCGUCC CAGGCAAAAU GGUUGACUGG UUGUCAGACC GGCCUGAGGC UACCUUCAGA

L S V P G K M V D W L S D R P E A T F R

nsp2

3640 3650 3660 3670 3680 3690

GCUCGGCUGG AUUUAGGCAU CCCAGGUGAU GUGCCCAAAU AUGACAUAAU AUUUGUUAAU

A R L D L G I P G D V P K Y D I I F V N

nsp2

3700 3710 3720 3730 3740 3750

GUGAGGACCC CAUAUAAAUA CCAUCACUAU CAGCAGUGUG AAGACCAUGC CAUUAAGCUA

V R T P Y K Y H H Y Q Q C E D H A I K L

nsp2

3760 3770 3780 3790 3800 3810

AGCAUGUUGA CCAAGAAAGC AUGUCUGCAU CUGAAUCCCG GCGGAACCUG UGUCAGCAUA

S M L T K K A C L H L N P G G T C V S I

nsp2

3820 3830 3840 3850 3860 3870

GGUUAUGGUU ACGCUGACAG GGCCAGCGAA AGCAUCAUUG GUGCUAUAGC GCGGCAGUUC

G Y G Y A D R A S E S I I G A I A R Q F

nsp2

3880 3890 3900 3910 3920 3930

AAGUUUUCCC GAGUAUGCAA ACCGAAAUCC UCACUUGAGG AGACGGAAGU UCUGUUUGUA

K F S R V C K P K S S L E E T E V L F V

nsp2

3940 3950 3960 3970 3980 3990

UUCAUUGGGU ACGAUCGCAA GGCCCGUACG CACAAUCCUU ACAAGCUAUC AUCAACCUUG

F I G Y D R K A R T H N P Y K L S S T L

nsp2

4000 4010 4020 4030 4032

ACCAACAUUU AUACAGGUUC CAGACUCCAC GAAGCCGGAU GU

T N I Y T G S R L H E A G C

nsp2

4042 4052 4062 4072 4082 4092

GCACCCUCAU AUCAUGUGGU GCGAGGGGAU AUUGCCACGG CCACCGAAGG AGUGAUUAUA

A P S Y H V V R G D I A T A T E G V I I

nsp3

4102 4112 4122 4132 4142 4152

AAUGCUGCUA ACAGCAAAGG ACAACCUGGC GGAGGGGUGU GCGGAGCGCU GUAUAAGAAA

N A A N S K G Q P G G G V C G A L Y K K

nsp3

4162 4172 4182 4192 4202 4212

UUCCCGGAAA GUUUCGAUUU ACAGCCGAUC GAAGUAGGAA AAGCGCGACU GGUCAAAGGU

F P E S F D L Q P I E V G K A R L V K G

nsp3

4222 4232 4242 4252 4262 4272

GCAGCUAAAC AUAUCAUUCA UGCCGUAGGA CCAAACUUCA ACAAAGUUUC GGAGGUUGAA

A A K H I I H A V G P N F N K V S E V E

nsp3

4282 4292 4302 4312 4322 4332

GGUGACAAAC AGUUGGCAGA GGCUUAUGAG UCCAUCGCUA AGAUUGUCAA CGAUAACAAU

G D K Q L A E A Y E S I A K I V N D N N

nsp3

4342 4352 4362 4372 4382 4392

UACAAGUCAG UAGCGAUUCC ACUGUUGUCC ACCGGCAUCU UUUCCGGGAA CAAAGAUCGA

Y K S V A I P L L S T G I F S G N K D R

nsp3

4402 4412 4422 4432 4442 4452

CUAACCCAAU CAUUGAACCA UUUGCUGACA GCUUUAGACA CCACUGAUGC AGAUGUAGCC

L T Q S L N H L L T A L D T T D A D V A

nsp3

4462 4472 4482 4492 4502 4512

AUAUACUGCA GGGACAAGAA AUGGGAAAUG ACUCUCAAGG AAGCAGUGGC UAGGAGAGAA

I Y C R D K K W E M T L K E A V A R R E

nsp3

4522 4532 4542 4552 4562 4572

GCAGUGGAGG AGAUAUGCAU AUCCGACGAU UCUUCAGUGA CAGAACCUGA UGCAGAGCUG

A V E E I C I S D D S S V T E P D A E L

nsp3

4582 4592 4602 4612 4622 4632

GUGAGGGUGC AUCCCAAGAG UUCUUUGGCU GGAAGGAAGG GCUACAGCAC AAGCGAUGGC

V R V H P K S S L A G R K G Y S T S D G

nsp3

4642 4652 4662 4672 4682 4692

AAAACUUUCU CAUAUUUGGA AGGGACCAAG UUUCACCAGG CGGCCAAGGA UAUAGCAGAA

K T F S Y L E G T K F H Q A A K D I A E

nsp3

4702 4712 4722 4732 4742 4752

AUUAAUGCCA UGUGGCCCGU UGCAACGGAG GCCAAUGAGC AGGUAUGCAU GUAUAUCCUC

I N A M W P V A T E A N E Q V C M Y I L

nsp3

4762 4772 4782 4792 4802 4812

GGAGAAAGCA UGAGCAGUAU UAGGUCGAAA UGCCCCGUCG AGGAGUCGGA AGCCUCCACA

G E S M S S I R S K C P V E E S E A S T

nsp3

4822 4832 4842 4852 4862 4872

CCACCUAGCA CGCUGCCUUG CUUGUGCAUC CAUGCCAUGA CUCCAGAAAG AGUACAGCGC

P P S T L P C L C I H A M T P E R V Q R

nsp3

4882 4892 4902 4912 4922 4932

CUAAAAGCCU CACGUCCAGA ACAAAUUACU GUGUGCUCAU CCUUUCCAUU GCCGAAGUAU

L K A S R P E Q I T V C S S F P L P K Y

nsp3

4942 4952 4962 4972 4982 4992

AGAAUCACUG GUGUGCAGAA GAUCCAAUGC UCCCAGCCUA UAUUGUUCUC ACCGAAAGUG

R I T G V Q K I Q C S Q P I L F S P K V

nsp3

5002 5012 5022 5032 5042 5052

CCUGCGUAUA UUCAUCCAAG GAAGUAUCUC GUGGAAACAC CACCGGUAGA CGAGACUCCG

P A Y I H P R K Y L V E T P P V D E T P

nsp3

5062 5072 5082 5092 5102 5112

GAGCCAUCGG CAGAGAACCA AUCCACAGAG GGGACACCUG AACAACCACC ACUUAUAACC

E P S A E N Q S T E G T P E Q P P L I T

nsp3

5122 5132 5142 5152 5162 5172

GAGGAUGAGA CCAGGACUAG AACGCCUGAG CCGAUCAUCA UCGAAGAAGA AGAAGAAGAU

E D E T R T R T P E P I I I E E E E E D

nsp3

5182 5192 5202 5212 5222 5232

AGCAUAAGUU UGCUGUCAGA UGGCCCGACC CACCAGGUGC UGCAAGUCGA GGCAGACAUU

S I S L L S D G P T H Q V L Q V E A D I

nsp3

5242 5252 5262 5272 5282 5292

CACGGGCCGC CCUCUGUAUC UAGCUCAUCC UGGUCCAUUC CUCAUGCAUC CGACUUUGAU

H G P P S V S S S S W S I P H A S D F D

nsp3

5302 5312 5322 5332 5342 5352

GUGGACAGUU UAUCCAUACU UGACACCCUG GAGGGAGCUA GCGUGACCAG CGGGGCAACG

V D S L S I L D T L E G A S V T S G A T

nsp3

5362 5372 5382 5392 5402 5412

UCAGCCGAGA CUAACUCUUA CUUCGCAAAG AGUAUGGAGU UUCUGGCGCG ACCGGUGCCU

S A E T N S Y F A K S M E F L A R P V P

nsp3

5422 5432 5442 5452 5462 5472

GCGCCUCGAA CAGUAUUCAG GAACCCUCCA CAUCCCGCUC CGCGCACAAG AACACCGUCA

A P R T V F R N P P H P A P R T R T P S

nsp3

5482 5492 5502 5512 5522 5532

CUUGCACCCA GCAGGGCCUG CUCCAGAACC AGCCUAGUUU CCACCCCGCC AGGCGUGAAU

L A P S R A C S R T S L V S T P P G V N

nsp3

5542 5552 5562 5572 5582 5592

AGGGUGAUCA CUAGAGAGGA GCUCGAAGCG CUUACCCCGU CACGCACUCC UAGCAGGUCG

R V I T R E E L E A L T P S R T P S R S

nsp3

5602 5612 5622 5632 5642 5652

GUCUCCAGAA CCAGCCUGGU CUCCAACCCG CCAGGCGUAA AUAGGGUGAU UACAAGAGAG

V S R T S L V S N P P G V N R V I T R E

nsp3

5662 5672 5682 5692 5702 5703

GAGUUUGAGG CGUUCGUAGC ACAACAACAA UGACGGUUUG AUGCGGGUGC A

*E F E A F V A Q Q Q * R F D A G A*

nsp3

5713 5723 5733 5743 5753 5763

UACAUCUUUU CCUCCGACAC CGGUCAAGGG CAUUUACAAC AAAAAUCAGU AAGGCAAACG

Y I F S S D T G Q G H L Q Q K S V R Q T

nsp4

5773 5783 5793 5803 5813 5823

GUGCUAUCCG AAGUGGUGUU GGAGAGGACC GAAUUGGAGA UUUCGUAUGC CCCGCGCCUC

V L S E V V L E R T E L E I S Y A P R L

nsp4

5833 5843 5853 5863 5873 5883

GACCAAGAAA AAGAAGAAUU ACUACGCAAG AAAUUACAGU UAAAUCCCAC ACCUGCUAAC

D Q E K E E L L R K K L Q L N P T P A N

nsp4

5893 5903 5913 5923 5933 5943

AGAAGCAGAU ACCAGUCCAG GAAGGUGGAG AACAUGAAAG CCAUAACAGC UAGACGUAUU

R S R Y Q S R K V E N M K A I T A R R I

nsp4

5953 5963 5973 5983 5993 6003

CUGCAAGGCC UAGGGCAUUA UUUGAAGGCA GAAGGAAAAG UGGAGUGCUA CCGAACCCUG

L Q G L G H Y L K A E G K V E C Y R T L

nsp4

6013 6023 6033 6043 6053 6063

CAUCCUGUUC CUUUGUAUUC AUCUAGUGUG AACCGUGCCU UUUCAAGCCC CAAGGUCGCA

H P V P L Y S S S V N R A F S S P K V A

nsp4

6073 6083 6093 6103 6113 6123

GUGGAAGCCU GUAACGCCAU GUUGAAAGAG AACUUUCCGA CUGUGGCUUC UUACUGUAUU

V E A C N A M L K E N F P T V A S Y C I

nsp4

6133 6143 6153 6163 6173 6183

AUUCCAGAGU ACGAUGCCUA UUUGGACAUG GUUGACGGAG CUUCAUGCUG CUUAGACACU

I P E Y D A Y L D M V D G A S C C L D T

nsp4

6193 6203 6213 6223 6233 6243

GCCAGUUUUU GCCCUGCAAA GCUGCGCAGC UUUCCAAAGA AACACUCCUA UUUGGAACCC

A S F C P A K L R S F P K K H S Y L E P

nsp4

6253 6263 6273 6283 6293 6303

ACAAUACGAU CGGCAGUGCC UUCAGCGAUC CAGAACACGC UCCAGAACGU CCUGGCAGCU

T I R S A V P S A I Q N T L Q N V L A A

nsp4

6313 6323 6333 6343 6353 6363

GCCACAAAAA GAAAUUGCAA UGUCACGCAA AUGAGAGAAU UGCCCGUAUU GGAUUCGGCG

A T K R N C N V T Q M R E L P V L D S A

nsp4

6373 6383 6393 6403 6413 6423

GCCUUUAAUG UGGAAUGCUU CAAGAAAUAU GCGUGUAAUA AUGAAUAUUG GGAAACGUUU

A F N V E C F K K Y A C N N E Y W E T F

nsp4

6433 6443 6453 6463 6473 6483

AAAGAAAACC CCAUCAGGCU UACUGAAGAA AACGUGGUAA AUUACAUUAC CAAAUUAAAA

K E N P I R L T E E N V V N Y I T K L K

nsp4

6493 6503 6513 6523 6533 6543

GGACCAAAAG CUGCUGCUCU UUUUGCGAAG ACACAUAAUU UGAAUAUGUU GCAGGACAUA

G P K A A A L F A K T H N L N M L Q D I

nsp4

6553 6563 6573 6583 6593 6603

CCAAUGGACA GGUUUGUAAU GGACUUAAAG AGAGACGUGA AAGUGACUCC AGGAACAAAA

P M D R F V M D L K R D V K V T P G T K

nsp4

6613 6623 6633 6643 6653 6663

CAUACUGAAG AACGGCCCAA GGUACAGGUG AUCCAGGCUG CCGAUCCGCU AGCAACAGCG

H T E E R P K V Q V I Q A A D P L A T A

nsp4

6673 6683 6693 6703 6713 6723

UAUCUGUGCG GAAUCCACCG AGAGCUGGUU AGGAGAUUAA AUGCGGUCCU GCUUCCGAAC

Y L C G I H R E L V R R L N A V L L P N

nsp4

6733 6743 6753 6763 6773 6783

AUUCAUACAC UGUUUGAUAU GUCGGCUGAA GACUUUGACG CUAUUAUAGC CGAGCACUUC

I H T L F D M S A E D F D A I I A E H F

nsp4

6793 6803 6813 6823 6833 6843

CAGCCUGGGG AUUGUGUUCU GGAAACUGAC AUCGCGUCGU UUGAUAAAAG UGAGGACGAC

Q P G D C V L E T D I A S F D K S E D D

nsp4

6853 6863 6873 6883 6893 6903

GCCAUGGCUC UGACCGCGUU AAUGAUUCUG GAAGACUUAG GUGUGGACGC AGAGCUGUUG

A M A L T A L M I L E D L G V D A E L L

nsp4

6913 6923 6933 6943 6953 6963

ACGCUGAUUG AGGCGGCUUU CGGCGAAAUU UCAUCAAUAC AUUUGCCCAC UAAAACUAAA

T L I E A A F G E I S S I H L P T K T K

nsp4

6973 6983 6993 7003 7013 7023

UUUAAAUUCG GAGCCAUGAU GAAAUCUGGA AUGUUCCUCA CACUGUUUGU GAACACAGUC

F K F G A M M K S G M F L T L F V N T V

nsp4

7033 7043 7053 7063 7073 7083

AUUAACAUUG UAAUCGCAAG CAGAGUGUUG AGAGAACGGC UAACCGGAUC ACCAUGUGCA

I N I V I A S R V L R E R L T G S P C A

nsp4

7093 7103 7113 7123 7133 7143

GCAUUCAUUG GAGAUGACAA UAUCGUGAAA GGAGUCAAAU CGGACAAAUU AAUGGCAGAC

A F I G D D N I V K G V K S D K L M A D

nsp4

7153 7163 7173 7183 7193 7203

AGGUGCGCCA CCUGGUUGAA UAUGGAAGUC AAGAUUAUAG AUGCUGUGGU GGGCGAGAAA

R C A T W L N M E V K I I D A V V G E K

nsp4

7213 7223 7233 7243 7253 7263

GCGCCUUAUU UCUGUGGAGG GUUUAUUUUG UGUGACUCCG UGACCGGCAC AGCGUGCCGU

A P Y F C G G F I L C D S V T G T A C R

nsp4

7273 7283 7293 7303 7313 7323

GUGGCAGACC CCCUAAAAAG GCUGUUUAAG CUAGGCAAAC CUCUGGCAGC AGACGAUGAA

V A D P L K R L F K L G K P L A A D D E

nsp4

7333 7343 7353 7363 7373 7383

CAUGAUGAUG ACAGGAGAAG GGCAUUGCAU GAGGAGUCAA CACGCUGGAA CCGAGUGGGU

H D D D R R R A L H E E S T R W N R V G

nsp4

7393 7403 7413 7423 7433 7443

AUUCUUUCAG AGCUGUGCAA GGCAGUAGAA UCAAGGUAUG AAACCGUAGG AACUUCCAUC

I L S E L C K A V E S R Y E T V G T S I

nsp4

7453 7463 7473 7483 7493 7503

AUAGUUAUGG CCAUGACUAC UCUAGCUAGC AGUGUUAAAU CAUUCAGCUA CCUGAGAGGG

I V M A M T T L A S S V K S F S Y L R G

nsp4

7513 7523 7527

GCCCCUAUAA CUCUCUACGG CUAA

*A P I T L Y G **

nsp4

```
      7537        7547        7557        7567  7568
CCUGAAUGGA CUACGACAUA GUCUAGUCCG CCAAGACUAG U
```

virUTR

```
      7578        7588        7598        7608        7618        7628
AUGUUCGUGU UCCUGGUGCU GCUGCCUCUG GUGUCCAGCC AGUGUGUGAA CCUGACCACC
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   N  L  T  T
```

S protein

```
      7638        7648        7658        7668        7678        7688
AGAACACAGC UGCCUCCAGC CUACACCAAC AGCUUUACCA GAGGCGUGUA CUACCCCGAC
  R  T  Q   L  P  P   A  Y  T  N   S  F  T   R  G  V   Y  Y  P  D
```

S protein

```
      7698        7708        7718        7728        7738        7748
AAGGUGUUCA GAUCCAGCGU GCUGCACUCU ACCCAGGACC UGUUCCUGCC UUUCUUCAGC
  K  V  F   R  S  S   V  L  H  S   T  Q  D   L  F  L   P  F  F  S
```

S protein

```
      7758        7768        7778        7788        7798        7808
AACGUGACCU GGUUCCACGC CAUCCACGUG UCCGGCACCA AUGGCACCAA GAGAUUCGAC
  N  V  T   W  F  H   A  I  H  V   S  G  T   N  G  T   K  R  F  D
```

S protein

```
      7818        7828        7838        7848        7858        7868
AACCCCGUGC UGCCCUUCAA CGACGGGGUG UACUUUGCCA GCACCGAGAA GUCCAACAUC
  N  P  V   L  P  F   N  D  G  V   Y  F  A   S  T  E   K  S  N  I
```

S protein

```
      7878        7888        7898        7908        7918        7928
AUCAGAGGCU GGAUCUUCGG CACCACACUG GACAGCAAGA CCCAGAGCCU GCUGAUCGUG
  I  R  G   W  I  F   G  T  T  L   D  S  K   T  Q  S   L  L  I  V
```

S protein

```
      7938        7948        7958        7968        7978        7988
AACAACGCCA CCAACGUGGU CAUCAAAGUG UGCGAGUUCC AGUUCUGCAA CGACCCCUUC
  N  N  A   T  N  V   V  I  K  V   C  E  F   Q  F  C   N  D  P  F
```

S protein

```
      7998        8008        8018        8028        8038        8048
CUGGGCGUCU ACUACCACAA GAACAACAAG AGCUGGAUGG AAAGCGAGUU CCGGGUGUAC
```

L G V Y Y H K N N K S W M E S E F R V Y

S protein

8058 8068 8078 8088 8098 8108

AGCAGCGCCA ACAACUGCAC CUUCGAGUAC GUGUCCCAGC CUUUCCUGAU GGACCUGGAA

S S A N N C T F E Y V S Q P F L M D L E

S protein

8118 8128 8138 8148 8158 8168

GGCAAGCAGG GCAACUUCAA GAACCUGCGC GAGUUCGUGU UUAAGAACAU CGACGGCUAC

G K Q G N F K N L R E F V F K N I D G Y

S protein

8178 8188 8198 8208 8218 8228

UUCAAGAUCU ACAGCAAGCA CACCCCUAUC AACCUCGUGC GGGAUCUGCC UCAGGGCUUC

F K I Y S K H T P I N L V R D L P Q G F

S protein

8238 8248 8258 8268 8278 8288

UCUGCUCUGG AACCCCUGGU GGAUCUGCCC AUCGGCAUCA ACAUCACCCG GUUUCAGACA

S A L E P L V D L P I G I N I T R F Q T

S protein

8298 8308 8318 8328 8338 8348

CUGCUGGCCC UGCACAGAAG CUACCUGACA CCUGGCGAUA GCAGCAGCGG AUGGACAGCU

L L A L H R S Y L T P G D S S S G W T A

S protein

8358 8368 8378 8388 8398 8408

GGUGCCGCCG CUUACUAUGU GGGCUACCUG CAGCCUAGAA CCUUCCUGCU GAAGUACAAC

G A A A Y Y V G Y L Q P R T F L L K Y N

S protein

8418 8428 8438 8448 8458 8468

GAGAACGGCA CCAUCACCGA CGCCGUGGAU UGUGCUCUGG AUCCUCUGAG CGAGACAAAG

E N G T I T D A V D C A L D P L S E T K

S protein

8478 8488 8498 8508 8518 8528

UGCACCCUGA AGUCCUUCAC CGUGGAAAAG GGCAUCUACC AGACCAGCAA CUUCCGGGUG

C T L K S F T V E K G I Y Q T S N F R V

S protein

```
     8538       8548       8558       8568       8578       8588
CAGCCCACCG AAUCCAUCGU GCGGUUCCCC AAUAUCACCA AUCUGUGCCC CUUCGGCGAG
  Q  P  T   E  S  I   V  R  F  P   N  I  T   N  L  C   P  F  G  E
```

S protein

```
     8598       8608       8618       8628       8638       8648
GUGUUCAAUG CCACCAGAUU CGCCUCUGUG UACGCCUGGA ACCGGAAGCG GAUCAGCAAU
  V  F  N   A  T  R   F  A  S  V   Y  A  W   N  R  K   R  I  S  N
```

S protein

```
     8658       8668       8678       8688       8698       8708
UGCGUGGCCG ACUACUCCGU GCUGUACAAC UCCGCCAGCU UCAGCACCUU CAAGUGCUAC
  C  V  A   D  Y  S   V  L  Y  N   S  A  S   F  S  T   F  K  C  Y
```

S protein

```
     8718       8728       8738       8748       8758       8768
GGCGUGUCCC CUACCAAGCU GAACGACCUG UGCUUCACAA ACGUGUACGC CGACAGCUUC
  G  V  S   P  T  K   L  N  D  L   C  F  T   N  V  Y   A  D  S  F
```

S protein

```
     8778       8788       8798       8808       8818       8828
GUGAUCCGGG GAGAUGAAGU GCGGCAGAUU GCCCCUGGAC AGACAGGCAA GAUCGCCGAC
  V  I  R   G  D  E   V  R  Q  I   A  P  G   Q  T  G   K  I  A  D
```

S protein

```
     8838       8848       8858       8868       8878       8888
UACAACUACA AGCUGCCCGA CGACUUCACC GGCUGUGUGA UUGCCUGGAA CAGCAACAAC
  Y  N  Y   K  L  P   D  D  F  T   G  C  V   I  A  W   N  S  N  N
```

S protein

```
     8898       8908       8918       8928       8938       8948
CUGGACUCCA AAGUCGGCGG CAACUACAAU UACCUGUACC GGCUGUUCCG GAAGUCCAAU
  L  D  S   K  V  G   G  N  Y  N   Y  L  Y   R  L  F   R  K  S  N
```

S protein

```
     8958       8968       8978       8988       8998       9008
CUGAAGCCCU UCGAGCGGGA CAUCUCCACC GAGAUCUAUC AGGCCGGCAG CACCCCUUGU
  L  K  P   F  E  R   D  I  S  T   E  I  Y   Q  A  G   S  T  P  C
```

S protein

```
     9018       9028       9038       9048       9058       9068
AACGGCGUGG AAGGCUUCAA CUGCUACUUC CCACUGCAGU CCUACGGCUU UCAGCCCACA
  N  G  V   E  G  F   N  C  Y  F   P  L  Q   S  Y  G   F  Q  P  T
```

S protein

9078 9088 9098 9108 9118 9128

AAUGGCGUGG GCUAUCAGCC CUACAGAGUG GUGGUGCUGA GCUUCGAACU GCUGCAUGCC

N G V G Y Q P Y R V V V L S F E L L H A

S protein

9138 9148 9158 9168 9178 9188

CCUGCCACAG UGUGCGGCCC UAAGAAAAGC ACCAAUCUCG UGAAGAACAA AUGCGUGAAC

P A T V C G P K K S T N L V K N K C V N

S protein

9198 9208 9218 9228 9238 9248

UUCAACUUCA ACGGCCUGAC CGGCACCGGC GUGCUGACAG AGAGCAACAA GAAGUUCCUG

F N F N G L T G T G V L T E S N K K F L

S protein

9258 9268 9278 9288 9298 9308

CCAUUCCAGC AGUUUGGCCG GGAUAUCGCC GAUACCACAG ACGCCGUUAG AGAUCCCCAG

P F Q Q F G R D I A D T T D A V R D P Q

S protein

9318 9328 9338 9348 9358 9368

ACACUGGAAA UCCUGGACAU CACCCCUUGC AGCUUCGGCG GAGUGUCUGU GAUCACCCCU

T L E I L D I T P C S F G G V S V I T P

S protein

9378 9388 9398 9408 9418 9428

GGCACCAACA CCAGCAAUCA GGUGGCAGUG CUGUACCAGG ACGUGAACUG UACCGAAGUG

G T N T S N Q V A V L Y Q D V N C T E V

S protein

9438 9448 9458 9468 9478 9488

CCCGUGGCCA UUCACGCCGA UCAGCUGACA CCUACAUGGC GGGUGUACUC CACCGGCAGC

P V A I H A D Q L T P T W R V Y S T G S

S protein

9498 9508 9518 9528 9538 9548

AAUGUGUUUC AGACCAGAGC CGGCUGUCUG AUCGGAGCCG AGCACGUGAA CAAUAGCUAC

N V F Q T R A G C L I G A E H V N N S Y

S protein

9558 9568 9578 9588 9598 9608

GAGUGCGACA UCCCCAUCGG CGCUGGAAUC UGCGCCAGCU ACCAGACACA GACAAACAGC

E C D I P I G A G I C A S Y Q T Q T N S

S protein

9618 9628 9638 9648 9658 9668

CCUCGGAGAG CCAGAAGCGU GGCCAGCCAG AGCAUCAUUG CCUACACAAU GUCUCUGGGC

P R R A R S V A S Q S I I A Y T M S L G

S protein

9678 9688 9698 9708 9718 9728

GCCGAGAACA GCGUGGCCUA CUCCAACAAC UCUAUCGCUA UCCCCACCAA CUUCACCAUC

A E N S V A Y S N N S I A I P T N F T I

S protein

9738 9748 9758 9768 9778 9788

AGCGUGACCA CAGAGAUCCU GCCUGUGUCC AUGACCAAGA CCAGCGUGGA CUGCACCAUG

S V T T E I L P V S M T K T S V D C T M

S protein

9798 9808 9818 9828 9838 9848

UACAUCUGCG GCGAUUCCAC CGAGUGCUCC AACCUGCUGC UGCAGUACGG CAGCUUCUGC

Y I C G D S T E C S N L L L Q Y G S F C

S protein

9858 9868 9878 9888 9898 9908

ACCCAGCUGA AUAGAGCCCU GACAGGGAUC GCCGUGGAAC AGGACAAGAA CACCCAAGAG

T Q L N R A L T G I A V E Q D K N T Q E

S protein

9918 9928 9938 9948 9958 9968

GUGUUCGCCC AAGUGAAGCA GAUCUACAAG ACCCCUCCUA UCAAGGACUU CGGCGGCUUC

V F A Q V K Q I Y K T P P I K D F G G F

S protein

9978 9988 9998 10008 10018 10028

AAUUUCAGCC AGAUUCUGCC CGAUCCUAGC AAGCCCAGCA AGCGGAGCUU CAUCGAGGAC

N F S Q I L P D P S K P S K R S F I E D

S protein

10038 10048 10058 10068 10078 10088

CUGCUGUUCA ACAAAGUGAC ACUGGCCGAC GCCGGCUUCA UCAAGCAGUA UGGCGAUUGU

L L F N K V T L A D A G F I K Q Y G D C

S protein

10098 10108 10118 10128 10138 10148

CUGGGCGACA UUGCCGCCAG GGAUCUGAUU UGCGCCCAGA AGUUUAACGG ACUGACAGUG

L G D I A A R D L I C A Q K F N G L T V

S protein

10158 10168 10178 10188 10198 10208

CUGCCUCCUC UGCUGACCGA UGAGAUGAUC GCCCAGUACA CAUCUGCCCU GCUGGCCGGC

L P P L L T D E M I A Q Y T S A L L A G

S protein

10218 10228 10238 10248 10258 10268

ACAAUCACAA GCGGCUGGAC AUUUGGAGCA GGCGCCGCUC UGCAGAUCCC CUUUGCUAUG

T I T S G W T F G A G A A L Q I P F A M

S protein

10278 10288 10298 10308 10318 10328

CAGAUGGCCU ACCGGUUCAA CGGCAUCGGA GUGACCCAGA AUGUGCUGUA CGAGAACCAG

Q M A Y R F N G I G V T Q N V L Y E N Q

S protein

10338 10348 10358 10368 10378 10388

AAGCUGAUCG CCAACCAGUU CAACAGCGCC AUCGGCAAGA UCCAGGACAG CCUGAGCAGC

K L I A N Q F N S A I G K I Q D S L S S

S protein

10398 10408 10418 10428 10438 10448

ACAGCAAGCG CCCUGGGAAA GCUGCAGGAC GUGGUCAACC AGAAUGCCCA GGCACUGAAC

T A S A L G K L Q D V V N Q N A Q A L N

S protein

10458 10468 10478 10488 10498 10508

ACCCUGGUCA AGCAGCUGUC CUCCAACUUC GGCGCCAUCA GCUCUGUGCU GAACGAUAUC

T L V K Q L S S N F G A I S S V L N D I

S protein

10518 10528 10538 10548 10558 10568

CUGAGCAGAC UGGACCCTCC TGAGGCCGAG GUGCAGAUCG ACAGACUGAU CACAGGCAGA

L S R L D ***P P*** *E A E V Q I D R L I T G R*

S protein

10578 10588 10598 10608 10618 10628

CUGCAGAGCC UCCAGACAUA CGUGACCCAG CAGCUGAUCA GAGCCGCCGA GAUUAGAGCC

L Q S L Q T Y V T Q Q L I R A A E I R A

S protein

10638 10648 10658 10668 10678 10688

UCUGCCAAUC UGGCCGCCAC CAAGAUGUCU GAGUGUGUGC UGGGCCAGAG CAAGAGAGUG

S A N L A A T K M S E C V L G Q S K R V

S protein

10698 10708 10718 10728 10738 10748

GACUUUUGCG GCAAGGGCUA CCACCUGAUG AGCUUCCCUC AGUCUGCCCC UCACGGCGUG

D F C G K G Y H L M S F P Q S A P H G V

S protein

10758 10768 10778 10788 10798 10808

GUGUUUCUGC ACGUGACAUA UGUGCCCGCU CAAGAGAAGA AUUUCACCAC CGCUCCAGCC

V F L H V T Y V P A Q E K N F T T A P A

S protein

10818 10828 10838 10848 10858 10868

AUCUGCCACG ACGGCAAAGC CCACUUUCCU AGAGAAGGCG UGUUCGUGUC CAACGGCACC

I C H D G K A H F P R E G V F V S N G T

S protein

10878 10888 10898 10908 10918 10928

CAUUGGUUCG UGACACAGCG GAACUUCUAC GAGCCCCAGA UCAUCACCAC CGACAACACC

H W F V T Q R N F Y E P Q I I T T D N T

S protein

10938 10948 10958 10968 10978 10988

UUCGUGUCUG GCAACUGCGA CGUCGUGAUC GGCAUUGUGA ACAAUACCGU GUACGACCCU

F V S G N C D V V I G I V N N T V Y D P

S protein

10998 11008 11018 11028 11038 11048

CUGCAGCCCG AGCUGGACAG CUUCAAAGAG GAACUGGACA AGUACUUUAA GAACCACACA

L Q P E L D S F K E E L D K Y F K N H T

S protein

11058 11068 11078 11088 11098 11108

AGCCCCGACG UGGACCUGGG CGAUAUCAGC GGAAUCAAUG CCAGCGUCGU GAACAUCCAG

S P D V D L G D I S G I N A S V V N I Q

S protein

11118 11128 11138 11148 11158 11168

AAAGAGAUCG ACCGGCUGAA CGAGGUGGCC AAGAAUCUGA ACGAGAGCCU GAUCGACCUG

K E I D R L N E V A K N L N E S L I D L

S protein

11178 11188 11198 11208 11218 11228

CAAGAACUGG GGAAGUACGA GCAGUACAUC AAGUGGCCCU GGUACAUCUG GCUGGGCUUU

Q E L G K Y E Q Y I K W P W Y I W L G F

S protein

11238 11248 11258 11268 11278 11288

AUCGCCGGAC UGAUUGCCAU CGUGAUGGUC ACAAUCAUGC UGUGUUGCAU GACCAGCUGC

I A G L I A I V M V T I M L C C M T S C

S protein

11298 11308 11318 11328 11338 11348

UGUAGCUGCC UGAAGGGCUG UUGUAGCUGU GGCAGCUGCU GCAAGUUCGA CGAGGACGAU

C S C L K G C C S C G S C C K F D E D D

S protein

11358 11368 11378 11388 11393

UCUGAGCCCG UGCUGAAGGG CGUGAAACUG CACUACACAU GAUGA

*S E P V L K G V K L H Y T * *

S protein

11403 11413 11423 11433 11443 11453

CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG

FI element

11463 11473 11483 11493 11503 11513

AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC

FI element

11523 11533 11543 11553 11563 11573

UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG

FI element

11583 11593 11603 11613 11623 11633

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

11643 11653 11663 11673 11683 11693

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCGCGGCC GCAUGAAUAC

FI element

11703 11713 11723 11733 11743 11753

AGCAGCAAUU GGCAAGCUGC UUACAUAGAA CUCGCGGCGA UUGGCAUGCC GCCUUAAAAU

FI element

11763 11773 11783 11793 11803 11807

UUUUAUUUUA UUUUUUCUUU UCUUUUCCGA AUCGGAUUUU GUUUUUAAUA UUUC

FI element

11817 11827 11837 11847 11857 11867

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

11877 11887 11897 11907 11917

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Nucleotide Sequence of RBS004.3

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
        10         20         30         40    45
GAUGGGCGGC GCAUGAGAGA AGCCCAGACC AAUUACCUAC CCAAA
                                5' UTR
        55         65         75         85         95        105
AUGGAGAAAG UUCACGUUGA CAUCGAGGAA GACAGCCCAU UCCUCAGAGC UUUGCAGCGG
  M  E  K   V  H  V   D  I  E  E   D  S  P   F  L  R   A  L  Q  R
                                nsp1
       115        125        135        145        155        165
AGCUUCCCGC AGUUUGAGGU AGAAGCCAAG CAGGUCACUG AUAAUGACCA UGCUAAUGCC
  S  F  P   Q  F  E   V  E  A  K   Q  V  T   D  N  D   H  A  N  A
                                nsp1
       175        185        195        205        215        225
AGAGCGUUUU CGCAUCUGGC UUCAAAACUG AUCGAAACGG AGGUGGACCC AUCCGACACG
  R  A  F   S  H  L   A  S  K  L   I  E  T   E  V  D   P  S  D  T
                                nsp1
       235        245        255        265        275        285
AUCCUUGACA UUGGAAGUGC GCCCGCCCGC AGAAUGUAUU CUAAGCACAA GUAUCAUUGU
  I  L  D   I  G  S   A  P  A  R   R  M  Y   S  K  H   K  Y  H  C
                                nsp1
       295        305        315        325        335        345
AUCUGUCCGA UGAGAUGUGC GGAAGAUCCG GACAGAUUGU AUAAGUAUGC AACUAAGCUG
  I  C  P   M  R  C   A  E  D  P   D  R  L   Y  K  Y   A  T  K  L
                                nsp1
       355        365        375        385        395        405
AAGAAAAACU GUAAGGAAAU AACUGAUAAG GAAUUGGACA AGAAAAUGAA GGAGCUCGCC
  K  K  N   C  K  E   I  T  D  K   E  L  D   K  K  M   K  E  L  A
                                nsp1
       415        425        435        445        455        465
GCCGUCAUGA GCGACCCUGA CCUGGAAACU GAGACUAUGU GCCUCCACGA CGACGAGUCG
```

A V M S D P D L E T E T M C L H D D E S

nsp1

475 485 495 505 515 525

UGUCGCUACG AAGGGCAAGU CGCUGUUUAC CAGGAUGUAU ACGCGGUUGA CGGACCGACA

C R Y E G Q V A V Y Q D V Y A V D G P T

nsp1

535 545 555 565 575 585

AGUCUCUAUC ACCAAGCCAA UAAGGGAGUU AGAGUCGCCU ACUGGAUAGG CUUUGACACC

S L Y H Q A N K G V R V A Y W I G F D T

nsp1

595 605 615 625 635 645

ACCCCUUUUA UGUUUAAGAA CUUGGCUGGA GCAUAUCCAU CAUACUCUAC CAACUGGGCC

T P F M F K N L A G A Y P S Y S T N W A

nsp1

655 665 675 685 695 705

GACGAAACCG UGUUAACGGC UCGUAACAUA GGCCUAUGCA GCUCUGACGU UAUGGAGCGG

D E T V L T A R N I G L C S S D V M E R

nsp1

715 725 735 745 755 765

UCACGUAGAG GGAUGUCCAU UCUUAGAAAG AAGUAUUUGA AACCAUCCAA CAAUGUUCUA

S R R G M S I L R K K Y L K P S N N V L

nsp1

775 785 795 805 815 825

UUCUCUGUUG GCUCGACCAU CUACCACGAA AAGAGGGACU UACUGAGGAG CUGGCACCUG

F S V G S T I Y H E K R D L L R S W H L

nsp1

835 845 855 865 875 885

CCGUCUGUAU UUCACUUACG UGGCAAGCAA AAUUACACAU GUCGGUGUGA GACUAUAGUU

P S V F H L R G K Q N Y T C R C E T I V

nsp1

895 905 915 925 935 945

AGUUGCGACG GGUACGUCGU UAAAAGAAUA GCUAUCAGUC CAGGCCUGUA UGGGAAGCCU

S C D G Y V V K R I A I S P G L Y G K P

nsp1

955 965 975 985 995 1005
UCAGGCUAUG CUGCUACGAU GCACCGCGAG GGAUUCUUGU GCUGCAAAGU GACAGACACA
S G Y A A T M H R E G F L C C K V T D T

nsp1

1015 1025 1035 1045 1055 1065
UUGAACGGGG AGAGGGUCUC UUUUCCCGUG UGCACGUAUG UGCCAGCUAC AUUGUGUGAC
L N G E R V S F P V C T Y V P A T L C D

nsp1

1075 1085 1095 1105 1115 1125
CAAAUGACUG GCAUACUGGC AACAGAUGUC AGUGCGGACG ACGCGCAAAA ACUGCUGGUU
Q M T G I L A T D V S A D D A Q K L L V

nsp1

1135 1145 1155 1165 1175 1185
GGGCUCAACC AGCGUAUAGU CGUCAACGGU CGCACCCAGA GAAACACCAA UACCAUGAAA
G L N Q R I V V N G R T Q R N T N T M K

nsp1

1195 1205 1215 1225 1235 1245
AAUUACCUUU UGCCCGUAGU GGCCCAGGCA UUUGCUAGGU GGGCAAAGGA AUAUAAGGAA
N Y L L P V V A Q A F A R W A K E Y K E

nsp1

1255 1265 1275 1285 1295 1305
GAUCAAGAAG AUGAAAGGCC ACUAGGACUA CGAGAUAGAC AGUUAGUCAU GGGGUGUUGU
D Q E D E R P L G L R D R Q L V M G C C

nsp1

1315 1325 1335 1345 1355 1365
UGGGCUUUUA GAAGGCACAA GAUAACAUCU AUUUAUAAGC GCCCGGAUAC CCAAACCAUC
W A F R R H K I T S I Y K R P D T Q T I

nsp1

1375 1385 1395 1405 1415 1425
AUCAAAGUGA ACAGCGAUUU CCACUCAUUC GUGCUGCCCA GGAUAGGCAG UAACACAUUG
I K V N S D F H S F V L P R I G S N T L

nsp1

1435 1445 1455 1465 1475 1485
GAGAUCGGGC UGAGAACAAG AAUCAGGAAA AUGUUAGAGG AGCACAAGGA GCCGUCACCU
E I G L R T R I R K M L E E H K E P S P

nsp1

1495 1505 1515 1525 1535 1545

CUCAUUACCG CCGAGGACGU ACAAGAAGCU AAGUGCGCAG CCGAUGAGGC UAAGGAGGUG

L I T A E D V Q E A K C A A D E A K E V

nsp1

1555 1565 1575 1585 1595 1605

CGUGAAGCCG AGGAGUUGCG CGCAGCUCUA CCACCUUUGG CAGCUGAUGU UGAGGAGCCC

R E A E E L R A A L P P L A A D V E E P

nsp1

1615 1625 1635 1645 1650

ACUCUGGAAG CCGAUGUCGA CUUGAUGUUA CAAGAGGCUG GGGCC

T L E A D V D L M L Q E A G A

nsp1

1660 1670 1680 1690 1700 1710

GGCUCAGUGG AGACACCUCG UGGCUUGAUA AAGGUUACCA GCUACGCUGG CGAGGACAAG

G S V E T P R G L I K V T S Y A G E D K

nsp2

1720 1730 1740 1750 1760 1770

AUCGGCUCUU ACGCUGUGCU UUCUCCGCAG GCUGUACUCA AGAGUGAAAA AUUAUCUUGC

I G S Y A V L S P Q A V L K S E K L S C

nsp2

1780 1790 1800 1810 1820 1830

AUCCACCCUC UCGCUGAACA AGUCAUAGUG AUAACACACU CUGGCCGAAA AGGGCGUUAU

I H P L A E Q V I V I T H S G R K G R Y

nsp2

1840 1850 1860 1870 1880 1890

GCCGUGGAAC CAUACCAUGG UAAAGUAGUG GUGCCAGAGG GACAUGCAAU ACCCGUCCAG

A V E P Y H G K V V V P E G H A I P V Q

nsp2

1900 1910 1920 1930 1940 1950

GACUUUCAAG CUCUGAGUGA AAGUGCCACC AUUGUGUACA ACGAACGUGA GUUCGUAAAC

D F Q A L S E S A T I V Y N E R E F V N

nsp2

1960 1970 1980 1990 2000 2010

AGGUACCUGC ACCAUAUUGC CACACAUGGA GGAGCGCUGA ACACUGAUGA AGAAUAUUAC

R Y L H H I A T H G G A L N T D E E Y Y

nsp2

2020 2030 2040 2050 2060 2070

AAAACUGUCA AGCCCAGCGA GCACGACGGC GAAUACCUGU ACGACAUCGA CAGGAAACAG

K T V K P S E H D G E Y L Y D I D R K Q

nsp2

2080 2090 2100 2110 2120 2130

UGCGUCAAGA AAGAGCUAGU CACUGGGCUA GGGCUCACAG GCGAGCUGGU CGAUCCUCCC

C V K K E L V T G L G L T G E L V D P P

nsp2

2140 2150 2160 2170 2180 2190

UUCCAUGAAU UCGCCUACGA GAGUCUGAGA ACACGACCAG CCGCUCCUUA CCAAGUACCA

F H E F A Y E S L R T R P A A P Y Q V P

nsp2

2200 2210 2220 2230 2240 2250

ACCAUAGGGG UGUAUGGCGU GCCAGGAUCA GGCAAGUCUG GCAUCAUUAA AAGCGCAGUC

T I G V Y G V P G S G K S G I I K S A V

nsp2

2260 2270 2280 2290 2300 2310

ACCAAAAAAG AUCUAGUGGU GAGCGCCAAG AAAGAAAACU GUGCAGAAAU UAUAAGGGAC

T K K D L V V S A K K E N C A E I I R D

nsp2

2320 2330 2340 2350 2360 2370

GUCAAGAAAA UGAAAGGGCU GGACGUCAAU GCCAGAACUG UGGACUCAGU GCUCUUGAAU

V K K M K G L D V N A R T V D S V L L N

nsp2

2380 2390 2400 2410 2420 2430

GGAUGCAAAC ACCCCGUAGA GACCCUGUAU AUUGACGAGG CUUUUGCUUG UCAUGCAGGU

G C K H P V E T L Y I D E A F A C H A G

nsp2

2440 2450 2460 2470 2480 2490

ACUCUCAGAG CGCUCAUAGC CAUUAUAAGA CCUAAAAAGG CAGUGCUCUG CGGAGAUCCC

T L R A L I A I I R P K K A V L C G D P

nsp2

2500 2510 2520 2530 2540 2550

AAACAGUGCG GUUUUUUUAA CAUGAUGUGC CUGAAAGUGC AUUUUAACCA CGAGAUUUGC

K Q C G F F N M M C L K V H F N H E I C

nsp2

2560 2570 2580 2590 2600 2610

ACACAAGUCU UCCACAAAAG CAUCUCUCGC CGUUGCACUA AAUCUGUGAC UUCGGUCGUC

T Q V F H K S I S R R C T K S V T S V V

nsp2

2620 2630 2640 2650 2660 2670

UCAACCUUGU UUUACGACAA AAAAAUGAGA ACGACGAAUC CGAAAGAGAC UAAGAUUGUG

S T L F Y D K K M R T T N P K E T K I V

nsp2

2680 2690 2700 2710 2720 2730

AUUGACACUA CCGGCAGUAC CAAACCUAAG CAGGACGAUC UCAUUCUCAC UUGUUUCAGA

I D T T G S T K P K Q D D L I L T C F R

nsp2

2740 2750 2760 2770 2780 2790

GGGUGGGUGA AGCAGUUGCA AAUAGAUUAC AAAGGCAACG AAAUAAUGAC GGCAGCUGCC

G W V K Q L Q I D Y K G N E I M T A A A

nsp2

2800 2810 2820 2830 2840 2850

UCUCAAGGGC UGACCCGUAA AGGUGUGUAU GCCGUUCGGU ACAAGGUGAA UGAAAAUCCU

S Q G L T R K G V Y A V R Y K V N E N P

nsp2

2860 2870 2880 2890 2900 2910

CUGUACGCAC CCACCUCAGA ACAUGUGAAC GUCCUACUGA CCCGCACGGA GGACCGCAUC

L Y A P T S E H V N V L L T R T E D R I

nsp2

2920 2930 2940 2950 2960 2970

GUGUGGAAAA CACUAGCCGG CGACCCAUGG AUAAAAACAC UGACUGCCAA GUACCCUGGG

V W K T L A G D P W I K T L T A K Y P G

nsp2

2980 2990 3000 3010 3020 3030

AAUUUCACUG CCACGAUAGA GGAGUGGCAA GCAGAGCAUG AUGCCAUCAU GAGGCACAUC

N F T A T I E E W Q A E H D A I M R H I

nsp2

3040 3050 3060 3070 3080 3090

UUGGAGAGAC CGGACCCUAC CGACGUCUUC CAGAAUAAGG CAAACGUGUG UUGGGCCAAG

L E R P D P T D V F Q N K A N V C W A K

nsp2

3100 3110 3120 3130 3140 3150

GCUUUAGUGC CGGUGCUGAA GACCGCUGGC AUAGACAUGA CCACUGAACA AUGGAACACU

A L V P V L K T A G I D M T T E Q W N T

nsp2

3160 3170 3180 3190 3200 3210

GUGGAUUAUU UUGAAACGGA CAAAGCUCAC UCAGCAGAGA UAGUAUUGAA CCAACUAUGC

V D Y F E T D K A H S A E I V L N Q L C

nsp2

3220 3230 3240 3250 3260 3270

GUGAGGUUCU UUGGACUCGA UCUGGACUCC GGUCUAUUUU CUGCACCCAC UGUUCCGUUA

V R F F G L D L D S G L F S A P T V P L

nsp2

3280 3290 3300 3310 3320 3330

UCCAUUAGGA AUAAUCACUG GGAUAACUCC CCGUCGCCUA ACAUGUACGG GCUGAAUAAA

S I R N N H W D N S P S P N M Y G L N K

nsp2

3340 3350 3360 3370 3380 3390

GAAGUGGUCC GUCAGCUCUC UCGCAGGUAC CCACAACUGC CUCGGGCAGU UGCCACUGGU

E V V R Q L S R R Y P Q L P R A V A T G

nsp2

3400 3410 3420 3430 3440 3450

AGAGUCUAUG ACAUGAACAC UGGUACACUG CGCAAUUAUG AUCCGCGCAU AAACCUAGUA

R V Y D M N T G T L R N Y D P R I N L V

nsp2

3460 3470 3480 3490 3500 3510

CCUGUAAACA GAAGACUGCC UCAUGCUUUA GUCCUCCACC AUAAUGAACA CCCACAGAGU

P V N R R L P H A L V L H H N E H P Q S

nsp2

3520 3530 3540 3550 3560 3570

GACUUUUCUU CAUUCGUCAG CAAAUUGAAG GGCAGAACUG UCCUGGUGGU CGGGGAAAAG

D F S S F V S K L K G R T V L V V G E K

nsp2

3580 3590 3600 3610 3620 3630

UUGUCCGUCC CAGGCAAAAU GGUUGACUGG UUGUCAGACC GGCCUGAGGC UACCUUCAGA

L S V P G K M V D W L S D R P E A T F R

nsp2

3640 3650 3660 3670 3680 3690

GCUCGGCUGG AUUUAGGCAU CCCAGGUGAU GUGCCCAAAU AUGACAUAAU AUUUGUUAAU

A R L D L G I P G D V P K Y D I I F V N

nsp2

3700 3710 3720 3730 3740 3750

GUGAGGACCC CAUAUAAAUA CCAUCACUAU CAGCAGUGUG AAGACCAUGC CAUUAAGCUA

V R T P Y K Y H H Y Q Q C E D H A I K L

nsp2

3760 3770 3780 3790 3800 3810

AGCAUGUUGA CCAAGAAAGC AUGUCUGCAU CUGAAUCCCG GCGGAACCUG UGUCAGCAUA

S M L T K K A C L H L N P G G T C V S I

nsp2

3820 3830 3840 3850 3860 3870

GGUUAUGGUU ACGCUGACAG GGCCAGCGAA AGCAUCAUUG GUGCUAUAGC GCGGCAGUUC

G Y G Y A D R A S E S I I G A I A R Q F

nsp2

3880 3890 3900 3910 3920 3930

AAGUUUUCCC GAGUAUGCAA ACCGAAAUCC UCACUUGAGG AGACGGAAGU UCUGUUUGUA

K F S R V C K P K S S L E E T E V L F V

nsp2

3940 3950 3960 3970 3980 3990

UUCAUUGGGU ACGAUCGCAA GGCCCGUACG CACAAUCCUU ACAAGCUAUC AUCAACCUUG

F I G Y D R K A R T H N P Y K L S S T L

nsp2

4000 4010 4020 4030 4032

ACCAACAUUU AUACAGGUUC CAGACUCCAC GAAGCCGGAU GU

T N I Y T G S R L H E A G C

nsp2

4042 4052 4062 4072 4082 4092

GCACCCUCAU AUCAUGUGGU GCGAGGGGAU AUUGCCACGG CCACCGAAGG AGUGAUUAUA

A P S Y H V V R G D I A T A T E G V I I

nsp3

4102 4112 4122 4132 4142 4152

AAUGCUGCUA ACAGCAAAGG ACAACCUGGC GGAGGGGUGU GCGGAGCGCU GUAUAAGAAA

N A A N S K G Q P G G G V C G A L Y K K

nsp3

4162 4172 4182 4192 4202 4212

UUCCCGGAAA GUUUCGAUUU ACAGCCGAUC GAAGUAGGAA AAGCGCGACU GGUCAAAGGU

F P E S F D L Q P I E V G K A R L V K G

nsp3

4222 4232 4242 4252 4262 4272

GCAGCUAAAC AUAUCAUUCA UGCCGUAGGA CCAAACUUCA ACAAAGUUUC GGAGGUUGAA

A A K H I I H A V G P N F N K V S E V E

nsp3

4282 4292 4302 4312 4322 4332

GGUGACAAAC AGUUGGCAGA GGCUUAUGAG UCCAUCGCUA AGAUUGUCAA CGAUAACAAU

G D K Q L A E A Y E S I A K I V N D N N

nsp3

4342 4352 4362 4372 4382 4392

UACAAGUCAG UAGCGAUUCC ACUGUUGUCC ACCGGCAUCU UUUCCGGGAA CAAAGAUCGA

Y K S V A I P L L S T G I F S G N K D R

nsp3

4402 4412 4422 4432 4442 4452

CUAACCCAAU CAUUGAACCA UUUGCUGACA GCUUUAGACA CCACUGAUGC AGAUGUAGCC

L T Q S L N H L L T A L D T T D A D V A

nsp3

4462 4472 4482 4492 4502 4512

AUAUACUGCA GGGACAAGAA AUGGGAAAUG ACUCUCAAGG AAGCAGUGGC UAGGAGAGAA

I Y C R D K K W E M T L K E A V A R R E

nsp3

4522 4532 4542 4552 4562 4572

GCAGUGGAGG AGAUAUGCAU AUCCGACGAU UCUUCAGUGA CAGAACCUGA UGCAGAGCUG

A V E E I C I S D D S S V T E P D A E L

nsp3

4582 4592 4602 4612 4622 4632

GUGAGGGUGC AUCCCAAGAG UUCUUUGGCU GGAAGGAAGG GCUACAGCAC AAGCGAUGGC

V R V H P K S S L A G R K G Y S T S D G

nsp3

4642 4652 4662 4672 4682 4692

AAAACUUUCU CAUAUUUGGA AGGGACCAAG UUUCACCAGG CGGCCAAGGA UAUAGCAGAA

K T F S Y L E G T K F H Q A A K D I A E

nsp3

4702 4712 4722 4732 4742 4752

AUUAAUGCCA UGUGGCCCGU UGCAACGGAG GCCAAUGAGC AGGUAUGCAU GUAUAUCCUC

I N A M W P V A T E A N E Q V C M Y I L

nsp3

4762 4772 4782 4792 4802 4812

GGAGAAAGCA UGAGCAGUAU UAGGUCGAAA UGCCCCGUCG AGGAGUCGGA AGCCUCCACA

G E S M S S I R S K C P V E E S E A S T

nsp3

4822 4832 4842 4852 4862 4872

CCACCUAGCA CGCUGCCUUG CUUGUGCAUC CAUGCCAUGA CUCCAGAAAG AGUACAGCGC

P P S T L P C L C I H A M T P E R V Q R

nsp3

4882 4892 4902 4912 4922 4932

CUAAAAGCCU CACGUCCAGA ACAAAUUACU GUGUGCUCAU CCUUUCCAUU GCCGAAGUAU

L K A S R P E Q I T V C S S F P L P K Y

nsp3

4942 4952 4962 4972 4982 4992

AGAAUCACUG GUGUGCAGAA GAUCCAAUGC UCCCAGCCUA UAUUGUUCUC ACCGAAAGUG

R I T G V Q K I Q C S Q P I L F S P K V

nsp3

5002 5012 5022 5032 5042 5052

CCUGCGUAUA UUCAUCCAAG GAAGUAUCUC GUGGAAACAC CACCGGUAGA CGAGACUCCG

P A Y I H P R K Y L V E T P P V D E T P

nsp3

5062 5072 5082 5092 5102 5112

GAGCCAUCGG CAGAGAACCA AUCCACAGAG GGGACACCUG AACAACCACC ACUUAUAACC

E P S A E N Q S T E G T P E Q P P L I T

nsp3

5122 5132 5142 5152 5162 5172

GAGGAUGAGA CCAGGACUAG AACGCCUGAG CCGAUCAUCA UCGAAGAAGA AGAAGAAGAU

E D E T R T R T P E P I I I E E E E E D

nsp3

5182 5192 5202 5212 5222 5232

AGCAUAAGUU UGCUGUCAGA UGGCCCGACC CACCAGGUGC UGCAAGUCGA GGCAGACAUU

S I S L L S D G P T H Q V L Q V E A D I

nsp3

5242 5252 5262 5272 5282 5292

CACGGGCCGC CCUCUGUAUC UAGCUCAUCC UGGUCCAUUC CUCAUGCAUC CGACUUUGAU

H G P P S V S S S S W S I P H A S D F D

nsp3

5302 5312 5322 5332 5342 5352

GUGGACAGUU UAUCCAUACU UGACACCCUG GAGGGAGCUA GCGUGACCAG CGGGGCAACG

V D S L S I L D T L E G A S V T S G A T

nsp3

5362 5372 5382 5392 5402 5412

UCAGCCGAGA CUAACUCUUA CUUCGCAAAG AGUAUGGAGU UUCUGGCGCG ACCGGUGCCU

S A E T N S Y F A K S M E F L A R P V P

nsp3

5422 5432 5442 5452 5462 5472

GCGCCUCGAA CAGUAUUCAG GAACCCUCCA CAUCCCGCUC CGCGCACAAG AACACCGUCA

A P R T V F R N P P H P A P R T R T P S

nsp3

5482 5492 5502 5512 5522 5532

CUUGCACCCA GCAGGGCCUG CUCCAGAACC AGCCUAGUUU CCACCCCGCC AGGCGUGAAU

L A P S R A C S R T S L V S T P P G V N

nsp3

```
     5542       5552       5562       5572       5582       5592
AGGGUGAUCA CUAGAGAGGA GCUCGAAGCG CUUACCCCGU CACGCACUCC UAGCAGGUCG
  R  V  I  T  R  E  E  L  E  A  L  T  P  S  R  T  P  S  R  S
```

nsp3

```
     5602       5612       5622       5632       5642       5652
GUCUCCAGAA CCAGCCUGGU CUCCAACCCG CCAGGCGUAA AUAGGGUGAU UACAAGAGAG
  V  S  R  T  S  L  V  S  N  P  P  G  V  N  R  V  I  T  R  E
```

nsp3

```
     5662       5672       5682       5692       5702 5703
GAGUUUGAGG CGUUCGUAGC ACAACAACAA UGACGGUUUG AUGCGGGUGC A
  E  F  E  A  F  V  A  Q  Q  Q  *  R  F  D  A  G  A
```

nsp3

```
     5713       5723       5733       5743       5753       5763
UACAUCUUUU CCUCCGACAC CGGUCAAGGG CAUUUACAAC AAAAAUCAGU AAGGCAAACG
  Y  I  F  S  S  D  T  G  Q  G  H  L  Q  Q  K  S  V  R  Q  T
```

nsp4

```
     5773       5783       5793       5803       5813       5823
GUGCUAUCCG AAGUGGUGUU GGAGAGGACC GAAUUGGAGA UUUCGUAUGC CCCGCGCCUC
  V  L  S  E  V  V  L  E  R  T  E  L  E  I  S  Y  A  P  R  L
```

nsp4

```
     5833       5843       5853       5863       5873       5883
GACCAAGAAA AAGAAGAAUU ACUACGCAAG AAAUUACAGU UAAAUCCCAC ACCUGCUAAC
  D  Q  E  K  E  E  L  L  R  K  K  L  Q  L  N  P  T  P  A  N
```

nsp4

```
     5893       5903       5913       5923       5933       5943
AGAAGCAGAU ACCAGUCCAG GAAGGUGGAG AACAUGAAAG CCAUAACAGC UAGACGUAUU
  R  S  R  Y  Q  S  R  K  V  E  N  M  K  A  I  T  A  R  R  I
```

nsp4

```
     5953       5963       5973       5983       5993       6003
CUGCAAGGCC UAGGGCAUUA UUUGAAGGCA GAAGGAAAAG UGGAGUGCUA CCGAACCCUG
  L  Q  G  L  G  H  Y  L  K  A  E  G  K  V  E  C  Y  R  T  L
```

nsp4

```
     6013       6023       6033       6043       6053       6063
```

CAUCCUGUUC CUUUGUAUUC AUCUAGUGUG AACCGUGCCU UUUCAAGCCC CAAGGUCGCA

H P V P L Y S S S V N R A F S S P K V A

nsp4

6073 6083 6093 6103 6113 6123

GUGGAAGCCU GUAACGCCAU GUUGAAAGAG AACUUUCCGA CUGUGGCUUC UUACUGUAUU

V E A C N A M L K E N F P T V A S Y C I

nsp4

6133 6143 6153 6163 6173 6183

AUUCCAGAGU ACGAUGCCUA UUUGGACAUG GUUGACGGAG CUUCAUGCUG CUUAGACACU

I P E Y D A Y L D M V D G A S C C L D T

nsp4

6193 6203 6213 6223 6233 6243

GCCAGUUUUU GCCCUGCAAA GCUGCGCAGC UUUCCAAAGA AACACUCCUA UUUGGAACCC

A S F C P A K L R S F P K K H S Y L E P

nsp4

6253 6263 6273 6283 6293 6303

ACAAUACGAU CGGCAGUGCC UUCAGCGAUC CAGAACACGC UCCAGAACGU CCUGGCAGCU

T I R S A V P S A I Q N T L Q N V L A A

nsp4

6313 6323 6333 6343 6353 6363

GCCACAAAAA GAAAUUGCAA UGUCACGCAA AUGAGAGAAU UGCCCGUAUU GGAUUCGGCG

A T K R N C N V T Q M R E L P V L D S A

nsp4

6373 6383 6393 6403 6413 6423

GCCUUUAAUG UGGAAUGCUU CAAGAAAUAU GCGUGUAAUA AUGAAUAUUG GGAAACGUUU

A F N V E C F K K Y A C N N E Y W E T F

nsp4

6433 6443 6453 6463 6473 6483

AAAGAAAACC CCAUCAGGCU UACUGAAGAA AACGUGGUAA AUUACAUUAC CAAAUUAAAA

K E N P I R L T E E N V V N Y I T K L K

nsp4

6493 6503 6513 6523 6533 6543

GGACCAAAAG CUGCUGCUCU UUUUGCGAAG ACACAUAAUU UGAAUAUGUU GCAGGACAUA

G P K A A A L F A K T H N L N M L Q D I

nsp4

6553 6563 6573 6583 6593 6603

CCAAUGGACA GGUUUGUAAU GGACUUAAAG AGAGACGUGA AAGUGACUCC AGGAACAAAA

P M D R F V M D L K R D V K V T P G T K

nsp4

6613 6623 6633 6643 6653 6663

CAUACUGAAG AACGGCCCAA GGUACAGGUG AUCCAGGCUG CCGAUCCGCU AGCAACAGCG

H T E E R P K V Q V I Q A A D P L A T A

nsp4

6673 6683 6693 6703 6713 6723

UAUCUGUGCG GAAUCCACCG AGAGCUGGUU AGGAGAUUAA AUGCGGUCCU GCUUCCGAAC

Y L C G I H R E L V R R L N A V L L P N

nsp4

6733 6743 6753 6763 6773 6783

AUUCAUACAC UGUUUGAUAU GUCGGCUGAA GACUUUGACG CUAUUAUAGC CGAGCACUUC

I H T L F D M S A E D F D A I I A E H F

nsp4

6793 6803 6813 6823 6833 6843

CAGCCUGGGG AUUGUGUUCU GGAAACUGAC AUCGCGUCGU UUGAUAAAAG UGAGGACGAC

Q P G D C V L E T D I A S F D K S E D D

nsp4

6853 6863 6873 6883 6893 6903

GCCAUGGCUC UGACCGCGUU AAUGAUUCUG GAAGACUUAG GUGUGGACGC AGAGCUGUUG

A M A L T A L M I L E D L G V D A E L L

nsp4

6913 6923 6933 6943 6953 6963

ACGCUGAUUG AGGCGGCUUU CGGCGAAAUU UCAUCAAUAC AUUUGCCCAC UAAAACUAAA

T L I E A A F G E I S S I H L P T K T K

nsp4

6973 6983 6993 7003 7013 7023

UUUAAAUUCG GAGCCAUGAU GAAAUCUGGA AUGUUCCUCA CACUGUUUGU GAACACAGUC

F K F G A M M K S G M F L T L F V N T V

nsp4

7033 7043 7053 7063 7073 7083

AUUAACAUUG UAAUCGCAAG CAGAGUGUUG AGAGAACGGC UAACCGGAUC ACCAUGUGCA

I N I V I A S R V L R E R L T G S P C A

nsp4

7093 7103 7113 7123 7133 7143

GCAUUCAUUG GAGAUGACAA UAUCGUGAAA GGAGUCAAAU CGGACAAAUU AAUGGCAGAC

A F I G D D N I V K G V K S D K L M A D

nsp4

7153 7163 7173 7183 7193 7203

AGGUGCGCCA CCUGGUUGAA UAUGGAAGUC AAGAUUAUAG AUGCUGUGGU GGGCGAGAAA

R C A T W L N M E V K I I D A V V G E K

nsp4

7213 7223 7233 7243 7253 7263

GCGCCUUAUU UCUGUGGAGG GUUUAUUUUG UGUGACUCCG UGACCGGCAC AGCGUGCCGU

A P Y F C G G F I L C D S V T G T A C R

nsp4

7273 7283 7293 7303 7313 7323

GUGGCAGACC CCCUAAAAAG GCUGUUUAAG CUAGGCAAAC CUCUGGCAGC AGACGAUGAA

V A D P L K R L F K L G K P L A A D D E

nsp4

7333 7343 7353 7363 7373 7383

CAUGAUGAUG ACAGGAGAAG GGCAUUGCAU GAGGAGUCAA CACGCUGGAA CCGAGUGGGU

H D D D R R R A L H E E S T R W N R V G

nsp4

7393 7403 7413 7423 7433 7443

AUUCUUUCAG AGCUGUGCAA GGCAGUAGAA UCAAGGUAUG AAACCGUAGG AACUUCCAUC

I L S E L C K A V E S R Y E T V G T S I

nsp4

7453 7463 7473 7483 7493 7503

AUAGUUAUGG CCAUGACUAC UCUAGCUAGC AGUGUUAAAU CAUUCAGCUA CCUGAGAGGG

I V M A M T T L A S S V K S F S Y L R G

nsp4

7513 7523 7527

GCCCCUAUAA CUCUCUACGG CUAA

A P I T L Y G *

nsp4

7537 7547 7557 7567 7568

CCUGAAUGGA CUACGACAUA GUCUAGUCCG CCAAGACUAG U

virUTR

7578 7588 7598 7608 7618 7628

AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGGU GAGAUUUCCA

M F V F L V L L P L V S S Q C V V R F P

RBD (S protein)

7638 7648 7658 7668 7678 7688

AAUAUUACAA AUCUGUGUCC AUUUGGAGAA GUGUUUAAUG CAACAAGAUU UGCAUCUGUG

N I T N L C P F G E V F N A T R F A S V

RBD (S protein)

7698 7708 7718 7728 7738 7748

UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU

Y A W N R K R I S N C V A D Y S V L Y N

RBD (S protein)

7758 7768 7778 7788 7798 7808

AGUGCUUCUU UUUCCACAUU UAAAUGUUAU GGAGUGUCUC CAACAAAAUU AAAUGAUUUA

S A S F S T F K C Y G V S P T K L N D L

RBD (S protein)

7818 7828 7838 7848 7858 7868

UGUUUUACAA AUGUGUAUGC UGAUUCUUUU GUGAUCAGAG GUGAUGAAGU GAGACAGAUU

C F T N V Y A D S F V I R G D E V R Q I

RBD (S protein)

7878 7888 7898 7908 7918 7928

GCCCCCGGAC AGACAGGAAA AAUUGCUGAU UACAAUUACA AACUGCCUGA UGAUUUUACA

A P G Q T G K I A D Y N Y K L P D D F T

RBD (S protein)

7938 7948 7958 7968 7978 7988

GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU UUAGAUUCUA AAGUGGGAGG AAAUUACAAU

G C V I A W N S N N L D S K V G G N Y N

RBD (S protein)

7998 8008 8018 8028 8038 8048

UAUCUGUACA GACUGUUUAG AAAAUCAAAU CUGAAACCUU UUGAAAGAGA UAUUUCAACA

Y L Y R L F R K S N L K P F E R D I S T

RBD (S protein)

8058 8068 8078 8088 8098 8108

GAAAUUUAUC AGGCUGGAUC AACACCUUGU AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU

E I Y Q A G S T P C N G V E G F N C Y F

RBD (S protein)

8118 8128 8138 8148 8158 8168

CCAUUACAGA GCUAUGGAUU UCAGCCAACC AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG

P L Q S Y G F Q P T N G V G Y Q P Y R V

RBD (S protein)

8178 8188 8198 8208 8218 8222

GUGGUGCUGU CUUUUGAACU GCUGCAUGCA CCUGCAACAG UGUGUGGACC UAAA

V V L S F E L L H A P A T V C G P K

RBD (S protein)

8232 8242 8249

GGCUCCCCCG GCUCCGGCUC CGGAUCU

G S P G S G S G S

GS linker

8259 8269 8279 8289 8299 8309

GGUUAUAUUC CUGAAGCUCC AAGAGAUGGG CAAGCUUACG UUCGUAAAGA UGGCGAAUGG

G Y I P E A P R D G Q A Y V R K D G E W

fibritin

8319 8329 8339 8349 8359 8369

GUAUUACUUU CUACCUUUUU AGGCCGGUCC CUGGAGGUGC UGUUCCAGGG CCCCGGCUGA

*V L L S T F L G R S L E V L F Q G P G **

fibritin

8372

UGA

*

fibritin

8382 8392 8402 8412 8422 8432

CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG

FI element

8442 8452 8462 8472 8482 8492

AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC

FI element

8502 8512 8522 8532 8542 8552

UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG

FI element

8562 8572 8582 8592 8602 8612

CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA

FI element

8622 8632 8642 8652 8662 8672

GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCGCGGCC GCAUGAAUAC

FI element

8682 8692 8702 8712 8722 8732

AGCAGCAAUU GGCAAGCUGC UUACAUAGAA CUCGCGGCGA UUGGCAUGCC GCCUUAAAAU

FI element

8742 8752 8762 8772 8782 8786

UUUUAUUUUA UUUUUUCUUU UCUUUUCCGA AUCGGAUUUU GUUUUUAAUA UUUC

FI element

8796 8806 8816 8826 8836 8846

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

8856 8866 8876 8886 8896

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

Nucleotide Sequence of RBS004.4

Nucleotide sequence is shown with individual sequence elements as indicated in bold letters. In addition, the sequence of the translated protein is shown in italic letters below the coding nucleotide sequence (* = stop codon).

```
         10         20         30         40     45
GAUGGGCGGC GCAUGAGAGA AGCCCAGACC AAUUACCUAC CCAAA
                                5' UTR
        55         65         75         85         95        105
AUGGAGAAAG UUCACGUUGA CAUCGAGGAA GACAGCCCAU UCCUCAGAGC UUUGCAGCGG
  M  E  K   V  H  V   D  I  E  E   D  S  P   F  L  R   A  L  Q  R
                               nsp1
       115        125        135        145        155        165
AGCUUCCCGC AGUUUGAGGU AGAAGCCAAG CAGGUCACUG AUAAUGACCA UGCUAAUGCC
  S  F  P   Q  F  E   V  E  A  K   Q  V  T   D  N  D   H  A  N  A
                               nsp1
       175        185        195        205        215        225
AGAGCGUUUU CGCAUCUGGC UUCAAAACUG AUCGAAACGG AGGUGGACCC AUCCGACACG
  R  A  F   S  H  L   A  S  K  L   I  E  T   E  V  D   P  S  D  T
                               nsp1
       235        245        255        265        275        285
AUCCUUGACA UUGGAAGUGC GCCCGCCCGC AGAAUGUAUU CUAAGCACAA GUAUCAUUGU
  I  L  D   I  G  S   A  P  A  R   R  M  Y   S  K  H   K  Y  H  C
                               nsp1
       295        305        315        325        335        345
AUCUGUCCGA UGAGAUGUGC GGAAGAUCCG GACAGAUUGU AUAAGUAUGC AACUAAGCUG
  I  C  P   M  R  C   A  E  D  P   D  R  L   Y  K  Y   A  T  K  L
                               nsp1
       355        365        375        385        395        405
AAGAAAAACU GUAAGGAAAU AACUGAUAAG GAAUUGGACA AGAAAAUGAA GGAGCUCGCC
  K  K  N   C  K  E   I  T  D  K   E  L  D   K  K  M   K  E  L  A
                               nsp1
       415        425        435        445        455        465
GCCGUCAUGA GCGACCCUGA CCUGGAAACU GAGACUAUGU GCCUCCACGA CGACGAGUCG
```

A V M S D P D L E T E T M C L H D D E S

nsp1

475 485 495 505 515 525

UGUCGCUACG AAGGGCAAGU CGCUGUUUAC CAGGAUGUAU ACGCGGUUGA CGGACCGACA

C R Y E G Q V A V Y Q D V Y A V D G P T

nsp1

535 545 555 565 575 585

AGUCUCUAUC ACCAAGCCAA UAAGGGAGUU AGAGUCGCCU ACUGGAUAGG CUUUGACACC

S L Y H Q A N K G V R V A Y W I G F D T

nsp1

595 605 615 625 635 645

ACCCCUUUUA UGUUUAAGAA CUUGGCUGGA GCAUAUCCAU CAUACUCUAC CAACUGGGCC

T P F M F K N L A G A Y P S Y S T N W A

nsp1

655 665 675 685 695 705

GACGAAACCG UGUUAACGGC UCGUAACAUA GGCCUAUGCA GCUCUGACGU UAUGGAGCGG

D E T V L T A R N I G L C S S D V M E R

nsp1

715 725 735 745 755 765

UCACGUAGAG GGAUGUCCAU UCUUAGAAAG AAGUAUUUGA AACCAUCCAA CAAUGUUCUA

S R R G M S I L R K K Y L K P S N N V L

nsp1

775 785 795 805 815 825

UUCUCUGUUG GCUCGACCAU CUACCACGAA AAGAGGGACU UACUGAGGAG CUGGCACCUG

F S V G S T I Y H E K R D L L R S W H L

nsp1

835 845 855 865 875 885

CCGUCUGUAU UUCACUUACG UGGCAAGCAA AAUUACACAU GUCGGUGUGA GACUAUAGUU

P S V F H L R G K Q N Y T C R C E T I V

nsp1

895 905 915 925 935 945

AGUUGCGACG GGUACGUCGU UAAAAGAAUA GCUAUCAGUC CAGGCCUGUA UGGGAAGCCU

S C D G Y V V K R I A I S P G L Y G K P

nsp1

955 965 975 985 995 1005
UCAGGCUAUG CUGCUACGAU GCACCGCGAG GGAUUCUUGU GCUGCAAAGU GACAGACACA
S G Y A A T M H R E G F L C C K V T D T

nsp1

1015 1025 1035 1045 1055 1065
UUGAACGGGG AGAGGGUCUC UUUUCCCGUG UGCACGUAUG UGCCAGCUAC AUUGUGUGAC
L N G E R V S F P V C T Y V P A T L C D

nsp1

1075 1085 1095 1105 1115 1125
CAAAUGACUG GCAUACUGGC AACAGAUGUC AGUGCGGACG ACGCGCAAAA ACUGCUGGUU
Q M T G I L A T D V S A D D A Q K L L V

nsp1

1135 1145 1155 1165 1175 1185
GGGCUCAACC AGCGUAUAGU CGUCAACGGU CGCACCCAGA GAAACACCAA UACCAUGAAA
G L N Q R I V V N G R T Q R N T N T M K

nsp1

1195 1205 1215 1225 1235 1245
AAUUACCUUU UGCCCGUAGU GGCCCAGGCA UUUGCUAGGU GGGCAAAGGA AUAUAAGGAA
N Y L L P V V A Q A F A R W A K E Y K E

nsp1

1255 1265 1275 1285 1295 1305
GAUCAAGAAG AUGAAAGGCC ACUAGGACUA CGAGAUAGAC AGUUAGUCAU GGGGUGUUGU
D Q E D E R P L G L R D R Q L V M G C C

nsp1

1315 1325 1335 1345 1355 1365
UGGGCUUUUA GAAGGCACAA GAUAACAUCU AUUUAUAAGC GCCCGGAUAC CCAAACCAUC
W A F R R H K I T S I Y K R P D T Q T I

nsp1

1375 1385 1395 1405 1415 1425
AUCAAAGUGA ACAGCGAUUU CCACUCAUUC GUGCUGCCCA GGAUAGGCAG UAACACAUUG
I K V N S D F H S F V L P R I G S N T L

nsp1

1435 1445 1455 1465 1475 1485
GAGAUCGGGC UGAGAACAAG AAUCAGGAAA AUGUUAGAGG AGCACAAGGA GCCGUCACCU
E I G L R T R I R K M L E E H K E P S P

nsp1

1495 1505 1515 1525 1535 1545

CUCAUUACCG CCGAGGACGU ACAAGAAGCU AAGUGCGCAG CCGAUGAGGC UAAGGAGGUG

L I T A E D V Q E A K C A A D E A K E V

nsp1

1555 1565 1575 1585 1595 1605

CGUGAAGCCG AGGAGUUGCG CGCAGCUCUA CCACCUUUGG CAGCUGAUGU UGAGGAGCCC

R E A E E L R A A L P P L A A D V E E P

nsp1

1615 1625 1635 1645 1650

ACUCUGGAAG CCGAUGUCGA CUUGAUGUUA CAAGAGGCUG GGGCC

T L E A D V D L M L Q E A G A

nsp1

1660 1670 1680 1690 1700 1710

GGCUCAGUGG AGACACCUCG UGGCUUGAUA AAGGUUACCA GCUACGCUGG CGAGGACAAG

G S V E T P R G L I K V T S Y A G E D K

nsp2

1720 1730 1740 1750 1760 1770

AUCGGCUCUU ACGCUGUGCU UUCUCCGCAG GCUGUACUCA AGAGUGAAAA AUUAUCUUGC

I G S Y A V L S P Q A V L K S E K L S C

nsp2

1780 1790 1800 1810 1820 1830

AUCCACCCUC UCGCUGAACA AGUCAUAGUG AUAACACACU CUGGCCGAAA AGGGCGUUAU

I H P L A E Q V I V I T H S G R K G R Y

nsp2

1840 1850 1860 1870 1880 1890

GCCGUGGAAC CAUACCAUGG UAAAGUAGUG GUGCCAGAGG GACAUGCAAU ACCCGUCCAG

A V E P Y H G K V V V P E G H A I P V Q

nsp2

1900 1910 1920 1930 1940 1950

GACUUUCAAG CUCUGAGUGA AAGUGCCACC AUUGUGUACA ACGAACGUGA GUUCGUAAAC

D F Q A L S E S A T I V Y N E R E F V N

nsp2

1960 1970 1980 1990 2000 2010

AGGUACCUGC ACCAUAUUGC CACACAUGGA GGAGCGCUGA ACACUGAUGA AGAAUAUUAC

R Y L H H I A T H G G A L N T D E E Y Y

nsp2

2020 2030 2040 2050 2060 2070

AAAACUGUCA AGCCCAGCGA GCACGACGGC GAAUACCUGU ACGACAUCGA CAGGAAACAG

K T V K P S E H D G E Y L Y D I D R K Q

nsp2

2080 2090 2100 2110 2120 2130

UGCGUCAAGA AAGAGCUAGU CACUGGGCUA GGGCUCACAG GCGAGCUGGU CGAUCCUCCC

C V K K E L V T G L G L T G E L V D P P

nsp2

2140 2150 2160 2170 2180 2190

UUCCAUGAAU UCGCCUACGA GAGUCUGAGA ACACGACCAG CCGCUCCUUA CCAAGUACCA

F H E F A Y E S L R T R P A A P Y Q V P

nsp2

2200 2210 2220 2230 2240 2250

ACCAUAGGGG UGUAUGGCGU GCCAGGAUCA GGCAAGUCUG GCAUCAUUAA AAGCGCAGUC

T I G V Y G V P G S G K S G I I K S A V

nsp2

2260 2270 2280 2290 2300 2310

ACCAAAAAAG AUCUAGUGGU GAGCGCCAAG AAAGAAAACU GUGCAGAAAU UAUAAGGGAC

T K K D L V V S A K K E N C A E I I R D

nsp2

2320 2330 2340 2350 2360 2370

GUCAAGAAAA UGAAAGGGCU GGACGUCAAU GCCAGAACUG UGGACUCAGU GCUCUUGAAU

V K K M K G L D V N A R T V D S V L L N

nsp2

2380 2390 2400 2410 2420 2430

GGAUGCAAAC ACCCCGUAGA GACCCUGUAU AUUGACGAGG CUUUUGCUUG UCAUGCAGGU

G C K H P V E T L Y I D E A F A C H A G

nsp2

2440 2450 2460 2470 2480 2490

ACUCUCAGAG CGCUCAUAGC CAUUAUAAGA CCUAAAAAGG CAGUGCUCUG CGGAGAUCCC

T L R A L I A I I R P K K A V L C G D P

nsp2

2500 2510 2520 2530 2540 2550

AAACAGUGCG GUUUUUUUAA CAUGAUGUGC CUGAAAGUGC AUUUUAACCA CGAGAUUUGC

K Q C G F F N M M C L K V H F N H E I C

nsp2

2560 2570 2580 2590 2600 2610

ACACAAGUCU UCCACAAAAG CAUCUCUCGC CGUUGCACUA AAUCUGUGAC UUCGGUCGUC

T Q V F H K S I S R R C T K S V T S V V

nsp2

2620 2630 2640 2650 2660 2670

UCAACCUUGU UUUACGACAA AAAAAUGAGA ACGACGAAUC CGAAAGAGAC UAAGAUUGUG

S T L F Y D K K M R T T N P K E T K I V

nsp2

2680 2690 2700 2710 2720 2730

AUUGACACUA CCGGCAGUAC CAAACCUAAG CAGGACGAUC UCAUUCUCAC UUGUUUCAGA

I D T T G S T K P K Q D D L I L T C F R

nsp2

2740 2750 2760 2770 2780 2790

GGGUGGGUGA AGCAGUUGCA AAUAGAUUAC AAAGGCAACG AAAUAAUGAC GGCAGCUGCC

G W V K Q L Q I D Y K G N E I M T A A A

nsp2

2800 2810 2820 2830 2840 2850

UCUCAAGGGC UGACCCGUAA AGGUGUGUAU GCCGUUCGGU ACAAGGUGAA UGAAAAUCCU

S Q G L T R K G V Y A V R Y K V N E N P

nsp2

2860 2870 2880 2890 2900 2910

CUGUACGCAC CCACCUCAGA ACAUGUGAAC GUCCUACUGA CCCGCACGGA GGACCGCAUC

L Y A P T S E H V N V L L T R T E D R I

nsp2

2920 2930 2940 2950 2960 2970

GUGUGGAAAA CACUAGCCGG CGACCCAUGG AUAAAAACAC UGACUGCCAA GUACCCUGGG

V W K T L A G D P W I K T L T A K Y P G

nsp2

2980 2990 3000 3010 3020 3030

AAUUUCACUG CCACGAUAGA GGAGUGGCAA GCAGAGCAUG AUGCCAUCAU GAGGCACAUC

N F T A T I E E W Q A E H D A I M R H I

nsp2

3040 3050 3060 3070 3080 3090

UUGGAGAGAC CGGACCCUAC CGACGUCUUC CAGAAUAAGG CAAACGUGUG UUGGGCCAAG

L E R P D P T D V F Q N K A N V C W A K

nsp2

3100 3110 3120 3130 3140 3150

GCUUUAGUGC CGGUGCUGAA GACCGCUGGC AUAGACAUGA CCACUGAACA AUGGAACACU

A L V P V L K T A G I D M T T E Q W N T

nsp2

3160 3170 3180 3190 3200 3210

GUGGAUUAUU UUGAAACGGA CAAAGCUCAC UCAGCAGAGA UAGUAUUGAA CCAACUAUGC

V D Y F E T D K A H S A E I V L N Q L C

nsp2

3220 3230 3240 3250 3260 3270

GUGAGGUUCU UUGGACUCGA UCUGGACUCC GGUCUAUUUU CUGCACCCAC UGUUCCGUUA

V R F F G L D L D S G L F S A P T V P L

nsp2

3280 3290 3300 3310 3320 3330

UCCAUUAGGA AUAAUCACUG GGAUAACUCC CCGUCGCCUA ACAUGUACGG GCUGAAUAAA

S I R N N H W D N S P S P N M Y G L N K

nsp2

3340 3350 3360 3370 3380 3390

GAAGUGGUCC GUCAGCUCUC UCGCAGGUAC CCACAACUGC CUCGGGCAGU UGCCACUGGU

E V V R Q L S R R Y P Q L P R A V A T G

nsp2

3400 3410 3420 3430 3440 3450

AGAGUCUAUG ACAUGAACAC UGGUACACUG CGCAAUUAUG AUCCGCGCAU AAACCUAGUA

R V Y D M N T G T L R N Y D P R I N L V

nsp2

3460 3470 3480 3490 3500 3510

CCUGUAAACA GAAGACUGCC UCAUGCUUUA GUCCUCCACC AUAAUGAACA CCCACAGAGU

P V N R R L P H A L V L H H N E H P Q S

nsp2

3520 3530 3540 3550 3560 3570

GACUUUUCUU CAUUCGUCAG CAAAUUGAAG GGCAGAACUG UCCUGGUGGU CGGGGAAAAG

D F S S F V S K L K G R T V L V V G E K

nsp2

3580 3590 3600 3610 3620 3630

UUGUCCGUCC CAGGCAAAAU GGUUGACUGG UUGUCAGACC GGCCUGAGGC UACCUUCAGA

L S V P G K M V D W L S D R P E A T F R

nsp2

3640 3650 3660 3670 3680 3690

GCUCGGCUGG AUUUAGGCAU CCCAGGUGAU GUGCCCAAAU AUGACAUAAU AUUUGUUAAU

A R L D L G I P G D V P K Y D I I F V N

nsp2

3700 3710 3720 3730 3740 3750

GUGAGGACCC CAUAUAAAUA CCAUCACUAU CAGCAGUGUG AAGACCAUGC CAUUAAGCUA

V R T P Y K Y H H Y Q Q C E D H A I K L

nsp2

3760 3770 3780 3790 3800 3810

AGCAUGUUGA CCAAGAAAGC AUGUCUGCAU CUGAAUCCCG GCGGAACCUG UGUCAGCAUA

S M L T K K A C L H L N P G G T C V S I

nsp2

3820 3830 3840 3850 3860 3870

GGUUAUGGUU ACGCUGACAG GGCCAGCGAA AGCAUCAUUG GUGCUAUAGC GCGGCAGUUC

G Y G Y A D R A S E S I I G A I A R Q F

nsp2

3880 3890 3900 3910 3920 3930

AAGUUUUCCC GAGUAUGCAA ACCGAAAUCC UCACUUGAGG AGACGGAAGU UCUGUUUGUA

K F S R V C K P K S S L E E T E V L F V

nsp2

3940 3950 3960 3970 3980 3990

UUCAUUGGGU ACGAUCGCAA GGCCCGUACG CACAAUCCUU ACAAGCUAUC AUCAACCUUG

F I G Y D R K A R T H N P Y K L S S T L

nsp2

4000 4010 4020 4030 4032

ACCAACAUUU AUACAGGUUC CAGACUCCAC GAAGCCGGAU GU

T N I Y T G S R L H E A G C

nsp2

4042 4052 4062 4072 4082 4092

GCACCCUCAU AUCAUGUGGU GCGAGGGGAU AUUGCCACGG CCACCGAAGG AGUGAUUAUA

A P S Y H V V R G D I A T A T E G V I I

nsp3

4102 4112 4122 4132 4142 4152

AAUGCUGCUA ACAGCAAAGG ACAACCUGGC GGAGGGGUGU GCGGAGCGCU GUAUAAGAAA

N A A N S K G Q P G G G V C G A L Y K K

nsp3

4162 4172 4182 4192 4202 4212

UUCCCGGAAA GUUUCGAUUU ACAGCCGAUC GAAGUAGGAA AAGCGCGACU GGUCAAAGGU

F P E S F D L Q P I E V G K A R L V K G

nsp3

4222 4232 4242 4252 4262 4272

GCAGCUAAAC AUAUCAUUCA UGCCGUAGGA CCAAACUUCA ACAAAGUUUC GGAGGUUGAA

A A K H I I H A V G P N F N K V S E V E

nsp3

4282 4292 4302 4312 4322 4332

GGUGACAAAC AGUUGGCAGA GGCUUAUGAG UCCAUCGCUA AGAUUGUCAA CGAUAACAAU

G D K Q L A E A Y E S I A K I V N D N N

nsp3

4342 4352 4362 4372 4382 4392

UACAAGUCAG UAGCGAUUCC ACUGUUGUCC ACCGGCAUCU UUUCCGGGAA CAAAGAUCGA

Y K S V A I P L L S T G I F S G N K D R

nsp3

4402 4412 4422 4432 4442 4452

CUAACCCAAU CAUUGAACCA UUUGCUGACA GCUUUAGACA CCACUGAUGC AGAUGUAGCC

L T Q S L N H L L T A L D T T D A D V A

nsp3

4462 4472 4482 4492 4502 4512

AUAUACUGCA GGGACAAGAA AUGGGAAAUG ACUCUCAAGG AAGCAGUGGC UAGGAGAGAA

I Y C R D K K W E M T L K E A V A R R E

nsp3

4522 4532 4542 4552 4562 4572

GCAGUGGAGG AGAUAUGCAU AUCCGACGAU UCUUCAGUGA CAGAACCUGA UGCAGAGCUG

A V E E I C I S D D S S V T E P D A E L

nsp3

4582 4592 4602 4612 4622 4632

GUGAGGGUGC AUCCCAAGAG UUCUUUGGCU GGAAGGAAGG GCUACAGCAC AAGCGAUGGC

V R V H P K S S L A G R K G Y S T S D G

nsp3

4642 4652 4662 4672 4682 4692

AAAACUUUCU CAUAUUUGGA AGGGACCAAG UUUCACCAGG CGGCCAAGGA UAUAGCAGAA

K T F S Y L E G T K F H Q A A K D I A E

nsp3

4702 4712 4722 4732 4742 4752

AUUAAUGCCA UGUGGCCCGU UGCAACGGAG GCCAAUGAGC AGGUAUGCAU GUAUAUCCUC

I N A M W P V A T E A N E Q V C M Y I L

nsp3

4762 4772 4782 4792 4802 4812

GGAGAAAGCA UGAGCAGUAU UAGGUCGAAA UGCCCCGUCG AGGAGUCGGA AGCCUCCACA

G E S M S S I R S K C P V E E S E A S T

nsp3

4822 4832 4842 4852 4862 4872

CCACCUAGCA CGCUGCCUUG CUUGUGCAUC CAUGCCAUGA CUCCAGAAAG AGUACAGCGC

P P S T L P C L C I H A M T P E R V Q R

nsp3

4882 4892 4902 4912 4922 4932

CUAAAAGCCU CACGUCCAGA ACAAAUUACU GUGUGCUCAU CCUUUCCAUU GCCGAAGUAU

L K A S R P E Q I T V C S S F P L P K Y

nsp3

4942 4952 4962 4972 4982 4992

AGAAUCACUG GUGUGCAGAA GAUCCAAUGC UCCCAGCCUA UAUUGUUCUC ACCGAAAGUG

R I T G V Q K I Q C S Q P I L F S P K V

nsp3

5002 5012 5022 5032 5042 5052

CCUGCGUAUA UUCAUCCAAG GAAGUAUCUC GUGGAAACAC CACCGGUAGA CGAGACUCCG

P A Y I H P R K Y L V E T P P V D E T P

nsp3

5062 5072 5082 5092 5102 5112

GAGCCAUCGG CAGAGAACCA AUCCACAGAG GGGACACCUG AACAACCACC ACUUAUAACC

E P S A E N Q S T E G T P E Q P P L I T

nsp3

5122 5132 5142 5152 5162 5172

GAGGAUGAGA CCAGGACUAG AACGCCUGAG CCGAUCAUCA UCGAAGAAGA AGAAGAAGAU

E D E T R T R T P E P I I I E E E E E D

nsp3

5182 5192 5202 5212 5222 5232

AGCAUAAGUU UGCUGUCAGA UGGCCCGACC CACCAGGUGC UGCAAGUCGA GGCAGACAUU

S I S L L S D G P T H Q V L Q V E A D I

nsp3

5242 5252 5262 5272 5282 5292

CACGGGCCGC CCUCUGUAUC UAGCUCAUCC UGGUCCAUUC CUCAUGCAUC CGACUUUGAU

H G P P S V S S S S W S I P H A S D F D

nsp3

5302 5312 5322 5332 5342 5352

GUGGACAGUU UAUCCAUACU UGACACCCUG GAGGGAGCUA GCGUGACCAG CGGGGCAACG

V D S L S I L D T L E G A S V T S G A T

nsp3

5362 5372 5382 5392 5402 5412

UCAGCCGAGA CUAACUCUUA CUUCGCAAAG AGUAUGGAGU UUCUGGCGCG ACCGGUGCCU

S A E T N S Y F A K S M E F L A R P V P

nsp3

5422 5432 5442 5452 5462 5472

GCGCCUCGAA CAGUAUUCAG GAACCCUCCA CAUCCCGCUC CGCGCACAAG AACACCGUCA

A P R T V F R N P P H P A P R T R T P S

nsp3

5482 5492 5502 5512 5522 5532

CUUGCACCCA GCAGGGCCUG CUCCAGAACC AGCCUAGUUU CCACCCCGCC AGGCGUGAAU

L A P S R A C S R T S L V S T P P G V N

nsp3

```
     5542       5552       5562       5572       5582       5592
AGGGUGAUCA CUAGAGAGGA GCUCGAAGCG CUUACCCCGU CACGCACUCC UAGCAGGUCG
  R  V  I   T  R  E   E  L  E  A   L  T  P   S  R  T   P  S  R  S
```

nsp3

```
     5602       5612       5622       5632       5642       5652
GUCUCCAGAA CCAGCCUGGU CUCCAACCCG CCAGGCGUAA AUAGGGUGAU UACAAGAGAG
  V  S  R   T  S  L   V  S  N  P   P  G  V   N  R  V   I  T  R  E
```

nsp3

```
     5662       5672       5682       5692       5702 5703
GAGUUUGAGG CGUUCGUAGC ACAACAACAA UGACGGUUUG AUGCGGGUGC A
  E  F  E   A  F  V   A  Q  Q  Q   *  R  F   D  A  G   A
```

nsp3

```
     5713       5723       5733       5743       5753       5763
UACAUCUUUU CCUCCGACAC CGGUCAAGGG CAUUUACAAC AAAAAUCAGU AAGGCAAACG
  Y  I  F   S  S  D   T  G  Q  G   H  L  Q   Q  K  S   V  R  Q  T
```

nsp4

```
     5773       5783       5793       5803       5813       5823
GUGCUAUCCG AAGUGGUGUU GGAGAGGACC GAAUUGGAGA UUUCGUAUGC CCCGCGCCUC
  V  L  S   E  V  V   L  E  R  T   E  L  E   I  S  Y   A  P  R  L
```

nsp4

```
     5833       5843       5853       5863       5873       5883
GACCAAGAAA AAGAAGAAUU ACUACGCAAG AAAUUACAGU UAAAUCCCAC ACCUGCUAAC
  D  Q  E   K  E  E   L  L  R  K   K  L  Q   L  N  P   T  P  A  N
```

nsp4

```
     5893       5903       5913       5923       5933       5943
AGAAGCAGAU ACCAGUCCAG GAAGGUGGAG AACAUGAAAG CCAUAACAGC UAGACGUAUU
  R  S  R   Y  Q  S   R  K  V  E   N  M  K   A  I  T   A  R  R  I
```

nsp4

```
     5953       5963       5973       5983       5993       6003
CUGCAAGGCC UAGGGCAUUA UUUGAAGGCA GAAGGAAAAG UGGAGUGCUA CCGAACCCUG
  L  Q  G   L  G  H   Y  L  K  A   E  G  K   V  E  C   Y  R  T  L
```

nsp4

```
     6013       6023       6033       6043       6053       6063
```

CAUCCUGUUC CUUUGUAUUC AUCUAGUGUG AACCGUGCCU UUUCAAGCCC CAAGGUCGCA

H P V P L Y S S S V N R A F S S P K V A

nsp4

6073 6083 6093 6103 6113 6123

GUGGAAGCCU GUAACGCCAU GUUGAAAGAG AACUUUCCGA CUGUGGCUUC UUACUGUAUU

V E A C N A M L K E N F P T V A S Y C I

nsp4

6133 6143 6153 6163 6173 6183

AUUCCAGAGU ACGAUGCCUA UUUGGACAUG GUUGACGGAG CUUCAUGCUG CUUAGACACU

I P E Y D A Y L D M V D G A S C C L D T

nsp4

6193 6203 6213 6223 6233 6243

GCCAGUUUUU GCCCUGCAAA GCUGCGCAGC UUUCCAAAGA AACACUCCUA UUUGGAACCC

A S F C P A K L R S F P K K H S Y L E P

nsp4

6253 6263 6273 6283 6293 6303

ACAAUACGAU CGGCAGUGCC UUCAGCGAUC CAGAACACGC UCCAGAACGU CCUGGCAGCU

T I R S A V P S A I Q N T L Q N V L A A

nsp4

6313 6323 6333 6343 6353 6363

GCCACAAAAA GAAAUUGCAA UGUCACGCAA AUGAGAGAAU UGCCCGUAUU GGAUUCGGCG

A T K R N C N V T Q M R E L P V L D S A

nsp4

6373 6383 6393 6403 6413 6423

GCCUUUAAUG UGGAAUGCUU CAAGAAAUAU GCGUGUAAUA AUGAAUAUUG GGAAACGUUU

A F N V E C F K K Y A C N N E Y W E T F

nsp4

6433 6443 6453 6463 6473 6483

AAAGAAAACC CCAUCAGGCU UACUGAAGAA AACGUGGUAA AUUACAUUAC CAAAUUAAAA

K E N P I R L T E E N V V N Y I T K L K

nsp4

6493 6503 6513 6523 6533 6543

GGACCAAAAG CUGCUGCUCU UUUUGCGAAG ACACAUAAUU UGAAUAUGUU GCAGGACAUA

G P K A A A L F A K T H N L N M L Q D I

nsp4

6553 6563 6573 6583 6593 6603

CCAAUGGACA GGUUUGUAAU GGACUUAAAG AGAGACGUGA AAGUGACUCC AGGAACAAAA

P M D R F V M D L K R D V K V T P G T K

nsp4

6613 6623 6633 6643 6653 6663

CAUACUGAAG AACGGCCCAA GGUACAGGUG AUCCAGGCUG CCGAUCCGCU AGCAACAGCG

H T E E R P K V Q V I Q A A D P L A T A

nsp4

6673 6683 6693 6703 6713 6723

UAUCUGUGCG GAAUCCACCG AGAGCUGGUU AGGAGAUUAA AUGCGGUCCU GCUUCCGAAC

Y L C G I H R E L V R R L N A V L L P N

nsp4

6733 6743 6753 6763 6773 6783

AUUCAUACAC UGUUUGAUAU GUCGGCUGAA GACUUUGACG CUAUUAUAGC CGAGCACUUC

I H T L F D M S A E D F D A I I A E H F

nsp4

6793 6803 6813 6823 6833 6843

CAGCCUGGGG AUUGUGUUCU GGAAACUGAC AUCGCGUCGU UUGAUAAAAG UGAGGACGAC

Q P G D C V L E T D I A S F D K S E D D

nsp4

6853 6863 6873 6883 6893 6903

GCCAUGGCUC UGACCGCGUU AAUGAUUCUG GAAGACUUAG GUGUGGACGC AGAGCUGUUG

A M A L T A L M I L E D L G V D A E L L

nsp4

6913 6923 6933 6943 6953 6963

ACGCUGAUUG AGGCGGCUUU CGGCGAAAUU UCAUCAAUAC AUUUGCCCAC UAAAACUAAA

T L I E A A F G E I S S I H L P T K T K

nsp4

6973 6983 6993 7003 7013 7023

UUUAAAUUCG GAGCCAUGAU GAAAUCUGGA AUGUUCCUCA CACUGUUUGU GAACACAGUC

F K F G A M M K S G M F L T L F V N T V

nsp4

7033 7043 7053 7063 7073 7083

AUUAACAUUG UAAUCGCAAG CAGAGUGUUG AGAGAACGGC UAACCGGAUC ACCAUGUGCA

I N I V I A S R V L R E R L T G S P C A

nsp4

7093 7103 7113 7123 7133 7143

GCAUUCAUUG GAGAUGACAA UAUCGUGAAA GGAGUCAAAU CGGACAAAUU AAUGGCAGAC

A F I G D D N I V K G V K S D K L M A D

nsp4

7153 7163 7173 7183 7193 7203

AGGUGCGCCA CCUGGUUGAA UAUGGAAGUC AAGAUUAUAG AUGCUGUGGU GGGCGAGAAA

R C A T W L N M E V K I I D A V V G E K

nsp4

7213 7223 7233 7243 7253 7263

GCGCCUUAUU UCUGUGGAGG GUUUAUUUUG UGUGACUCCG UGACCGGCAC AGCGUGCCGU

A P Y F C G G F I L C D S V T G T A C R

nsp4

7273 7283 7293 7303 7313 7323

GUGGCAGACC CCCUAAAAAG GCUGUUUAAG CUAGGCAAAC CUCUGGCAGC AGACGAUGAA

V A D P L K R L F K L G K P L A A D D E

nsp4

7333 7343 7353 7363 7373 7383

CAUGAUGAUG ACAGGAGAAG GGCAUUGCAU GAGGAGUCAA CACGCUGGAA CCGAGUGGGU

H D D D R R R A L H E E S T R W N R V G

nsp4

7393 7403 7413 7423 7433 7443

AUUCUUUCAG AGCUGUGCAA GGCAGUAGAA UCAAGGUAUG AAACCGUAGG AACUUCCAUC

I L S E L C K A V E S R Y E T V G T S I

nsp4

7453 7463 7473 7483 7493 7503

AUAGUUAUGG CCAUGACUAC UCUAGCUAGC AGUGUUAAAU CAUUCAGCUA CCUGAGAGGG

I V M A M T T L A S S V K S F S Y L R G

nsp4

7513 7523 7527

GCCCCUAUAA CUCUCUACGG CUAA

*A P I T L Y G **

nsp4

```
      7537        7547        7557        7567  7568
CCUGAAUGGA CUACGACAUA GUCUAGUCCG CCAAGACUAG U
```

virUTR

```
      7578        7588        7598        7608        7618        7628
AUGUUUGUGU UUCUUGUGCU GCUGCCUCUU GUGUCUUCUC AGUGUGUGGU GAGAUUUCCA
  M  F  V   F  L  V   L  L  P  L   V  S  S   Q  C  V   V  R  F  P
```

RBD (S protein)

```
      7638        7648        7658        7668        7678        7688
AAUAUUACAA AUCUGUGUCC AUUUGGAGAA GUGUUUAAUG CAACAAGAUU UGCAUCUGUG
  N  I  T   N  L  C   P  F  G  E   V  F  N   A  T  R   F  A  S  V
```

RBD (S protein)

```
      7698        7708        7718        7728        7738        7748
UAUGCAUGGA AUAGAAAAAG AAUUUCUAAU UGUGUGGCUG AUUAUUCUGU GCUGUAUAAU
  Y  A  W   N  R  K   R  I  S  N   C  V  A   D  Y  S   V  L  Y  N
```

RBD (S protein)

```
      7758        7768        7778        7788        7798        7808
AGUGCUUCUU UUUCCACAUU UAAAUGUUAU GGAGUGUCUC CAACAAAAUU AAAUGAUUUA
  S  A  S   F  S  T   F  K  C  Y   G  V  S   P  T  K   L  N  D  L
```

RBD (S protein)

```
      7818        7828        7838        7848        7858        7868
UGUUUUACAA AUGUGUAUGC UGAUUCUUUU GUGAUCAGAG GUGAUGAAGU GAGACAGAUU
  C  F  T   N  V  Y   A  D  S  F   V  I  R   G  D  E   V  R  Q  I
```

RBD (S protein)

```
      7878        7888        7898        7908        7918        7928
GCCCCCGGAC AGACAGGAAA AAUUGCUGAU UACAAUUACA AACUGCCUGA UGAUUUUACA
  A  P  G   Q  T  G   K  I  A  D   Y  N  Y   K  L  P   D  D  F  T
```

RBD (S protein)

```
      7938        7948        7958        7968        7978        7988
GGAUGUGUGA UUGCUUGGAA UUCUAAUAAU UUAGAUUCUA AAGUGGGAGG AAAUUACAAU
  G  C  V   I  A  W   N  S  N  N   L  D  S   K  V  G   G  N  Y  N
```

RBD (S protein)

```
      7998        8008        8018        8028        8038        8048
UAUCUGUACA GACUGUUUAG AAAAUCAAAU CUGAAACCUU UUGAAAGAGA UAUUUCAACA
```

```
  Y  L  Y   R  L  F   R  K  S  N   L  K  P   F  E  R   D  I  S  T
```

RBD (S protein)

```
     8058        8068        8078        8088        8098        8108
GAAAUUUAUC AGGCUGGAUC AACACCUUGU AAUGGAGUGG AAGGAUUUAA UUGUUAUUUU
  E  I  Y   Q  A  G   S  T  P  C   N  G  V   E  G  F   N  C  Y  F
```

RBD (S protein)

```
     8118        8128        8138        8148        8158        8168
CCAUUACAGA GCUAUGGAUU UCAGCCAACC AAUGGUGUGG GAUAUCAGCC AUAUAGAGUG
  P  L  Q   S  Y  G   F  Q  P  T   N  G  V   G  Y  Q   P  Y  R  V
```

RBD (S protein)

```
     8178        8188        8198        8208        8218     8222
GUGGUGCUGU CUUUUGAACU GCUGCAUGCA CCUGCAACAG UGUGUGGACC UAAA
  V  V  L   S  F  E   L  L  H  A   P  A  T   V  C  G   P  K
```

RBD (S protein)

```
     8232        8242    8249
GGCUCCCCCG GCUCCGGCUC CGGAUCU
  G  S  P   G  S  G   S  G  S
```

GS linker

```
     8259        8269        8279        8289        8299        8309
GGUUAUAUUC CUGAAGCUCC AAGAGAUGGG CAAGCUUACG UUCGUAAAGA UGGCGAAUGG
  G  Y  I   P  E  A   P  R  D  G   Q  A  Y   V  R  K   D  G  E  W
```

fibritin

```
     8319        8329 8330
GUAUUACUUU CUACCUUUUU A
  V  L  L   S  T  F   L
```

fibritin

```
     8340    8345
GGAAGCGGCA GCGGA
  G  S  G   S  G
```

GS linker

```
     8355        8365        8375        8385        8395        8405
UCUGAACAGU ACAUUAAAUG GCCUUGGUAC AUUUGGCUUG GAUUUAUUGC AGGAUUAAUU
  S  E  Q   Y  I  K   W  P  W  Y   I  W  L   G  F  I   A  G  L  I
```

TM

```
      8415        8425        8435        8445        8455        8465
GCAAUUGUGA UGGUGACAAU UAUGUUAUGU UGUAUGACAU CAUGUUGUUC UUGUUUAAAA
  A  I  V   M  V  T   I  M  L  C   C  M  T   S  C  C   S  C  L  K
```

TM

```
      8475        8485        8495        8505        8515        8525
GGAUGUUGUU CUUGUGGAAG CUGUUGUAAA UUUGAUGAAG AUGAUUCUGA ACCUGUGUUA
  G  C  C   S  C  G   S  C  C  K   F  D  E   D  D  S   E  P  V  L
```

TM

```
      8535        8545        8555
AAAGGAGUGA AAUUGCAUUA CACAUGAUGA
  K  G  V   K  L  H   Y  T  *  *
```

TM

```
      8565        8575        8585        8595        8605        8615
CUCGAGCUGG UACUGCAUGC ACGCAAUGCU AGCUGCCCCU UUCCCGUCCU GGGUACCCCG
```

FI element

```
      8625        8635        8645        8655        8665        8675
AGUCUCCCCC GACCUCGGGU CCCAGGUAUG CUCCCACCUC CACCUGCCCC ACUCACCACC
```

FI element

```
      8685        8695        8705        8715        8725        8735
UCUGCUAGUU CCAGACACCU CCCAAGCACG CAGCAAUGCA GCUCAAAACG CUUAGCCUAG
```

FI element

```
      8745        8755        8765        8775        8785        8795
CCACACCCCC ACGGGAAACA GCAGUGAUUA ACCUUUAGCA AUAAACGAAA GUUUAACUAA
```

FI element

```
      8805        8815        8825        8835        8845        8855
GCUAUACUAA CCCCAGGGUU GGUCAAUUUC GUGCCAGCCA CACCGCGGCC GCAUGAAUAC
```

FI element

```
      8865        8875        8885        8895        8905        8915
AGCAGCAAUU GGCAAGCUGC UUACAUAGAA CUCGCGGCGA UUGGCAUGCC GCCUUAAAAU
```

FI element

```
      8925        8935        8945        8955        8965    8969
UUUUAUUUUA UUUUUUCUUU UCUUUUCCGA AUCGGAUUUU GUUUUUAAUA UUUC
```

FI element

```
      8979        8989        8999        9009        9019        9029
```

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA GCAUAUGACU AAAAAAAAAA AAAAAAAAAA

Poly(A)

9039 9049 9059 9069 9079

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA

Poly(A)

In some embodiments, vaccine RNA described herein comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 15, 16, 17, 19, 20, 21, 24, 25, 26, 27, 30, and 32. A particularly preferred vaccine RNA described herein comprises a nucleotide sequence selected from the group consisting of SEQ ID NO: 15, 17, 19, 21, 25, 26, 30, and 32 such as selected from the group consisting of SEQ ID NO: 17, 19, 21, 26, 30, and 32.

RNA described herein is preferably formulated in lipid nanoparticles (LNP). In one embodiment, the LNP comprise a cationic lipid, a neutral lipid, a steroid, a polymer conjugated lipid; and the RNA. In one embodiment, the cationic lipid is ALC-0315, the neutral lipid is DSPC, the steroid is cholesterol, and the polymer conjugated lipid is ALC-0159. The preferred mode of administration is intramuscular administration, more preferably in aqueous cryoprotectant buffer for intramuscular administration. The drug product is a preferably a preservative-free, sterile dispersion of RNA formulated in lipid nanoparticles (LNP) in aqueous cryoprotectant buffer for intramuscular administration.

In different embodiments, the drug product comprises the components shown below, preferably at the proportions or concentrations shown below:

Component	**Function**	**Proportion (mol%)**
ALC-0315 [1]	Functional lipid	47.5
ALC-0159 [2]	Functional lipid	1.8
DSPC [3]	Structural lipid	10.0
Cholesterol, synthetic	Structural lipid	40.7

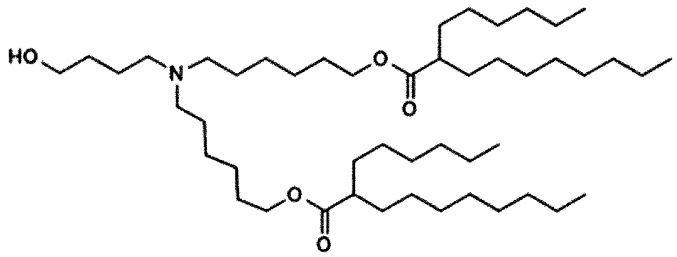
Component	**Function**	**Concentration (mg/mL)**
Drug Substance	Active	0.5
ALC-0315 [1]	Functional lipid	7.17
ALC-0159 [2]	Functional lipid	0.89
DSPC [3]	Structural lipid	1.56

Cholesterol, synthetic	Structural lipid	3.1
Sucrose	Cryoprotectant	102.69
NaCl	Buffer	6.0
KCl	Buffer	0.15
Na_2HPO_4	Buffer	1.08
KH_2PO_4	Buffer	0.18
Water for injection	Solvent/Vehicle	q.s.

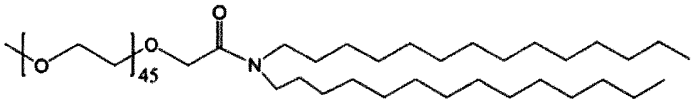
Component	**Function**	**Concentration (mg/mL)**
Drug Substance	Active	1.0
ALC-0315 [1]	Functional lipid	13.56
ALC-0159 [2]	Functional lipid	1.77
DSPC [3]	Structural lipid	3.11
Cholesterol, synthetic	Structural lipid	6.20
Sucrose	Cryoprotectant	102.69
NaCl	Buffer	6.0
KCl	Buffer	0.15
Na_2HPO_4	Buffer	1.08
KH_2PO_4	Buffer	0.15
Water for injection	Solvent/Vehicle	q.s.

[1] ALC-0315 = ((4-hydroxybutyl)azanediyl)bis(hexane-6,1-diyl)bis(2-hexyldecanoate) / 6-[N-6-(2-hexyldecanoyloxy)hexyl-N-(4-hydroxybutyl)amino]hexyl 2-hexyldecanoate
[2] ALC-0159 = 2-[(polyethylene glycol)-2000]-*N,N*-ditetradecylacetamide / 2-[2-(ω-methoxy (polyethyleneglycol2000) ethoxy]-N,N-ditetradecylacetamide
[3] DSPC = 1,2-Distearoyl-*sn*-glycero-3-phosphocholine
q.s. = quantum satis (as much as may suffice)

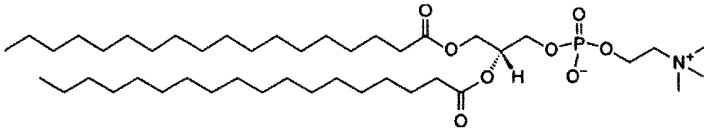
ALC-0315:



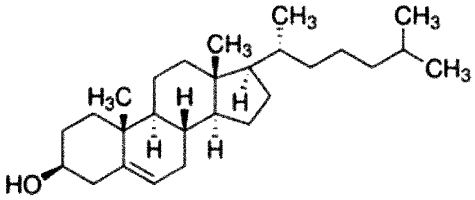
ALC-0159:



DSPC:



Cholesterol:



In one embodiment, the ratio of mRNA to total lipid (N/P) is between 6.0 and 6.5 such as about 6.0 or about 6.3.

Nucleic acid containing particles

Nucleic acids described herein such as RNA encoding a vaccine antigen may be administered formulated as particles.

In the context of the present disclosure, the term "particle" relates to a structured entity formed by molecules or molecule complexes. In one embodiment, the term "particle" relates to a micro- or nano-sized structure, such as a micro- or nano-sized compact structure dispersed in a medium. In one embodiment, a particle is a nucleic acid containing particle such as a particle comprising DNA, RNA or a mixture thereof.

Electrostatic interactions between positively charged molecules such as polymers and lipids and negatively charged nucleic acid are involved in particle formation. This results in

complexation and spontaneous formation of nucleic acid particles. In one embodiment, a nucleic acid particle is a nanoparticle.

As used in the present disclosure, "nanoparticle" refers to a particle having an average diameter suitable for parenteral administration.

A "nucleic acid particle" can be used to deliver nucleic acid to a target site of interest (e.g., cell, tissue, organ, and the like). A nucleic acid particle may be formed from at least one cationic or cationically ionizable lipid or lipid-like material, at least one cationic polymer such as protamine, or a mixture thereof and nucleic acid. Nucleic acid particles include lipid nanoparticle (LNP)-based and lipoplex (LPX)-based formulations.

Without intending to be bound by any theory, it is believed that the cationic or cationically ionizable lipid or lipid-like material and/or the cationic polymer combine together with the nucleic acid to form aggregates, and this aggregation results in colloidally stable particles.

In one embodiment, particles described herein further comprise at least one lipid or lipid-like material other than a cationic or cationically ionizable lipid or lipid-like material, at least one polymer other than a cationic polymer, or a mixture thereof

In some embodiments, nucleic acid particles comprise more than one type of nucleic acid molecules, where the molecular parameters of the nucleic acid molecules may be similar or different from each other, like with respect to molar mass or fundamental structural elements such as molecular architecture, capping, coding regions or other features,

Nucleic acid particles described herein may have an average diameter that in one embodiment ranges from about 30 nm to about 1000 nm, from about 50 nm to about 800 nm, from about 70 nm to about 600 nm, from about 90 nm to about 400 nm, or from about 100 nm to about 300 nm.

Nucleic acid particles described herein may exhibit a polydispersity index less than about 0.5, less than about 0.4, less than about 0.3, or about 0.2 or less. By way of example, the nucleic acid particles can exhibit a polydispersity index in a range of about 0.1 to about 0.3 or about 0.2 to about 0.3.

With respect to RNA lipid particles, the N/P ratio gives the ratio of the nitrogen groups in the lipid to the number of phosphate groups in the RNA. It is correlated to the charge ratio, as the nitrogen atoms (depending on the pH) are usually positively charged and the phosphate groups are negatively charged. The N/P ratio, where a charge equilibrium exists, depends on the pH. Lipid formulations are frequently formed at N/P ratios larger than four up to twelve, because positively charged nanoparticles are considered favorable for transfection. In that case, RNA is considered to be completely bound to nanoparticles.

Nucleic acid particles described herein can be prepared using a wide range of methods that may involve obtaining a colloid from at least one cationic or cationically ionizable lipid or lipid-like material and/or at least one cationic polymer and mixing the colloid with nucleic acid to obtain nucleic acid particles.

The term "colloid" as used herein relates to a type of homogeneous mixture in which dispersed particles do not settle out. The insoluble particles in the mixture are microscopic, with particle sizes between 1 and 1000 nanometers. The mixture may be termed a colloid or a colloidal suspension. Sometimes the term "colloid" only refers to the particles in the mixture and not the entire suspension.

For the preparation of colloids comprising at least one cationic or cationically ionizable lipid or lipid-like material and/or at least one cationic polymer methods are applicable herein that are conventionally used for preparing liposomal vesicles and are appropriately adapted. The most commonly used methods for preparing liposomal vesicles share the following fundamental stages: (i) lipids dissolution in organic solvents, (ii) drying of the resultant solution, and (iii) hydration of dried lipid (using various aqueous media).

In the film hydration method, lipids are firstly dissolved in a suitable organic solvent, and dried down to yield a thin film at the bottom of the flask. The obtained lipid film is hydrated using an appropriate aqueous medium to produce a liposomal dispersion. Furthermore, an additional downsizing step may be included.

Reverse phase evaporation is an alternative method to the film hydration for preparing liposomal vesicles that involves formation of a water-in-oil emulsion between an aqueous phase and an organic phase containing lipids. A brief sonication of this mixture is required for system homogenization. The removal of the organic phase under reduced pressure yields a milky gel that turns subsequently into a liposomal suspension.

The term "ethanol injection technique" refers to a process, in which an ethanol solution comprising lipids is rapidly injected into an aqueous solution through a needle. This action disperses the lipids throughout the solution and promotes lipid structure formation, for example lipid vesicle formation such as liposome formation. Generally, the RNA lipoplex particles described herein are obtainable by adding RNA to a colloidal liposome dispersion. Using the ethanol injection technique, such colloidal liposome dispersion is, in one embodiment, formed as follows: an ethanol solution comprising lipids, such as cationic lipids and additional lipids, is injected into an aqueous solution under stirring. In one embodiment, the RNA lipoplex particles described herein are obtainable without a step of extrusion.

The term "extruding" or "extrusion" refers to the creation of particles having a fixed, cross-sectional profile. In particular, it refers to the downsizing of a particle, whereby the particle is forced through filters with defined pores.

Other methods having organic solvent free characteristics may also be used according to the present disclosure for preparing a colloid.

LNPs typically comprise four components: ionizable cationic lipids, neutral lipids such as phospholipids, a steroid such as cholesterol, and a polymer conjugated lipid such as polyethylene glycol (PEG)-lipids. Each component is responsible for payload protection, and enables effective intracellular delivery. LNPs may be prepared by mixing lipids dissolved in ethanol rapidly with nucleic acid in an aqueous buffer.

The term "average diameter" refers to the mean hydrodynamic diameter of particles as measured by dynamic laser light scattering (DLS) with data analysis using the so-called cumulant algorithm, which provides as results the so-called $Z_{average}$ with the dimension of a

length, and the polydispersity index (PI), which is dimensionless (Koppel, D., J. Chem. Phys. 57, 1972, pp 4814-4820, ISO 13321). Here "average diameter", "diameter" or "size" for particles is used synonymously with this value of the $Z_{average}$.

The "polydispersity index" is preferably calculated based on dynamic light scattering measurements by the so-called cumulant analysis as mentioned in the definition of the "average diameter". Under certain prerequisites, it can be taken as a measure of the size distribution of an ensemble of nanoparticles.

Different types of nucleic acid containing particles have been described previously to be suitable for delivery of nucleic acid in particulate form (e.g. Kaczmarek, J. C. et al., 2017, Genome Medicine 9, 60). For non-viral nucleic acid delivery vehicles, nanoparticle encapsulation of nucleic acid physically protects nucleic acid from degradation and, depending on the specific chemistry, can aid in cellular uptake and endosomal escape.

The present disclosure describes particles comprising nucleic acid, at least one cationic or cationically ionizable lipid or lipid-like material, and/or at least one cationic polymer which associate with nucleic acid to form nucleic acid particles and compositions comprising such particles. The nucleic acid particles may comprise nucleic acid which is complexed in different forms by non-covalent interactions to the particle. The particles described herein are not viral particles, in particular infectious viral particles, i.e., they are not able to virally infect cells.

Suitable cationic or cationically ionizable lipids or lipid-like materials and cationic polymers are those that form nucleic acid particles and are included by the term "particle forming components" or "particle forming agents". The term "particle forming components" or "particle forming agents" relates to any components which associate with nucleic acid to form nucleic acid particles. Such components include any component which can be part of nucleic acid particles.

Cationic polymer

Given their high degree of chemical flexibility, polymers are commonly used materials for nanoparticle-based delivery. Typically, cationic polymers are used to electrostatically condense the negatively charged nucleic acid into nanoparticles. These positively charged groups often consist of amines that change their state of protonation in the pH range between 5.5 and 7.5, thought to lead to an ion imbalance that results in endosomal rupture. Polymers such as poly-L-lysine, polyamidoamine, protamine and polyethyleneimine, as well as naturally occurring polymers such as chitosan have all been applied to nucleic acid delivery and are suitable as cationic polymers herein. In addition, some investigators have synthesized polymers specifically for nucleic acid delivery. Poly(β-amino esters), in particular, have gained widespread use in nucleic acid delivery owing to their ease of synthesis and biodegradability. Such synthetic polymers are also suitable as cationic polymers herein.

A "polymer," as used herein, is given its ordinary meaning, i.e., a molecular structure comprising one or more repeat units (monomers), connected by covalent bonds. The repeat units can all be identical, or in some cases, there can be more than one type of repeat unit present within the polymer. In some cases, the polymer is biologically derived, i.e., a biopolymer such as a protein. In some cases, additional moieties can also be present in the polymer, for example targeting moieties such as those described herein.

If more than one type of repeat unit is present within the polymer, then the polymer is said to be a "copolymer." It is to be understood that the polymer being employed herein can be a copolymer. The repeat units forming the copolymer can be arranged in any fashion. For example, the repeat units can be arranged in a random order, in an alternating order, or as a "block" copolymer, i.e., comprising one or more regions each comprising a first repeat unit (e.g., a first block), and one or more regions each comprising a second repeat unit (e.g., a second block), etc. Block copolymers can have two (a diblock copolymer), three (a triblock copolymer), or more numbers of distinct blocks.

In certain embodiments, the polymer is biocompatible. Biocompatible polymers are polymers that typically do not result in significant cell death at moderate concentrations. In certain embodiments, the biocompatible polymer is biodegradable, i.e., the polymer is able to degrade, chemically and/or biologically, within a physiological environment, such as within the body.

In certain embodiments, polymer may be protamine or polyalkyleneimine, in particular protamine.

The term "protamine" refers to any of various strongly basic proteins of relatively low molecular weight that are rich in arginine and are found associated especially with DNA in place of somatic histones in the sperm cells of various animals (as fish). In particular, the term "protamine" refers to proteins found in fish sperm that are strongly basic, are soluble in water, are not coagulated by heat, and yield chiefly arginine upon hydrolysis. In purified form, they are used in a long-acting formulation of insulin and to neutralize the anticoagulant effects of heparin.

According to the disclosure, the term "protamine" as used herein is meant to comprise any protamine amino acid sequence obtained or derived from natural or biological sources including fragments thereof and multimeric forms of said amino acid sequence or fragment thereof as well as (synthesized) polypeptides which are artificial and specifically designed for specific purposes and cannot be isolated from native or biological sources.

In one embodiment, the polyalkyleneimine comprises polyethylenimine and/or polypropylenimine, preferably polyethyleneimine. A preferred polyalkyleneimine is polyethyleneimine (PEI). The average molecular weight of PEI is preferably $0.75 \cdot 10^2$ to 10^7 Da, preferably 1000 to 10^5 Da, more preferably 10000 to 40000 Da, more preferably 15000 to 30000 Da, even more preferably 20000 to 25000 Da.

Preferred according to the disclosure is linear polyalkyleneimine such as linear polyethyleneimine (PEI).

Cationic polymers (including polycationic polymers) contemplated for use herein include any cationic polymers which are able to electrostatically bind nucleic acid. In one embodiment, cationic polymers contemplated for use herein include any cationic polymers with which nucleic acid can be associated, e.g. by forming complexes with the nucleic acid or forming vesicles in which the nucleic acid is enclosed or encapsulated.

Particles described herein may also comprise polymers other than cationic polymers, i.e., non-cationic polymers and/or anionic polymers. Collectively, anionic and neutral polymers are referred to herein as non-cationic polymers.

Lipid and lipid-like material

The terms "lipid" and "lipid-like material" are broadly defined herein as molecules which comprise one or more hydrophobic moieties or groups and optionally also one or more hydrophilic moieties or groups. Molecules comprising hydrophobic moieties and hydrophilic moieties are also frequently denoted as amphiphiles. Lipids are usually poorly soluble in water. In an aqueous environment, the amphiphilic nature allows the molecules to self-assemble into organized structures and different phases. One of those phases consists of lipid bilayers, as they are present in vesicles, multilamellar/unilamellar liposomes, or membranes in an aqueous environment. Hydrophobicity can be conferred by the inclusion of apolar groups that include, but are not limited to, long-chain saturated and unsaturated aliphatic hydrocarbon groups and such groups substituted by one or more aromatic, cycloaliphatic, or heterocyclic group(s). The hydrophilic groups may comprise polar and/or charged groups and include carbohydrates, phosphate, carboxylic, sulfate, amino, sulfhydryl, nitro, hydroxyl, and other like groups.

As used herein, the term "amphiphilic" refers to a molecule having both a polar portion and a non-polar portion. Often, an amphiphilic compound has a polar head attached to a long hydrophobic tail. In some embodiments, the polar portion is soluble in water, while the non-polar portion is insoluble in water. In addition, the polar portion may have either a formal

positive charge, or a formal negative charge. Alternatively, the polar portion may have both a formal positive and a negative charge, and be a zwitterion or inner salt. For purposes of the disclosure, the amphiphilic compound can be, but is not limited to, one or a plurality of natural or non-natural lipids and lipid-like compounds.

The term "lipid-like material", "lipid-like compound" or "lipid-like molecule" relates to substances that structurally and/or functionally relate to lipids but may not be considered as lipids in a strict sense. For example, the term includes compounds that are able to form amphiphilic layers as they are present in vesicles, multilamellar/unilamellar liposomes, or membranes in an aqueous environment and includes surfactants, or synthesized compounds with both hydrophilic and hydrophobic moieties. Generally speaking, the term refers to molecules, which comprise hydrophilic and hydrophobic moieties with different structural organization, which may or may not be similar to that of lipids. As used herein, the term "lipid" is to be construed to cover both lipids and lipid-like materials unless otherwise indicated herein or clearly contradicted by context.

Specific examples of amphiphilic compounds that may be included in an amphiphilic layer include, but are not limited to, phospholipids, aminolipids and sphingolipids.

In certain embodiments, the amphiphilic compound is a lipid. The term "lipid" refers to a group of organic compounds that are characterized by being insoluble in water, but soluble in many organic solvents. Generally, lipids may be divided into eight categories: fatty acids, glycerolipids, glycerophospholipids, sphingolipids, saccharolipids, polyketides (derived from condensation of ketoacyl subunits), sterol lipids and prenol lipids (derived from condensation of isoprene subunits). Although the term "lipid" is sometimes used as a synonym for fats, fats are a subgroup of lipids called triglycerides. Lipids also encompass molecules such as fatty acids and their derivatives (including tri-, di-, monoglycerides, and phospholipids), as well as sterol-containing metabolites such as cholesterol.

Fatty acids, or fatty acid residues are a diverse group of molecules made of a hydrocarbon chain that terminates with a carboxylic acid group; this arrangement confers the molecule

with a polar, hydrophilic end, and a nonpolar, hydrophobic end that is insoluble in water. The carbon chain, typically between four and 24 carbons long, may be saturated or unsaturated, and may be attached to functional groups containing oxygen, halogens, nitrogen, and sulfur. If a fatty acid contains a double bond, there is the possibility of either a cis or trans geometric isomerism, which significantly affects the molecule's configuration. Cis-double bonds cause the fatty acid chain to bend, an effect that is compounded with more double bonds in the chain. Other major lipid classes in the fatty acid category are the fatty esters and fatty amides. Glycerolipids are composed of mono-, di-, and tri-substituted glycerols, the best-known being the fatty acid triesters of glycerol, called triglycerides. The word "triacylglycerol" is sometimes used synonymously with "triglyceride". In these compounds, the three hydroxyl groups of glycerol are each esterified, typically by different fatty acids. Additional subclasses of glycerolipids are represented by glycosylglycerols, which are characterized by the presence of one or more sugar residues attached to glycerol via a glycosidic linkage.

The glycerophospholipids are amphipathic molecules (containing both hydrophobic and hydrophilic regions) that contain a glycerol core linked to two fatty acid-derived "tails" by ester linkages and to one "head" group by a phosphate ester linkage. Examples of glycerophospholipids, usually referred to as phospholipids (though sphingomyelins are also classified as phospholipids) are phosphatidylcholine (also known as PC, GPCho or lecithin), phosphatidylethanolamine (PE or GPEtn) and phosphatidylserine (PS or GPSer).

Sphingolipids are a complex family of compounds that share a common structural feature, a sphingoid base backbone. The major sphingoid base in mammals is commonly referred to as sphingosine. Ceramides (N-acyl-sphingoid bases) are a major subclass of sphingoid base derivatives with an amide-linked fatty acid. The fatty acids are typically saturated or mono-unsaturated with chain lengths from 16 to 26 carbon atoms. The major phosphosphingolipids of mammals are sphingomyelins (ceramide phosphocholines), whereas insects contain mainly ceramide phosphoethanolamines and fungi have phytoceramide phosphoinositols and mannose-containing headgroups. The glycosphingolipids are a diverse family of molecules

composed of one or more sugar residues linked via a glycosidic bond to the sphingoid base. Examples of these are the simple and complex glycosphingolipids such as cerebrosides and gangliosides.

Sterol lipids, such as cholesterol and its derivatives, or tocopherol and its derivatives, are an important component of membrane lipids, along with the glycerophospholipids and sphingomyelins.

Saccharolipids describe compounds in which fatty acids are linked directly to a sugar backbone, forming structures that are compatible with membrane bilayers. In the saccharolipids, a monosaccharide substitutes for the glycerol backbone present in glycerolipids and glycerophospholipids. The most familiar saccharolipids are the acylated glucosamine precursors of the Lipid A component of the lipopolysaccharides in Gram-negative bacteria. Typical lipid A molecules are disaccharides of glucosamine, which are derivatized with as many as seven fatty-acyl chains. The minimal lipopolysaccharide required for growth in E. coli is Kdo2-Lipid A, a hexa-acylated disaccharide of glucosamine that is glycosylated with two 3-deoxy-D-manno-octulosonic acid (Kdo) residues.

Polyketides are synthesized by polymerization of acetyl and propionyl subunits by classic enzymes as well as iterative and multimodular enzymes that share mechanistic features with the fatty acid synthases. They comprise a large number of secondary metabolites and natural products from animal, plant, bacterial, fungal and marine sources, and have great structural diversity. Many polyketides are cyclic molecules whose backbones are often further modified by glycosylation, methylation, hydroxylation, oxidation, or other processes.

According to the disclosure, lipids and lipid-like materials may be cationic, anionic or neutral. Neutral lipids or lipid-like materials exist in an uncharged or neutral zwitterionic form at a selected pH.

Cationic or cationically ionizable lipids or lipid-like materials

The nucleic acid particles described herein may comprise at least one cationic or cationically ionizable lipid or lipid-like material as particle forming agent. Cationic or cationically ionizable lipids or lipid-like materials contemplated for use herein include any cationic or cationically ionizable lipids or lipid-like materials which are able to electrostatically bind nucleic acid. In one embodiment, cationic or cationically ionizable lipids or lipid-like materials contemplated for use herein can be associated with nucleic acid, e.g. by forming complexes with the nucleic acid or forming vesicles in which the nucleic acid is enclosed or encapsulated.

As used herein, a "cationic lipid" or "cationic lipid-like material" refers to a lipid or lipid-like material having a net positive charge. Cationic lipids or lipid-like materials bind negatively charged nucleic acid by electrostatic interaction. Generally, cationic lipids possess a lipophilic moiety, such as a sterol, an acyl chain, a diacyl or more acyl chains, and the head group of the lipid typically carries the positive charge.

In certain embodiments, a cationic lipid or lipid-like material has a net positive charge only at certain pH, in particular acidic pH, while it has preferably no net positive charge, preferably has no charge, i.e., it is neutral, at a different, preferably higher pH such as physiological pH. This ionizable behavior is thought to enhance efficacy through helping with endosomal escape and reducing toxicity as compared with particles that remain cationic at physiological pH.

For purposes of the present disclosure, such "cationically ionizable" lipids or lipid-like materials are comprised by the term "cationic lipid or lipid-like material" unless contradicted by the circumstances.

In one embodiment, the cationic or cationically ionizable lipid or lipid-like material comprises a head group which includes at least one nitrogen atom (N) which is positive charged or capable of being protonated.

Examples of cationic lipids include, but are not limited to 1,2-dioleoyl-3-trimethylammonium propane (DOTAP); N,N-dimethyl-2,3-dioleyloxypropylamine (DODMA), 1,2-di-O-octadecenyl-3-trimethylammonium propane (DOTMA), 3-(N—(N',N'-dimethylaminoethane)-

carbamoyl)cholesterol (DC-Chol), dimethyldioctadecylammonium (DDAB); 1,2-dioleoyl-3-dimethylammonium-propane (DODAP); 1,2-diacyloxy-3-dimethylammonium propanes; 1,2-dialkyloxy-3-dimethylammonium propanes; dioctadecyldimethyl ammonium chloride (DODAC), 1,2-distearyloxy-N,N-dimethyl-3-aminopropane (DSDMA), 2,3-di(tetradecoxy)propyl-(2-hydroxyethyl)-dimethylazanium (DMRIE), 1,2-dimyristoyl-sn-glycero-3-ethylphosphocholine (DMEPC), l,2-dimyristoyl-3-trimethylammonium propane (DMTAP), 1,2-dioleyloxypropyl-3-dimethyl-hydroxyethyl ammonium bromide (DORIE), and 2,3-dioleoyloxy- N-[2(spermine carboxamide)ethyl]-N,N-dimethyl-l-propanamium trifluoroacetate (DOSPA), 1,2-dilinoleyloxy-N,N-dimethylaminopropane (DLinDMA), 1,2-dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA), dioctadecylamidoglycyl spermine (DOGS), 3-dimethylamino-2-(cholest-5-en-3-beta-oxybutan-4-oxy)-1-(cis,cis-9,12-octadecadienoxy)propane (CLinDMA), 2-[5'-(cholest-5-en-3-beta-oxy)-3'-oxapentoxy)-3-dimethyl-1-(cis,cis-9',12'-octadecadienoxy)propane (CpLinDMA), N,N-dimethyl-3,4-dioleyloxybenzylamine (DMOBA), 1,2-N,N'-dioleylcarbamyl-3-dimethylaminopropane (DOcarbDAP), 2,3-Dilinoleoyloxy-N,N-dimethylpropylamine (DLinDAP), 1,2-N,N'-Dilinoleylcarbamyl-3-dimethylaminopropane (DLincarbDAP), 1,2-Dilinoleoylcarbamyl-3-dimethylaminopropane (DLinCDAP), 2,2-dilinoleyl-4-dimethylaminomethyl-[1,3]-dioxolane (DLin-K-DMA), 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-K-XTC2-DMA), 2,2-dilinoleyl-4-(2-dimethylaminoethyl)-[1,3]-dioxolane (DLin-KC2-DMA), heptatriaconta-6,9,28,31-tetraen-19-yl-4-(dimethylamino)butanoate (DLin-MC3-DMA), N-(2-Hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (DMRIE), (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(cis-9-tetradecenyloxy)-1-propanaminium bromide (GAP-DMORIE), (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-1-propanaminium bromide (GAP-DLRIE), (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (GAP-DMRIE), N-(2-Aminoethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (βAE-DMRIE), N-(4-carboxybenzyl)-N,N-dimethyl-2,3-bis(oleoyloxy)propan-1-aminium (DOBAQ), 2-({8-[(3β)-cholest-5-en-3-

yloxy]octyl}oxy)-N,N-dimethyl-3-[(9Z,12Z)-octadeca-9,12-dien-1-yloxy]propan-1-amine (Octyl-CLinDMA), 1,2-dimyristoyl-3-dimethylammonium-propane (DMDAP), 1,2-dipalmitoyl-3-dimethylammonium-propane (DPDAP), N1-[2-((1S)-1-[(3-aminopropyl)amino]-4-[di(3-amino-propyl)amino]butylcarboxamido)ethyl]-3,4-di[oleyloxy]-benzamide (MVL5), 1,2-dioleoyl-sn-glycero-3-ethylphosphocholine (DOEPC), 2,3-bis(dodecyloxy)-N-(2-hydroxyethyl)-N,N-dimethylpropan-1-amonium bromide (DLRIE), N-(2-aminoethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)propan-1-aminium bromide (DMORIE), di((Z)-non-2-en-1-yl) 8,8'-((((2(dimethylamino)ethyl)thio)carbonyl)azanediyl)dioctanoate (ATX), N,N-dimethyl-2,3-bis(dodecyloxy)propan-1-amine (DLDMA), N,N-dimethyl-2,3-bis(tetradecyloxy)propan-1-amine (DMDMA), Di((Z)-non-2-en-1-yl)-9-((4-(dimethylaminobutanoyl)oxy)heptadecanedioate (L319), N-Dodecyl-3-((2-dodecylcarbamoyl-ethyl)-{2-[(2-dodecylcarbamoyl-ethyl)-2-{(2-dodecylcarbamoyl-ethyl)-[2-(2-dodecylcarbamoyl-ethylamino)-ethyl]-amino}-ethylamino)propionamide (lipidoid $98N_{12}$-5), 1-[2-[bis(2-hydroxydodecyl)amino]ethyl-[2-[4-[2-[bis(2 hydroxydodecyl)amino]ethyl]piperazin-1-yl]ethyl]amino]dodecan-2-ol (lipidoid C12-200).

In some embodiments, the cationic lipid may comprise from about 10 mol % to about 100 mol %, about 20 mol % to about 100 mol %, about 30 mol % to about 100 mol %, about 40 mol % to about 100 mol %, or about 50 mol % to about 100 mol % of the total lipid present in the particle.

Additional lipids or lipid-like materials

Particles described herein may also comprise lipids or lipid-like materials other than cationic or cationically ionizable lipids or lipid-like materials, i.e., non-cationic lipids or lipid-like materials (including non-cationically ionizable lipids or lipid-like materials). Collectively, anionic and neutral lipids or lipid-like materials are referred to herein as non-cationic lipids or lipid-like materials. Optimizing the formulation of nucleic acid particles by addition of other

hydrophobic moieties, such as cholesterol and lipids, in addition to an ionizable/cationic lipid or lipid-like material may enhance particle stability and efficacy of nucleic acid delivery.

An additional lipid or lipid-like material may be incorporated which may or may not affect the overall charge of the nucleic acid particles. In certain embodiments, the additional lipid or lipid-like material is a non-cationic lipid or lipid-like material. The non-cationic lipid may comprise, e.g., one or more anionic lipids and/or neutral lipids. As used herein, an "anionic lipid" refers to any lipid that is negatively charged at a selected pH. As used herein, a "neutral lipid" refers to any of a number of lipid species that exist either in an uncharged or neutral zwitterionic form at a selected pH. In preferred embodiments, the additional lipid comprises one of the following neutral lipid components: (1) a phospholipid, (2) cholesterol or a derivative thereof; or (3) a mixture of a phospholipid and cholesterol or a derivative thereof. Examples of cholesterol derivatives include, but are not limited to, cholestanol, cholestanone, cholestenone, coprostanol, cholesteryl-2'-hydroxyethyl ether, cholesteryl-4'- hydroxybutyl ether, tocopherol and derivatives thereof, and mixtures thereof.

Specific phospholipids that can be used include, but are not limited to, phosphatidylcholines, phosphatidylethanolamines, phosphatidylglycerols, phosphatidic acids, phosphatidylserines or sphingomyelin. Such phospholipids include in particular diacylphosphatidylcholines, such as distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dimyristoylphosphatidylcholine (DMPC), dipentadecanoylphosphatidylcholine, dilauroylphosphatidylcholine, dipalmitoylphosphatidylcholine (DPPC), diarachidoylphosphatidylcholine (DAPC), dibehenoylphosphatidylcholine (DBPC), ditricosanoylphosphatidylcholine (DTPC), dilignoceroylphatidylcholine (DLPC), palmitoyloleoyl-phosphatidylcholine (POPC), 1,2-di-O-octadecenyl-sn-glycero-3-phosphocholine (18:0 Diether PC), 1-oleoyl-2-cholesterylhemisuccinoyl-sn-glycero-3-phosphocholine (OChemsPC), 1-hexadecyl-sn-glycero-3-phosphocholine (C16 Lyso PC) and phosphatidylethanolamines, in particular diacylphosphatidylethanolamines, such as dioleoylphosphatidylethanolamine (DOPE), distearoyl-phosphatidylethanolamine (DSPE),

dipalmitoyl-phosphatidylethanolamine (DPPE), dimyristoyl-phosphatidylethanolamine (DMPE), dilauroyl-phosphatidylethanolamine (DLPE), diphytanoyl-phosphatidylethanolamine (DPyPE), and further phosphatidylethanolamine lipids with different hydrophobic chains.

In certain preferred embodiments, the additional lipid is DSPC or DSPC and cholesterol.

In certain embodiments, the nucleic acid particles include both a cationic lipid and an additional lipid.

In one embodiment, particles described herein include a polymer conjugated lipid such as a pegylated lipid. The term "pegylated lipid" refers to a molecule comprising both a lipid portion and a polyethylene glycol portion. Pegylated lipids are known in the art.

Without wishing to be bound by theory, the amount of the at least one cationic lipid compared to the amount of the at least one additional lipid may affect important nucleic acid particle characteristics, such as charge, particle size, stability, tissue selectivity, and bioactivity of the nucleic acid. Accordingly, in some embodiments, the molar ratio of the at least one cationic lipid to the at least one additional lipid is from about 10:0 to about 1:9, about 4:1 to about 1:2, or about 3:1 to about 1:1.

In some embodiments, the non-cationic lipid, in particular neutral lipid, (e.g., one or more phospholipids and/or cholesterol) may comprise from about 0 mol % to about 90 mol %, from about 0 mol % to about 80 mol %, from about 0 mol % to about 70 mol %, from about 0 mol % to about 60 mol %, or from about 0 mol % to about 50 mol %, of the total lipid present in the particle.

Lipoplex Particles

In certain embodiments of the present disclosure, the RNA described herein may be present in RNA lipoplex particles.

In the context of the present disclosure, the term "RNA lipoplex particle" relates to a particle that contains lipid, in particular cationic lipid, and RNA. Electrostatic interactions between positively charged liposomes and negatively charged RNA results in complexation and

spontaneous formation of RNA lipoplex particles. Positively charged liposomes may be generally synthesized using a cationic lipid, such as DOTMA, and additional lipids, such as DOPE. In one embodiment, a RNA lipoplex particle is a nanoparticle.

In certain embodiments, the RNA lipoplex particles include both a cationic lipid and an additional lipid. In an exemplary embodiment, the cationic lipid is DOTMA and the additional lipid is DOPE.

In some embodiments, the molar ratio of the at least one cationic lipid to the at least one additional lipid is from about 10:0 to about 1:9, about 4:1 to about 1:2, or about 3:1 to about 1:1. In specific embodiments, the molar ratio may be about 3:1, about 2.75:1, about 2.5:1, about 2.25:1, about 2:1, about 1.75:1, about 1.5:1, about 1.25:1, or about 1:1. In an exemplary embodiment, the molar ratio of the at least one cationic lipid to the at least one additional lipid is about 2:1.

RNA lipoplex particles described herein have an average diameter that in one embodiment ranges from about 200 nm to about 1000 nm, from about 200 nm to about 800 nm, from about 250 to about 700 nm, from about 400 to about 600 nm, from about 300 nm to about 500 nm, or from about 350 nm to about 400 nm. In specific embodiments, the RNA lipoplex particles have an average diameter of about 200 nm, about 225 nm, about 250 nm, about 275 nm, about 300 nm, about 325 nm, about 350 nm, about 375 nm, about 400 nm, about 425 nm, about 450 nm, about 475 nm, about 500 nm, about 525 nm, about 550 nm, about 575 nm, about 600 nm, about 625 nm, about 650 nm, about 700 nm, about 725 nm, about 750 nm, about 775 nm, about 800 nm, about 825 nm, about 850 nm, about 875 nm, about 900 nm, about 925 nm, about 950 nm, about 975 nm, or about 1000 nm. In an embodiment, the RNA lipoplex particles have an average diameter that ranges from about 250 nm to about 700 nm. In another embodiment, the RNA lipoplex particles have an average diameter that ranges from about 300 nm to about 500 nm. In an exemplary embodiment, the RNA lipoplex particles have an average diameter of about 400 nm.

The RNA lipoplex particles and compositions comprising RNA lipoplex particles described herein are useful for delivery of RNA to a target tissue after parenteral administration, in particular after intravenous administration. The RNA lipoplex particles may be prepared using liposomes that may be obtained by injecting a solution of the lipids in ethanol into water or a suitable aqueous phase. In one embodiment, the aqueous phase has an acidic pH. In one embodiment, the aqueous phase comprises acetic acid, e.g., in an amount of about 5 mM. Liposomes may be used for preparing RNA lipoplex particles by mixing the liposomes with RNA. In one embodiment, the liposomes and RNA lipoplex particles comprise at least one cationic lipid and at least one additional lipid. In one embodiment, the at least one cationic lipid comprises 1,2-di-O-octadecenyl-3-trimethylammonium propane (DOTMA) and/or 1,2-dioleoyl-3-trimethylammonium-propane (DOTAP). In one embodiment, the at least one additional lipid comprises 1,2-di-(9Z-octadecenoyl)-sn-glycero-3-phosphoethanolamine (DOPE), cholesterol (Chol) and/or 1,2-dioleoyl-sn-glycero-3-phosphocholine (DOPC). In one embodiment, the at least one cationic lipid comprises 1,2-di-O-octadecenyl-3-trimethylammonium propane (DOTMA) and the at least one additional lipid comprises 1,2-di-(9Z-octadecenoyl)-sn-glycero-3-phosphoethanolamine (DOPE). In one embodiment, the liposomes and RNA lipoplex particles comprise 1,2-di-O-octadecenyl-3-trimethylammonium propane (DOTMA) and 1,2-di-(9Z-octadecenoyl)-sn-glycero-3-phosphoethanolamine (DOPE). Spleen targeting RNA lipoplex particles are described in WO 2013/143683, herein incorporated by reference. It has been found that RNA lipoplex particles having a net negative charge may be used to preferentially target spleen tissue or spleen cells such as antigen-presenting cells, in particular dendritic cells. Accordingly, following administration of the RNA lipoplex particles, RNA accumulation and/or RNA expression in the spleen occurs. Thus, RNA lipoplex particles of the disclosure may be used for expressing RNA in the spleen. In an embodiment, after administration of the RNA lipoplex particles, no or essentially no RNA accumulation and/or RNA expression in the lung and/or liver occurs. In one embodiment, after administration of the RNA lipoplex particles, RNA accumulation and/or RNA expression in

antigen presenting cells, such as professional antigen presenting cells in the spleen occurs. Thus, RNA lipoplex particles of the disclosure may be used for expressing RNA in such antigen presenting cells. In one embodiment, the antigen presenting cells are dendritic cells and/or macrophages.

Lipid nanoparticles (LNPs)

In one embodiment, nucleic acid such as RNA described herein is administered in the form of lipid nanoparticles (LNPs). The LNP may comprise any lipid capable of forming a particle to which the one or more nucleic acid molecules are attached, or in which the one or more nucleic acid molecules are encapsulated.

In one embodiment, the LNP comprises one or more cationic lipids, and one or more stabilizing lipids. Stabilizing lipids include neutral lipids and pegylated lipids.

In one embodiment, the LNP comprises a cationic lipid, a neutral lipid, a steroid, a polymer conjugated lipid; and the RNA, encapsulated within or associated with the lipid nanoparticle.

In one embodiment, the LNP comprises from 40 to 55 mol percent, from 40 to 50 mol percent, from 41 to 49 mol percent, from 41 to 48 mol percent, from 42 to 48 mol percent, from 43 to 48 mol percent, from 44 to 48 mol percent, from 45 to 48 mol percent, from 46 to 48 mol percent, from 47 to 48 mol percent, or from 47.2 to 47.8 mol percent of the cationic lipid. In one embodiment, the LNP comprises about 47.0, 47.1, 47.2, 47.3, 47.4, 47.5, 47.6, 47.7, 47.8, 47.9 or 48.0 mol percent of the cationic lipid.

In one embodiment, the neutral lipid is present in a concentration ranging from 5 to 15 mol percent, from 7 to 13 mol percent, or from 9 to 11 mol percent. In one embodiment, the neutral lipid is present in a concentration of about 9.5, 10 or 10.5 mol percent.

In one embodiment, the steroid is present in a concentration ranging from 30 to 50 mol percent, from 35 to 45 mol percent or from 38 to 43 mol percent. In one embodiment, the steroid is present in a concentration of about 40, 41, 42, 43, 44, 45 or 46 mol percent.

In one embodiment, the LNP comprises from 1 to 10 mol percent, from 1 to 5 mol percent, or from 1 to 2.5 mol percent of the polymer conjugated lipid.

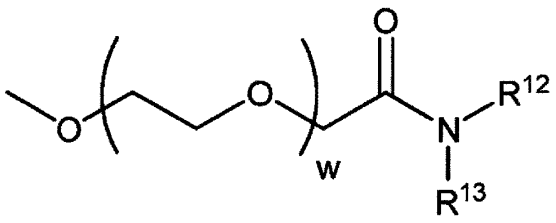
In one embodiment, the LNP comprises from 40 to 50 mol percent a cationic lipid; from 5 to 15 mol percent of a neutral lipid; from 35 to 45 mol percent of a steroid; from 1 to 10 mol percent of a polymer conjugated lipid; and the RNA, encapsulated within or associated with the lipid nanoparticle.

In one embodiment, the mol percent is determined based on total mol of lipid present in the lipid nanoparticle.

In one embodiment, the neutral lipid is selected from the group consisting of DSPC, DPPC, DMPC, DOPC, POPC, DOPE, DOPG, DPPG, POPE, DPPE, DMPE, DSPE, and SM. In one embodiment, the neutral lipid is selected from the group consisting of DSPC, DPPC, DMPC, DOPC, POPC, DOPE and SM. In one embodiment, the neutral lipid is DSPC.

In one embodiment, the steroid is cholesterol.

In one embodiment, the polymer conjugated lipid is a pegylated lipid. In one embodiment, the pegylated lipid has the following structure:

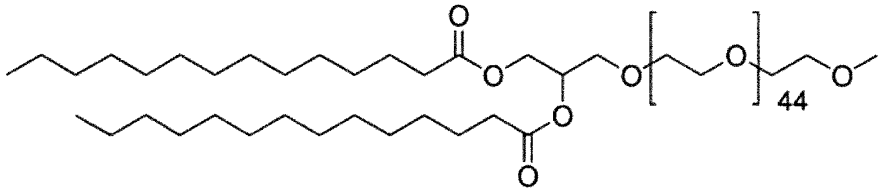


or a pharmaceutically acceptable salt, tautomer or stereoisomer thereof, wherein:

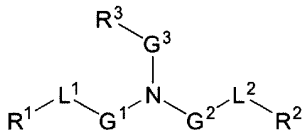
R^{12} and R^{13} are each independently a straight or branched, saturated or unsaturated alkyl chain containing from 10 to 30 carbon atoms, wherein the alkyl chain is optionally interrupted by one or more ester bonds; and w has a mean value ranging from 30 to 60. In one embodiment, R^{12} and R^{13} are each independently straight, saturated alkyl chains containing from 12 to 16 carbon atoms. In one embodiment, w has a mean value ranging from 40 to 55. In one embodiment, the average w is about 45. In one embodiment, R^{12} and R^{13} are each

independently a straight, saturated alkyl chain containing about 14 carbon atoms, and w has a mean value of about 45.

In one embodiment, the pegylated lipid is DMG-PEG 2000, e.g., having the following structure:



In some embodiments, the cationic lipid component of the LNPs has the structure of Formula (III):



(III)

or a pharmaceutically acceptable salt, tautomer, prodrug or stereoisomer thereof, wherein:

one of L^1 or L^2 is –O(C=O)-, -(C=O)O-, -C(=O)-, -O-, -$S(O)_x$-, -S-S-, -C(=O)S-, SC(=O)-, -$NR^aC(=O)$-, -$C(=O)NR^a$-, $NR^aC(=O)NR^a$-, -$OC(=O)NR^a$- or -$NR^aC(=O)O$-, and the other of L^1 or L^2 is –O(C=O)-, -(C=O)O-, -C(=O)-, -O-, -$S(O)_x$-, -S-S-, -C(=O)S-, SC(=O)-, -$NR^aC(=O)$-, -$C(=O)NR^a$-, $NR^aC(=O)NR^a$-, -$OC(=O)NR^a$- or -$NR^aC(=O)O$- or a direct bond;

G^1 and G^2 are each independently unsubstituted C_1-C_{12} alkylene or C_1-C_{12} alkenylene;

G^3 is C_1-C_{24} alkylene, C_1-C_{24} alkenylene, C_3-C_8 cycloalkylene, C_3-C_8 cycloalkenylene;

R^a is H or C_1-C_{12} alkyl;

R^1 and R^2 are each independently C_6-C_{24} alkyl or C_6-C_{24} alkenyl;

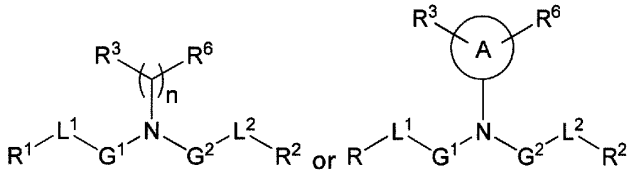
R^3 is H, OR^5, CN, -$C(=O)OR^4$, -$OC(=O)R^4$ or –$NR^5C(=O)R^4$;

R^4 is C_1-C_{12} alkyl;

R^5 is H or C_1-C_6 alkyl; and

x is 0, 1 or 2.

In some of the foregoing embodiments of Formula (III), the lipid has one of the following structures (IIIA) or (IIIB):



(IIIA) (IIIB)

wherein:

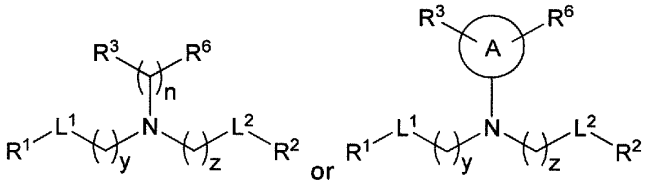
A is a 3 to 8-membered cycloalkyl or cycloalkylene ring;

R^6 is, at each occurrence, independently H, OH or C_1-C_{24} alkyl;

n is an integer ranging from 1 to 15.

In some of the foregoing embodiments of Formula (III), the lipid has structure (IIIA), and in other embodiments, the lipid has structure (IIIB).

In other embodiments of Formula (III), the lipid has one of the following structures (IIIC) or (IIID):

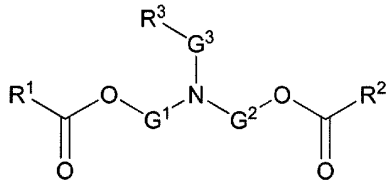


(IIIC) (IIID)

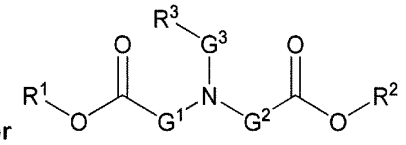
wherein y and z are each independently integers ranging from 1 to 12.

In any of the foregoing embodiments of Formula (III), one of L^1 or L^2 is -O(C=O)-. For example, in some embodiments each of L^1 and L^2 are -O(C=O)-. In some different embodiments of any of the foregoing, L^1 and L^2 are each independently -(C=O)O- or -O(C=O)-. For example, in some embodiments each of L^1 and L^2 is -(C=O)O-.

In some different embodiments of Formula (III), the lipid has one of the following structures (IIIE) or (IIIF):

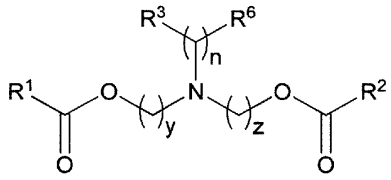


or

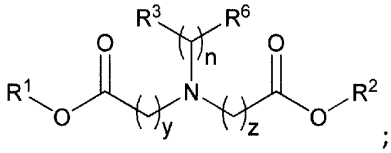


(IIIE) (IIIF)

In some of the foregoing embodiments of Formula (III), the lipid has one of the following structures (IIIG), (IIIH), (IIII), or (IIIJ):

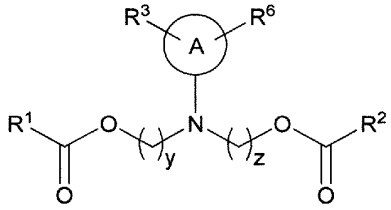


;

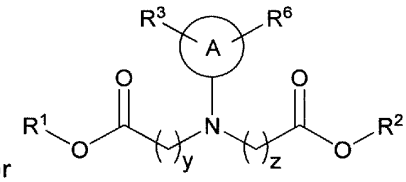


;

(IIIG) (IIIH)



or



(IIII) (IIIJ)

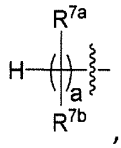
In some of the foregoing embodiments of Formula (III), n is an integer ranging from 2 to 12, for example from 2 to 8 or from 2 to 4. For example, in some embodiments, n is 3, 4, 5 or 6. In some embodiments, n is 3. In some embodiments, n is 4. In some embodiments, n is 5. In some embodiments, n is 6.

In some other of the foregoing embodiments of Formula (III), y and z are each independently an integer ranging from 2 to 10. For example, in some embodiments, y and z are each independently an integer ranging from 4 to 9 or from 4 to 6.

In some of the foregoing embodiments of Formula (III), R^6 is H. In other of the foregoing embodiments, R^6 is C_1-C_{24} alkyl. In other embodiments, R^6 is OH.

In some embodiments of Formula (III), G^3 is unsubstituted. In other embodiments, G3 is substituted. In various different embodiments, G^3 is linear C_1-C_{24} alkylene or linear C_1-C_{24} alkenylene.

In some other foregoing embodiments of Formula (III), R^1 or R^2, or both, is C_6-C_{24} alkenyl. For example, in some embodiments, R^1 and R^2 each, independently have the following structure:



,

wherein:

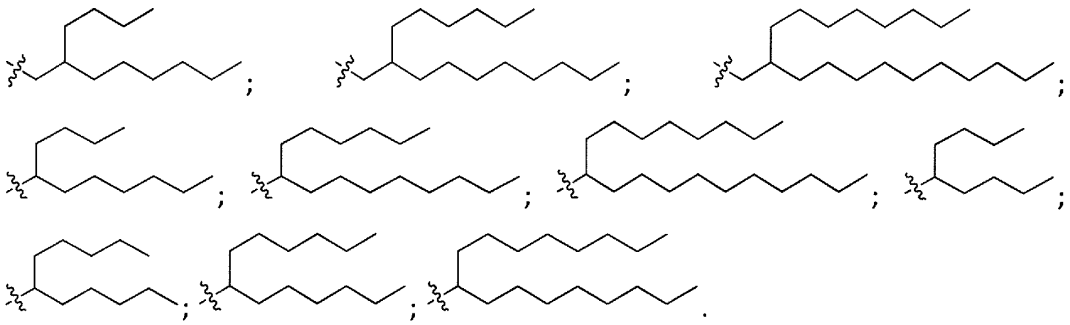
R^{7a} and R^{7b} are, at each occurrence, independently H or C_1-C_{12} alkyl; and

a is an integer from 2 to 12,

wherein R^{7a}, R^{7b} and a are each selected such that R^1 and R^2 each independently comprise from 6 to 20 carbon atoms. For example, in some embodiments a is an integer ranging from 5 to 9 or from 8 to 12.

In some of the foregoing embodiments of Formula (III), at least one occurrence of R^{7a} is H. For example, in some embodiments, R^{7a} is H at each occurrence. In other different embodiments of the foregoing, at least one occurrence of R^{7b} is C_1-C_8 alkyl. For example, in some embodiments, C_1-C_8 alkyl is methyl, ethyl, n-propyl, iso-propyl, n-butyl, iso-butyl, tert-butyl, n-hexyl or n-octyl.

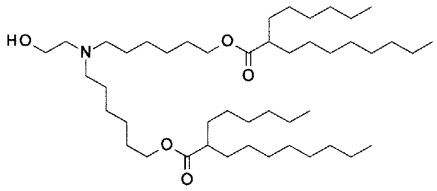
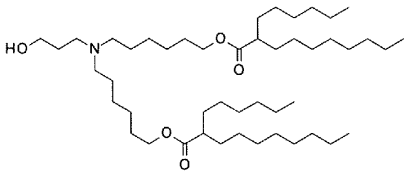
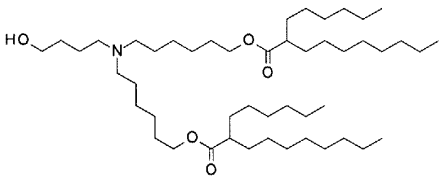
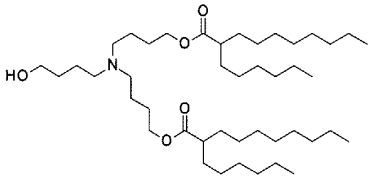
In different embodiments of Formula (III), R^1 or R^2, or both, has one of the following structures:

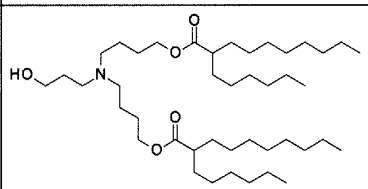
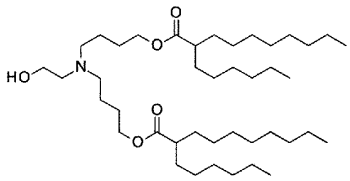
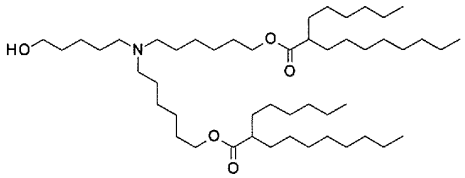
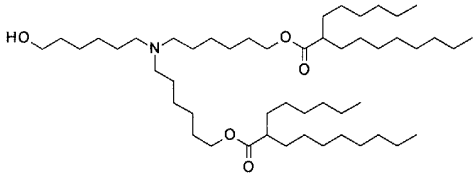
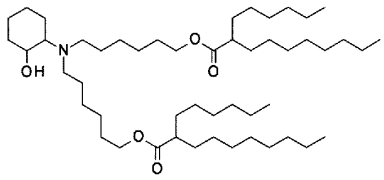
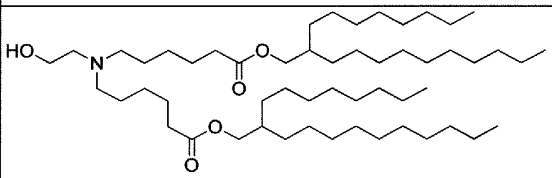


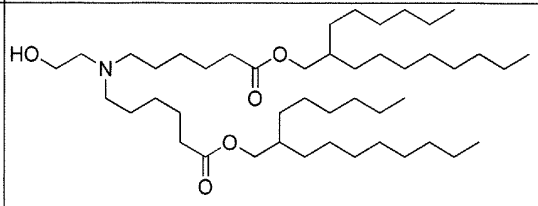
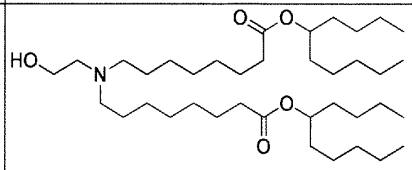
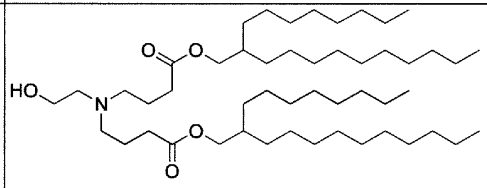
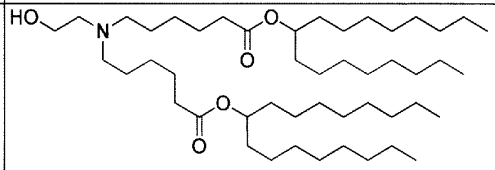
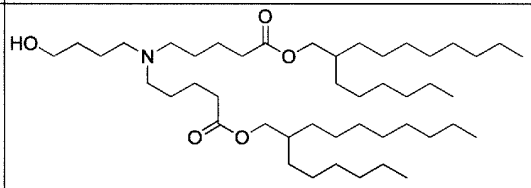
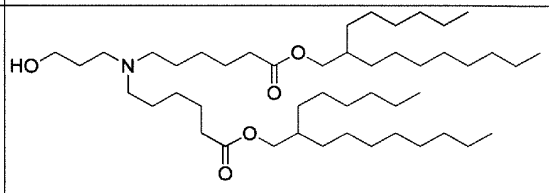
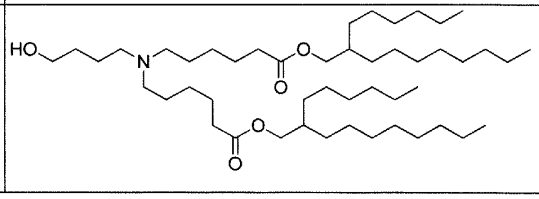
In some of the foregoing embodiments of Formula (III), R^3 is OH, CN, -C(=O)OR^4, -OC(=O)R^4 or –NHC(=O)R^4. In some embodiments, R^4 is methyl or ethyl.

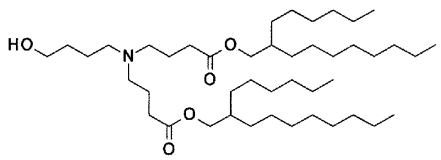
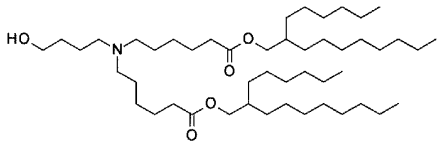
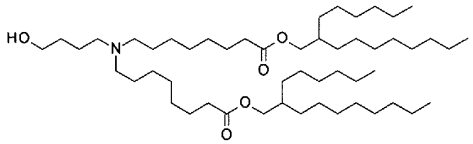
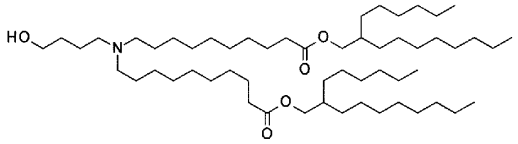
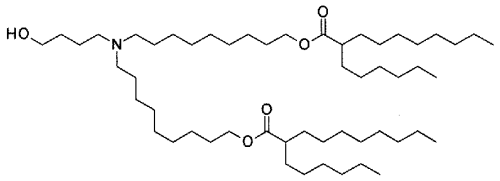
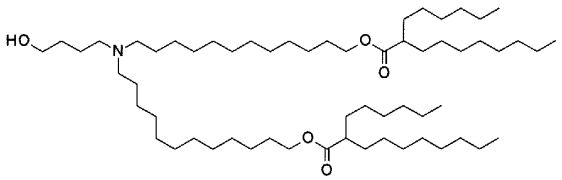
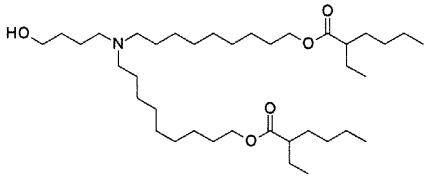
In various different embodiments, the cationic lipid of Formula (III) has one of the structures set forth in the table below.

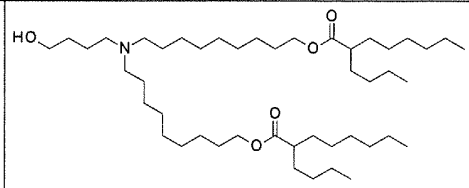
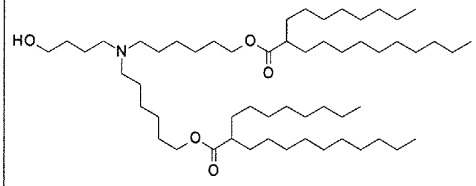
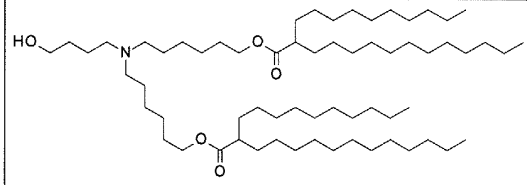
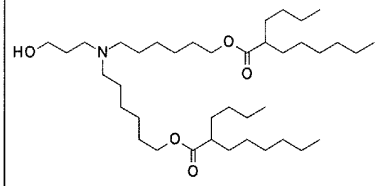
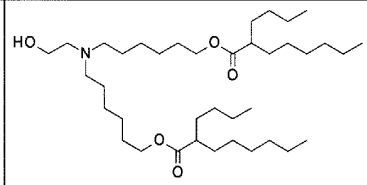
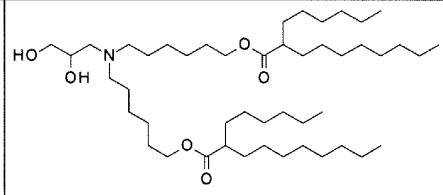
Representative Compounds of Formula (III).

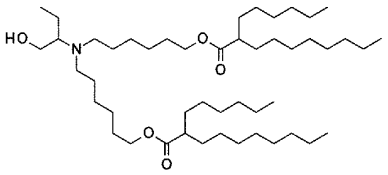
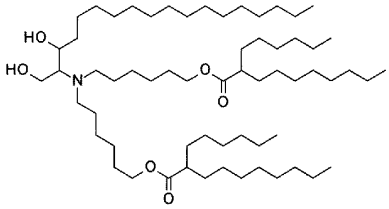
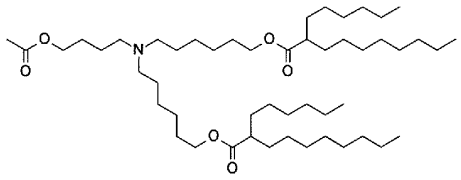
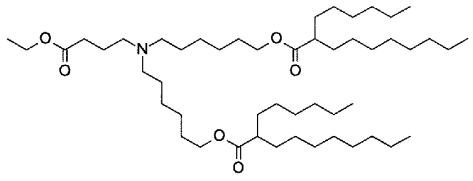
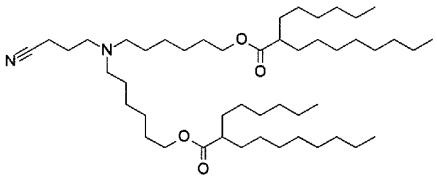
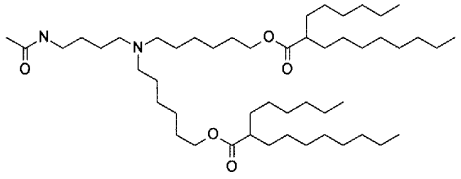
No.	Structure
III-1	
III-2	
III-3	
III-4	

No.	Structure
III-5	
III-6	
III-7	
III-8	
III-9	
III-10	

No.	Structure
III-11	
III-12	
III-13	
III-14	
III-15	
III-16	
III-17	

No.	Structure
III-18	
III-19	
III-20	
III-21	
III-22	
III-23	
III-24	

No.	Structure
III-25	
III-26	
III-27	
III-28	
III-29	
III-30	

No.	Structure
III-31	
III-32	
III-33	
III-34	
III-35	
III-36	

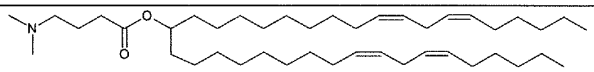
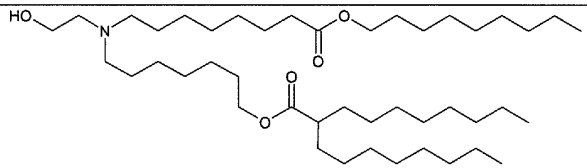
In some embodiments, the LNP comprises a lipid of Formula (III), RNA, a neutral lipid, a steroid and a pegylated lipid. In some embodiments, the lipid of Formula (III) is compound III-3. In some embodiments, the neutral lipid is DSPC. In some embodiments, the steroid is cholesterol. In some embodiments, the pegylated lipid is ALC-0159.

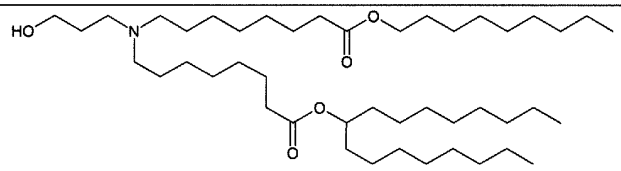
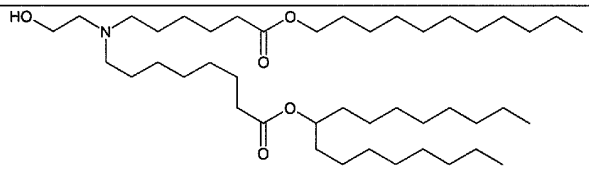
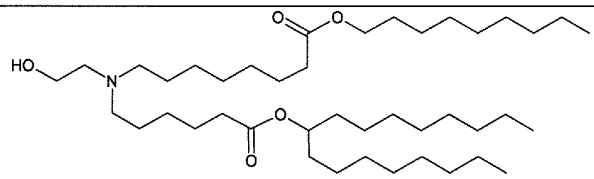
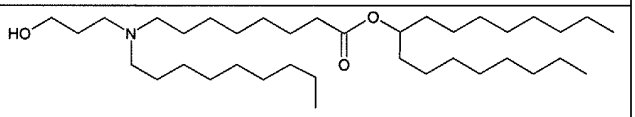
In some embodiments, the cationic lipid is present in the LNP in an amount from about 40 to about 50 mole percent. In one embodiment, the neutral lipid is present in the LNP in an amount from about 5 to about 15 mole percent. In one embodiment, the steroid is present in the LNP in an amount from about 35 to about 45 mole percent. In one embodiment, the pegylated lipid is present in the LNP in an amount from about 1 to about 10 mole percent.

In some embodiments, the LNP comprises compound III-3 in an amount from about 40 to about 50 mole percent, DSPC in an amount from about 5 to about 15 mole percent, cholesterol in an amount from about 35 to about 45 mole percent, and ALC-0159 in an amount from about 1 to about 10 mole percent.

In some embodiments, the LNP comprises compound III-3 in an amount of about 47.5 mole percent, DSPC in an amount of about 10 mole percent, cholesterol in an amount of about 40.7 mole percent, and ALC-0159 in an amount of about 1.8 mole percent.

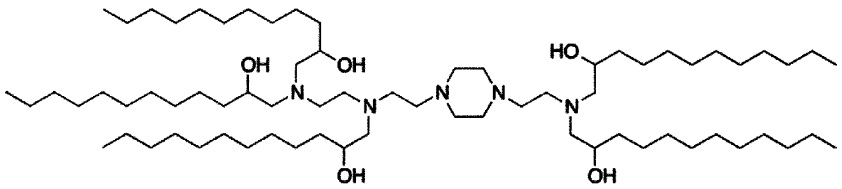
In various different embodiments, the cationic lipid has one of the structures set forth in the table below.

No.	Structure
A	
B	

No.	Structure
C	
D	
E	
F	

In some embodiments, the LNP comprises a cationic lipid shown in the above table, e.g., a cationic lipid of Formula (B) or Formula (D), in particular a cationic lipid of Formula (D), RNA, a neutral lipid, a steroid and a pegylated lipid. In some embodiments, the neutral lipid is DSPC. In some embodiments, the steroid is cholesterol. In some embodiments, the pegylated lipid is DMG-PEG 2000.

In one embodiment, the LNP comprises a cationic lipid that is an ionizable lipid-like material (lipidoid). In one embodiment, the cationic lipid has the following structure:



The N/P value is preferably at least about 4. In some embodiments, the N/P value ranges from 4 to 20, 4 to 12, 4 to 10, 4 to 8, or 5 to 7. In one embodiment, the N/P value is about 6.
LNP described herein may have an average diameter that in one embodiment ranges from about 30 nm to about 200 nm, or from about 60 nm to about 120 nm.

RNA Targeting

Some aspects of the disclosure involve the targeted delivery of the RNA disclosed herein (e.g., RNA encoding vaccine antigens and/or immunostimulants).
In one embodiment, the disclosure involves targeting lung. Targeting lung is in particular preferred if the RNA administered is RNA encoding vaccine antigen. RNA may be delivered to lung, for example, by administering the RNA which may be formulated as particles as described herein, e.g., lipid particles, by inhalation.
In one embodiment, the disclosure involves targeting the lymphatic system, in particular secondary lymphoid organs, more specifically spleen. Targeting the lymphatic system, in particular secondary lymphoid organs, more specifically spleen is in particular preferred if the RNA administered is RNA encoding vaccine antigen.
In one embodiment, the target cell is a spleen cell. In one embodiment, the target cell is an antigen presenting cell such as a professional antigen presenting cell in the spleen. In one embodiment, the target cell is a dendritic cell in the spleen.
The "lymphatic system" is part of the circulatory system and an important part of the immune system, comprising a network of lymphatic vessels that carry lymph. The lymphatic system consists of lymphatic organs, a conducting network of lymphatic vessels, and the circulating lymph. The primary or central lymphoid organs generate lymphocytes from immature progenitor cells. The thymus and the bone marrow constitute the primary lymphoid organs. Secondary or peripheral lymphoid organs, which include lymph nodes and the spleen, maintain mature naïve lymphocytes and initiate an adaptive immune response.

RNA may be delivered to spleen by so-called lipoplex formulations, in which the RNA is bound to liposomes comprising a cationic lipid and optionally an additional or helper lipid to form injectable nanoparticle formulations. The liposomes may be obtained by injecting a solution of the lipids in ethanol into water or a suitable aqueous phase. RNA lipoplex particles may be prepared by mixing the liposomes with RNA. Spleen targeting RNA lipoplex particles are described in WO 2013/143683, herein incorporated by reference. It has been found that RNA lipoplex particles having a net negative charge may be used to preferentially target spleen tissue or spleen cells such as antigen-presenting cells, in particular dendritic cells. Accordingly, following administration of the RNA lipoplex particles, RNA accumulation and/or RNA expression in the spleen occurs. Thus, RNA lipoplex particles of the disclosure may be used for expressing RNA in the spleen. In an embodiment, after administration of the RNA lipoplex particles, no or essentially no RNA accumulation and/or RNA expression in the lung and/or liver occurs. In one embodiment, after administration of the RNA lipoplex particles, RNA accumulation and/or RNA expression in antigen presenting cells, such as professional antigen presenting cells in the spleen occurs. Thus, RNA lipoplex particles of the disclosure may be used for expressing RNA in such antigen presenting cells. In one embodiment, the antigen presenting cells are dendritic cells and/or macrophages.

The electric charge of the RNA lipoplex particles of the present disclosure is the sum of the electric charges present in the at least one cationic lipid and the electric charges present in the RNA. The charge ratio is the ratio of the positive charges present in the at least one cationic lipid to the negative charges present in the RNA. The charge ratio of the positive charges present in the at least one cationic lipid to the negative charges present in the RNA is calculated by the following equation: charge ratio=[(cationic lipid concentration (mol)) * (the total number of positive charges in the cationic lipid)] / [(RNA concentration (mol)) * (the total number of negative charges in RNA)].

The spleen targeting RNA lipoplex particles described herein at physiological pH preferably have a net negative charge such as a charge ratio of positive charges to negative charges from

about 1.9:2 to about 1:2, or about 1.6:2 to about 1:2, or about 1.6:2 to about 1.1:2. In specific embodiments, the charge ratio of positive charges to negative charges in the RNA lipoplex particles at physiological pH is about 1.9:2.0, about 1.8:2.0, about 1.7:2.0, about 1.6:2.0, about 1.5:2.0, about 1.4:2.0, about 1.3:2.0, about 1.2:2.0, about 1.1:2.0, or about 1:2.0.

Immunostimulants may be provided to a subject by administering to the subject RNA encoding an immunostimulant in a formulation for preferential delivery of RNA to liver or liver tissue. The delivery of RNA to such target organ or tissue is preferred, in particular, if it is desired to express large amounts of the immunostimulant and/or if systemic presence of the immunostimulant, in particular in significant amounts, is desired or required.

RNA delivery systems have an inherent preference to the liver. This pertains to lipid-based particles, cationic and neutral nanoparticles, in particular lipid nanoparticles such as liposomes, nanomicelles and lipophilic ligands in bioconjugates. Liver accumulation is caused by the discontinuous nature of the hepatic vasculature or the lipid metabolism (liposomes and lipid or cholesterol conjugates).

For *in vivo* delivery of RNA to the liver, a drug delivery system may be used to transport the RNA into the liver by preventing its degradation. For example, polyplex nanomicelles consisting of a poly(ethylene glycol) (PEG)-coated surface and an mRNA-containing core is a useful system because the nanomicelles provide excellent *in vivo* stability of the RNA, under physiological conditions. Furthermore, the stealth property provided by the polyplex nanomicelle surface, composed of dense PEG palisades, effectively evades host immune defenses.

Examples of suitable immunostimulants for targeting liver are cytokines involved in T cell proliferation and/or maintenance. Examples of suitable cytokines include IL2 or IL7, fragments and variants thereof, and fusion proteins of these cytokines, fragments and variants, such as extended-PK cytokines.

In another embodiment, RNA encoding an immunostimulant may be administered in a formulation for preferential delivery of RNA to the lymphatic system, in particular secondary

lymphoid organs, more specifically spleen. The delivery of an immunostimulant to such target tissue is preferred, in particular, if presence of the immunostimulant in this organ or tissue is desired (e.g., for inducing an immune response, in particular in case immunostimulants such as cytokines are required during T-cell priming or for activation of resident immune cells), while it is not desired that the immunostimulant is present systemically, in particular in significant amounts (e.g., because the immunostimulant has systemic toxicity).

Examples of suitable immunostimulants are cytokines involved in T cell priming. Examples of suitable cytokines include IL12, IL15, IFN-α, or IFN-β, fragments and variants thereof, and fusion proteins of these cytokines, fragments and variants, such as extended-PK cytokines.

Immunostimulants

In one embodiment, the RNA encoding vaccine antigen may be non-immunogenic. In this and other embodiments, the RNA encoding vaccine antigen may be co-administered with an immunostimulant or RNA encoding an immunostimulant. The methods and agents described herein are particularly effective if the immunostimulant is attached to a pharmacokinetic modifying group (hereafter referred to as "extended-pharmacokinetic (PK)" immunostimulant). The methods and agents described herein are particularly effective if the immunostimulant is administered in the form of RNA encoding an immunostimulant. In one embodiment, said RNA is targeted to the liver for systemic availability. Liver cells can be efficiently transfected and are able to produce large amounts of protein.

An "immunostimulant" is any substance that stimulates the immune system by inducing activation or increasing activity of any of the immune system's components, in particular immune effector cells. The immunostimulant may be pro-inflammatory.

According to one aspect, the immunostimulant is a cytokine or a variant thereof. Examples of cytokines include interferons, such as interferon-alpha (IFN-α) or interferon-gamma (IFN-γ), interleukins, such as IL2, IL7, IL12, IL15 and IL23, colony stimulating factors, such as M-CSF and GM-CSF, and tumor necrosis factor. According to another aspect, the immunostimulant

includes an adjuvant-type immunostimulatory agent such as APC Toll-like Receptor agonists or costimulatory/cell adhesion membrane proteins. Examples of Toll-like Receptor agonists include costimulatory/adhesion proteins such as CD80, CD86, and ICAM-1.

Cytokines are a category of small proteins (~5–20 kDa) that are important in cell signaling. Their release has an effect on the behavior of cells around them. Cytokines are involved in autocrine signaling, paracrine signaling and endocrine signaling as immunomodulating agents. Cytokines include chemokines, interferons, interleukins, lymphokines, and tumour necrosis factors but generally not hormones or growth factors (despite some overlap in the terminology). Cytokines are produced by a broad range of cells, including immune cells like macrophages, B lymphocytes, T lymphocytes and mast cells, as well as endothelial cells, fibroblasts, and various stromal cells. A given cytokine may be produced by more than one type of cell. Cytokines act through receptors, and are especially important in the immune system; cytokines modulate the balance between humoral and cell-based immune responses, and they regulate the maturation, growth, and responsiveness of particular cell populations. Some cytokines enhance or inhibit the action of other cytokines in complex ways.

According to the disclosure, a cytokine may be a naturally occurring cytokine or a functional fragment or variant thereof. A cytokine may be human cytokine and may be derived from any vertebrate, especially any mammal. One particularly preferred cytokine is interferon-α.

Interferons

Interferons (IFNs) are a group of signaling proteins made and released by host cells in response to the presence of several pathogens, such as viruses, bacteria, parasites, and also tumor cells. In a typical scenario, a virus-infected cell will release interferons causing nearby cells to heighten their anti-viral defenses.

Based on the type of receptor through which they signal, interferons are typically divided among three classes: type I interferon, type II interferon, and type III interferon.

All type I interferons bind to a specific cell surface receptor complex known as the IFN-α/β receptor (IFNAR) that consists of IFNAR1 and IFNAR2 chains.

The type I interferons present in humans are IFNα, IFNβ, IFNε, IFNκ and IFNω. In general, type I interferons are produced when the body recognizes a virus that has invaded it. They are produced by fibroblasts and monocytes. Once released, type I interferons bind to specific receptors on target cells, which leads to expression of proteins that will prevent the virus from producing and replicating its RNA and DNA.

The IFNα proteins are produced mainly by plasmacytoid dendritic cells (pDCs). They are mainly involved in innate immunity against viral infection. The genes responsible for their synthesis come in 13 subtypes that are called IFNA1, IFNA2, IFNA4, IFNA5, IFNA6, IFNA7, IFNA8, IFNA10, IFNA13, IFNA14, IFNA16, IFNA17, IFNA21. These genes are found together in a cluster on chromosome 9.

The IFNβ proteins are produced in large quantities by fibroblasts. They have antiviral activity that is involved mainly in innate immune response. Two types of IFNβ have been described, IFNβ1 and IFNβ3. The natural and recombinant forms of IFNβ1 have antiviral, antibacterial, and anticancer properties.

Type II interferon (IFNγ in humans) is also known as immune interferon and is activated by IL12. Furthermore, type II interferons are released by cytotoxic T cells and T helper cells.

Type III interferons signal through a receptor complex consisting of IL10R2 (also called CRF2-4) and IFNLR1 (also called CRF2-12). Although discovered more recently than type I and type II IFNs, recent information demonstrates the importance of type III IFNs in some types of virus or fungal infections.

In general, type I and II interferons are responsible for regulating and activating the immune response.

According to the disclosure, a type I interferon is preferably IFNα or IFNβ, more preferably IFNα.

According to the disclosure, an interferon may be a naturally occurring interferon or a functional fragment or variant thereof. An interferon may be human interferon and may be derived from any vertebrate, especially any mammal.

Interleukins

Interleukins (ILs) are a group of cytokines (secreted proteins and signal molecules) that can be divided into four major groups based on distinguishing structural features. However, their amino acid sequence similarity is rather weak (typically 15–25% identity). The human genome encodes more than 50 interleukins and related proteins.

According to the disclosure, an interleukin may be a naturally occurring interleukin or a functional fragment or variant thereof. An interleukin may be human interleukin and may be derived from any vertebrate, especially any mammal.

Extended-PK group

Immunostimulant polypeptides described herein can be prepared as fusion or chimeric polypeptides that include an immunostimulant portion and a heterologous polypeptide (i.e., a polypeptide that is not an immunostimulant). The immunostimulant may be fused to an extended-PK group, which increases circulation half-life. Non-limiting examples of extended-PK groups are described infra. It should be understood that other PK groups that increase the circulation half-life of immunostimulants such as cytokines, or variants thereof, are also applicable to the present disclosure. In certain embodiments, the extended-PK group is a serum albumin domain (e.g., mouse serum albumin, human serum albumin).

As used herein, the term "PK" is an acronym for "pharmacokinetic" and encompasses properties of a compound including, by way of example, absorption, distribution, metabolism, and elimination by a subject. As used herein, an "extended-PK group" refers to a protein, peptide, or moiety that increases the circulation half-life of a biologically active molecule when fused to or administered together with the biologically active molecule. Examples of an

extended-PK group include serum albumin (e.g., HSA), Immunoglobulin Fc or Fc fragments and variants thereof, transferrin and variants thereof, and human serum albumin (HSA) binders (as disclosed in U.S. Publication Nos. 2005/0287153 and 2007/0003549). Other exemplary extended-PK groups are disclosed in Kontermann, Expert Opin Biol Ther, 2016 Jul;16(7):903-15 which is herein incorporated by reference in its entirety. As used herein, an "extended-PK" immunostimulant refers to an immunostimulant moiety in combination with an extended-PK group. In one embodiment, the extended-PK immunostimulant is a fusion protein in which an immunostimulant moiety is linked or fused to an extended-PK group.

In certain embodiments, the serum half-life of an extended-PK immunostimulant is increased relative to the immunostimulant alone (i.e., the immunostimulant not fused to an extended-PK group). In certain embodiments, the serum half-life of the extended-PK immunostimulant is at least 20, 40, 60, 80, 100, 120, 150, 180, 200, 400, 600, 800, or 1000% longer relative to the serum half-life of the immunostimulant alone. In certain embodiments, the serum half-life of the extended-PK immunostimulant is at least 1.5-fold, 2-fold, 2.5-fold, 3-fold, 3.5 fold, 4-fold, 4.5-fold, 5-fold, 6-fold, 7-fold, 8-fold, 10- fold, 12-fold, 13-fold, 15-fold, 17-fold, 20-fold, 22- fold, 25-fold, 27-fold, 30-fold, 35-fold, 40-fold, or 50-fold greater than the serum half-life of the immunostimulant alone. In certain embodiments, the serum half-life of the extended-PK immunostimulant is at least 10 hours, 15 hours, 20 hours, 25 hours, 30 hours, 35 hours, 40 hours, 50 hours, 60 hours, 70 hours, 80 hours, 90 hours, 100 hours, 110 hours, 120 hours, 130 hours, 135 hours, 140 hours, 150 hours, 160 hours, or 200 hours.

As used herein, "half-life" refers to the time taken for the serum or plasma concentration of a compound such as a peptide or protein to reduce by 50%, *in vivo*, for example due to degradation and/or clearance or sequestration by natural mechanisms. An extended-PK immunostimulant suitable for use herein is stabilized *in vivo* and its half-life increased by, e.g., fusion to serum albumin (e.g., HSA or MSA), which resist degradation and/or clearance or sequestration. The half-life can be determined in any manner known per se, such as by pharmacokinetic analysis. Suitable techniques will be clear to the person skilled in the art, and

may for example generally involve the steps of suitably administering a suitable dose of the amino acid sequence or compound to a subject; collecting blood samples or other samples from said subject at regular intervals; determining the level or concentration of the amino acid sequence or compound in said blood sample; and calculating, from (a plot of) the data thus obtained, the time until the level or concentration of the amino acid sequence or compound has been reduced by 50% compared to the initial level upon dosing. Further details are provided in, e.g., standard handbooks, such as Kenneth, A. et al., Chemical Stability of Pharmaceuticals: A Handbook for Pharmacists and in Peters et al., Pharmacokinetic Analysis: A Practical Approach (1996). Reference is also made to Gibaldi, M. et al., Pharmacokinetics, 2nd Rev. Edition, Marcel Dekker (1982).

In certain embodiments, the extended-PK group includes serum albumin, or fragments thereof or variants of the serum albumin or fragments thereof (all of which for the purpose of the present disclosure are comprised by the term "albumin"). Polypeptides described herein may be fused to albumin (or a fragment or variant thereof) to form albumin fusion proteins. Such albumin fusion proteins are described in U.S. Publication No. 20070048282.

As used herein, "albumin fusion protein" refers to a protein formed by the fusion of at least one molecule of albumin (or a fragment or variant thereof) to at least one molecule of a protein such as a therapeutic protein, in particular an immunostimulant. The albumin fusion protein may be generated by translation of a nucleic acid in which a polynucleotide encoding a therapeutic protein is joined in-frame with a polynucleotide encoding an albumin. The therapeutic protein and albumin, once part of the albumin fusion protein, may each be referred to as a "portion", "region" or "moiety" of the albumin fusion protein (e.g., a "therapeutic protein portion" or an "albumin protein portion"). In a highly preferred embodiment, an albumin fusion protein comprises at least one molecule of a therapeutic protein (including, but not limited to a mature form of the therapeutic protein) and at least one molecule of albumin (including but not limited to a mature form of albumin). In one embodiment, an albumin fusion protein is processed by a host cell such as a cell of the target

organ for administered RNA, e.g. a liver cell, and secreted into the circulation. Processing of the nascent albumin fusion protein that occurs in the secretory pathways of the host cell used for expression of the RNA may include, but is not limited to signal peptide cleavage; formation of disulfide bonds; proper folding; addition and processing of carbohydrates (such as for example, N- and O-linked glycosylation); specific proteolytic cleavages; and/or assembly into multimeric proteins. An albumin fusion protein is preferably encoded by RNA in a non-processed form which in particular has a signal peptide at its N-terminus and following secretion by a cell is preferably present in the processed form wherein in particular the signal peptide has been cleaved off. In a most preferred embodiment, the "processed form of an albumin fusion protein" refers to an albumin fusion protein product which has undergone N-terminal signal peptide cleavage, herein also referred to as a "mature albumin fusion protein". In preferred embodiments, albumin fusion proteins comprising a therapeutic protein have a higher plasma stability compared to the plasma stability of the same therapeutic protein when not fused to albumin. Plasma stability typically refers to the time period between when the therapeutic protein is administered *in vivo* and carried into the bloodstream and when the therapeutic protein is degraded and cleared from the bloodstream, into an organ, such as the kidney or liver, that ultimately clears the therapeutic protein from the body. Plasma stability is calculated in terms of the half-life of the therapeutic protein in the bloodstream. The half-life of the therapeutic protein in the bloodstream can be readily determined by common assays known in the art.

As used herein, "albumin" refers collectively to albumin protein or amino acid sequence, or an albumin fragment or variant, having one or more functional activities (e.g., biological activities) of albumin. In particular, "albumin" refers to human albumin or fragments or variants thereof especially the mature form of human albumin, or albumin from other vertebrates or fragments thereof, or variants of these molecules. The albumin may be derived from any vertebrate, especially any mammal, for example human, cow, sheep, or pig. Non-mammalian albumins include, but are not limited to, hen and salmon. The albumin portion of

the albumin fusion protein may be from a different animal than the therapeutic protein portion.

In certain embodiments, the albumin is human serum albumin (HSA), or fragments or variants thereof, such as those disclosed in US 5,876,969, WO 2011/124718, WO 2013/075066, and WO 2011/0514789.

The terms, human serum albumin (HSA) and human albumin (HA) are used interchangeably herein. The terms, "albumin and "serum albumin" are broader, and encompass human serum albumin (and fragments and variants thereof) as well as albumin from other species (and fragments and variants thereof).

As used herein, a fragment of albumin sufficient to prolong the therapeutic activity or plasma stability of the therapeutic protein refers to a fragment of albumin sufficient in length or structure to stabilize or prolong the therapeutic activity or plasma stability of the protein so that the plasma stability of the therapeutic protein portion of the albumin fusion protein is prolonged or extended compared to the plasma stability in the non-fusion state.

The albumin portion of the albumin fusion proteins may comprise the full length of the albumin sequence, or may include one or more fragments thereof that are capable of stabilizing or prolonging the therapeutic activity or plasma stability. Such fragments may be of 10 or more amino acids in length or may include about 15, 20, 25, 30, 50, or more contiguous amino acids from the albumin sequence or may include part or all of specific domains of albumin. For instance, one or more fragments of HSA spanning the first two immunoglobulin-like domains may be used. In a preferred embodiment, the HSA fragment is the mature form of HSA.

Generally speaking, an albumin fragment or variant will be at least 100 amino acids long, preferably at least 150 amino acids long.

According to the disclosure, albumin may be naturally occurring albumin or a fragment or variant thereof. Albumin may be human albumin and may be derived from any vertebrate, especially any mammal.

Preferably, the albumin fusion protein comprises albumin as the N-terminal portion, and a therapeutic protein as the C-terminal portion. Alternatively, an albumin fusion protein comprising albumin as the C-terminal portion, and a therapeutic protein as the N-terminal portion may also be used. In other embodiments, the albumin fusion protein has a therapeutic protein fused to both the N-terminus and the C-terminus of albumin. In a preferred embodiment, the therapeutic proteins fused at the N- and C-termini are the same therapeutic proteins. In another preferred embodiment, the therapeutic proteins fused at the N- and C-termini are different therapeutic proteins. In one embodiment, the different therapeutic proteins are both cytokines.

In one embodiment, the therapeutic protein(s) is (are) joined to the albumin through (a) peptide linker(s). A linker peptide between the fused portions may provide greater physical separation between the moieties and thus maximize the accessibility of the therapeutic protein portion, for instance, for binding to its cognate receptor. The linker peptide may consist of amino acids such that it is flexible or more rigid. The linker sequence may be cleavable by a protease or chemically.

As used herein, the term "Fc region" refers to the portion of a native immunoglobulin formed by the respective Fc domains (or Fc moieties) of its two heavy chains. As used herein, the term "Fc domain" refers to a portion or fragment of a single immunoglobulin (Ig) heavy chain wherein the Fc domain does not comprise an Fv domain. In certain embodiments, an Fc domain begins in the hinge region just upstream of the papain cleavage site and ends at the C-terminus of the antibody. Accordingly, a complete Fc domain comprises at least a hinge domain, a CH2 domain, and a CH3 domain. In certain embodiments, an Fc domain comprises at least one of: a hinge (e.g., upper, middle, and/or lower hinge region) domain, a CH2 domain, a CH3 domain, a CH4 domain, or a variant, portion, or fragment thereof. In certain embodiments, an Fc domain comprises a complete Fc domain (i.e., a hinge domain, a CH2 domain, and a CH3 domain). In certain embodiments, an Fc domain comprises a hinge domain (or portion thereof) fused to a CH3 domain (or portion thereof). In certain embodiments, an

Fc domain comprises a CH2 domain (or portion thereof) fused to a CH3 domain (or portion thereof). In certain embodiments, an Fc domain consists of a CH3 domain or portion thereof. In certain embodiments, an Fc domain consists of a hinge domain (or portion thereof) and a CH3 domain (or portion thereof). In certain embodiments, an Fc domain consists of a CH2 domain (or portion thereof) and a CH3 domain. In certain embodiments, an Fc domain consists of a hinge domain (or portion thereof) and a CH2 domain (or portion thereof). In certain embodiments, an Fc domain lacks at least a portion of a CH2 domain (e.g., all or part of a CH2 domain). An Fc domain herein generally refers to a polypeptide comprising all or part of the Fc domain of an immunoglobulin heavy-chain. This includes, but is not limited to, polypeptides comprising the entire CH1, hinge, CH2, and/or CH3 domains as well as fragments of such peptides comprising only, e.g., the hinge, CH2, and CH3 domain. The Fc domain may be derived from an immunoglobulin of any species and/or any subtype, including, but not limited to, a human IgG1, IgG2, IgG3, IgG4, IgD, IgA, IgE, or IgM antibody. The Fc domain encompasses native Fc and Fc variant molecules. As set forth herein, it will be understood by one of ordinary skill in the art that any Fc domain may be modified such that it varies in amino acid sequence from the native Fc domain of a naturally occurring immunoglobulin molecule. In certain embodiments, the Fc domain has reduced effector function (e.g., FcγR binding).

The Fc domains of a polypeptide described herein may be derived from different immunoglobulin molecules. For example, an Fc domain of a polypeptide may comprise a CH2 and/or CH3 domain derived from an IgG1 molecule and a hinge region derived from an IgG3 molecule. In another example, an Fc domain can comprise a chimeric hinge region derived, in part, from an IgG1 molecule and, in part, from an IgG3 molecule. In another example, an Fc domain can comprise a chimeric hinge derived, in part, from an IgG1 molecule and, in part, from an IgG4 molecule.

In certain embodiments, an extended-PK group includes an Fc domain or fragments thereof or variants of the Fc domain or fragments thereof (all of which for the purpose of the present disclosure are comprised by the term "Fc domain"). The Fc domain does not contain a variable

region that binds to antigen. Fc domains suitable for use in the present disclosure may be obtained from a number of different sources. In certain embodiments, an Fc domain is derived from a human immunoglobulin. In certain embodiments, the Fc domain is from a human IgG1 constant region. It is understood, however, that the Fc domain may be derived from an immunoglobulin of another mammalian species, including for example, a rodent (e.g. a mouse, rat, rabbit, guinea pig) or non- human primate (e.g. chimpanzee, macaque) species. Moreover, the Fc domain (or a fragment or variant thereof) may be derived from any immunoglobulin class, including IgM, IgG, IgD, IgA, and IgE, and any immunoglobulin isotype, including IgG1, IgG2, IgG3, and IgG4.

A variety of Fc domain gene sequences (e.g., mouse and human constant region gene sequences) are available in the form of publicly accessible deposits. Constant region domains comprising an Fc domain sequence can be selected lacking a particular effector function and/or with a particular modification to reduce immunogenicity. Many sequences of antibodies and antibody-encoding genes have been published and suitable Fc domain sequences (e.g. hinge, CH2, and/or CH3 sequences, or fragments or variants thereof) can be derived from these sequences using art recognized techniques.

In certain embodiments, the extended-PK group is a serum albumin binding protein such as those described in US2005/0287153, US2007/0003549, US2007/0178082, US2007/0269422, US2010/0113339, WO2009/083804, and WO2009/133208, which are herein incorporated by reference in their entirety. In certain embodiments, the extended-PK group is transferrin, as disclosed in US 7,176,278 and US 8,158,579, which are herein incorporated by reference in their entirety. In certain embodiments, the extended-PK group is a serum immunoglobulin binding protein such as those disclosed in US2007/0178082, US2014/0220017, and US2017/0145062, which are herein incorporated by reference in their entirety. In certain embodiments, the extended-PK group is a fibronectin (Fn)-based scaffold domain protein that binds to serum albumin, such as those disclosed in US2012/0094909, which is herein incorporated by reference in its entirety. Methods of making fibronectin-based scaffold

domain proteins are also disclosed in US2012/0094909. A non-limiting example of a Fn3-based extended-PK group is Fn3(HSA), i.e., a Fn3 protein that binds to human serum albumin.

In certain aspects, the extended-PK immunostimulant, suitable for use according to the disclosure, can employ one or more peptide linkers. As used herein, the term "peptide linker" refers to a peptide or polypeptide sequence which connects two or more domains (e.g., the extended-PK moiety and an immunostimulant moiety) in a linear amino acid sequence of a polypeptide chain. For example, peptide linkers may be used to connect an immunostimulant moiety to a HSA domain.

Linkers suitable for fusing the extended-PK group to e.g. an immunostimulant are well known in the art. Exemplary linkers include glycine-serine-polypeptide linkers, glycine-proline-polypeptide linkers, and proline-alanine polypeptide linkers. In certain embodiments, the linker is a glycine-serine-polypeptide linker, i.e., a peptide that consists of glycine and serine residues.

In addition to, or in place of, the heterologous polypeptides described above, an immunostimulant polypeptide described herein can contain sequences encoding a "marker" or "reporter". Examples of marker or reporter genes include β-lactamase, chloramphenicol acetyltransferase (CAT), adenosine deaminase (ADA), aminoglycoside phosphotransferase, dihydrofolate reductase (DHFR), hygromycin-B-hosphotransferase (HPH), thymidine kinase (TK), β-galactosidase, and xanthine guanine phosphoribosyltransferase (XGPRT).

Pharmaceutical compositions

The agents described herein may be administered in pharmaceutical compositions or medicaments and may be administered in the form of any suitable pharmaceutical composition.

In one embodiment, the pharmaceutical composition described herein is an immunogenic composition for inducing an immune response against coronavirus in a subject. For example, in one embodiment, the immunogenic composition is a vaccine.

In one embodiment of all aspects of the invention, the components described herein such as RNA encoding a vaccine antigen may be administered in a pharmaceutical composition which may comprise a pharmaceutically acceptable carrier and may optionally comprise one or more adjuvants, stabilizers etc. In one embodiment, the pharmaceutical composition is for therapeutic or prophylactic treatments, e.g., for use in treating or preventing a coronavirus infection.

The term "pharmaceutical composition" relates to a formulation comprising a therapeutically effective agent, preferably together with pharmaceutically acceptable carriers, diluents and/or excipients. Said pharmaceutical composition is useful for treating, preventing, or reducing the severity of a disease or disorder by administration of said pharmaceutical composition to a subject. A pharmaceutical composition is also known in the art as a pharmaceutical formulation.

The pharmaceutical compositions of the present disclosure may comprise one or more adjuvants or may be administered with one or more adjuvants. The term "adjuvant" relates to a compound which prolongs, enhances or accelerates an immune response. Adjuvants comprise a heterogeneous group of compounds such as oil emulsions (e.g., Freund's adjuvants), mineral compounds (such as alum), bacterial products (such as Bordetella pertussis toxin), or immune-stimulating complexes. Examples of adjuvants include, without limitation, LPS, GP96, CpG oligodeoxynucleotides, growth factors, and cytokines, such as monokines, lymphokines, interleukins, chemokines. The cytokines may be IL1, IL2, IL3, IL4, IL5, IL6, IL7, IL8, IL9, IL10, IL12, IFNα, IFNγ, GM-CSF, LT-a. Further known adjuvants are aluminium hydroxide, Freund's adjuvant or oil such as Montanide® ISA51. Other suitable adjuvants for use in the present disclosure include lipopeptides, such as Pam3Cys.

The pharmaceutical compositions according to the present disclosure are generally applied in a "pharmaceutically effective amount" and in "a pharmaceutically acceptable preparation".

The term "pharmaceutically acceptable" refers to the non-toxicity of a material which does not interact with the action of the active component of the pharmaceutical composition.

The term "pharmaceutically effective amount" or "therapeutically effective amount" refers to the amount which achieves a desired reaction or a desired effect alone or together with further doses. In the case of the treatment of a particular disease, the desired reaction preferably relates to inhibition of the course of the disease. This comprises slowing down the progress of the disease and, in particular, interrupting or reversing the progress of the disease. The desired reaction in a treatment of a disease may also be delay of the onset or a prevention of the onset of said disease or said condition. An effective amount of the compositions described herein will depend on the condition to be treated, the severeness of the disease, the individual parameters of the patient, including age, physiological condition, size and weight, the duration of treatment, the type of an accompanying therapy (if present), the specific route of administration and similar factors. Accordingly, the doses administered of the compositions described herein may depend on various of such parameters. In the case that a reaction in a patient is insufficient with an initial dose, higher doses (or effectively higher doses achieved by a different, more localized route of administration) may be used.

The pharmaceutical compositions of the present disclosure may contain salts, buffers, preservatives, and optionally other therapeutic agents. In one embodiment, the pharmaceutical compositions of the present disclosure comprise one or more pharmaceutically acceptable carriers, diluents and/or excipients.

Suitable preservatives for use in the pharmaceutical compositions of the present disclosure include, without limitation, benzalkonium chloride, chlorobutanol, paraben and thimerosal.

The term "excipient" as used herein refers to a substance which may be present in a pharmaceutical composition of the present disclosure but is not an active ingredient. Examples of excipients, include without limitation, carriers, binders, diluents, lubricants, thickeners, surface active agents, preservatives, stabilizers, emulsifiers, buffers, flavoring agents, or colorants.

The term "diluent" relates a diluting and/or thinning agent. Moreover, the term "diluent" includes any one or more of fluid, liquid or solid suspension and/or mixing media. Examples of suitable diluents include ethanol, glycerol and water.

The term "carrier" refers to a component which may be natural, synthetic, organic, inorganic in which the active component is combined in order to facilitate, enhance or enable administration of the pharmaceutical composition. A carrier as used herein may be one or more compatible solid or liquid fillers, diluents or encapsulating substances, which are suitable for administration to subject. Suitable carrier include, without limitation, sterile water, Ringer, Ringer lactate, sterile sodium chloride solution, isotonic saline, polyalkylene glycols, hydrogenated naphthalenes and, in particular, biocompatible lactide polymers, lactide/glycolide copolymers or polyoxyethylene/polyoxy-propylene copolymers. In one embodiment, the pharmaceutical composition of the present disclosure includes isotonic saline.

Pharmaceutically acceptable carriers, excipients or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in Remington's Pharmaceutical Sciences, Mack Publishing Co. (A. R Gennaro edit. 1985).

Pharmaceutical carriers, excipients or diluents can be selected with regard to the intended route of administration and standard pharmaceutical practice.

In one embodiment, pharmaceutical compositions described herein may be administered intravenously, intraarterially, subcutaneously, intradermally or intramuscularly. In certain embodiments, the pharmaceutical composition is formulated for local administration or systemic administration. Systemic administration may include enteral administration, which involves absorption through the gastrointestinal tract, or parenteral administration. As used herein, "parenteral administration" refers to the administration in any manner other than through the gastrointestinal tract, such as by intravenous injection. In a preferred embodiment, the pharmaceutical composition is formulated for intramuscular administration.

In another embodiment, the pharmaceutical composition is formulated for systemic administration, e.g., for intravenous administration.

The term "co-administering" as used herein means a process whereby different compounds or compositions (e.g., RNA encoding an antigen and RNA encoding an immunostimulant) are administered to the same patient. The different compounds or compositions may be administered simultaneously, at essentially the same time, or sequentially.

The pharmaceutical compositions and products described herein may be provided as a frozen concentrate for solution for injection, e.g., at a concentration of 0.50 mg/mL. In one embodiment, for preparation of solution for injection, a drug product is thawed and diluted with isotonic sodium chloride solution (e.g., 0.9% NaCl, saline), e.g., by a one-step dilution process. In some embodiments, bacteriostatic sodium chloride solution (e.g., 0.9% NaCl, saline) cannot be used as a diluent. In some embodiments, a diluted drug product is an off-white suspension. The concentration of the final solution for injection varies depending on the respective dose level to be administered.

In one embodiment, administration is performed within 6 h after begin of preparation due to the risk of microbial contamination and considering the multiple-dose approach of the preparation process. In one embodiment, in this period of 6 h, two conditions are allowed: room temperature for preparation, handling and transfer as well as 2 to 8°C for storage.

Compositions described herein may be shipped and/or stored under temperature-controlled conditions, e.g., temperature conditions of about 4-5°C or below, about -20°C or below, - 70°C±10°C (e.g., -80°C to -60°C), e.g., utilizing a cooling system (e.g., that may be or include dry ice) to maintain the desired temperature. In one embodiment, compositions described herein are shipped in temperature-controlled thermal shippers. Such shippers may contain a GPS-enabled thermal sensor to track the location and temperature of each shipment. The compositions can be stored by refilling with, e.g., dry ice.

Treatments

The present invention provides methods and agents for inducing an adaptive immune response against coronavirus in a subject comprising administering an effective amount of a composition comprising RNA encoding a coronavirus vaccine antigen described herein.

In one embodiment, the methods and agents described herein provide immunity in a subject to coronavirus, coronavirus infection, or to a disease or disorder associated with coronavirus. The present invention thus provides methods and agents for treating or preventing the infection, disease, or disorder associated with coronavirus.

In one embodiment, the methods and agents described herein are administered to a subject having an infection, disease, or disorder associated with coronavirus. In one embodiment, the methods and agents described herein are administered to a subject at risk for developing the infection, disease, or disorder associated with coronavirus. For example, the methods and agents described herein may be administered to a subject who is at risk for being in contact with coronavirus. In one embodiment, the methods and agents described herein are administered to a subject who lives in, traveled to, or is expected to travel to a geographic region in which coronavirus is prevalent. In one embodiment, the methods and agents described herein are administered to a subject who is in contact with or expected to be in contact with another person who lives in, traveled to, or is expected to travel to a geographic region in which coronavirus is prevalent. In one embodiment, the methods and agents described herein are administered to a subject who has knowingly been exposed to coronavirus through their occupation, or other contact. In one embodiment, a coronavirus is SARS-CoV-2. In some embodiments, methods and agents described herein are administered to a subject with evidence of prior exposure to and/or infection with SARS-CoV-2 and/or an antigen or epitope thereof or cross-reactive therewith. For example, in some embodiments, methods and agents described herein are administered to a subject in whom antibodies, B cells, and/or T cells reactive with one or more epitopes of a SARS-CoV-2 spike protein are detectable and/or have been detected.

For a composition to be useful as a vaccine, the composition must induce an immune response against the coronavirus antigen in a cell, tissue or subject (e.g., a human). In some embodiments, the composition induces an immune response against the coronavirus antigen in a cell, tissue or subject (e.g., a human). In some instances, the vaccine induces a protective immune response in a mammal. The therapeutic compounds or compositions of the invention may be administered prophylactically (i.e., to prevent a disease or disorder) or therapeutically (i.e., to treat a disease or disorder) to subjects suffering from, or at risk of (or susceptible to) developing a disease or disorder. Such subjects may be identified using standard clinical methods. In the context of the present invention, prophylactic administration occurs prior to the manifestation of overt clinical symptoms of disease, such that a disease or disorder is prevented or alternatively delayed in its progression. In the context of the field of medicine, the term "prevent" encompasses any activity, which reduces the burden of mortality or morbidity from disease. Prevention can occur at primary, secondary and tertiary prevention levels. While primary prevention avoids the development of a disease, secondary and tertiary levels of prevention encompass activities aimed at preventing the progression of a disease and the emergence of symptoms as well as reducing the negative impact of an already established disease by restoring function and reducing disease-related complications.

The present disclosure reports various characterization of provided compositions (see, e.g., Example 2; see also Examples thereafter) and furthermore establishes parameters for vaccines effective in humans.

In some embodiments, administration of an immunogenic composition or vaccine of the present invention may be performed by single administration or boosted by multiple administrations.

In some embodiments, an amount the RNA described herein from 0.1 μg to 300 μg, 0.5 μg to 200 μg, or 1 μg to 100 μg, such as about 1 μg, about 3 μg, about 10 μg, about 30 μg, about 50 μg, or about 100 μg may be administered per dose. In one embodiment, the invention envisions administration of a single dose. In one embodiment, the invention envisions

administration of a priming dose followed by one or more booster doses. The booster dose or the first booster dose may be administered 7 to 28 days or 14 to 24 days following administration of the priming dose.

In some embodiments, an amount of the RNA described herein of 60 µg or lower, 50 µg or lower, 40 µg or lower, 30 µg or lower, 20 µg or lower, 10 µg or lower, 5 µg or lower, 2.5 µg or lower, or 1 µg or lower may be administered per dose.

In some embodiments, an amount of the RNA described herein of at least 0.25 µg, at least 0.5 µg, at least 1 µg, at least 2 µg, at least 3 µg, at least 4 µg, at least 5 µg, at least 10 µg, at least 20 µg, at least 30 µg, or at least 40 µg may be administered per dose.

In some embodiments, an amount of the RNA described herein of 0.25 µg to 60 µg, 0.5 µg to 55 µg, 1 µg to 50 µg, 5 µg to 40 µg, or 10 µg to 30 µg may be administered per dose.

In one embodiment, an amount of the RNA described herein of about 30 µg is administered per dose. In one embodiment, at least two of such doses are administered. For example, a second dose may be administered about 21 days following administration of the first dose.

In some embodiments, the efficacy of the RNA vaccine described herein (e.g., administered in two doses, wherein a second dose may be administered about 21 days following administration of the first dose, and administered, for example, in an amount of about 30 µg per dose) is at least 70%, at least 80%, at least 90, or at least 95% beginning 7 days after administration of the second dose (e.g., beginning 28 days after administration of the first dose if a second dose is administered 21 days following administration of the first dose). In some embodiments, such efficacy is observed in populations of age of at least 50, at least 55, at least 60, at least 65, at least 70, or older. In some embodiments, the efficacy of the RNA vaccine described herein (e.g., administered in two doses, wherein a second dose may be administered about 21 days following administration of the first dose, and administered, for example, in an amount of about 30 µg per dose) beginning 7 days after administration of the second dose (e.g., beginning 28 days after administration of the first dose if a second dose is administered 21 days following administration of the first dose) in populations of age of at

least 65, such as 65 to 80, 65 to 75, or 65 to 70, is at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, or at least 95%. Such efficacy may be observed over time periods of up to 1 month, 2 months, 3 months, 6 months or even longer.

In one embodiment, vaccine efficacy is defined as the percent reduction in the number of subjects with evidence of infection (vaccinated subjects vs. non-vaccinated subjects).

In one embodiment, efficacy is assessed through surveillance for potential cases of COVID-19. If, at any time, a patient develops acute respiratory illness, for the purposes herein, the patient can be considered to potentially have COVID-19 illness. The assessments can include a nasal (midturbinate) swab, which may be tested using a reverse transcription-polymerase chain reaction (RT-PCR) test to detect SARS-CoV-2. In addition, clinical information and results from local standard-of-care tests can be assessed.

In some embodiments, efficacy assessments may utilize a definition of SARS-CoV-2-related cases wherein:

• Confirmed COVID-19: presence of at least 1 of the following symptoms and SARS-CoV-2 NAAT (nucleic acid amplification-based test) positive during, or within 4 days before or after, the symptomatic period: fever; new or increased cough; new or increased shortness of breath; chills; new or increased muscle pain; new loss of taste or smell; sore throat; diarrhea; vomiting.

Alternatively or additionally, in some embodiments, efficacy assessments may utilize a definition of SARS-CoV-2-related cases wherein one or more of the following additional symptoms defined by the CDC can be considered: fatigue; headache; nasal congestion or runny nose; nausea.

In some embodiments, efficacy assessments may utilize a definition of SARS-CoV-2-related severe cases

• Confirmed severe COVID-19: confirmed COVID-19 and presence of at least 1 of the following: clinical signs at rest indicative of severe systemic illness (e.g., RR ≥30 breaths per minute, HR ≥125 beats per minute, $SpO_2 \leq 93\%$ on room air at sea level, or $PaO_2/FiO_2 < 300$mm Hg);

respiratory failure (which can be defined as needing high-flow oxygen, noninvasive ventilation, mechanical ventilation, or ECMO); evidence of shock (e.g., SBP <90 mm Hg, DBP <60 mm Hg, or requiring vasopressors); significant acute renal, hepatic, or neurologic dysfunction; admission to an ICU; death.

Alternatively or additionally, in some embodiments a serological definition can be used for patients without clinical presentation of COVID-19: e.g., confirmed seroconversion to SARS-CoV-2 without confirmed COVID-19: e.g., positive N-binding antibody result in a patient with a prior negative N-binding antibody result.

In some embodiments, any or all of the following assays can be performed on serum samples: SARS-CoV-2 neutralization assay; S1-binding IgG level assay; RBD-binding IgG level assay; N-binding antibody assay.

In one embodiment, methods and agents described herein are administered to a paediatric population. In various embodiments, the paediatric population comprises or consists of subjects under 18 years, e.g., 5 to less than 18 years of age, 12 to less than 18 years of age, 16 to less than 18 years of age, 12 to less than 16 years of age, or 5 to less than 12 years of age. In various embodiments, the paediatric population comprises or consists of subjects under 5 years, e.g., 2 to less than 5 years of age, 12 to less than 24 months of age, 7 to less than 12 months of age, or less than 6 months of age.

In one embodiment, the paediatric population comprises or consists of subjects 12 to less than 18 years of age including subjects 16 to less than 18 years of age and/or subjects 12 to less than 16 years of age. In this embodiment, treatments may comprise 2 vaccinations 21 days apart, wherein, in one embodiment, the vaccine is administered in an amount of 30 μg RNA per dose, e.g., by intramuscular administration.

In one embodiment, the paediatric population comprises or consists of subjects 5 to less than 18 years of age including subjects 12 to less than 18 years of age and/or subjects 5 to less than 12 years of age. In this embodiment, treatments may comprise 2 vaccinations 21 days apart,

wherein, in various embodiments, the vaccine is administered in an amount of 10 µg, 20µg, or 30 µg RNA per dose, e.g., by intramuscular administration.

In one embodiment, the paediatric population comprises or consists of subjects less than 5 years of age including subjects 2 to less than 5 years of age, subjects 12 to less than 24 months of age, subjects 7 to less than 12 months of age, subjects 6 to less than 12 months of age and/or subjects less than 6 months of age. In this embodiment, treatments may comprise 2 vaccinations, e.g., 21 to 42 days apart, e.g., 21 days apart, wherein, in various embodiments, the vaccine is administered in an amount of 10 µg, 20µg, or 30 µg RNA per dose, e.g., by intramuscular administration.

In some embodiments, efficacy for mRNA compositions dsescribed in pediatric populations (e.g., described herein) may be assessed by various metrics described herein (including, e.g., but not limited to COVID-19 incidence per 1000 person-years in subjects with no serological or virological evidence of past SARS-CoV-2 infection; geometric mean ratio (GMR) of SARS CoV-2 neutr lizing titers measured, e.g., 7 days after a second dose; etc.)

In some embodiments, pediatric populations described herein (e.g., from 12 to less than 16 years of age) may be monitored for occurrence of multisystem inflammatory syndrome (MIS) (e.g., inflammation in different body parts such as, e.g., heart, lung, kidneys, brain, skin ,eyes, and/or gastrointestinal organs), after administration of an RNA composition (e.g., mRNA) described herein. Exemplary symponts of MIS in children may include, but are not limited to fever, abdominal pain, vomiting, diarrhea, neck pain, rash, bloodshot eyes, feeling extra tried, and combinations thereof.

In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) described herein as BNT162b1 (RBP020.3), BNT162b2 (RBP020.1 or RBP020.2). In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) described herein as RBP020.2.

In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 21, a nucleotide

sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 21, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 5. In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 21; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 5.

In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 19, or 20, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 19, or 20, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 19, or 20; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7.

In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 20, a nucleotide sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the nucleotide sequence of SEQ ID NO: 20, and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, or an amino acid sequence having at least 99%, 98%, 97%, 96%, 95%, 90%, 85%, or 80% identity to the amino acid sequence of SEQ ID NO: 7. In one embodiment, RNA administered as described above is nucleoside modified messenger RNA (modRNA) and (i) comprises the nucleotide sequence of SEQ ID NO: 20; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7.

In one embodiment, RNA administered is nucleoside modified messenger RNA (modRNA), (i) comprises the nucleotide sequence of SEQ ID NO: 20; and/or (ii) encodes an amino acid sequence comprising the amino acid sequence of SEQ ID NO: 7, and is administered in an amount of about 30 µg per dose. In one embodiment, at least two of such doses are administered. For example, a second dose may be administered about 21 days following administration of the first dose.

In some embodiments, populations to be treated with RNA described herein comprise, essentially consist of, or consist of subjects of age of at least 50, at least 55, at least 60, or at least 65. In some embodiments, populations to be treated with RNA described herein comprise, essentially consist of, or consist of subjects of age of between 55 to 90, 60 to 85, or 65 to 85.

In some embodiments, the period of time between the doses administered is at least 7 days, at least 14 days, or at least 21 days. In some embodiments, the period of time between the doses administered is between 7 days and 28 days such as between 14 days and 23 days.

In some embodiments, no more than 5 doses, no more than 4 doses, or no more than 3 doses of the RNA described herein may be administered to a subject.

In some embodiments, the methods and agents described herein are administered (in a regimen, e.g., at a dose, frequency of doses and/or number of doses) such that adverse events (AE), i.e., any unwanted medical occurrence in a patient, e.g., any unfavourable and unintended sign, symptom, or disease associated with the use of a medicinal product, whether or not related to the medicinal product, are mild or moderate in intensity. In some embodiments, the methods and agents described herein are administered such that adverse events (AE) can be managed with interventions such as treatment with, e.g., paracetamol or other drugs that provide analgesic, antipyretic (fever-reducing) and/or anti-inflammatory effects, e.g., nonsteroidal anti-inflammatory drugs (NSAIDs), e.g., aspirin, ibuprofen, and naproxen. Paracetamol or "acetaminophen" which is not classified as a NSAID exerts weak anti-inflammatory effects and can be administered as analgesic according to the invention.

In some embodiments, the methods and agents described herein provide a neutralizing effect in a subject to coronavirus, coronavirus infection, or to a disease or disorder associated with coronavirus.

In some embodiments, the methods and agents described herein following administration to a subject induce an immune response that blocks or neutralizes coronavirus in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce the generation of antibodies such as IgG antibodies that block or neutralize coronavirus in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce an immune response that blocks or neutralizes coronavirus S protein binding to ACE2 in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce the generation of antibodies that block or neutralize coronavirus S protein binding to ACE2 in the subject.

In some embodiments, the methods and agents described herein following administration to a subject induce geometric mean concentrations (GMCs) of RBD domain-binding antibodies such as IgG antibodies of at least 500 U/ml, 1000 U/ml, 2000 U/ml, 3000 U/ml, 4000 U/ml, 5000 U/ml, 10000 U/ml, 15000 U/ml, 20000 U/ml, 25000 U/ml, 30000 U/ml or even higher. In some embodiments, the elevated GMCs of RBD domain-binding antibodies persist for at least 14 days, 21 days, 28 days, 1 month, 3 months, 6 months, 12 months or even longer.

In some embodiments, the methods and agents described herein following administration to a subject induce geometric mean titers (GMTs) of neutralizing antibodies such as IgG antibodies of at least 100 U/ml, 200 U/ml, 300 U/ml, 400 U/ml, 500 U/ml, 1000 U/ml, 1500 U/ml, or even higher. In some embodiments, the elevated GMTs of neutralizing antibodies persist for at least 14 days, 21 days, 28 days, 1 month, 3 months, 6 months, 12 months or even longer.

As used herein, the term "neutralization" refers to an event in which binding agents such as antibodies bind to a biological active site of a virus such as a receptor binding protein, thereby inhibiting the viral infection of cells. As used herein, the term "neutralization" with respect to

coronavirus, in particular coronavirus S protein, refers to an event in which binding agents such as antibodies bind to the RBD domain of the S protein, thereby inhibiting the viral infection of cells. In particular, the term "neutralization" refers to an event in which binding agents eliminate or significantly reduce virulence (e.g. ability of infecting cells) of viruses of interest.

The type of immune response generated in response to an antigenic challenge can generally be distinguished by the subset of T helper (Th) cells involved in the response. Immune responses can be broadly divided into two types: Th1 and Th2. Th1 immune activation is optimized for intracellular infections such as viruses, whereas Th2 immune responses are optimized for humoral (antibody) responses. Th1 cells produce interleukin 2 (IL-2), tumor necrosis factor (TNFα) and interferon gamma (IFNγ). Th2 cells produce IL-4, IL-5, IL-6, IL-9, IL-10 and IL-13. Th1 immune activation is the most highly desired in many clinical situations. Vaccine compositions specialized in eliciting Th2 or humoral immune responses are generally not effective against most viral diseases.

In some embodiments, the methods and agents described herein following administration to a subject induce or promote a Th1-mediated immune response in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce or promote a cytokine profile that is typical for a Th1-mediated immune response in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce or promote the production of interleukin 2 (IL-2), tumor necrosis factor (TNFα) and/or interferon gamma (IFNγ) in the subject. In some embodiments, the methods and agents described herein following administration to a subject induce or promote the production of interleukin 2 (IL-2) and interferon gamma (IFNγ) in the subject. In some embodiments, the methods and agents described herein following administration to a subject do not induce or promote a Th2-mediated immune response in the subject, or induce or promote a Th2-mediated immune response in the subject to a significant lower extent compared to the induction or promotion of a Th1-mediated immune response. In some

embodiments, the methods and agents described herein following administration to a subject do not induce or promote a cytokine profile that is typical for a Th2-mediated immune response in the subject, or induce or promote a cytokine profile that is typical for a Th2-mediated immune response in the subject to a significant lower extent compared to the induction or promotion of a cytokine profile that is typical for a Th1-mediated immune response. In some embodiments, the methods and agents described herein following administration to a subject do not induce or promote the production of IL-4, IL-5, IL-6, IL-9, IL-10 and/or IL-13, or induce or promote the production of IL-4, IL-5, IL-6, IL-9, IL-10 and/or IL-13 in the subject to a significant lower extent compared to the induction or promotion of interleukin 2 (IL-2), tumor necrosis factor (TNFα) and/or interferon gamma (IFNγ) in the subject. In some embodiments, the methods and agents described herein following administration to a subject do not induce or promote the production of IL-4, or induce or promote the production of IL-4 in the subject to a significant lower extent compared to the induction or promotion of interleukin 2 (IL-2) and interferon gamma (IFNγ) in the subject.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a panel of different S protein variants such as SARS-CoV-2 S protein variants, in particular naturally occurring S protein variants. In some embodiments, the panel of different S protein variants comprises at least 5, at least 10, at least 15, or even more S protein variants. In some embodiments, such S protein variants comprise variants having amino acid modifications in the RBD domain and/or variants having amino acid modifications outside the RBD domain. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 321 (Q) in SEQ ID NO: 1 is S. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 321 (Q) in SEQ ID NO: 1 is L. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the

amino acid corresponding to position 341 (V) in SEQ ID NO: 1 is I. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 348 (A) in SEQ ID NO: 1 is T. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 354 (N) in SEQ ID NO: 1 is D. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 359 (S) in SEQ ID NO: 1 is N. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 367 (V) in SEQ ID NO: 1 is F. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 378 (K) in SEQ ID NO: 1 is S. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 378 (K) in SEQ ID NO: 1 is R. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 408 (R) in SEQ ID NO: 1 is I. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 409 (Q) in SEQ ID NO: 1 is E. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 435 (A) in SEQ ID NO: 1 is S. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 439 (N) in SEQ ID NO: 1 is K. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 458 (K) in SEQ ID NO: 1 is R. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 472 (I) in SEQ ID NO: 1 is V. In one embodiment, such S protein variant comprises

SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 476 (G) in SEQ ID NO: 1 is S. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 477 (S) in SEQ ID NO: 1 is N. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 483 (V) in SEQ ID NO: 1 is A. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 508 (Y) in SEQ ID NO: 1 is H. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 519 (H) in SEQ ID NO: 1 is P. In one embodiment, such S protein variant comprises SARS-CoV-2 S protein or a naturally occurring variant thereof wherein the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at a position corresponding to position 501 (N) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y.

Said S protein variant comprising a mutation at a position corresponding to position 501 (N) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), and 244 (L). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID

NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets VOC-202012/01.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y and A701V, and optionally: L18F, R246I, K417N, and deletion 242-244. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a deletion at a position corresponding to positions 69 (H) and 70 (V) in SEQ ID NO: 1.

In some embodiments, a S protein variant comprising a deletion at a position corresponding to positions 69 (H) and 70 (V) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 144 (Y), 501 (N), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), and 1229 (M). In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the

amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets VOC-202012/01.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "Cluster 5".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: deletion 69-70, Y453F, I692V, M1229I, and optionally S1147L.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at a position corresponding to position 614 (D) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G.

In some embodiments, a S protein variant comprising a mutation at a position corresponding to position 614 (D) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 501 (N), 570 (A), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), and 1229 (M). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the

amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets VOC-202012/01.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, D614G and A701V, and optionally: L18F, R246I, K417N, and deletion 242-244.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at positions corresponding to positions 501 (N) and 614 (D) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y and the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G.

In some embodiments, a S protein variant comprising a mutation at positions corresponding to positions 501 (N) and 614 (D) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 570 (A), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), and 1229 (M). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the

amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets VOC-202012/01.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: deletion 69-70, deletion 144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, D614G and A701V, and optionally: L18F, R246I, K417N, and deletion 242-244.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at a position corresponding to position 484 (E) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K.

In some embodiments, a S protein variant comprising a mutation at a position corresponding to position 484 (E) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 501 (N), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 417 (K), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID

NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y and A701V, and optionally: L18F, R246I, K417N, and deletion 242-244. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "B.1.1.28".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "B.1.1.248".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the

subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at positions corresponding to positions 501 (N) and 484 (E) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y and the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K.

In some embodiments, a S protein variant comprising a mutation at positions corresponding to positions 501 (N) and 484 (E) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 417 (K), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to

position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y and

A701V, and optionally: L18F, R246I, K417N, and deletion 242-244. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "B.1.1.248".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at positions corresponding to positions 501 (N), 484 (E) and 614 (D) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K and the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G.

In some embodiments, a S protein variant comprising a mutation at positions corresponding to positions 501 (N), 484 (E) and 614 (D) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 570 (A), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 701 (A), 18 (L), 246 (R), 417 (K), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 417 (K), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position

144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, A701V, and D614G, and optionally: L18F, R246I, K417N, and deletion 242-244.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a deletion at a position corresponding to positions 242 (L), 243 (A) and 244 (L) in SEQ ID NO: 1.

In some embodiments, a S protein variant comprising a deletion at a position corresponding to positions 242 (L), 243 (A) and 244 (L) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 501 (N), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 417 (K), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 417 (K), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to

position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, A701V

and deletion 242-244, and optionally: L18F, R246I, and K417N. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at a position corresponding to position 417 (K) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T.

In some embodiments, a S protein variant comprising a mutation at a position corresponding to position 417 (K) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 501 (N), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 484 (E), 701 (A), 18 (L), 246 (R), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID

NO: 1 is G. In one embodiment, the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, A701V, and K417N, and optionally: L18F, R246I, and deletion 242-244. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "B.1.1.248".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant such as SARS-CoV-2 S protein variant, in particular naturally occurring S protein variant comprising a mutation at positions corresponding to positions 417 (K) and 484 (E) and/or 501 (N) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is N, and the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K and/or the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 417 (K) in SEQ ID NO: 1 is T, and the amino acid corresponding to position 484 (E) in SEQ ID NO: 1 is K and/or the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y.

In some embodiments, a S protein variant comprising a mutation at positions corresponding to positions 417 (K) and 484 (E) and/or 501 (N) in SEQ ID NO: 1 may comprise one or more further mutations. Such one or more further mutations may be selected from mutations at positions corresponding to the following positions in SEQ ID NO: 1: 69 (H), 70 (V), 144 (Y), 570 (A), 614 (D), 681 (P), 716 (T), 982 (S), 1118 (D), 80 (D), 215 (D), 701 (A), 18 (L), 246 (R), 242 (L), 243 (A), 244 (L), 453 (Y), 692 (I), 1147 (S), 1229 (M), 20 (T), 26 (P), 138 (D), 190 (R), 655 (H), 1027 (T), and 1176 (V). In one embodiment, the amino acid corresponding to position 69 (H) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 70 (V) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position

144 (Y) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 570 (A) in SEQ ID NO: 1 is D. In one embodiment, the amino acid corresponding to position 614 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 681 (P) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 716 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 982 (S) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 1118 (D) in SEQ ID NO: 1 is H. In one embodiment, the amino acid corresponding to position 80 (D) in SEQ ID NO: 1 is A. In one embodiment, the amino acid corresponding to position 215 (D) in SEQ ID NO: 1 is G. In one embodiment, the amino acid corresponding to position 701 (A) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 18 (L) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 246 (R) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 242 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 243 (A) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 244 (L) in SEQ ID NO: 1 is deleted. In one embodiment, the amino acid corresponding to position 453 (Y) in SEQ ID NO: 1 is F. In one embodiment, the amino acid corresponding to position 692 (I) in SEQ ID NO: 1 is V. In one embodiment, the amino acid corresponding to position 1147 (S) in SEQ ID NO: 1 is L. In one embodiment, the amino acid corresponding to position 1229 (M) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 20 (T) in SEQ ID NO: 1 is N. In one embodiment, the amino acid corresponding to position 26 (P) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 138 (D) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 190 (R) in SEQ ID NO: 1 is S. In one embodiment, the amino acid corresponding to position 655 (H) in SEQ ID NO: 1 is Y. In one embodiment, the amino acid corresponding to position 1027 (T) in SEQ ID NO: 1 is I. In one embodiment, the amino acid corresponding to position 1176 (V) in SEQ ID NO: 1 is F.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets 501.V2.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: D80A, D215G, E484K, N501Y, A701V, and K417N and optionally: L18F, R246I, and deletion 242-244. Said S protein variant may also comprise a D->G mutation at a position corresponding to position 614 in SEQ ID NO: 1.

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets "B.1.1.248".

In some embodiments, the methods and agents described herein following administration to a subject induce an antibody response, in particular a neutralizing antibody response, in the subject that targets a S protein variant comprising the following mutations at positions corresponding to the following positions in SEQ ID NO: 1: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, H655Y, T1027I, and V1176F.

The term "amino acid corresponding to position..." as used herein refers to an amino acid position number corresponding to an amino acid position number in SARS-CoV-2 S protein, in particular the amino acid sequence shown in SEQ ID NO: 1. Corresponding amino acid positions in other coronavirus S protein variants such as SARS-CoV-2 S protein variants may be found by alignment with SARS-CoV-2 S protein, in particular the amino acid sequence shown in SEQ ID NO: 1. It is considered well-known in the art how to align a sequence or segment in a sequence and thereby determine the corresponding position in a sequence to an amino acid position according to the present invention. Standard sequence alignment programs such as ALIGN, ClustalW or similar, typically at default settings may be used.

In some embodiments, the panel of different S protein variants to which an antibody response is targeted comprises at least 5, at least 10, at least 15, or even more S protein variants selected from the group consisting of the Q321S, V341I, A348T, N354D, S359N, V367F, K378S, R408I, Q409E, A435S, K458R, I472V, G476S, V483A, Y508H, H519P and D614G variants described above. In some embodiments, the panel of different S protein variants to which an antibody response is targeted comprises all S protein variants from the group consisting of the Q321S, V341I, A348T, N354D, S359N, V367F, K378S, R408I, Q409E, A435S, K458R, I472V, G476S, V483A, Y508H, H519P and D614G variants described above.

In some embodiments, the panel of different S protein variants to which an antibody response is targeted comprises at least 5, at least 10, at least 15, or even more S protein variants selected from the group consisting of the Q321L, V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P and D614G variants described above. In some embodiments, the panel of different S protein variants to which an antibody response is targeted comprises all S protein variants from the group consisting of the Q321L, V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, H519P and D614G variants described above.

In some embodiments, a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof, e.g., as encoded by the RNA described herein, comprises one or more of the mutations described herein for S protein variants such as SARS-CoV-2 S protein variants, in particular naturally occurring S protein variants. In one embodiment, a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof, e.g., as encoded by the RNA described herein, comprises a mutation at a position corresponding to position 501 (N) in SEQ ID NO: 1. In one embodiment, the amino acid corresponding to position 501 (N) in SEQ ID NO: 1 is Y. In some embodiments, a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-

CoV-2 S protein or the immunogenic variant thereof, e.g., as encoded by the RNA described herein, comprises one or more mutations, such as all mutations, of a SARS-CoV-2 S protein of a SARS-CoV-2 variant selected from the group consisting of VOC-202012/01, 501.V2, Cluster 5 and B.1.1.248. In some embodiments, a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof, e.g., as encoded by the RNA described herein, comprises an amino acid sequence with alanine substitution at position 80, glycine substitution at position 215, lysine substitution at position 484, tyrosine substitution at position 501, valine substitution at position 701, phenylalanine substitution at position 18, isoleucine substitution at position 246, asparagine substitution at position 417, glycine substitution at position 614, deletions at positions 242 to 244, and proline substitutions at positions 986 and 987 of SEQ ID NO:1.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration to a subject induce a cell-mediated immune response (e.g., CD4+ and/or CD8+ T cell response). In some embodiments, T cells are induced that recognize one or more eptiopes (e.g., MHC class I-restricted epitopes) selected from the group consisting of LPFNDGVYF, GVYFASTEK, YLQPRTFLL, QPTESIVRF, CVADYSVLY, KCYGVSPTK, NYNYLYRLF, FQPTNGVGY, IPFAMQMAY, RLQSLQTYV, GTHWFVTQR, VYDPLQPEL, QYIKWPWYI, and KWPWYIWLGF. In one embodiment, T cells are induced that recognize the eptiope YLQPRTFLL. In one embodiment, T cells are induced that recognize the eptiope NYNYLYRLF. In one embodiment, T cells are induced that recognize the eptiope QYIKWPWYI. In one embodiment, T cells are induced that recognize the eptiope KCYGVSPTK. In one embodiment, T cells are induced that recognize the eptiope RLQSLQTYV. In some embodiments, the methods and agents, e.g., mRNA compositions, described herein are administered according to a regimen which achieves such induction of T cells.

In some embodiments, the methods and agents, e.g., mRNA compositions, described herein following administration to a subject induce a cell-mediated immune response (e.g., CD4+ and/or CD8+ T cell response) that is detectable 15 weeks or later, 16 weeks or later, 17 weeks

or later, 18 weeks or later, 19 weeks or later, 20 weeks or later, 21 weeks or later, 22 weeks or later, 23 weeks or later, 24 weeks or later or 25 weeks or later after administration, e.g., using two doses of the RNA described herein (wherein the second dose may be administered about 21 days following administration of the first dose). In some embodiments, the methods and agents, e.g., mRNA compositions, described herein are administered according to a regimen which achieves such induction of a cell-mediated immune response.

In one embodiment, vaccination against Coronavirus described herein, e.g., using RNA described herein which may be administered in the amounts and regimens described herein, e.g., at two doses of 30 µg per dose e.g. administered 21 days apart, may be repated after a certain period of time, e.g., once it is observed that protection against Coronavirus infection diminishes, using the same or a different vaccine as used for the first vaccination. Such certain period of time may be at least 6 months, 1 year, two years etc. In one embodiment, the same RNA as used for the first vaccination is used for the second or further vaccination, however, at a lower dose or a lower frequency of administration. For example, the first vaccination may comprise vaccination using a dose of about 30 µg per dose, wherein in one embodiment, at least two of such doses are administered, (for example, a second dose may be administered about 21 days following administration of the first dose) and the second or further vaccination may comprise vaccination using a dose of less than about 30 µg per dose, wherein in one embodiment, only one of such doses is administered. In one embodiment, a different RNA as used for the first vaccination is used for the second or further vaccination, e.g., BNT162b2 is used for the first vaccination and BNT162B1 or BNT162b3 is used for the second or further vaccination.

In one embodiment, the vaccination regimen comprises a first vaccination using at least two doses of the RNA described herein, e.g., two doses of the RNA described herein (wherein the second dose may be administered about 21 days following administration of the first dose), and a second vaccination using a single dose or multiple doses, e.g., two doses, of the RNA described herein. In various embodiments, the second vaccination is administered 3 to 24

months, 6 to 18 months, 6 to 12 months, or 5 to 7 months after administration of the first vaccination, e.g., after the initial two-dose regimen. The amount of RNA used in each dose of the second vaccination may be equal or different to the amount of RNA used in each dose of the first vaccination. In one embodiment, the amount of RNA used in each dose of the second vaccination is equal to the amount of RNA used in each dose of the first vaccination. In one embodiment, the amount of RNA used in each dose of the second vaccination and the amount of RNA used in each dose of the first vaccination is about 30 µg per dose. In one embodiment, the same RNA as used for the first vaccination is used for the second vaccination. In one embodiment, the RNA used for the first vaccination and for the second vaccination is BNT162b2. In one embodiment, a different RNA as used for the first vaccination is used for the second vaccination. In one embodiment, the RNA used for the first vaccination is BNT162b2 and the RNA used for the second vaccination is RNA encoding a SARS-CoV-2 S protein of a SARS-CoV-2 variant strain, e.g., a strain discussed herein. In one embodiment, the RNA used for the first vaccination is BNT162b2 and the RNA used for the second vaccination is RNA encoding a SARS-CoV-2 S protein of a SARS-CoV-2 variant strain that is prevalent or rapidly spreading at the time of the second vaccination. In one embodiment, the RNA used for the first vaccination is BNT162b2 and the RNA used for the second vaccination is RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprising one or more of the mutations described herein for S protein variants such as SARS-CoV-2 S protein variants, in particular naturally occurring S protein variants. In one embodiment, the RNA used for the first vaccination is BNT162b2 and the RNA used for the second vaccination is RNA encoding a SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof comprising one or more mutations, such as all mutations, of a SARS-CoV-2 S protein of a SARS-CoV-2 variant selected from the group consisting of VOC-202012/01, 501.V2, Cluster 5 and B.1.1.248. In one embodiment, the RNA used for the first vaccination encodes a polypeptide comprising an amino acid sequence

with proline residue substitutions at positions 986 and 987 of SEQ ID NO:1 and the RNA used for the second vaccination is RNA encoding a polypeptide comprising an amino acid sequence with alanine substitution at position 80, glycine substitution at position 215, lysine substitution at position 484, tyrosine substitution at position 501, valine substitution at position 701, phenylalanine substitution at position 18, isoleucine substitution at position 246, asparagine substitution at position 417, glycine substitution at position 614, deletions at positions 242 to 244, and proline substitutions at positions 986 and 987 of SEQ ID NO:1.

In one embodiment, the vaccination regimen comprises a first vaccination using two doses of RNA encoding a polypeptide comprising an amino acid sequence with proline residue substitutions at positions 986 and 987 of SEQ ID NO:1 administered about 21 days apart and a second vaccination using a single dose or multiple doses of RNA encoding a polypeptide comprising an amino acid sequence with proline residue substitutions at positions 986 and 987 of SEQ ID NO:1 administered about 6 to 12 months after administration of the first vaccination, i.e., after the initial two-dose regimen. In one embodiment, each RNA dose comprises 30 μg RNA.

In one embodiment, the vaccination regimen comprises a first vaccination using two doses of RNA encoding a polypeptide comprising an amino acid sequence with proline residue substitutions at positions 986 and 987 of SEQ ID NO:1 administered about 21 days apart and a second vaccination using a single dose or multiple doses of RNA encoding a polypeptide comprising an amino acid sequence with alanine substitution at position 80, glycine substitution at position 215, lysine substitution at position 484, tyrosine substitution at position 501, valine substitution at position 701, phenylalanine substitution at position 18, isoleucine substitution at position 246, asparagine substitution at position 417, glycine substitution at position 614, deletions at positions 242 to 244, and proline substitutions at positions 986 and 987 of SEQ ID NO:1 administered about 6 to 12 months after administration of the first vaccination, i.e., after the initial two-dose regimen. In one embodiment, each RNA dose comprises 30 μg RNA.

In one embodiment, the second vaccination results in a boosting of the immune response.

In one embodiment, the RNA described herein is co-administered with other vaccines. In some embodiments, an RNA composition described herein is co-administered with an influenza vaccine. In some embodiments, an RNA composition provided herein and other injectable vaccine(s) are administered at different times. In some embodiments, an RNA composition provided herein is administered at the same time as other injectable vaccine(s). In some such embodiments, an RNA composition provided herein and at least one another injectable vaccine(s) are administered at different injection sites. In some embodiments, an RNA composition provided herein is not mixed with any other vaccine in the same syringe. In some embodiments, an RNA composition provided herein is not combined with other coronavirus vaccines as part of vaccination against coronavirus, e.g., SARS-CoV-2.

The term "disease" refers to an abnormal condition that affects the body of an individual. A disease is often construed as a medical condition associated with specific symptoms and signs. A disease may be caused by factors originally from an external source, such as infectious disease, or it may be caused by internal dysfunctions, such as autoimmune diseases. In humans, "disease" is often used more broadly to refer to any condition that causes pain, dysfunction, distress, social problems, or death to the individual afflicted, or similar problems for those in contact with the individual. In this broader sense, it sometimes includes injuries, disabilities, disorders, syndromes, infections, isolated symptoms, deviant behaviors, and atypical variations of structure and function, while in other contexts and for other purposes these may be considered distinguishable categories. Diseases usually affect individuals not only physically, but also emotionally, as contracting and living with many diseases can alter one's perspective on life, and one's personality.

In the present context, the term "treatment", "treating" or "therapeutic intervention" relates to the management and care of a subject for the purpose of combating a condition such as a disease or disorder. The term is intended to include the full spectrum of treatments for a given condition from which the subject is suffering, such as administration of the therapeutically

effective compound to alleviate the symptoms or complications, to delay the progression of the disease, disorder or condition, to alleviate or relief the symptoms and complications, and/or to cure or eliminate the disease, disorder or condition as well as to prevent the condition, wherein prevention is to be understood as the management and care of an individual for the purpose of combating the disease, condition or disorder and includes the administration of the active compounds to prevent the onset of the symptoms or complications.

The term "therapeutic treatment" relates to any treatment which improves the health status and/or prolongs (increases) the lifespan of an individual. Said treatment may eliminate the disease in an individual, arrest or slow the development of a disease in an individual, inhibit or slow the development of a disease in an individual, decrease the frequency or severity of symptoms in an individual, and/or decrease the recurrence in an individual who currently has or who previously has had a disease.

The terms "prophylactic treatment" or "preventive treatment" relate to any treatment that is intended to prevent a disease from occurring in an individual. The terms "prophylactic treatment" or "preventive treatment" are used herein interchangeably.

The terms "individual" and "subject" are used herein interchangeably. They refer to a human or another mammal (e.g. mouse, rat, rabbit, dog, cat, cattle, swine, sheep, horse or primate) that can be afflicted with or is susceptible to a disease or disorder but may or may not have the disease or disorder. In many embodiments, the individual is a human being. Unless otherwise stated, the terms "individual" and "subject" do not denote a particular age, and thus encompass adults, elderlies, children, and newborns. In some embodiments, the term "subject" includes humans of age of at least 50, at least 55, at least 60, at least 65, at least 70, or older. In some embodiments, the term "subject" includes humans of age of at least 65, such as 65 to 80, 65 to 75, or 65 to 70. In embodiments of the present disclosure, the "individual" or "subject" is a "patient".

The term "patient" means an individual or subject for treatment, in particular a diseased individual or subject.

In one embodiment of the disclosure, the aim is to provide an immune response against coronavirus, and to prevent or treat coronavirus infection.

A pharmaceutical composition comprising RNA encoding a peptide or protein comprising an epitope may be administered to a subject to elicit an immune response against an antigen comprising said epitope in the subject which may be therapeutic or partially or fully protective.

A person skilled in the art will know that one of the principles of immunotherapy and vaccination is based on the fact that an immunoprotective reaction to a disease is produced by immunizing a subject with an antigen or an epitope, which is immunologically relevant with respect to the disease to be treated. Accordingly, pharmaceutical compositions described herein are applicable for inducing or enhancing an immune response. Pharmaceutical compositions described herein are thus useful in a prophylactic and/or therapeutic treatment of a disease involving an antigen or epitope.

As used herein, "immune response" refers to an integrated bodily response to an antigen or a cell expressing an antigen and refers to a cellular immune response and/or a humoral immune response. The immune system is divided into a more primitive innate immune system, and acquired or adaptive immune system of vertebrates, each of which contains humoral and cellular components.

"Cell-mediated immunity", "cellular immunity", "cellular immune response", or similar terms are meant to include a cellular response directed to cells characterized by expression of an antigen, in particular characterized by presentation of an antigen with class I or class II MHC. The cellular response relates to immune effector cells, in particular to cells called T cells or T lymphocytes which act as either "helpers" or "killers". The helper T cells (also termed $CD4^+$ T cells) play a central role by regulating the immune response and the killer cells (also termed cytotoxic T cells, cytolytic T cells, $CD8^+$ T cells or CTLs) kill diseased cells such as virus-infected cells, preventing the production of more diseased cells.

An immune effector cell includes any cell which is responsive to vaccine antigen. Such responsiveness includes activation, differentiation, proliferation, survival and/or indication of one or more immune effector functions. The cells include, in particular, cells with lytic potential, in particular lymphoid cells, and are preferably T cells, in particular cytotoxic lymphocytes, preferably selected from cytotoxic T cells, natural killer (NK) cells, and lymphokine-activated killer (LAK) cells. Upon activation, each of these cytotoxic lymphocytes triggers the destruction of target cells. For example, cytotoxic T cells trigger the destruction of target cells by either or both of the following means. First, upon activation T cells release cytotoxins such as perforin, granzymes, and granulysin. Perforin and granulysin create pores in the target cell, and granzymes enter the cell and trigger a caspase cascade in the cytoplasm that induces apoptosis (programmed cell death) of the cell. Second, apoptosis can be induced via Fas-Fas ligand interaction between the T cells and target cells.

The term "effector functions" in the context of the present invention includes any functions mediated by components of the immune system that result, for example, in the neutralization of a pathogenic agent such as a virus and/or in the killing of diseased cells such as virus-infected cells. In one embodiment, the effector functions in the context of the present invention are T cell mediated effector functions. Such functions comprise in the case of a helper T cell ($CD4^+$ T cell) the release of cytokines and/or the activation of $CD8^+$ lymphocytes (CTLs) and/or B cells, and in the case of CTL the elimination of cells, i.e., cells characterized by expression of an antigen, for example, via apoptosis or perforin-mediated cell lysis, production of cytokines such as IFN-γ and TNF-α, and specific cytolytic killing of antigen expressing target cells.

The term "immune effector cell" or "immunoreactive cell" in the context of the present invention relates to a cell which exerts effector functions during an immune reaction. An "immune effector cell" in one embodiment is capable of binding an antigen such as an antigen presented in the context of MHC on a cell or expressed on the surface of a cell and mediating an immune response. For example, immune effector cells comprise T cells (cytotoxic T cells,

helper T cells, tumor infiltrating T cells), B cells, natural killer cells, neutrophils, macrophages, and dendritic cells. Preferably, in the context of the present invention, "immune effector cells" are T cells, preferably $CD4^+$ and/or $CD8^+$ T cells, most preferably $CD8^+$ T cells. According to the invention, the term "immune effector cell" also includes a cell which can mature into an immune cell (such as T cell, in particular T helper cell, or cytolytic T cell) with suitable stimulation. Immune effector cells comprise $CD34^+$ hematopoietic stem cells, immature and mature T cells and immature and mature B cells. The differentiation of T cell precursors into a cytolytic T cell, when exposed to an antigen, is similar to clonal selection of the immune system.

A "lymphoid cell" is a cell which is capable of producing an immune response such as a cellular immune response, or a precursor cell of such cell, and includes lymphocytes, preferably T lymphocytes, lymphoblasts, and plasma cells. A lymphoid cell may be an immune effector cell as described herein. A preferred lymphoid cell is a T cell.

The terms "T cell" and "T lymphocyte" are used interchangeably herein and include T helper cells (CD4+ T cells) and cytotoxic T cells (CTLs, CD8+ T cells) which comprise cytolytic T cells. The term "antigen-specific T cell" or similar terms relate to a T cell which recognizes the antigen to which the T cell is targeted and preferably exerts effector functions of T cells.

T cells belong to a group of white blood cells known as lymphocytes, and play a central role in cell-mediated immunity. They can be distinguished from other lymphocyte types, such as B cells and natural killer cells by the presence of a special receptor on their cell surface called T cell receptor (TCR). The thymus is the principal organ responsible for the maturation of T cells. Several different subsets of T cells have been discovered, each with a distinct function.

T helper cells assist other white blood cells in immunologic processes, including maturation of B cells into plasma cells and activation of cytotoxic T cells and macrophages, among other functions. These cells are also known as CD4+ T cells because they express the CD4 glycoprotein on their surface. Helper T cells become activated when they are presented with peptide antigens by MHC class II molecules that are expressed on the surface of antigen

presenting cells (APCs). Once activated, they divide rapidly and secrete small proteins called cytokines that regulate or assist in the active immune response.

Cytotoxic T cells destroy virally infected cells and tumor cells, and are also implicated in transplant rejection. These cells are also known as CD8+ T cells since they express the CD8 glycoprotein on their surface. These cells recognize their targets by binding to antigen associated with MHC class I, which is present on the surface of nearly every cell of the body.

A majority of T cells have a T cell receptor (TCR) existing as a complex of several proteins. The TCR of a T cell is able to interact with immunogenic peptides (epitopes) bound to major histocompatibility complex (MHC) molecules and presented on the surface of target cells. Specific binding of the TCR triggers a signal cascade inside the T cell leading to proliferation and differentiation into a maturated effector T cell. The actual T cell receptor is composed of two separate peptide chains, which are produced from the independent T cell receptor alpha and beta (TCRα and TCRβ) genes and are called α- and β-TCR chains. γδ T cells (gamma delta T cells) represent a small subset of T cells that possess a distinct T cell receptor (TCR) on their surface. However, in γδ T cells, the TCR is made up of one γ-chain and one δ-chain. This group of T cells is much less common (2% of total T cells) than the αβ T cells.

"Humoral immunity" or "humoral immune response" is the aspect of immunity that is mediated by macromolecules found in extracellular fluids such as secreted antibodies, complement proteins, and certain antimicrobial peptides. It contrasts with cell-mediated immunity. Its aspects involving antibodies are often called antibody-mediated immunity.

Humoral immunity refers to antibody production and the accessory processes that accompany it, including: Th2 activation and cytokine production, germinal center formation and isotype switching, affinity maturation and memory cell generation. It also refers to the effector functions of antibodies, which include pathogen neutralization, classical complement activation, and opsonin promotion of phagocytosis and pathogen elimination.

In humoral immune response, first the B cells mature in the bone marrow and gain B-cell receptors (BCR's) which are displayed in large number on the cell surface. These membrane-

bound protein complexes have antibodies which are specific for antigen detection. Each B cell has a unique antibody that binds with an antigen. The mature B cells migrate from the bone marrow to the lymph nodes or other lymphatic organs, where they begin to encounter pathogens. When a B cell encounters an antigen, the antigen is bound to the receptor and taken inside the B cell by endocytosis. The antigen is processed and presented on the B cell's surface again by MHC-II proteins. The B cell waits for a helper T cell (TH) to bind to the complex. This binding will activate the TH cell, which then releases cytokines that induce B cells to divide rapidly, making thousands of identical clones of the B cell. These daughter cells either become plasma cells or memory cells. The memory B cells remain inactive here; later when these memory B cells encounter the same antigen due to reinfection, they divide and form plasma cells. On the other hand, the plasma cells produce a large number of antibodies which are released free into the circulatory system. These antibodies will encounter antigens and bind with them. This will either interfere with the chemical interaction between host and foreign cells, or they may form bridges between their antigenic sites hindering their proper functioning, or their presence will attract macrophages or killer cells to attack and phagocytose them.

The term "antibody" includes an immunoglobulin comprising at least two heavy (H) chains and two light (L) chains inter-connected by disulfide bonds. Each heavy chain is comprised of a heavy chain variable region (abbreviated herein as VH) and a heavy chain constant region. Each light chain is comprised of a light chain variable region (abbreviated herein as VL) and a light chain constant region. The VH and VL regions can be further subdivided into regions of hypervariability, termed complementarity determining regions (CDR), interspersed with regions that are more conserved, termed framework regions (FR). Each VH and VL is composed of three CDRs and four FRs, arranged from amino-terminus to carboxy-terminus in the following order: FR1, CDR1, FR2, CDR2, FR3, CDR3, FR4. The variable regions of the heavy and light chains contain a binding domain that interacts with an antigen. The constant regions of the antibodies may mediate the binding of the immunoglobulin to host tissues or factors,

including various cells of the immune system (e.g., effector cells) and the first component (Clq) of the classical complement system. An antibody binds, preferably specifically binds with an antigen.

Antibodies expressed by B cells are sometimes referred to as the BCR (B cell receptor) or antigen receptor. The five members included in this class of proteins are IgA, IgG, IgM, IgD, and IgE. IgA is the primary antibody that is present in body secretions, such as saliva, tears, breast milk, gastrointestinal secretions and mucus secretions of the respiratory and genitourinary tracts. IgG is the most common circulating antibody. IgM is the main immunoglobulin produced in the primary immune response in most subjects. It is the most efficient immunoglobulin in agglutination, complement fixation, and other antibody responses, and is important in defense against bacteria and viruses. IgD is the immunoglobulin that has no known antibody function, but may serve as an antigen receptor. IgE is the immunoglobulin that mediates immediate hypersensitivity by causing release of mediators from mast cells and basophils upon exposure to allergen.

An "antibody heavy chain", as used herein, refers to the larger of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations.

An "antibody light chain", as used herein, refers to the smaller of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations, κ and λ light chains refer to the two major antibody light chain isotypes.

The present disclosure contemplates an immune response that may be protective, preventive, prophylactic and/or therapeutic. As used herein, "induces [or inducing] an immune response" may indicate that no immune response against a particular antigen was present before induction or it may indicate that there was a basal level of immune response against a particular antigen before induction, which was enhanced after induction. Therefore, "induces [or inducing] an immune response" includes "enhances [or enhancing] an immune response".

The term "immunotherapy" relates to the treatment of a disease or condition by inducing, or enhancing an immune response. The term "immunotherapy" includes antigen immunization or antigen vaccination.

The terms "immunization" or "vaccination" describe the process of administering an antigen to an individual with the purpose of inducing an immune response, for example, for therapeutic or prophylactic reasons.

The term "macrophage" refers to a subgroup of phagocytic cells produced by the differentiation of monocytes. Macrophages which are activated by inflammation, immune cytokines or microbial products nonspecifically engulf and kill foreign pathogens within the macrophage by hydrolytic and oxidative attack resulting in degradation of the pathogen. Peptides from degraded proteins are displayed on the macrophage cell surface where they can be recognized by T cells, and they can directly interact with antibodies on the B cell surface, resulting in T and B cell activation and further stimulation of the immune response. Macrophages belong to the class of antigen presenting cells. In one embodiment, the macrophages are splenic macrophages.

The term "dendritic cell" (DC) refers to another subtype of phagocytic cells belonging to the class of antigen presenting cells. In one embodiment, dendritic cells are derived from hematopoietic bone marrow progenitor cells. These progenitor cells initially transform into immature dendritic cells. These immature cells are characterized by high phagocytic activity and low T cell activation potential. Immature dendritic cells constantly sample the surrounding environment for pathogens such as viruses and bacteria. Once they have come into contact with a presentable antigen, they become activated into mature dendritic cells and begin to migrate to the spleen or to the lymph node. Immature dendritic cells phagocytose pathogens and degrade their proteins into small pieces and upon maturation present those fragments at their cell surface using MHC molecules. Simultaneously, they upregulate cell-surface receptors that act as co-receptors in T cell activation such as CD80, CD86, and CD40 greatly enhancing their ability to activate T cells. They also upregulate CCR7, a chemotactic receptor that induces

the dendritic cell to travel through the blood stream to the spleen or through the lymphatic system to a lymph node. Here they act as antigen-presenting cells and activate helper T cells and killer T cells as well as B cells by presenting them antigens, alongside non-antigen specific co-stimulatory signals. Thus, dendritic cells can actively induce a T cell- or B cell-related immune response. In one embodiment, the dendritic cells are splenic dendritic cells.

The term "antigen presenting cell" (APC) is a cell of a variety of cells capable of displaying, acquiring, and/or presenting at least one antigen or antigenic fragment on (or at) its cell surface. Antigen-presenting cells can be distinguished in professional antigen presenting cells and non-professional antigen presenting cells.

The term "professional antigen presenting cells" relates to antigen presenting cells which constitutively express the Major Histocompatibility Complex class II (MHC class II) molecules required for interaction with naive T cells. If a T cell interacts with the MHC class II molecule complex on the membrane of the antigen presenting cell, the antigen presenting cell produces a co-stimulatory molecule inducing activation of the T cell. Professional antigen presenting cells comprise dendritic cells and macrophages.

The term "non-professional antigen presenting cells" relates to antigen presenting cells which do not constitutively express MHC class II molecules, but upon stimulation by certain cytokines such as interferon-gamma. Exemplary, non-professional antigen presenting cells include fibroblasts, thymic epithelial cells, thyroid epithelial cells, glial cells, pancreatic beta cells or vascular endothelial cells.

"Antigen processing" refers to the degradation of an antigen into procession products, which are fragments of said antigen (e.g., the degradation of a protein into peptides) and the association of one or more of these fragments (e.g., via binding) with MHC molecules for presentation by cells, such as antigen presenting cells to specific T cells.

The term "disease involving an antigen" refers to any disease which implicates an antigen, e.g. a disease which is characterized by the presence of an antigen. The disease involving an antigen can be an infectious disease. As mentioned above, the antigen may be a disease-

associated antigen, such as a viral antigen. In one embodiment, a disease involving an antigen is a disease involving cells expressing an antigen, preferably on the cell surface.

The term "infectious disease" refers to any disease which can be transmitted from individual to individual or from organism to organism, and is caused by a microbial agent (e.g. common cold). Infectious diseases are known in the art and include, for example, a viral disease, a bacterial disease, or a parasitic disease, which diseases are caused by a virus, a bacterium, and a parasite, respectively. In this regard, the infectious disease can be, for example, hepatitis, sexually transmitted diseases (e.g. chlamydia or gonorrhea), tuberculosis, HIV/acquired immune deficiency syndrome (AIDS), diphtheria, hepatitis B, hepatitis C, cholera, severe acute respiratory syndrome (SARS), the bird flu, and influenza.

Packaging and Shipping

The present disclosure describes methods, kits, containers, container systems, and devices to improve delivery logistics of time and/or temperature-sensitive materials, particularly biological and pharmaceutical materials. The containers described herein can be thermally insulated containers intended for transporting and/or temporary storage of such temperature-sensitive materials. In some embodiments, the container and/or kit can have a separate payload container that contains the temperature-sensitive materials. The containers can be equipped with integrated electronics capable of measuring, storing, monitoring, tracking and communicating important information regarding the location of the container and the environment inside the container, such as the temperature.

The size of the kits and container systems can be designed to taking into consideration the various constraints that can be involved with the shipping and storage logistics relevant to a particular material that is being transported. For example, considerations include maximizing the capacity of the shipping containers (including the payload container and trays) while still being capable of maintaining a particular low temperature of the temperature-sensitive material. Further considerations include maximizing the amount of space within the shipping

container that is capable keeping materials at a particular low temperature, and to maximize the amount of containers that can be stored in a warehouse facility, for example. Further for example, the trays of the present disclosure can be designed to maximize the number of vials (or other storage media) that can be placed within such trays while maintaining a sufficiently low temperature of the vials in the middle section of the tray, as well as the vials at the edges of the tray. Further considerations include minimizing the amount of dry ice (or other cooling mechanism) that is required within the kit and/or container system to maintain the temperature-sensitive material at or below a particular low temperature. Accordingly, the kits, container systems, and methods of the present disclosure have been contemplated and designed with these considerations in mind.

In some embodiments, temperature-sensitive materials described herein may be shipped and/or stored under temperature-controlled conditions, e.g., temperature conditions of −70°C ± 10°C, e.g., utilizing dry ice to maintain the desired temperature. In one embodiment, materials are shipped in temperature-controlled thermal shippers. Such shippers may contain a GPS-enabled thermal sensor to track the location and temperature of each shipment. The materials can be stored by refilling with dry ice.

In some embodiments, a kit as provided herein may comprise a real-time monitoring logging device, which, for example in some embodiments, is capable of providing shipment temperatures, shipment time and/or location. The containers can be part of a logistics system, including methods of real-time monitoring of the location, internal temperature, and other parameters of the container or the temperature-sensitive materials within the container. The integrated electronics can be capable of broadcasting information regarding the container through the use of a global positioning system (GPS) and/or other wireless technologies, such as local area wireless communication (Wi-Fi), Bluetooth, cellular network, or other wireless networks.

In some embodiments, information regarding the container is wirelessly exchanged with cloud-based data storage or other communication networks. Such information can include

real-time and/or historical location and temperature data, which can be processed for users on multiple platforms in various formats. For example, the information from the container may be provided to users via mobile devices through short message service (SMS) and/or multimedia messaging service (MMS). In other embodiments, the information may be accessible via a cloud-based database or from generated reports. Embodiments of the present invention may be implemented in a cloud computing environment or with any other type of known or future developed computing environment.

A computer system/server may be utilized in connection with the methods and kits described herein, for example distributed cloud computing environments where tasks are performed by remote processing devices linked through a communications network. In a distributed cloud computing environment, program modules may be located in both local and remote computer system storage media including memory storage devices. A computer system/server computer may also communicate with one or more external devices, such as device computers. The computer system/server computer typically includes a variety of computer system readable media. This media may be any available media that is accessible by computer system/server computer, and includes both volatile and non-volatile media, as well as removable and non-removable media. Cloud computing enables convenient, on-demand network access to a shared pool of configurable computing resources (e.g. networks, network bandwidth, servers, processing, memory, storage, applications, virtual machines, and services) that can be rapidly provisioned and released with minimal management effort or interaction with a provider of the service.

The kit and/or container may also communicate information regarding the container/kit itself (e.g. temperature history, location information) to a local user or network during non-transit periods.

In some embodiments, alerts are sent to appropriate parties if the temperature of the material is outside the desired range. In other embodiments, a countdown timer is used to keep track

of the time that the temperature-sensitive material has been in transit, and ensure that the amount of time does not exceed a certain limit.

In still other embodiments, the payload container is equipped with its own sensors, such as temperature sensors and with close range communication devices, capable of transmitting information regarding a range of parameters, including, but not limited to, temperature, humidity, location, and time, from the payload container to an end user via a mobile device application, the cloud hosted application, or another receiving system.

The temperature-sensitive material being transported may be any biological or pharmaceutical product, including, but not limited to, specimens, vaccines, medicines, pharmaceuticals, blood samples, cells, stem cells, tissues, engineered tissue products, manufactured cell and gene therapies, organs, or any fluid, bone or cellular or metabolic byproduct, intermediary, or derivative.

In some embodiments, the containers disclosed herein (e.g. the primary container, the payload container, the container for dry ice, the tray, etc.) can be made of suitable materials that will meet the requirements of maintaining the temperature-sensitive material at a sufficiently low temperature, and will further meet the requirements of shipping space, storage capacity, etc. Materials useful for producing the kits and/or container systems of the present disclosure can include materials such as corrugated cardboard, corrugated plastics, or high density plastics foam. For example, corrugated translucent or white polypropylene (e.g. Akylux®, Biplex®, or equivalent thereof) can be used. The containers can have a lining of either Styrofoam or resilient foam in the form of formed, molded or precut pads, and at least one pre-chilled gel pack, which is a sealed bag-like container of heavy plastic filled with a gel which freezes upon chilling and maintains a relatively low temperature in the container. Other methods and materials used to provide insulation for the kit or container system include vacuum insulation panels, expanded or extruded polystyrene, or polyurethane foam. Other methods and materials, such as use of dry ice, can also be used in order to maintain the temperature-sensitive material at or below an appropriate temperature.

Materials used in the container for maintaining an ultra-low temperature, for example dry ice, should be placed in the insulated shipping container correctly in order to provide the correct temperature and temperature stability required for shipment. Similarly, the payload container (the container housing the temperature-sensitive material being transported) should be placed correctly within the shipping container. The payload container can be of any shape that can safely ship the material. The payload container can be a larger container preferably containing packing material to protect the payload from mechanical vibration, shock, or other forms of stress during transit. The payload container can contain a smaller container, such as a vial, a specimen tube, a bag, or a syringe, that is placed within the payload container. In other embodiments, the payload container could be the container that houses the temperature-sensitive materials.

In some embodiments, the insulated shipping container and/or the payload container include one or more temperature sensors. In embodiments where temperature sensors are used, they may come into contact with, be in direct contact with, or be in close proximity to whatever they are measuring in order to sense the temperature of that item or its environment. If the insulated materials being used in the packing were not conditioned or frozen sufficiently, these sensors alert a user regarding the improper preconditioning of the insulating materials, halting further packaging and shipping of the materials until such errors are corrected.

The sensors are preferably at least partially embedded or fully embedded into one or more of the walls of an insulated shipping container. These sensors communicate either via hard wires or near field communication methods to a long-range communications device which itself is embedded into the body of the insulated shipping container. The long-range communications device may utilize cellular communication or other communication networks to communicate with a user. In some embodiments, a cellular modem is integrated into the communications device. In some embodiments, the sensor in the insulating material is an RFID tag, a temperature sensor, or a magnet. Some examples of the communications devices include, but are not limited to, cellular communication devices (e.g.--cellular phones, cellular modems,

code division multiple access systems, global system for mobile communications, and other cellular portions of the spectrum), RF transmitters, active RFID devices, RFID tags, iBeacon® transmitters, ZigBee® transmitters, Bluetooth® transmitters, Wi-Fi radios, other wireless transmitters, or other near field communication signals or devices.

The logistics/tracking system may contain the ability to complete shipping air bills, and communicate with appropriate users as to the status and location of a particular shipping container. The logistics/tracking system may also prevent the completion of an air bill if the pack out procedures are not properly followed, resulting in activation of the built-in sensors and/or switches. The logistics/tracking system may be cloud-based, a client application, and/or a mobile application.

In some embodiments with a communications device in the payload container, the communications device in the payload container is a near field communication device that provides information and may communicate, for example with the shipping or storage container or a smartphone device, using low power communications including Bluetooth®, iBeacon®, ZigBee®, Wi-Fi or other forms of near field communication (NFC).

In some embodiments, the temperature-sensitive materials may have been prepared, stored, transported, characterized, and/or used under conditions where temperature does not exceed a particular threshold. Alternatively or additionally, in some embodiments, the temperature-sensitive materials may have been protected from light (e.g., from certain wavelengths) during some or all of their preparation, storage, transport, characterization, and/or use.

In some embodiments, the temperature-sensitive material as described herein may be shipped, stored, and/or utilized, in a container (such as a vial or syringe), e.g., a glass container (such as a glass vial or syringe), which, in some embodiments, may be a single-dose container or a multi-dose container (e.g., may be arranged and constructed to hold, and/or in some embodiments may hold, a single dose, or multiple doses of a product for administration). In some embodiments, a multi-dose container (such as a multi-dose vial or syringe) may be

arranged and constructed to hold, and/or may hold 2, 3, 4, 5, 6, 7, 8, 9, 10 or more doses; in some particular embodiments, it may be designed to hold and/or may hold 5 doses. In some embodiments, a single-dose or multi-dose container (such as a single-dose or multi-dose vial or syringe) may be arranged and constructed to hold and/or may hold a volume or amount greater than the indicated number of doses, e.g., in order to permit some loss in transfer and/or administration. In some embodiments, the temperature-sensitive material may be shipped, stored, and/or utilized, in a preservative-free glass container (e.g., a preservative-free glass vial or syringe, e.g., a single-dose or multi-dose preservative-free glass vial or syringe). In some embodiments, the temperature-sensitive material may be shipped, stored, and/or utilized, in a preservative-free glass container (e.g., a preservative-free glass vial or syringe, e.g., a single-dose or multi-dose preservative-free glass vial or syringe) that contains 0.45 mL of frozen liquid (e.g., including 5 doses). In some embodiments, the temperature-sensitive material and/or a container (e.g., a vial or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature below room temperature, at or below 4°C, at or below 0°C, at or below −20°C, at or below −60°C, at or below −70°C, at or below −80°C , at or below −90°C, etc. In some embodiments, the temperature-sensitive material and/or a container (e.g., a viral or syringe) in which it is disposed, is shipped, stored, and/or utilized may be maintained at a temperature between −80°C and −60°C, or between −90°C and −60°C, or between −90°C and −50°C, or between −80°C and −50°C. In some embodiments, the temperature-sensitive material and/or a container (e.g., a vial or syringe) in which it is disposed is shipped, stored, and/or utilized together with and/or in the context of a thermally protective material or container and/or of a temperature adjusting material. For example, in some embodiments, the temperature-sensitive material and/or a container (e.g., a vial or syringe) in which it is disposed is shipped, stored, and/or utilized together with ice and/or dry ice and/or with an insulating material. In some particular embodiments, a container (e.g., a vial or syringe) in which the temperature-sensitive material is disposed is positioned in a tray or other retaining device and is further contacted with (or otherwise in

the presence of) temperature adjusting (e.g., ice and/or dry ice) material and/or insulating material.

In some embodiments, multiple containers (e.g., multiple vials or syringes such as single use or multi-use vials or syringes as described herein) in which a provided temperature-sensitive material is disposed are co-localized (e.g., in a common tray, rack, box, etc.) and packaged with (or otherwise in the presence of) temperature adjusting (e.g., ice and/or dry ice) material and/or insulating material. To give but one example, in some embodiments, multiple containers (e.g., multiple vials or syringes such as single use or multi-use vials or syringes as described herein) in which the temperature-sensitive material is disposed are positioned in a common tray or rack, and multiple such trays or racks are stacked in a carton that is surrounded by a temperature adjusting material (e.g., dry ice) in a thermal (e.g., insulated) shipper.

In some embodiments, temperature adjusting material is replenished periodically (e.g., within 24 hours of arrival at a site, and/or every 2 hours, 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 14 hours, 16 hours, 18 hours, 20 hours, 22 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, 10 days, etc.). Preferably, re-entry into a thermal shipper should be infrequent, and desirably should not occur more than twice a day. In some embodiments, a thermal shipper is re-closed within 5, 4, 3, 2, or 1 minute, or less, of having been opened. In some embodiments, a provided temperature-sensitive material that has been stored within a thermal shipper for a period of time, optionally within a particular temperature range remains useful. For example, in some embodiments, if a thermal shipper as described herein containing a temperature-sensitive material is or has been maintained (e.g., stored) at a temperature within a range of about 15°C to about 25°C, material may be used for up to 10 days; that is, in some embodiments, a provided temperature-sensitive material that has been maintained within a thermal shipper, which thermal shipper is at a temperature within a range of about 15°C to about 25°C, for a period of not more than 10 days is administered to a subject. Alternatively or additionally, in some embodiments, if a temperature-sensitive material is or

has been maintained (e.g., stored) within a thermal shipper, which thermal shipper has been maintained (e.g., stored) at a temperature within a range of about 15°C to about 25°C, it may be used for up to 10 days; that is, in some embodiments, a provided temperature-sensitive material that has been maintained within a thermal shipper, which thermal shipper has been maintained at a temperature within a range of about 15°C to about 25°C for a period of not more than 10 days is administered to a subject. In some embodiments, a provided temperature-sensitive material is shipped and/or stored in a frozen state. In some embodiments, a frozen temperature-sensitive material is thawed. In some embodiments, a thawed material may be used for up to a small number (e.g., 1, 2, 3, 4, 5, or 6) of days after thawing if maintained (e.g., stored) at a temperature at or below room temperature (e.g., below about 30°C, 25°C, 20°C, 15°C, 10°C, 8°C, 4°C, etc). In some embodiments, a thawed temperature-sensitive material may be used after being stored (e.g., for such small number of days) at a temperature between about 2°C and about 8°C; alternatively or additionally, a material may be used within a small number (e.g., 1, 2, 3, 4, 5, 6) of hours after thawing at room temperature. Thus, in some embodiments, a provided temperature-sensitive material that has been thawed and maintained at a temperature at or below room temperature, and in some embodiments between about 2°C and about 8°C, for not more than 6, 5, 4, 3, 2, or 1 days is administered to a subject. Alternatively or additionally, in some embodiments, a temperature-sensitive material that has been thawed and maintained at room temperature for not more than 6, 5, 4, 3, 2, or 1 hours is administered to a subject.

In some embodiments, a provided temperature-sensitive material is shipped and/or stored in a concentrated state. In some embodiments, such a concentrated composition is diluted prior to administration. In some embodiments, a diluted composition is administered within a period of about 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 hour(s) post-dilution; in some embodiments, such administration is within 6 hours post-dilution. Thus, in some embodiments, diluted preparation of a temperature-sensitive material is administered to a subject within 6 hours post-dilution (e.g., as described herein after having been maintained at an appropriate

temperature, e.g., at a temperature below room temperature, at or below 4°C, at or below 0°C, at or below −20°C, at or below −60°C, at or below −70°C, at or below −80°C, etc, and typically at or above about 2°C, for example between about 2°C and about 8°C or between about 2°C and about 25°C).

In some embodiments, a temperature-sensitive material that is stored, shipped or utilized (e.g., a frozen composition, a liquid concentrated composition, a diluted liquid composition, etc.) may be protected from light. In some embodiments, one or more steps may be taken to reduce or minimize exposure to light for such materials (e.g., which may be disposed within a container such as a vial or a syringe). In some embodiments, exposure to direct sunlight and/or to ultraviolent light is avoided. In some embodiments, a diluted solution may be handled and/or utilized under normal room light conditions (e.g., without particular steps taken to minimize or reduce exposure to room light). It should be understood that strict adherence to aseptic techniques is desirable during handling (e.g., diluting and/or administration) of the materials as described herein.

Certain exemplary embodiments:

1. A method of immunizing against SARS-CoV-2, the method comprising steps of:

administering a composition comprising a lipid nanoparticle encapsulated mRNA that encodes at least an epitope of a SARS-CoV-2-encoded polypeptide, according to a regimen established to achieve detectable antibody titer against the epitope in serum within 7 days, which regimen comprises administration of at least one dose of the composition.

2. The method of embodiment 1, wherein the regimen comprises administration of at least two doses of the composition.

3. The method of embodiment 1, wherein the regimen consists of administration of two doses of the composition.

4. The method of embodiment 2 or embodiment 3, wherein the first dose is a different amount that one or more subsequent doses.

5. The method of embodiment 1 or embodiment 4, wherein the first dose is administered a period of time before the subsequent dose, which period of time is at least 1 week, 1 month, 2 months, 3 months, 6 months, 1 year, 2 years, 3 years or more.

6. The method of any one of embodiments 1-6, wherein the regimen has been established to have an incidence of adverse events below 60% when administered to a relevant population of adults.7. The method of embodiment 6, wherein the regimen has been established not to elicit local injection site reactions above moderate severity with an incidence greater than about 1 in 75.

8. The method of any one of embodiments 1-7, wherein each dose is no more than 60 ug or lower, including, e.g., no more than 50 ug, no more than 40 ug, no more than 30 ug, no more than 20 ug, no more than 10 ug, no more than 5 ug, no more than 2.5 ug, no more than 1 ug.

9. The method of any one of embodiments 1-8, wherein each dose is at least 1 ug or higher, including, e.g., at least 2 ug, at least 5 ug, at least 10 ug, at least 20 ug, at least 30 ug, at least 40 ug, or more.

10. A method comprising administering to a subject a composition comprising a lipid nanoparticle encapsulated mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition is administered in an effective amount to induce in the subject a SARS-COV-2 S-protein specific immune response, wherein the effective amount is sufficient to provide sterilizing immunity in the subject at an at least 2-fold (including, e.g., at least 3-fold, at least 4-fold, at least 5-fold) lower dose relative to a reference composition (e.g., a reference RNA vaccine or composition).

11. A method comprising administering to a subject a composition comprising a lipid nanoparticle encapsulated mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition is administered in an effective amount to reduce viral load in the subject by at least 80%, relative to a control, at 2 days or more (including, e.g., 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9

days, or more) following exposure to SARS-COV2, wherein the control is the viral load in a subject administered a reference composition (e.g., a reference RNA vaccine or composition).

12. A method comprising administering to a subject a composition comprising a lipid nanoparticle encapsulated mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition is administered in an effective amount to induce in the subject a SARS-COV-2 S-protein specific immune response, wherein efficacy of the RNA vaccine is at least 80% relative to unvaccinated control subjects.

13. The method of any one of embodiments 10-12, wherein the effective amount is sufficient to produce detectable levels of SARS-COV-2 S protein or a fragment thereof as measured in serum of the subject at 1-72 hours post administration.

14. The method of any one of embodiments 10-12, wherein the effective amount is sufficient to produce a 1,000-10,000 neutralization titer produced by neutralizing antibody against the SARS-COV-2 S protein as measured in serum of the subject at 1-72 hours post administration.

15. The method of any one of embodiments 10-14, wherein an anti-SARS-COV-2 S protein antibody titer produced in the subject is increased by at least 1 log relative to a control, wherein the control is an anti-SARS-COV-2 S protein antibody titer produced in a subject who has not been administered a vaccine against SARS-COV-2.

16. The method of any one of embodiments 10-15, wherein the anti-SARS-COV-2 S protein antibody titer produced in the subject is increased at least 2 times relative to a control, wherein the control is an anti-SARS-COV-2 S protein antibody titer produced in a subject who has not been administered a vaccine against SARS-COV-2.

17. The method of any one of embodiments 1-16, wherein the administering is performed by intramuscular injection.

18. An immunogenic composition comprising a lipid nanoparticle encapsulated RNA (e.g., mRNA) that encodes at least an epitope of a SARS-CoV-2-encoded polypeptide, which vaccine composition has been established to achieve detectable antibody titer against the epitope in

serum within 7 days after administration to a population of adult human subjects according to a regimen that includes administration of at least one dose of the vaccine composition.

19. The immunogenic composition of embodiment 18, wherein at least 80% of the uridines in the RNA have a chemical modification.

20. The immunogenic composition of embodiment 18 or 19, wherein 100% of the uridines in the RNA have a chemical modification.

21. The immunogenic composition of any one of embodiments 18-20, wherein the 5' terminal cap is 7mG(5')ppp(5')NlmpNp.

22. The immunogenic composition of any one of embodiments 18-21, wherein the lipid nanoparticles in the composition comprise a cationic lipid, a PEG-modified lipid, a sterol and a non-cationic lipid.

23. The immunogenic composition of any one of embodiments 18-22, wherein lipid nanoparticles in the composition comprise a molar ratio of about 20-60% cationic lipid, 0.5-15% PEG-modified lipid, 25-55% sterol, and 5-25% non-cationic lipid.

24. The immunogenic composition of embodiment 22 or 23, wherein the cationic lipid is an ionizable cationic lipid, the non-cationic lipid is a neutral lipid, and the sterol is a cholesterol.

25. The immunogenic composition of any one of embodiments 22 or 23, wherein the cationic lipid is selected from the group consisting of 2,2-dilinoleyl-4-dimethylaminoethyl-[1,3]-dioxolane (DLin-KC2-DMA), dilinoleyl-methyl-4-dimethylaminobutyrate (DLin-MC3-DMA), and di((Z)-non-2-en-1-yl) 9-((4-(dimethylamino)butanoyl)oxy)heptadecanedioate.

26. The immunogenic composition of any one of embodiments 18-25, wherein the RNA comprises a 5' terminal cap and a chemical modification, and the RNA is formulated or is to be formulated as an lipid nanoparticle.

27. The immunogenic composition of any one of embodiments 18-26, wherein the SARS-CoV-2 S protein, an immunogenic variant thereof, or an immunogenic fragment of the SARS-CoV-2 S protein or the immunogenic variant thereof is linked to a signal peptide.

28. The immunogenic composition of embodiment 27, wherein the signal peptide is selected from the group consisting of: a HuIgGk signal peptide (METPAQLLFLLLLWLPDTTG); an IgE heavy chain epsilon-1signal peptide (MDWTWILFLVAAATRVHS); a Japanese encephalitis PRM signal sequence (MLGSNSGQRVVFTILLLLVAPAYS) and a VSVg protein signal sequence (MKCLLYLAFLFIGVNCA).

29. A method for eliciting an immune response in a subject by activating T cells in vivo, comprising administering to the subject a composition comprising a lipid nanoparticle encapsulated modified nucleoside mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, thereby activating T cells in vivo against infection by SARS-COV2 in the subject.

30. A method for eliciting an immune response against SARS-COV-2 in a subject, comprising administering to the subject a composition comprising a lipid nanoparticle encapsulated modified nucleoside mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition elicits an increased production of the SARS-COV2 polypeptide or fragment thereof production, as compared to a composition comprising a corresponding unmodified mRNA.

31. A method for eliciting an immune response against SARS-COV-2 in a subject, comprising administering to the subject a composition comprising a lipid nanoparticle encapsulated modified nucleoside mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition elicits increased antibody titers, as compared to a composition comprising a corresponding unmodified mRNA.

32. A method for eliciting an immune response against SARS-COV-2 in a subject, comprising administering at least one dose to the subject a composition comprising a lipid nanoparticle encapsulated modified nucleoside mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition elicits increased antibody titers in the subject at least 7 days after the first dose, as compared to the antibody titers against SARS-COV-2 prior to administration of the composition.

33. A method for eliciting an immune response against SARS-COV-2 in a subject, comprising administering at least one dose to the subject a composition comprising a lipid nanoparticle encapsulated modified nucleoside mRNA, wherein the mRNA encodes an amino acid sequence comprising SARS-COV2 S protein or a fragment thereof, wherein the composition elicits increased antibody titers in the subject at least 7 days after the first dose, as compared to a composition comprising a corresponding unmodified mRNA.

34. The method according to any one of embodiments 29-33, wherein the mRNA is present at a purity of 90% or greater.

35. The method according to any one of embodiments 29-34, wherein the composition does not further comprise a unmodified RNA encoding SARS-COV2 S protein or a fragment thereof.

36. The method according to any one of embodiments 29-35, wherein the composition is administered at least 2 times, the first and second administrations being at least 7 days apart.

37. The method according to any one of embodiments 29-36, wherein the subject is at risk for a SARS-CoV-2 infection.

38. The method according to any one of embodiments 29-37, wherein the subject is undergoing treatment for cardiovascular disease.

39. The method according to any one of embodiments 29-37, wherein the subject is undergoing treatment for diabetes.

40. The method according to any one of embodiments 29-37, wherein the subject is undergoing treatment for chronic cardiopulmonary disease.

41. The method according to any one of embodiments 29-37, wherein the subject is undergoing treatment for chronic renal disease.

42. The method according to any one of embodiments 29-41, wherein the immune response is sustained for at least about 30 days.

43. The method according to any one of embodiments 29-42, wherein the immune response is sustained for at least about 60 days.

44. The method according to any one of embodiments 29-43, wherein the immune response is sustained for at least about 180 days.

45. The method according to any one of embodiments 29-44, wherein the immune response comprises virus neutralizing titer.

46. The method according to any one of embodiments 29-45, wherein the subject is at least 18 years of age.

47. The method according to any one of embodiments 29-46, wherein the dose comprises 100 ug or less of mRNA.

48. The method according to any one of embodiments 29-47, wherein the dose comprises less than 100 ug of mRNA and the composition elicits an immune response that is greater than the immune response elicited by a composition comprising at least 100 ug of mRNA.

49. The method according to any one of embodiments 29-48, wherein the dose comprises about 30 ug of mRNA.

50. The method according to any one of embodiments 29-49, wherein the immune response comprises antibodies against the receptor binding domain of the S protein of SARS-CoV-2.

51. The method according to any one of embodiments 29-50, wherein the immune response comprises RBD-binding IgG.

52. The method according to any one of embodiments 29-50, wherein the SARS-CoV-2 S protein or a fragment thereof comprises a receptor binding domain.

53. A kit comprising a) a composition comprising a lipid nanoparticle encapsulated mRNA; and b) a temperature monitoring system.

54. The kit according to embodiment 53, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein when the temperature monitoring system displays or warns when the temperature of the composition attains a temperature above about −80° C.

55. The kit according to embodiment 53, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein when the temperature monitoring

system displays or warns when the temperature of the composition attains a temperature above about −60° C.

56. A kit comprising a) a composition comprising a lipid nanoparticle encapsulated mRNA; and b) a light sensor.

57. The kit according to embodiment 56, wherein the light sensor comprises a photosensitive element configured to react to exposure to light, resulting in a change in a material property of the photosensitive element.

58. The method according to any one of embodiments 29-35, wherein the composition is administered at least 2 times, the first and second administrations being at least 14 days apart.

59. The method according to any one of embodiments 29-35, wherein the composition is administered at least 2 times, the first and second administrations being at least 21 days apart.

60. The method according to any one of embodiments 29-48, wherein the dose comprises about 10 ug of mRNA.

61. The method according to any one of embodiments 29-35, wherein the composition is administered at least 2 times, the first and second administrations being at least 28 days apart.

62. The method according to any one of embodiments 29-35, wherein the mRNA encodes any one of the amino acid sequences SEQ ID NO: 3, SEQ ID NO: 5, and SEQ ID NO: 7.

63. An immunogenic composition comprising a messenger ribonucleic acid (mRNA) polynucleotide comprising an open reading frame encoding a polypeptide that comprises a receptor-binding portion of a SARs-CoV-2 S protein formulated in at least one lipid nanoparticle comprising a cationic lipid, in an effective amount to induce an immune response in a subject administered at least one dose of the immunogenic composition, wherein the isolated mRNA polynucleotide is not self-replicating RNA.

64. The immunogenic composition of embodiment 63, wherein the lipid nanoparticle further comprises any one of a non-cationic lipid, sterol, and PEG-modified lipid.

65. The immunogenic composition of embodiment 63, comprising

an isolated messenger ribonucleic acid (mRNA) polynucleotide comprising an open reading frame encoding a polypeptide that comprises a receptor-binding portion of a SARs-CoV-2 S protein; formulated in at least one lipid nanoparticle that comprises a molar ratio of 20-60% ionizable cationic lipid, 5-25% non-cationic lipid, 25-55% sterol, and 0.5-15% PEG-modified lipid, in an effective amount to induce an immune response in a subject administered at least one dose of the immunogenic composition, wherein the isolated mRNA polynucleotide is not self-replicating RNA.

66. The immunogenic composition of embodiment 63, wherein the polypeptide does not comprise the complete S protein.

67. The immunogenic composition of embodiment 63, wherein the polypeptide comprises the receptor binding domain (RBD) of a SARs-CoV-2 S protein.

68. The immunogenic composition of embodiment 63, wherein the polypeptide comprises SEQ ID NO: 5.

69. The immunogenic composition of embodiment 63, wherein the polypeptide comprises SEQ ID NO: 29 or 31.

70. The immunogenic composition of embodiment 63, wherein the polypeptide comprises SEQ ID NO: 3.

71. The immunogenic composition of embodiment 63, wherein the polypeptide comprises SEQ ID NO: 7.

72. The immunogenic composition of any one of embodiments 63-71, wherein the isolated mRNA polynucleotide further comprises a 5' terminal cap, 7mG(5')ppp(5')NlmpNp.

73. The immunogenic composition of any one of embodiments 63-72, wherein at least 80% of the uracil in the open reading frame have a chemical modification selected from N1-methyl-pseudouridine or N1-ethyl-pseudouridine.

74. The immunogenic composition of any one of embodiments 63-73, wherein the chemical modification is in the 5-position of the uracil.

75. The immunogenic composition of any one of embodiments 63-74, wherein the efficacy of the immunogenic composition in vaccinated subjects is at least 60%, relative to unvaccinated subjects, following a single dose of the immunogenic composition.

76. The immunogenic composition of embodiment 75, wherein the efficacy of the immunogenic composition in vaccinated subjects is at least 70%, relative to unvaccinated subjects, following a single dose of the immunogenic composition.

77. The immunogenic composition of embodiment 75, wherein the efficacy of the immunogenic composition in vaccinated subjects is at least 80%, relative to unvaccinated subjects, following a single dose of the immunogenic composition.

78. The immunogenic composition of embodiment 75, wherein the efficacy of the immunogenic composition in vaccinated subjects is at least 90%, relative to unvaccinated subjects, following a single dose of the immunogenic composition.

79. The immunogenic composition of any one of embodiments 63-78, wherein the effective amount is sufficient to produce detectable levels of a polypeptide that comprises a receptor-binding portion of a SARS-CoV-2 S protein as measured in serum of a subject vaccinated with at least one dose of the immunogenic composition at 1-72 hours post administration.

80. The immunogenic composition of any one of embodiments 63-79, wherein the effective amount is sufficient to produce a 1,000-10,000 neutralization titer produced by neutralizing antibody against the antigenic polypeptide that comprises a receptor-binding portion of a SARS-CoV-2 S protein as measured in serum of a subject vaccinated with at least one dose of the immunogenic composition at 1-72 hours post administration.

81. The immunogenic composition of embodiment 80, wherein the 1,000-10,000 neutralization titer is produced in the absence of antibody-dependent enhancement (ADE) of a SARS-CoV-2-associated disease.

82. The immunogenic composition of any one of embodiments 63-81, wherein the effective amount does not induce the immunogenic composition-associated enhanced respiratory disease (ERD).

83. The immunogenic composition of any one of embodiments 63-82, wherein the effective amount reduces the amount of SARS-CoV-2 viral RNA in a lung of the subject after infection with a SARS-CoV-2 virus, as compared to the amount of SARS-CoV-2 viral RNA in a lung of an unvaccinated subject after infection with a SARS-CoV-2 virus.

84. The immunogenic composition of any one of embodiments 63-82, wherein the effective amount reduces the amount of SARS-CoV-2 viral RNA in a lung of the subject at least 3 days after infection with a SARS-CoV-2 virus, as compared to the amount of SARS-CoV-2 viral RNA in a lung of the subject 3 days after infection with a SARS-CoV-2 virus.

85. The immunogenic composition of any one of embodiments 63-82, wherein the effective amount reduces the amount of SARS-CoV-2 viral RNA in a nasal swab sample of the subject after infection with a SARS-CoV-2 virus, as compared to the amount of SARS-CoV-2 viral RNA in a nasal swab sample of an unvaccinated subject after infection with a SARS-CoV-2 virus.

86. The immunogenic composition of any one of embodiments 63-82, wherein the effective amount does not increase the amount of SARS-CoV-2 viral RNA in a nasal swab sample of the subject 3 days after infection with a SARS-CoV-2 virus, as compared to the amount of SARS-CoV-2 viral RNA in a nasal swab sample of the subject 1 day after infection with a SARS-CoV-2 virus.

87. The immunogenic composition of any one of embodiments 63-87, wherein an anti-SARS-CoV-2 antibody titer produced in a subject vaccinated with at least one dose of the immunogenic composition is increased by at least 1 log relative to a control, wherein the control is an anti-SARS-CoV-2 antibody titer produced in a subject who has not been administered an immunogenic composition against SARS-CoV-2.

88. The immunogenic composition of any one of embodiments 63-87, wherein an anti-SARS-CoV-2 antibody titer produced in a subject vaccinated with at least one dose of the immunogenic composition is increased at least 2 times relative to a control, wherein the control is an anti-SARS-CoV-2 antibody titer produced in a subject who has not been administered an immunogenic composition against SARS-CoV-2.

89. The immunogenic composition of any one of embodiments 63-88, wherein the effective amount is a total dose of 2 μg-100 μg.

90. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 100 μg.

91. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 20 μg-50 μg.

92. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 10 μg-30 μg.

93. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 10 μg.

94. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 20 μg.

95. The immunogenic composition of embodiment 89, wherein the effective amount is a total dose of 30 μg.

96. The immunogenic composition of any one of embodiments 63-95, wherein the composition is formulated in a single-dose vial.

97. The immunogenic composition of any one of embodiments 63-95, wherein the composition is formulated in a multi-dose vial.

98. The immunogenic composition of any one of embodiments 63-97, wherein intramuscular administration of the effective amount of the immunogenic composition to a subject induces a neutralizing antibody titer in a subject.

99. The immunogenic composition of embodiment 98, wherein the neutralizing antibody titer is sufficient to reduce viral infection of B cells by at least 50% relative to a neutralizing antibody titer of an unvaccinated control subject or relative to a neutralizing antibody titer of a subject vaccinated with a live attenuated viral vaccine, an inactivated viral vaccine, or a protein subunit viral vaccine.

100. The immunogenic composition of embodiment 98 or 99, wherein the neutralizing antibody titer is induced in the subject following fewer than three doses of the immunogenic composition.

101. The immunogenic composition of any one of embodiments 98-100, wherein the neutralizing antibody titer and/or a T cell immune response is sufficient to reduce the rate of asymptomatic viral infection relative to the neutralizing antibody titer of unvaccinated control subjects.

102. The immunogenic composition of any one of embodiments 98-101, wherein the neutralizing antibody titer and/or a T cell immune response is sufficient to prevent viral latency in the subject.

103. The immunogenic composition of any one of embodiments 98-102, wherein the neutralizing antibody titer is sufficient to block fusion of virus with epithelial cells and/or B cells of the subject.

104. The immunogenic composition of any one of embodiments 63-103, wherein intramuscular administration of the effective amount of the immunogenic composition to a subject induces a T cell immune response in the subject.

105. The immunogenic composition of embodiment 104, wherein the T cell immune response comprises a $CD4^+$ T cell immune response and/or a $CD8^+$ T cell immune response.

106. The immunogenic composition of any one of embodiments 63-105, wherein the encoded polypeptide is presented on the surface of cells of the subject.

107. A method comprising administering to a subject an immunogenic composition of any one of embodiments 63-106, wherein the immunogenic composition is administered to the subject in an effective amount to induce an immune response in the subject.

108. The method of embodiment 107, wherein the immune response is induced against a SARs-CoV-2 virus having a mutation in the RBD, as compared to SEQ ID NO: 5.

109. The method of embodiment 107, wherein the immune response is induced against a SARs-CoV-2 virus having a mutation in the spike protein, as compared to SEQ ID NO: 1.

110. The method of embodiment 108 or 109, wherein the immune response is induced against a SARs-CoV-2 virus having any one of the following mutations in the RBD: Q321L, V341I, A348T, N354D, S359N, V367F, K378R, R408I, Q409E, A435S, N439K, K458R, I472V, G476S, S477N, V483A, Y508H, and H519P, as compared to SEQ ID NO: 1.

111. The method of embodiment 109, wherein the immune response is induced against a SARs-CoV-2 virus having a D614G mutation in the spike protein, as compared to SEQ ID NO: 1.

112. The method of embodiment 107, wherein the immunogenic composition is administered to the subject annually.

113. An RNA, optionally complexed by a (poly)cationic polymer, polyplex(es), protein(s) or peptide(s), which RNA: (a) comprises an open reading frame encoding a polypeptide that comprises a receptor-binding-portion of a SARS-CoV-2 S protein; and (b) is suitable for intracellular expression of the polypeptide.

114. The RNA of embodiment 113, wherein the polypeptide does not comprise the complete S protein.

115. The RNA of embodiment 113 or 114, wherein the RNA further comprises a 5′ terminal cap, 7mG(5′)ppp(5′)NlmpNp.

116. The RNA of any one of embodiments 113-115, wherein at least 80% of the uracil in the open reading frame have a chemical modification selected from N1-methyl-pseudouridine or N1-ethyl-pseudouridine.

117. The RNA of any one of embodiments 113-116, wherein the chemical modification is in the 5-position of the uracil.

118. The RNA of any one of embodiments 113-117 for use in inducing an immune response in humans or vaccinating humans.

119. The RNA for use of embodiment 118, wherein the humans comprise humans known to have been exposed to SARS-CoV-2.

120. The RNA for use of embodiment 118, wherein the humans comprise humans known to have been infected by SARS-CoV-2.

121. The RNA for use of embodiment 118, wherein the humans comprise humans not known to have been exposed to SARS-CoV-2.

122. Use of the RNA of any one of embodiments 113-117 for vaccinating humans.

123. The use of embodiment 122, wherein the humans comprise humans known to have been exposed to SARS-CoV-2.

124. The use of embodiment 122, wherein the humans comprise humans known to have been infected by SARS-CoV-2.

125. The use of embodiment 122, wherein the humans comprise humans not known to have been exposed to SARS-CoV-2.

126. A single-dose formulation comprising the immunogenic composition of any one of embodiments 63-106.

127. A multi-dose formulation comprising the immunogenic composition of any one of embodiments 63-106 in one vial.

128. The formulation according to embodiment 126, comprising at least 2 doses per vial.

129. The formulation according to embodiment 126, comprising a total of 2-12 doses per vial.

130. The formulation according to any one of embodiments 126-129, wherein each dose is equal in volume.

131. The formulation according to any one of embodiments 126-130, wherein each formulation comprises a total volume of 1-3 mL in the vial.

132. The formulation according to any one of embodiments 126-131, wherein the immunogenic composition is frozen.

133. A pre-filled vaccine delivery device comprising the immunogenic composition of any one of embodiments 63-106.

134. According to one aspect of the present disclosure, there is provided a kit comprising: a) a primary container; b) a payload container; c) at least one tray for placement within the payload container, wherein the at least one tray contains a temperature-sensitive material; and d) a dry ice container; wherein the at least one tray has dimensions A x B x H, where A is

about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

135. The kit according to embodiment 134, wherein the payload container has the dimensions of about 229 mm x 229 mm x 229 mm.

136. The kit according to embodiment 134, wherein the kit is capable of maintaining the temperature of the material within the tray at −50°C or lower for at least 10 days.

137. The kit according to embodiment 136, wherein the kit is capable of maintaining the temperature of the material within the tray at −70°C or lower for at least 10 days.

138. The kit according to embodiment 136, wherein the kit is capable of maintaining the temperature of the material within the tray at −80°C for at least 10 days.

139. The kit according to embodiment 134, further comprising a temperature monitoring system.

140. The kit according to embodiment 139 wherein the temperature monitoring system comprises a temperature sensor and a display, wherein the temperature monitoring system displays or warns when the temperature of the material attains a temperature greater than about −80° C.

141. The kit according to embodiment 134, wherein the payload container is placed at the bottom of the primary container, and further wherein the dry ice container is placed on top of the payload container.

142. The kit according to embodiment 141, wherein the at least one tray is placed inside the payload container.

143. The kit according to embodiment 142, wherein there are 1, 2, 3, 4, or 5 trays within the payload container.

144. The kit according to embodiment 134, wherein the temperature-sensitive material is contained within at least one glass vial, and wherein the at least one glass vial is placed within the tray.

145. The kit according to embodiment 144, where the at least one glass vial is a multi-dose vial.

146. The kit according to embodiment 144, wherein each tray contains at least 25 vials.

147. The kit according to embodiment 146, wherein each tray contains at least 50 vials.

148. The kit according to embodiment 147, wherein each tray contains at least 75 vials.

149. The kit according to embodiment 148, wherein each tray contains at least 125 vials.

150. The kit according to embodiment 149, wherein each tray contains at least 150 vials.

151. The kit according to embodiment 150, wherein each tray contains at least 195 vials.

152. A container system comprising: a) a primary container; b) a payload container; c) at least one tray for placement within the payload container, wherein the at least one tray contains a temperature-sensitive material; and d) a dry ice container; wherein the at least one tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

153. The container system according to embodiment 152, wherein the payload container has the dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 228 to about 233 mm.

154. The container system according to embodiment 153, wherein the payload container has the dimensions of about 229 mm x 229 mm x 229 mm.

155. The container system according to embodiment 152, wherein the system is capable of maintaining the temperature of the material within the tray at −50°C or lower for at least 10 days.

156. The container system according to embodiment 155, wherein the system is capable of maintaining the temperature of the material within the tray at −70°C or lower for at least 10 days.

157. The container system according to embodiment 156, wherein the system is capable of maintaining the temperature of the material within the tray at −80°C or lower for at least 10 days.

158. The container system according to embodiment 152, wherein the payload container is placed at the bottom of the primary container, and further wherein the dry ice container is placed on top of the payload container.

159. The container system according to embodiment 158, wherein the at least one tray is placed inside the payload container.

160. The container system according to embodiment 159, wherein there are 1, 2, 3, 4, or 5 trays within the payload container.

161. The container system according to embodiment 160, wherein the temperature-sensitive material is contained within at least one glass vial, and wherein the at least one glass vial is placed within the tray.

162. The container system according to embodiment 161, wherein the at least one glass vial is a multi-dose vial.

163. The container system according to embodiment 162, wherein each tray contains at least 25 vials.

164. The container system according to embodiment 163, wherein each tray contains at least 195 vials.

165. A method of transporting a temperature-sensitive material comprising the steps of: a) placing the material in a kit according to embodiment 134, or in a container system according to embodiment 152; and b) transporting the kit or container system to an intended destination.

166. The method according to embodiment 165, wherein the temperature inside the payload container is continuously monitored throughout the duration of the transportation.

167. The method according to embodiment 166, where the transportation is carried out on land, air, and/or water.

168. The method according to embodiment 166, where the transportation is carried out via land vehicle, airplane, and/or boat.

169. The method according to embodiment 165, wherein the temperature inside the payload container is maintained at −70°C or lower throughout the duration of the transportation.

170. The method according to embodiment 169, wherein the temperature inside the payload container is maintained at −80°C or lower throughout the duration of the transportation.

171. The method according to embodiment 165, wherein there are at least 150 vials in each tray.

172. The method according to embodiment 171, wherein there are 195 vials in each tray.

173. The method according to embodiment 172, wherein there are at least 5 trays within the payload container.

174. The method according to embodiment 165, wherein the location of the kit or container system is periodically monitored through use of a global positioning system (GPS).

175. A payload container having dimensions of about 229 mm x 229 mm x 229 mm, wherein at least five trays are placed within the payload container, and wherein each tray contains at least 100 vials of temperature-sensitive material.

176. The payload container according to embodiment 175, wherein each tray contains at least 150 vials of temperature-sensitive material.

177. The payload container according to embodiment 176, wherein each tray contains 195 vials of temperature-sensitive material.

178. A tray for carrying temperature-sensitive material, wherein the tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

179. The tray according to embodiment 178, wherein at least 150 vials are placed within the tray.

180. The tray according to embodiment 179, wherein 195 vials are placed within the tray.

Citation of documents and studies referenced herein is not intended as an admission that any of the foregoing is pertinent prior art. All statements as to the contents of these documents

are based on the information available to the applicants and do not constitute any admission as to the correctness of the contents of these documents.

The following description is presented to enable a person of ordinary skill in the art to make and use the various embodiments. Descriptions of specific devices, techniques, and applications are provided only as examples. Various modifications to the examples described herein will be readily apparent to those of ordinary skill in the art, and the general principles defined herein may be applied to other examples and applications without departing from the spirit and scope of the various embodiments. Thus, the various embodiments are not intended to be limited to the examples described herein and shown, but are to be accorded the scope consistent with the claims.

Examples

Example 1: *In vivo* immunogenicity using Influenza Hemagglutinin (HA) as a model antigen

The potency of the RNA platforms to be used for the coronavirus vaccine described herein has been tested by performing extensive immunogenicity and virus challenge studies using Influenza HA as a model antigen. The studies investigated the induction of antibody responses determined with antigen specific enzyme-linked immunosorbent assay (ELISA) test and functional studies applying virus-neutralization (VNT) assays.One study evaluated the potency of the LNP formulation using a modRNA-LNP vaccine that encodes Influenza HA. Mice were injected IM with 1 µg on days 0 ad 28 with an LNP-formulated Influenza HA modRNA. On days 14, 28 and 49 blood samples were taken, and tested for immunogenicity. The analysis showed a high antibody immune response, resulting in very high titers of antigen-specific IgG in serum and high viral-neutralization activity (Figure 3). Moreover, strong Th1 CD4 and CD8 T cell responses (Figure 4) were induced by the modRNA vaccine.

Example 2: Immunogenicity studies for Coronavirus vaccine candidates

Primary pharmacodynamics studies were performed in BALB/c mice to test the immunogenicity of the vaccine candidates shown in the following table.

Table 2: Vaccine candidates

Vaccine	mRNA type	Vaccine encoded antigen
BNT162a1	uRNA	RBD (Receptor Binding Domain) of SARS-CoV-2 Spike protein (S protein)
BNT162b1	modRNA	RBD (Receptor Binding Domain) of SARS-CoV-2 Spike protein (S protein)
BNT162b2	modRNA	Modified version of SARS-CoV-2 Spike protein (S protein)

BNT162c1	saRNA	RBD (Receptor Binding Domain) of SARS-CoV-2 Spike protein (S protein)

Thus, as can be seen, embodiments of multiple formats were assessed in parallel. This described approach and system achieved remarkable and efficient success, enabling development of an effective clinical candidate within several months of provision of antigen (e.g., SARS-CoV-2 S1 protein and/or RBD thereof) sequence (as described herein, relevant sequence information (e.g., GenBank: MN908947.3) became available in Jan 2020)

In the study, four groups of each eight female BALB/c mice were immunized once with the animal trial material at three different doses, or with buffer (control group; see Table 3). While the clinical trial material will be diluted in saline, the animal trial material was diluted in PBS including 300mM sucrose. As this is the storage buffer of the material itself, the test items are representative for the vaccine that will be used in the planned clinical trials. Immunizations were given IM using a dose volume of 20 µL.

Table 3: Study design

Group No	No of animals	Vaccine dose	Immunization Day	Dose volume [µL] / route	Blood collection Day	End of in-life phase
1	8	buffer	0	20 / IM	7, 14, 21	28
2	8	Low	0	20 / IM	7, 14, 21	28
3	8	Medium	0	20 / IM	7, 14, 21	28
4	8	High	0	20 / IM	7, 14, 21	28

Blood of immunized animals was collected on days 7, 14, 21 and 28, and analyzed for the antibody immune response by ELISA and pseudovirus-based neutralization assay (pVNT).

SARS-CoV-2-S specific antibody responses directed against the recombinant S1 subunit or the RBD were detected by ELISA. In brief, high protein-binding 96-well plates (MaxiSorp ELISA plates, VWR International GmbH, Cat. No. 7341284) were coated with 100 ng recombinant S1

subunit (Sino Biological Inc., Cat. No. 40591-V08H) or RBD (Sino Biological Inc., Cat. No. 40592-V02H) per well in 100 µL coating buffer (50 mM sodium carbonate-bicarbonate buffer, pH9.6) overnight at 4 °C. Plates were washed three times with 300 µL/well 1x phosphate-buffered saline (PBS, VWR International GmbH, Cat. No. 0780-10L) supplemented with 0.01% Tween 20 (Carl Roth GmbH & Co. KG, Cat. No. 9127.1) and blocked with 250 µL/well 1x Casein Blocking Buffer (Sigma-Aldrich GmbH, Cat No. B6429-500ml) for 1 hour at 37°C on a microplate shaker. Plates were again washed three times with 300 µL/well 1x PBS supplemented with 0.01% Tween 20 and incubated with mouse serum samples diluted in 1x Casein Blocking Buffer for 1 hour at 37°C on a microplate shaker. Plates were washed three times with 300 µL/well 1x PBS supplemented with 0.01% Tween 20 and subsequently incubated with Peroxidase-conjugated goat anti-mouse secondary antibody (Jackson ImmunoResearch Ltd., Cat. No. 115-036-071; diluted 1:7500 in 1x Casein Blocking Buffer) for 45 minutes at 37°C on a microplate shaker. Plates were washed three times with 300 µL/well 1x PBS supplemented with 0.01% Tween 20 and 100 µL/well TMB substrate (Biotrend Chemiekalien GmbH, Cat. No. 4380A) was added. Plates were incubated for 8 min at room temperature and the reaction stopped by addition of 100 µL 25% sulphuric acid (VWR International GmbH, Cat. No. 1007161000). Plates were read on a microplate reader and the recorded absorbance at 450 nm corrected by subtracting the reference absorbance at 620 nM.

Functional antibody responses to the vaccine candidates were detected by pVNT. The pVNT uses a replication-deficient vesicular stomatitis virus (VSV) that lacks the genetic information for the VSV envelope glycoprotein G but contains an open-reading frame (ORF) for green fluorescent protein (GFP). VSV/SARS-CoV-2 pseudovirus was generated according to a published protocol (Hoffmann et al., Cell, 2020; PMID 32142651). The pseudotype virus bears the SARS-CoV-2 S protein, which mediates cell entry. Therefore, the pseudovirus can be inactivated by neutralizing antibodies that bind SARS-CoV-2 S. This inactivation can be analyzed via *in vitro* methods.

In brief, $4x10^4$ Vero 76 cells (ATCC® CRL-1587™) per well were seeded in a 96-well plate (Greiner Bio-One GmbH, Cat. No. 655160) in 150 µL/well DMEM (Thermo Fisher Scientific, Cat. No. 61965059) supplemented with 10% fetal bovine serum (FBS, Sigma-Aldrich GmbH, Cat. No. F7524). Cells were incubated for 4 to 6 hours at 37°C and 7.5% CO_2. Meanwhile, mouse serum samples were diluted 1:6 up to 1:768 in DMEM/10% FBS in two-fold dilution steps. Diluted serum samples were combined with an equal volume of titrated and pre-diluted VSV/SARS CoV-2 pseudovirus supernatant, resulting in a serum dilution ranging from 1:12 up to 1:1536. The pseudovirus/serum dilution mix was incubated for 5 min at RT on a microplate shaker at 750 rpm with an additional 5 min incubation at RT without agitation. 50 µL/well pseudovirus/serum dilution mix was added to the seeded Vero-76 cells with the applied pseudovirus volume per well corresponding to 200 infectious units (IU). Each dilution of serum samples was tested in duplicate wells. Cells were incubated for 16 to 24 hours at 37°C and 7.5% CO_2. Vero 76 cells incubated with pseudovirus in the absence of mouse sera were used as positive controls. Vero 76 cells incubated without pseudovirus were used as negative controls. After the incubation, the cell culture plates were removed from the incubator, placed in an IncuCyte Live Cell Analysis system (Essen Bioscience) and incubated for 30 min prior to the analysis. Whole well scanning for brightfield and GFP fluorescence was performed using a 4× objective. To calculate the neutralizing titer, infected GFP-positive cell number per well was compared with the pseudovirus positive control. Mean values of the pseudovirus positive control multiplied by 0.5 represent the pseudovirus neutralization 50% (pVN50). Serum samples with mean values below this cut-off exhibit >50% virus neutralization activity, respectively.

Immunogenicity study of BNT162a1 (RBL063.3)

To dissect the potency of the LNP-formulated uRNA vaccine coding for BNT162a1, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine will be investigated by focusing on the antibody immune response.

ELISA data 7, 14, 21 and 28 d after the first immunization show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 5).

Immunogenicity study of BNT162b1 (RBP020.3)

To dissect the potency of the LNP-formulated modRNA vaccine coding for BNT162b1, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine will be investigated by focusing on the antibody immune response.

ELISA data 7, 14, 21 and 28 d after the first immunization show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 6). Sera obtained 14, 21, and 28 d after immunization show high SARS-CoV-2 pseudovirus neutralization, especially sera from mice immunized with 1 or 5 µg BNT162b1 and correlating with the strong increase of IgG antibody titers (Figure 7).

Immunogenicity study of BNT162c1 (RBS004.3)

To dissect the potency of the LNP-formulated saRNA vaccine coding for BNT162c1, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine will be investigated by focusing on the antibody immune response.

ELISA data 7, 14 and 21 d after the first immunization show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 8). Sera obtained 14, and 21 d after immunization show dose-dependent SARS-CoV-2 pseudovirus neutralization activity (Figure 9).

Immunogenicity study of LNP-formulated uRNA encoding the viral S protein-V8 (SEQ ID NO: 7, 8) (RBL063.1)

To dissect the potency of the LNP-formulated uRNA vaccine coding for the viral S protein-V8 (RBL063.1), BALB/c mice were immunized IM once as outlined inTable 3. The immunogenicity of the RNA vaccine will be investigated by focusing on the antibody immune response.
ELISA data 7, 14, 21 and 28 d after the first immunization are available that show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 10). Sera obtained 14, 21 and 28 d after immunization show dose-dependent SARS-CoV-2 pseudovirus neutralization activity (Figure 11).

Immunogenicity study of BNT162b2 (RBP020.1)

To dissect the potency of the vaccine BNT162b2 (RBP020.1), the immunogenicity of the construct was investigated. For this purpose, a dose titration study in BALB/c mice was initiated where the immune response will be analyzed focusing on the antibody immune response.
ELISA data 7, 14, and 21 d after the first immunization are available that show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 12). Sera obtained 14, and 21 d after immunization show dose-dependent SARS-CoV-2 pseudovirus neutralization activity (Figure 13).

Immunogenicity study of the LNP-formulated saRNA encoding the viral S protein-V9 (SEQ ID NO: 7, 9) (RBS004.2)

To dissect the potency of the LNP-formulated saRNA vaccine coding for V9, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine will be investigated by focusing on the antibody immune response.
ELISA data 7, 14, and 21 d after the first immunization are available that show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 14). Sera obtained 14, and 21 d after immunization show dose-dependent SARS-CoV-2 pseudovirus neutralization activity (Figure 15).

The above data demonstrate an immune response for both the RBD with a trimerization domain ("V5") and the mutated full-length S protein ("V8"/"V9") *in vivo* in all tested platforms (including the vaccines BNT162a1, BNT162b1, BNT162b2, and BNT162c1). The antibody immune response was already seen at very early time points by ELISA (i.e., at 7 d post-immunization) Importantly, induced antibodies were able to efficiently neutralize SARS-COV-2 pseudovirus infection *in vitro*. Also, the induction of an antibody response using a very low immunization dose of 0.2 µg/mouse when using the modRNA platform (BNT162b1, BNT162b2) as well as the saRNA platform (BNT162c1) indicates a high potency of the vaccine candidates.

In mice, BNT162b2 induced a higher antigen-specific titer compared to BNT162b1 encoded with the identical RNA platform. As expected, the immunogenicity in mice against the antigens differs between the RNA platforms. In mice, the most immunogenic platform based on antigen-specific antibody induction is the modRNA followed by saRNA. The uRNA platform induces the lowest antigen-specific antibody titer.

Example 3: Selection of Formulation

The LNP delivery system was in general developed to effectively and safely deliver therapeutic nucleic acids into the cytosol of various cell types after local administration *in vivo*. The early formulation work was performed with several promising LNP formulations and surrogate RNA coding for luciferase. The aim of the experiments was to correlate the effect of different ionizable cationic lipids on the efficacy of RNA delivery by LNPs *in vivo.* Formulations were compared in terms of RNA encapsulation efficiency, apparent pKa, LNP size and polydispersity. Among the screened cationic lipids, ALC-0315 exhibited suitable physical characteristics regarding particle size, homogeneity, and RNA encapsulation efficiency.

Based on this the ALC-0315/DSPC/CHOL/ALC-0159 prototype was submitted for *in vivo* screening. The results presented in Figure 16 summarize the *in vivo* testing of two independent pilot batches using luciferase (Luc) RNA. The results demonstrate improved potency of the ALC-0315 prototype as compared to an internal benchmark (ALC-0218). On the basis of these studies, ALC-0315 was identified as a highly potent cationic lipid and brought forward for further product development studies.

The formulation screening procedure described above involves intravenous administration resulting in delivery primarily to the liver. The mechanism of LNP uptake into hepatocytes is driven by binding of endogenous apolipoproteins to the LNP followed by receptor-mediated endocytosis e.g. through low density lipoprotein receptors. In order to investigate whether the same mechanism is involved for an intramuscular administration, Luc RNA containing LNPs comprising ALC-0315 were injected intravenously (0.3 mg/kg) and intramuscularly (0.2 mg/kg) into ApoE knockout mice in the presence or absence of recombinant human ApoE3. As control, wild-type C57Bl/6 mice were also treated by the different routes of administration. RNA-LNP were pre-incubated with recombinant human ApoE3 (1 mg encapsulated mRNA with 1 mg ApoE3) for 1 hour at room temperature (RT) prior to administration. Luc expression was monitored at 4, 24, 72 and 96 hours post administration (Figure 17).

When mice were administered intravenously, Luc expression was detected in the wild-type C57Bl/6 mice. In the ApoE knockout mice Luc expression was significantly reduced however when preincubated with exogenous ApoE the expression of Luc was recovered to similar expression levels as wild-type mice (Figure 18).

In vivo Luc expression experiments using mouse models showed, that similar mechanisms are involved in the uptake of RNA-LNP in case of intramuscular administration as for intravenous administration, and this is not only true for hepatocytes but also for the cells local to the administration site.

In vivo experiments after intramuscular administration of the final ALC-0315/DSPC/CHOL/ALC-0159, confirmed minimal drainage with regards to biodistribution, immunogenicity (vaccine activity) and tolerability.

Example 4: Immunogenicity studies for Coronavirus vaccine candidates

Functional cellular immune responses to the vaccine candidates were detected by ELISpot assay using the IFN-γ ELISpot^{PLUS} kit (Mabtech, Cat. No. 3321-4APT-2). In brief, spleens were removed from animals after sacrifice at day 28 after vaccination. Spleens were mechanically dissociated using the plunger of a syringe and a 70 µM cell strainer (Greiner Bio-One GmbH, Cat. No. 542070). Splenocytes were washed with an excess volume of DPBS (Thermo Fisher Scientific, Cat. No. 14190-094) followed by centrifugation at 300 × g for 6 min at RT and discarding the supernatants. Erythrocytes were then lysed with erythrocyte lysis buffer (154 mM NH_4Cl, 10 mM $KHCO_3$, 0.1 mM EDTA) for 5 min at RT. The reaction was stopped with an excess volume of DPBS. After another washing step, cells were resuspended in RPMI 1640 medium (Gibco, Cat. no. 61870-010) supplemented with 10% FBS, 1% MEM Non-Essential Amino Acids Solution (Gibco, Cat. No. 11140-035), 1% sodium pyruvate (Gibco, Cat. No. 11360-039), 0.5% penicillin/streptomycin (Gibco, Cat. No. 15140-122), passed through a 70 µm cell mesh again and counted. CD8+ or CD4+ T cells were isolated from splenocyte cell suspensions using CD8a or CD4 MACS® MicroBeads (Miltenyi Biotec, Cat. No. 130-117-044 and 130-117-043) according to the manufacturer's instructions. In parallel, 96-well ELISpot plates were washed with PBS and blocked with medium (RPMI 1640 medium supplemented with 10% FBS, 1% MEM Non-Essential Amino Acids Solution, 1% sodium pyruvate, 0.5% penicillin/streptomycinmedium) for at least 30 min at 37°C. 1×10^5 CD8+ or CD4+ T cells in 100 µL medium were subsequently re-stimulated by addition of 50 µL peptide solution (irrelevant control peptide AH1 (2 µg/mL; sequence: SPSYVYHQF), PepMix™ SARS-CoV-2 S-RBD (0.025 µg/mL per peptide; JPT, customized) or PepMix™ SARS-CoV-2 Spike Glycoprotein (0.1 µg/mL per peptide; JPT, Cat. No. PM-WCPV-S-2) and 50 µL of autologous bone marrow-

derived dendritic cells in the IFN-γ ELISpot assay. Each condition was tested in duplicate. Plates were incubated overnight in a 37°C humidified incubator with 5% CO_2 and after approximately 18 h, cells were removed from the plates. IFN-γ spots were detected according to the manufacturer's protocol. After plate drying for 2–3 h under the laminar flow, an ELISpot plate reader (ImmunoSpot® S6 Core Analyzer, CTL) was used to count and analyze spot numbers per well.

In addition to ELISpot assay, Luminex analyses were conducted to inform about the T_H1 or T_H2 nature of the detected T cell response. 5×10^5 splenocytes in 100 µL RPMI 1640 medium supplemented with 10% FBS, 1% MEM Non-Essential Amino Acids Solution, 1% sodium pyruvate, 0.5% penicillin/streptomycinmedium were transferred to a 96-well flat bottom cell culture plate. 100 µL irrelevant control peptide AH1 (2 µg/mL; sequence: SPSYVYHQF), or PepMix™ SARS-CoV-2 Spike Glycoprotein (0.1 µg/mL per peptide; JPT, Cat. No. PM-WCPV-S-2) were added. The plates were incubated for 48 hours and supernatant thereafter was harvested for cytokine profiling. Cytokine concentrations in supernatants of the re-stimulated splenocytes were determined using a bead-based T_H1/T_H2 ProcartaPlex immunoassay (Thermo Fisher Scientific, Cat. No. EPX110-20820-901) according to the manufacturer's instructions. Fluorescence was measured with the Bioplex200 System (Biorad) and analyzed with ProcartaPlex Analyst 1.0 software (Thermo Fisher Scientific). The following analytes were measured: IFN-γ; IL-12p70; IL-13; IL-1 beta; IL-2; IL-4; IL-5; IL-6; TNF alpha; GM-CSF; IL-18.

For immunophenotyping, flow cytometry analysis was performed. Briefly, erythrocytes from 50 µL freshly drawn blood were lysed with ACK lysing buffer (Gibco) and cells were stained with fixable viability dye (eBioscience) and anti-CXCR5 (rat IgG2a) antibody in the presence of Fc block (both BD Bioscience) in flow buffer (DPBS (Gibco) supplemented with 2% FCS, 2 mM EDTA (both Sigma) and 0.01% sodium azide (Morphisto) for 20 minutes at room temperature. After staining with anti-rat IgG2a biotin in flow buffer for 20 minutes at 2-8 °C, cells were stained extracellularly with antibodies against CD3, CD4, CD8α, CD38, CD44, PD-1, ICOS, CD62L, CXCR5, CD19 and streptavidin in Brilliant Stain Buffer Plus (BD Bioscience) diluted in

flow buffer for 20 minutes at 2-8 °C. Cells were fixed with 2% RotiHistofix (Roth) for 15 minutes at room temperature. Cells were resuspended in Perm buffer (FoxP3/Transcription Factor Staining Buffer Set, eBioscience) and incubated over night at 2-8 °C. Permeabilized cells were intracellularly treated with Fc block for 10 minutes at 2-8 °C and stained with T-bet and GATA (BD Bioscience) antibodies for 30 minutes at 2-8 °C. Cells were resuspended in flow buffer and acquired on a BD Symphony A3 flow cytometer (BD Bioscience) and analyzed with FlowJo 10.6.2.

For mouse B cell subtyping in draining lymph nodes, $2.5x10^5$ lymph node cells were treated with Fc block for 15 minutes and stained extracellularly with antibodies against CD19, CD45R/B220, IgD, CD138, IgM, CD38, CD95/FAS, IgG1, IgG2a, CD73, GR-1, F4/80, CD4, CD8 in Brilliant Stain Buffer (BD Bioscience) for 20 minutes at 2-8 °C. Cells were fixed with 2% RotiHistofix and incubated over night at 2-8 °C.

Immunogenicity study of BNT162b1 (RBP020.3)

To dissect the potency of the LNP-formulated modRNA vaccine coding for BNT162b1, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine was investigated by focusing on the cellular immune response.

After stimulation with an S protein- or RBD-specific peptide pool, but not after stimulation with irrelevant peptide AH1, both CD4+ and CD8+ T cells displayed IFN-γ responses in the IFN-γ ELISpot assay (Figure 22). In Luminex analysis, cytokine production after peptide stimulation was confirmed for analytes that indicate a T_H1-driven immune response (Figure 23).

Immunophenotyping analysis of blood 7 days after immunization (Figure 24) revealed a significant increase in circulating T follicular helper cells (Tfh) and activated T cells. At day 12 after immunization, draining lymph nodes from immunized BALB/c mice were dissected and B cell subpopulation analysis was performed (Figure 25). A significant increase in B cells was found in lymph nodes with detectable numbers of plasma cells, class switched B cells and IgG1

or IgG2a positive germinal center B cells. Both in blood and draining lymph node, an activation and maturation of the adaptive immune response was confirmed.

Immunogenicity study of the LNP-formulated modRNA encoding the viral P2-S protein V8 (RBP020.1)

To dissect the potency of the LNP-formulated modRNA vaccine coding for RBP020.1, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine was investigated by focusing on the cellular immune response.

After stimulation with an S protein-specific peptide pool, but not after stimulation with irrelevant peptide AH1, both CD4+ and CD8+ T cells displayed IFN-γ responses in the IFN-γ ELISpot assay (Figure 26). In Luminex analysis, cytokine production after peptide stimulation was confirmed for analytes that indicate a T_H1-driven immune response (Figure 27).

Immunogenicity study of the LNP-formulated saRNA encoding the viral P2-S protein V9 (RBS004.2)

To dissect the potency of the LNP-formulated saRNA vaccine coding for RBS004.2, BALB/c mice were immunized IM once as outlined in Table 3. The immunogenicity of the RNA vaccine was investigated by focusing on the cellular immune response.

After stimulation with an S protein-specific peptide pool, but not after stimulation with irrelevant peptide AH1, both CD4+ and CD8+ T cells displayed IFN-γ responses in the IFN-γ ELISpot assay (Figure 28). In Luminex analysis, cytokine production after peptide stimulation was confirmed for analytes that indicate a T_H1-driven immune response (Figure 29).

Immunogenicity study of BNT162b3 variants BNT162b3c and BNT162b3d

To get an idea about the potential potency of transmembrane-anchored RBD-based vaccine antigens (Schematic in Figure 30; BNT162b3c (1) and BNT162b3d (2)), BALB/c mice were immunized IM once with 4 µg LNP-C12 formulated mRNA or with buffer as control. The non-

clinical LNP-C12 formulated mRNAs were used as surrogate for the BNT162b3 variants BNT162b3c and BNT162b3d. The immunogenicity of the RNA vaccine was investigated by focusing on the antibody immune response.

ELISA data 6, 14 and 21 d after the first immunization show an early, dose-dependent immune activation against the S1 protein and the receptor binding domain (Figure 31). Sera obtained 6, 14 and 21 d after immunization show high SARS-CoV-2 pseudovirus neutralization, correlating with the increase of IgG antibody titers (Figure 32).

Example 5: Immunogenicity studies for Coronavirus vaccine candidates in non-human primates (NHP)

Six rhesus macaques per group were immunized IM with 30 or 100 µg of BNT162b1 or with buffer on days 0 and 21. By 14 days after the first dose, antibodies that bound a recombinant S1 were readily detectable, and levels of S1-binding antibodies exceeded the upper limit of quantification of the assay (10,000 U/mL) by day 28. For comparison, S1-binding antibodies of 62 human COVID-19 convalescent sera, obtained after the onset of symptoms were analyzed. All timepoints throughout the two NHP groups significantly exceeded the mean of the human COVID-19 convalescent sera of 422 U/mL (Fig. 33a). The VNT geometric mean titers (GMTs) of sera from rhesus macaques immunized with either dose level of BNT162b1 were detectable by 14 days after a single immunization and reached a geometric mean of 768 (30 µg dose level) or 1,714 (100 µg) by day 28 (Fig. 33b). The neutralization GMTs were 282 (30 µg) and 975 (100 µg) on day 35 (14 days after the boost) (Fig. 33b). Flow cytometry analysis of $CD4^+$ T cells from blood samples stimulated with a S peptide mix on day 42 revealed significant secretion of the T_H1 cytokines IFNγ, IL-2 and TNFα. Additionally, IL-21 secretion was significantly increased. IL-21 is known to play a critical role in B cell activation, expansion and plasma cell generation as well as the generation of Tfh. In contrast, no significant amounts of the T_H2 cytokine IL-4 were detected (Fig. 33c). In summary and in alignment to the results

obtained in mice, BNT162b1 induced a high antibody immune with an early affinity maturation coming with a T_H1 biased immune response.

In summary, we demonstrate that the methyl-nucleoside m1Ψ-modified mRNA encoding the trimeric receptor binding domain from the SARS-CoV-2 S protein is protective in non-human primates.

Example 6: Phase 1/2 Study to Describe the Safety, Tolerability, and Immunogenicity of a COVID-19 RNA Vaccine Candidate (BNT162b1) in Healthy Adults 18 to 55 Years of Age

We report safety, tolerability, and immunogenicity from a placebo-controlled, observer-blinded dose escalation trial among healthy adults randomized to receive 2 doses of 10 µg, 30 µg, or 100 µg of BNT162b1, a lipid nanoparticle (LNP)-formulated, nucleoside-modified, mRNA vaccine candidate that encodes trimerized SARS-CoV-2 spike glycoprotein RBD antigen. Local reactions and systemic events were dose-dependent, generally mild to moderate, and transient. RBD-binding IgG concentrations and SARS-CoV-2 neutralizing titers increased with dose level and after a second dose. Geometric mean neutralizing titers reached 1.8- to 2.8-fold that of a COVID-19 convalescent human serum panel.

The BNT162b1 vaccine candidate now being tested clinically incorporates nucleoside 1-methyl-pseudouridine modified RNA (modRNA) and encodes the receptor binding domain of the SARS-CoV-2 spike, a key target of neutralizing antibodies. The RBD antigen expressed by BNT162b1 is modified by the addition of a T4 fibritin-derived "foldon" trimerization domain to increase its immunogenicity. This RNA vaccine candidate is being tested in parallel in coordinated studies in Germany and in the US. Here, we present data obtained in the US study.

Methods

Study design and participants: This Phase 1/2, randomized, placebo-controlled, observer-blinded trial was conducted in the United States to assess the safety, tolerability, and immunogenicity of ascending dose levels of various BNT162 mRNA vaccine candidates.

Assessment of three dose levels (10, 30, or 100 μg) of the BNT162b1 candidate was conducted at two sites in the United States. This study utilized a sentinel cohort design with progression and dose escalation taking place after review of data from the sentinel cohort at each dose level. Healthy men and nonpregnant women 18 to 55 years of age were enrolled. Key exclusion criteria included individuals with known infection with human immunodeficiency virus, hepatitis C virus, or hepatitis B virus; immunocompromised individuals and those with a history of autoimmune disease; those with increased risk for severe COVID-19; previous clinical or microbiological diagnosis of COVID-19; receipt of medications intended to prevent COVID-19; previous vaccination with any coronavirus vaccine; and a SARS-CoV-2 NAAT-positive nasal swab within 24 hours before study vaccination.

The final protocol and informed consent document were approved by institutional review boards for each of the investigational centers participating in this study, and this study was conducted in compliance with all International Council for Harmonisation (ICH) Good Clinical Practice (GCP) guidelines and the ethical principles of the Declaration of Helsinki. A signed and dated informed consent was required before any study-specific activity was performed.

Endpoints: The study's primary endpoints included: the proportion of participants reporting prompted local reactions, systemic events, and use of antipyretic and/or pain medication within 7 days after vaccination, AEs through 1 month after the last dose, and SAEs through 6 months after vaccination, and the proportion of sentinel cohort participants with clinical laboratory abnormalities 1 week after vaccination and grading shifts in laboratory assessments between baseline and 1 and 7 days after Dose 1 and between Dose 2 and 7 days after Dose 2. Secondary endpoints included: SARS-CoV-2 neutralizing geometric mean titers (GMTs); SARS-CoV-2 S1- binding IgG and RBD-binding IgG geometric mean concentrations (GMCs) 7 and 21 days after Dose 1 and 7 and 14 days after Dose 2; geometric mean fold rise (GMFR), ≥ 4-fold rise from baseline and geometric mean ratio (GMR) of SARS-CoV-2 serum neutralizing GMTs to SARS-CoV-2–antigen binding antibody GMCs at each time point.

Procedures: Study participants were randomly assigned to a vaccine group using an interactive web-based response technology system with each group comprising 15 participants (12 active vaccine recipients and 3 placebo recipients). Participants received two 0.5-mL doses of either BNT162b1 or placebo, administered by intramuscular injection into the deltoid muscle.

BNT162b1 incorporates a Good Manufacturing Process (GMP)-grade mRNA drug substance that encodes the trimerized SARS-CoV-2 spike glycoprotein RBD antigen. The mRNA is formulated with lipids as the mRNA-LNP drug product. The vaccine was supplied as a buffered-liquid solution for IM injection and was stored at -80 °C. The placebo was a sterile saline solution for injection (0.9% sodium chloride injection, in a 0.5-mL dose).

Safety assessments for all participants included 4-hour observation after vaccination (for the first 5 participants vaccinated in each sentinel group, and a 30-minute observation (for the remainder of participants) for immediate AEs. The safety assessments also included self-reporting of prompted local reactions (redness, swelling, and pain at the injection site), systemic events (fever, fatigue, headache, chills, vomiting, diarrhea, muscle pain, and joint pain), and the use of antipyretic and/or pain medication in an electronic diary (e-diary) for 7 days after vaccination, reporting of unprompted AEs through 1 month after vaccination and SAEs through 6 months after the last vaccination. Hematology and chemistry assessments were conducted at screening, 1 and 7 days after Dose 1, and 7 days after Dose 2.

The protocol specified safety stopping rules for all sentinel-cohort participants. Both an internal review committee (IRC) and an external data monitoring committee (EDMC) reviewed all safety data.

Immunogenicity testing: 50 mL of blood was collected for immunogenicity assessments (SARS-CoV-2 serum neutralization assay, SARS-CoV-2 S1-specific IgG direct Luminex immunoassay, SARS-CoV-2 RBD-specific IgG direct Luminex immunoassay and nonvaccine antigen (NVA) Ig direct Luminex immunoassay) before each study vaccination, at 7 and 21 days after Dose 1 and at 7, 14, 1 month and 6 months after Dose 2.

The SARS-CoV-2 neutralization assay used a previously described strain of SARS-CoV-2 (USA_WA1/2020) that had been rescued by reverse genetics and engineered by the insertion of an mNeonGreen (mNG) gene into open reading frame 7 of the viral genome. This reporter virus generates similar plaque morphologies and indistinguishable growth curves from wild-type virus. Serial dilutions of heat inactivated sera were incubated with the reporter virus for 1 hour at 37°C before inoculating Vero E6 cell monolayers. Infected foci were detected by fluorescence between 16-24 hours after inoculation by the addition of Hoechst 33342 Solution and counted with a Cytation 7 Cell Imaging Multi-Mode Reader.

Statistical analysis: The sample size for the sentinel cohort of the study was not based on statistical hypothesis testing. The primary safety objective was evaluated by descriptive summary statistics for local reactions, systemic events, abnormal hematology and chemistry laboratory parameters, and AEs and SAEs for each vaccine group. A 3-tier approach was used to summarize AEs. The secondary immunogenicity objectives were descriptively summarized at the various time points.

Results

Between 04 May 2020 and 19 June 2020, 76 subjects were screened, and 45 participants were randomized and vaccinated. Twelve participants per dose level (10 µg, 30 µg, or 100 µg) were vaccinated with BNT162b1 on Days 0 and 21, and 9 participants received placebo (Figure 34). The study population consisted of healthy male and nonpregnant female participants, 18 to 55 years of age with a mean age of 35.4 years (minimum 19 and maximum 54 years). Overall, 51.1% of participants were male and 48.9% were female. Most participants were white (82.2%) and non-Hispanic/non-Latino (93.3%).

Safety and Tolerability

In the 7 days after either vaccination, pain at the injection site was the most frequently local reaction, reported by 58.3% (7/12) in the 10 µg and 100.0% (12/12 each) in the 30 µg and 100

µg BNT162b1 groups and by 22.2% (2/9) of placebo recipients after Dose 1 and by 83.3% and 100.0% of BNT162b1 recipients at the 10 µg and 30 µg dose levels, respectively, after Dose 2. All local reactions were mild or moderate in severity except for one report of severe pain following Dose 1 of 100 µg BNT162b1.

The most common systemic events reported in the 7 days after vaccination were mild to moderate fatigue and headache in both BNT162b1 and placebo recipients. Systemic events increased with dose level and were reported in a greater number of subjects after the second dose (10 µg and 30 µg groups). Following Dose 1, fever ≥38.0 °C was reported by 50.0% (6/12) of BNT162b1 recipients in the 100 µg group and 8.3% (1/12) of participants each in the 10 µg and 30 µg groups. Following Dose 2, 8.3% (1/12) of participants in the 10 µg group and 75.0% (9/12) of participants in the 30 µg group reported fever ≥38.0 °C. No Grade 4 systemic events or fever were reported. (Figures 35 & 36). Most local reactions and systemic events peaked by Day 2 after vaccination and resolved by Day 7. Based on the reactogenicity profile, participants who received an initial 100 µg dose did not receive a second vaccination.

Adverse events were reported by 50.0% (6/12) of participants who received 10 µg or 30 µg of BNT162b1, by 58.3% (7/12) of those who received 100 µg of BNT162b1, and by 11.1% (1/9) of placebo recipients. Two participants reported a severe AE, one at the 30 µg dose level (Grade 3 pyrexia 2 days after vaccination) and one at the 100 µg dose level (sleep disturbance 1 day after vaccination). Related AEs were reported by 25% (3/12) to 50% (6/12) of BNT162b1 recipients and by 11.1% (1/6) of those who received placebo. No serious adverse events were reported.

No Grade 1 or greater change in routine clinical laboratory values or laboratory abnormalities were observed for most subjects after either of the BNT162b1 vaccinations. The most notable changes were decreases in lymphocyte count in 8.3% (1/12), 45.5% (5/11), and 50.0% (6/12) of participants who received 10 µg, 30 µg, or 100 µg, respectively, of BNT162b1. One participant each at the 10 µg (8.3%) and 30 µg (9.1%) dose levels and 4 participants at the 100 µg dose level (33.3%) had Grade 3 decreases in lymphocytes. These hematological changes,

which were noted in blood drawn 1-3 days after Dose 1, returned to normal 6-8 days after vaccination. None of the changes in laboratory values after vaccination were associated with clinical findings. In addition, Grade 2 neutropenia was noted 6-9 days after the second dose of 10 μg or 30 μg BNT162b1, in 1 participant each. The neutrophil count was not repeated for these two subjects however they continue be followed in the study and no adverse events or clinical manifestation of neutropenia have been reported to date.

Immunogenicity

RBD-binding IgG concentrations and SARS-CoV-2 neutralizing titers were assessed in sera drawn at baseline and at 7 and 21 days after the first dose and 7 days (Day 28) after the second dose of BNT162b1 (Figure 37a). By 21 days after the first dose (for all three dose levels), geometric mean concentrations (GMCs) of RBD-binding IgG were 534-1,778 units/mL, compared to 602 units/mL for a panel of COVID-19 convalescent human sera. By 7 days after the second dose (for the 10 μg and 30 μg dose levels) RBD-binding IgG GMCs had increased to 4,813-30,207 units/mL. Because the participants who received a first dose of 100 μg BNT162b1 did not receive a second dose, the development of the antibody response without a second dose could not be evaluated, and there was no further increase in RBD-binding antibody concentration beyond 21 days after the first dose among participants in this dosing group. Highly elevated RBD-binding antibody concentrations persisted to Day 35 (two weeks after the second dose) in the participants who received 10 μg and 30 μg dose levels of BNT162b1.

Modest increases in SARS-CoV-2 neutralizing geometric mean titers (GMTs) were observed 21 days after Dose 1 (Figure 37b). Substantially greater serum neutralizing GMTs were achieved 7 days after participants received a second 10 μg or 30 μg dose, reaching 168-267, compared to 94 for the COVID-19 convalescent serum panel.

Discussion

The RNA-based vaccine candidate BNT162b1 was safe and well tolerated. All dose levels exhibited a tolerability and safety profile consistent with those previously observed for mRNA-based vaccines. A clear dose level response was observed after Doses 1 and 2 in adults 18-55 years of age. Reactogenicity was generally higher after the second dose, but symptoms resolved within a few days after presentation. Based on the tolerability profile of the first dose at the 100 µg dose level, participants randomized to the 100 µg group did not receive a second vaccination. Transient decreases in lymphocytes (Grades 1-3) were observed within a few days after vaccination; however, lymphocyte counts returned to baseline within 6-8 days in all participants. These laboratory abnormalities were not associated with clinical findings. Lymphopenia following vaccination is most likely explained by transient migration of lymphocytes into the tissues.

Robust immunogenicity was observed after vaccination with BNT162b1. RBD-binding IgG concentrations were detected at Day 21 and substantially increased 7 days after the booster dose given at Day 21. After the first dose, the RBD-binding IgG GMCs in vaccinated participants (10 µg dose level) were similar to those observed in a panel of 38 sera from COVID-19 convalescing humans obtained 20-40 days after the onset of symptoms and at least 14 days after the start of asymptomatic convalescence. In sera drawn from the 30 µg and 100 µg dose level cohorts, GMCs were substantially higher than in the convalescent serum panel. After the booster vaccinations (Dose 2) with 10 µg or 30 µg BNT162b1, the RBD-binding IgG GMCs were 8.0-fold to 50-fold higher than the convalescent serum panel GMC.

Sera from vaccinated participants were also tested in the SARS-CoV-2 neutralization assay. Neutralization titers were measurable at Day 21 for all dose levels. At Day 28 (7 days after the booster dose), substantial SARS-CoV-2 neutralization titers were observed. The virus neutralizing GMTs after the 10 µg and 30 µg booster vaccinations (Dose 2) were, respectively, 1.8-fold and 2.8-fold higher than the neutralizing GMT of the convalescent serum panel. As the 100 µg dose level cohort was not boosted, no corresponding data for immunogenicity after a second vaccination are available.

These clinical findings for the BNT162b1 vaccine candidate are very encouraging and provide strong evidence supporting accelerated development and at-risk manufacturing to maximize the opportunity for the soonest availability of a prophylactic vaccine to prevent COVID-19.

Example 7: Concurrent antibody and, T cell and cytokine responses elicited by a COVID-19 RNA vaccine

In this example, we present characterisation of antibody and T cell responses after BNT162b1 vaccination from a non-randomized open-label phase I/II trial in healthy adults, 18-55 years of age. Two doses, of 1 µg, 10 µg, 30 µg and 50 µg of BNT162b1 administered 21 days apart elicited concomitant antibody, and robust $CD4^+$ and $CD8^+$ T cell responses. All subjects exhibited strong antibody responses with IgG concentrations significantly above those observed in COVID-19 convalescent human sera. Day 43 SARS-CoV-2 serum neutralising geometric mean titers were in the range of 0.7-fold (1 µg) to 3.3-fold (50 µg) compared to those of a panel of COVID-19 convalescent human sera, and were broadly active against diverse SARS-CoV-2 spike variants. Interferon (IFN)γ, an immune stimulatory cytokine with anti-viral properties, was produced by a high frequency of RBD-antigen specific $CD8^+$ T and numerous $CD4^+$ T cells. IL-12p70, which reinforces a T_H1 immune cell profile, was detected in RBD-stimulated immune cells. The robust RBD-specific antibody, T-cell and favorable cytokine responses by the BNT162b1 mRNA vaccine suggests a potential for multiple beneficial protective mechanisms against COVID-19.

Materials and Methods

Clinical trial design

Study BNT162-01 (NCT04380701 – Germany trial) is an ongoing, first-in-human, Phase I/II, open-label dose-finding clinical trial to assess the safety, tolerability, and immunogenicity of ascending dose levels of various intramuscularly administered BNT162 mRNA vaccine

candidates. Healthy men and non-pregnant women 18 to 55 years (amended to add 56 -85 of age) of age are eligible. Key exclusion criteria included previous clinical or microbiological diagnosis of COVID-19; receipt of medications to prevent COVID-19; previous vaccination with any coronavirus vaccine; a positive serological test for SARS-CoV-2 IgM and/or IgG at the screening visit; and a SARS-CoV-2 NAAT-positive nasal swab within 24 hours before study vaccination; those with increased risk for severe COVID-19; immunocompromised individuals, those with known infection with HIV, hepatitis C virus, or hepatitis B virus and those with a history of autoimmune disease. The primary endpoints of the study are safety and immunogenicity.

In the part of the study reported here five dose levels (1 µg, 10 µg, 30 µg, 50 µg or 60 µg) of the BNT162b1 candidate were assessed at one site in Germany with 12 healthy volunteers per dose level in a dose escalation and de-escalation design. Sentinel dosing was performed in each dose-escalation cohort. Progression in that cohort and dose escalation required data review by a safety review committee. Subjects received a BNT162b1 prime dose on day 1, and a boost dose on day 22±2. Serum for antibody assays was obtained on day 1 (pre-prime), 8±1 (post-prime), 22±2 (pre-boost), 29±3 and 43±4 (post-boost). PBMCs for T cell studies were obtained on day 1 (pre-prime) and 29±3 (post-boost). One subject of the 10 µg, and one subject of the 50 µg dose cohort left the study prior to the boost immunisation due to withdrawal of consent and private reasons.

The presented data comprise the BNT162b1-immunised cohorts only and are based on a preliminary analysis with a data extraction date of July 13th, 2020, focused on analysis of vaccine-induced immunogenicity (secondary endpoint) descriptively summarised at the various time points. All participants with data available were included in the immunogenicity analyses.

The trial was carried out in Germany in accordance with the Declaration of Helsinki and Good Clinical Practice Guidelines and with approval by an independent ethics committee (Ethik-Kommission of the Landesärztekammer Baden-Württemberg, Stuttgart, Germany) and the

competent regulatory authority (Paul-Ehrlich Institute, Langen, Germany). All subjects provided written informed consent.

Manufacturing of RNA

BNT162b1 incorporates a Good Manufacturing Practice (GMP)-grade mRNA drug substance that encodes the trimerized SARS-CoV-2 spike glycoprotein RBD antigen. The RNA is generated from a DNA template by *in vitro* transcription in the presence of 1-methylpseudouridine-5'-triphosphate (m1YTP; Thermo Fisher Scientific) instead of uridine-5'-triphosphate (UTP). Capping is performed co-transcriptionally using a trinucleotide cap 1 analogue ($(m_2^{7,3'-O})$Gppp($m^{2'-O}$)ApG; TriLink). The antigen-encoding RNA contains sequence elements that increase RNA stability and translation efficiency in human dendritic cells (Holtkamp, S. et al., Blood 108, 4009–4017 (2006); Orlandini von Niessen, A. G. et al., Mol. Ther. 27, 824–836 (2019)). The mRNA is formulated with lipids to obtain the RNA-LNP drug product. The vaccine was transported and supplied as a buffered-liquid solution for IM injection and was stored at -80 °C.

Proteins and peptides

A pool of 15-mer peptides overlapping by 11 aa and covering the whole sequence of the BNT162b1-encoded SARS-CoV-2 RBD, was used for *ex vivo* stimulation of PBMCs for flow cytometry, IFNγ ELISpot and cytokine profiling. CEF (CMV, EBV, influenza virus; HLA class I epitope peptide pool) and CEFT (CMV, EBV, influenza virus, tetanus toxoid; HLA class II epitope peptide pool) (both JPT Peptide Technologies) were used as controls for general T-cell reactivity.

Human convalescent sera and PBMC panel

Human SARS-CoV-2 infection/COVID-19 convalescent sera (*n*=38) were drawn from subjects 18-83 years of age at least 14 days after PCR-confirmed diagnosis and at a time when the subjects were asymptomatic. Serum donors had symptomatic infections (*n*=35), or had been hospitalized (*n*=1). Sera were obtained from Sanguine Biosciences (Sherman Oaks, CA), the MT Group (Van Nuys, CA) and Pfizer Occupational Health and Wellness (Pearl River, NY).

Human SARS-CoV-2 infection/COVID-19 convalescent PBMC samples (*n*=6) were collected from subjects 41-79 years of age 45-59 days after PCR-confirmed diagnosis when subjects were asymptomatic. PBMC donors had asymptomatic/mild infections (*n*= 4; clinical score 1 and 2) or had been hospitalized (*n*=2; clinical score 4 and 5). Blood samples were obtained from the Frankfurt University Hospital (Germany).

Cell culture and primary cell isolation

Vero cells (ATCC CCL-81) and Vero E6 cells (ATCC CRL-1586) were cultured in Dulbecco's modified Eagle's medium (DMEM) with GlutaMAX™ (Gibco) supplemented with 10% fetal bovine serum (FBS) (Sigma-Aldrich). Cell lines were tested for mycoplasma contamination after receipt and before expansion and cryopreservation. Peripheral blood mononuclear cells (PBMCs) were isolated by Ficoll-Hypaque (Amersham Biosciences) density gradient centrifugation and cryopreserved prior to subsequent analysis.

RBD binding IgG antibody assay

A recombinant SARS-CoV-2 RBD containing a C-terminal Avitag™ (Acro Biosystems) was bound to streptavidin-coated Luminex microspheres. Heat-inactivated subject sera were diluted 1:500, 1:5,000, and 1:50,000. Following an overnight incubation at 2-8 °C while shaking, plates were washed in a solution containing 0.05% Tween-20. A secondary fluorescently labelled goat anti-human polyclonal antibody (Jackson Labs) was added for 90 minutes at room temperature while shaking, before plates were washed once more in a solution containing 0.05% Tween-20. Data were captured as median fluorescent intensities (MFIs) using a Luminex reader and converted to U/mL antibody concentrations using a reference standard curve with arbitrary assigned concentrations of 100 U/mL and accounting for the serum dilution factor. Three dilutions are used to increase the likelihood that at least one result for any sample will fall within the useable range of the standard curve. Assay results were reported in U/mL of IgG. The final assay results are expressed as the geometric mean concentration of all sample dilutions that produced a valid assay result within the assay range.

SARS-CoV-2 neutralisation assay

The neutralisation assay used a previously described strain of SARS-CoV-2 (USA_WA1/2020) that had been rescued by reverse genetics and engineered by the insertion of an mNeonGreen (mNG) gene into open reading frame 7 of the viral genome (Xie, X. et al., Cell Host Microbe 27, 841-848.e3 (2020)). This reporter virus generates similar plaque morphologies and indistinguishable growth curves from wild-type virus. Viral master stocks (2 x 10^7 PFU/mL) were grown in Vero E6 cells as previously described (Xie, X. et al., Cell Host Microbe 27, 841-848.e3 (2020)). Serial dilutions of heat-inactivated sera were incubated with the reporter virus (2 x 10^4 PFU per well for a final multiplicity of infection (MOI) of 0.5 to yield approximately a 10-30% infection rate of the Vero monolayer) for 1 hour at 37 °C before inoculating Vero CCL81 cell monolayers (targeted to have 8,000 to 15,000 cells per well) in 96-well plates to allow accurate quantification of infected cells. Total cell counts per well were enumerated by nuclear stain (Hoechst 33342) and fluorescent virally infected foci were detected 16-24 hours after inoculation with a Cytation 7 Cell Imaging Multi-Mode Reader (Biotek) with Gen5 Image Prime version 3.09. Titers were calculated in GraphPad Prism version 8.4.2 by generating a 4-parameter (4PL) logistical fit of the percent neutralisation at each serial serum dilution. The 50% neutralisation titre (VNT_{50}) was reported as the interpolated reciprocal of the dilution yielding a 50% reduction in fluorescent viral foci.

VSV-SARS-CoV-2 spike variant pseudovirus neutralisation assay

VSV-SARS-CoV-2-S pseudoparticle generation and neutralisation assays were performed as previously described (Baum, A. et al., Science, eabd0831 (2020). doi:10.1126/science.abd0831). Briefly, human codon optimized SARS-CoV-2 spike (GenBank: MN908947.3) was synthesised (Genscript) and cloned into an expression plasmid. SARS-CoV-2 complete genome sequences were downloaded from GISAID Nucleotide database (https://www.gisaid.org) (last accessed 24 Aug 2020). Sequences were curated and genetic diversity of the Spike-encoding gene was assessed across high quality genome sequences using custom pipelines. Amino acid substitutions were cloned into the spike expression plasmid using site-directed mutagenesis. HEK293T cells (ATCC CRL-3216) were seeded (culture

medium: DMEM high glucose (Life Technologies) supplemented with 10% heat-inactivated fetal bovine serum (FBS; Life Technologies) and Penicillin/Streptomycin/L-Glutamine (Life Technologies)) and transfected the following day with spike expression plasmid using Lipofectamine LTX (Life Technologies) following the manufacturer's protocol. At 24 hours post-transfection at 37°C, cells were infected with the VSVΔG:mNeon/VSV-G virus diluted in Opti-MEM (Life Technologies) at a multiplicity of infection of 1. Cells were incubated 1 hour at 37°C, washed to remove residual input virus and overlaid with infection medium (DMEM high glucose supplemented with 0.7% Low IgG BSA (Sigma), sodium pyruvate (Life Technologies) and 0.5% Gentamicin (Life Technologies)). After 24 hours at 37°C, the supernatant containing VSV-SARS-CoV-2-S pseudoparticles was collected, centrifuged at 3000xg for 5 minutes to clarify and stored at -80°C until further use.

For pseudovirus neutralisation assays, Vero cells (ATCC CCL-81) were seeded in 96-well plates in culture medium and allowed to reach approximately 85% confluence before use in the assay (24 hours later). Sera were serially diluted 1:2 in infection medium starting with a 1:40 dilution. VSV-SARS-CoV-2-S pseudoparticles were diluted 1:1 in infection medium for a fluorescent focus unit (ffu) count in the assay of ~1000. Serum dilutions were mixed 1:1 with pseudoparticles for 30 minutes at room temperature prior to addition to Vero cells and incubation at 37°C for 24 hours. Supernatants were removed and replaced with PBS (Gibco), and fluorescent foci were quantified using the SpectraMax i3 plate reader with MiniMax imaging cytometer (Molecular Devices). Neutralisation titers were calculated in GraphPad Prism version 8.4.2 by generating a 4-parameter logistical (4PL) fit of the percent neutralisation at each serial serum dilution. The 50% pseudovirus neutralisation titre ($pVNT_{50}$) was reported as the interpolated reciprocal of the dilution yielding a 50% reduction in fluorescent viral foci.

IFN γ ELISpot.

IFNγ ELISpot analysis was performed *ex vivo* (without further *in vitro* culturing for expansion) using PBMCs depleted of $CD4^+$ and enriched for $CD8^+$ T cells ($CD8^+$ effectors), or depleted of $CD8^+$ and enriched for $CD4^+$ T cells ($CD4^+$ effectors). Tests were performed in duplicate and with a positive control (anti-CD3 monoclonal antibody CD3-2 (1:1,000; Mabtech)). Multiscreen filter plates (Merck Millipore) pre-coated with IFNγ-specific antibodies (ELISpotPro kit, Mabtech) were washed with PBS and blocked with X-VIVO 15 medium (Lonza) containing 2% human serum albumin (CSL-Behring) for 1-5 hours. Per well, 3.3×10^5 effector cells were stimulated for 16-20 hours with an overlapping peptide pool representing the vaccine-encoded RBD. Bound IFNγ was visualized using a secondary antibody directly conjugated with alkaline phosphatase followed by incubation with BCIP/NBT substrate (ELISpotPro kit, Mabtech). Plates were scanned using an AID Classic Robot ELISPOT Reader and analysed by ImmunoCapture V6.3 (Cellular Technology Limited) or AID ELISPOT 7.0 software (AID Autoimmun Diagnostika). Spot counts were displayed as mean values of each duplicate. T-cell responses stimulated by peptides were compared to effectors incubated with medium only as negative control using an in-house ELISpot data analysis tool (EDA), based on two statistical tests (distribution-free resampling) according to Moodie et al. (Moodie, Z., et al., J. Immunol. Methods 315, 121–32 (2006); Moodie, Z. et al., Cancer Immunol. Immunother. 59, 1489–501 (2010)), to provide sensitivity while maintaining control over false positives.

To account for varying sample quality reflected in the number of spots in response to anti-CD3 antibody stimulation, a normalisation method was applied to enable direct comparison of spot counts/strength of response between individuals. This dependency was modelled in a log-linear fashion with a Bayesian model including a noise component (unpublished). For a robust normalization, each normalisation was sampled 1000 times from the model and the median taken as normalized spot count value. Likelihood of the model: $\log \lambda_E = \alpha \log \lambda_P + \log \beta_j + \sigma\varepsilon$, where λ_E is the normalized spot count of the sample, α is a stable factor (normally distributed) common among all positive controls λ_P, β_j a sample j specific component

(normally distributed) and $\sigma\varepsilon$ is the noise component, of which σ is Cauchy distributed and ε is Student's-t distributed. β_j ensures that each sample is treated as a different batch.

Flow cytometry

Cytokine-producing T cells were identified by intracellular cytokine staining. PBMCs thawed and rested for 4 hours in OpTmizer medium supplemented with 2 µg/mL DNAseI (Roche), were restimulated with a peptide pool representing the vaccine-encoded SARS-CoV-2 RBD (2 µg/mL/peptide; JPT Peptide Technologies) in the presence of GolgiPlug (BD) for 18 hours at 37 °C. Controls were treated with DMSO-containing medium. Cells were stained for viability and surface markers in flow buffer ((DPBS (Gibco) supplemented with 2% FCS (Biochrom), 2 mM EDTA (Sigma-Aldrich)) for 20 minutes at 4 °C. Afterwards, samples were fixed and permeabilized using the Cytofix/Cytoperm kit according to manufacturer's instructions (BD Biosciences). Intracellular staining was performed in Perm/Wash buffer for 30 minutes at 4 °C. Samples were acquired on a FACS VERSE instrument (BD Biosciences) and analysed with FlowJo software version 10.5.3 (FlowJo LLC, BD Biosciences). RBD-specific cytokine production was corrected for background by subtraction of values obtained with DMSO-containing medium. Negative values were set to zero. Cytokine production in Figure 42b was calculated by summing up the fractions of all $CD4^+$ T cells positive for either IFNγ, IL-2 or IL-4, setting this sum to 100% and calculating the fraction of each specific cytokine-producing subset thereof.

Cytokine profiling

Human PBMCs were restimulated for 48 hours with SARS-CoV-2 RBD peptide pool (2 µg/mL final concentration per peptide). Stimulation with DMSO-containing medium served as negative controls. Concentrations of TNF, IL-1β and IL-12p70 in supernatants were determined using a bead-based, 11-plex T_H1/T_H2 human ProcartaPlex immunoassay (Thermo Fisher Scientific) according to the manufacturer's instructions. Fluorescence was measured with a Bioplex200 system (Bio-Rad) and analysed with ProcartaPlex Analyst 1.0 software (Thermo Fisher Scientific). RBD-specific cytokine production was corrected for background by

subtraction of values obtained with DMSO-containing medium. Negative values were set to zero.

Results

Study design and analysis set

Between April 23rd 2020 and May 22nd 2020, 60 subjects were vaccinated with BNT162b1. Twelve participants per 1 µg, 10 µg, 30 µg, and 50 µg dose levels received a first dose on day 1 and were boosted on day 22, and 12 participants received a 60 µg prime dose on Day 1 only (Figure 43). The study population consisted of healthy males and non-pregnant females with a mean age of 41 years (range 19 to 55 years) with equal gender distribution. Most participants were Caucasian (96.7%) with one African American and one Asian subject (1.7% each). Preliminary data analysis was focussed on immunogenicity (Table 4).

Table 4. Subject disposition and analysis sets.

	BNT162b1		Antibody analysis					T-cell analysis	
Cohort	**Prime**	**Boost**	**Day 1**	**Day 8±1**	**Day 22±2**	**Day 29±3**	**Day 43±4**	**Day 1**	**Day 29±3**
1 µg	12	12	12	12	12	12	12	8	8
10 µg	12	11	12	12	12	11	11 (10)	10 (6)	10 (6)
30 µg	12	12	12	12	12	12	12 (10)	10 (7)	10 (7)
50 µg	12	11	12	12	12	11	6	8 (5)	8 (5)
60 µg	12	N/A	12	12	11	12	N/A	N/A	N/A

Antibody analysis: Values indicated number of subjects for which virus neutralisation assay was performed. Values in parentheses indicate number of subjects for which RBD binding IgG antibody assay was performed. T-cell analysis: Values indicated number of subjects for which IFNγ ELISpot was performed. Values in parentheses indicate number of subjects for which flow cytometry was performed. N/A: Samples not yet available.

Briefly, no serious adverse events (SAE), no unexpected toxicities, and no withdrawals due to related AEs were observed. Most reported solicited AEs were signs and symptoms of vaccine reactogenicity, typically with onset within the first 24 hours post immunisation, such as systemic, and injection site reactions, chiefly symptoms of pain and tenderness (Figure 44). Symptomatology was mostly mild or moderate in intensity with occasional severe (Grade 3) AEs such as fever, chills, headache, muscle and joint pain, and injection site reactions. All AEs resolved spontaneously, mostly within 24 hours of onset and could be managed with simple measures (*e.g.* paracetamol). Based on the reactogenicity reported after the first dose, participants who had received an initial 60 µg dose did not receive a second 60 µg dose.

Whereas no relevant change in routine clinical laboratory values occurred after BNT162b1 vaccination, a transient increase of the inflammatory marker C-reactive protein (CRP) and temporary reduction of blood lymphocyte counts were observed in a dose-dependent manner in vaccinated subjects (Figure 45). Based on our previous clinical experience with RNA vaccines, the latter is likely attributable to innate immune stimulation-related transient redistribution of lymphocytes (Kamphuis, E., et al., Blood 108, 3253–61 (2006)).

Vaccine-induced antibody response

RBD-binding IgG concentrations and SARS-CoV-2 neutralising titers were assessed at baseline, 7 and 21 days after the BNT162b1 prime dose (days 8 and 22), and 7 and 21 days after the boost dose (days 29 and 43), except for the 60 µg cohort, which received prime only (Figure 39).

All subjects including those who received the 1 µg dose showed a strong, dose-dependent vaccine-induced antibody response. Twenty-one days after the priming dose (for the four dose levels ranging from 1-50 µg), geometric mean concentrations (GMCs) of RBD-binding IgG were dose dependently about 265-1,672 U/mL (Figure 39). Seven days after the boosting dose (day 29) RBD-binding IgG GMCs in subjects treated with 1-50 µg BNT162b1 strongly increased dose-dependently to about 2,015-25,006 U/mL. At day 43 (21 days after boost), RBD-binding antibody GMCs were in the range of about 3,920-22,700 U/mL in BNT162b1 vaccinated

individuals as compared to about 602 U/mL measured in a panel of sera from 38 SARS-CoV-2 infection convalescent patients (18-83 years of age) drawn at least 14 days after PCR-confirmed diagnosis. In the 60 µg dose cohort with prime dose only, RBD-binding IgG GMCs were about 1,058 U/mL by day 29 indicating the necessity of the second dose for boosting the antibody titer.

SARS-CoV-2 neutralising antibody geometric mean titers (GMTs) increased modestly in a dose-dependent manner 21 days after the priming dose (Figure 40a). Substantially higher serum neutralizing GMTs were achieved 7 days after the boost dose, reaching about 36 (1 µg dose level), about 158 (10 µg dose level), about 308 (30 µg dose level), and about 578 (50 µg dose level), compared to about 94 for the convalescent serum panel. On day 43 (21 days after the boost), depending on the dose level, the neutralising antibody GMT were further increased to about 62 (1 µg dose), were relatively stable at about 126 (10 µg dose), or decreased slightly to about 157 (30 µg dose), and about 309 (50 µg dose). Neutralising antibody GMTs were strongly correlated with RBD-binding IgG GMC (Figure 40b). In summary, neutralising antibody titers were largely in the range of those previously reported in the US study with BNT162b1.

Further, by 7 days after the second dose, sera of vaccinated subjects displayed broad neutralising activity across a panel of seventeen SARS-CoV-2 spike variants identified in publicly available SARS-CoV-2 sequences, including sixteen RBD mutants (Baum, A. et al., Science, eabd0831 (2020). doi:10.1126/science.abd0831) and the dominant spike variant D614G (Baum, A. et al., Science, eabd0831 (2020). doi:10.1126/science.abd0831) (Figure 40c).

Vaccine-induced T cell responses

$CD4^+$ and $CD8^+$ T cell responses in BNT162b1 immunized subjects were characterized prior to prime vaccination (day 1) and on day 29 after prime (7 days after boost vaccination) using direct *ex vivo* IFNγ ELISPOT with PBMCs from 36 subjects across the 1 µg to 50 µg dose cohorts (Figure 41). In this assay, $CD4^+$ or $CD8^+$ T cell effectors were stimulated overnight with overlapping peptides representing the full-length sequence of the vaccine-encoded RBD.

Of 36 subjects, 34 (94.4%, including all subjects treated with ≥ 10 µg BNT162b1) mounted RBD-specific $CD4^+$ T cell responses. The magnitude varied between individuals with the strongest CD4 T cell responses being more than 10-fold of the memory responses observed against a panel of cytomegalovirus (CMV), Epstein Barr virus (EBV), influenza virus and tetanus toxoid-derived immuno-dominant peptides in the same subjects (Fig 41a-c). No $CD4^+$ T cell responses were detectable at baseline, except for one subject with a low number of preexisting RBD-reactive $CD4^+$ T cells, which increased significantly after vaccination (normalized mean spot count from 63 to 1,519, in the 50 µg dose cohort). The strength of RBD-specific $CD4^+$ T cell responses correlated positively with both RBD-binding IgG and with SARS-CoV-2 neutralising antibody titers (Figure 41d, Figure 46a), in line with the concept of intramolecular help (Sette, A. et al., Immunity 28, 847–58 (2008)). The two subjects lacking $CD4^+$ response had no detectable VNT_{50} titers either (Figure 41d).

Vaccine-induced $CD8^+$ T cell responses, some strong ones were mounted by the majority of subjects (29/36, 80.6%) (Figure 41a) and were quite comparable with memory responses against CMV, EBV, Influenza virus and tetanus toxoid in the same subjects (Figure 41b, c). The strength of RBD-specific $CD8^+$ T cell responses correlated positively with vaccine-induced $CD4^+$ T cell responses but did not significantly correlate with SARS-CoV-2 neutralizing antibody titers (Figure 46b, c).

Of note, although at 1 µg BNT162b1 the immunogenicity rate was lower (6/8 responding subjects), the magnitude of vaccine-induced $CD4^+$ and $CD8^+$ T cells in some subjects was almost as high as with 50 µg BNT162b1 (Figure 41a). To assess functionality and polarization of RBD-specific T cells, cytokines secreted in response to stimulation with the vaccine antigen were determined by intracellular staining (ICS) with IFNγ, IL-2 and IL-4 specific antibodies in pre- and post-vaccination PBMCs of 18 BNT162b1 immunised subjects. RBD-specific $CD4^+$ T cells secreted IFNγ, IL-2, or both, but did not secrete IL-4 (Figure 42a-c). Similarly, a fraction of RBD-specific $IFN\gamma^+$ $CD8^+$ T cells also secreted IL-2.

The mean fraction of RBD-specific T cells within total circulating T cells obtained by BNT162b1 vaccination was substantially higher than that observed in six subjects recovered from COVID-19. Frequency of RBD-specific IFNγ$^+$ CD8$^+$ T cells reached up to several percent of total peripheral blood CD8$^+$ T cells (Figure 42c). Analysis of supernatants of PBMCs stimulated *ex vivo* with overlapping RBD peptides from a subgroup of five vaccinated subjects showed cognate release of proinflammatory cytokines TNF, IL-1β and IL-12p70 (Figure 42d).

In summary, these findings indicate that BNT162b1 induces functional and proinflammatory CD4$^+$/CD8$^+$ T cell responses in almost all subjects, with T_H1 polarized helper response.

Discussion

We observed concurrent production of neutralising antibodies, activation of virus-specific CD4$^+$ and CD8$^+$ T cells, and robust release of immune-modulatory cytokines such as IFNγ, which represents a coordinated immune response to counter a viral intrusion (for review Vabret, N. et al., Immunity 52, 910–941 (2020)). IFNγ represents a key cytokine for several anti-viral responses. Indeed, patients with IFNγ gene polymorphism related to impaired IFNγ activity have been shown to display 5-fold increased susceptibility to SARS (Chong, W. P. et al., BMC Infect. Dis. 6, 82 (2006)). Also, IFNγ acts in synergy with type I interferons to inhibit replication of SARS-CoV-2 (Sainz, B., et al., Virology 329, 11–7 (2004)). The robust production of IFNγ from CD8$^+$ T cells indicates a favourable immune response with both anti-viral and immune-augmenting properties.

Importantly, the detection of IFNγ, IL-2 and IL-12p70 but not IL-4 indicates a favorable T_H1 profile and the absence of a potentially deleterious T_H2 immune response. CD4$^+$ and CD8$^+$ T cells may confer long lasting immunity against corona viruses as indicated in SARS-CoV-1 survivors, where CD8$^+$ T-cell immunity persisted for 6-11 years (Vabret, N. et al., Immunity 52, 910–941 (2020); Ng, O.-W. et al., Vaccine 34, 2008–14 (2016)).

Some cases of asymptomatic virus exposure have been associated with cellular immune response without seroconversion indicating that SARS-Cov-2 specific T cells could be relevant

in disease control even in the absence of neutralising antibodies (Gallais, F. et al. (2020). doi:medRxiv: 10.1101/2020.06.21.20132449). Almost all vaccinated volunteers mounted RBD-specific T cell responses detected with an *ex vivo* ELISpot assay, which was performed without prior expansion of T cells that captures only high-magnitude T cell responses. Although the strength of the T-cell responses varied considerably between subjects, we observed no clear dose dependency of the T-cell response strength in the dose range of 1 µg to 50 µg, indicating that stimulation and robust expansion of T cells might be accomplished at the lowest mRNA-encoded immunogen levels.

The study confirms the dose-dependency of RBD-binding IgG and neutralisation responses, reproduces our previous findings for 10 and 30 µg dose levels in the US trial, and shows that neutralising antibody titers are further increased by a prime/boost regimen at 50 µg.

A notable observation is that two injections of BNT162b1 at a dose level as low as 1 µg are capable of inducing RBD-binding IgG levels higher than those observed in convalescent sera, and serum neutralising antibody titers that are still increasing up to day 43. Considering that the magnitude of a protective neutralising antibody titer is not known, and given the substantial T-cell responses we observed for some subjects in the 1 µg cohort may hold the promise that a considerable fraction of individuals may benefit even from this lowest tested dose level.

A purely RBD-directed immunity might be considered prone to escape of the virus by single amino acid changes in this small domain. However, neutralisation of 17 pseudo-typed viruses, 16 of which enter cells using a spike with a different RBD variant found in circulating strains and one of which uses the dominant spike variant D614G, alleviates this potential concern.

Example 8: Summary of Safety and Immunogenicity Data from Stage 1 of COVID-19 Vaccine BNT162

This example provides additional safety and immunogenicity data for the BNT162b1 and BNT162b2 vaccine candidates. These safety and tolerability data, as well as immunoglobulin

G (IgG) binding and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) neutralization titer data, are coming from US participants in a Stage 1 US Study of these vaccine candidates.

For BNT162b1, the following is observed:

For 10 µg to 30 µg dose levels, reactogenicity (particularly systemic events) increases with increasing dose level in 18 to 55-year-old and 65 to 85-year-old participants. Reactogenicity (particularly systemic events) increased after Dose 2 compared to Dose 1.

For BNT162b2, the following is observed:

Dose level- and dose number-dependent increases in reactogenicity were minimal to modest in either age group. Based on all available data, the reactogenicity profile observed with BNT162b2 (and particularly SEQ ID NO:20) is quite favorable.

The immunogenicity data presented herein, focusing on SARS-CoV-2 neutralizing responses post-dose 2, allow to conclude the following:

For BNT162b1 at Day 28 (7 days post-dose 2):

Neutralizing antibody responses elicited after immunization with 10 µg and 30 µg dosages (where data are available in both age groups) are higher in adults 18 to 55 years of age compared to the 65 to 85-year-old group. In the 65 to 85 year old group, neutralizing antibody responses after 20 µg and 30 µg dosages were similar, although numerically higher at the 20 µg dose level.

For BNT162b2 (particularly, SEQ ID NO:20) at Day 28 (7 days post-dose 2):

Neutralizing antibody responses after the 20 µg dosage (where data are available in both age groups) were higher in the 18 to 55 year old group compared to the 65 to 85-year-old group. In the 18 to 55 year-old group, neutralizing antibody responses were higher after receiving 20 µg compared to 10 µg dose levels. The S1 IgG binding antibody data in Figure 56, and comparisons of post-dose 1 responses across dose levels that are highest at the 30 µg dose level, suggest that neutralizing antibody levels will likely also be higher for the 30 µg dose level

post-dose 2, as levels of binding antibody correlate well with neutralizing antibody levels. In the 65 to 85 year old group, neutralizing antibody responses after 20 µg and 30 µg doses were higher at the 30 µg dose level.

The data overall show similar neutralizing antibody responses post-dose 2 between BNT162b1 and BNT162b2.

Safety and Tolerability of BNT162b1

18-55 Years of Age Groups

Safety data are available for this age group through post-dose 2 for all dose levels, except for 20 µg, which for now has partial data available through post-dose 2 (and 100 µg where a second dose has not been administered at the recommendation of the Internal Review Committee (IRC)). Local reactions are shown in Figure 48. Systemic events are shown in Figure 49.

Immunogenicity of BNT162b1

65-85 Years of Age Groups

Immunogenicity data are available for this age group through post-dose 2 for all dose levels. RBD-binding IgG geometric mean concentrations (GMCs) are shown in Figure 50. SARS-CoV-2 neutralizing geometric mean titers (GMTs) are shown in Figure 51.

Safety and Tolerability of BNT162b2

18-55 Years of Age Groups

Safety data are available for this age group through post-dose 2 for all dose levels. Local reactions are shown in Figure 52. Systemic events are shown in Figure 53.

65-85 Years of Age Groups

Safety data are available for this age group through post-dose 2 for all dose levels, however, the data for the 10 µg dose level are only partial. Local reactions are shown in Figure 54. Systemic events are shown in Figure 55.

Immunogenicity of BNT162b2

18-55 Years of Age Groups

Immunogenicity data are available for this age group through post-dose 1 for the 30 µg dose level and post-dose 2 for the 10 µg and 20 µg dose levels. S1-binding IgG GMCs are shown in Figure 56. SARS-CoV-2 neutralizing GMTs are shown in Figure 57.

65-85 Years of Age Groups

Immunogenicity data are available for this age group through post-dose 2 for the 20 µg and 30 µg dose levels. S1-binding IgG GMCs are shown in Figure 58. SARS-CoV-2 neutralizing GMTs are shown in Figure 59.

CONCLUSIONS

The local tolerability profiles of BNT162b1 and BNT162b2 (and particularly SEQ ID NO:20) and the immune response data are similar between the 2 candidates. BNT162b2 (particularly SEQ ID NO:20) may show a favorable systemic reactogenicity profile (particularly in the 65 to 85-year-old group). When selecting the dose level for BNT162b2 (particularly SEQ ID NO:20), the SARS-CoV-2 neutralizing antibody response level in the 65 to 85-year-old group could be of weight to maximize the neutralizing antibody responses in this age group, which is at highest risk of severe disease. Comparing the neutralizing antibody levels in the 20 µg and 30 µg older adult cohorts in this study, the 30 µg dose level showed higher neutralizing antibody levels than those in the 20 µg cohort (Figure 59). In comparison to the neutralizing antibody level of a human convalescent serum panel (HCS) with a GMT of 94, the GMT at the 30 µg dose level was 1.6 times the GMT of the HCS; the GMT at the 20 µg dose level was 0.9 times the GMT of HCS. Thus, both showed neutralizing antibody titres at least comparable to that of the human convalescent serum panel. The 38 human SARS-CoV-2 infection/COVID-19 convalescent sera were drawn from participants 18 to 83 years of age, at least 14 days after PCR-confirmed diagnosis, and at a time when participants were asymptomatic. The serum donors predominantly had symptomatic infections (35/38), and one had been hospitalized. The sera

were obtained from Sanguine Biosciences (Sherman Oaks, CA), the MT Group (Van Nuys, CA), and Pfizer Occupational Health and Wellness (Pearl River, NY). In addition, S1-IgG antibody binding concentrations in both older (Figure 58, post-dose 2) and younger (Figure 56, post-dose 1) adult cohorts also favored the selection of the 30 µg dose level. Preliminary human T cell data that are being generated in a German trial with BNT162b2 are confirming the robust CD4+ and CD8+ expected for the RNA platform. With these considerations, it is proposed to use BNT162b2 (particularly SEQ ID NO:20) at the 30 µg dose level to proceed into Phase 2b/3 because this dose and construct provides the optimum combination of a favorable reactogenicity profile and a robust immune response, likely to afford protection against COVID-19 in younger and older adults.

Example 9: Immunology of COVID-19 Vaccine BNT162

To support progression to Phase 2/3 in adults 18-85 years of age, provided herein are nonclinical and clinical data summarizing the T cell response following BNT162b2 immunization in mice and in humans enrolled in a trial with BNT162. The following immunogenicity data are provided:

1. Preliminary and unaudited mouse immunogenicity data: IFNγ ELISpot (Figure 60), intracellular cytokine staining, and Luminex quantification of cytokines produced following BNT162b2 immunization.
2. From a German trial (BNT162-01): IFNγ ELISpot (Figure 61, Figure 62, Figure 63) for BNT162b2 at the 10 µg dose level in 18-55 year old participants before the first dose and 7 days after dose 2.

T cell responses for BNT162b2 in mice

Four groups of eight female BALB/c mice were immunized on day 0 with doses of 0.2 µg, 1 µg or 5 µg per animal BNT162b2 (particularly SEQ ID NO:20), or with the buffer alone (control group), by intramuscular (IM) injection. On days 12 and 28, spleens were collected for

splenocyte isolation and analysis of T-cell responses using IFNγ ELISpot assays. Luminex assays and intracellular cytokine staining (ICS) were performed to assess cytokine responses. A high fraction of splenocytes of both CD4+ and CD8+ T-cell phenotypes isolated from BNT162b2-immunized mice on days 12 and 28 after immunization, when re-stimulated *ex vivo* with a full-length S peptide mix, exerted a strong antigen-specific IFNγ- and IL-2-response in ELISpot and flow cytometry assays (Figure 60a and b). Splenocytes harvested on day 28 and stimulated with the full-length S peptide pool produced high levels of the T_H1 cytokines IL-2 and IFNγ with correspondingly minimal levels of the T_H2 cytokines IL-4, IL-5, and IL-13 in multiplex immunoassays (Figure 60c).

T cell responses in humans for BNT162b2 from German Study

To evaluate the T cell phenotype elicited by immunization of humans with BNT162b2 (particularly SEQ ID NO:20), IFNγ ELISpot was performed on peripheral blood mononuclear cells (PBMCs) obtained from participants in a German study.

IFN γ ELISpot

Vaccine-elicited T cell responses were determined using CD4- or CD8-depleted PBMCs obtained from subjects prior to dose 1 and on day 29 (7 days after dose 2). IFNγ ELISpot data were generated for 5 subjects immunized with 10 µg of BNT162b2 (particularly SEQ ID NO:20) at day 1 and 22. Post-vaccination spike-specific *ex vivo* CD4+ and CD8+ T cell responses were detected in 5/5 (100%) subjects, respectively. All responses were minimal or undetectable in the prevaccination samples. The responses are considered vaccine induced (Figure 61, Figure 62, Figure 63).

The BNT162b2 vaccine-elicited, antigen specific CD8+ and CD4+ T cell responses stimulated by S peptide pool 1 (N-terminal portion of the spike, which includes the receptor binding domain [RBD]) and S peptide pool 2 (C-terminal portion of the spike) were comparable to or higher than the memory responses in the same subjects against CMV, EBV, influenza virus, and tetanus toxoid (Figure 63).

CONCLUSIONS

These data for the BNT162b2 vaccine candidate confirm prior results obtained in preclinical models and in humans immunized with modRNA (nucleoside-modified) platforms. The data indicate that modRNA elicits substantial Th1-type CD4+ and CD8+ T cell responses.

Example 10: A trimeric SARS-CoV-2 receptor-binding domain RNA vaccine is highly immunogenic and protective in non-human primates

Here, we report the design and non-clinical development of the BNT162b1 vaccine candidate. We demonstrate that nucleoside-modified mRNA encoding a structurally stable, trimerised receptor-binding domain (RBD) of SARS-CoV-2, encapsulated in lipid nanoparticles (LNP) for effective intramuscular delivery, elicits strong antibody and T_H1-dominated cellular immune responses in mice. Immunisation of mice with single doses of BNT162b1 elicited substantial dose level-dependent increases in pseudovirus neutralisation titers and strong IFNγ-positive $CD4^+$ and $CD8^+$ T-cell responses. Prime-boost vaccination of rhesus macaques with BNT162b1 elicited authentic SARS-CoV-2 neutralising geometric mean titers, 2.6 to 6.0 times those of a SARS-CoV-2 convalescent human serum panel. Upon SARS-CoV-2 infectious challenge, the immunised macaques had either no or more transient presence of viral RNA in the nose and lungs than did non-immunised control macaques.

Materials and Methods

Ethics statement.

All mouse studies were performed at BioNTech SE, and protocols were approved by the local authorities (local welfare committee), conducted according to FELASA recommendations and in compliance with the German Animal Welfare Act and Directive 2010/63/EU. Only animals with an unobjectionable health status were selected for testing procedures.

Immunisations for the non-human primate (NHP) study were performed at the University of Louisiana at Lafayette-New Iberia Research Center (NIRC), which is accredited by the Association for Assessment and Accreditation of Laboratory Animal Care (AAALAC, Animal Assurance #: 000452). The work was in accordance with USDA Animal Welfare Act and Regulations and the NIH Guidelines for Research Involving Recombinant DNA Molecules, and Biosafety in Microbiological and Biomedical Laboratories. All procedures performed on these animals were in accordance with regulations and established guidelines and were reviewed and approved by an Institutional Animal Care and Use Committee or through an ethical review process. Infectious SARS-CoV-2 challenge for the NHP study was performed at the Southwest National Primate Research Center. Animal husbandry followed standards recommended by AAALAC International and the NIH Guide for the Care of Use of Laboratory Animals. This study was approved by the Texas Biomedical Research Institute Animal Care and Use Committee.

Protein and peptide reagents.

A purified recombinant SARS-CoV-2 RBD fusion with a mouse IgG1 constant region was used as a target for Western Blot and tagged with a human Fc-tag (both Sino Biological) was used in ELISA to detect SARS-CoV-2 S-specific IgG. A purified recombinant RBD with a histidine tag (Sino Biological) was used for surface plasmon resonance (SPR) spectroscopy. An overlapping 15-mer peptide pool of the S protein was used for ELISpot, cytokine profiling and intracellular cytokine staining. A peptide control (SPSYVYHQF, derived from gp70 AH-1 (Slansky, J. E. et al., Immunity 13, 529–538, 2000)) was used as control for ELISpot assays. All peptides were obtained from JPT Peptide Technologies.

Human convalescent sera.

Human COVID-19 convalescent sera (n=38) were drawn from donors 18-83 years of age at least 14 days after PCR-confirmed diagnosis and at a time when the participants were asymptomatic. Serum donors had symptomatic infections (35/38), or had had been hospitalised (1/38). Sera were obtained from Sanguine Biosciences (Sherman Oaks, CA), the MT group (Van Nuys, CA) and Pfizer Occupational Health and Wellness (Pearl River, NY).

Cell culture.

Human embryonic kidney (HEK)293T/17 and Vero-76 cells (both ATCC) were cultured in Dulbecco's modified Eagle's medium (DMEM) with GlutaMAX™ (Gibco) supplemented with 10% fetal bovine serum (Sigma-Aldrich). Cell lines were tested for mycoplasma contamination after receipt, before expansion and cryopreservation. Vero E6 and Vero CCL81 (both ATCC) cells were cultured in DMEM (Gibco) containing 2% HyClone fetal bovine serum and 100 U/mL penicillium/streptomycin (Gibco). Expi293F™ cells were grown in Expi293™ media and transiently transfected using ExpiFectamine™293 (all from Thermo Fisher Scientific).

Manufacturing of *in vitro* transcribed RNA.

To generate the template for RNA synthesis, a DNA fragment encoding a fusion protein composed of the signal peptide (SP, amino acids 1-16), the SARS-CoV-2 S RBD (GenBank: MN908947) and a T4 fibritintrimerisation motif ('foldon'), was cloned into a starting plasmid vector with backbone sequence elements for improved RNA stability and translational efficiency (Orlandini von Niessen, A. G. et al., Mol Ther 27, 824–836; 2019; Holtkamp, S. et al., Blood 108, 4009–4017, 2006). Non-coding backbone elements included the regions from the T7 promoter to the 5' and 3' UTR plus a poly(A) tail (100 nucleotides) interrupted by a linker (A30LA70, 10 nucleotides). The DNA was purified, spectrophotometrically quantified, and *in vitro* transcribed by T7 RNA polymerase in the presence of a trinucleotide cap1 analogue ($(m_2^{7,3'-O})$Gppp($m^{2'-O}$)ApG; TriLink) and of N^1-methylpseudouridine-5'-triphosphate (m1ΨTP; Thermo Fisher Scientific) instead of uridine-5'-triphosphate (UTP) (Grudzien-Nogalska, E. et al., Methods in molecular biology (Clifton, N.J.) 969, 55–72, 2013). RNA was purified using magnetic particles (Berensmeier, S., Appl.Microbiol.Biotechnol. 73, 495–504, 2006), integrity assessed by microfluidic capillary electrophoresis (Agilent Fragment Analyser), and concentration, pH, osmolality, endotoxin level and bioburden determined.

Lipid-nanoparticle formulation of the RNA.

Purified RNA was formulated into LNPs using an ethanolic lipid mixture ofionisable cationic lipid and transferred into an aqueous buffer system via diafiltration to yield an LNP

composition similar to one previously described (Maier, M. A. et al., Molecular therapy : the journal of the American Society of Gene Therapy 21, 1570–1578, 2013). BNT162b1 was stored at -70 °C at a concentration of 0.5 mg/mL.

mRNA transfection.

HEK293T/17 cells were transfected with transfection reagent-mixed BNT162b1 RNA or BNT162b1 by incubation for 18 hours. Non-LNP formulated mRNA (1 µg for Western blot and flow cytometry, 2.5 µg for immunofluorescence) was diluted in Opti-MEM medium (Thermo Fisher Scientific) and mixed with the transfection reagents according to the manufacturer's instructions (RiboJuice, Merck Millipore).

Western blot analysis.

A lysate of BNT162b1 RNA transfected HEK293T/17 cells was analysed by denaturing SDS-PAGE with 10% Mini-Protean TGX precast polyacrylamide gels (Bio-Rad) and Western blot. Transfer to a nitrocellulose membrane (Carl Roth) was performed using a semi-dry transfer system (Trans-Blot Turbo Transfer System, Bio-Rad). Blotted proteins were detected with a primary rabbit polyclonal antibody elicited by a recombinant S1 fragment of the SARS-CoV S (SinoBiological) and a secondary anti-rabbit horse raddish peroxidase (HRP)-conjugated antibody (Sigma Aldrich). Blots were developed with SuperSignal West Femto chemiluminescent substrate (Thermo Fisher Scientific) and imaged with a Bio-Rad ChemiDoc system using the Image Lab software version 5.0.

Immunofluorescence.

Transfected HEK293T/17 cells were fixed in 4% paraformaledehyde (PFA) and permeabilised in phosphate-buffered saline (PBS)/0.2% Triton X-100. Free binding sites were blocked and cells incubated with a rabbit polyclonal antibody recognising the S1 Subunit (SinoBiological) and anti-rabbit IgG secondary antibody (Jackson ImmunoResearch), or labelled Concanavalin A (Invitrogen). DNA was stained with Hoechst (Life Technologies). Images were acquired with a Leica SP8 confocal microscope.

Flow cytometry.

Transfected HEK293T/17 cells were stained with Fixable Viability Dye (eBioscience). After fixation (Fixation Buffer, Biolegend), cells were permeabilised (Perm Buffer, eBioscience) and stained with a monoclonal SARS-CoV-2 spike S1 antibody (SinoBiological). Cells were acquired on a FACSCanto II flow cytometer (BD Biosciences) using BD FACSDiva software version 8.0.1 and analysed by FlowJo software version 10.6.2 (FlowJo LLC, BD Biosciences).

For mouse T-cell analysis in peripheral blood, erythrocytes from 50 µL freshly drawn blood were lysed (ACK lysing buffer, Gibco), and cells were stained with Fixable Viability Dye (eBioscience) and primary antibodies in the presence of Fc block in flow buffer (DPBS [Gibco] supplemented with 2% FCS, 2 mM EDTA [both Sigma] and 0.01% sodium azide [Morphisto]). After staining with secondary biotin-coupled antibodies in flow buffer, cells were stained extracellularly against surface markers with directly labelled antibodies and streptavidin in Brilliant Stain Buffer Plus (BD Bioscience) diluted in flow buffer. Cells were fixed with 2% RotiHistofix (Carl Roth) and permeabilised (Perm Buffer, FoxP3/Transcription Factor Staining Buffer Set, eBioscience) overnight. Permeabilised cells were intracellularly treated with Fc block and stained with antibodies against transcription factors in Perm Buffer.

For mouse T-cell analysis in lymphoid tissues, 1×10^6 lymph node and 4×10^6 spleen cells were stained for viability and extracellular antigens with directly labelled antibodies. Cells were washed in 2% RotiHistofix and fixed (Fix/Perm Buffer, FoxP3/Transcription Factor Staining Buffer Set, eBioscience) overnight. Intracellular staining was performed as described for blood T-cell staining. For mouse B-cell subtyping in lymphoid tissues, 2.5×10^5 lymph node and 1×10^6 spleen cells were treated with Fc block, stained for viability and extracellular antigens as described for blood T-cell staining and fixed with 2% RotiHistofix overnight. For mouse intracellular cytokine staining in T cells, 1×10^6 lymph node and 4×10^6 spleen cells were *ex vivo* restimulated with 0.2 µg/mL final concentration per peptide of full-length S peptide mix in the presence of GolgiStop and GolgiPlug (both BD Bioscience) for 5 hours. Cells were stained for viability and extracellular antigens as described for lymphoid T-cell staining. Cells were

fixed with 2% RotiHistofix and permeabilised overnight. Intracellular staining was performed as described for blood T-cell staining.

Mouse cells were acquired on a BD Symphony A3 or BD Celesta (B-cell subtyping) flow cytometer (BD Bioscience) using BD FACSDiva software version 9.1 or 8.0.1.1, respectively, and analysed with FlowJo 10.6 (FlowJo LLC, BD Biosciences).

Protein expression and purification.

To express the RBD-foldon encoded by BNT162b1 for biochemical and structural analysis, DNA corresponding to the RNA coding sequence was cloned into the pMCG1309 vector. A plasmid encoding amino acids 1–615 of human ACE2 with C-terminal His-10 and Avi tags was generated for transient expression of the ACE2 peptidase domain (ACE2 PD) in Expi293F cells. The ACE2/B^0AT1 complex was produced by co-expression of two plasmids in Expi293F cells, one of them encoding ACE2 amino acids 1–17 followed by haemagglutinin and Strep II tags and ACE2 amino acids 18–805, and the other containing a methionine followed by a FLAG tag and amino acids 2–634 of human B^0AT1.

Secreted ACE2 PD was isolated from conditioned cell culture medium using Nickel Excel resin (GE Healthcare) followed by gel filtration chromatography on a Superdex200 10/30 column (GE Healthcare) in PBS. Approximately 5 mg of purified ACE2 PD was covalently attached per 1 mL of 4% beaded agarose by amine coupling using AminoLink Plus resin (Thermo Fisher Scientific). The RBD-trimer was purified from conditioned medium by affinity capture with the ACE2 PD crosslinked agarose and was eluted from the resin with 3 M $MgCl_2$. Following dialysis, the protein was concentrated and purified by gel filtration using a Superdex200 10/300 column in HEPES-buffered saline (HBS) with 10% glycerol. Purification of the ACE2/B^0AT1 complex was based on the procedure described previously (Yan, R. et al., Science (New York, N.Y.) 367, 1444–1448, 2020). To form the ACE2/B^0AT1/RBD-trimer complex, ACE2/B^0AT1 aliquots were combined with purified RBD-foldon diluted in ACE2/B^0AT1 size exclusion chromatography buffer (25 mM Tris pH 8.0, 150 mM NaCl, 0.02% glyco diosgenin) for a 3:1 molar ratio of RBD-trimers to ACE2 protomers. After incubation at 4 °C for 30 minutes, the

sample was concentrated and resolved on a Superose 6 Increase 10/300 GL column. Peak fractions containing the complex were pooled and concentrated.

Surface plasmon resonance spectroscopy.

Binding kinetics of murine RBD-specific serum IgGs was determined using a Biacore T200 device (Cytiva) with HBS-EP running buffer (BR100669, Cytiva) at 25 °C. Carboxyl groups on the CM5 sensor chip matrix were activated with a mixture of 1-ethyl-3-(3-dimethylaminopropyl) carbodiimidehydrochloride (EDC) and N-hydroxysuccinimide (NHS) to form active esters for the reaction with amine groups. Anti-mouse-Fc-antibody (Jackson ImmunoResearch) was diluted in 10 mM sodium acetate buffer pH 5 (30 µg/mL) for covalent coupling to immobilisation level of ~10,000 response units (RU). Free N-hydroxysuccinimide esters on the sensor surface were deactivated with ethanolamine.

Mouse serum was diluted 1:50 in HBS-EP buffer and applied at 10 µL/min for 30 seconds to the active flow cell for capture by immobilised antibody, while the reference flow cell was treated with buffer. Binding analysis of captured murine IgG antibodies to RBD-His (Sino Biological Inc.) was performed using a multi-cycle kinetic method with concentrations ranging from 1.5625 to 50 nM. An association period of 180 seconds was followed by a dissociation period of 600 seconds with a constant flow rate of 40 µL/min and a final regeneration step. Binding kinetics were calculated using a global kinetic fit model (1:1 Langmuir, Biacore T200 Evaluation Software Version 3.1, Cytiva).

Biolayer interferometry.

Binding of RBD-foldon to the ACE2-PD was measured by biolayer interferometry on an Octet RED384 (FortéBio) in a buffer composed of 10 mM HEPES pH 7.5, 150 mM NaCl and 1 mM EDTA at 25 °C. Avi-tagged human ACE2 PD was immobilised on streptavidin-coated sensors. Binding data were collected for 10 minutes of association and 15 minutes of dissociation for a concentration series of RBD-trimer. Data were reference-subtracted and fit to a 1:1 binding model with R^2 value greater than 0.96 to determine kinetics and affinity of binding, using Octet Data Analysis Software v10.0 (FortéBio). The dissociation rate of interaction (k_d) was slower

than the limit of measurement of the instrument, and the binding affinity (K_D) was estimated using an assumed dissociation rate k_d of 1×10^{-6} s^{-1}.

Electron microscopy of negatively stained samples.

Purified RBD-trimer protein in 4 µL was applied to a glow-discharged copper grid overlaid with formvar and amorphous carbon (Ted Pella). Staining was performed with Nano-W organotungstate stain (Nanoprobes) according to the manufacturer's protocol, and the sample imaged using an FEI TF-20 microscope operating at 200 kV, with a magnification of 62,000x and defocus of -2.5 µm. Micrographs were contrast transfer function (CTF)-corrected in RELION using CTFFIND-4.1 (Rohou, A. & Grigorieff, N., Journal of structural biology 192, 216–221, 2015). A small manually picked dataset was used to generate 2D references for auto-picking. The resulting particle set was subjected to 2D classification in RELION 3.0.6 (Zivanov, J. et al., eLife 7; 10.7554/eLife.42166 (2018)).

Cryo-electron microscopy.

Purified ACE2/B^{0}AT1/RBD-trimer complex at 6 mg/mL in 4 µL was applied to gold Quantifoil R1.2/1.3 200 mesh grids glow discharged in residual air for 30 seconds at 20 mA using a Pelco Easiglow. The sample was blotted using a Vitrobot Mark IV for 5 seconds with a force of -3 before being plunged into liquid ethane cooled by liquid nitrogen. In total, 7,455 micrographs were collected from a single grid on a Titan Krios operating at 300 keV equipped with a Gatan K2 Summit direct electron detector in super-resolution mode at a magnification of 165,000x, for a magnified pixel size of 0.435 Å at the specimen level. Data were collected over a defocus range of -1.2 to -3.4 µm with a total electron dose of 52.06 $e^-/Å^2$ fractionated into 40 frames over a 6-second exposure for 1.30 $e^-/Å^2$/frame. Initial motion correction was performed in Warp (Tegunov, D. & Cramer, P., Nature methods 16, 1146–1152, 2019), during which super-resolution data were binned to give a pixel size of 0.87 Å. Corrected micrographs were imported into RELION 3.1-beta (Zivanov, J. et al., eLife 7; 10.7554/eLife.42166 (2018)) for CTF estimation with CTFFIND-4.1 (Rohou, A. & Grigorieff, N., Journal of structural biology 192, 216–221, 2015). Particles were picked using the LaPlacian-of-Gaussian particle picking

algorithm as implemented in RELION and extracted with a box size of 450 pixels. References obtained by 2D classification were used for a second round of reference-based auto-picking, yielding a dataset of 715,356 particles. Particle heterogeneity was filtered out with 2D and 3D classification with a mask size of 280 nm to filter out the non-ACE2-bound RBD copies in each RBD-trimer, yielding a set of 87,487 particles, which refined to 3.73 Å with C2 symmetry. Refinement after subtraction of micelle and B^0AT1 density from the particles yielded an improved map of 3.24 Å. The atomic model from PDB ID 6M17 (Yan, R. et al., Science (New York, N.Y.) 367, 1444–1448, 2020) was rigid-body fitted into the 3.24 Å density, then flexibly fitted to the density using real-space refinement in Phenix (Adams, P. D. et al., Acta crystallographica. Section D, Biological crystallography 66, 213–221, 2010) alternating with manual building in Coot (Emsley, P. et al., Acta crystallographica. Section D, Biological crystallography 66, 486–501, 2010). The microscope was operated for image acquisition using SerialEM software version 3.8.0 beta (Mastronarde, D. N., Journal of structural biology 152, 36–51, 2005). Biolayer interferometry data was collected with Octet Data Acquisition software version 10.0.0.87 and processing was performed using ForteBio Data Analysis software version 10.0.

Immunisation.

Mice. Female BALB/c mice (Janvier; 8-12 weeks) were randomly allocated to groups. BNT162b1 was diluted in PBS, 300 mM sucrose or saline (0.9% NaCl) and injected IM into the gastrocnemius muscle at a volume of 20 µL under isoflurane anaesthesia.

Rhesus macaques (*Macaca mulatta*). Male rhesus macaques (2–4 years) were randomly assigned to receive either BNT162b1 or saline placebo control in 0.5 mL volume administered by IM injection in the left quadriceps muscle on Days 0 and 21. Blood for serum and PBMCs was collected in compliance with animal protocol 2017-8725-023 approved by the NIRC Institutional Animal Care and Use Committee. Animals were anesthetised with ketamine HCl (10 mg/kg; IM) during blood collection and immunisation, and monitored for adequate sedation.

SARS-CoV-2 challenge of rhesus macaques.

The SARS-CoV-2 inoculum was obtained from a stock of 2.1×10^6 PFU/mL previously prepared at Texas Biomedical Research Institute (San Antonio, Texas), aliquoted into single use vials, and stored at -70 °C. The working virus stock was generated from two passages of the SARS-CoV-2 USA-WA1/2020 isolate (a 4th passage seed stock purchased from BEI Resources; NR-52281) in Vero E6 cells. The virus was confirmed to be SARS-CoV-2 by deep sequencing and identical to the published sequence (GenBank accession number MN985325.1).

BNT162b1-immunised (n=6) and age-matched saline control-immunised (n=6) male rhesus macaques (control) were challenged with 1×10^6 plaque forming units of SARS-CoV-2 USA-WA1/2020 isolate, split equally between the intranasal (IN; 0.2 mL) and intratracheal (IT; 0.2 mL) routes as previously described (Singh, D. K. et al., SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species, 2020). The challenge was performed 41 to 48 days after the second immunisation. A separate sentinel group of non-immunised age- and sex-matched animals (n=3) received only DMEM supplemented with 10% FCS IN (0.2 mL) and IT (0.2 mL). Approximately two weeks prior to challenge, animals were moved to the Animal Biosafety Level 3 (ABSL-3) facility at Southwest National Primate Research Center (SNPRC; San Antonio, TX). Animals were monitored regularly by a board-certified veterinary clinician for rectal body temperature, weight and physical examination. Specimen collection was performed under tiletamine zolazepam (Telazol) anaesthesia as described (Singh, D. K. et al., SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species, 2020). Nasal swabs were collected from macaques at 0, 1, 3, and 6 days after inoculation to assess viral titers. Bronchoalveolar lavage (BAL) was performed the week before challenge and at Days 3 and 6 post-inoculation by instilling four times 20 mL of saline. These washings were pooled, aliquoted and stored frozen at -70 °C.

Reverse-transcription quantitative polymerase chain reaction.

To detect and quantify SARS-CoV-2, viral RNA was extracted from nasal swabs and BAL specimens as previously described (Mehra, S. et al., The Journal of infectious diseases 207, 1115–1127, 2013; Gautam, U. S. et al., Proceedings of the National Academy of Sciences of the United States of America 115, E62-E71; 2018; Joosten, S. A. et al., PLoS pathogens 6, e1000782, 2010) and tested by RT-qPCR as previously described (Singh, D. K. et al., SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species, 2020). Briefly, 10 µg yeast tRNA and 1×10^3 PFU of MS2 phage (*Escherichia coli* bacteriophage MS2, ATCC) were added to each thawed sample, and RNA extraction performed using the NucleoMag Pathogen kit (Macherey-Nagel). The SARS-CoV-2 RT-qPCR was performed on extracted RNA using a CDC-developed 2019-nCoV_N1 assay on a QuantStudio 3 instrument (Applied Biosystems). The cut-off for positivity (limit of detection, LOD) was established at 10 gene equivalents (GE) per reaction (800 GE/mL). Samples were tested in duplicate. On day 6, one BAL specimen from the control group and one day 1 nasal swab from the BNT162b1-immunised group had, on repeated measurements, viral RNA levels on either side of the LLOD. These specimens were categorised as indeterminate and excluded from the graphs and the analysis.

Tissue preparation.

Mice. Peripheral blood was collected from the retro-orbital venous plexus or *vena facialis* under isoflurane anaesthesia. Blood was centrifuged for 5 minutes at 16.000 x g, and the serum was immediately used for downstream assays or stored at -20 °C. Spleen single-cell suspensions were prepared in PBS by mashing tissue against the surface of a 70 µm cell strainer (BD Falcon) using the plunger of a 3-mL syringe (BD Biosciences). Erythrocytes were removed by hypotonic lysis. Popliteal, inguinal and iliac lymph nodes were pooled, cut into pieces, digested with collagenase D (1 mg/mL; Roche) and passed through cell strainers.

Rhesus macaques (*Macaca mulatta*). Blood for serum and PBMCs was collected in compliance with animal protocol 2017-8725-023 approved by the NIRC Institutional Animal Care and Use Committee.

RBD-binding IgG antibody assay.

For mouse sera, MaxiSorp plates (Thermo Fisher Scientific) were coated with recombinant RBD (100 ng/100 µL) in sodium carbonate buffer, and bound IgG was detected using an HRP-conjugated secondary antibody and TMB substrate (Biotrend). Data collection was performed using a BioTek Epoch reader and Gen5 software version 3.0.9. For concentration analysis, the signal of the specific samples was correlated to a standard curve of an isotype control. For rhesus macaque and human sera, a recombinant SARS-CoV-2 RBD containing a C-terminal Avitag™ (Acro Biosystems) was bound to streptavidin-coated Luminex microspheres. Bound rhesus macaque or human anti-RBD antibodies present in the serum were detected with a fluorescently labelled goat anti-human polyclonal secondary antibody (Jackson ImmunoResearch). Data were captured as median fluorescent intensities (MFIs) using a Bioplex200 system (Bio-Rad) and converted to U/mL antibody concentrations using a reference standard curve consisting of 5 pooled human COVID-19 convalescent serum samples (obtained >14 days PCR diagnosis), diluted in antibody depleted human serum, with arbitrary assigned concentrations of 100 U/mL and accounting for the serum dilution factor.

VSV-SARS-CoV-2 spike variant pseudovirus neutralisation.

A recombinant replication-deficient vesicular stomatitis virus (VSV) vector that encodes GFP instead of VSV-G (VSVΔG-GFP) was pseudotyped with SARS-CoV-2 S protein according to published pseudotyping protocols (Berger Rentsch, M. & Zimmer, G., PLoS ONE 6, e25858, 2011; Lester, S. et al., Access Microbiology 1, 20290, 2019). In brief, HEK293T/17 monolayers transfected to express SARS-CoV-2 S truncated of the C-terminal cytoplasmic 19 amino acids (SARS-CoV-2-S-CΔ19) were inoculated with VSVΔG-GFP vector. After incubation for 1 hour at 37 °C, the inoculum was removed and cells were washed with PBS before medium supplemented with anti-VSV-G antibody (clone 8G5F11, Kerafast Inc.) was added to neutralise residual input virus. VSV/SARS-CoV-2 pseudovirus-containing medium was harvested 20 hours after inoculation, 0.2 µm filtered and stored at -80 °C.

Vero-76 cells were seeded in 96-well plates. Serial dilutions of mouse serum samples were prepared and pre-incubated for 10 minutes at room temperature with VSV/SARS-CoV-2 pseudovirus suspension (4.8×10^3 infectious units [IU]/mL) before transferring the mix to Vero-76 cells. Inoculated Vero-76 cells were incubated for 20 hours at 37 °C. Plates were placed in an IncuCyte Live Cell Analysis system (Sartorius) and incubated for 30 minutes prior to the analysis (IncuCyte 2019B Rev2 software). Whole well scanning for brightfield and GFP fluorescence was performed using a 4× objective. The 50% pseudovirus neutralisation titre ($pVNT_{50}$) was reported as the reciprocal of the first serum dilution yielding a 50% reduction in GFP-positive infected cell number per well compared to the mean of the no serum pseudovirus positive control. Each serum sample dilution was tested in duplicates.

SARS-CoV-2 neutralisation by human convalescent and rhesus macaque sera.

The SARS-CoV-2 neutralisation assay used a previously described strain of SARS-CoV-2 (USA_WA1/2020) that had been rescued by reverse genetics and engineered by the insertion of an mNeonGreen (mNG) gene into open reading frame 7 of the viral genome (Xie, X. et al., Cell host & microbe 27, 841-848.e3, 2020). This reporter virus generates similar plaque morphologies and indistinguishable growth curves from wild-type virus. Viral master stocks were grown in Vero E6 cells as previously described (Lester, S. et al., Access Microbiology 1, 20290, 2019). When testing human convalescent serum specimens, the fluorescent neutralisation assay produced comparable results as the conventional plaque reduction neutralisation assay. Serial dilutions of heat-inactivated sera were incubated with the reporter virus (2×10^4 PFU per well) to yield approximately a 10-30% infection rate of the Vero CCL81 monolayer) for 1 hour at 37 °C before inoculating Vero CCL81 cell monolayers (targeted to have 8,000 to 15,000 cells per well) in 96-well plates to allow accurate quantification of infected cells. Total cell counts per well were enumerated by nuclear stain (Hoechst 33342) and fluorescent virally infected foci were detected 16-24 hours after inoculation with a Cytation 7 Cell Imaging Multi-Mode Reader (Biotek) with Gen5 Image Prime version 3.09. Titers were calculated in GraphPad Prism version 8.4.2 by generating a 4- parameter (4PL)

logistical fit of the percent neutralisation at each serial serum dilution. The 50% neutralisation titre (VNT_{50}) was reported as the interpolated reciprocal of the dilution yielding a 50% reduction in fluorescent viral foci.

IFNγ ELISpot.

ELISpot assays were performed with mouse IFNγ ELISpot^{PLUS} kits according to the manufacturer's instructions (Mabtech). A total of 5×10^5 splenocytes was *ex vivo* were restimulated with the full-length S peptide mix (0.1 µg/mL final concentration per peptide, JPT) or controls (gp70-AH1 [SPSYVYHQF] (Slansky, J. E. et al., Immunity 13, 529–538, 2000), JPT, 4 µg/mL; Concanavalin A (ConA), Sigma, 2 µg/mL). Streptavidin-ALP and BCIP/NBT-plus substrate were added, and spots counted using an ELISpot plate reader (ImmunoSpot® S6 Core Analyzer, CTL). Spot numbers were evaluated using ImmunoCapture Image Aquision Software V7.0 and ImmunoSpot 7.0.17.0 Professional. For T-cell subtyping, $CD8^+$ T cells were isolated from splenocyte suspensions using MACS MicroBeads (CD8a [Ly-2], Miltenyi Biotec) according to the manufacturer's instructions. The flow-through served as a source of $CD4^+$ T cells. $CD8^+$ or $CD4^+$ T cells were subsequently restimulated with syngeneic bone marrow-derived dendritic cells loaded with full-length S peptide mix (0.1 µg/mL final concentration per peptide) or medium as control. Purity of isolated T-cell subsets was determined by flow cytometry to calculate spot counts per 1×10^5 $CD8^+$ or $CD4^+$ T cells.

Cytokine profiling.

Mouse splenocytes were re-stimulated for 48 hours with full-length S peptide mix (0.2 µg/mL final concentration per peptide) or medium only. Concentrations of IFNγ, IL-2, IL-4 and IL-5 in supernatants were determined using a bead-based, 11-plex T_H1/T_H2 mouse ProcartaPlex multiplex immunoassay (Thermo Fisher Scientific) according to the manufacturer's instructions. Fluorescence was measured with a Bioplex200 system (Bio-Rad) and analysed with ProcartaPlex Analyst 1.0 software (Thermo Fisher Scientific).

Statistics and reproducibility.

No statistical methods were used to predetermine group and samples sizes (n). All experiments were performed once. P-values reported for RT-qPCR analysis were determined by categorical analysis for binomial response (undetectable viral RNA after challenge as success, measurable viral RNA after challenge as failure) with logit link to treatment and day effects using PROC GENMOD from SAS® 9.4. Samples from post challenge days (Days 3 and 6 for BAL; Days 1, 3 and 6 for nasal swab) were included in the analysis. Indeterminate results were excluded from this analysis. All remaining analyses were carried out using GraphPad Prism 8.4.

Results

We designed a SARS-CoV-2 vaccine named BNT162b1, which is composed of an LNP-encapsulated N^1-methyl-pseudouridine (m1Ψ) nucleoside-modified mRNA that encodes the RBD fused at its C-terminus to the natural trimerisation domain (foldon) of T4 fibritin (Meier, S. et al., Journal of molecular biology 344, 1051–1069, 2004) (Fig. 64a). The SARS-CoV-2 S signal peptide (SP) enables ER translocation and secretion of the trimeric RBD. The m1Ψ-modification of the RNA dampens innate immune sensing and, together with optimized non-coding sequence elements, increases RNA translation *in vivo* (Orlandini von Niessen, A. G. et al., Mol Ther 27, 824–836, 2019; Karikó, K. et al., Molecular therapy: the journal of the American Society of Gene Therapy 16, 1833–1840, 2008).

BNT162b1 RNA *in vitro* transcribed by T7 polymerase from a plasmid DNA template had a single, sharp peak microfluidic capillary electrophoresis profile, consistent with its calculated length of 1262 nucleotides, indicating purity and integrity (data not shown). Western blot analysis of a lysate of BNT162b1 RNA-transfected HEK293T/17 cells demonstrated that the RBD was expressed from the RNA and had an apparent molecular weight consistent with its calculated weight of 29.46 kDa (data not shown). Protein expression and endoplasmic reticulum localisation on the secretory pathway in transfected cells were confirmed by flow cytometry and immunofluorescence microscopy, respectively (data not shown).

For structural characterization, the trimerised RBD was expressed from a DNA sequence corresponding to the coding sequence of BNT162b1 RNA in Expi293F cells and purified by affinity capture with the ACE2 peptidase domain immobilized on agarose beads. The trimerised RBD bound to the human ACE2 peptidase domain (PD) with high affinity (5 pM K_D), which is approximately 1,000-fold the reported K_D of 5.09 nM for monomeric RBD and consistent with the avidity effect of multimeric binding (data not shown). The trimeric valency of the RBD-foldon and its flexibility were visualized by electron microscopy (EM) of negatively stained specimens, which revealed a range of conformations (Fig. 64b). Although the flexibility of the RBD-foldon precluded direct structural analysis at high resolution, the RBD domains could be immobilized by binding to a complex of ACE2 and the B^0AT1 neutral amino acid transporter, which ACE2 chaperones, when that complex was in the previously reported closed conformation (Yan, R. et al., Science (New York, N.Y.) 367, 1444–1448, 2020). The size and symmetry of the RBD-foldon/ACE2/B^0AT1 ternary complex aided image reconstruction by electron cryomicroscopy (cryoEM), and the structure of the RBD domains in the complex was determined to 3.24 Å resolution (Fig. 64c). One copy of the RBD was resolved for each bound trimer. The binding interface between the resolved RBD and the ACE2 extracellular domain was fitted to a previously reported structure and showed good agreement (He, Y. et al., Biochemical and Biophysical Research Communications 324, 773–781, 2004; Yi, C. et al., Cellular & molecular immunology; 10.1038/s41423-020-0458-z, 2020). The high affinity binding to ACE2 and well-resolved structure in complex with ACE2 demonstrate that the recombinant RBD-foldon authentically presents the ACE2 binding site targeted by many SARS-CoV-2 neutralising antibodies (Brouwer, P. J. M. et al., Science (New York, N.Y.); 10.1126/science.abc5902 (2020); Zost, S. J. et al., Nature medicine; 10.1038/s41591-020-0998-x (2020)).

BNT162b1-elicited B- and T-cell immune responses were characterised in a series of experiments in BALB/c mice after a single intramuscular (IM) immunisation with 0.2, 1, or 5 µg BNT162b1 or with buffer alone. RBD-specific serum IgG developed quickly at all dose levels in

a dose-dependent manner and plateaued around day 21 (at 1.63 ± 0.13 mg/mL for the 5 µg dose level; Fig. 65a). Vaccine-elicited IgG had high RBD-binding affinity (geometric mean K_D 48.0 pM) with high on-rate (geometric mean k_{on} 1.72 x 10^6/Ms) and low off-rate (geometric mean K_{off} 8.27 x 10^{-5}/s; Fig. 65b). SARS-CoV-2 neutralising activity in mouse serum was measured by a vesicular stomatitis virus (VSV)-based SARS-CoV-2 pseudovirus neutralisation assay. Mean 50% pseudovirus neutralisation titers ($pVNT_{50}$) increased steadily after immunisation to 102, 192, and 1,056 on day 28 for the 0.2, 1, and 5 µg dose levels, respectively (Fig. 65c).

A high fraction of splenocytes of both $CD4^+$ and $CD8^+$ T-cell phenotypes isolated from BNT162b1-immunised mice on days 12 and 28 after immunisation, when re-stimulated *ex vivo* with a full-length S peptide mix, exerted a strong antigen-specific IFNγ-response in ELISpot assays (Fig. 65d). Full-length S peptide-stimulated bulk splenocytes and $CD4^+$ and $CD8^+$ subsets also show high IFNγ production at day 12 and significant IL-2 responses but much lower IL-4 responses in flow cytometric cytokine release analyses, indicating a T_H1 phenotype response (Fig. 65e). The T_H1 phenotype persists, with total splenocytes harvested on day 28 and stimulated with the full-length S peptide pool producing high levels of IL-2 and IFNγ but undetectable amounts of the T_H2 cytokines IL-4 and IL-5 in multiplex immunoassays (Fig. 65f). In draining lymph nodes (dLN) and spleens obtained 12 days after immunisation of mice with BNT162b1 or buffer, much higher numbers of B cells (including plasma cells, class switched IgG1- and IgG2a-positive B cells, and germinal center B cells) were observed in the samples from mice that received BNT162b1 (data not shown). In blood obtained 7 days after immunisation, the number of circulating B cells was lower than in buffer-immunised mice, most likely due to B-cell homing to lymphoid compartments (data not shown). dLNs from BNT162b1-immunised mice also displayed an elevation in T-cell counts, particularly numbers of T follicular helper (T_{FH}) cells, including subsets with ICOS upregulation, which are known to play an essential role in the formation of germinal centers (Hutloff, A., Oncotarget 6, 21785–21786, 2015) (data not shown). BNT162b1-induced elevation of T_{FH} cells was also detected in

the spleen and blood (data not shown). In aggregate, these data indicate a strong and concurrent induction of SARS-CoV-2 S-specific neutralising antibody titers and a T_H1-driven T-cell response by BNT162b1. Intramuscularly administered BNT162b1 appears to be delivered to dLNs as immune-educated sites for proficient vaccine priming, with migration of lymphocytes from the blood to lymphoid tissues to participate in the vaccine response.

The immunogenicity of BNT162b1 was next tested in 2–4 year old male rhesus macaques. Groups of six were immunised IM with 30 or 100 µg of BNT162b1 or with saline control on Days 0 and 21. RBD-binding IgG was readily detectable by Day 14 after a single immunisation, and levels increased further through Day 21, when the boosting dose was given (Fig. 66a). Seven days after the second immunisation (Day 28), the geometric mean RBD-binding IgG concentrations (GMCs) were 20,962 units (U)/mL (30 µg dose level) and 48,575 U/mL (100 µg dose level). For comparison, the RBD-binding IgG GMC of a panel of 38 SARS-CoV-2 convalescent human sera was 602 U/mL, substantially lower than the GMC of the immunised rhesus macaques after one or two doses. Fifty percent neutralisation titers (VNT_{50}), measured by an authentic SARS-CoV-2 neutralisation assay (Muruato, A. E. et al., bioRxiv : the preprint server for biology; 10.1101/2020.05.21.109546, 2020), were detectable in rhesus sera by Day 14 after a single immunisation and reached geometric mean titers (GMTs) of 768 (30 µg dose level) or 1,714 (100 µg dose level) 7 days after the boost (Day 28, Fig. 66b). Robust neutralisation GMTs of 247 for 30 µg and 564 for 100 µg dose levels persisted to at least Day 42 (most recent time point tested). For comparison, the 50% neutralisation GMT of the human convalescent serum panel was 93.6.

The groups of rhesus macaques (n=6) that had received two immunisations with 100 µg BNT162b1 or buffer control were challenged 41 to 48 days after the second immunisation with 1×10^6 plaque forming units of SARS-CoV-2 (strain USA-WA1/2020), split equally between the intranasal and intratracheal routes, as previously described (Singh, D. K. et al. SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species, 2020). Three non-immunised, age-

matched, male rhesus macaques (sentinel) were mock-challenged with cell culture medium. At the time of challenge, SARS-CoV-2 neutralising titers ranged from 208 to 1,185 in the BNT162b1-immunised animals and were undetectable in animals from the control-immunised and sentinel groups.

SARS-CoV-2 RNA was measured in bronchoalveolar lavage (BAL) and nasal swab samples by reverse-transcription quantitative polymerase chain reaction (RT-qPCR). All BAL and nasal swab samples obtained before the infectious challenge and all those obtained from sentinel animals lacked detectable SARS-CoV-2 RNA (Fig. 67). Three days after SARS-CoV-2 challenge, viral RNA was detected in BAL fluid from 5/6 control-immunised and 2/6 BNT162b1-immunised animals (Fig. 67a). By 6 days after challenge, all six BNT162b1-immunised macaques had undetectable viral RNA in their lungs; of the control-immunised macaques, three had a high level of viral RNA in BAL fluid, two had cleared, and one had an indeterminate RT-qPCR result. At the time of necropsy (7-23 days after challenge), no viral RNA was detectable in BAL fluid from any animal. After SARS-CoV-2 challenge, viral RNA was detected in nasal swabs of the control-immunised group at each time point: two animals at Day 1, three animals at Days 3 and 6 after challenge (Fig. 67b), and two animals at the time of necropsy (not shown). In BNT162b1-immunised animals, all nasal swabs were negative or indeterminate at Day 1, and all were negative at Day 3 and at the time of necropsy; at Day 6, swabs from two were positive, indicating a more transient course of viral RNA detection compared to non-immunised rhesus macaques. The difference in the proportion of animals with detectable viral RNA between BNT162b1-immunised animals and control-immunised animals is statistically significant ($p=0.0037$ for BAL, and 0.0212 for nasal swab). None of the challenged animals showed clinical or radiographic signs of significant illness, indicating that the 2-4 years old male rhesus challenge model is primarily an infection model for SARS-CoV-2, not a COVID-19 disease model.

Discussion

We demonstrate that BNT162b1, an LNP-formulated m1Ψ nucleoside-modified mRNA encoding the trimeric RBD antigen, is highly immunogenic in mice and rhesus macaques and limits infection in rhesus macaques challenged with infectious SARS-CoV-2. The RBD-foldon coding sequence directs the expression of a flexible, trimeric protein that binds ACE2 with high affinity and has a structurally intact ACE2 receptor binding site. One key finding is that in mice, a single sub-microgram immunisation rapidly induces high neutralising antibody titers that are in the range or above recently reported SARS-CoV-2 vaccine candidates (van Doremalen, N. et al., bioRxiv : the preprint server for biology; 10.1101/2020.05.13.093195 (2020); Corbett, K. S. et al., bioRxiv : the preprint server for biology; 10.1101/2020.06.11.145920 (2020)). The strong $CD4^+$ and stronger $CD8^+$ T-cell responses, both skewing towards a T_H1-bias, and T_{FH} generation may imply a strong protection capacity induced by the vaccine candidate (Pardi, N. et al., The Journal of Experimental Medicine 215, 1571–1588, 2018). Proliferation of T_{FH} in germinal centres is integral for generation of an adaptive B-cell response. In humans, T_{FH} occurring in the circulation after vaccination were correlated with a high frequency of antigen-specific antibodies (Farooq, F. et al., Scientific reports 6, 27944, 2016). Immunisation with BNT162b1 triggered redistribution of B cells and T_{FH} cells from the blood to lymphoid tissues, where antigen presentation occurs.

Another significant finding is that in rhesus macaques two doses of m1Ψ nucleoside-modified mRNA encoding the trimeric SARS-CoV-2 S RBD-foldon elicited SARS-CoV-2 neutralising GMTs 8.2 to 18.2-fold the GMT of a SARS-CoV-2 convalescent human serum panel. Results in nonhuman primates confirm the vaccine's high potency and ability to protect against SARS-CoV-2 challenge in a preclinical model of acute SARS-CoV-2 infection.

Example 11: A RNA vaccine encoding the prefusion-stable SARS-CoV-2 S is highly immunogenic in mice and non human primates

Here, we report a SARS-CoV-2 infectious challenge of immunised macaques with BNT162b2 vaccine.

Materials and Methods

Manufacturing of *in vitro* transcribed RNA.

To generate the template for RNA synthesis, a DNA fragment encoding the full-length SARS-CoV-2 S protein (GenBank: MN908947), with amino acid exchanges K986P and V987P, was cloned into a starting plasmid vector with backbone sequence elements for improved RNA stability and translational efficiency (Orlandini von Niessen, A. G. et al., Mol Ther 27, 824–836, 2019; Holtkamp, S. et al., Blood 108, 4009–4017, 2006). Non-coding backbone elements included the regions from the T7 promoter to the 5' and 3' UTR plus a poly(A) tail (100 nucleotides) interrupted by a linker (A30LA70, 10 nucleotides). The DNA was purified, spectrophotometrically quantified, and *in vitro* transcribed by T7 RNA polymerase in the presence of a trinucleotide cap1 analogue ($(m_2^{7,3'-O})Gppp(m^{2'-O})ApG$; TriLink) and of N^1-methylpseudouridine-5'-triphosphate (m1ΨTP; Thermo Fisher Scientific) instead of uridine-5'-triphosphate (UTP) (Grudzien-Nogalska, E. et al., Methods in molecular biology (Clifton, N.J.) 969, 55–72, 2013). RNA was purified using magnetic particles (Berensmeier, S., Appl.Microbiol.Biotechnol. 73, 495–504, 2006), integrity assessed by microfluidic capillary electrophoresis (Agilent Fragment Analyser), and concentration, pH, osmolality, endotoxin level and bioburden determined.

Lipid-nanoparticle formulation of the RNA.

Purified RNA was formulated into LNPs using an ethanolic lipid mixture ofionisable cationic lipid and transferred into an aqueous buffer system via diafiltration to yield an LNP composition similar to one previously described (Maier, M. A. et al., Molecular therapy : the journal of the American Society of Gene Therapy 21, 1570–1578, 2013). BNT162b2 was stored at -70 °C at a concentration of 0.5 mg/mL.

Immunisation.

Male rhesus macaques (2–4 years) were randomly assigned to receive either BNT162b2 or saline placebo control in 0.5 mL volume administered by IM injection in the left quadriceps

muscle on Days 0 and 21. Blood for serum and PBMCs was collected in compliance with animal protocol 2017-8725-023 approved by the NIRC Institutional Animal Care and Use Committee. Animals were anesthetised with ketamine HCl (10 mg/kg; IM) during blood collection and immunisation, and monitored for adequate sedation.

SARS-CoV-2 challenge of Rhesus macaques.

The SARS-CoV-2 inoculum was obtained from a stock of 2.1×10^6 PFU/mL previously prepared at Texas Biomedical Research Institute (San Antonio, TX), aliquoted into single use vials, and stored at -70 °C. The working virus stock was generated from two passages of the SARS-CoV-2 USA-WA1/2020 isolate (a 4th passage seed stock purchased from BEI Resources; NR-52281) in Vero E6 cells. The virus was confirmed to be SARS-CoV-2 by deep sequencing and identical to the published sequence (GenBank accession number MN985325.1).

BNT162b2-immunised (n=6) and age-matched saline control-immunised (n=6) male rhesus macaques (control) were challenged with 1×10^6 plaque forming units of SARS-CoV-2 USA-WA1/2020 isolate, split equally between the intranasal (IN; 0.2 mL) and intratracheal (IT; 0.2 mL) routes as previously described (Singh, D. K. et al. SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species (2020)). The challenge was performed 41 to 48 days after the second immunisation. A separate sentinel group of non-immunised age- and sex-matched animals (n=3) received only DMEM supplemented with 10% FCS IN (0.2 mL) and IT (0.2 mL). Approximately two weeks prior to challenge, animals were moved to the ABSL-3 facility at Southwest National Primate Research Center (SNPRC; San Antonio, TX). Animals were monitored regularly by a board-certified veterinary clinician for rectal body temperature, weight and physical examination. Specimen collection was performed under tiletamine zolazepam (Telazol) anaesthesia as described (Singh, D. K. et al. SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species (2020)). Nasal swabs were collected from macaques at 0, 1, 3, and 6 days after inoculation to assess viral titers. Bronchoalveolar lavage (BAL) was performed the

week before challenge and at Days 3 and 6 post-inoculation by instilling four times 20 mL of saline. These washings were pooled, aliquoted and stored frozen at -70 °C.

Reverse-transcription quantitative polymerase chain reaction.

SARS-CoV-2 was detected and quantified in NHP essentially as described above in Example 10.

Results

Results showed COVID-19 mRNA Vaccine BNT162b2 was immunogenic eliciting IgG responses after a single dose which were boosted by a second dose. These also showed a dose-response. At 30 μg BNT162, the neutralizing geometric mean titre was compared to that seen in covalescent plasma from human patients with SARS CoV-2 and found to be ~8-fold higher with seven days after Dose of the higher dose of 100 μg giving a higher excess of ~18-fold and remaining 3.3-times higher than this benchmark five weeks after the last immunization.. In monkeys the response was also characterised as Th1-dominant with IFN-γ and IL-2, but no IL-4 response. CD4 and CD8 positive cellular responses were also observed in monkeys too. Such cellular immune response was characterized as a strongly Th1-biased CD4+ T cell response with a concurrent interferon-γ (IFN-γ)+ CD8+ T cell response.

The groups of rhesus macaques (n=6) that had received two immunisations with 100 μg BNT162b2 or buffer control were challenged 41 to 48 days after the second immunisation with 1×10^6 plaque forming units of SARS-CoV-2 (strain USA-WA1/2020), split equally between the intranasal and intratracheal routes, as previously described (Singh, D. K. et al. SARS-CoV-2 infection leads to acute infection with dynamic cellular and inflammatory flux in the lung that varies across nonhuman primate species, 2020). Three non-immunised, age-matched, male rhesus macaques (sentinel) were mock-challenged with cell culture medium. At the time of challenge, SARS-CoV-2 neutralising titers ranged from 204 to 938 in the BNT162b2-immunised animals and were undetectable in animals from the control-immunised and sentinel groups.

SARS-CoV-2 RNA was measured in bronchoalveolar lavage (BAL) and nasal swab samples by reverse-transcription quantitative polymerase chain reaction (RT-qPCR). All BAL and nasal swab samples obtained before the infectious challenge and all those obtained from sentinel animals lacked detectable SARS-CoV-2 RNA (Fig. 68). Three days after SARS-CoV-2 challenge, viral RNA was detected in BAL fluid from 5/6 control-immunised and 2/6 BNT162b2-immunised animals (Fig. 68). By 6 days after challenge, all six BNT162b2-immunised macaques had undetectable viral RNA in their lungs; of the control-immunised macaques, three had a high level of viral RNA in BAL fluid, two had cleared, and one had an indeterminate RT-qPCR result. After SARS-CoV-2 challenge, viral RNA was detected in nasal swabs of the control-immunised group at each time point: two animals at Day 1, three animals at Days 3 and 6 after challenge (Fig. 68). In BNT162b2-immunised animals, all nasal swabs were negative at Day 3 and at Day 6.

In lung tissues, control monkeys had evidence of pulmonary disease indicated by their increased scores on computed tomography scans with a suggestion of recovery in that scores at day 10 were less than those at day 3; in contrast, the monkeys given COVID-19 mRNA Vaccine BNT162b2 had lower scores. Microscopic analysis of lung tissues showed that lung inflammation was similar between control and BNT162b2-immunized monkeys, and there was no evidence of enhanced respiratory disease.

Discussion

Results in nonhuman primates confirm the potency and ability of BNT162b2, an LNP-formulated m1Ψ nucleoside-modified mRNA encoding the S antigen captured in a prefusion conformation, to protect against SARS-CoV-2 challenge in a preclinical model of acute SARS-CoV-2 infection.

Example 12: Storage, shipping and dose preparation

This example illustrates storage, shipping and dose preparation of a multi-dose vial of BNT162b2 concentrate for injection.

As shown in Fig. 69, at the stage of primary packing, 2 ml type 1 glass, preservative-free, multi-dose vial (MDV) is used, wherein the MDV has 0.45 ml frozen liquid drug product and there are 5 doses per vial. At the stage of secondary packing, a single tray holds 195 vials, such as 975 doses per tray. The tray (white box) dimensions are 229 X 229 x 40 mm. At the stage of teriary packing, a minimum of 1 tray (975 doses) (or up to 5 trays (max 4875 doses)) is stacked in a payload carton. The payload carton is submerged in 23 Kg of dry ice pellets (10 mm - 16 mm pellets). The thermal shipper dimensions are as follows: internal dimensions: 245mm X 245mm X 241mm; external dimensions: 400mm X 400mm X 560mm. The total weight of the thermal shipper is ~ 35 Kg.

Different sizes of Ultra-Low Temperature (ULT) freezers are available in the market. Fig. 70 shows an example for a small volume storage (about 90 litres; about 30K doses (left)) and for a large volume storage (about 500 litres; about 200K doses (right)). Thermal shipper keeps ULT (e.g., -90°C to -60°C) up to 10 days if stored at 15 °C to 25 °C temperatures without opening and such storage period of time can be extended further by consistently refilling to the top of the container with dry ice. Upon receipt and after opening, the box should be replenished with dry ice within 24 hours (23 Kg of dry ice pellets (10 mm - 16 mm pellets). Thermal shipper should be re-iced every 5 days. It is recommended that the thermal shipper is opened not more than twice a day. Thermal shipper should be closed within 1 minute (or less) after opening. The vaccine can be stored at 2 °C to 8 °C up to 2 days or at room temperature for no more than 2 hours after thawing. Post-dilution in use period is 6 hours.

Fig. 71 shows an exemplary dose preparation for a BNT162b2 5-dose vial which contains a frozen concentrated solution that is preservative-free and must be thawed and diluted prior to administration. The preparation steps are as follows:

Remove a 5-dose vial of BNT162b2 concentrate for injection from its carton in frozen storage and allow to thaw for approximately 30 minutes at room temperature (e.g., up to 25°C). In some embodiments, such a multi-dose vial of BNT162b2 may be thawed and stored in a refrigerator (e.g., 2°C - 8°C), for example, for up to 5 days. Vials thawed at room temperature must be diluted within 2 hours or transferred to a refrigerator. Undiluted vials may be stored for up to 48 hours in the refrigerator. Do not refreeze thawed vials. During storage, minimize exposure to room light, and avoid exposure to direct sunlight and ultraviolet light. Thawed vials can be handled in room light conditions.

After thawing and prior to use, ensure the vial is equilibrated to room temperature, and invert gently 10 times to mix. Do not shake.

Using aseptic technique, cleanse the vial stopper with a single-use antiseptic swab, then dilute the thawed vial of BNT162b2 by adding 1.8 mL of 0.9% Sodium Chloride Injection, USP into the vial. Needles 21 gauge or narrower needles are recommended. However, those skill in the art will understand that in some embodiments, wider needeles may be used. For example, in some embodiments, needles 20, 19, 18, 17, 16, 15 or wider needles may be used.

You may feel some pressure in the vial as you add the diluent. Ensure vial pressure is equalized by withdrawing 1.8 mL air into the empty diluent syringe before removing the needle from the vial.

Gently invert the diluted vial 10 times to mix. Do not shake.

Record the date and time of dilution in the appropriate place on the BNT162b2 vial label. Expiry is 6 hours from the time of dilution. Diluted multi-dose vials are stored between 2°C and 25°C. Do not freeze. Discard if frozen.

Using aseptic technique, cleanse the vial stopper with a single-use antiseptic swab, and draw up 0.3 mL of the diluted dosing solution into a new sterile dosing syringe with a needle appropriate for intramuscular injection. Adjustments to remove air bubbles should be done with the needle still in the vial to avoid loss of dosing solution. It is recommended to use the same needle to withdraw and administer the dose whenever possible. If a second needle is

required for administration, pull back on the syringe plunger until a small amount of air enters the syringe prior to removing the first needle to avoid loss of dosing solution during the needle change. Take care when priming the administration needle to prevent any loss of dose.
For each additional dose, use a new sterile syringe and needle and ensure the vial stopper is cleansed with antiseptic before each withdrawal. Prepared syringes should be administered immediately. If they cannot be administered immediately, they must be administered within 6 hours of the initial vial dilution. Before administration, ensure a final injection volume in the syringe of 0.3 mL.

Example 13: Vaccine Candidate Against COVID-19 Achieved Success in First Interim Analysis from Phase 3 Study

The Phase 3 clinical trial of BNT162b2 has enrolled more than 43,000 participants to date, almost 39,000 of whom have received a second dose of the vaccine candidate as of November 8, 2020. Approximately 42% of global participants and 30% of U.S. participants have racially (e.g., including White, Black or African American, American Indian or Alaska native, Asian, native Hawaiian or other Pacific Islander, multiracial) and ethnically (e.g., including Hispanic/Latino and non-Hispanic/non-Latino) diverse backgrounds. The trial is continuing to enroll and is expected to continue through the final analysis when a total of 164 confirmed COVID-19 cases have accrued.
Vaccine candidate BNT162b2 achieved success in First Interim Analysis from Phase 3 Study. The vaccine candidate was found to be more than 90% effective in preventing COVID-19 in participants without evidence of prior SARS-CoV-2 infection in the first interim efficacy analysis. Analysis evaluated 94 confirmed cases of COVID-19 in trial participants. No serious safety concerns have been observed.
A set of results from the Phase 3 COVID-19 vaccine trial, assembled by November 4, 2020, provides evidence of the ability of BNT162b2 to prevent COVID-19. The case split between vaccinated individuals and those who received the placebo indicates a vaccine efficacy rate

above 90%, at 7 days after the second dose. In particular, early analysis of the results showed that individuals who received two injections of the vaccine three weeks apart experienced more than 90% fewer cases of symptomatic COVID-19 than those who received a placebo. This confirms that protection is achieved 28 days after the initiation of the vaccination, which consists of a 2-dose schedule.

Preliminary such data includes the following tables:

Table 5. Vaccine Efficacy – First COVID-19 Occurrence From 7 Days After Dose 2 – Subjects Without Evidence of Infection Prior to 7 Days After Dose 2 – Evaluable Efficacy Population (7 Days) – Interim Analysis 1.

	Vaccine Group (as Randomized)						
	BNT162b2 (30 µg) (N[a]=16061)		Placebo (N[a]=16218)				
Efficacy Endpoint	n1[b]	Surveillance Time[c] (n2[d])	n1[b]	Surveillance Time[c] (n2[d])	VE (%)	(95% CI[e])	Pr (VE >30% | data)[f]
First COVID-19 occurrence from 7 days after Dose 2	4	1.72161 (15899)	90	1.73212 (16010)	95.5	(88.8, 98.4)	>0.9999

Abbreviations: N-binding = SARS-CoV-2 nucleoprotein-binding; NAAT = nucleic acid amplification test; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; VE = vaccine efficacy.

Note: Subjects who had no serological or virological evidence (prior to 7 days after receipt of the last dose) of past SARS-CoV-2 infection (ie, N-binding antibody [serum] negative at Visit 1 and SARS-CoV-2 not detected by NAAT [nasal swab] at Visits 1 and 2), and had negative NAAT at any unscheduled visit prior to 7 days after Dose 2 were included in the analysis.

Note: Data from subjects who are not confirmed 7 days post dose 2 cases are included in the analysis to comprehensively show all data reported and/or contribute to the total surveillance time calculation but may be subject to change with additional follow-up.

a. N = number of subjects in the specified group.

b. n1 = Number of subjects meeting the endpoint definition.

c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from 7 days after Dose 2 to the end of the surveillance period.

d. n2 = Number of subjects at risk for the endpoint.

e. Credible interval for VE was calculated using a beta-binomial model adjusted for surveillance time.

f. Posterior probability (Pr) was calculated using a beta-binomial model adjusted for surveillance time. This probability must be at least 99.5% at the interim analysis in order to conclude that the vaccine is efficacious.

Table 6. Severe COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population – Interim Analysis 1.

	Vaccine Group (as Randomized)	
	BNT162b2 (30 µg) (N[a]=21617)	Placebo (N[a]=21633)
Efficacy Endpoint	**n[b]**	**n[b]**
Severe COVID-19 occurrence after Dose 1	0	7

Note: Data from subjects who are not confirmed 7 days post dose 2 cases are included in the analysis to comprehensively show all data reported and/or contribute to the total surveillance time calculation but may be subject to change with additional follow-up.

a. N = number of subjects in the specified group.

b. n = Number of subjects meeting the endpoint definition.

Example 14: Efficacy and Immunogenicity evaluation

Efficacy Results

Vaccine efficacy of BNT162b2 against COVID-19 among participants without evidence of past SARS-CoV-2 infection was demonstrated at the first interim analysis conducted after accrual of at least 62 cases following the protocol and SAP. The primary efficacy results presented in this section are from that interim analysis.

Only the vaccine efficacy of BNT162b2 for the first primary efficacy endpoint (COVID-19 incidence based on central laboratory or locally confirmed NAAT in participants without serological or virological evidence of past SARS-CoV-2 infection prior to 7 days after receipt of the second dose) is analyzed and presented at this interim analysis.

First Primary Efficacy Endpoint

Among participants included in the evaluable efficacy population, 32,279 participants (16,061 in BNT162b2 group and 16,218 in placebo group) did not have evidence of infection with SARS-CoV-2 through 7 days after the second dose. There were 4 COVID-19 cases in the BNT162b2 group compared to 90 COVID-19 cases reported in the placebo group. These data give an estimated vaccine efficacy of 95.5% for BNT162b2. The posterior probability of >99.99% met the prespecified interim analysis success criterion of > 99.5% (Table 7). The 95% credible interval for the vaccine efficacy was 88.8% to 98.4%, indicating that given the current observed data there is a 95% probability that the true VE lies in this interval. Also, note that the posterior probability that true VE > 86.0% is 99.5% and VE > 88.8% is 97.5%.

Table 7. Vaccine Efficacy – First COVID-19 Occurrence From 7 Days After Dose 2 – Subjects Without Evidence of Infection Prior to 7 Days After Dose 2 – Evaluable Efficacy Population (7 Days) – Interim Analysis 1

	Vaccine Group (as Randomized)						
	BNT162b2 (30 µg) (N^a=16061)		Placebo (N^a=16218)				
Efficacy Endpoint	n1[b]	Surveillance Time[c] (n2[d])	n1[b]	Surveillance Time[c] (n2[d])	VE (%)	(95% CI[e])	Pr (VE >30% | data)[f]

First COVID-19 occurrence from 7 days after Dose 2	4	1.722 (15899)	90	1.732 (16010)	95.5	(88.8, 98.4)	>0.9999

Abbreviations: N-binding = SARS-CoV-2 nucleoprotein-binding; NAAT = nucleic acid amplification test; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; VE = vaccine efficacy.
Note: Subjects who had no serological or virological evidence (prior to 7 days after receipt of the last dose) of past SARS-CoV-2 infection (ie, N-binding antibody [serum] negative at Visit 1 and SARS-CoV-2 not detected by NAAT [nasal swab] at Visits 1 and 2), and had negative NAAT at any unscheduled visit prior to 7 days after Dose 2 were included in the analysis.
Note: Data from subjects who are not confirmed 7 days post dose 2 cases are included in the analysis to comprehensively show all data reported and/or contribute to the total surveillance time calculation but may be subject to change with additional follow-up.
a. N = number of subjects in the specified group.
b. n1 = Number of subjects meeting the endpoint definition.
c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from 7 days after Dose 2 to the end of the surveillance period.
d. n2 = Number of subjects at risk for the endpoint.
e. Credible interval for VE was calculated using a beta-binomial model adjusted for surveillance time.
f. Posterior probability (Pr) was calculated using a beta-binomial model adjusted for surveillance time. This probability must be at least 99.5% at the interim analysis in order to conclude that the vaccine is efficacious.

The vaccine efficacy of BNT162b2 for the same primary efficacy endpoint based on the all-available efficacy population was 95.7%, with 4 and 93 cases in the BNT162b2 and placebo groups, respectively.

No clinically meaningful differences in VE by subgroup were observed by age group, country, ethnicity, sex, or race in the in the Dose 2 evaluable efficacy population, with VE estimates that ranged from 91.2% to 100.0% (Table 8).

Table 8. Vaccine Efficacy – First COVID-19 Occurrence From 7 Days After Dose 2, by Subgroup – Subjects Without Evidence of Infection Prior to 7 Days After Dose 2 – Evaluable Efficacy Population (7 Days) – Interim Analysis 1

	Vaccine Group (as Randomized)					
	BNT162b2 (30 µg) (N[a]=16061)		Placebo (N[a]=16218)			
Efficacy Endpoint Subgroup	**n1[b]**	**Surveillance Time[c] (n2[d])**	**n1[b]**	**Surveillance Time[c] (n2[d])**	**VE (%)**	**(95% CI[e])**
First COVID-19 occurrence from 7 days after Dose 2						
Overall	4	1.722 (15899)	90	1.732 (16010)	95.5	(88.1, 98.8)
Age group (years)						
16 to 55	2	0.954 (8994)	67	0.959 (9040)	97.0	(88.7, 99.6)

>55	2	0.767 (6905)	23	0.773 (6970)	91.2	(64.6, 99.0)
Sex						
Male	2	0.874 (8115)	38	0.865 (8029)	94.8	(79.8, 99.4)
Female	2	0.848 (7784)	52	0.867 (7981)	96.1	(85.1, 99.5)
Race						
White	4	1.477 (13399)	85	1.491 (13530)	95.3	(87.4, 98.7)
Black or African American	0	0.124 (1263)	4	0.124 (1277)	100.0	(-51.8, 100.0)
All others[f]	0	0.121 (1237)	1	0.118 (1203)	100.0	(-3690.1, 100.0)
Ethnicity						
Hispanic/Latino	1	0.464 (4389)	34	0.459 (4342)	97.1	(82.7, 99.9)
Non-Hispanic/non-Latino	3	1.247 (11418)	56	1.262 (11570)	94.6	(83.3, 98.9)
Country						
Argentina	0	0.271 (2436)	28	0.266 (2402)	100.0	(86.2, 100.0)
Brazil	0	0.087 (878)	2	0.087 (879)	100.0	(-432.5, 100.0)
USA	4	1.360 (12384)	60	1.376 (12530)	93.3	(81.8, 98.2)

Abbreviations: N-binding = SARS-CoV-2 nucleoprotein-binding; NAAT = nucleic acid amplification test; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; VE = vaccine efficacy.
Note: Subjects who had no serological or virological evidence (prior to 7 days after receipt of the last dose) of past SARS-CoV-2 infection (ie, N-binding antibody [serum] negative at Visit 1 and SARS-CoV-2 not detected by NAAT [nasal swab] at Visits 1 and 2), and had negative NAAT at any unscheduled visit prior to 7 days after Dose 2 were included in the analysis.
Note: Data from subjects who are not confirmed 7 days post dose 2 cases are included in the analysis to comprehensively show all data reported and/or contribute to the total surveillance time calculation but may be subject to change with additional follow-up.
a. N = number of subjects in the specified group.
b. n1 = Number of subjects meeting the endpoint definition.
c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from 7 days after Dose 2 to the end of the surveillance period.
d. n2 = Number of subjects at risk for the endpoint.
e. Confidence interval (CI) for VE is derived based on the Clopper and Pearson method adjusted to the surveillance time.
f. American Indian or Alaska native, Asian, Native Hawaiian or other Pacific Islander, multiracial, not reported race categories are presented as "All others".

Severe COVID-19 Cases

Severe COVID-19 cases were reported in a total of 7 participants in Phase 3, all in the placebo group, as of the data cutoff date of 04 November 2020 for the first interim analysis (Table 9). Five of these cases were reported between Dose 1 and Dose 2, none were reported less than 7 days after Dose 2, and 2 cases were reported at least 7 days after Dose 2.

Table 9. Severe COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population – Interim Analysis 1

	Vaccine Group (as Randomized)

Efficacy Endpoint	BNT162b2 (30 µg) (N^a=21617) n^b	Placebo (N^a=21633) n^b
Severe COVID-19 occurrence after Dose 1	0	7

Note: Data from subjects who are not confirmed 7 days post dose 2 cases are included in the analysis to comprehensively show all data reported and/or contribute to the total surveillance time calculation but may be subject to change with additional follow-up.
a. N = number of subjects in the specified group.
b. n = Number of subjects meeting the endpoint definition.

Efficacy Conclusions

The first primary efficacy objective met success criteria. BNT162b2 achieved vaccine efficacy of 95.5% with a 2-sided 95% credible interval of 88.8% to 98.4% among participants without evidence of infection up to 7 days after Dose 2, and a >99.99% posterior probability for the true vaccine efficacy greater than 30% conditioning on available data.

All 7 severe COVID-19 cases (after Dose 1) were observed in the placebo group, as of the interim analysis cutoff date.

Immunogenicity Results

Phase 1

This Phase 1 interim Clinical Study Report (CSR) presents immunogenicity results for both adult age groups up to 1 month after Dose 2 for the BNT162b1 and BNT162b2 vaccine candidates at the 10-µg, 20-µg, and 30-µg dose levels, and up to 7 weeks after Dose 1 of BNT162b1 at the 100-µg dose level (younger age group only).

Results for the 7 days after Dose 1 time point are only analyzed and presented in the younger age group (18 to 55 years of age) for 10 µg and 30 µg BNT162b1.

SARS-CoV-2 Neutralizing Titers – Phase 1

GMTs

Overall, for both the BNT162b1 and the BNT162b2 recipients in both age groups, SARS-CoV-2 50% neutralizing GMTs modestly increased by Day 21 after Dose 1 and were substantially increased 7 days after Dose 2. Generally, GMTs in the older age

group tended to be somewhat lower than the GMTs in the younger age group at most time points for both BNT162b1 and BNT162b2 recipients.

BNT162b1

In the younger age group, SARS-CoV-2 50% neutralizing GMTs modestly increased by Day 21 after Dose 1 and were substantially increased 7 days after Dose 2 (Day 28) of BNT162b1, with higher GMTs observed in the 30-µg dose group compared to the 10-µg and 20-µg dose groups (Figure 72). GMTs increased at 14 days after Dose 2 (Day 35) for all dose groups, and although GMTs decreased at 1 month after Dose 2 (Day 52), the Day 52 GMTs remained substantially higher than those at the earlier time points after Dose 1.

In the 100-µg dose group, SARS-CoV-2 50% neutralizing GMTs modestly increased by Day 21 after Dose 1 of BNT162b1 and decreased to a near baseline value by Day 52.

Generally similar trends were observed in the older age group, with higher GMTs observed in the 20-µg and 30-µg dose groups of BNT162b1 compared to the 10-µg dose group (Figure 73).

Similar trends were observed for the SARS-CoV-2 90% neutralizing GMTs.

Results for the all-available immunogenicity population in the younger age and older age groups were similar to those observed for the evaluable immunogenicity population.

RCDCs of SARS-CoV-2 50% and 90% neutralizing titers after BNT162b1 for the younger and older age groups show that the majority of participants responded by 7 days after Dose 2 of BNT162b1.

BNT162b2

In the younger age group, SARS-CoV-2 50% neutralizing GMTs increased by Day 21 after Dose 1 and were substantially increased 7 days after Dose 2 (Day 28) of BNT162b2, with higher GMTs observed in the 20-µg and 30-µg dose groups compared

to the 10-µg dose group (Figure 74). The GMTs decreased at 14 days after Dose 2 (Day 35) and 1 month after Dose 2 (Day 52) of BNT162b2; however, the GMTs remained substantially higher than those at the earlier time points after Dose 1.

Similar trends were generally observed in the older age group, with higher GMTs observed in the 30-µg dose groups compared to the 20-µg and 10-µg dose groups (Figure 75). SARS-CoV-2 50% neutralizing GMTs were increased 7 days after Dose 2 and were similar in the 10-µg and 20-µg dose groups and higher in the 30-µg dose group. At 1 month after Dose 2, GMTs remained substantially higher than those at the earlier time points after Dose 1. In the older age group, SARS-CoV-2 50% neutralizing GMTs were generally lower than the GMTs in the younger age group. Similar trends were observed for the SARS-CoV-2 90% neutralizing GMTs.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population. RCDCs of SARS-CoV-2 50% and 90% neutralizing titers for the younger and older age groups show that the majority of participants responded by 7 days after Dose 2 of BNT162b2.

GMFRs

Overall, for both the BNT162b1 and the BNT162b2 recipients, and in both age groups, GMFRs of SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2 (Day 28) were substantially higher compared to the respective GMFRs after Dose 1. GMFRs in the older age group were generally lower than the those in the younger age group for both BNT162b1 and BNT162b2 recipients.

BNT162b1

In the younger age group, GMFRs of SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b1 were substantially high compared to GMFRs at earlier time points after Dose 1 of BNT162b1 in all dose groups, with GMFRs being highest in the 30-µg dose group. At 1 month after Dose 2, the GMFRs remained higher than those at the earlier time points after Dose 1.

In the 100-µg dose group, the GMFRs of SARS-CoV-2 50% neutralizing titers were not substantially increased through Day 52 after Dose 1 of BNT162b1.

In the older age group, GMFRs of SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b1 were substantially high compared to GMFRs at the earlier time point after Dose 1 of BNT162b1 in the 20-µg and 30-µg dose groups with GMFRs being highest in the 20-µg dose group. The GMFRs remained high in the 20-µg and 30-µg dose groups at 1 month after Dose 2 (Day 52) of BNT162b1 compared to GMFRs at the earlier time point after Dose 1.

Similar trends were observed for GMFRs of SARS-CoV-2 90% neutralizing titers in the younger age group and older age group.

Results for the all-available immunogenicity population in the younger age and older age groups were similar to those observed for the evaluable immunogenicity population.

BNT162b2

In the younger age group, GMFRs of SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b2 were substantially high compared to GMFRs at the earlier time point after Dose 1 of BNT162b2 for all dose groups, with GMFRs being similar and highest in the 20-µg and 30-µg dose groups. GMFRs remained high through 1 month after Dose 2 of BNT162b2 compared to GMFRs 21 days after Dose 1 of BNT162b2.

In the older age group, GMFRs of SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b2 were substantially high compared to GMFRs at the earlier time point after Dose 1 of BNT162b2 in all dose groups, with GMFRs being highest in the 30-µg dose group. GMFRs remained high through 1 month after Dose 2 of BNT162b2 compared to GMFRs at 21 days after Dose 1 of BNT162b2.

Similar trends were observed for GMFRs of SARS-CoV-2 90% neutralizing titers in the younger and older age groups.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

Number (%) of Participants Achieving a ≥4-Fold Rise

Overall, for both the BNT162b1 and the BNT162b2 recipients, and in both age groups, most participants achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers from before vaccination to 7 days after Dose 2, except in the older participants in the 10-µg BNT162b1 dose group.

BNT162b1

In the younger age group, from before vaccination to 21 days after Dose 1 of BNT162b1, no participants in the 10-µg dose group and ≤3 participants in the 20-µg and the 30-µg dose groups achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers. From before vaccination to both 7 days and 1 month after Dose 2 of BNT162b1 most or all participants in the 10-µg, 20-µg, and 30-µg dose groups achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers.

In the older age group, from before vaccination to 21 days after Dose 1 of BNT162b1, only 1 participant in the 30-µg dose group achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers. From before vaccination to both 7 days and 1 month after Dose 2 of BNT162b1, ≤2 participants in the 10-µg group and 9 to 11 participants in the 20-µg and 30-µg dose groups achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

BNT162b2

In the younger age group, from before vaccination to 21 days after Dose 1 of BNT162b2, 2 (18.2%) participants in the 10-µg dose group, 3 (25.0%) participants in the 20-µg dose group, and none in the 30-µg group achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers. From before vaccination to 7 days after Dose 2 of BNT162b2, all participants achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers, which was maintained through 1 month after Dose 2 of BNT162b2.

In the older age group, from before vaccination to 21 days after Dose 1 of BNT162b2, no participants achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers in any dose group. From before vaccination to 7 days after Dose 2 of BNT162b2, 10 (83.3%), 9 (81.8%), and 10 (90.9%) participants achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers in the 10-µg, 20-µg, and 30-µg dose groups, respectively. From before vaccination to 1 month after Dose 2 of BNT162b2, 9 (75.0%), 6 (54.5%), and 11 (100.0%) participants achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers in the 10-µg, 20-µg, and 30-µg dose groups, respectively.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

SARS-CoV-2 Antigen-Specific Binding Antibody Levels – Phase 1

Vaccine candidate BNT162b1 encodes for the RBD of SARS-CoV-2. RBD-binding IgG responses for each dose level and age group for this candidate are described in this section. RBD-binding IgG levels were also assessed for candidate BNT62b2 which encodes the P2 S of SARS-CoV-2.

Vaccine candidate BNT162b2 encodes for the P2 S of SARS-CoV-2. S1-binding IgG responses for each dose level and age group for this candidate are described in this section. S1-binding IgG levels were also assessed for candidate BNT62b1 which encodes the RBD of SARS-CoV-2.

GMCs

Overall, for both the BNT162b1 and the BNT162b2 recipients, and in both age groups, RBD- and S1-binding GMCs increased substantially by Day 21 after Dose 1 and were further increased 7 days after Dose 2. Responses were maintained through Day 52. GMCs in the older age group were generally lower than the GMCs in the younger age group, with the exception of Day 28 in the 20-µg BNT162b1 dose group for both RBD- and S1-binding IgG levels.

BNT162b1

In the younger age group, RBD-binding GMCs increased substantially by Day 21 after Dose 1 of BNT162b1 and further increased 7 days after Dose 2 (Day 28) of BNT162b1,

with higher GMCs observed in the 30-µg dose group compared to the 10-µg and 20-µg dose groups (Figure 76). At 1 month after Dose 2 (Day 52), the GMCs remained substantially higher than at the earlier time points after Dose 1.

In the 100-µg BNT162b1 group, the RBD-binding GMC increased substantially by 21 days after BNT162b1 and remained higher through Day 52 compared to the Day 7 GMC.

In the older age group, RBD-binding GMCs increased substantially by Day 21 after Dose 1 of BNT162b1 and further increased 7 days after Dose 2 (Day 28) of BNT162b1, with higher GMCs observed in the 20-µg and 30-µg dose groups compared to the 10-µg group (Figure 77). At 1 month after Dose 2 (Day 52), the GMCs remained substantially higher than at the earlier time point after Dose 1.

S1-binding IgG GMC results for BNT162b1 were similar to those observed for RBD-binding IgG GMCs in the younger (Figure 78) and older age groups (Figure 79), and in the 100-µg BNT162b1 group.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

RCDCs of RBD- and S1-binding IgG levels show that the majority of participants responded by 21 days after Dose 1 of BNT162b1.

BNT162b2

In the younger age group, S1-binding GMCs increased substantially by Day 21 after Dose 1 of BNT162b2 and were substantially increased by 7 days after Dose 2 (Day 28) of BNT162b2, with higher GMCs observed in the 20-µg and 30-µg dose groups compared to the 10-µg dose group (Figure 80). At 1 month after Dose 2 (Day 52), the GMCs remained substantially higher than at the earlier time point after Dose 1.

Similar trends were observed in the older age group, with higher S1-binding GMCs observed in the 30-µg dose group compared to the 10-µg and 20-µg dose groups (Figure 81).

RBD-binding IgG GMC results for BNT162b2 were similar to those observed for S1-binding IgG GMCs in the younger (Figure 82) and older age groups (Figure 83).

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

RCDCs of RBD- and S1-binding IgG levels after BNT162b2 show that the majority of participants responded by 21 days after Dose 1 of BNT162b2.

GMFRs

Overall, for the BNT162b1 and the BNT162b2 recipients, and in both age groups, GMFRs of RBD-binding IgG levels and GMFRs of S1-binding IgG levels were substantially high from before vaccination to 21 days after Dose 1, with greater GMFRs observed from before vaccination to 7 days after Dose 2.

BNT162b1

GMFRs of RBD-binding IgG levels were substantially high from before vaccination to Day 21 (before Dose 2) after Dose 1 of BNT162b1, with greater GMFRs observed from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b1 in both the younger and older age groups, for the 10-µg, 20-µg, and 30-µg dose groups. GMFRs remained substantially high in the 10-µg, 20-µg, and 30-µg BNT162b1 groups from before vaccination to 1 month after Dose 2 compared to the earlier time points after Dose 1 for both age groups.

In the 100-µg BNT162b1 group, GMFR of RBD-binding IgG levels was substantially high from before vaccination by 21 days after BNT162b1 and remained higher through Day 52 compared to the Day 7 GMFR.

Similar trends were observed for GMFRs of S1-binding IgG levels for BNT162b1.

Results for the all-available immunogenicity population in the younger age and older age groups were similar to those observed for the evaluable immunogenicity population.

BNT162b2

GMFRs of S1-binding IgG levels were substantially high from before vaccination to Day 21 (before Dose 2) after Dose 1 of BNT162b2, with greater GMFRs observed from before vaccination to 7 days after Dose 2 (Day 28) of BNT162b2 in both the younger and older age groups, for the 10-µg, 20-µg, and 30-µg dose groups. GMFRs remained

substantially high in all BNT162b2 groups from before vaccination to 1 month after Dose 2 compared to the earlier time point after Dose 1 for both age groups.

Similar trends were observed for GMFRs of RBD-binding IgG levels for BNT162b2.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

Number (%) of Participants Achieving a ≥4-Fold Rise

Overall, for the BNT162b1 and the BNT162b2 recipients, and in both age groups, all participants achieved a ≥4-fold rise in S1- and RBD-binding IgG levels from before vaccination to 7 days after Dose 2, with the exception of 1 participant in the younger 20-µg BNT162b1 group.

BNT162b1

In the younger age group, from before vaccination to 21 days following Dose 1 of BNT162b1, all participants (except 1 in the 20- µg dose group) across all dose groups achieved a ≥4-fold rise in RBD-binding IgG levels. All participants in the 20-µg dose group achieved a ≥4-fold rise in RBD-binding IgG levels from before vaccination to 14 days after Dose 2 (Day 35).

In the older age group, from before vaccination to 21 days following Dose 1 of BNT162b1, all participants in the 20-µg and 30-µg dose groups and 8 (72.7%) participants in the 10-µg dose group achieved a ≥4-fold rise in RBD-binding IgG levels. All participants in the 10-µg dose group achieved a ≥4-fold rise in RBD-binding IgG levels from before vaccination to 7 days after Dose 2 (Day 28).

Similar trends were generally observed for participants achieving a ≥4-fold rise in S1-binding IgG levels for BNT162b1.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

BNT162b2

In the younger age group, from before vaccination to 21 days following Dose 1 of BNT162b2, all participants in each dose group achieved a ≥4-fold rise in S1-binding IgG levels.

In the older age group, from before vaccination to 21 days following Dose 1 of BNT162b2, all participants in the 10-µg, and 30-µg dose groups and 11 (91.7%) participants in the 20-µg dose group achieved a ≥4-fold rise in S1-binding IgG levels. All participants in the 20-µg dose group achieved a ≥4-fold rise in S1-binding IgG levels from before vaccination to 7 days after Dose 2 (Day 28).

Similar trends were generally observed for participants achieving a ≥4-fold rise in RBD-binding IgG levels for BNT162b2.

Results for the all-available immunogenicity population were similar to those observed for the evaluable immunogenicity population in the younger and older age groups.

GMRs of SARS-CoV-2-Neutralizing Titers to SARS-CoV-2 Antigen-Specific Binding Antibody Levels

Overall, for BNT162b1 and BNT162b2 recipients, GMRs of SARS-CoV-2 50% neutralizing titers to RBD- or S1-binding IgG levels show a more robust RBD- or S1-binding levels relative to neutralizing titers, which were similar within each age group.

BNT162b1

At 21 days after Dose 1 at 10 µg, 20 µg, or 30 µg, GMRs of SARS-CoV-2 50% neutralizing titers to RBD-binding IgG levels were ≤0.035 in the younger age group and ≤0.183 in the older age group. At 14 days after Dose 2, the GMRs were ≤0.032 in the younger age group and ≤0.018 in the older age group.

For the 100-µg dose group, the GMR was 0.018 at 21 days after Dose 1 and 0.014 at 35 days after Dose 1.

GMRs of SARS-CoV-2 50% neutralizing titers to S1-binding IgG levels were similar to GMRs of SARS-CoV-2 50% neutralizing titers to RBD-binding IgG levels in the younger and older age groups after BNT162b1.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

BNT162b2

At 21 days after Dose 1, GMRs of SARS-CoV-2 50% neutralizing titers to S1-binding IgG levels were ≤ 0.035 in the younger age group and ≤0.124 in the older age group. At 14 days after Dose 2, the GMRs were ≤0.040 in the younger age group and ≤0.037 in the older age group.

Results for the all-available immunogenicity population in the younger and older age groups were similar to those observed for the evaluable immunogenicity population.

Evaluating BNT162b1 and BNT162b2 GMRs

In the younger age group at 21 days after Dose 1, GMRs of SARS-CoV-2 50% neutralizing titers to RBD-binding IgG levels were ≤0.035 after BNT162b1 and ≤0.054 after BNT162b2. At 14 days after Dose 2, the GMRs were ≤0.032 after BNT162b1 and ≤0.046 after BNT162b2.

In the older age group at 21 days after Dose 1, GMRs of SARS-CoV-2 50% neutralizing titers to RBD-binding IgG levels were ≤0.183 after BNT162b1 and ≤0.196 after BNT162b2. At 14 days after Dose 2, the GMRs were ≤0.018 after BNT162b1 and ≤0.043 after BNT162b2.

In the younger age group at 21 days after Dose 1, GMRs of SARS-CoV-2 50% neutralizing titers to S1-binding IgG levels were ≤0.061 after BNT162b1 and ≤0.035 after BNT162b2. At 14 days after Dose 2, the GMRs were ≤0.035 after BNT162b1 and ≤0.040 after BNT162b2.

In the older age group at 21 days after Dose 1, GMRs of SARS-CoV-2 50% neutralizing titers to S1-binding IgG levels were ≤0.328 after BNT162b1 and ≤0.124 after BNT162b2. At 14 days after Dose 2, the GMRs were ≤0.022 after BNT162b1 and ≤0.037 after BNT162b2.

Phase 1 Summary of Immunogenicity Results Evaluating BNT162b1 and BNT162b2

In general, a modest neutralizing immune response was observed in both the younger and older age groups after the first dose. A much more robust immune response was observed 7 days after the second dose of either BNT162b1 or BNT162b2 at all dose levels in both the younger and older age groups. Antibody levels at the last time point tested were still substantially above those at baseline.

In the younger age group:

At 7 days after Dose 2, SARS-CoV-2 50% neutralizing GMTs in the 20-µg and 30-µg dose groups were higher for BNT162b2 recipients than for BNT162b1 recipients. The GMTs were similar in the 10-µg dose group for both recipients. At 1 month after Dose 2 (Day 52), GMTs remained substantially higher than those at the earlier time points after Dose 1 for both BNT162b1 and BNT162b2 recipients.

From before vaccination to 7 days after Dose 2, GMFRs of SARS-CoV-2 50% neutralizing titers were substantially high for BNT162b1 and BNT162b2 recipients at the 30µg dose level.

From before vaccination to 7 days after Dose 2, all participants at the 30-µg dose level who received BNT162b1 or BNT162b2 achieved a ≥4-fold rise in SARS CoV-2 50% neutralizing titers.

In the older age group:

At 7 days after Dose 2, SARS-CoV-2 50% neutralizing GMT in the 30-µg dose group was higher for BNT162b2 recipients than for BNT162b1 recipients. At 1 month after Dose 2 (Day 52), the SARS-CoV-2 50% neutralizing GMTs in the 30-µg dose group were similar for both BNT162b1 and BNT162b2 recipients.

From before vaccination to 7 days after Dose 2, the GMFR of SARS-CoV-2 50% neutralizing titers were substantially high for BNT162b1 and BNT162b2 recipients at the 30-µg dose level.

From before vaccination to 7 days after Dose 2, most participants who received BNT162b1 or BNT162b2 at the 30-µg dose level achieved a ≥4-fold rise in SARS-CoV-2 50% neutralizing titers.

Phase 1 Immunogenicity Conclusions

Both BNT162b1 and BNT162b2 elicited robust SARS-CoV-2 neutralizing antibody response 7 days after Dose 2 in younger and older adults, based on GMTs, GMFRs, proportions of participants achieving a ≥4-fold rise in neutralizing titers, and RCDCs. Neutralizing antibody response was maintained through Day 52 and was similar for the candidates within the corresponding age and dose groups.

Both BNT162b1 and BNT162b2 elicited substantial rises in antigen binding IgG levels 7 days after Dose 2, based on GMCs, GMFRs, and proportions of participants achieving a ≥4-fold rise in IgG-antigen specific binding. Responses were maintained through Day 52.

In the 100-µg dose group, SARS-CoV-2 neutralizing antibody response modestly increased by 3 weeks after Dose 1 of BNT162b1, but neutralizing antibody response returned to levels similar to baseline by 7 weeks after Dose 1.

These data support the need for a 2-dose vaccination series.

Phase 2

Immunogenicity is an exploratory endpoint for the Phase 2 part of the study.

Phase 3

Immunogenicity is a secondary (12 to 15 year olds compared with 16 to 25 year olds) and an exploratory endpoint for the Phase 3 part of the study.

Example 15: Safety evaluation

In this interim CSR, all participants in Phase 1 and the first 6610 participants in Phase 2/3 (360 participants from Phase 2 included) used an e-diary for reporting local reactions and systemic events. A total of 1125 participants in Phase 2/3 were identified as baseline SARS-CoV-2 positive, defined as having a positive N-binding antibody test result or positive nucleic acid amplification test (NAAT) result on the day of Dose 1; of these, 545 received BNT162b2 and 580 received placebo.

Phase 1

Safety data are available up through the date cutoff date (24 August 2020) and are summarized at various time points relative to Dose 1 or Dose 2. Safety results for Phase 1 vaccine candidates BNT162b1 and BNT162b2 for both adult age groups are presented up to 1 month after Dose 2 (or data cutoff date) at the 10-µg, 20-µg, and 30-µg dose levels. Safety results for BNT162b1 at the 100-µg dose level in the younger age group are presented up to 3 weeks after Dose 1 or to before Dose 2 based on the data cutoff date. Note that the group of participants 18 to 55 years of age who

received 100 µg BNT162b1 did not receive a second dose of 100 µg BNT162b2 per IRC decision.

Local Reactions – Phase 1

Overall, for both the BNT162b1 and the BNT162b2 recipients, and in both age groups, pain at the injection site was the most frequent local reaction. Redness and swelling occurred less frequently in the BNT162b2 group and in the BNT162b1 group. In both the BNT162b1 and BNT162b2 groups, the frequency of local reactions was lower in the older age group compared to the younger age group, and there was a trend of a higher frequency of local reactions with increased dose.

BNT162b1

In the younger age group, pain at the injection site was the most frequently reported local reaction within 7 days after Dose 1 of BNT162b1. As dose level increased from 10 µg to 30 µg, increasing frequencies of pain at the injection site (58.3% to 100.0%, 7 and 12 participants, respectively) were observed compared to none in the placebo group (Figure 84). Redness was reported in 2 (16.7%) participants in the 30-µg dose group, and swelling was reported in 3 (25.0%) participants in the 20-µg dose group and 2 (16.7%) participants in the 30-µg dose group. In the 100-µg dose group, pain at the injection site (12 [100.0%] participants), swelling (5 [41.7%] participants), and redness (4 [33.3%] participants) were reported, and 1 [8.3%] participant had severe injection site pain (note: per IRC decision, Dose 2 was later administered to participants at the 10-µg dose level).

Within 7 days after Dose 2 of BNT162b1 in the younger age group, pain at the injection site remained the most frequently reported local reaction reaching 12 (100.0%) participants with the 30-µg dose group compared to the placebo group (2 [22.2%] participants), while the proportions of participants with redness (2 [16.7%] participants) and swelling (3 [25.0%] participants) were highest in the 30-µg dose group (Figure 84). No redness or swelling was reported in the placebo group.

In the older age group, pain at the injection site was the most frequently reported local reaction within 7 days after Dose 1 of BNT162b1 in both the 20-µg and 30-µg

dose groups (11 [91.7%] participants each) compared to the placebo group (1 [11.1%] participant) (Figure 85). No redness was reported, and the maximal frequency of swelling (2 [16.7%] participants) was in the 30-µg group. No redness or swelling was reported in the placebo group.

Within 7 days after Dose 2 of BNT162b1 in the older age group, pain at the injection site was the most frequently reported local reaction in both the 20-µg and 30-µg dose groups (9 [75.0%] participants each). The frequency of swelling (3 [25.0%] participants) was maximal at 30 µg, while redness (1 [8.3%] participant each) was reported in the 20-µg and 30-µg dose groups. No redness or swelling was reported in the placebo group.

After the first and second dose and in both age groups, the majority of local reactions were mild or moderate in severity, and no Grade 4 local reactions were reported.

Overall, for BNT162b1 recipients and in both age groups, pain at the injection site was the most frequent local reaction (58.3% to 100.0%), and redness (0% to 16.7%) and swelling (0% to 25.0%) occurred at a lower frequency. Notably, the frequency of local reactions was lower in the older age group compared to the younger age group, and there was a trend of a higher frequency of local reactions with increased dose.

In the younger age group, pain at the injection site had median onset day of Day 1.0 (day of vaccination) after either dose of BNT162b1 across doses 10 µg to 30 µg and after Dose 1 of BNT162b1 100 µg. Median onset day for redness and swelling was between Day 1.0 and Day 3.0 in all dose groups.

In the older age group, pain at the injection site had median onset day of Day 1.0 (day of vaccination) after Dose 1 of BNT162b1 across all dose groups and after Dose 2 for the 20-µg and 30-µg dose groups (median onset day was on Day 1.5 in the 10-µg dose group after Dose 2). With the exception of redness on Day 4 (20-µg dose group) and Day 5 (30-µg dose group) in 1 participant each after Dose 2, all other local reactions of redness or swelling reported had median onset day between Day 1.0 and Day 3.0 for all dose groups.

Local reactions resolved with median durations between 1.0 and 4.0 days in the younger age group and older age group across dose levels.

BNT162b2

In the younger age group, pain at the injection site was the most frequently reported local reaction within 7 days after Dose 1, which was maximal in the 30-µg dose group (11 [91.7%] participants) (Figure 86). One [8.3%] participant had severe injection site pain after Dose 1 of 30 µg. Most participants did not report swelling and redness. After Dose 2, pain at the injection site remained the most frequently reported local reaction (83.3%, 10 participants in each) in the 20-µg and 30-µg dose groups compared to the placebo group (2 [22.2%] participants). No participants reported redness and swelling for any dose group including placebo.

In the older age group, pain at the injection site was reported within 7 days after Dose 1 of BNT162b2 in all dose groups and was maximal in the 30-µg dose group (75.0%, 9 participants), while no redness and swelling was reported in any group (Figure 87). Local reactions were not reported in the placebo group. After Dose 2, pain at the injection site (8 [66.7%] participants) was reported in the 30-µg group compared to the placebo group (9 [11.1%] participants); no participants who received BNT162b2 or placebo reported redness and swelling.

After the first and second dose and in both age groups, the majority of local reactions were mild or moderate in severity, and no Grade 4 local reactions were reported.

Overall, for BNT162b2 recipients and in both age groups, pain at the injection site was the most frequent local reaction (33.3% to 91.7%), and redness (0% to 8.3%) and swelling (0% to 16.7%) were infrequent. The frequency of local reactions was lower in the older age group compared to the younger age group, and there was a trend of a higher frequency of local reactions with increased dose.

In the younger age group, median onset day for local reactions occurred between Day 1.0 (day of vaccination) to Day 2.0 after any dose of BNT162b2 across any dose level. In the older age group, median onset day for local reactions occurred between Day 1.0 (day of vaccination) to Day 2.0 after any dose of BNT162b2 across any dose

level. Local reactions generally resolved with median durations between 1.0 to 2.0 days in the younger and older age groups across dose levels.

Systemic Events – Phase 1

Overall, within 7 days after Dose 1, fatigue was generally the most frequently reported systemic event in the both the younger and older BNT162b1 groups and in the older BNT162b2 group; while headache and fatigue were most frequently reported in the younger BNT162b2 dose group. Overall, within 7 days after Dose 2, headache was the most frequently reported systemic event in the both the younger and older BNT162b1 groups and fatigue was the most frequently reported systemic event in the both the younger and older BNT162b2 groups. Chills was generally reported at a higher frequency after Dose 2 and at a higher frequency in the BNT162b1 group than in the BNT162b2 group. Fever was reported more frequently in the younger BNT162b1 group after Dose 2 than in the older BNT162b2 group. For both the BNT162b1 and the BNT162b2 recipients, after the first and second dose and in both age groups, the majority of systemic events were mild or moderate in severity, and no Grade 4 systemic events were reported.

BNT162b1

In the younger age group, fatigue was the most frequently reported systemic event within 7 days after Dose 1 of BNT162b1, reported by 4 (33.3%), 8 (66.7%), and 6 (50.0%) participants in the 10-µg, 20-µg, and 30-µg dose groups, respectively (Figure 88), compared to the placebo group (2 [22.2%] participants). Headache (6 [50.0%] participants) and chills (7 [58.3%] participants) were reported in the 30-µg dose group, and ≤1 (8.1%) participant reported fever in each group through 30 µg. In the placebo group, headache (1 [11.1%]) participant) was reported and none reported fever or chills. In the 100-µg dose group, higher frequencies were reported compared to the 30-µg dose group: fatigue (10 [83.3%] participants), headache (9 [75.0%] participants), chills (10 [83.3%] participants), and fever (6 [50.0%] participants).

Within 7 days after Dose 2 of BNT162b1 in the younger age group, headache was the most frequently reported systemic event, reported by all 12 (100.0%) participants in

the 30-μg dose group compared to none in the placebo group, while fatigue and chills were reported by 10 (83.3% participants) and 8 (66.7%) participants in the 30-μg dose group, respectively. Fever was reported in 17% and 75% of participants in the 20-μg and 30-μg dose groups, respectively. In the placebo group, 2 (22.2%) participants reported fatigue, and none reported fever and chills.

In the older age group, fatigue was the most frequently reported systemic event within 7 days after Dose 1 of BNT162b1, with 7 (58.3%) and 6 (50.0)% of participants reporting fatigue in the 20-μg and 30-μg dose groups, respectively (Figure 89), compared to 4 (44.4%) participants in the placebo group. Headache (6 [50.0%] participants) and chills (2 [16.7%] participants) were reported in the 30-μg dose group, and fever (3 [25.0%] participants) was reported only in the 30-μg dose group. In the placebo group, chills (2 [22.2%] participants) was reported and none reported headache or fever. One participant each reported severe muscle pain (20-μg dose group) and severe fatigue (30-μg dose group) (the former was pain related to onset of herpes zoster).

Within 7 days after Dose 2 of BNT162b1 in the older age group, headache was the most frequent systemic event reported in both the 20-μg and 30-μg dose groups (9 [75.0%] participants each) compared to the placebo group (1 [11.1%] participant). Chills was reported in 7 (58.3%) and 4 (33.3%) participants at the 20-μg and 30-μg dose groups, respectively. Fever was reported in 6 (50.0%) participants in the 20-μg dose group and in 4 (33.3%) participants in the 30-μg dose group, with 1 participant reporting fever >38.9°C to 40.0°C. In the placebo group, fatigue (2 [22.2%] participants) was reported and none reported fever and chills.

After the first and second dose and in both age groups, the majority of systemic events were mild or moderate in severity, and no Grade 4 systemic events were reported. In the older age group, prompted systemic events after each dose were milder and less frequent than those observed in the younger age group.

Systemic events had the highest frequency and/or severity with the 100-μg dose group after Dose 1. Use of antipyretic/pain medication also increased with increasing

dose level and number of doses in both age groups. For these reasons, the IRC decided that the younger age group participants should not receive a second dose of 100 µg of BNT162b1.

In the younger age group, median onset day for most systemic events after either dose of BNT162b1 across doses 10 µg to 30 µg and after Dose 1 of BNT162b1 100 µg was between Day 1.0 and Day 2.0. Most systemic events generally resolved with median durations between 1.0 to 2.0 days. For fatigue, median duration after Dose 1 was 4.0 days in the 10-µg dose group compared with 2.0 days in the 30-µg dose group.

In the older age group, median onset day for most systemic events after either dose of BNT162b1, and across any dose group, was between Day 1.0 and Day 3.5. Most systemic events generally resolved with median durations between 1.0 to 3.0 days.

BNT162b2

In the younger age group, headache (4 [33.3%] to 6 [50.0%] participants) and fatigue (3 [25.0%] to 5 [41.7%] participants) were the most frequently reported systemic events within 7 days after Dose 1 of BNT162b2 compared to the placebo group (3 [33.3%] participants each) (Figure 90). Fever (2 [16.7%] participants) and chills (4 [33.3%] participants) were reported only in the 30-µg dose group. One participant in the 30-µg group with a prior history of migraine reported a severe migraine headache on Day 7 after Dose 1.

Within 7 days after Dose 2 of BNT162b2 in the younger age group, fatigue was the most frequently reported systemic event in the 20-µg and 30-µg dose groups (7 [58.3%] and 9 [75.0%] participants, respectively) compared to the placebo group (5 [55.6%] participants). Headache (8 [66.7%] participants), chills (7 [58.3%] participants), and muscle pain (7 [58.3%] participants), and fever (2 [16.7%] participants) were reported in the 30-µg dose group. Of these events, fatigue (5 [55.6%] participants), headache (1 [11.1%] participant), and chills (1 [11.1%] participant) were reported in the placebo group, and none were reported for muscle pain.

In the older age group, the most frequently reported systemic event within 7 days after Dose 1 of BNT162b2 was fatigue in the 20-µg and at 30-µg dose groups (4 [33.3%] and 3 [25.0%] participants, respectively) compared to the placebo group (2 [22.2%] participants) (Figure 91). Headache (3 [25.0%] participants), chills (2 [16.7%] participants), and muscle pain (1 [8.3%] participant) were maximal in the 20-µg dose group. Of these events, only headache (1 [11.1%] participant) and muscle pain (2 [22.2%] participants) were reported in the placebo group. Fever was not reported. Within 7 days after Dose 2 of BNT162b2 in the older age group, fatigue remained the most frequent systemic event in the 20-µg and 30-µg dose groups (6 [50.0%] and 5 [41.7%] participants, respectively), compared to the placebo group (1 [11.1%] participant). Headache was reported in the 20-µg and 30-µg dose groups (4 [33.3%] and 3 [25.0%] participants, respectively), while muscle pain and chills were reported in the 30-µg dose group (3 [25.0%] and 2 [16.7%] participants, respectively). Fever (1 [8.3%] participant) was reported in the 30-µg dose group. Of these events, headache and muscle pain were reported in the placebo group (1 [11.1%] participant each).

After the first and second dose and in both age groups, the majority of systemic events were mild or moderate in severity, and no Grade 4 systemic events were reported.

In the younger age group, median onset day for most systemic events after either dose of BNT162b2, and across any dose group, was between Day 1.0 and Day 4.0. Most systemic events generally resolved with median durations between 1.0 to 2.5 days.

In the older age group, median onset day for any systemic event after either dose of BNT162b2, and across any dose level, was between Day 1.5 and Day 2.0, except for systemic events in the 10-µg dose group after Dose 1, which had a median onset day of Day 5.5. Most systemic events generally resolved with median durations between 1.0 to 3.0 days.

Adverse Events – Phase 1

Summary of Adverse Events – Phase 1

All AEs from Dose 1 through the data cutoff date of 24 August 2020 were included in the summary for all dose levels for each vaccine candidate and age group other than BNT162b1 100-µg group for which AEs from Dose 1 to before Dose 2 were summarized.

Overall, fewer participants reported at least 1 AE after Dose 1 in the older BNT162b2 group (8.3% to 25.0%) compared to the younger (41.7% to 50.0%) and older (25.0% to 58.3%) BNT162b1 groups and the younger BNT162b2 group (33.3% to 41.7%).

BNT162b1

In the younger age group, 5 (41.7%) to 6 (50%) participants reported at least 1 AE after Dose 1 of BNT162b1 up to 30 µg, compared to 2 (22.2%) participants in the placebo group. Related AEs increased with increasing BNT162b1 dose level (25.0% to 50.0%); six (50%) participants reported at least 1 related AE in the 30-µg dose group. One (8.3%) participant reported a severe AE (pyrexia) in the 30-µg dose group.

In the 100-µg dose group, 8 (66.7%) participants reported at least 1 AE after Dose 1 to before Dose 2 of BNT162b1, compared to 1 (33.3%) participant in the placebo group. Six (50.0%) participants had at least 1 related AE, and 1 (8.3%) participant reported a severe AE (sleep disorder).

In the older group, 3 (25.0%) participants (30-µg dose group) and 7 (58.3%) participants each (10-µg and 20-µg dose groups) reported at least 1 AE after Dose 1 of BNT162b1, compared to 4 (44.4%) participants in the placebo group. Two (16.7%) to 4 (33.3%) participants reported at least 1 related AE, with the highest frequency in the 20-µg dose group. One participant each reported a severe AE in the 20-µg (herpes zoster) and 30-µg (fatigue) dose groups.

No SAEs, AEs leading to withdrawals, or deaths were reported in either age group.

BNT162b2

In the younger age group, 4 (33.3%) to 5 (41.7%) participants reported at least 1 AE after Dose 1 of BNT162b2, compared to 2 (22.2%) participants in the placebo group. Two (16.7%) to 4 (33.3%) participants reported at least 1 related AE, with the highest

frequency in the 20-µg dose group. One participant reported a severe AE (migraine) in the 30-µg dose group.

In the older group, 1 (8.3%) to 3 (25.0%) participants reported at least 1 AE after Dose 1 of BNT162b2, compared to 2 (22.2%) participants in the placebo group. Only 1 (8.3%) participant reported at least 1 related AE (20-µg dose group). One participant each reported a severe AE in the 30-µg dose group (muscle spasms) and placebo group (radiculopathy).

No SAEs, AEs leading to withdrawals, or deaths were reported in either age group.

Analysis of Adverse Events – Phase 1

Adverse Events by System Organ Class and Preferred Term – Phase 1

AE by SOC and PT summaries in this section included AEs from Dose 1 to 1 month after Dose 2 for all groups other than BNT162b1 100-ug group for which AEs from Dose 1 to 3 weeks after Dose 1 or from Dose 1 to before Dose 2 were summarized.

General disorders and administration site conditions was the most commonly reported SOC in the older BNT162b1 group and the younger BNT162b2 group. The most commonly reported SOC was gastrointestinal disorders in the younger BNT162b1 group and nervous system disorders in the older BNT162b2 group. Generally, most PTs were reported by ≤2 participants per dose group.

BNT162b1

In the younger age group, from Dose 1 to 1 month after Dose 2 of BNT162b1, gastrointestinal disorders was the most commonly reported SOC (2 [16.7%] participants each dose group) in the BNT162b1 groups up to 30 µg. In the 20-µg dose group only, paraesthesia (3 [25.0%]) was the most common AE by PT. All other AEs were reported by ≤2 participants per dose group, including those in the placebo group.

In the 100-µg dose group, from Dose 1 to 3 weeks after Dose 1 of BNT162b1, psychiatric disorders was the most commonly reported SOC (3 [25.0%] participants), and sleep disorder (3 [25%] participants) was the most common AE by PT. All other AEs were reported by ≤2 participants, including those in the placebo group.

In the older age group, from Dose 1 to 1 month after Dose 2 of BNT162b1, general disorders and administration site conditions was the most commonly reported SOC in the BNT162b1 groups, reported in a total of 6 participants: 1 (8.3%) participant in the 10-µg dose group, 2 (16.7%) participants in the 20-µg dose group, and 3 (25.0%) participants in the 30-µg dose group. Any AEs by PT were reported by no more than 1 participant per dose group.

BNT162b2

In the younger age group, general disorders and administration site conditions was the most commonly reported SOC. These events included injection site pain and injection site erythema. Any AEs by PT were reported by no more than 1 participant per dose group.

In the older age group, nervous system disorders was the most commonly reported SOC, reported in 1 participant each in the 30-µg group (sciatica) and the placebo group (radiculopathy). Any AEs by PT were reported by no more than 1 participant per dose group.

Related Adverse Events – Phase 1

Overall, general disorders and administration site conditions was the most commonly reported SOC for the younger and older BNT162b1 groups and the younger BNT162b2 group. In the older BNT162b2 group, nausea, reported in 1 (8.3%) participant, was the only related AE.

BNT162b1

In the younger age group, general disorders and administration site conditions was the most commonly reported SOC (injection site pain, pyrexia, chills, fatigue, and injection site swelling). Two (16.7%) participants each in the 30-µg dose group reported related AEs of tachycardia and pyrexia. All other related AEs were reported by ≤2 participants per dose group.

In the 100-µg BNT162b1 group, psychiatric disorders were the most commonly reported SOC. Three (25.0%) participants reported sleep disorder as their psychiatric disorder. All other related AEs were reported by ≤2 participants each.

In the older age group, general disorders and administration site conditions was the most commonly reported SOC (fatigue, injection site bruising, injection site pain, and peripheral swelling). Any related AEs by PT were reported by no more than 1 participant per dose group.

BNT162b2

In the younger age group, general disorders and administration site conditions was the most commonly reported SOC (injection site pain and injection site erythema). Any related AEs by PT were reported by no more than 1 participant per dose group, including those in the placebo group.

In the older age group, only 1 (8.3%) participant reported a related AE of nausea in the 20-µg dose group.

Immediate Adverse Events – Phase 1

BNT162b1

In the younger age group, 1 participant reported an immediate AE of paraesthesia after Dose 1 of 20 µg BNT162b1. In the 100-µg group, no participants reported an immediate AE after Dose 1.

In the older age group, 1 participant reported an immediate AE of eye paraesthesia after Dose 1 of 10 µg BNT162b1.

There were no participants in either age group who reported any immediate AEs after Dose 2 of BNT162b1.

BNT162b2

In the younger age group, after Dose 1 of BNT162b2, there were 3 participants who reported an immediate AE: injection site erythema (10-µg dose group), ageusia (20-µg dose group), and injection site pain (30-µg dose group). After Dose 2 of BNT162b2, there was 1 participant who reported an immediate AE of taste disorder (20-µg dose group).

There were no participants in the older age group who reported any immediate AE after any dose of BNT162b2.

Severe Adverse Events – Phase 1

BNT162b1

In the younger age group, there was 1 participant who reported a severe AE of pyrexia (102.4°F) 2 days after Dose 2 (30-µg dose group) and 1 participant who reported a severe AE of sleep disorder 1 day after Dose 1 (100-µg dose group). Both AEs were determined by the investigator to be related to study intervention.

In the older age group, 2 participants reported a severe AE: herpes zoster which occurred 2 days after Dose 1 (20-µg dose group, considered unrelated to BNT162b1) and fatigue 1 day after Dose 2 (30-µg dose group, considered related to BNT162b1).

BNT162b2

In the younger age group, 1 participant with a history of migraines reported a severe migraine 7 days after Dose 1 (30-µg dose group, considered unrelated). In the older age group, 2 participants reported a severe AE: muscle spasms 2 days after Dose 2 (30-µg dose group, considered unrelated to BNT162b2) and radiculopathy 3 days after Dose 1 (placebo), considered unrelated to study intervention.

Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 1

Deaths – Phase 1

There were no Phase 1 participants who died through the data cutoff date of 24 August 2020 in this interim CSR.

Serious Adverse Events – Phase 1

There were no Phase 1 participants who reported any SAEs during the period covered in this interim CSR.

Safety-Related Participant Withdrawals – Phase 1

There were no Phase 1 participants with any AEs leading to withdrawal from the study through the data cutoff date of 24 August 2020 in this interim CSR.

Other Significant Adverse Events – Phase 1

AEs of special interest were not defined for Phase 1 of this study.

Other Safety Assessments – Phase 1

Severe COVID-19 Illness – Phase 1

There were no COVID-19 cases reported in the Phase 1 participants through the data cutoff date of 24 August 2020.

Pregnancy – Phase 1

Pregnancy was not reported in any Phase 1 participants through the data cutoff date of 24 August 2020.

Analysis and Discussion of Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 1

During the period covered in this interim CSR, there were no SAEs, AEs leading to withdrawals, or deaths reported in either age group.

Clinical Laboratory Evaluation – Phase 1

Overall, 1 to 3 days after Dose 1, there were transient decreases in lymphocytes (<0.8 × LLN), which returned to normal by 6 to 8 days after Dose 1, in the younger and older BNT162b1 and BNT162b2 groups. Most shifts were from normal or Grade 1 to Grade 1, 2, or 3 decrease in lymphocyte counts, which returned to normal by 6 to 8 days after Dose 1, and were observed in all age and dose groups. Shifts from normal to Grade 1 (younger BNT162b1 group) or Grade 2 (older BNT162b2 group) neutrophil decrease were also observed but were infrequent.

Overall, other clinical chemistry abnormalities reported or shifts of laboratory results were infrequent. The incidence of decreased lymphocyte counts was lower for BNT162b2 recipients compared with BNT162b1 recipients. None of the laboratory abnormalities were associated with clinical findings.

BNT162b1

In the younger age group, laboratory abnormalities of transient decreases in lymphocytes (<0.8 × LLN) were observed in 1 (8.3%), 4 (33.3%), and 6 (54.5%) of participants 1 to 3 days after Dose 1 of BNT162b1 10 µg, 20 µg, or 30 µg, respectively, which returned to normal by 6 to 8 days after Dose 1. A shift from normal to Grade 3 decrease in lymphocyte counts was observed in 1 participant each in the 10-µg and 30-µg dose groups and 2 (16.7%) participants the 20-µg dose group. No Grade 3 decrease in lymphocyte counts was observed by 6 to 8 days after Dose 1. After Dose

1, a shift from normal to Grade 2 neutrophil decrease was observed in 1 (11.1%) participant in the placebo group, which was not observed by 19 to 23 days after Dose 1. At 6 to 8 days after Dose 2, a shift in neutrophil decrease was observed in 1 participant each in the 10-µg dose group (Grade 1 to Grade 2) and in the 30-µg dose group (normal to Grade 2). Both participants had a shift to Grade 1 at the unplanned visit approximately 1 month after Dose 2.

In the 100-µg BNT162b1 group, laboratory abnormalities of transient decreases in lymphocytes (<0.8 × LLN) were observed in 9 (75.0%) participants 1 to 3 days after Dose 1, which returned to normal by 6 to 8 days after Dose 1. A shift from normal to Grade 3 decrease in lymphocyte counts was observed in 4 (33.3%) participants 1 to 3 days after Dose 1, which returned to normal by 6 to 8 days after Dose 1. A shift from normal to Grade 1 neutrophil decrease was observed in 3 (25.0%) participants at 6 to 8 days after Dose 1, which returned to normal by 19 to 23 days after Dose 1.

In the older age group, laboratory abnormalities of transient decreases in lymphocytes (<0.8 × LLN) were also observed in 1 (8.3%), 3 (25.0%), and 2 (16.7%) participants 1 to 3 days after Dose 1 of BNT162b1 10 µg, 20 µg, or 30 µg, respectively, which returned to normal by 6 to 8 days after Dose 1. At 1 to 3 days after Dose 1 of BNT162b1, shifts from normal to Grade 3 or Grade 4 decrease in lymphocyte counts were observed in 1 (8.3%) participant each in the 30-µg and 10-µg dose groups, respectively, and both returned to normal by 6 to 8 days after Dose 1.

Overall, other clinical chemistry abnormalities reported or shifts of laboratory results were infrequent. None of the abnormalities were associated with clinical findings.

BNT162b2

In the younger age group, laboratory abnormalities of transient decreases in lymphocytes (<0.8 × LLN) were observed in 1 (8.3%) participant each 1 to 3 days after Dose 1 of BNT162b2 in the 20-µg and 30-µg dose groups, which returned to normal by 6 to 8 days after Dose 1. At 1 to 3 days after Dose 1 of BNT162b2, shifts from normal to Grade 1 decrease in lymphocyte counts were observed in 3 (25.0%), 2 (16.7%), and 4 (33.3%) participants in the 10-µg, 20-µg, and 30-µg dose groups,

respectively, and shifts from normal to Grade 2 decrease in lymphocyte counts were observed in 1 (8.3%) participant each in the 20-µg and 30-µg dose groups. By 6 to 8 days after Dose 1, no Grade 2 or Grade 3 decrease in lymphocyte counts were observed.

In the older age group, laboratory abnormalities of transient decreases in lymphocytes (<0.8 × LLN) were also observed in 1 (8.3%) participant each 1 to 3 days after Dose 1 of BNT162b2 across all dose levels, which returned to normal by 6 to 8 days after Dose 1. A shift from normal to Grade 3 (10-µg dose group) and a Grade 1 to Grade 3 (30-µg dose group) decrease in lymphocyte counts was observed in 1 (8.3%) participant each after Dose 1. A shift from normal to Grade 2 neutrophil decrease was observed in 2 (16.7%) participants in the 20-µg dose group at 1 to 3 days after Dose 1, and no shifts to Grade 2 were observed by 6 to 8 days after Dose 1. A shift from normal to Grade 2 neutrophil decrease was observed in 1 (8.3%) participant in the 10-µg dose group at 6 to 8 days after Dose 1. By 19 to 23 days after Dose 1, no shifts to Grade 2 neutrophil decrease were observed for any dose group.

Overall, other clinical chemistry abnormalities reported or shifts of laboratory results were infrequent. The incidence of decreased lymphocyte counts was lower for BNT162b2 recipients compared with BNT162b1 recipients. None of the laboratory abnormalities were associated with clinical findings.

Physical Examination Findings – Phase 1

Overall, there were fewer abnormalities noted during physical examinations after BNT162b2 than after BNT162b1 in both age groups. Abnormalities were generally observed 1 to 3 days after Dose 1 and most were of the extremities, musculoskeletal system, or skin.

BNT162b1

In the younger age group, there were no abnormalities noted during baseline physical examinations. Overall, after randomization, most abnormalities were observed 1 to 3 days after Dose 1 of 10 µg, 20 µg, or 30 µg BNT162b1 (9 [20.0%] participants) and 6 to 8 days after Dose 2 (7 [15.6%] participants). In the 30-µg dose group, a maximum of

6 (50.0%) participants had abnormalities 1 to 3 days after Dose 1, and most abnormalities were of the extremities.

In the 100-µg dose group, only 1 (8.3%) participant had an abnormality at baseline. From Dose 1 to 3 weeks after Dose 1, 9 (75.0%) participants had abnormalities 1 to 3 days after BNT162b1, and most abnormalities were of the extremities.

In the older age group, there were 5 (11.1%) participants with abnormalities noted during baseline physical examinations, with ≤2 participants in any dose group. Overall, after randomization, most abnormalities were observed 1 to 3 days after Dose 1 of BNT162b1 (15 [33.3%] participants). In the 20-µg and 30-µg dose groups, 6 (50.0%) and 4 (33.3%) participants had abnormalities 1 to 3 days after Dose 1, and most abnormalities involved either the musculoskeletal system or extremities.

There were no clinically important findings from physical examinations.

BNT162b2

In the younger age group, there were 5 (11.1%) participants with abnormalities noted during baseline physical examinations, with ≤2 participants in any dose group. Overall, after randomization, most abnormalities were observed 1 to 3 days after Dose 1 of 10 µg, 20 µg, or 30 µg BNT162b2 (5 [11.1%] participants) and 6 to 8 days after Dose 2 (4 [8.9%] participants), with most being abnormalities of the extremities or skin.

In the older age group, there was 1 (8.3%) participant in the 30-µg dose group with an abnormality noted during the baseline physical examination. After randomization, ≤2 participants in any dose group overall had an abnormality in physical examination during any visit window.

There were no clinically important findings from physical examinations at baseline.

Phase 1 Summary of Safety Results Evaluating BNT162b1 and BNT162b2

Overall, reactogenicity events were well tolerated and short-lived (median durations 1.0 to 4.0 days). All participants returned to receive their second dose. All AEs as a result of reactogenicity events resolved without sequelae.

For local reactions in both age groups, pain at the injection site (58.3% to 100.0%), redness (0% to 16.7%), and swelling (0% to 25.0%) were reported for BNT162b1

recipients, which were more frequent than for BNT162b2 recipients: pain at the injection site (33.3% to 91.7%), redness (0% to 8.3%), and swelling (0% to 16.7%). In general, frequencies of local reactions were observed to be higher with increased dose level.

The frequency of local reactions was lower in the older age group compared to the younger age group. The frequency of pain at the injection site, the most frequently reported local reaction, was lower in the older age groups after 30 µg BNT162b1 (91.7% and 75.0%) and after 30 µg of BNT162b2 (75.0% and 66.7% for Dose 1 and Dose 2, respectively), compared to the younger age groups after 30 µg of BNT162b1 (100.0% for both Dose 1 and Dose 2) and 30 µg of BNT162b2 (91.7% and 83.3% for Dose 1 and Dose 2, respectively).

BNT162b2 recipients in the older age group reported lower frequencies of local reactions compared with BNT162b1 recipients in the older age group. In the older 30-µg BNT162b2 group, pain at the injection site was lower after Dose 1 (75.0%) and Dose 2 (66.7%) than in the older 30-µg BNT162b1 group after Dose 1 (91.7%) and Dose 2 (75.0%).

Common systemic events in both age groups after either Dose 1 or Dose 2 included fatigue (16.7% to 83.3%), headache (25.0% to 100%), chills (8.3% to 66.7%), fever (0% to 75.0%), and muscle pain (8.3% to 75.0%) for BNT162b1 recipients up to 30 µg, which were more frequent than BNT162b2 recipients up to 30 µg: fatigue (8.3% to 75.0%), headache (0% to 66.7%), chills (0% to 58.3%), fever (0% to 16.7%), and muscle pain (0% to 58.3%). In general, frequencies of systemic events were observed to be higher with increased dose level.

The frequency of systemic events was lower in the older age group compared to the younger age group. The frequency of fatigue was lower in the older age groups after 30 µg of BNT162b1 (50.0% and 66.7%) and after 30 µg of BNT162b2 (25.0% and 41.7% for Dose 1 and Dose 2, respectively), compared to the younger age groups after 30 µg of BNT162b1 (50.0% and 83.3%) and after 30 µg of BNT162b2 (41.7% and 75.0%) for Dose 1 and Dose 2, respectively.

BNT162b2 recipients in the older age group reported lower frequencies of systemic events compared with BNT162b1 recipients in the older age group. The frequency of fatigue was lower in the older 30-µg BNT162b2 group (25.0% and 41.7% for Dose 1 and Dose 2, respectively) than in the older 30-µg BNT162b1 group (50.0% and 66.7% for Dose 1 and Dose 2, respectively).

Most AEs were mild or moderate in severity. Most related AEs were similar to the solicited reactogenicity events reported in the e-diary. Few severe AE were reported but were considered not related to study intervention.

There were no SAEs, deaths, or discontinuations because of AEs.

Transient decrease in lymphocytes were observed in all age and dose groups 1 to 3 days after Dose 1, which resolved by 6 to 8 days after Dose 1.

There were no clinically important findings from physical examinations.

BNT162b2 demonstrated a favorable reactogenicity and safety profile compared with BNT162b1, contributing to the selection of BNT162b2 for Phase 2/3 development.

Phase 1 Safety Conclusions

All doses tested for BNT162b1 and BNT162b2 (10 µg, 20 µg, and 30 µg) were safe and well tolerated except for BNT162b1 at 100 µg, which was discontinued after the first dose due to the reactogenicity profile.

Reactogenicity was generally higher after Dose 2 than Dose 1.

The frequency of local and systemic reactogenicity was generally lower for BNT162b2 compared to BNT162b1 especially after the second dose.

Reactogenicity events after each dose for both BNT162b1 and BNT162b2 in older adults were milder and less frequent than those observed in younger adults. The majority of reactogenicity events were mild or moderate in severity.

Most AEs were mild or moderate. There were no SAEs or discontinuations because of AEs.

Overall, fewer AEs were experienced by participants who received BNT162b2 compared with those who received BNT162b1, with the least number of participants experiencing AEs in the BNT162b2 older age group. Few severe AEs in the older age

group after BNT162b2 were observed, and all were considered unrelated to study intervention.

Clinical laboratory evaluations showed a transient decrease in lymphocytes that was observed in all age and dose groups after Dose 1, which resolved within a few days, were not associated with any other clinical sequelae, and were not considered clinically relevant.

BNT162b2 at 30 µg was selected to proceed into the Phase 2/3 portion of the study because this dose and construct provided the optimum combination of a favorable reactogenicity profile and a robust immune response.

Phase 2

Safety data are available up to the data cutoff date (02 September 2020) and are summarized up to the data cutoff date for the 360 participants in Phase 2. All participants in Phase 2 used an e-diary for reporting local reactions and systemic events.

Local Reactions – Phase 2

After the first and second dose of BNT162b2 and in both age groups, the majority of local reactions were mild or moderate in severity, and no Grade 4 (potentially life-threatening) local reactions were reported.

In the BNT162b2 group, pain at the injection site was reported more frequently in the younger age group (Figure 92) than in the older age group (Figure 93), and frequency was similar after Dose 1 compared with Dose 2 of BNT162b2 in the younger age group (85.2% vs. 80.2%, respectively) and in the older age group (70.7% vs. 72.5%, respectively). In the placebo group, pain at the injection site was reported at similar frequencies (7.8% to 10.2%) in the younger and older age groups after Dose 1 and Dose 2.

In the BNT162b2 group, redness and swelling were similar in the younger and older age group after Dose 1. After Dose 2, the frequency of redness and swelling was slightly higher in the older age group (7.7% and 12.1%, respectively) than in the younger age group (3.5% and 3.5%, respectively). In the placebo group, only

1 participant in the older age group reported redness after Dose 1, and no swelling was reported.

One participant in the BNT162b2 group (older age group) reported severe injection site pain after Dose 1, and 1 participant in the younger age group reported severe injection site pain after Dose 2. One participant in the BNT162b2 group (older age group) reported severe redness after Dose 2.

Overall, across age groups, pain at the injection site was the most frequent local reaction and did not increase after Dose 2, and redness and swelling were generally similar in frequency after Dose 1 and Dose 2.

Across age groups, local reactions for the BNT162b2 group after either dose had a median onset day between Day 1.0 and Day 3.0 (Day 1.0 was the day of vaccination), and ranges were generally similar in the younger and older age groups. Across age groups, after either dose of BNT162b2, local reactions resolved after a median duration of 1.0 to 3.0 days, which was generally similar in the younger and older age groups.

Systemic Events – Phase 2

In the BNT162b2 group, systemic events were generally reported more frequently and were of higher severity in the younger group (Figure 94) compared with the older group (Figure 95), with frequencies and severity increasing with number of doses (Dose 1 vs Dose 2). Vomiting and diarrhea were exceptions with vomiting infrequent and similar in both age groups and vomiting and diarrhea similar after each dose. Frequencies of systemic events in the younger and older BNT162b2 groups (Dose 1 vs Dose 2) are listed below:

fatigue: younger group (50.0% vs 59.3%) compared to older group (35.9% vs 52.7%)

headache: younger group (31.8% vs 51.2%) compared to older group (27.2% vs 36.3%)

muscle pain: younger group (23.9% vs 45.3%) compared to older group (14.1% vs 28.6%)

chills: younger group (9.1% vs 40.7%) compared to older group (7.6% vs 20.9%)

joint pain: younger group (9.1% vs 17.4%) compared to older group (4.3% vs 16.5%)

fever: younger group (3.4% vs 17.4%) compared to older group (0.0% vs 11.0%).

vomiting: similar in both age groups and after either dose.

diarrhea: reported less frequently in the older group and was similar after each dose.

Systemic events were generally reported less frequently in the placebo group than in the BNT162b2 group, for both age groups and doses, with some exceptions. In the younger age group, fever, headache, chills, vomiting, and diarrhea after Dose 1, and vomiting after Dose 2 were reported at similar frequencies in both the placebo and BNT162b2 groups (Figure 94). In the older age group, vomiting, diarrhea, muscle pain, and joint pain after Dose 1, and vomiting and diarrhea after Dose 2 were reported at similar frequencies in the placebo and BNT162b2 groups (Figure 95).

Use of antipyretic/pain medication was slightly less frequent in the older age group after both doses but increased in both age groups overall after Dose 2 as compared with after Dose 1. Use of antipyretic/pain medication was less frequent in the placebo group than in the BNT162b2 group.

After the first and second dose and in both age groups, the majority of systemic events were mild or moderate in severity, and no Grade 4 (potentially life-threatening) systemic events were reported. Across age groups, severe systemic events were only reported after Dose 2 of BNT162b2 overall and included fever (1.1%), fatigue (4.0%), headache (2.8%), chills (2.3%), and muscle pain (1.7%).

Across age groups, systemic events after both doses of BNT162b2 had a median onset day between Day 2.0 to Day 3.0 (Day 1.0 was the day of vaccination), and ranges were similar in the younger and older age groups. Across age groups, systemic events for this group after either dose resolved with a median duration of 1 day, which was similar in the younger and older age groups. There was no clear difference in the durations of systemic events that occurred after Dose 1 compared to those that occurred after Dose 2.

Adverse Events – Phase 2

Summary of Adverse Events – Phase 2

The number of participants who reported at least 1 AE was similar in the BNT162b2 group compared with the placebo group, which was generally similar in the 2 vaccine groups in the younger and older age groups (Table 10 and Table 11, respectively).

Two severe events were reported for 2 participants in the BNT162b2 younger age group: myalgia (AE) and gastric adenocarcinoma (SAE) The SAE of gastric adenocarcinoma occurred 23 days after receiving Dose 1. Both events were assessed by the investigator as not related to study intervention.

From 7 days after Dose 2 to the data cutoff date (02 September 2020), no additional participants reported any AE.

Table 10. Number (%) of Subjects Reporting at Least 1 Adverse Event From Dose 1 to 7 Days After Dose 2, by Age Group – Phase 2 – Safety Population Age Group: 18-55 Years

	Vaccine Group (as Administered)	
Adverse Event	BNT162b2 (30 µg) (N^a=88) n^b (%)	Placebo (N^a=90) n^b (%)
Any event	8 (9.1)	10 (11.1)
Related[c]	3 (3.4)	6 (6.7)
Severe	2 (2.3)	0
Life-threatening	0	0
Any serious adverse event	1 (1.1)	0
Related[c]	0	0
Severe	1 (1.1)	0
Life-threatening	0	0
Any adverse event leading to withdrawal	1 (1.1)	0
Related[c]	0	0
Severe	1 (1.1)	0
Life-threatening	0	0
Death	0	0

a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified adverse event category. For "any event", n = the number of subjects reporting at least 1 occurrence of any adverse event.
c. Assessed by the investigator as related to investigational product.

Table 11. Number (%) of Subjects Reporting at Least 1 Adverse Event From Dose 1 to 7 Days After Dose 2, by Age Group – Phase 2 – Safety Population Age Group: 56-85 Years

	Vaccine Group (as Administered)	
Adverse Event	BNT162b2 (30 µg) (N^a=92) n^b (%)	Placebo (N^a=90) n^b (%)
Any event	4 (4.3)	8 (8.9)
Related[c]	2 (2.2)	2 (2.2)
Severe	0	0
Life-threatening	0	0
Any serious adverse event	0	0
Related[c]	0	0
Severe	0	0
Life-threatening	0	0
Any adverse event leading to withdrawal	0	0
Related[c]	0	0
Severe	0	0
Life-threatening	0	0
Death	0	0

a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified adverse event category. For "any event", n = the number of subjects reporting at least 1 occurrence of any adverse event.
c. Assessed by the investigator as related to investigational product.

Analysis of Adverse Events – Phase 2

Adverse Events by System Organ Class and Preferred Term – Phase 2

Table 12 presents the number of participants who reported at least 1 AE from Dose 1 to 7 days after Dose 2 by SOC and PT.

The number of participants who reported at least 1 AE was similar in the BNT162b2 group compared to the placebo group from Dose 1 to 7 days after Dose 2.

In the younger age group, 8 (9.1%) and 10 (11.1%) participants reported at least 1 AE in the BNT162b2 group and the placebo group, respectively. In the older age group, 4 (4.3%) and 8 (8.9%) participants reported at least 1 AE in the BNT162b2 group and the placebo group, respectively.

Overall, most AEs reported up to 7 days after Dose 2 were in the SOCs of gastrointestinal disorders (3 [1.7%] in the BNT162b2 group and 2 [1.1%] in the placebo group), general disorders and administration site conditions (3 [1.7%] in the BNT162b2 group and 7 [3.9%] in the placebo group), and musculoskeletal and connective tissue disorders (3 [1.7%] in the BNT162b2 group and 1 [0.6%] in the placebo group).

The most frequently reported AE by PT was injection site pain (3 [3.4%]) in the younger BNT162b2 group, which all occurred on the day of vaccination with Dose 1 during the reporting period for local reactions. Two events resolved within 3 days, and 1 event resolved 11 days later. All other AEs by PT were reported in ≤2 participants in each vaccine group.

One participant in the older BNT162b2 group had an AE of contusion in the upper left arm deltoid region, which was assessed by the investigator as related to study intervention.

Table 12. Number (%) of Subjects Reporting at Least 1 Adverse Event From Dose 1 to 7 Days After Dose 2, by System Organ Class and Preferred Term – Phase 2 – Safety Population

	Vaccine Group (as Administered)							
	BNT162b2 (30 µg)						Placebo	
	18-55 Years (N^a=88)		56-85 Years (N^a=92)		18-85 Years (N^a=180)		18-85 Years (N^a=180)	
System Organ Class Preferred Term	n^b (%)	(95% CI[c])	n^b (%)	(95% CI[c])	n^b (%)	(95% CI[c])	n^b (%)	(95% CI[c])
Any event	8 (9.1)	(4.0, 17.1)	4 (4.3)	(1.2, 10.8)	12 (6.7)	(3.5, 11.4)	18 (10.0)	(6.0, 15.3)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Lymphadenopathy	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
GASTROINTESTINAL DISORDERS	1 (1.1)	(0.0, 6.2)	2 (2.2)	(0.3, 7.6)	3 (1.7)	(0.3, 4.8)	2 (1.1)	(0.1, 4.0)
Diarrhoea	1 (1.1)	(0.0, 6.2)	1 (1.1)	(0.0, 5.9)	2 (1.1)	(0.1, 4.0)	1 (0.6)	(0.0, 3.1)
Odynophagia	0	(0.0, 4.1)	1 (1.1)	(0.0, 5.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Tongue discomfort	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
GENERAL DISORDERS AND ADMINISTRATION SITE CONDITIONS	3 (3.4)	(0.7, 9.6)	0	(0.0, 3.9)	3 (1.7)	(0.3, 4.8)	7 (3.9)	(1.6, 7.8)

Injection site erythema	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	2 (1.1)	(0.1, 4.0)
Injection site pain	3 (3.4)	(0.7, 9.6)	0	(0.0, 3.9)	3 (1.7)	(0.3, 4.8)	0	(0.0, 2.0)
Fatigue	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	2 (1.1)	(0.1, 4.0)
Chills	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Injection site discolouration	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Injection site swelling	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
INFECTIONS AND INFESTATIONS	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Vulvovaginal mycotic infection	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
INJURY, POISONING AND PROCEDURAL COMPLICATIONS	0	(0.0, 4.1)	1 (1.1)	(0.0, 5.9)	1 (0.6)	(0.0, 3.1)	3 (1.7)	(0.3, 4.8)
Contusion	0	(0.0, 4.1)	1 (1.1)	(0.0, 5.9)	1 (0.6)	(0.0, 3.1)	1 (0.6)	(0.0, 3.1)
Fall	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Muscle rupture	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Tendon rupture	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
INVESTIGATIONS	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
White blood cell count increased	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
MUSCULOSKELETAL AND CONNECTIVE TISSUE DISORDERS	2 (2.3)	(0.3, 8.0)	1 (1.1)	(0.0, 5.9)	3 (1.7)	(0.3, 4.8)	1 (0.6)	(0.0, 3.1)
Myalgia	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	1 (0.6)	(0.0, 3.1)
Arthralgia	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Neck pain	0	(0.0, 4.1)	1 (1.1)	(0.0, 5.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Adenocarcinoma gastric	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
NERVOUS SYSTEM DISORDERS	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Headache	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
RESPIRATORY, THORACIC AND MEDIASTINAL DISORDERS	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	2 (1.1)	(0.1, 4.0)
Oropharyngeal pain	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Productive cough	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Rhinorrhoea	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
SKIN AND SUBCUTANEOUS TISSUE DISORDERS	1 (1.1)	(0.0, 6.2)	1 (1.1)	(0.0, 5.9)	2 (1.1)	(0.1, 4.0)	1 (0.6)	(0.0, 3.1)
Dermatitis	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)
Hangnail	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Macule	0	(0.0, 4.1)	1 (1.1)	(0.0, 5.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Rash macular	0	(0.0, 4.1)	0	(0.0, 3.9)	0	(0.0, 2.0)	1 (0.6)	(0.0, 3.1)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified event. For "any event", n = number of subjects reporting at least 1 occurrence of any event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

Related Adverse Events by System Organ Class and Preferred Term – Phase 2

The number of participants with AEs assessed by the investigator as related to study intervention from Dose 1 to 7 days after Dose 2 were low in frequency and similar in the BNT162b2 group and placebo group. Within the BNT162b2 group, a similar proportion of participants in the young and old age groups reported related AEs. Most investigator-assessed related AEs were reactogenicity events in the SOC of general disorders and administration site conditions, and they were reported by a similar proportion of participants in the BNT162b2 group overall compared with the placebo group, with injection site pain being the PT reported most frequently and exclusively in the BNT162b2 younger age group.

Immediate Adverse Events – Phase 2

There were no immediate AEs after any dose of BNT162b2 30 µg or placebo.

Severe or Life-Threatening Adverse Events – Phase 2

Two participants (both in the BNT162b2 younger age group) reported severe events of myalgia (AE) and gastric adenocarcinoma (SAE). The participant who reported myalgia had scapular muscle pain, which began 2 days after Dose 2 and was ongoing at the time of the data cutoff. Both events were assessed by the investigator as not related to study intervention.

Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 2

Deaths – Phase 2

There were no Phase 2 participants who died through the data cutoff date of 02 September 2020 in this interim CSR.

Serious Adverse Events – Phase 2

One participant had an SAE from Dose 1 to 7 days after Dose 2 (Table 13). One participant, who was in the BNT162b2 younger age group, had an SAE of gastric adenocarcinoma 23 days after Dose 1, which was assessed by the investigator as not related to study intervention (Table 13). The SAE was ongoing at the time of the data cutoff, and the participant was withdrawn from the study because of the SAE.

From 7 days after Dose 2 to the data cutoff date (02 September 2020), no additional participants reported any SAE.

Table 13. Number (%) of Subjects Reporting at Least 1 Serious Adverse Event From Dose 1 to 7 Days After Dose 2, by System Organ Class and Preferred Term – Phase 2 – Safety Population

	Vaccine Group (as Administered)							
	BNT162b2 (30 µg)						Placebo	
	18-55 Years (N^a=88)		56-85 Years (N^a=92)		18-85 Years (N^a=180)		18-85 Years (N^a=180)	
System Organ Class Preferred Term	n^b (%)	(95% CI^c)	n^b (%)	(95% CI^c)	n^b (%)	(95% CI^c)	n^b (%)	(95% CI^c)
Any event	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)
Adenocarcinoma gastric	1 (1.1)	(0.0, 6.2)	0	(0.0, 3.9)	1 (0.6)	(0.0, 3.1)	0	(0.0, 2.0)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified adverse event. For "any event", n = number of subjects reporting at least 1 occurrence of any adverse event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

Safety-Related Participant Withdrawals – Phase 2

The participant in the BNT162b2 younger age group who reported an SAE of gastric adenocarcinoma was discontinued from the study on Day 23 after Dose 1 of BNT162b2.

Narratives of Safety-Related Participant Withdrawals – Phase 2

A narrative for the Phase 2 participant who was withdrawn from the study because of an SAE through the data cutoff date (02 September 2020) was provided.

Other Significant Adverse Events – Phase 2

AEs of special interest were not defined for Phase 2 of this study; however, targeted medical events were monitored throughout the study.

Analysis and Discussion of Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 2

Up to the data cutoff date of 02 September 2020, there was 1 participant in the younger age group (BNT162b2 group) withdrawn from the study because of an SAE of gastric adenocarcinoma, which was assessed by the investigator as not related to study intervention.

Phase 2 Safety Conclusions

Across age groups, local reactions were generally similar in frequency after each dose, and systemic events generally increased in frequency and severity after Dose 2 compared to Dose 1. Local and systemic reactogenicity events were well-tolerated and short-lived.

Reactogenicity events after each dose of BNT162b2 in older adults were generally milder and less frequent than those observed in younger adults. The majority of reactogenicity events were mild or moderate in severity. No Grade 4 events were reported.

AEs in participants were low in frequency, and most AEs were mild or moderate in severity. There were no SAEs or discontinuations because of AEs that were assessed as related by the investigator.

The reactogenicity and AE profile after BNT162b2 30 µg evaluated in 360 participants was consistent with the safety profile observed after BNT162b2 30 µg in Phase 1.

BNT162b2 at 30 µg was safe and well tolerated up to 7 days after Dose 2.

Phase 2/3

In this interim CSR, safety results for Phase 3 included 36,855 older adolescent and adult participants (16 to 91 years of age) up through the safety data cutoff date of 06

October 2020. AE summaries included any AE reported, regardless of whether participants completed the visit at 1 month after Dose 2. The first 6610 adult participants (18 to 85 years of age, which included the 360 participants in Phase 2) used an e-diary for reporting local reactions and systemic events and had safety data summarized through at least 1 month after Dose 2.

During the Phase 2/3 portion of the study, a stopping rule for the theoretical concern of vaccine enhanced disease was to be triggered if the 1-sided probability of observing the same or more extreme adverse severe case split was 5% or less, given the same true incidence for vaccine and placebo recipients, and alert criteria were to be triggered if this probability was less than 11%. It is also noted that, with ~18,000 per arm, the study has > 83% probability of detecting at least 1 adverse event.

Local Reactions – Phase 2/3

In the BNT162b2 group, pain at the injection site was reported more frequently in the younger age group (Figure 96) than in the older age group (Figure 97), and frequency was similar after Dose 1 compared with Dose 2 of BNT162b2 in the younger age group (85.3% vs. 79.5%, respectively) and in the older age group (71.7% vs. 66.6%, respectively). In the placebo group, pain at the injection site after Doses 1 and 2 was reported at slightly higher frequencies in the younger age group (13.8% and 11.9%, respectively) than in the older age group (8.8% and 7.7%, respectively).

In the BNT162b2 group, frequencies of redness and swelling were similar in the younger and older age group after Doses 1 and 2. Frequencies of redness were similar after Dose 1 compared with Dose 2 of BNT162b2 in the younger age group (4.3% vs 5.4%, respectively) and in the older age group (4.5% vs 6.6%, respectively). Frequencies of swelling were similar after Dose 1 compared with Dose 2 of BNT162b2 in the younger age group (5.5% vs 5.9%, respectively) and in the older age group (6.5% vs 7.0%, respectively). In the placebo group, redness and swelling were reported infrequently in the younger (≤0.8%) and older (≤1.3%) age groups after Doses 1 and 2. Overall, across age groups, pain at the injection site did not increase after Dose 2, and redness and swelling were generally similar in frequency after Dose 1 and Dose 2.

Severe local reactions (≤0.8%) were reported infrequently in the BNT162b2 group after either dose overall but occurred more frequently in the younger group. After the first and second dose and in both age groups, the majority of local reactions were mild or moderate in severity, and no Grade 4 local reactions were reported.

Subgroup Analyses

No clinically meaningful differences in local reactions were observed by country, sex, race, or ethnicity.

Across age groups, local reactions for the BNT162b2 group after either dose had a median onset day between Day 1.0 and Day 3.0 (Day 1.0 was the day of vaccination), and ranges were similar in the younger and older age groups. Across age groups, local reactions for this group after either dose resolved with median durations between 1.0 to 2.0 days, which were similar in the younger and older age groups.

Systemic Events – Phase 2/3

Systemic events were generally increased in frequency and severity in the younger group (Figure 98) compared with the older group (Figure 99), with frequencies and severity increasing with number of doses (Dose 1 vs Dose 2) Vomiting and diarrhea were exceptions with vomiting reported similarly infrequently in both age groups and both vomiting and diarrhea similar after each dose. Frequencies of systemic events in the younger and older BNT162b2 groups (Dose 1 vs Dose 2) are listed below:

fatigue: younger group (49.0% vs 61.6%) compared to older group (34.3% vs 51.2%)

headache: younger group (42.9% vs 53.1%) compared to older group (25.4% vs 39.5%)

muscle pain: younger group (22.0% vs. 38.6%) compared to older group (14.0% vs 28.5%)

chills: younger group (14.4% vs 36.5%) compared to older group (6.2% vs 22.8%)

joint pain: younger group (10.9% vs 22.4%) compared to older group (8.3% vs 18.9%)

fever: younger group (3.7% vs 16.6%) compared to older group (1.4% vs 11.5%).

vomiting: similar in both age groups and after either dose.

diarrhea: reported less frequently in the older group and was similar after each dose.

Systemic events were generally reported less frequently in the placebo group than in the BNT162b2 group, for both age groups and doses, with some exceptions. In the younger age group, fever and joint pain (after Dose 1) and vomiting and diarrhea (after Dose 1 and Dose 2) were reported at similar frequencies in the placebo group and the BNT162b2 group (Figure 98). In the older age group, fever and joint pain (after Dose 1) and vomiting and diarrhea (after Dose 1 and Dose 2) were reported at similar frequencies in the placebo group and the BNT162b2 group (Figure 99).

Use of antipyretic/pain medication was slightly less frequent in the older age group (20.1% to 37.4%) than in the younger age group (28.1% to 45.8%) after both doses, and medication use increased in both age groups after Dose 2 as compared with after Dose 1. Use of antipyretic/pain medication was less frequent in the placebo group than in the BNT162b2 group and was similar after Dose 1 and Dose 2 in the younger and older placebo groups (9.8% to 13.7%).

Severe systemic events across age groups after Dose 1 of BNT162b2 were generally lower in frequency than after Dose 2: fever (0.1% vs 0.8%), fatigue (0.8% vs 3.7%), headache (0.5% vs 1.9%), chills (0.2% vs 1.7%), muscle pain (0.3% vs. 1.6%), and joint pain (0.1% vs 0.6%). Diarrhea and vomiting frequencies were generally similar.

In the placebo group, severe fever was reported at a similar frequency (0.1%) after Dose 1 and Dose 2. One participant in the younger BNT162b2 group reported fever of 41.2°C only on Day 2 after Dose 2 and was nonfebrile for all other days of the reporting period.

After the first and second dose and in both age groups, the majority of systemic events were mild or moderate in severity, and no Grade 4 (potentially life-threatening) systemic events were reported other than fever occurring only 1 day in 1 participant (41.2°C) in the BNT162b2 group.

Subgroup Analyses

No clinically meaningful differences in systemic events were observed by country, ethnicity, sex, or race.

Across age groups, median onset day for most systemic events after either dose of BNT162b2 was Day 2.0 (Day 1.0 was the day of vaccination), and ranges were similar in the younger and older age groups. Across age groups, all systemic events resolved with median duration of 1.0 day, which was similar in the younger and older age groups.

Adverse Events – Phase 2/3

In this interim CSR, the first 6610 adult participants (which included the 360 participants in Phase 2) had safety data summarized through at least 1 month after Dose 2. AE summaries for all 36,855 participants up to the cutoff date (06 October 2020) included any event reported, regardless of whether participants completed the visit at 1 month after Dose 2. At the time of the data cutoff date, there was a small percentage (≤0.7%) of participants with at least 1 uncoded term.

Summary of Adverse Events – Phase 2/3

First 6610 Participants – Phase 2/3

Table 14 presents a summary of the first 6610 participants reporting at least 1 AE from Dose 1 to 1 month after Dose 2.

The number of participants who reported at least 1 AE was similar in the BNT162b2 group as compared with the placebo group. Severe AEs, SAEs, and AEs leading to withdrawal were reported by ≤1.1%, 0.5%, and 0.2%, respectively, in both groups.

In the younger and older age groups, the numbers of participants who reported at least 1 AE from Dose 1 to 1 month after Dose 2 were similar in the BNT162b2 group and the corresponding placebo group. Rates of related AEs, severe AEs, SAEs, and AEs leading to withdrawal in the younger and older age groups were also similar to the corresponding placebo group.

The first 6610 participants who reported at least 1 AE from Dose 1 to the data cutoff date in the BNT162b2 group and the placebo group were similar to those in the corresponding groups at 1 month after Dose 2 (Table 14). From 1 month after Dose 2 to the data cutoff date, 4 additional participants in the younger age group (3 in BNT162b2 and 1 in placebo) and 10 additional participants in the older age group (3

in BNT162b2 and 7 in placebo) reported at least 1 AE. There were no additional related AEs, severe AEs, SAEs, or AEs leading to withdrawal reported in either group.

Table 14. Number (%) of Subjects Reporting at Least 1 Adverse Event From Dose 1 to 1 Month After Dose 2 – ~6000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)	
Adverse Event	BNT162b2 (30 µg) (N^a=3314) n^b (%)	Placebo (N^a=3296) n^b (%)
Any event	374 (11.3)	316 (9.6)
Related[c]	135 (4.1)	68 (2.1)
Severe	35 (1.1)	19 (0.6)
Life-threatening	4 (0.1)	7 (0.2)
Any serious adverse event	18 (0.5)	17 (0.5)
Related[c]	0	0
Severe	9 (0.3)	8 (0.2)
Life-threatening	4 (0.1)	7 (0.2)
Any adverse event leading to withdrawal	6 (0.2)	5 (0.2)
Related[c]	2 (0.1)	1 (0.0)
Severe	2 (0.1)	1 (0.0)
Life-threatening	1 (0.0)	2 (0.1)
Death	0	0

a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified adverse event category. For "any event", n = the number of subjects reporting at least 1 occurrence of any adverse event.
c. Assessed by the investigator as related to investigational product.

All Participants – Phase 2/3

From Dose 1 to the data cutoff date, the number of overall participants who reported at least 1 AE was higher in the BNT162b2 group as compared with the placebo group. Severe AEs, SAEs, and AEs leading to withdrawal were reported by ≤0.8%, 0.3%, and 0.1%, respectively, in both groups. Discontinuations due to related AEs were reported in 6 participants in the BNT162b2 group and 4 participants in the placebo group.

Three Phase 3 participants died: 1 participant in the BNT162b2 group and 2 participants in the placebo group. The participant in the BNT162b2 group who died

experienced an SAE of arteriosclerosis which was assessed by the investigator as not related to study intervention.

In the younger age group, the number of participants who reported at least 1 AE was 1920 (18.1%) and 880 (8.3%) in the BNT162b2 and placebo groups, respectively. In the older age group, the number of participants who reported at least 1 AE was 1166 (14.9%) and 582 (7.4%) in the BNT162b2 and placebo groups, respectively.

Analysis of Adverse Events – Phase 2/3

Adverse Events by System Organ Class and Preferred Term – Phase 2/3

First 6610 Participants – Phase 2/3

There are no Tier 1 AEs identified for this program.

There were no Tier 2 AEs (defined as an event rate ≥1.0% in any vaccine group [PT level]) reported from Dose 1 to 1 month after Dose 2.

Most AEs reported up to 1 month after Dose 2 overall were reactogenicity and in the SOCs of general disorders and administration site conditions (81 [2.4%] in the BNT162b2 group and 57 [1.7%] in the placebo group), musculoskeletal and connective tissue disorders (81 [2.4%] in the BNT162b2 group and 56 [1.7%] in the placebo group), infections and infestations (56 [1.7%] in the BNT162b2 group and 48 [1.5%] in the placebo group), and gastrointestinal disorders (54 [1.6%] in the BNT162b2 group and 41 [1.2%] in the placebo group) (Table 15). In the younger BNT162b2 group, rates of AEs in these SOCs were: general disorders and administration site conditions (54 [3.0%]), musculoskeletal and connective tissue disorders (53 [3.0%]), infections and infestations (31 [1.7%]), and gastrointestinal disorders (32 [1.8%]). In the older BNT162b2 group, rates of AEs in these SOCs were: general disorders and administration site conditions (27 [1.8%]), musculoskeletal and connective tissue disorders (28 [1.8%]), infections and infestations (25 [1.6%]), and gastrointestinal disorders (22 [1.4%]).

In the BNT162b2 group, the most frequently reported AEs by PT overall were injection site pain (30 [0.9%]), headache (30 [0.9%]), and fatigue (27 [0.8%]) (Table 15), and during this time period (from Dose 1 to 1 month after Dose 2) most of these AEs were

reported during the e-diary 1 week reporting period. The majority of these PTs were reported in the younger age group: headache (21[1.2%]), and fatigue (17 [1.0%]). Injection site pain was reported at a similar frequency in the younger (16 [0.9%]) and older (14 [0.9%]) age groups.

In the BNT162b2 group, there were 10 (0.3%) participants who reported an AE of lymphadenopathy: 6 in the younger age group and 4 in the older age group compared to none in the placebo group; 1 (0.1%) was male and 9 (0.5%) were females. AEs of lymphadenopathy occurred in the arm and neck region (in axillary, left axillary, left para clavicular, left supra clavicular, bilateral cervical, or unspecified lymph nodes). Most lymphadenopathy events were reported within 2 to 4 days after vaccination (2 events were reported 8 days after vaccination). Five of the events lasted ≤4 days, 3 events lasted between 12 to 16 days, and 2 events were ongoing at the time of the data cutoff date.

In the younger age group, an AE of angioedema 13 days after Dose 1 (both eyes) and hypersensitivity (allergy attack [no additional information available at the time of this report], unrelated to study intervention) were reported in 1 participant each (BNT162b2 group), and an AE of drug hypersensitivity (oral penicillin reaction) was reported in 1 participant (placebo). None of these events were assessed by the investigator as related to study intervention. Three participants in the younger BNT162b2 group reported appendicitis compared to 1 participant in the older placebo group with perforated appendicitis; all were assessed by the investigator as unrelated to study intervention.

Table 15. Number (%) of Subjects Reporting at Least 1 Adverse Event From Dose 1 to 1 Month After Dose 2, by System Organ Class and Preferred Term – ~6000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)	
	BNT162b2 (30 µg) (N^a=3314)	Placebo (N^a=3296)

System Organ Class Preferred Term	n[b] (%)	(95% CI[c])	n[b] (%)	(95% CI[c])
Any event	374 (11.3)	(10.2, 12.4)	316 (9.6)	(8.6, 10.6)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	14 (0.4)	(0.2, 0.7)	0	(0.0, 0.1)
Lymphadenopathy	10 (0.3)	(0.1, 0.6)	0	(0.0, 0.1)
Anaemia	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Iron deficiency anaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Lymph node pain	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
CARDIAC DISORDERS	6 (0.2)	(0.1, 0.4)	4 (0.1)	(0.0, 0.3)
Atrial fibrillation	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Mitral valve incompetence	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Palpitations	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Acute coronary syndrome	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Acute myocardial infarction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Angina pectoris	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Angina unstable	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Atrial flutter	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Cardiac failure congestive	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery dissection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery occlusion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Left atrial enlargement	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Left ventricular hypertrophy	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Mitral valve prolapse	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tachycardia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
CONGENITAL, FAMILIAL AND GENETIC DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Congenital cystic kidney disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
EAR AND LABYRINTH DISORDERS	7 (0.2)	(0.1, 0.4)	6 (0.2)	(0.1, 0.4)
Vertigo	2 (0.1)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Vertigo positional	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Ear discomfort	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Deafness unilateral	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Ear pain	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tinnitus	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Tympanic membrane perforation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
ENDOCRINE DISORDERS	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Goitre	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypogonadism	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
EYE DISORDERS	8 (0.2)	(0.1, 0.5)	6 (0.2)	(0.1, 0.4)
Cataract	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Chalazion	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Vision blurred	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Blepharitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Conjunctival hyperaemia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Dacryostenosis acquired	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Diplopia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Eye pain	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Lacrimation increased	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Retinal detachment	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vitreous detachment	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
GASTROINTESTINAL DISORDERS	54 (1.6)	(1.2, 2.1)	41 (1.2)	(0.9, 1.7)
Diarrhoea	17 (0.5)	(0.3, 0.8)	15 (0.5)	(0.3, 0.7)
Nausea	12 (0.4)	(0.2, 0.6)	5 (0.2)	(0.0, 0.4)
Toothache	5 (0.2)	(0.0, 0.4)	2 (0.1)	(0.0, 0.2)
Vomiting	4 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Abdominal pain	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Constipation	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Dyspepsia	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Gastrooesophageal reflux disease	0	(0.0, 0.1)	3 (0.1)	(0.0, 0.3)
Odynophagia	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Dental caries	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Inguinal hernia	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Small intestinal obstruction	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Abdominal adhesions	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Abdominal pain upper	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Abdominal rigidity	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Angular cheilitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Colitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Diverticular perforation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Faeces soft	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Gastric ulcer haemorrhage	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Gastrointestinal disorder	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Gingival discomfort	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Haematochezia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hiatus hernia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypoaesthesia oral	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Intestinal obstruction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Irritable bowel syndrome	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Mouth ulceration	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Parotid duct obstruction	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Rectal haemorrhage	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Salivary gland calculus	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tongue discomfort	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tongue ulceration	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
GENERAL DISORDERS AND ADMINISTRATION SITE CONDITIONS	81 (2.4)	(1.9, 3.0)	57 (1.7)	(1.3, 2.2)
Fatigue	27 (0.8)	(0.5, 1.2)	17 (0.5)	(0.3, 0.8)
Injection site pain	30 (0.9)	(0.6, 1.3)	14 (0.4)	(0.2, 0.7)
Chills	15 (0.5)	(0.3, 0.7)	7 (0.2)	(0.1, 0.4)
Injection site erythema	10 (0.3)	(0.1, 0.6)	6 (0.2)	(0.1, 0.4)
Pyrexia	13 (0.4)	(0.2, 0.7)	2 (0.1)	(0.0, 0.2)

Injection site swelling	4 (0.1)	(0.0, 0.3)	4 (0.1)	(0.0, 0.3)
Pain	4 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Malaise	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Injection site bruising	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Injection site reaction	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Asthenia	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Injection site pruritus	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Chest discomfort	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Chest pain	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Face oedema	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Inflammation	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Injection site discolouration	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Injection site discomfort	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Injection site hyperaesthesia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Non-cardiac chest pain	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Swelling	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Unevaluable event	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vaccination site nodule	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Vascular stent occlusion	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
HEPATOBILIARY DISORDERS	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Cholelithiasis	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Cholecystitis acute	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
IMMUNE SYSTEM DISORDERS	4 (0.1)	(0.0, 0.3)	6 (0.2)	(0.1, 0.4)
Seasonal allergy	1 (0.0)	(0.0, 0.2)	3 (0.1)	(0.0, 0.3)
Food allergy	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Allergy to vaccine	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Anaphylactic reaction	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Drug hypersensitivity	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hypersensitivity	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Milk allergy	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
INFECTIONS AND INFESTATIONS	56 (1.7)	(1.3, 2.2)	48 (1.5)	(1.1, 1.9)
Urinary tract infection	10 (0.3)	(0.1, 0.6)	7 (0.2)	(0.1, 0.4)
Sinusitis	8 (0.2)	(0.1, 0.5)	1 (0.0)	(0.0, 0.2)
Diverticulitis	3 (0.1)	(0.0, 0.3)	4 (0.1)	(0.0, 0.3)
Tooth infection	2 (0.1)	(0.0, 0.2)	3 (0.1)	(0.0, 0.3)
Otitis media	0	(0.0, 0.1)	4 (0.1)	(0.0, 0.3)
Upper respiratory tract infection	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Appendicitis	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Cellulitis	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Ear infection	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Herpes zoster	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Pneumonia	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Tonsillitis	0	(0.0, 0.1)	3 (0.1)	(0.0, 0.3)
Conjunctivitis	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Gastroenteritis	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Infected bite	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Otitis externa	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)

Otitis media acute	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Skin infection	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Tooth abscess	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Acute sinusitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Appendicitis perforated	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Cystitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Dermatitis infected	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Eye infection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Folliculitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Fungal infection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Fungal skin infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Genital herpes	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Genital herpes simplex	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Gingivitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hordeolum	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Kidney infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Lower respiratory tract infection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Oral candidiasis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Oral fungal infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Parotitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Peritoneal abscess	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Peritonitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Pharyngitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Pharyngitis streptococcal	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Respiratory tract infection viral	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Rhinitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Sepsis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Skin bacterial infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Soft tissue infection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Subcutaneous abscess	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vulvovaginal candidiasis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Vulvovaginal mycotic infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
INJURY, POISONING AND PROCEDURAL COMPLICATIONS	28 (0.8)	(0.6, 1.2)	42 (1.3)	(0.9, 1.7)
Fall	8 (0.2)	(0.1, 0.5)	16 (0.5)	(0.3, 0.8)
Arthropod bite	5 (0.2)	(0.0, 0.4)	3 (0.1)	(0.0, 0.3)
Muscle strain	4 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Contusion	2 (0.1)	(0.0, 0.2)	4 (0.1)	(0.0, 0.3)
Skin abrasion	1 (0.0)	(0.0, 0.2)	4 (0.1)	(0.0, 0.3)
Skin laceration	0	(0.0, 0.1)	4 (0.1)	(0.0, 0.3)
Ankle fracture	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Joint dislocation	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Tooth fracture	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Fibula fracture	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Foot fracture	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Joint injury	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Ligament sprain	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Limb injury	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)

Meniscus injury	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Muscle rupture	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Rib fracture	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Bone contusion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Chest injury	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Corneal abrasion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Craniocerebral injury	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Forearm fracture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hand fracture	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Humerus fracture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Lumbar vertebral fracture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Muscle injury	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Postoperative ileus	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Procedural pain	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Radius fracture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Road traffic accident	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Sunburn	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Tendon rupture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Thermal burn	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
INVESTIGATIONS	9 (0.3)	(0.1, 0.5)	4 (0.1)	(0.0, 0.3)
Body temperature increased	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Blood glucose increased	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Blood cholesterol increased	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Blood pressure increased	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Blood triglycerides increased	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Cardiac stress test abnormal	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Electrocardiogram QT prolonged	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Heart rate increased	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Weight decreased	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
White blood cell count increased	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
METABOLISM AND NUTRITION DISORDERS	12 (0.4)	(0.2, 0.6)	7 (0.2)	(0.1, 0.4)
Decreased appetite	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Hypercholesterolaemia	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Type 2 diabetes mellitus	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Dehydration	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Diabetes mellitus inadequate control	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Dyslipidaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Glucose tolerance impaired	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hyperlipidaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypertriglyceridaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypoglycaemia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hypokalaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Iron deficiency	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Obesity	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Vitamin D deficiency	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
MUSCULOSKELETAL AND CONNECTIVE TISSUE DISORDERS	81 (2.4)	(1.9, 3.0)	56 (1.7)	(1.3, 2.2)

Arthralgia	20 (0.6)	(0.4, 0.9)	15 (0.5)	(0.3, 0.7)
Myalgia	20 (0.6)	(0.4, 0.9)	12 (0.4)	(0.2, 0.6)
Back pain	8 (0.2)	(0.1, 0.5)	8 (0.2)	(0.1, 0.5)
Pain in extremity	10 (0.3)	(0.1, 0.6)	4 (0.1)	(0.0, 0.3)
Neck pain	5 (0.2)	(0.0, 0.4)	5 (0.2)	(0.0, 0.4)
Muscle spasms	4 (0.1)	(0.0, 0.3)	2 (0.1)	(0.0, 0.2)
Musculoskeletal pain	2 (0.1)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Osteoarthritis	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Tendonitis	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Arthritis	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Flank pain	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Joint effusion	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Plantar fasciitis	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Bursitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Exostosis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Limb discomfort	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Muscle twitching	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Muscular weakness	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Musculoskeletal discomfort	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Musculoskeletal stiffness	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Osteitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Osteopenia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Pain in jaw	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Rotator cuff syndrome	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tenosynovitis stenosans	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Torticollis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	4 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Basal cell carcinoma	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Adenocarcinoma gastric	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Breast cancer	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Seborrhoeic keratosis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Uterine leiomyoma	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vaginal neoplasm	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NERVOUS SYSTEM DISORDERS	44 (1.3)	(1.0, 1.8)	32 (1.0)	(0.7, 1.4)
Headache	30 (0.9)	(0.6, 1.3)	24 (0.7)	(0.5, 1.1)
Dizziness	3 (0.1)	(0.0, 0.3)	2 (0.1)	(0.0, 0.2)
Migraine	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Paraesthesia	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Syncope	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Burning sensation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Cervical radiculopathy	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Dysgeusia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hypoaesthesia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Radiculopathy	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Sciatica	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Transient ischaemic attack	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)

Tremor	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
PSYCHIATRIC DISORDERS	13 (0.4)	(0.2, 0.7)	13 (0.4)	(0.2, 0.7)
Anxiety	4 (0.1)	(0.0, 0.3)	4 (0.1)	(0.0, 0.3)
Depression	2 (0.1)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Anxiety disorder	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Irritability	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Mental status changes	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Bipolar disorder	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Depressed mood	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Disorientation	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Gastrointestinal somatic symptom disorder	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Insomnia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Mental disorder	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Mood swings	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Panic reaction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Sleep disorder	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Suicidal ideation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
RENAL AND URINARY DISORDERS	3 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Acute kidney injury	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Chronic kidney disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Dysuria	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Haematuria	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Nephrolithiasis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Urinary retention	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
REPRODUCTIVE SYSTEM AND BREAST DISORDERS	4 (0.1)	(0.0, 0.3)	2 (0.1)	(0.0, 0.2)
Dysmenorrhoea	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Cervical dysplasia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Menorrhagia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Prostatitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
RESPIRATORY, THORACIC AND MEDIASTINAL DISORDERS	21 (0.6)	(0.4, 1.0)	26 (0.8)	(0.5, 1.2)
Oropharyngeal pain	4 (0.1)	(0.0, 0.3)	7 (0.2)	(0.1, 0.4)
Cough	5 (0.2)	(0.0, 0.4)	5 (0.2)	(0.0, 0.4)
Rhinitis allergic	3 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Rhinorrhoea	1 (0.0)	(0.0, 0.2)	4 (0.1)	(0.0, 0.3)
Nasal congestion	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Dyspnoea	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Dyspnoea exertional	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Upper-airway cough syndrome	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Acute respiratory failure	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Allergic respiratory disease	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Asthma	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Bronchospasm	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Chronic obstructive pulmonary disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Productive cough	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Pulmonary embolism	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Sinus congestion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Throat irritation	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
SKIN AND SUBCUTANEOUS TISSUE DISORDERS	32 (1.0)	(0.7, 1.4)	19 (0.6)	(0.3, 0.9)
Dermatitis contact	10 (0.3)	(0.1, 0.6)	3 (0.1)	(0.0, 0.3)
Rash	7 (0.2)	(0.1, 0.4)	2 (0.1)	(0.0, 0.2)
Erythema	3 (0.1)	(0.0, 0.3)	1 (0.0)	(0.0, 0.2)
Urticaria	2 (0.1)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Dermatitis	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Pruritus	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Hyperhidrosis	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Macule	1 (0.0)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Angioedema	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Dermatitis atopic	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Dermatitis bullous	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Drug eruption	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Ecchymosis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Hangnail	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Papule	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Rash erythematous	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Rash maculo-papular	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Rosacea	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Skin discolouration	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Skin ulcer	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
SURGICAL AND MEDICAL PROCEDURES	5 (0.2)	(0.0, 0.4)	4 (0.1)	(0.0, 0.3)
Dental care	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Dental operation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Gingival operation	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hip surgery	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Inguinal hernia repair	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Laryngeal operation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Postoperative care	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Sclerotherapy	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Tooth extraction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
VASCULAR DISORDERS	8 (0.2)	(0.1, 0.5)	15 (0.5)	(0.3, 0.7)
Hypertension	5 (0.2)	(0.0, 0.4)	6 (0.2)	(0.1, 0.4)
Haematoma	1 (0.0)	(0.0, 0.2)	3 (0.1)	(0.0, 0.3)
Aortic aneurysm	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Deep vein thrombosis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Essential hypertension	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypotension	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
LYMPHOEDEMA	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Lymphorrhoea	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Orthostatic hypotension	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Raynaud's phenomenon	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified event. For "any event", n = number of subjects reporting at least 1 occurrence of any event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

All Participants – Phase 2/3

For all 36,855 participants up to the data cutoff date, there were a total of 121 (0.7%) participants in the BNT162b2 group and 51 (0.3%) participants in the placebo group with at least 1 uncoded term. As a result, uncoded terms are also present in other AE tables summarized by SOC and PT.

From Dose 1 to the data cutoff date, the number of overall participants who reported at least 1 AE was higher in the BNT162b2 group (3086 [16.8%]) as compared with the placebo group (1462 [7.9%]). Most AEs reported in all participants from Dose 1 to the data cutoff date were reactogenicity and in the SOCs of general disorders and administration site conditions (1941 [10.5%] in the BNT162b2 group and 438 [2.4%] in the placebo group), musculoskeletal and connective tissue disorders (742 [4.0%] in the BNT162b2 group and 227 [1.2%] in the placebo group), and nervous system disorders (567 [3.1%] in the BNT162b2 group and 251 [1.4%] in the placebo group).

In the BNT162b2 group, the most frequently reported AEs by PT were injection site pain (1222 [6.6%]), pyrexia (504 [2.7%]), fatigue (481 [2.6%]), headache (470 [2.6%]), chills (458 [2.5%]), and myalgia (454 [2.5%]). The majority of these PTs were reported in the younger age group: injection site pain (787 [7.4%]), pyrexia (351 [3.3%]), fatigue (309 [2.9%]), headache (303 [2.9%]), chills (316 [3.0%]), and myalgia (304 [2.9%]).

Beyond the first 6610 participants, events related to reactogenicity are no longer reported using an e-diary but are instead reported as AEs. Therefore, a post hoc analysis was conducted to evaluate if the imbalance in AEs observed in the overall participants from Dose 1 to the data cutoff date but not observed in the first 6610 participants from Dose 1 to 1 month after Dose 2 was attributed to reactogenicity events. The analysis examined the AEs reported within 7 days after each dose, which represented the reactogenicity reporting period. The time period was chosen because

many AEs were reported in the SOCs of general disorders and administration site conditions, musculoskeletal and connective tissue disorders, and nervous system disorders, which contains AEs consistent with reactogenicity events, and could only be attributed to reactogenicity if they occurred during this time period as opposed to occurring up to a month from each dose.

From Dose 1 to 7 days after Dose 1 (as of the data cutoff date), 1494 (8.1%) participants reported at least 1 AE in the BNT162b2 group, which represented approximately half of the total number of the 3086 [16.8%] participants who reported at least 1 AE up to the data cutoff date. In the placebo group, 555 (3.0%) participants reported at least 1 AE from Dose 1 to 7 days after Dose 1, compared with the total number of 1462 (7.9%) participants who reported at least 1 AE up to the data cutoff date.

From Dose 2 to 7 days after Dose 2 (as of the data cutoff date), 1165 (6.3%) participants reported at least 1 AE in the BNT162b2 group, which represented approximately 38% of the total number of the 3086 [16.8%] participants who reported at least 1 AE up to the data cutoff date. From Dose 2 to 7 days after Dose 2, fewer participants reported AEs in the placebo group than the BNT162b2 group. In the placebo group, 268 (1.5%) participants reported at least 1 AE from Dose 2 to 7 days after Dose 2, compared with the total number of 1462 (7.9%) participants who reported at least 1 AE up to the data cutoff date.

AEs were reported from Dose 1 to 7 days after Dose 1 in the SOC of general disorders and administration site conditions (1127 [6.1%] in the BNT162b2 group and 251 [1.4%] in the placebo group), which represented more than half of the total number of participants reporting at least 1 AE in this SOC (1941 [10.5%] in the BNT162b2 group and 438 [2.4%] in the placebo group) up to the data cutoff date. Musculoskeletal and connective tissue disorders (252 [1.4%] in the BNT162b2 group and 76 [0.4%] in the placebo group) and nervous system disorders (220 [1.2%] in the BNT162b2 group and 115 [0.6%] in the placebo group) were also commonly reported, representing a smaller proportion of the total number of participants reporting AEs for these SOCs.

In the BNT162b2 group, the most frequently reported AEs from Dose 1 to 7 days after Dose 1 by PT were injection site pain (881 [4.8%]), fatigue (231 [1.3%]), headache (181 [1.0%]), myalgia (147 [0.8%]), pyrexia (110 [0.6%]), and chills (100 [0.5%]). The majority of these PTs were reported in the younger age group: injection site pain (566 [5.3%]), fatigue (153 [1.4%]), headache (118 [1.1%]), myalgia (99 [0.9%]), pyrexia (82 [0.8%]), and chills (75 [0.7%]). Injection site pain reported from Dose 1 to 7 days after Dose 1 (881 [4.8%]) represented a large proportion of the total participants who reported AEs for this PT (1222 [6.6%]).

AEs were reported from Dose 2 to 7 days after Dose 2 in the SOCs of general disorders and administration site conditions (828 [4.5%] in the BNT162b2 group and 93 [0.5%] in the placebo group), musculoskeletal and connective tissue disorders (377 [2.0%] in the BNT162b2 group and 38 [0.2%] in the placebo group), and nervous system disorders (294 [1.6%] in the BNT162b2 group and 40 [0.2%] in the placebo group). Musculoskeletal and connective tissue disorders and nervous system disorders reported from Dose 2 to 7 days after Dose 2 represented at least half of the total number of participants who reported at least 1 AE in these SOCs.

In the BNT162b2 group, the most frequently reported AEs from Dose 2 to 7 days after Dose 2 by PT were pyrexia (375 [2.0%]), chills (327 [1.8%]), injection site pain (313 [1.7%]), myalgia (282 [1.5%]), headache (258 [1.4%]), and fatigue (227 [1.2%]). The majority of these PTs were reported in the younger age group: pyrexia (251 [2.4%]), chills (216 [2.0%]), myalgia (185 [1.7%]), injection site pain (183 [1.7%]), headache (154 [1.5%]), and fatigue (134 [1.3%]). AEs for most of these PTs reported from Dose 2 to 7 days after Dose 2 represented at least half of the total number of participants who reported an AE for these PTs: pyrexia (504 [2.7%]), chills (458 [2.5%]), myalgia (454 [2.5%]), headache (470 [2.6%]), and fatigue (481 [2.6%]).

Overall, AEs reported from Dose 1 to 7 days after Dose 1 and from Dose 2 to 7 days after Dose 2 were largely attributable to reactogenicity events. This observation provides a reasonable explanation for the greater rates of AEs observed overall in the BNT162b2 group compared with the placebo group.

From Dose 1 to the data cutoff date, there were a total of 44 (0.2%) participants in the BNT162b2 group who reported an AE of lymphadenopathy, inclusive of those reported in the first 6610 participants (10 [0.3%]). Up to the data cutoff date, 34 additional participants in the BNT162b2 group and 4 additional participants in the placebo group reported an AE of lymphadenopathy. In the BNT162b2 group, lymphadenopathy was reported in 34 (0.3%) participants in the younger age group and 10 (0.1%) participants in the older age group compared to 4 (0.0%) in the placebo group (3 in the younger age group and 1 in the older age group). Lymphadenopathy occurred predominantly in the arm and neck region with most events reported in left axillary lymph node(s). Most lymphadenopathy events occurred after Dose 2, ≤3 days after Dose 1 or Dose 2, were Grade 1 or Grade 2 in severity, and 32 of 48 events were resolved by the data cutoff date. In 1 participant in the younger BNT162b2 age group, Grade 1 lymphadenopathy (swollen right axillary lymph nodes) was an immediate AE, which occurred after Dose 1 and was continuing at the data cutoff date.

In the younger age group, there was 1 participant each with an AE of suspected COVID-19 in the BNT162b2 (SAE) and placebo groups.

In the BNT162b2 group, 6 participants reported immunization reactions (vaccine reaction or systemic vaccine reaction [no additional information currently available at the time of this report]) assessed as related to study intervention. Three participants reported drug hypersensitivity in the BNT162b2 group in addition to the drug hypersensitivity in a participant in the placebo group. Drug hypersensitivity (allergic reaction) was assessed as related in 1 participant in the BNT162b2 group and drug hypersensitivity (drug allergy or allergic reaction to dipyrone) was assessed as unrelated to study intervention in 2 participants in the BNT162b2 group.

Nineteen (0.1%) participants in the BNT162b2 group (14 in the younger age group and 5 in the older age group reported at least 1 vaccine complication (most were descriptive of reactogenicity events) compared to none in the placebo group. All were assessed as related to the study intervention and included: post vaccination myalgia, fever, body aches, headache, chills, nausea, adverse reaction, arthralgia, fatigue,

aches, muscle aches, malaise, and sore left shoulder. Most events were Grade 1, started within 3 days of vaccination, and lasted from 1 to 3 days.

In addition to the 4 participants with appendicitis (including 1 appendicitis perforated in the placebo group) in the first 6610 participants, there were an additional 3 participants with appendicitis (including 1 participant with appendicitis perforated) reported in the BNT162b2 group from Dose 1 through the data cutoff date for all participants. Therefore, a total of 6 participants in the BNT162b2 group reported appendicitis (including 1 appendicitis perforated) with 4 in the younger age group and 2 in the older age group, and 1 participant in the placebo group (older age group) reported appendicitis (perforated). All events were severe or life-threatening and none were assessed as related to study intervention.

Related Adverse Events by System Organ Class and Preferred Term – Phase 2/3

First 6610 Participants – Phase 2/3

From Dose 1 to 1 month after Dose 2, 135 (4.1%) participants reported at least 1 AE assessed as related by the investigator in the BNT162b2 group, and 68 (2.1%) participants reported at least 1 related AE in the placebo group. Most related AEs were reactogenicity events and in the SOC of general disorders and administration site conditions (69 [2.1%] in the BNT162b2 group and 40 [1.2%] in the placebo group).

The AEs of lymphadenopathy reported in 8 of 10 participants were assessed by the investigator as related to study intervention.

All Participants – Phase 2/3

From Dose 1 to the data cutoff date, 2303 (12.5%) participants in the BNT162b2 group and 593 (3.2%) participants in the placebo group reported at least 1 AE assessed as related by the investigator, inclusive of the related AEs for the first 6610 participants. Most related AEs were reactogenicity events and in the SOC of general disorders and administration site conditions (1869 [10.1%] in the BNT162b2 group and 365 [2.0%] in the placebo group).

The AEs of lymphadenopathy reported in 30 of 44 participants in the BNT162b2 group and 2 of 4 participants in the placebo group were assessed by the investigator as related to study intervention.

In the BNT162b2 group, based on all information currently available at the time of this report:

Six participants reported immunization reaction (vaccine reaction or systemic vaccine reaction) assessed as related to the study intervention. In most participants, immunization reactions occurred 1 or 2 days after Dose 2, lasted 2 or 3 days (1 participant was recovering at data cutoff date), and were Grade 1 or Grade 2 in severity. In 1 participant, immunization reactions (systemic vaccine reactions) occurred 2 days after Dose 1 (Grade 1) and lasted 2 days, and 1 day after Dose 2 (Grade 3) and lasted 4 days.

One participant reported an AE each of drug hypersensitivity (allergic reaction), urticaria (allergic reaction), and headache, which were all Grade 2 and assessed by the investigator as related to study intervention. The AEs of drug hypersensitivity and urticaria both occurred within 1 day after Dose 1 and resolved that same day. The AE of headache occurred the following day after vaccination and lasted 4 days.

Immediate Adverse Events – Phase 2/3

First 6610 Participants – Phase 2/3

After Dose 1, ≤0.3% of participants reported immediate AEs. Most immediate AEs were in the SOC of general disorders and administration site conditions and were events related to injection site reactions (injection site pain, injection site erythema and injection site swelling).

After Dose 2, 0.1% of participants in each group reported immediate AEs. Most immediate AEs were in the SOC of general disorders and administration site conditions and were events related to injection site reactions (injection site pain, injection site hyperaesthesia, and injection site pruritus).

After either dose of BNT162b2, no participant reported an immediate allergic reaction to the vaccine.

All Participants – Phase 2/3

After Dose 1, 0.3% of participants in each group reported immediate AEs. Most immediate AEs were in the SOC of general disorders and administration site conditions and most events were related to injection site reactions with injection site pain most frequently reported (40 [0.2%] participants in the BNT162b2 group and 27 (0.1%) participants in the placebo group). One participant had an immediate AE of lymphadenopathy after Dose 1. All other immediate AEs were reported by ≤3 participants each in the BNT162b2 group.

After Dose 2, 0.1% of participants in each group reported immediate AEs. Most immediate AEs were in the SOC of general disorders and administration site conditions and most events were injection site reactions with injection site pain most frequently reported (10 [0.1%] participants in the BNT162b2 group and 7 [0.0%] participants in the placebo group). All other immediate AEs were reported by ≤2 participants each.

After either dose of BNT162b2, no participant reported an immediate allergic reaction to the vaccine.

Severe or Life-Threatening Adverse Events – Phase 2/3

First 6610 Participants – Phase 2/3

From Dose 1 to 1 month after Dose 2, severe AEs reported were reported by 35 (1.1%) participants in the BNT162b2 group and 19 (0.6%) in the placebo group.

Four (0.1%) participants in the BNT162b2 group and 7 (0.2%) participants in the placebo group had at least 1 life-threatening AE from Dose 1 to 1 month after Dose 2. None of these events were assessed by the investigator as related to study intervention.

In the BNT162b2 group:

One participant from Phase 2 had a severe event of gastric adenocarcinoma (SAE), which is discussed in a previous section.

Two participants had severe events of appendicitis: 1 event began 9 days after Dose 1 and the other event began 15 days after Dose 2 (SAEs) which were assessed by the investigator as not related to study intervention.

One participant had 2 life-threatening AEs of appendicitis and peritoneal abscess 7 days after Dose 1 (both SAEs); both events were assessed by the investigator as not related to study intervention.

One participant had 8 severe events: anemia, cardiac failure congestive, abdominal adhesions, sepsis, hypokalaemia, mental status changes, acute kidney injury, and acute respiratory failure (all SAEs). None of the events were assessed by the investigator as related to study intervention.

All Participants – Phase 2/3

Severe AEs reported up to the data cutoff date, inclusive of those discussed for the first 6610 participants, were reported by 142 [0.8%] participants in the BNT162b2 group and 70 (0.4%) in the placebo group. Additional events included:

Two participants in the BNT162b2 group had a severe event each of appendicitis: 1 event began 17 days after Dose 1 and the other event began 11 days after Dose 1 (SAE) which were assessed by the investigator as not related to study intervention.

One participant in the BNT162b2 group had a severe event of perforated appendicitis on the same day after Dose 1 (SAE) which was assessed by the investigator as not related to study intervention.

Nine participants (0.0%) in the BNT162b2 group and 12 (0.1%) participants in the placebo group had at least 1 life-threatening AE from Dose 1 to the data cutoff date, inclusive of those discussed for the first 6610 participants. None of these events were assessed by the investigator as related to study intervention.

Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 2/3

Deaths – Phase 2/3

There were 3 Phase 3 participants (1 in the BNT162b2 group and 2 in the placebo group) who died through the data cutoff date of 06 October 2020. None of these deaths were among the first 6610 participants (Table 14) and none were assessed by the investigator as related to study intervention.

One participant in the older BNT162b2 group experienced a Grade 4 SAE of arteriosclerosis 4 days after Dose 1 and died 15 days after Dose 1.

One participant in the younger placebo group experienced a Grade 4 SAE of unevaluable event (unknown of unknown origin [no additional information currently available at the time of this report) 8 days after Dose 1 and died the same day.

One participant in the older placebo group experienced a Grade 4 SAE of hemorrhagic stroke 15 days after Dose 2 and died 35 days after Dose 2.

Death Narratives

Narratives for the participants who died through the data cutoff date (06 October 2020) were provided.

Serious Adverse Events – Phase 2/3

First 6610 Participants – Phase 2/3

From Dose 1 to 1 month after Dose 2, the number of participants who reported at least 1 SAE was similar in the BNT162b2 group (18 (0.5%]) and in the placebo group (17 [0.5%]) (Table 16). None of the SAEs were assessed by the investigator as related to study intervention. Most PTs for SAEs were reported by only 1 participant (3 participants reported an SAE of appendicitis).

From Dose 1 to 1 month after Dose 2, the number of participants who reported at least 1 SAE in the younger and older age groups was similar.

In the BNT162b2 group:

Two participants had an SAE each of appendicitis: 1 event began 9 days after Dose 1 and the other event began 15 days after Dose 2.

One participant had an SAE each of appendicitis and peritoneal abscess 7 days after Dose 1, which was considered life-threatening. Both events lasted for 17 days.

One participant had 8 SAEs 17 days after Dose 1: anemia, cardiac failure congestive, abdominal adhesions, sepsis, hypokalaemia, mental status changes, acute kidney injury, and acute respiratory failure (all were severe). The SAEs of abdominal adhesions and acute respiratory failure lasted for 2 and 14 days, respectively. All other SAEs lasted for 19 days.

One participant had an SAE of anaphylactic reaction 9 days after Dose 2 as a result of a bee sting which was considered life threatening. The event resolved on the same day.

In the placebo group, 1 participant had an SAE each of appendicitis perforated and peritonitis 13 and 15 days after Dose 2, respectively (both severe). Both events lasted 4 and 5 days, respectively.

From 1 month after Dose 2 to the data cutoff date, no additional SAEs were reported for these first 6610 participants.

Table 16. Number (%) of Subjects Reporting at Least 1 Serious Adverse Event From Dose 1 to 1 Month After Dose 2, by System Organ Class and Preferred Term – ~6000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)			
	BNT162b2 (30 µg) (N[a]=3314)		Placebo (N[a]=3296)	
System Organ Class Preferred Term	n[b] (%)	(95% CI[c])	n[b] (%)	(95% CI[c])
Any event	18 (0.5)	(0.3, 0.9)	17 (0.5)	(0.3, 0.8)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Anaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
CARDIAC DISORDERS	3 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Acute coronary syndrome	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Atrial fibrillation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Cardiac failure congestive	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery dissection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery occlusion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
EAR AND LABYRINTH DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Vertigo	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
EYE DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Diplopia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
GASTROINTESTINAL DISORDERS	3 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Abdominal adhesions	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Colitis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Diarrhoea	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Diverticular perforation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Intestinal obstruction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Small intestinal obstruction	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
GENERAL DISORDERS AND ADMINISTRATION SITE CONDITIONS	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Chest pain	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Non-cardiac chest pain	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Unevaluable event	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vascular stent occlusion	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
HEPATOBILIARY DISORDERS	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Cholelithiasis	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Cholecystitis acute	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
IMMUNE SYSTEM DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Anaphylactic reaction	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
INFECTIONS AND INFESTATIONS	4 (0.1)	(0.0, 0.3)	3 (0.1)	(0.0, 0.3)
Appendicitis	3 (0.1)	(0.0, 0.3)	0	(0.0, 0.1)
Appendicitis perforated	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Peritoneal abscess	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Peritonitis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Pneumonia	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Sepsis	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Urinary tract infection	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
INJURY, POISONING AND PROCEDURAL COMPLICATIONS	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Forearm fracture	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Skin laceration	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
INVESTIGATIONS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Cardiac stress test abnormal	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
METABOLISM AND NUTRITION DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Hypokalaemia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	2 (0.1)	(0.0, 0.2)	1 (0.0)	(0.0, 0.2)
Adenocarcinoma gastric	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Breast cancer	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Vaginal neoplasm	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NERVOUS SYSTEM DISORDERS	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Syncope	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
PSYCHIATRIC DISORDERS	2 (0.1)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Bipolar disorder	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Mental disorder	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Mental status changes	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Suicidal ideation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
RENAL AND URINARY DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Acute kidney injury	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
RESPIRATORY, THORACIC AND MEDIASTINAL DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Acute respiratory failure	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)

VASCULAR DISORDERS	0	(0.0, 0.1)	2 (0.1)	(0.0, 0.2)
Deep vein thrombosis	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Orthostatic hypotension	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified event. For "any event", n = number of subjects reporting at least 1 occurrence of any event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

All Participants – Phase 2/3

From Dose 1 to the data cutoff date, inclusive of those discussed for the first 6610 participants, the number of participants who reported at least 1 SAE was similar in the BNT162b2 group (63 [0.3%]) and in the placebo group (49 [0.3%]) (Table 17).

Additional events included:

In the BNT162b2 group, there were 2 participants in the younger age group with an SAE each assessed by the investigator as related to study intervention:

One participant had an SAE of lymphadenopathy (right axilla) 13 days after Dose 1, which was not resolved at the time of the data cutoff. The participant was a 48-year-old woman with a relevant medical history of eczema and topical crisaborole use who was administered BNT162b2 vaccine in the left deltoid and had right axillary pain and lymphadenopathy. She had no injuries to the right arm, no fever, and no history of a similar incident. Her WBC was normal with a normal lymphocyte count and a right axilla ultrasound showed 4 enlarged lymph nodes (largest 2.5 × 1.1 × 2.4 cm). A biopsy was performed and was reported to be normal and without markers for lymphoma or other cancer. A follow-up visit with oncology (and possible repeat ultrasound) was planned for 3 months time.

One participant had an SAE of shoulder injury related to vaccine administration (SIRVA, erroneously administered into or near the shoulder joint capsule) after Dose 2, which was recovering at the time of the data cutoff.

From Dose 1 to the data cutoff date, a total of 6 participants in the BNT162b2 group reported an SAE of appendicitis. Three of these SAEs of appendicitis occurred in the first 6610 participants. The 3 additional SAEs of appendicitis are described below

along with other specified SAEs that were assessed as not related to study intervention in the BNT162b2 group:

Two participants had an SAE each of appendicitis: 1 event began 17 days after Dose 1 which lasted for 3 days (younger age group), and the other event began 11 days after Dose 1 which lasted 5 days (older age group).

One participant in the older age group had an SAE of appendicitis perforated on the same day after Dose 1, which was resolving at the time of the data cutoff.

One participant in the younger age group had an SAE of suspected COVID-19 on the same day after Dose 2, which lasted for 6 days. The nasal swab result was negative.

Table 17. Number (%) of Subjects Reporting at Least 1 Serious Adverse Event From Dose 1 to Data Cutoff Date (06OCT2020), by System Organ Class and Preferred Term – Phase 2/3 (All Participants) – Safety Population

	Vaccine Group (as Administered)			
	BNT162b2 (30 µg) (N[a]=18419)		Placebo (N[a]=18436)	
System Organ Class Preferred Term	n[b] (%)	(95% CI[c])	n[b] (%)	(95% CI[c])
Any event	63 (0.3)	(0.3, 0.4)	49 (0.3)	(0.2, 0.4)
BLOOD AND LYMPHATIC SYSTEM DISORDERS	2 (0.0)	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Anaemia	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Leukocytosis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Lymphadenopathy	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Neutropenia	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Thrombocytosis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
CARDIAC DISORDERS	10 (0.1)	(0.0, 0.1)	6 (0.0)	(0.0, 0.1)
Cardiac failure congestive	2 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Acute coronary syndrome	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Atrial fibrillation	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Acute myocardial infarction	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Angina pectoris	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Arrhythmia	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Arrhythmia supraventricular	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Arteriospasm coronary	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Coronary artery disease	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Coronary artery dissection	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Coronary artery occlusion	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)

Myocardial infarction	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
EAR AND LABYRINTH DISORDERS	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Vertigo	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
EYE DISORDERS	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Diplopia	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Retinal artery occlusion	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
GASTROINTESTINAL DISORDERS	7 (0.0)	(0.0, 0.1)	5 (0.0)	(0.0, 0.1)
Small intestinal obstruction	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Abdominal adhesions	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Colitis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Diarrhoea	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Diverticular perforation	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Gastrointestinal haemorrhage	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Intestinal obstruction	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Obstructive pancreatitis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Oesophageal food impaction	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Pancreatitis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Salivary gland calculus	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
GENERAL DISORDERS AND ADMINISTRATION SITE CONDITIONS	3 (0.0)	(0.0, 0.0)	3 (0.0)	(0.0, 0.0)
Unevaluable event	0	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Chest pain	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Influenza like illness	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Non-cardiac chest pain	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Shoulder injury related to vaccine administration	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Vascular stent occlusion	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
HEPATOBILIARY DISORDERS	3 (0.0)	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Cholecystitis acute	0	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Cholelithiasis	2 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Bile duct stone	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
IMMUNE SYSTEM DISORDERS	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Anaphylactic reaction	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
INFECTIONS AND INFESTATIONS	15 (0.1)	(0.0, 0.1)	9 (0.0)	(0.0, 0.1)
Appendicitis	5 (0.0)	(0.0, 0.1)	0	(0.0, 0.0)
Pneumonia	1 (0.0)	(0.0, 0.0)	4 (0.0)	(0.0, 0.1)
Appendicitis perforated	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Cellulitis	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Diverticulitis	2 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Pyelonephritis	2 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Osteomyelitis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Peritoneal abscess	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Peritonitis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Pharyngitis streptococcal	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Sepsis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Suspected COVID-19	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Urinary tract infection	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)

Urosepsis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
INJURY, POISONING AND PROCEDURAL COMPLICATIONS	2 (0.0)	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Forearm fracture	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Head injury	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hip fracture	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Skin laceration	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
INVESTIGATIONS	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Cardiac stress test abnormal	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hepatic enzyme increased	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
METABOLISM AND NUTRITION DISORDERS	3 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Fluid retention	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hyperglycaemia	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hypoglycaemia	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Hypokalaemia	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
MUSCULOSKELETAL AND CONNECTIVE TISSUE DISORDERS	1 (0.0)	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Musculoskeletal chest pain	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Osteoarthritis	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Osteochondritis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	3 (0.0)	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Adenocarcinoma gastric	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Breast cancer	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Metastases to central nervous system	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Uterine leiomyoma	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Vaginal neoplasm	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
NERVOUS SYSTEM DISORDERS	5 (0.0)	(0.0, 0.1)	7 (0.0)	(0.0, 0.1)
Syncope	0	(0.0, 0.0)	3 (0.0)	(0.0, 0.0)
Subarachnoid haemorrhage	2 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Cerebrovascular accident	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Diplegia	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Haemorrhagic stroke	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Ischaemic stroke	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Loss of consciousness	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Paraesthesia	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Transient ischaemic attack	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
PREGNANCY, PUERPERIUM AND PERINATAL CONDITIONS	0	(0.0, 0.0)	3 (0.0)	(0.0, 0.0)
Pregnancy	0	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Abortion spontaneous incomplete	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
PSYCHIATRIC DISORDERS	3 (0.0)	(0.0, 0.0)	3 (0.0)	(0.0, 0.0)
Suicidal ideation	0	(0.0, 0.0)	2 (0.0)	(0.0, 0.0)
Bipolar disorder	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Mental disorder	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Mental status changes	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Psychotic disorder	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)

RENAL AND URINARY DISORDERS	4 (0.0)	(0.0, 0.1)	0	(0.0, 0.0)
Nephrolithiasis	2 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Acute kidney injury	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Renal colic	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
RESPIRATORY, THORACIC AND MEDIASTINAL DISORDERS	2 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Acute respiratory failure	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Pneumonitis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Pulmonary embolism	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
SURGICAL AND MEDICAL PROCEDURES	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Breast conserving surgery	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
UNCODED TERM	3 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
INVASIVE DUCTAL CARCINOMA STAGE 1B, LEFT BREAST@@	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
LEFT OVARIAN CYST, BENIGN TUMOR@@	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
MRSA INFECTION RIGHT STUMP@@	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
PROLAPSED UTERUS@@	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
STEMI: ST ELEVATION MYOCARDIAL INFARCTION@@	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
VASCULAR DISORDERS	4 (0.0)	(0.0, 0.1)	2 (0.0)	(0.0, 0.0)
Deep vein thrombosis	1 (0.0)	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)
Arteriosclerosis	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hypertension	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Hypertensive urgency	1 (0.0)	(0.0, 0.0)	0	(0.0, 0.0)
Orthostatic hypotension	0	(0.0, 0.0)	1 (0.0)	(0.0, 0.0)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified event. For "any event", n = number of subjects reporting at least 1 occurrence of any event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

Serious Adverse Event Narratives – Phase 2/3

Narratives for the Phase 3 participants who reported SAEs assessed as related to study intervention by the investigator who completed their visit at 1 month after Dose 2 and through the data cutoff date (06 October 2020) were provided.

Safety-Related Participant Withdrawals – Phase 2/3

First 6610 Participants – Phase 2/3

From Dose 1 to 1 month after Dose 2, 6 (0.2%) participants in the BNT162b2 group and 5 (0.2%) participants in the placebo group were withdrawn because of AEs (Table

18), and no additional withdrawals were reported for these participants from 1 month after Dose 2 until the data cutoff date.

Withdrawals of interest in the BNT162b2 group:

Two participants were withdrawn because of AEs that were assessed by the investigator as related to study intervention. One participant in the younger age group had an AE of myalgia 8 days after Dose 1 which was recovering at the time of the data cutoff. One participant in the older age group had an AE of pruritus and an AE of tachycardia 2 days after Dose 1; both events had a duration of 1 day and both were severe.

Three participants each had an SAE and were withdrawn from the study: younger age group (gastric adenocarcinoma), and in the older age group (coronary artery disease and coronary artery dissection).

Withdrawals of interest in the placebo group:

One participant (younger age group) was withdrawn because of an AE of allergy to vaccine (study intervention) and an AE of erythematous rash 2 days after Dose 1; both AEs resolved 18 days later, and both were assessed by the investigator as related to study intervention.

One participant in the older group had an SAE (coronary artery occlusion) assessed by the investigator as not related and was withdrawn from the study.

One participant in the older group was withdrawn from the study because of an AE of urticaria 10 days after Dose 1. The event resolved on the same day and was assessed by the investigator as not related to study intervention.

Table 18. Number (%) of Subjects Withdrawn Because of Adverse Events From Dose 1 to 1 Month After Dose 2, by System Organ Class and Preferred Term – ~6000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)	
	BNT162b2 (30 µg) (N^a=3314)	Placebo (N^a=3296)

System Organ Class Preferred Term	n[b] (%)	(95% CI[c])	n[b] (%)	(95% CI[c])
Any event	6 (0.2)	(0.1, 0.4)	5 (0.2)	(0.0, 0.4)
CARDIAC DISORDERS	3 (0.1)	(0.0, 0.3)	2 (0.1)	(0.0, 0.2)
Atrial fibrillation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Coronary artery disease	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery dissection	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Coronary artery occlusion	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Left ventricular hypertrophy	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Tachycardia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
GASTROINTESTINAL DISORDERS	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Diverticular perforation	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
IMMUNE SYSTEM DISORDERS	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Allergy to vaccine	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
INJURY, POISONING AND PROCEDURAL COMPLICATIONS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Ankle fracture	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Fall	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
MUSCULOSKELETAL AND CONNECTIVE TISSUE DISORDERS	2 (0.1)	(0.0, 0.2)	0	(0.0, 0.1)
Muscular weakness	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Myalgia	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NEOPLASMS BENIGN, MALIGNANT AND UNSPECIFIED (INCL CYSTS AND POLYPS)	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Adenocarcinoma gastric	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
NERVOUS SYSTEM DISORDERS	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Transient ischaemic attack	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
SKIN AND SUBCUTANEOUS TISSUE DISORDERS	1 (0.0)	(0.0, 0.2)	2 (0.1)	(0.0, 0.2)
Pruritus	1 (0.0)	(0.0, 0.2)	0	(0.0, 0.1)
Rash erythematous	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)
Urticaria	0	(0.0, 0.1)	1 (0.0)	(0.0, 0.2)

Note: MedDRA (v23.0) coding dictionary applied.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects reporting at least 1 occurrence of the specified event. For "any event", n = number of subjects reporting at least 1 occurrence of any event.
c. Exact 2-sided CI based on the Clopper and Pearson method.

All Participants – Phase 2/3

From Dose 1 to the data cutoff date, 18 (0.1%) participants in the BNT162b2 group and 14 (0.1%) participants in the placebo group were withdrawn because of AEs. In addition to withdrawals discussed for the first 6610 participants, other withdrawals included:

One participant in the younger BNT162b2 group had an SAE of lymphadenopathy (right axilla) 13 days after Dose 1 assessed by the investigator as related to study intervention and was withdrawn, which was not resolved at the time of the data cutoff.

Three participants in the younger age group (1 BNT162b2 and 2 placebo) became pregnant after Dose 1 and were withdrawn.

One participant in the younger placebo group had a positive pregnancy test (exposure during pregnancy) 39 days after Dose 1 and was withdrawn.

Narratives of Safety-Related Participant Withdrawals – Phase 2/3

Narratives for the Phase 2/3 participants with any AEs leading to withdrawal from the study through the data cutoff date (06 October 2020) were provided.

Other Significant Adverse Events – Phase 2/3

AEs of special interest were not defined for Phase 2/3 of this study; however, targeted medical events were monitored throughout the study.

Other Safety Assessments – Phase 2/3

Severe COVID-19 Illness – Phase 2/3

At the time of the efficacy interim analysis cutoff date of 04 November 2020, all 7 severe COVID-19 cases were reported in the placebo group.

Pregnancy – Phase 2/3

Pregnancy was reported in 5 Phase 3 participants through the data cutoff date of 06 October 2020: in 1 participant in the BNT162b2 group and 4 participants in the placebo group. Incomplete spontaneous abortion occurred in 1 participant in the placebo group.

Narratives for pregnancy were provided.

Analysis and Discussion of Deaths, Serious Adverse Events, Safety-Related Participant Withdrawals, and Other Significant Adverse Events – Phase 2/3

Up to the data cutoff date of 06 October 2020, the numbers of SAEs were similar in the BNT162b2 group (63 [0.3%]) and in the placebo group (49 [0.3%]). Two

participants in the BNT162b2 group reported SAEs that were assessed by the investigator as related to study intervention.

Few participants in the BNT162b2 group (18 [0.1%]) and in the placebo group (14 [0.1%]) were withdrawn because of AEs.

There were 3 deaths (1 in the BNT162b2 group and 2 in the placebo group); none of the deaths were assessed by the investigator as related to study intervention.

Phase 2/3 Safety Conclusions

Across age groups, local reactions were generally similar in frequency after each dose, and systemic events generally increased in frequency and severity after Dose 2 compared to Dose 1. Local and systemic reactogenicity events were well-tolerated and short-lived (median durations of 1.0 to 2.0 days).

Reactogenicity events after each dose of BNT162b2 in older adults were generally milder and less frequent than those observed in younger adults. The majority of reactogenicity events were mild or moderate in severity. No Grade 4 events were reported other than fever in 1 participant in the BNT162b2 group that began 1 day after Dose 2 and lasted 1 day.

The reactogenicity and AE profile after BNT162b2 30 μg evaluated in 6610 participants was consistent with the safety profile observed after BNT162b2 30 μg in Phase 1 and Phase 2.

AEs were reported in 16.8% of participants in the BNT162b2 group, and most AEs were mild or moderate in severity. At the time of the data cutoff date, the number of participants with AEs in the BNT162b2 group was greater as compared with the placebo group (7.9%), which upon analysis, was attributed to reactogenicity events reported as AEs within 7 days after each dose.

At the time of the data cutoff date, there were 2 related SAEs in the BNT162b2 group (lymphadenopathy and shoulder injury related to vaccine administration (SIRVA, erroneously administered into or near the shoulder joint capsule), and there were 6 discontinuations because of related AEs. There was 1 death in the BNT162b2 group

(arteriosclerosis) and 2 deaths in the placebo group that were assessed as not related to study intervention.

Overall, BNT162b2 at 30 µg was well tolerated when measured up to 1 month after Dose 2 following dosing regimen.

Example 16: Conclusion of Phase 3 Study of COVID-19 Vaccine, Meeting All Primary Efficacy Endpoints

After conducting the final efficacy analysis in the ongoing Phase 3 study, the mRNA-based COVID-19 vaccine, BNT162b2, met all of the study's primary efficacy endpoints. Analysis of the data indicated a vaccine efficacy rate of 95% ($p<0.0001$) in participants without prior SARS-CoV-2 infection (first primary objective) and also in participants with and without prior SARS-CoV-2 infection (second primary objective), in each case measured from 28 days after the first dose, 7 days after the second dose. The first primary objective analysis is based on 170 cases of COVID-19 of which 162 cases of COVID-19 were observed in the placebo group versus 8 cases in the BNT162b2 group. Efficacy was consistent across age, gender, race and ethnicity demographics. The observed efficacy in adults over 65 years of age was over 94%.

There were 10 severe cases of COVID-19 observed in the trial, with nine of the cases occurring in the placebo group and one in the BNT162b2 vaccinated group. No serious safety concerns related to the vaccine were reported. A review of unblinded reactogenicity data from the final analysis which consisted of a randomized subset of at least 8,000 participants 18 years and older in the Phase 2/3 study demonstrated that the vaccine was well tolerated, with most solicited adverse events resolving shortly after vaccination. The only Grade 3 (severe) solicited adverse events greater than or equal to 2% in frequency after the first or second dose were fatigue at 3.8% and headache at 2.0% following dose 2. Consistent with earlier shared results, older adults tended to report fewer and milder solicited adverse events following vaccination. The local reactogenicity profile among SARS-CoV-2 positive participants was consistent with that of the overall reactogenicity subset; similarly, on comparison

of AE data with that of the 'All subjects', there is no indication of a worse safety profile in baseline positive participants. Indeed, there is no indication of a worse safety profile in baseline positive participants; therefore, BNT162b2 can be used irrespective of COVID-19 history or SARS-CoV-2 serological status.

In addition, the safety milestone required by the U.S. Food and Drug Administration (FDA) for Emergency Use Authorization (EUA) has been achieved.

The results of this first global trial to reach the final efficacy analysis mark indicated that a high rate of protection against COVID-19 can be achieved very fast after the first 30 µg dose, underscoring the potential of BNT162 to provide early protection.

In summary:

- *Primary efficacy analysis demonstrated BNT162b2 to be 95% effective against COVID-19 beginning 28 days after the first dose; 170 confirmed cases of COVID-19 were evaluated, with 162 observed in the placebo group versus 8 in the vaccine group*
- *Efficacy was consistent across age, gender, race and ethnicity demographics; observed efficacy in adults over 65 years of age was over 94%*
- *Safety data milestone required by U.S. Food and Drug Administration (FDA) for Emergency Use Authorization (EUA) has been achieved*
- *Data demonstrates vaccine was well tolerated across all populations with over 43,000 participants enrolled; no serious safety concerns observed; the only Grade 3 adverse event greater than 2% in frequency was fatigue at 3.8% and headache at 2.0%*

Example 17: All Confirmed Cases of COVID-19 After Dose 1

A number of confirmed cases of COVID-19 are not captured in the analyses of the first primary endpoint for the evaluable efficacy population because they occurred less than 7 days after Dose 2, or because they occurred in participants who were excluded

from the evaluable efficacy population or who had evidence of infection before or during the vaccination regimen.

All reports of COVID-19 with onset at any time after Dose 1 are accounted for in Table 19, which provides a summary of cases for all participants in the Dose 1 all-available efficacy (modified intention-to-treat) population, regardless of evidence of infection before or during the vaccination regimen. Among these participants, 50 cases of COVID-19 occurred after Dose 1 in the BNT162b2 group compared to 275 cases in the placebo group (Table 19). Notably, in the BNT162b2 group, most cases occurred before Dose 2. The estimated VE against confirmed COVID-19 occurring after Dose 1 was 82% (2-sided 95% CI: 75.6 %, 86.9%), with an estimated VE of 52.4% (2-sided 95% CI: 29.5%, 68.4%) against confirmed COVID-19 occurring after Dose 1 but before Dose 2.

Table 19. COVID-19 Occurrence After Dose 1 – Dose 1 All-Available Efficacy Population

Efficacy Endpoint	BNT162b2 (30 µg) (N[a]=21669) n[b]	Placebo (N[a]=21686) n[b]
COVID-19 occurrence after Dose 1	50	275
After Dose 1 to before Dose 2	39	82
Dose 2 to 7 days after Dose 2	2	21
≥7 days after Dose 2	9	172

a. N = number of subjects in the specified group.
b. n1 = Number of subjects meeting the endpoint definition.

The early onset of protection is readily apparent in Figure 100, which displays cumulative incidence for the first COVID-19 occurrence after Dose 1 among all vaccinated participants based on Dose 1 all-available efficacy (modified intention-to-treat) population. Disease onset appears to track together for BNT162b2 and placebo until approximately 14 days after Dose 1, at which point the curves diverge, with cases steadily accumulating in the placebo group, while remaining virtually flat in the BNT162b2 group.

The cumulative incidence of COVID-19 cases over time among placebo and vaccine recipients begins to diverge by 14 days after Dose 1, approximately 9 days after the estimated median incubation period of 5 days, indicating the early onset of a partially protective effect of immunization. In the interval between Dose 1 and Dose 2, the observed vaccine efficacy was 52%, and in the first 7 days after Dose 2, it was 91%, reaching full efficacy for COVID-19 with onset at least 7 days after Dose 2.

Example 18: Secondary Efficacy Results – Final Analysis

Vaccine Efficacy For COVID-19 Occurring Within 14 Days After Dose 2 – Final Analysis

Participants Without Evidence of Infection Before Vaccination

For this efficacy endpoint, participants with positive or unknown NAAT results at any illness visit prior to 14 days after Dose 2 were not included in the evaluation for efficacy.

Among participants without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against confirmed COVID-19 occurring at least 14 days after Dose 2 was 94.2%, with 8 and 139 cases in the BNT162b2 and placebo groups respectively. The posterior probability of >99.99% for the true VE greater than 30% met the prespecified success criterion of >98.6% for this endpoint. The 95% credible interval for the vaccine efficacy was 88.7% to 97.2%, indicating that the true VE is at least 88.7% with a 97.5% probability given the available data.

Participants With or Without Evidence of Infection Before Vaccination

Among participants with or without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against confirmed COVID-19 occurring at least 14 days after Dose 2 was 94.4%, with 8 and 144 cases in the BNT162b2 and placebo groups respectively. The posterior probability of >99.99% for the true VE greater than 30% met the prespecified success criterion of >98.6% for this endpoint. The 95% credible interval for the vaccine efficacy was 89.1% to 97.3%, indicating that the true VE is at least 89.1% with a 97.5% probability given the available data.

Vaccine Efficacy for Severe COVID-19 Cases – Final Analysis

Efficacy Against Severe COVID-19 (≥7 Days After Dose 2)

Participants Without Evidence of Infection Before and During Vaccination Regimen

For this efficacy endpoint, participants with positive or unknown NAAT results at any illness visit prior to 7 days after Dose 2 were not included in the evaluation for efficacy. Among participants without evidence of severe SARS-CoV-2 infection before and during vaccination regimen, the estimated VE against severe COVID-19 occurring at least 7 days after Dose 2 was 66.4%, with 1 and 3 cases in the BNT162b2 and placebo groups respectively. The posterior probability for the true vaccine efficacy greater than 30% is 74.29%, which did not meet the prespecified success criterion of >98.6% for this endpoint due to the small number of severe cases observed after Dose 2 in the study.

Participants With and Without Evidence of Infection Before and During Vaccination Regimen

Among participants with or without evidence of severe SARS-CoV-2 infection prior to 7 days after Dose 2, VE against severe COVID-19 occurring at least 7 days after Dose 2 was 66.3%, with 1 and 3 cases in the BNT162b2 and placebo groups respectively. The posterior probability for the true vaccine efficacy greater than 30% is 74.19%.

All Confirmed Cases of Severe COVID-19 After Dose 1 – All-Available Population

Among participants in the all-available efficacy population, 1 case of COVID-19 occurred after Dose 1 in the BNT162b2 group compared to 9 cases in the placebo group. The estimated VE against severe COVID-19 occurring after Dose 1 was 88.9% (2-sided 95% CI: 20.1%, 99.7%), with an estimated VE of 75.0% against severe COVID-19 occurring at least 7 days after Dose 2.

Efficacy Against Severe COVID-19 (≥14 Days After Dose 2)

Participants Without Evidence of Infection Before and During Vaccination Regimen (14 Days) – Severe

Among participants without evidence of severe SARS-CoV-2 infection before and during vaccination regimen, the estimated VE against severe COVID-19 occurring at

least 14 days after Dose 2 was 66.4%, with 1 and 3 cases in the BNT162b2 and placebo groups respectively. The posterior probability for the true vaccine efficacy greater than 30% is 74.32%.

Participants With or Without Evidence of Infection Before and During Vaccination Regimen (14 Days) – Severe

Among participants with or without evidence of severe SARS-CoV-2 infection before and during vaccination phase, VE against severe COVID-19 occurring at least 14 days after Dose 2 was 66.3%, with 1 and 3 cases in the BNT162b2 and placebo groups respectively. The posterior probability for the true vaccine efficacy greater than 30% is 74.18%.

Vaccine Efficacy for COVID-19 Cases per CDC Definition – Final Analysis

Efficacy Against COVID-19 Based on CDC-Defined Symptoms (≥7 Days After Dose 2)

Participants Without Evidence of Infection Before and During Vaccination Regimen – CDC Defined – 7 Days

Among participants without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against CDC-defined COVID-19 occurring at least 7 days after Dose 2 was 95.1% (2-sided 95% CI: 90.2%, 97.9%), with 8 and 165 cases in the BNT162b2 and placebo groups, respectively.

Participants With and Without Evidence of Infection Before and During Vaccination Regimen – CDC Defined – 7 Days

Among participants with and without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against CDC-defined COVID-19 occurring at least 7 days after Dose 2 was 94.7% (2-sided 95% CI: 89.8% - 97.6%), with 9 and 172 cases in the BNT162b2 and placebo groups, respectively.

Efficacy Against COVID-19 Based on CDC-Defined Symptoms (≥14 Days After Dose 2)

Among participants without and with or without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against CDC-defined COVID-19 occurring

at least 14 days after Dose 2 were similar to those occurring at least 7 days after Dose 2.

Example 19: Efficacy Conclusions – Final Analysis

In the final efficacy analysis, among participants without evidence of SARS-CoV-2 infection before and during vaccination regimen, VE against confirmed COVID-19 occurring at least 7 days after Dose 2 was 95.0%, with 8 COVID-19 cases in the BNT162b2 group compared to 162 COVID-19 cases in the placebo group. The 95% credible interval for the vaccine efficacy was 90.3% to 97.6%. For the second primary endpoint, VE against confirmed COVID-19 occurring at least 7 days after Dose 2 in participants with and without evidence of SARS-CoV-2 infection before and during vaccination regimen was 94.6%, with 9 and 169 cases in the BNT162b2 and placebo groups respectively. The posterior probability of >99.99% for the true VE greater than 30% met the prespecified success criterion of >98.6% for this endpoint. The 95% credible interval for the vaccine efficacy was 89.9% to 97.3%, indicating that the true VE is at least 89.9% with a 97.5% probability given the available data

Observed VE was very high for the first primary efficacy endpoint across subgroups of age, sex, race/ethnicity, and country, as VE was >93% in all subgroups, with the exception of "all others" race group (89.3% VE) and Brazil (87.7% VE).

A total of 10 cases of severe COVID-19 occurred after Dose 1, 1 in the BNT162b2 group, compared with 9 cases in the placebo group.

Among all participants (regardless of evidence of infection before or during the vaccination regimen) 50 cases of COVID-19 occurred after Dose 1 in the BNT162b2 group compared with 275 cases in the placebo group, indicating an estimated VE of 82% (95% CI: 75.6%, 86.9%) against confirmed COVID-19 occurring after Dose 1.

The early onset of protection is readily apparent from cumulative incidence curves, which show that disease onset tracks conjointly for BNT162b2 and placebo until approximately 14 days after Dose 1, at which point the curves diverge, with cases

steadily accumulating in the placebo group, while remaining virtually flat after BNT162b2.

In conclusion, the final efficacy results show that BNT162b2 at 30 µg provided protection against COVID-19 in participants who had no evidence of prior infection with SARS-CoV-2, including across demographic subgroups, with severe cases observed predominantly in the placebo group.

Details of demographic populations assessed are presented below in Tables 20 and 21.

Table 20. Demographic Characteristics – ~38000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)		
	BNT162b2 (30 µg) (N^a=18860) n^b (%)	Placebo (N^a=18846) n^b (%)	Total (N^a=37706) n^b (%)
Sex			
Male	9639 (51.1)	9436 (50.1)	19075 (50.6)
Female	9221 (48.9)	9410 (49.9)	18631 (49.4)
Race			
White	15636 (82.9)	15630 (82.9)	31266 (82.9)
Black or African American	1729 (9.2)	1763 (9.4)	3492 (9.3)
American Indian or Alaska native	102 (0.5)	99 (0.5)	201 (0.5)
Asian	801 (4.2)	807 (4.3)	1608 (4.3)
Native Hawaiian or other Pacific Islander	50 (0.3)	26 (0.1)	76 (0.2)
Multiracial	449 (2.4)	406 (2.2)	855 (2.3)
Not reported	93 (0.5)	115 (0.6)	208 (0.6)
Ethnicity			
Hispanic/Latino	5266 (27.9)	5277 (28.0)	10543 (28.0)
Non-Hispanic/non-Latino	13482 (71.5)	13459 (71.4)	26941 (71.5)
Not reported	112 (0.6)	110 (0.6)	222 (0.6)
Country			
Argentina	2883 (15.3)	2881 (15.3)	5764 (15.3)
Brazil	1145 (6.1)	1139 (6.0)	2284 (6.1)
South Africa	372 (2.0)	372 (2.0)	744 (2.0)
USA	14460 (76.7)	14454 (76.7)	28914 (76.7)
Age group			

16-55 Years	10889 (57.7)	10896 (57.8)	21785 (57.8)
>55 Years	7971 (42.3)	7950 (42.2)	15921 (42.2)
Age at vaccination (years)			
Mean (SD)	50.5 (15.65)	50.3 (15.72)	50.4 (15.68)
Median	52.0	52.0	52.0
Min, max	(16, 89)	(16, 91)	(16, 91)
Body mass index (BMI)			
Underweight (<18.5 kg/m^2)	201 (1.1)	235 (1.2)	436 (1.2)
Normal weight (≥18.5 kg/m^2 - 24.9 kg/m^2)	5517 (29.3)	5460 (29.0)	10977 (29.1)
Overweight (≥25.0 kg/m^2 - 29.9 kg/m^2)	6578 (34.9)	6481 (34.4)	13059 (34.6)
Obese (≥30.0 kg/m^2)	6556 (34.8)	6662 (35.3)	13218 (35.1)
Missing	8 (0.0)	8 (0.0)	16 (0.0)

Note: HIV-positive subjects are included in this summary but not included in the analyses of the overall study objectives.
a. N = number of subjects in the specified group, or the total sample. This value is the denominator for the percentage calculations.
b. n = Number of subjects with the specified characteristic.

Table 21. Baseline Charlson Comorbidities – ~38000 Subjects for Phase 2/3 Analysis – Safety Population

	Vaccine Group (as Administered)		
Charlson Comorbidity Index Category	**BNT162b2 (30 µg) (N[a]=18860) n[b] (%)**	**Placebo (N[a]=18846) n[b] (%)**	**Total (N[a]=37706) n[b] (%)**
Subjects with any Charlson comorbidity	3934 (20.9)	3809 (20.2)	7743 (20.5)
AIDS/HIV	59 (0.3)	62 (0.3)	121 (0.3)
Any Malignancy	733 (3.9)	662 (3.5)	1395 (3.7)
Cerebrovascular Disease	195 (1.0)	166 (0.9)	361 (1.0)
Chronic Pulmonary Disease	1478 (7.8)	1453 (7.7)	2931 (7.8)
Congestive Heart Failure	88 (0.5)	83 (0.4)	171 (0.5)
Dementia	7 (0.0)	11 (0.1)	18 (0.0)
Diabetes With Chronic Complication	99 (0.5)	113 (0.6)	212 (0.6)
Diabetes Without Chronic Complication	1473 (7.8)	1478 (7.8)	2951 (7.8)
Hemiplegia or Paraplegia	13 (0.1)	21 (0.1)	34 (0.1)
Leukemia	12 (0.1)	10 (0.1)	22 (0.1)
Lymphoma	22 (0.1)	32 (0.2)	54 (0.1)
Metastatic Solid Tumor	4 (0.0)	3 (0.0)	7 (0.0)
Mild Liver Disease	125 (0.7)	89 (0.5)	214 (0.6)
Moderate or Severe Liver Disease	1 (0.0)	2 (0.0)	3 (0.0)
Myocardial Infarction	194 (1.0)	188 (1.0)	382 (1.0)

Peptic Ulcer Disease	52 (0.3)	71 (0.4)	123 (0.3)
Peripheral Vascular Disease	124 (0.7)	117 (0.6)	241 (0.6)
Renal Disease	123 (0.7)	133 (0.7)	256 (0.7)
Rheumatic Disease	62 (0.3)	56 (0.3)	118 (0.3)

Note: MedDRA (v23.1) coding dictionary applied.
Note: HIV-positive subjects are included in this summary but not included in the analyses of the overall study objectives.
a. N = number of subjects in the specified group. This value is the denominator for the percentage calculations.
b. n = Number of subjects with the specified characteristic. Subjects with multiple occurrences within each category are counted only once. For 'Subjects with any Charlson comorbidity', n = number of subjects reporting at least 1 occurrence of any Charlson comorbidity.

Example 20: Certain Observations Regarding Response of Young Adolescent Populations to Immunization with BNT162b2

In clinical trials described in Examples 13-19, the following were observed in younger adolescent populations.

Local Reactions in Younger Adolescents

Younger adolescents 12 to 15 years of age (N=100; 49 in the BNT162b2 group and 51 in the placebo group) contributed preliminary data to the reactogenicity subset and were analyzed separately. In this age group, pain at the injection site was the most frequently prompted local reaction in the BNT162b2 group, reported in 71.4% of participants compared to 17.6% in the placebo group after Dose 1. The incidence of pain was reduced in the BNT162b2 group and placebo group after Dose 2 (down to 58.7% vs 8.7%). Redness was reported in 1 participant in the BNT162b2 group after Dose 1 and in 2 participants after Dose 2, and in none in the placebo group after either dose. Swelling was reported in 2 participants in the BNT162b2 group after Dose 1 and in 3 participants after Dose 2, and in 1 in the placebo group after Dose 1 and none after Dose 2. Most local reactions were mild to moderate in severity. Two severe reactions were reported, both in the BNT162b2 group: severe redness and severe pain at the injection site.

Systemic Reactions in Younger Adolescents

Younger adolescents 12 to 15 years of age (N=100; 49 in the BNT162b2 group and 51 in the placebo group) contributed preliminary data to the reactogenicity subset and were analyzed separately. Most systemic events (other than vomiting and diarrhea, which had low incidences across groups) were reported at higher incidence in the BNT162b2 group than in the placebo group. However, there was no clear trend for increasing incidence or severity after Dose 1 compared to after Dose 2. In this age group, the most frequent prompted systemic events after Dose 1 compared to Dose 2 were (Dose 1 vs Dose 2):

- fatigue: BNT162b2 (49.0% vs 50.0%) compared to placebo (25.5% vs 6.5%)
- headache: BNT162b2 (42.9% vs 45.7%) compared to placebo (35.3% vs 21.7%)
- muscle pain: BNT162b2 (22.4% vs 30.4%) compared to placebo (13.7% vs 4.3%)
- chills: BNT162b2 (30.6% vs 28.3%) compared to placebo (7.8% vs 8.7%)
- joint pain: BNT162b2 (12.2% vs 17.4%) compared to placebo (9.8% vs 6.5%)
- fever: BNT162b2 (14.3% vs 19.6%) compared to placebo (0% vs 0%)
- vomiting: reported at similar frequencies in both groups and similar after each dose
- diarrhea: reported at similar frequencies in both groups and similar after each dose.

Most systemic events in younger adolescents were mild to moderate in severity. Severe events were relatively infrequent in both groups, occurring in no more than 1 or 2 participants after either dose.

Antipyretic/pain medication use in the younger adolescent group was modestly increased after Dose 2 compared to Dose 1 (30.6% vs 41.3%) and was greater than use in the placebo group (9.8% vs 13%).

In summary, as observed in older age groups (e.g., greater than 16 years of age such as 16-85 years of age), reactogenicity was mostly mild to moderate and short-lived

after dosing for younger adolescents 12 to 15 years of age, and the adverse event profile did not suggest any serious safety concerns.

Examples 21-24 below further confirm that neutralizing antibody responses and/or cell-mediated immune responses can be achieved with mRNA compositions described herein (including, e.g., BNT162b1 and BNT162b2) administered according to various dosing regimens described herein, including for example dosing regimens that involve administration of one or more doses lower than 30 ug, including, e.g., 20 ug, 10 ug, 3 ug, etc. Among other things, data provided in these Examples 21-24 further confirm induction of an immune response (e.g., as described herein) against SARS-CoV-2 upon administration of certain mRNA compositions described herein (including, e.g., BNT162b1 and BNT162b2) with one or more doses of 3 ug or above.

Those of ordinary skill in the art, reading the present disclosure, will appreciate that it demonstrates among other things, that administration of various mRNA compositions described herein can induce immune responses that include neutralizing antibodies against SARS-CoV-2; it furthermore confirms that certain such compositions (i.e., that induce neutralizing antibodies and/or that induce cell-mediated immune response such as T cell response) can induce protective immune responses that reduce SARS-CoV-2 infection and/or incidence of COVID19 sickness in organisms, specifically including primate organisms in which they have induced such neutralizing antibodies and/or cell-mediated immune response and furthermore including humans. In some embodiments, it also confirms that certain such compositions (e.g., described herein) do not significantly induce vaccine-mediated disease enhancement, for example, as evidenced by only one of the 10 cases of severe COVID-19 that were observed after a first dose. Indeed, the present disclosure documents that such compositions can effectively vaccinate humans (see, for example, clinical trial results included in Examples 13-19), for example, against severe COVID-19 disease.

Example 21: Immunogenicity studies for functional antibody responses

In clinical trials described in Example 7, the following were observed in healthy younger adults (18-55 years of age) and older adults (56-85 years of age) after BNT162b1 or BNT162b2 vaccination. Two doses, of 1 μg, 3 μg, 10 μg, 20 μg, or 30 μg were administered 21 days apart in younger adults. Two doses of 20 μg was administered 21 days apart in older adults. Functional antibody data for younger adult cohorts was determined up until Day 50 after an initial dose was administered for dose groups 1 μg and 3 μg, and up until Day 85 for dose groups 10, 20, and 30 μg. For BNT162b2-dosed older adults, data is available until Day 29 after an initial dose was administered.

For virus neutralizing antibody GMTs (neutralizing GMTs) and 95% confidence intervals for participants aged 18 to 55 years after dosing with BNT162b1, see Figure 40.

For virus neutralizing antibody GMTs (neutralizing GMTs) and 95% confidence intervals for younger participants aged 18 to 55 yrs and older participants aged 56 to 85 yrs after dosing with BNT162b2, see Figure 101 (50% neutralizing titer).

Geometric means fold increase (GMFI) from baseline in fuctional antibody titer data are shown in Figure 102 (BNT162b1) and Figure 103 (BNT162b2).

Participants dosed with BNT162b1 showed a strong dose-dependent antibody response. On Day 22, at 21 days after dose 1, virus neutralising antibody GMTs had increased in a dose-dependent manner for the 1, 10, 30 and 50 μg dose groups. At Day 29 (7 days after Dose 2), neutralising GMTs showed a strong, dose level dependent booster response. In the single, 60 μg dose group, neutralising GMTs remained at a lower level, indicating a booster dose is necessary to increase functional antibody titers.

On Day 43 (21 days after Dose 2 of BNT162b1), neutralising GMTs decreased (with the exception of the 1 μg dose level). Day 43 virus neutralising GMTs were 0.7-fold (1 μg) to 3.6-fold (50 μg) those of a COVID-19 HCS panel.

The COVID-19 HCS panel is comprised of 38 human COVID-19 HCS sera drawn from individuals aged 18 to 85 yrs, at least 14 d after confirmed diagnosis, and at a time

when the individuals were asymptomatic. The serum donors predominantly had symptomatic infections (35/38), and one had been hospitalized. The sera were obtained from Sanguine Biosciences (Sherman Oaks, CA), the MT Group (Van Nuys, CA), and Pfizer Occupational Health and Wellness (Pearl River, NY).

Participants dosed with BNT162b2 showed a strong antibody response induced by BNT162b2. Virus neutralizing GMTs were detected at 21 days after Dose 1 (Day 22) and had increased substantially in younger participants (aged 18 to 55 years) immunized with ≥3 µg of BNT162b2, and older participants (aged 56-85 years) immunized with 20 µg BNT162b2 by 7 days after Dose 2 (Day 29). Day 29 virus neutralizing GMTs were comparable between the younger and odler adult 20 µg dose level cohorts. The lowest treated dose of 1 µg BNT162b2 elicited a minimal neutralising response in participants aged 18 to 55 years.

On Day 43 (21 days after Dose two of BNT162b2), virus neutralising GMTs in the younger adult cohorts decreased for the 3, 20, and 30 µg dose levels. Thereafter, neutralising GMTs in between Days 29 and 43, neutralizing GMTs remained stable up to Day 85 (63 days after Dose two) for younger adult dose groups 10, 20 and 30 µg and were 1.3-fold to 1.9-fold those of a COVID-19 HCS panel.

Seroconversion in this context is defined as a minimum of a 4-fold increase of antibody GMT as compared to baseline. The frequency of participants with seroconversion is shown in Figures 104 (BNT162b1) and 105 (BNT162b2).

All participants dosed with Dose 1 at ≥ 30 µg BNT162b1 or BNT162b2 seroconverted either by 7 days or 21 days after Dose 2 (Day 29 or Day 43). All participants dosed with 30 µg BNT162b2 remained seropositive throughout the follow-up until Day 85.

Example 22: Immunogenicity studies for binding antibody concentrations

In clinical trials described in Example 7, the following were observed in healthy younger adults (18-55 years of age) and older adults (56-85 years of age) after BNT162b1 or BNT162b2 vaccination. Binding antibody concentration data is available up until Day 43 for BNT162b1-dosed younger participants aged 18 to 55 yrs dosed

with 1, 10, 30, 50, or 60 µg on Days 1 (all dose levels) and 22 (all dose levels except 60 µg) (n=12 per group).

For BNT162b2-dosed participants, data is available for younger participants aged 18 to 55 yrs dosed with 1, 3, 10, 20, or 30 µg, and older participants aged 56 to 85 yrs dosed with 20 µg on Days 1 and 22 (n=12 per group). Binding antibody concentration data for younger participant dose groups is available up until Day 50 for dose groups 1 µg and 3 µg, and up until Day 85 for dose groups 10, 20, and 30 µg. For the BNT162b2-dosed older participants, data is available up until Day 29.

The fold increase from baseline in binding antibody concentrations after dosing with BNT162b1 and BNT162b2 are shown in Figure 106 and Figure 107, respectively.

Participants dosed with BNT162b1 showed a strong dose-dependent antibody response against the SARS-CoV-2 spike (S) protein S1 subunit at Day 21 after Dose 1 (Day 22). At 7 days after Dose 2 (Day 29), S1-binding immunoglobulin (IgG) GMCs showed a strong, dose-dependent booster response. In the 60 µg dose group, which was only dosed once, S1-binding IgG GMCs remained at a lower level, indicating that a booster dose is necessary to increase antibody concentrations.

At 21 days after Dose 2 of BNT162b1 (Day 43), S1-binding IgG GMCs decreased (with exception of the 1 µg dose group), but were clearly above those of a COVID-19 HSC panel for all doses tested.

BNT162b2 dosed participants showed a strong BNT162b2-induced S1-binding IgG response at 21 days after Dose 1 (Day 22) with evidence of a dose-dependent response only between the 1 µg and 10 µg dose levels. S1-binding IgG GMCs showed a substantial boster response by 7 days after Dose 2 (Day 29). Day 29 S1-binding IgG GMCs were comparable between the younger and older participants at the 20 µg dose level.

Across all dose-level cohorts antibody levels decreased over time, but with S1-binding antibody GMCs well above that observed in a COVID-19 HCS panel at Day 85 (63 days after Dose 2; 10 to 30 µg dose level) (Figure 107).

Almost all BNT162b1- and BNT162b2-immunized participants seroconverted with regard to the S1-binding antibody response as early as 21 days after Dose 1 (Day 22). Frequency of participants with seroconversion after dosing with BNT162b1 is shown in Figure 108 and with BNT162b2 is shown in Figure 109. Similar observations were made using only the RBD domain as the target antigen.

Example 23: Exemplary Cell-Mediated Immune Responses: SARS-CoV-2-specific $CD4^+$ and $CD8^+$ T-cell responses

In clinical trials described in Example 7, the following were observed in healthy younger adults (18-55 years of age) and older adults (56-85 years of age) after BNT162b1 or BNT162b2 vaccination. CD4+ and CD8+ T-cell response data were available from 97 study participants receiving BNT162b1, 70 younger participants at dose levels of 1, 3, 10, 20, 30, 50, or 60 µg (note: Dose 2 was not given in the 60 µg dose group), and 27 older participants at dose levels of 10, 20, or 30 µg, as well as 76 participants receiving BNT162b2 at dose levels of 1, 3, 10, 20, or 30 µg (47 younger participants), or 10, 20, or 30 µg (older participants).

BNT162b1 induced strong RBD-specific $CD4^+$ T-cell responses in the majority of participants given both dose one and dose two (86 of 88 [97.7%]), including all older participants (27 of 27 [100%]); $CD8^+$ responses were induced in 47 of 61 (77.0%) younger participants and in 21 of 27 (77.7%) of older participants. In contrast, T-cell responses were detected less often and were lower in magnitude in 9 younger participants who received only Dose 1 in the 60 µg dose group, indicating the importance of a booster dose

BNT162b2 induced strong SARS-CoV-2 S protein-specific $CD4^+$ T-cell responses in all of the dosed younger or older participants (76 of 76 [100%]); $CD8^+$ T-cell responses were induced in 45/47 (95.7%) of younger participants and 24/29 (82.8%) older participants. Despite the slightly lower $CD8^+$ immunogenicity rate in older participants, the magnitude of the BNT162b2-induced responses was comparable to those induced in younger participants receiving 30 µg of BNT162b2. These T-cell

responses were directed against different parts of the antigen including non-RBD sequences, indicating the induction of multi-epitopic responses by BNT162b2 in both age groups.

Dosing twice with BNT162b1 or BNT162b2 led to a substantial increase in incidence and magnitude of T-cell responses in both age groups, and across all dose levels for BNT162b1. While the magnitude of $CD4^+$ T-cell responses induced by BNT162b2 was also similar across different dose levels, the magnitude of $CD8^+$ T-cell responses was highest at the 30 µg dose level. The participants with the strongest $CD4^+$ T-cell responses had more than 10-fold of the memory responses observed in the same participants against immunodominant peptides from cytomegalovirus, Epstein Barr virus, influenza virus, and tetanus toxoid in the same participants. The same participants also had strong $CD8^+$ T-cell responses that were comparable to memory responses against the above mentioned viral antigens.
RBD- and S protein-specific $CD4^+$ T-cell responses observed after vaccination were induced *de novo* by BNT162b1 in 97.5% of participants and by BNT162b2 in 100% of participants. RBD- and S protein-specific $CD8^+$ T-cell responses observed after vaccination were induced *de novo* by BNT162b1 in 95.5% of participants and by BNT162b2 in 96.6% of participants.

Example 24: Exemplary Cell-Mediated Immune Responses: funtional and pro-inflammatory $CD4^+/CD8^+$ T-cell responses

In clinical trials described in Example 7, the following were observed in healthy younger adults (18-55 years of age) and older adults (56-85 years of age) after BNT162b1 or BNT162b2 vaccination. *De novo* induction of SARS-CoV-2 S protein or RBD protein directed T-cells was confirmed using intracellular cytokine staining (ICS). As described in Example 7 for BNT162b1, similar cell-mediated immune responses were also observed with BNT162b2 as described below.

For example, IFNγ-producing CD4+ and CD8+ T-cells against SARS-CoV-2 S protein or RBD were induced robustly by both BNT162b1 and BNT162b2. No clear dose dependency was observed for both BNT162b1 and BNT162b2. The cytokine responses elicited after dosing with either BNT162b1 or BNT162b2 in older participants was mostly identical in response pattern and intensity with that in younger participants.

BNT162b1 and BNT162 induced poly-functional and pro-inflammatory CD4+/CD8+ T-cell responses in almost all participants. The detection of interferon (IFN)γ, interleukin (IL)-2 but not IL-4 indicates a favorable Th1 profile and the absence of a potentially deleterious Th2 immune response.

Regarding BNT162b2, peripheral blood mononuclear cell (PBMC) fractions isolated from blood of study participants collected at baseline (pre-Dose 1) and 29±3 d after Dose 1 BNT162b2 were analyzed. This includes data for a total of 74 study participants:

- Younger participants aged 18 to 55 yrs per dose group: 1 µg (n=8), 3 µg (n=9), 10 µg (n=10), 20 µg (n=9), 30 µg (n=10).
- Older participants aged 56 to 85 yrs per dose group: 10 µg (n=11), 20 µg (n=8), 30 µg (n=9).

The functionality and polarization of vaccine-induced SARS-CoV-2 S-specific T cells were assessed by intracellular accumulation of cytokines IFN-gamma, IL-2, and IL-4 in response to stimulation with overlapping peptides representing the full-length sequence of the vaccine-encoded RBD and the wild-type SARS CoV-2 protein, respectively. As a control, PMBCs from 18 COVID-19 convalescent virologically confirmed patients were used.

Two doses of BNT162b2 (dose range 1 to 30 µg), induced vaccine-specific T-cell responses in both age groups analyzed (Figures 110 and 111). Testing for SARS-CoV-2 S protein specific T-cell responses was performed with two different peptide pools, S pool 1 comprising overlapping peptides from the N-terminal region of the S protein

(which is not equilvalent to structural domains) and S pool 2 comprising C-terminal regions of the S protein. S-specific $CD4^+$ T-cell responses analyzed in 74 participants dosed with BNT162b2 were characterized by a Th1 cytokine profile secreting IFN-gamma, or IL-2, or both.

Almost no Th2 cytokine IL-4 secreting T cells were detectable in response to S peptide sub-pool stimulations (mean fractions: 0.01% and 0.02% of antigen-specific circulating $CD4^+$ T cells in the 20 and 30 µg adult cohort, respectively; separate stimulation with S protein sub-pool 1 and sub-pool 2). S-specific $CD8^+$ T cells secreted IFNγ in 61 of the 74 analyzed participants (adults: 40 of 46 participants and older adults: 21 of 28 participants) and also IL-2 secreting $CD8^+$ T cells were detectable. Fractions of S-specific $IFN\gamma^+$ $CD8^+$ T cells targeting the N-terminal domain of the S protein reached up to 1% of total peripheral blood $CD8^+$ T cells in the 20 and 30 µg younger participant dose groups and up to 2.4% in the 30 µg older participant dose group. Pre-existing $CD8^+$ T-cell responses against the C-terminal region of the S protein were detected in 17 of 74 dosed participants (range: 0.07 to 5.59% IFNγ-producing $CD8^+$ T cells). In 6 of 17 participants, these pre-existing responses were slightly amplified upon BNT162b2 dosing.

Overall, the mean fractions of S-specific $CD4^+$ and $CD8^+$ T cells were substantially higher (e.g., the S protein pool 1 IFNγ $CD8^+$ response of 30 µg dosed participants was 12.5-fold higher) than that observed in 18 patients who recovered from COVID-19. Importantly, for the clinically targeted 30 µg dose group, the cytokine responses elicited after vaccination with BNT162b2 in older participants was mostly identical in response pattern and intensity with that of the younger participants.

BNT162b2-induced T-cell responses, especially for $CD8^+$ T cells, were not limited to the RBD, and pronounced and strong T cell recognition of non-RBD regions of the S protein were observed.

BNT162b2 induced poly-functional and pro-inflammatory $CD4^+$/$CD8^+$ T-cell responses in almost all participants. The Th1 polarization of the helper response was

characterized by a robust IFNγ/IL-2 and only minor IL-4 production upon antigen-specific (wild-type SARS-CoV-2 S protein peptide pools) re-stimulation.

Example 25: Certain T cell responses induced by BNT162b2

In addition to Examples 23 and 24, which describe certain T cell responses induced by immunization with BNT162b2 as observed in the German trial (Study BNT162-01; NCT04380701), the present Example further demonstrates immunogenicity of prime-boost vaccination with 1, 10, 20 and 30 µg BNT162b2 in participants 19-55 years of age, including detailed characterisation of T cell responses, e.g., the first identification of epitopes recognised by CD8+ T cells induced by a COVID-19 vaccine described herein. Without wishing to be bound by any particular theory, it is noted that identity of epitopes to which a response is raised in a subject, and/or extent of response to particular epitope or combination of epitopes may impact one or more features (e.g., effectiveness and/or duration) of an immune response and/or of immune protection provided by an administered vaccine. In some embodiments, an administration regimen may involve one or more steps of monitoring one or more features of an immune response, including, for example, presence and/or level of response (e.g., of T cells and/or antibodies) that recognize one or more particular epitopes. In some embodiments, need for, timing of, and/or magnitude of a subsequent dose may be determined in light of such monitoring.

As further described below, the present Example demonstrates, in part, that the epitopes recognised by several BNT162b2-induced $CD8^+$ T cells when presented on frequent MHC alleles were identified using peptide MHC multimers; and that $CD8^+$ T cells were shown to be of the early-differentiated effector-memory phenotype, with single specificities reaching 0.01-3% of circulating $CD8^+$ T cells. Without wishing to be bound by any particular theory, it is noted that cells that exhibit "effector-memory" phenotype may provide longer term protection.

The present Example also documents that certain participants receiving BNT162b2 had pre-existing T cell responses. Thus, among other things, this example confirms that compositions as described herein, and particularly BNT162b2 may well be useful even in subjects who have already been exposed to one or more related viruses, including potentially the same virus – i.e., SARS-CoV-2 and/or to an antigen thereof or another antigen that shares one or more epitopes with SARS-CoV2 spike protein.

Prevalence and magnitude of vaccine-induced T cell responses

T cell responses of 37 BNT162b2 immunised participants from whom sufficient peripheral blood mononuclear cells (PBMCs) were available were analysed pre-vaccination (day 1) and seven days after the booster dose (day 29) by direct ex vivo IFNγ enzyme-linked immunosorbent spot (ELISpot) assay (Figure 112 and Figure 113). One of ordinary skill in the art will understand that SARS-CoV-2 S protein is composed of a signal peptide (aa 1-13), the N-terminal S1 protease fragment (aa 14-685), and the C-terminal S2 protease fragment (aa 686-1273); and that S1 contains the RBD (aa 319-541), which binds to the host receptor, and that S2 mediates fusion between the viral envelope and cell membrane. To deconvolute reactivity against S protein, $CD4^+$ or $CD8^+$ T cell effectors were stimulated overnight with overlapping peptides representing different portions of the wild-type sequence of SARS-CoV-2 S, namely N-terminal pools 'S pool 1' (aa 1-643) and 'RBD' (aa 1-16 fused to aa 327-528 of S), and the C-terminal 'S pool 2' (aa 633-1273).

Seven days after the boost with BNT162b2 at any of the indicated doses, robustly expanded SARS-CoV-2 S-specific $CD4^+$ T-cells were detectable in all 37 participants (Figure 112a, Figure 113a). In 34 of these participants, comparison to pre-vaccination PBMCs was possible. Thirty of the 34 subjects (88.2%) had de novo (not existent at baseline) $CD4^+$ T cell responses against both S pool 1 and S pool 2 of SARS-CoV-2. One participant had de novo response only against pool 2. The remaining three participants had de novo responses against S pool 1 and low numbers of pre-existing S pool 2-reactive $CD4^+$ T cells. In two of these three participants, the pre-existing

responses against S pool 2 were amplified by vaccination (from 91 and 188 spots/10^6 cells pre-vaccination to 1391 and 965 spots after vaccination, respectively), whereas in one of the three participants, the pre-existing responses against S pool 2 remained stable (53 to 140 spots/10^6 cells). These data demonstrate that in 94.1% (32/34) of participants, two doses of BNT162b2 induce poly-epitopic $CD4^+$ T cell responses (de novo or amplified) directed against both N- and C-terminal portions of S and thus against epitopes outside the RBD (Figure 113b).

Although for dose levels ≥10 µg the magnitude of $CD4^+$ T cell responses did not appear to be dose-dependent, it varied between individuals. In the strongest responders, the S-specific $CD4^+$ T cell responses were more than 10-fold of the individual memory responses to common viruses and recall antigens (those from cytomegalovirus, Epstein Barr virus, influenza virus and tetanus toxoid) (Figure 112b,c).

Vaccine-induced S-specific $CD8^+$ T cell responses were detected in 34 of 37 vaccinated participants (91.9%). The majority were strong responses (Figure 112a, Figure 113a) comparable to individual memory responses against cytomegalovirus (CMV), Epstein Barr virus (EBV) and influenza virus (Figure 112b,c). De novo S -specific $CD8^+$ T cell responses were induced in 33 participants, these were either directed against both (22 participants), or one of the S pools (S pool 1 in ten participants, and S pool 2 in two participants), indicating a preponderance of a poly-epitopic response including non-RBD S-specific T cells (Figure 113b). In seven participants, pre-existing $CD8^+$ T cell responses to S pool 2 were detected that were not further augmented by vaccination. Six out of these seven participants had a concurrent de novo response to pool 1 of S, which in strength did not differ significantly from those observed in individuals without pre-existing responses to S pool 2 (Figure 113c). Of note, the strongest responses (higher than third quartile) against S pool 1 among the 34 participants with detectable $CD8^+$ T cell responses were observed in those without pre-existing S pool 2-specific responses.

The magnitude of S-specific $CD4^+$ T cell responses correlated positively with S1-binding IgG (Figure 114a), and, in line with the concept of intramolecular help (e.g., a CD4

response to one eptiope in an antigen can support development of a CD8 response to an epitope in the same antigen), also with the strength of S-specific $CD8^+$ T cell responses (Figure 114b). S-specific $CD8^+$ T cell responses also correlated positively with S1-binding IgG (Figure 114c), indicating a convergent development of the humoral and cellular adaptive immunity.

Polarisation of vaccine-induced T cell responses

To assess functionality and polarisation of S-specific T cells, cytokines secreted in response to stimulation with S pool 1, S pool 2 and RBD pool were determined by intracellular staining (ICS) for IFNγ, IL-2 and IL-4 specific responses in pre- and post-vaccination PBMCs of 37 BNT162b2-immunised participants receiving different doses. A considerable fraction of vaccine-induced, S-specific $CD4^+$ T cells secreted IFNγ, IL-2, or both, while T cells secreting the T_H2 cytokine IL-4 were barely detectable (Figure 115a-c, Figure 113d-e). Vaccine-induced S-specific $CD8^+$ T cells secreted predominantly IFNγ and lower levels of IL-2 in response to S pool 1 and S pool 2 stimulation. Fractions of $IFN\gamma^+$ $CD8^+$ T cells specific to S pool 1 constituted up to about 1% of total peripheral blood $CD8^+$ T cells (Figure 115d). Of note, several of the analysed participants (*n*=3 in the 20 µg dose cohort and *n*=3 in the 30 µg dose cohort) displayed pre-existing S pool 2 specific $CD8^+$ T cell responses, which in 5 out of the 6 participants were not further amplified after vaccination. A strong pre-existing S pool 2 specific $IFN\gamma^+$ $CD4^+$ T cell response was detectable in one participant (20 µg dose cohort) (Figure 115c).

In both assay systems, cytokine production of $CD4^+$ as well as $CD8^+$ T cells in response to peptide pools comprising the full SARS-CoV-2 S exceeded the responses against the RBD peptide pool, further confirming the poly-epitopic nature of T cell responses elicited by BNT162b2. The mean fraction of BNT162b2-induced S-specific $IFN\gamma^+$ or $IL\text{-}2^+$ $CD4^+$ and $CD8^+$ T cells within total circulating T cells was higher than that detected in eighteen control subjects who had recovered from COVID-19 (HCS) (Figure 115c,d).

Epitope specificity and phenotype of CD8+ T cells observed in immunization with BNT162b2

$CD8^+$ T cell responses were characterised on the epitope level in three participants vaccinated with a 2-dose regimen with two doses (e.g., 10 μg/dose or 30 μg/dose) given 21 days apart.

Pre- and post-vaccination peripheral blood mononuclear cells (PBMCs) collected from the participants were stained with individualised peptide/MHC multimer staining cocktails for flow cytometry analysis. Twenty-three (4 for HLA-B*0702, 19 for HLA-A*2402), 14 (HLA-B*3501) and twenty-three (7 for HLA-B*4401, 16 for HLA-A*0201) diverse peptide/MHC allele pairs were used for participant 1, 2 and 3, respectively, thus probing a selected set of potential reactivities rather than comprehensively capturing the poly-epitopic T cell response.For each participant, de novo induced $CD8^+$ T cell reactivities against multiple epitopes were identified adding up to a total of eight different epitope/MHC pairs spread across the full length of S protein (Figure 116 a, c). The magnitude of epitope-specific T cell responses ranged between 0.01-3.09% of peripheral $CD8^+$ T cells and the most profound expansion was observed for HLA-A*0201 YLQPRTFLL (3.09% $multimer^+$ of $CD8^+$), HLA-A*2402 QYIKWPWYI (1.27% $multimer^+$ of $CD8^+$) and HLA-B*3501 QPTESIVRF (0.17% $multimer^+$ of $CD8^+$). Comparison with the bulk $IFN\gamma^+$ $CD8^+$ T cell response against full S protein in these individuals determined by ELISpot and intracellular staining (ICS) indicated that pMHC technology may be more useful to assess the true extent of the cellular immune response (Figure 113f).

Phenotyping of the identified pMHC $multimer^+$ S antigen-experienced $CD8^+$ T cell specificities revealed an early differentiated effector memory phenotype characterized by low expression of CCR7 and CD45RA and high expression of the costimulatory molecules CD28 and CD27. $CD8^+$ T cells also expressed markers associated with cognate activation, such as CD38, HLA-DR and PD-1 (Figure 116b).

Discussion

Effectors of the adaptive immune system have complementary roles in the defense of viral infections. While neutralising antibodies are the first line of defense, CD8+ cytotoxic T lymphocytes (CTLs) contribute to virus clearance from intracellular compartments that are inaccessible to neutralising antibodies. Antigen-specific CD4+ T cells have immune orchestrating functions, including provision of cognate help to B cells and CD8+ T cells, support of memory generation, as well as indirect (e.g. via IFNγ) or direct (against MHC class II-expressing target cells) cytotoxic activity.

This Example shows that vaccination with BNT162b2 induces a coordinated immune response with SARS-CoV-2 S-specific neutralising antibodies (as described in other Examples), CD4+ T cells, CD8+ T cells, and immune-modulatory cytokines such as IFNγ. All participants vaccinated with BNT162b2 mounted de novo S-specific CD4+ T cell responses and almost 92% of participants mounted CD8+ T cell responses, as detected with an ex vivo ELISpot assay. The magnitude of the T cell responses varied inter-individually and showed no clear dose dependency. Even with the lowest dose of 1 μg BNT162b2, most of the vaccinated participants demonstrated robust expansion of CD4+ and CD8+ T cells. T cell responses were directed against RBD, S1 and S2 regions of S protein, indicating immune recognition of multiple independent MHC I and II epitopes.

Expression of IFNγ and IL-2 but only low levels of IL-4 in BNT162b2-induced CD4+ T cells indicated a TH1 profile and the absence of a potentially deleterious TH2 immune response.

While all CD8+ T cell responses against the S1 subunit of S protein were de novo and not detected at baseline, pre-existing immune responses against the S2 subunit were identified in several individuals. The S1 fragment has less sequence similarity to the corresponding seasonal coronavirus sequences than the S2 fragment does; without wishing to be bound by theory, it is proposed that this finding indicates that pre-existing cross-reactive CD8+ T cells may have been detected.

Peptide MHC (pMHC) multimer technology enabled the identification of S protein epitopes recognised by vaccine-induced $CD8^+$ T cells as well as direct quantification

of the respective epitope-specific T cells. The cumulative T cell frequencies in each participant exceeded the overall T cell response measured in ELISpot and ICS assays, indicating that those assays underestimate the true magnitude of the poly-epitopic response. One of skill in the art will appreciate that single peptide analyses are known to yield higher T cell frequencies as compared to functional T cell assays that stimulate with peptide pools, with a multitude of immunogenic epitopes competing. A high proportion of induced $CD8^+$ T cells were early differentiated effector memory cells. This favourable phenotype has the potential to respond rapidly, but has a limited capacity to produce IFNγ, and thus is less likely to be detected in functional T cell assays. While epitopes in SARS-CoV-2 S against which infected individuals raise CD8+ T cells were identified and known in the art (see, e.g., Shomuradova et al., Immunity (2020) doi:10.1016/j.immuni.2020.11.004; and Peng et al. Nat. Immunol. 21, 1336-1345 (2020)), the data presented herein is the first demonstration of epitopes recognised by COVID-19 vaccine-induced T cells. Of note, the immunodominant HLA-A*02:01 restricted peptide YLQPRTFLL identified in this stidy has previously been described in convalescent COVID-19 patients. *Id.*

Materials and Methods

Proteins and peptides.

Two pools of 15-mer peptides overlapping by 11 amino acids (aa) and together covering the whole sequence of wild-type SARS-CoV-2 S (S pool 1 featuring aa 1-643, S pool 2 featuring aa 633-1273) and one pool covering the SARS-CoV-2 RBD (aa 327-528) with the signal peptide of S (aa 1-16) fused to its N-terminus were used for ex vivo stimulation of PBMCs for flow cytometry and IFNγ ELISpot. CEF (CMV, EBV, influenza virus; human leukocyte antigen [HLA] class I epitope peptide pool) and CEFT (CMV, EBV, influenza virus, tetanus toxoid; HLA class II epitope peptide pool) were used as controls for general T-cell reactivity and to benchmark the magnitude of memory T cell responses. All peptides were obtained from JPT Peptide Technologies.

Human convalescent serum and PBMC panel.

Human SARS-CoV-2 infection/COVID-19 convalescent sera (*n*=38) were drawn from donors 18-83 years of age at least 14 days after PCR-confirmed diagnosis and at a time when the participants were asymptomatic. The mean age of the donors was 45 years. Neutralising GMTs in subgroups of the donors were as follows: symptomatic infections, 90 (*n*=35); asymptomatic infections, 156 (*n*=3); hospitalized, 618 (*n*=1). Sera were obtained from Sanguine Biosciences (Sherman Oaks, CA), the MT Group (Van Nuys, CA) and Pfizer Occupational Health and Wellness (Pearl River, NY). Human SARS-CoV-2 infection/COVID-19 convalescent PBMC samples (*n*=18) were collected from donors 22-79 years of age 30-62 days after PCR-confirmed diagnosis, when donors were asymptomatic. PBMC donors had asymptomatic or mild infections (*n*=16, clinical score 1 and 2) or had been hospitalized (*n*=2, clinical score 4 and 5). Blood samples were obtained from the Frankfurt University Hospital.

Primary cell isolation.

PBMCs were isolated by Ficoll-Paque™ PLUS (Cytiva) density gradient centrifugation and cryopreserved prior to analysis.

IFNγ ELISpot.

IFNγ ELISpot analysis was performed ex vivo (without further in vitro culturing for expansion) using PBMCs depleted of $CD4^+$ and enriched for $CD8^+$ T cells ($CD8^+$ effectors) or depleted of $CD8^+$ and enriched for $CD4^+$ T cells ($CD4^+$ effectors). Tests were performed in duplicate and with a positive control (anti-CD3 monoclonal antibody CD3-2 [1:1,000; Mabtech]). Multiscreen filter plates (Merck Millipore) pre-coated with IFNγ-specific antibodies (ELISpotPro kit, Mabtech) were washed with PBS and blocked with X-VIVO 15 medium (Lonza) containing 2% human serum albumin (CSL-Behring) for 1-5 hours. Per well, 3.3 x 10^5 effector cells were stimulated for 16-20 hours with three overlapping peptide pools representing different portions of the wild-type sequence of SARS-CoV-2 S (N-terminal pools S pool 1 [aa 1-643] and RBD

[aa1-16 fused to aa 327-528], and the C-terminal S pool 2 [aa 633-1273]). Bound IFNγ was visualised using a secondary antibody directly conjugated with alkaline phosphatase followed by incubation with 5-bromo-4-chloro-3'-indolyl phosphate (BCIP)/ nitro blue tetrazolium (NBT) substrate (ELISpotPro kit, Mabtech). Plates were scanned using an AID Classic Robot ELISPOT Reader and analysed by AID ELISPOT 7.0 software (AID Autoimmun Diagnostika). Spot counts were displayed as mean values of each duplicate. T-cell responses stimulated by peptides were compared to effectors incubated with medium only as a negative control using an in-house ELISpot data analysis tool (EDA), based on two statistical tests (distribution-free resampling), to provide sensitivity while maintaining control over false positives.

To account for varying sample quality reflected in the number of spots in response to anti-CD3 antibody stimulation, a normalisation method was applied, enabling direct comparison of spot counts and strength of response between individuals. This dependency was modelled in a log-linear fashion with a Bayesian model including a noise component (unpublished). For a robust normalization, each normalisation was sampled 1000 times from the model and the median taken as normalized spot count value. Likelihood of the model: $\log \lambda_E = \alpha \log \lambda_P + \log \beta_j + \sigma\varepsilon$, where λ_E is the normalized spot count of the sample; α is a stable factor (normally distributed) common among all positive controls λ_P; β_j is a sample j specific component (normally distributed); and $\sigma\varepsilon$ is the noise component, of which σ is Cauchy distributed, and ε is Student's-t distributed. β_j ensures that each sample is treated as a different batch.

Flow cytometry.

Cytokine-producing T cells were identified by intracellular cytokine staining. PBMCs thawed and rested for 4 hours in OpTmizer medium supplemented with 2 µg/mL DNase I (Roche), were restimulated with different portions of the wild-type sequence of SARS-CoV-2 S in peptide pools described in the ELISpot section (2 µg/mL/peptide; JPT Peptide Technologies) in the presence of GolgiPlug (BD) for 18 hours at 37 °C. Controls were treated with DMSO-containing medium. Cells were stained for viability

and surface markers (CD3 BV421, 1:250; CD4 BV480, 1:50; CD8 BB515, 1:100; all BD Biosciences) in flow buffer (DPBS [Gibco] supplemented with 2% FBS [Biochrom], 2 mM ethylenediaminetetraacetic acid [EDTA; Sigma-Aldrich]) for 20 minutes at 4 °C. Afterwards, samples were fixed and permeabilised using the Cytofix/Cytoperm kit according to manufacturer's instructions (BD Biosciences). Intracellular staining (CD3 BV421, 1:250; CD4 BV480, 1:50; CD8 BB515, 1:100; IFNγ PE-Cy7, 1:50 [for HCS]; IFNγ BB700, 1:250 [for participants]; IL-2 PE, 1:10; IL-4 APC, 1:500; all BD Biosciences) was performed in Perm/Wash buffer for 30 minutes at 4 °C. Samples were acquired on a fluorescence-activated cell sorter (FACS) VERSE instrument (BD Biosciences) and analysed with FlowJo software version 10.6.2 (FlowJo LLC, BD Biosciences). S- and RBD-specific cytokine production was corrected for background by subtraction of values obtained with dimethyl sulfoxide (DMSO)-containing medium. Negative values were set to zero. Cytokine production in Figure 116b was calculated by summing up the fractions of all $CD4^+$ T cells positive for either IFNγ, IL-2 or IL-4, setting this sum to 100% and calculating the fraction of each specific cytokine-producing subset thereof. Pseudocolor plot axes are in log10 scale.

Peptide/MHC multimer staining.

In order to select MHC-class I epitopes for multimer analysis, a mass spectrometry-based binding and presentation predictor (e.g., as described in Abelin et al., Immunity 46, 315-326 (2017); and Poran et al., Genome Med. 12, 70 (2020)) was applied to 8-12 amino acid long peptide sequences from the Spike glycoprotein derived from the GenBank reference sequence for SARS-CoV-2 (accession: NC_045512.2, https://www.ncbi.nlm.nih.gov/nuccore/NC_045512) and paired with 18 MHC-class-I alleles with >5% frequency in the European population. Top predicted epitopes were identified by setting thresholds to the binding percent-rank (≤1%) and presentation scores ($\geq 10^{-2.2}$) and considered for synthesis of peptides of >90% purity. pMHC complexes were refolded with the easYmer technology (easYmer® kit, ImmuneAware Aps), and complex formation was validated in a bead-based flow cytometry assay

according to the manufacturer's instructions. Combinatorial labeling was used for dissecting the antigen specificity of T cells utilizing two-color combinations of five different fluorescent labels to enable detection of up to ten different T cell populations per sample. For tetramerisation, streptavidin (SA)-fluorochrome conjugates were added: SA BV421, SA BV711, SA PE, SA PE-Cy7, SA APC (all BD Biosciences). For three BNT162b2 vaccinated participants, individualized pMHC multimer staining cocktails contained up to ten pMHC complexes, with each pMHC complex encoded by a unique two-color combination. PBMCs ($2x10^6$) were stained ex vivo for 20 minutes at room temperature with each pMHC multimer cocktail at a final concentration of 4 nM in Brilliant Staining Buffer Plus (BSB Plus [BD Horizon™]). Surface and viability staining was carried out in flow buffer (DPBS [Gibco] with 2% FBS [Biochrom], 2 mM EDTA [Sigma-Aldrich]) supplemented with BSB Plus for 30 minutes at 4 °C (CD3 BUV395, 1:50; CD45RA BUV563, 1:200; CD27 BUV737, 1:200; CD8 BV480, 1:200; CD279 BV650, 1:20; CD197 BV786, 1:15; CD4 BB515, 1:50; CD28 BB700, 1:100; CD38 PE-CF594, 1:600; HLA-DR APC-R700, 1:150; all BD Biosciences; DUMP channel: CD14 APC-eFluor780, 1:100; CD16 APC-eFluor780, 1:100; CD19 APC-eFluor780, 1:100; fixable viability dye eFluor780, 1:1,667; all ThermoFisher Scientific). Cells were fixed for 15 minutes at 4 °C in 1x Stabilization Fixative (BD), acquired on a FACSymphony™ A3 flow cytometer (BD Biosciences) and analysed with FlowJo software version 10.6.2 (FlowJo LLC, BD Biosciences). $CD8^+$ T cell reactivities were considered positive, when a clustered population was observed that was labelled with only two pMHC multimer colors.

Example 26: Evidence suggesting possibility of re-infection

The primary endpoint was evaluated in individuals without prior evidence of COVID-19 disease, and very few cases of confirmed COVID-19 occurred among participants with evidence of infection prior to vaccination (although more cases occurred in the placebo group compared with the vaccine group). However, available data, while

limited, as shown in Tables 22-23 suggest that previously infected individuals can be at risk of COVID-19 (i.e., reinfection) and could benefit from vaccination.

Table 22. Vaccine Efficacy – First COVID-19 Occurrence From 7 Days After Dose 2, by Test Status – Subjects With or Without Evidence of Infection Prior to 7 Days After Dose 2 – Evaluable Efficacy (7 Days) Population

RT-PCR NP Swab Results and Serostatus: Time Points	**Vaccine Group** N[a]= 19965 Cases n1[b] surveillance time[c] (n2[d])	**Control Group** N[a]= 20172 Cases n1[b] surveillance time[c] (n2[d])	**Vaccine Efficacy % (95% CI[e])**
Pre-dose 1 SARS-CoV-2 RT-PCR (NP swab)			
Positive	0 0.013 (119)	0 0.015 (137)	NE (NE, NE)
Negative	9 2.301 (18259)	166 2.314 (18410)	94.5 (89.4, 97.6)
Unknown	0 0.017 (181)	3 0.016 (161)	100.0 (-126.2, 100.0)
Pre-dose 2 SARS-CoV-2 RT-PCR (NP swab)			
Positive	0 0.009 (83)	1 0.012 (106)	100 (-4916.4, 100.0)
Negative	9 2.301 (18263)	167 2.315 (18408)	94.6 (89.5, 97.6)
Unknown	0 0.022 (213)	1 0.018 (194)	100.0 (-3173.8, 100.0)
Subjects with negative RT-PCR pre-dose 1 and positive RT-PCR pre-dose 2			
Subjects with documented COVID-19 symptoms between dose 1 and 2	0 0.000 (0)	0 0.000 (1)	--
Subjects with no documented COVID-19 symptoms between dose 1 and 2	0 0.004 (44)	1 0.006 (52)	--
Pre-dose 1 serostatus[f]			

Positive	1 0.052 (488)	1 0.056 (525)	-8.0 (-8378.1, 98.6)
Negative	8 2.255 (17823)	167 2.260 (17894)	95.2 (90.3, 98.0)
Unknown	0 0.025 (248)	1 0.030 (289)	100.0 (-4527.0, 100.0)
1-month post-dose 2 (Visit 3) serostatus*	**No data shown**		
Positive			
Negative			
Subjects who seroconverted between dose 1 and 1-month post-dose 2**	**No data shown**		
Subjects with documented COVID-19 symptoms during time period			
Subjects with no documented COVID-19 symptoms during time period (protocol-defined vaccine efficacy against asymptomatic infection)			

Abbreviations: N-binding = SARS-CoV-2 nucleoprotein-binding; RT-PCR = reverse transcription–polymerase chain reaction; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; VE = vaccine efficacy; NP = nasopharyngeal; NE = Not estimable.

a. N = number of subjects in the specified group.

b. n1 = Number of subjects meeting the endpoint definition.

c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from 7 days after Dose 2 to the end of the surveillance period.

d. n2 = Number of subjects at risk for the endpoint.

e. Confidence interval (CI) for VE is derived based on the Clopper and Pearson method adjusted for surveillance time.

f. Based on N-binding test result.

Table 23. Vaccine Efficacy – First COVID-19 Occurrence From 7 Days After Dose 2, by Test Status – Subjects With or Without Evidence of Infection Prior to 7 Days After Dose 2 – All Available Efficacy Population

RT-PCR NP Swab Results and Serostatus: Time Points	**Vaccine Group** N[a]= 20488 Cases n1[b] surveillance time[c] (n2[d])	**Control Group** N[a]= 20459 Cases n1[b] surveillance time[c] (n2[d])	**Vaccine Efficacy % (95% CI[e])**
Pre-dose 1 SARS-CoV-2 RT-PCR (NP swab)			
Positive	0 0.014 (122)	0 0.015 (138)	NE (NE, NE)
Negative	9 2.358 (18740)	169 2.338 (18668)	94.7 (89.7, 97.6)
Unknown	0 0.018 (187)	3 0.016 (165)	100.0 (-125.3, 100.0)
Pre-dose 2 SARS-CoV-2 RT-PCR (NP swab)			
Positive	0 0.010 (86)	1 0.012 (107)	100.0 (-4739.5, 100.0)
Negative	9 2.357 (18743)	170 2.339 (18660)	94.7 (89.8, 97.6)
Unknown	0 0.022 (220)	1 0.019 (204)	100.0 (-3290.7, 100.0)
Subjects with negative RT-PCR pre-dose 1 and positive RT-PCR pre-dose 2			
Subjects with documented COVID-19 symptoms between dose 1 and 2	0 0.000 (0)	0 0.000 (1)	--
Subjects with no documented COVID-19 symptoms between dose 1 and 2	0 0.005 (47)	1 0.006 (53)	--
Pre-dose 1 serostatus[f]			
Positive	1 0.053 (500)	1 0.057 (537)	-7.5 (-8335.1, 98.6)
Negative	8 2.308 (18278)	170 2.283 (18144)	95.3 (90.6, 98.0)

Unknown	0 0.028 (271)	1 0.030 (290)	100.0 (-4081.4, 100.0)
1-month post-dose 2 (Visit 3) serostatus*	**No data shown**		
Positive			
Negative			
Subjects who seroconverted between dose 1 and 1-month post-dose 2**	**No data shown**		
Subjects with documented COVID-19 symptoms during time period			
Subjects with no documented COVID-19 symptoms during time period (protocol-defined vaccine efficacy against asymptomatic infection)			

Abbreviations: N-binding = SARS-CoV-2 nucleoprotein-binding; RT-PCR = reverse transcription–polymerase chain reaction; SARS-CoV-2 = severe acute respiratory syndrome coronavirus 2; VE = vaccine efficacy; NP = nasopharyngeal; NE = Not estimable.

a. N = number of subjects in the specified group.
b. n1 = Number of subjects meeting the endpoint definition.
c. Total surveillance time in 1000 person-years for the given endpoint across all subjects within each group at risk for the endpoint. Time period for COVID-19 case accrual is from 7 days after Dose 2 to the end of the surveillance period.
d. n2 = Number of subjects at risk for the endpoint.
e. Confidence interval (CI) for VE is derived based on the Clopper and Pearson method adjusted for surveillance time.
f. Based on N-binding test result.

Example 27: Pharmacokinetics (PK) and Absorption, Distribution, Metabolism, and Excretion (ADME) Analysis of Certain Lipid Excipients

The present Example describes various assessed characteristics (e.g., PK/ADME characteristics) of lipids used in a vaccine composition as described herein. Without wishing to be bound by any particular theory it is noted that such characteristics of lipid components may contribute to relevant features (e.g., distribution, expression, etc) of administered vaccines, including to efficacy generally and/or in particular

circumstances (e.g., when administered according to particular regimens and/or to particular populations, etc).

Absorption

A single dose PK study of ALC-0315 and ALC-0319 following intravenous (IV) bolus injection of a nanparticle formulation in rats was conducted to assess the PK and metabolism of lipid excipients ALC-0315 and ALC-0159. This study used LNPs containing surrogate luciferase RNA, with the lipid composition being identical to BNT162b2, to investigate the *in vivo* disposition of ALC-0159 and ALC-0315.

Concentrations of ALC-0159 dropped approximately 8000- and >250-fold in plasma and liver, respectively, during this 2-week study. For ALC-0315, the elimination of the molecule from plasma and liver was slower, but concentrations fell approximately 7000- and 4-fold in two weeks for plasma and liver, respectively. Overall, the apparent terminal t½ in plasma and liver were similar in both tissues and were 2-3 and 6-8 days for ALC-0159 and ALC-0315, respectively. The apparent terminal t½ in plasma likely represents the re-distribution of the respective lipids from the tissues into which they have distributed as the LNP, back to plasma where they are eliminated.

Metabolism

In vitro metabolism of ALC-0315 and ALC-0159 was evaluated in blood, liver microsomes, S9 fractions, and hepatocytes from mice, rats, monkeys, and humans. *In vivo* metabolism was examined in rat plasma, urine, faeces, and liver samples from the PK study. Metabolism of ALC-0315 and ALC-0159 appears to occur relatively slowly *in vitro* and *in vivo*. ALC-0315 and ALC-0159 are apparently metabolised by hydrolytic metabolism of the ester and amide functionalities, respectively, and this hydrolytic metabolism is observed across the species evaluated.

Excretion

Excretion studies appeared to demonstrate that 50% of ALC-0159 was eliminated unchanged in faeces, and that metabolism played a role in the elimination of ALC-0315, as little to no unchanged material was detected in either urine or faeces.

Investigations of urine, faeces and plasma from the rat PK study identified a series of ester cleavage products of ALC-0315. Without wishing to be bound by any particular theory, it is proposed that this likely represents the primary clearance mechanism acting on this molecule *in vivo*. *In vitro*, ALC-0159 was metabolized slowly by hydrolytic metabolism of the amide functionality.

Example 28: Distribution analysis of administered vaccine composition

In vivo biodistribution of COVID-19 mRNA Vaccine BNT162b2 was evaluated using mice as a model system and assessing luciferase expression as a surrogate reporter. Protein expression was demonstrated at the site of injection and to a lesser extent, and more transiently, in the liver after mice received an IM injection of RNA encoding luciferase in an LNP formulation like BNT162b2. Luciferase expression was identified at the injection site at 6 hours after injection and diminsihed to near near baseline levels by day 9. Expression in the liver was also present at 6 hours after injection and was not detected by 48 hours after injection. All other tissues than liver evaluated contain equal to or less than 1% of the dose.

Example 29: Repeat-dose toxicity study of various dosing regimens

A GLP-compliant repeat-dose study performed in rats to evaluate immunogenicity and toxicity of COVID-19 mRNA vaccines, including BNT162b2.

In certain studies, male and female Wistar Han rats were given a vaccine composition as described herein; compositions based on various RNA platforms (e.g., BNT162b2) were tested as IM injection(s) into the hind limb on three occasions each a week apart (dosing days 1, 8 and 15). Different doses (10, 30 and 100 µg) were tested; the lower doses were given as a single injection of 20-70 µl while the highest doses (100 µg) and controls were given as two injections (one in each hind limb) of 100 µl each. The

control was phosphate buffered saline/300 mM sucrose, corresponding to the storage buffer of the vaccine product. Each group had 18 male and 18 female rats, assigned as 10 to the main study, 5 for recovery groups and 3 as additional animals for cytokine analyses. The recovery period was 3 weeks after the last dose. Necropsy was performed on study day 17, ~48 hours after the last dose and after the 3-week recovery period.

No unscheduled deaths were observed.

Dosing was considered well tolerated and did not present any signs of systemic toxicity; there was a slight increase in body temperature in the hours after dosing and some loss in body weight over the same period but these were not of a magnitude to be considered adverse.

Local inflammatory reactions were observed at the intramuscular injection site. Injection site changes noted were oedema, erythema, and induration, more severe and more frequent after the second and/or third doses compared to the first; however, these resolved prior to subsequent dosing and were fully recovered at the end of the 3-week recovery period.

Macroscopic findings at the injection sites included induration or thickening, occasionally accompanied by encrustation, which was noted for nearly all rats. This correlated microscopically with inflammation and variable fibrosis, oedema, and myofibre degeneration. Inflammation at the injection site was accompanied by elevations in circulating white blood cells and acute phase proteins (fibrinogen, alpha-2 macroglobulin, and alpha-1 acid glycoprotein).

Inflammation was occasionally evident extending into tissues adjacent to the injection site. There was enlargement of the draining (iliac) lymph nodes evident at the end of dosing. This correlated with increased cellularity of germinal centres and increased plasma cells in the draining (iliac) lymph node and is an anticipated immune response to the administered vaccine.

Enlargement of spleen and increased spleen weights correlated microscopically to increased haematopoiesis and increased haematopoiesis was also evident in the bone

marrow. These findings are likely secondary to the immune/inflammatory responses to the vaccine.

At the end of the recovery period, injection sites were normal, clinical pathology findings and macroscopic observations had resolved and there was evidence of recovery of the injection site inflammation on microscopy.

Microscopic vacuolation of portal hepatocytes was present after the dosing phase. This observation was absent after the recovery period. There were no elevations in alanine aminotransferase (ALAT). There were elevations in gamma-glutamyltransferase (GGT) in all vaccinated rats, but there were no macroscopic or microscopic findings consistent with cholestasis or hepatobiliary injury to explain the increased gamma-GT activity which was completely resolved at the end of the 3-week recovery period. The vacuolation may be related to hepatic distribution of the pegylated lipids in the LNP. No changes were seen in serum cytokine concentrations.

There were no effects noted on ophthalmological and auditory assessments, nor on external appearance or behaviour; in particular, gait was normal meaning that the changes seen did not affect the rats' mobility. No vaccine-related changes were seen in serum cytokine concentrations.

Testing for immunogenicity showed that COVID-19 mRNA Vaccines (including, e.g., BNT162b2 such as BNT162b2 v8) elicited a specific IgG antibody response to SARS CoV-2 spike protein directed against the S1 fragment and the receptor binding domain. A neutralizing antibody response was also observed with the vaccine in a pseudovirus neutralization assay.

Results from ELISA assays are shown in Figures 117 and 118 (from day 17 or day 10 as noted in the figures), in which the very top traces are those for COVID-19 mRNA Vaccine BNT162b2 and other traces are those for other COVID-19 mRNA vaccines using different constructs as described herein: similar results were shown for day 38 (not shown here). These translated into neutralising activity as seen in the VSV/SARS-CoV2-S pseudovirus neutralisation test using Vero 76 cells (Figure 119): similar results were presented for day 38 (not shown here). Across the vaccines tested in this study

those with a higher antigen-specific antibody titre also had a more pronounced virus neutralisation effect.

COVID-19 mRNA vaccines (e.g., BNT162b2) were well tolerated, and produced inflammatory changes at the injection sites and the draining lymph nodes, increased haematopoiesis in the bone marrow and spleen, and clinical pathology changes consistent with an immune response or inflammation in the injection sites.

Those skilled in the art, reading the present disclosure, will appreciate that the findings in this Example can be considered typical of those expected with dosing of various mRNA constructs and/or lipid nanoparticles as described herein.

Example 30: Toxicity and immunogenicity study of three-dose regimen

A study was performed to assess toxicity in rats given COVID-19 mRNA Vaccine (e.g., BNT162b2). This study was in compliance with Good Laboratory Practice.

Male and female Wistar Han rats were given BNT162b2 as an IM injection into the hind limb on three occasions, each a week apart (dosing days 1, 8 and 15). Necropsy was performed on study day 17, ~48 hours after the last dose, and after the 3-week recovery period. COVID-19 mRNA Vaccine BNT162b2 was supplied at 0.5 mg/ml and the dose volume was 60 µl, to give 30 µg per dose. Control rats received saline.

Blood was taken at various points during the assessment, prior to and during dosing, and also during recovery, and antibody responses to vaccine components were assessed.

All rats given COVID-19 mRNA Vaccine (e.g., BNT162b2) survived to their scheduled necropsy: there were no changes noted in clinical signs or body weight changes noted. A reduction in food intake was noted on days 4 and 11 (to 0.83x controls) and there was an increase in mean body temperature post-dose on day 1 (up to 0.54°C), day 8 (up to 0.98°C), and day 15 (up to 1.03°C) compared to controls.

At injection sites, there were instances of oedema and erythema on days 1 (maximum of slight oedema and very slight erythema), 8 (maximum of moderate oedema and

very slight erythema) and 15 (maximum of moderate oedema and very slight erythema) which fully resolved and were not noted prior to dosing on days 8 and 15. Haematological tests showed higher white blood cells (up to 2.95x controls), primarily involving neutrophils (up to 6.80x controls), monocytes (up to 3.30x controls), and large unstained cells, LUC, (up to 13.2x controls) and slightly higher eosinophils and basophils on days 4 and 17. White blood cells were higher on day 17 as compared with day 4. There were transiently lower reticulocytes on day 4 (to 0.27x controls) in both sexes and higher reticulocytes on day 17 (up to 1.31x controls) in females only. Lower red blood cell mass parameters (to 0.90x controls) were present on days 4 and 17. There were lower A:G ratios (to 0.82x) on days 4 and 17. Higher fibrinogen was noted on day 17 (up to 2.49x) compared to controls, consistent with an acute phase response. The acute phase proteins alpha-1-acid glycoprotein (up to 39x on day 17) and alpha-2 macroglobulin (up to 71x on Day 17) were elevated on days 4 and 17 with higher concentrations in males. There were no changes urinalysis parameters.

At post-mortem there were higher absolute and relative spleen weights in vaccinated rats (up to 1.42x in males and to 1.62x in females). There were no other changes in organ weights. Macroscopic findings included enlarged draining lymph nodes and pale/dark firm injection sites in a minority of vaccinated rats. The dosing was tolerated without inducing any systemic toxicity with all changes consistent with an inflammatory response and immune activation: findings are consistent with those typically associated with dosing of lipid nanoparticle-encapsulated mRNA vaccines.

Example 31: Reproduction Toxicity

A study was performed to assess reproduction toxicity in female rats given COVID-19 mRNA vaccines, including BNT162b2. Female rats were given a COVID-19 mRNA vaccine (e.g., BNT162b2) twice before the start of mating and twice during gestation at a human clinical dose (e.g., 30 µg RNA/dosing day). The COVID-19 mRNA vaccine was administered intramuscularly (IM) to F0 female Wistar rats 21 and 14 days before the start of mating (M-21 and M-14, respectively) and then on Gestation Day

(GD) 9 and GD20, for a total of 4 doses. A subgroup was terminated at GD21 and another (litter) group was terminated at PostNatal Day (PND) 21. SARS-CoV-2 neutralizing antibody titers were found in the majority of females just prior to mating (M-14), in most females and foetuses at the end of gestation (GD21), and in most offspring at the end of lactation (PND21). There was transient reduced body weight gain and food consumption after each dose. No effects on the estrous cycle or fertility index were observed. While there was an increase (~2x) of pre-implantation loss (as compared to control), the pre-implantation loss percent observed in the vaccinated group was within historical control data range (5.1%-11.5%). Among foetuses (from a total of n=21 dams/litters), there was a very low incidence of gastroschisis, mouth/jaw malformations, right sided aortic arch, and/or cervical vertebrae abnormalities. Regarding skeletal findings, the exposed group had comparable to control group levels of presacral vertebral arches supernumerary lumbar ribs, supernumerary lumbar short ribs, caudal vertebrae number <5). There were no signs of adverse effects on the postnatal pups (terminated at PND21). This study shows that there is no significant adverse effects on fertility and early embryogenesis.

Example 32: Safety and immunogenicity of the SARS-COV-2 BNT162b1 mRNA vaccine in younger and older Chinese adults: a randomized, placebo-controlled, observer-blind phase I study

The present Example reports initial results from a phase I trial testing BNT162b1 in 144 healthy Chinese participants. BNT162b1 encodes the SARS-CoV-2 spike glycoprotein receptor-binding domain (RBD) and is one of several RNA-based SARS-CoV-2 vaccine candidates described herein.

The present Example specifically reports on the observed safety profile, in whichfever >39ºC was the only Grade 3 adverse event reported. Prime-boost vaccination with 10 µg or 30 µg BNT162b1 induced robust antibody and T-cell

responses in both young (18 to 59 years of age) and older (65 to 85) Chinese adults. Both dose levels induced seroconversion after 41 d: Geometric mean titres of SARS-CoV-2 serum-neutralizing antibodies in younger participants in the 10 µg and 30 µg dose groups were 1.9 and 2.1 times that of convalescent sera from recovered COVID-19 patients; and in older participants 0.7 and 1.3 times. Interferon-γ T cell responses to RBD antigen challenge were significantly higher in participants receiving BNT162b1 than those in placebo group.

Increased reactogenicity as well as a more favorable vaccine-elicited virus-neutralizing response were associated with the 30 µg dose of BNT162b1 in both younger and older Chinese adults.

The safety and immunogenicity data provided in the present Example for BNT162b1, specifically with respect to vaccination of healthy, young and elderly Chinese participants, suggests that prime-boost vaccination with 10 µg and 30 µg dose levels of the BNT162b1 vaccine induces a strong humoral and cellular immunogenic response in both younger adults of 18 to 55 years of age and older adults of 65 to 85 years of age, with robust RBD-specific antibody and T-cell responses seen in in both younger and older participants, at least within 28 days following the prime-boost vaccination. Certain findings in this study further confirm aspects of the tolerability profile for BNT162b1, for example as also observed in American and German populations.

Methods

A randomized, placebo-controlled, observer-blind phase 1 trial was conducted in 144 healthy young adults, 18 to 59 years of age, and older adults 65 to 85 years of age in Taizhou, Jiangsu Province, China. Eligible participants were randomized to receive two doses, administered 21 days apart, of either BNT162b1 at a dose of 10 µg or 30 µg or placebo, administered as an intramuscular injection. Study participants, investigators, and laboratory staff were blinded to treatment administration. The primary safety endpoints were local reactions at injection site or systemic adverse reactions within 14 days after vaccination, and adverse events occurring up to 28 days after receiving

the boost vaccination. The immunogenic endpoints of virus-neutralizing antibody, and antigen-specific binding antibodies and cellular immune responses elicited by vaccine were measured at predefined timepoints.

Results

Study design and analysis set

A total of 296 adults aged between 18-55 years or 65-85 years were screened at Taizhou vaccine clinical research center in Jiangsu Province, in China. 144 eligible participants consented to participate in the trial and were randomized 1:1:1 to receive prime and boost doses of BNT162b1 at 10 μg or 30 μg, or two placebo doses 21 days apart. Following priming doses, two participants between the ages of 65 and 85 years had withdrawn from boost dose administration (one at 10 μg, one at 30 μg). The demographic characteristics of the participants are shown in Table 24. The mean age among the younger participants ranged from 37.9 to 42.0 years, and the mean age among the older participants ranged from 68.5 to 70.7 years in the treatment groups, with equal gender distribution across treatment groups. The medical history or existing underlying disorders of the participants were similar across treatment groups, with the exception of hypertension, which was noted in older participants at baseline.

Observed safety and tolerability data

Within 14 days after completion of dosing, 21 (88%) of the younger participants in the 10 μg BNT162b1 dose group and 24 (100%) of the younger participants in the 30 μg BNT162b1 dose group reported at least one solicited adverse reaction, versus 17% of the younger participants in the placebo group (Tables 25A-25B). Reactogenicity was dose level dependent and most evident in the 30 μg BNT162b1 dose group. The most common solicited adverse reactions reported were injection site pain, fever, headache, fatigue, malaise, joint pain, muscle pain chills. The adverse events were transient and either managed with simple standard of care management, or resolved spontaneously. Most of the reported adverse reactions were mild or moderate in severity, and resolved within the first seven days after each BNT162b1 dose. No injection site reactions were graded as severe (grade 3). All of the grade 3 systemic

adverse reactions associated with the vaccination were fever, predominantly observed in the younger participants . One male participant in the older age group experienced an episodic Grade 3 fever accompanied by pain and pruritus at the injection site after administration of the prime BNT162b1 dose at 30 µg, and electively withdrew from boost vaccination administration.

No pre-specified trial-halting rules were met during the study. Only one serious adverse event was reported by a participant of 67 years of age (a humerus fracture caused by a car accident, preventing the participant from receiving the boost dose) which was considered as not related to the vaccine or study procedure. The overall frequencies of injection site adverse reactions post-vaccination were comparable after the BNT162b1 prime and boost doses. Some systematic adverse reactions such as fever, headache, fatigue, and malaise occurred more commonly after the BNT162b1 boost dose than after the prime dose in younger adults . In contrast to the younger participants, elderly participants did not present with increased reactogenicity after the BNT162b1 boost dose.

There were no changes reported in blood pressure and respiratory rates among the participants across different treatment groups before and after BNT162b1 administration. Transient increases of temperature and pulse rate 24 hours post-vaccination were noted in both younger and older participants, especially in the 30 µg dose group. The most common abnormalities in laboratory values from baseline were transient decreases in lymphocyte and platelet counts and increases in C-reaction protein. All laboratory abnormalities were self-limited and resolved in a short period of time without clinical manifestations . These data are consistent with certain findings reported in other populations (e.g., as described elsewhere herein).

Vaccine-induced antibody responses

All participants were seronegative at baseline (day 1, pre-vaccination), and were monitored for seroconversion at days 8, 22, 29 and 43 by analyses of SARS-CoV-2 neutralizing antibodies and RBD and S1 protein binding antibodies. The BNT162b1 induced antibody responses in vaccinated participants were compared with a panel of

human COVID-19 convalescent serum obtained at least 14 days after PCR-confirmed diagnosis from 28 COVID-19 patients. The highest neutralization titers were observed on day 43 (i.e., 21 days after the BNT162b1 boost dose), indicating a continuous uptrend in this group of Asian participants after day 29, which seems to further increase in this Asian population at day 43 among older participants as compared with reports in other populations, showing peak titres occurring earlier and subsequently subsiding in this subject population. On day 43, both 10 µg and 30 µg BNT162b1 dose levels induced significant virus-neutralizing antibody responses after the BNT162b1 prime dose which was boosted by the second BNT162b1 dose, with geometric mean titers (GMTs) of 232.9 (95% CI 151.3 to 358.5) and 254.0 (184.6 to 349.4) in the younger participants, and 80.0 (49.2 to 130.2) and 160.0 (96.7 to 264.6) in the older participants in the 10 µg and 30 µg dose groups, respectively (Figure 120). The virus-neutralizing responses of younger participants in the 10 µg and 30 µg dose groups were 1.9 and 2.1 times the GMT of a panel of the convalescent sera (GMT, 119.9; 95% CI, 70.4 to 203.9). In the older participants, the corresponding ratios were 0.7 and 1.3 times in the 10 µg and 30 µg dose groups, respectively. All the younger recipients showed positive seroconversion on Day 43, and the seroconversion rate was 91% at the 10 µg dose and 96% at the 30 µg dose in the older recipients on Day 43, respectively . Participants who received the 30 µg dose appeared to have somewhat higher virus-neutralizing antibody responses than those received the 10 µg dose. However, the older participants between the ages of 65 and 85 generally showed a slower virus-neutralizing response and lower peak response than the younger participants between the ages 18 and 55.

Similarly, both doses of BNT162b1 induced high levels of S1- and RBD-binding IgG in the participants after the prime-boost regimen. The S1- and RBD-binding IgG levels after vaccination across all timepoints in the vaccine recipients were highly correlated with the neutralizing titers regardless of the age and dose groups, with a correlation coefficient of 0.85, and 0.79 ($p<0{\cdot}0001$), respectively .

Vaccine-induced T-cell responses

Vaccine-induced CD8+ T cell responses in individuals immunized with BNT162b1 were characterized before the priming vaccination (day 1), on day 29 (7 days after the boost vaccination) and on day 43 (21 days after the boost vaccination), using a direct *ex vivo* IFNγ enzyme-linked immunosorbent spot (ELISpot) assay with peripheral blood mononuclear cells (PBMCs). At day 29, specific IFN-γ ELISpot responses against the Sp1 peptide pool (covering RBD) were significantly higher in participants receiving BNT162b1 than those in placebo group (Figure 121). Younger participants aged 18 to 55 years had average spot-forming cells of 227.5 (95%CI, 146.5 to 308.5) in those who had received 10 µg vaccinations, and 223.5 (181.2 to 265.9) in those who had received the 30 µg vaccinations per 10^5 PBMCs. In older participants aged 65 to 85 years, a slightly lower spot-forming cells with averages of 156.5 (84.1 to 229.0) and 171.9 (113.4 to 230.3) were noted post-vaccination across the two dose groups. At day 43, younger participants receiving the prime-boost BNT162b1 regimen tended to show a mild decrease in their S1-specific IFN-γ ELISpot response compared to that seen on day 29; no blood samples were collected at this time point from the older participants, as so this data is not available. No differences between the BNT162b1 and the placebo groups were observed for IFN-γ ELISpot responses to the Sp2 peptide pool (which does not include peptides of the RBD encoded by BNT162b1) and minor non-specific responses to CD8+ T cells were observed in both dose groups.

Discussion

The trial described in this Example was conducted in China in parallel with other BNT162 vaccine candidates in multiple regions[14]. One focus of the study was to establish data with respect to safety and immunogenicity of mRNA vaccines in Asian populations. This Example reports a first evaluation of both the safety and immunogenicity profiles of such an mRNA vaccine in a Chinese population, and furthermore of younger and older Chinese populations.

This is a preliminary report for the clinical trial of the modified-RNA-based SARS-CoV-2 vaccine candidate BNT162b1, which encodes the SARS-CoV-2 RBD, administrated to

a healthy adult Chinese population. BNT162b1, like BNT162b2 (modRNA encoding the S protein derived from the same nucleoside-modified platform) induces strong vaccine-induced antibody responses and strong T cell responses. Clinical safety and immunogenicity for both BNT162b1 and BNT162b2 candidates have been evaluated in healthy adults in both German (younger adults; BNT162-01) and American (younger adults and elderly adults aged 65 to 85 years; BNT162-02) populations. In younger adult groups, severe local reactogenicity AEs within 7 days were fewer in American study (BNT162-02) and the present study (BNT162-03) as compared with the German study (BNT162-01). Systemic reactogenicity AEs within 7 days were broadly similar across studies. Systemic AEs (independent of relatedness) within 28 days post Dose 2 were slightly higher in the BNT162-02 and BNT162-03 studies, as compared to the BNT162-01 study.

In older adult groups, severe local reactogenicity AEs within 7 days were similar across studies. Systemic reactogenicity AEs within 7 days were slightly lower in the BNT162-03 study, as compared to the BNT162-01 and the BNT162-02 studies. Systemic AEs (independent of relatedness) within 28 days post Dose 2 were slightly higher in the BNT162-03 study as compared to the BNT162-02 study, however the severe AEs were lower. In summary, comparative analyses of the BNT162b1 safety profile between the BNT162-01, BNT162-02 and BNT162-03 studies at 30µg showed a generally comparable profile, and in the systemic reactogenicity /older population even a better safety profile in the Asian population vs non-Asian. Thus, findings reported here further complements and expands reporting of BNT162b1 and other RNA-based vaccine candidates from clinical trials conducted in Germany and the United States[7,8,15].

The rationale for this study was to evaluate whether intrinsic and extrinsic differences between German and Chinese population have any impact on tolerability or immune responses to this novel type of vaccine. The safety profile of the vaccine candidate BNT162b1 in healthy Chinese adults observed in our study appear to be better than that reported in other populations, in term of severe reactogenicity by local and

systemic reactions[7,15]. Body habitus, endogenous antibody repertoire may have an influence. The reactogenicity of BNT162b1 was dose-dependent. Increased frequencies of adverse events were observed after administration of the boost vaccination compared with those after the prime vaccination, especially in the younger participants. Older adults had lower incidences of adverse reactions than the younger participants. Grade 3 fever was reported by 17% of the younger participants and 8% of the older participants receiving 30 µg dose, respectively. Nearly all severe fever reactions were transient and self-limiting. One participant had withdrawn from the boost vaccination due to the reactions after the prime dose administration, having episodic fever or cold intolerance with or without temperature record accompanied by the injection site pain, itching and pruritus, which lasted over two weeks and resolved after taking Hydrocortisone Butyrate ointment. Transient decreases in lymphocyte counts as pharmacodynamic markers were predominantly observed in the younger recipients at 30 µg dose level of BNT162b1, which was associated with the redistribution of lymphocytes into lymphoid tissues by innate immune stimulation[16].

Both doses of the vaccine candidate BNT162b1 were effective at eliciting specific humoral and cellular immune responses, with a clear boost effect of the second vaccination on antibody titers found in both younger and older adults. BNT162b1 administered at a 30 µg dose following a prime-boost regimen induced an optimal level of immune responses in terms of virus-neutralizing antibody to SARS-CoV-2, which was higher than those in a panel of human convalescent serum samples, regardless of age. The humoral response in the Chinese participants showed a unique temporal pattern and peaked at day 43 in both age groups. Although the number of participants was small, and methodological differences in measurements that may occur can influence observed results, the findings reported here suggest that there may be a populational difference in response to the vaccine.

Since the vaccine candidate BNT162b1 is a modified RNA vaccine encoding a trimeric version of the RBD, the vaccine recipients in the study reported in the present Example

demonstrated significant T-cell responses specific to S1 peptide pool (containing 166 15-mer S1 peptides of from the human SARS-CoV-2 virus), but not to the S2 peptide pool. The results indicated the cellular responses elicited by BNT162b1 was antigen specific. By contrast, the vaccine candidate BNT162b2 spectrum was different from other RNA-based SARS-CoV-2 vaccine, inducing T-cell responses could recognize both S1 and S2 peptide pools[15]. Nevertheless, data showed BNT162b1 at the 30 μg dose was highly immunogenic capable of eliciting strong humoral and cell-mediated responses in healthy Chinese adults.

Those skilled in the art appreciate that small sample size and age restriction of 18 years and older may limit the conclusive rigor of findings observed in the present Example. Regardless, given that prophylactic RNA vaccines as described herein represent a novel approach to vaccination, safety assessments, including in particular populations (e.g., in children and adolescent populations) are particularly valuable. Also, although comparison of serum neutralizing responses elicited by the vaccine candidates described herein with that in human convalescent serum panels provides meaningful assessment of the vaccines, the level of serological immunity needed to protect against COVID-19 has not yet been rigorously established[17]. Those skilled in the art also recognize that the human convalescent serum panels that have been used in different trials are not standardized among laboratories, and thus may have a different distribution of patient characteristics and timepoints of collection, so that direct comparison of results (e.g., characterizing different vaccine candidates and/or characterizing vaccine candidates relative to different convalescent serum) may not be informative.

In summary, results described in the present Example confirmed the dose-dependency safety and good immunogenicity profile of the RNA-based SARS-CoV-2 vaccine candidate BNT162b1 and further expand the previous findings for BNT162b1 in the Germany and the United States trials[7,8,15]. Increased reactogenicity as well as a more favorable vaccine-elicited virus-neutralizing response were found associated with the 30 μg of the BNT162b1 in both younger and older adults. In contrast, another

vaccine candidate BNT162b2 manufactured from same platform, showed a more favorable safety profile[8]. BNT162b1 encodes a relatively small RBD immunogen, which might induce a narrower spectrum of neutralizing antibodies that are less robust to potential antigenic drift of SARS-CoV-2, compared with BNT162b2, which encodes a full-length spike immunogen[18]. It is worth noting that the candidate BNT162b2 has been found to be more than 95% effective in preventing COVID-19 in participants, with no decreasing efficacy in those over 65 years of age[19].

Methods

Study design and participants

This randomized, placebo-controlled, observer-blind phase I trial was performed in healthy young adults between 18 and 59 years old, and older adults between 65 and 85 years of age, in Taizhou, Jiangsu Province, China. Participants were in overall good health established by medical history, physical examination, and laboratory tests at the screening visit. Both males and females were included and agreed to use contraception during the trial. We excluded participants that were pregnant or breast-feeding. Participants that tested positive for SARS-CoV-2 via a commercial rapid diagnostic kit for IgM/IgG antibody to SARS-CoV-2 (manufactured by Livzon diagnostics inc., Zhuhai, China), or via testing with a pharyngeal swab nucleic acid diagnostic test (manufactured by Fosun pharma, Shanghai, China) were excluded. Imaging features of COVID-19 present in a chest CT scan was a further exclusion criteria. Participants with serious cardiovascular disease or chronic conditions such as uncontrolled diabetes and hypertension, human immunodeficiency virus, hepatitis B and hepatitis C were excluded. Written informed consent was obtained from each participant before the start of the study.

The study was conducted in accordance with the Declaration of Helsinki and Good Clinical Practice. The trial protocol was reviewed and approved by the National Medical Products Administration, China, and the institutional review board of the Jiangsu Provincial Center of Disease Control and Prevention.

Randomization and blinding

Eligible participants between 18 and 55 years of age were enrolled in the younger age group, and older participants aged greater than or equal to 65 years and less than or equal to 85 years were enrolled in the older age group. Participants were randomized in a ratio of 1:1:1 to receive the low-dose BNT126b1 or high-dose BNT126b1 or placebo. Participants were stratified by gender, using a Web-based interactive response technology (IRT) system. The blocked randomization list was generated by an independent statistician using SAS software (version 9.4).

Authorized unblinded pharmacists prepared the vaccines or placebo according to the allocation of participants through the IRT system, and nurses administrated the investigational products to participants. The unblinded staff had no further involvement in the trial, and were forbidden to disclosure allocation information to others. All other investigators, participants, laboratory staff and the sponsor remained blinded throughout the trial.

Vaccine and vaccination

BNT162b1 as administered consisted of a Good Manufacturing Practice (GMP)-grade mRNA drug substance encoding the trimerized SARS-CoV-2 spike glycoprotein RBD antigen, formulated with lipids to obtain the RNA–LNP drug product. Vaccine was transported and supplied as a buffered-liquid solution for intramuscular injection, and stored at -80 °C, e.g., as described herein.

The low-dose and high-dose BNT126b1 contained 10 µg and 30 µg active ingredient, respectively, and the placebo was a commercial saline solution. Each participant received a prime-boost dosing regimen of vaccine candidate BNT162b1 at either 10 µg/0.5 ml or at 30 µg/0.5 ml or placebo of 0.5 ml administered into the deltoid, 21 days apart.

Monitoring of safety and immunogenicity

Each participant was asked to remain at the study site for at least six hours post vaccine administration to donate blood samples prior to and 24 hours post prime vaccination and again prior to and 8 days post boost vaccination for laboratory testing.

Vital signs including temperature, blood pressure, pulse, and respiratory rate were measured at baseline, and one hour, three hours and six hours post-vaccination. Any adverse events following the vaccination were documented by participants using diaries until day 28 post-administration of the boost dose. Younger group participants were enrolled and received the vaccination first. Enrollment of the older age group was launched following evaluation of the preliminary safety data of the younger age group for the first 14 days post-prime vaccination. Severity of adverse events and laboratory abnormal changes are graded with both the scale issued by the China State Food and Drug Administration[20] and the U.S. Food and Drug Administration (FDA)[21]. Serum and PBMCs were collected before the vaccination, at day 8 and/or day 22 after the boost dose, to facilitate measurement of specific IgG antibody responses to RBD and spike glycoprotein S1, neutralizing antibody to SARS-CoV-2, and T-cell responses. All reported adverse events were reviewed by investigators. Adverse events were categorized as either possibly, probably, or definitely related to the vaccine candidate.

Human convalescent sera

The neutralizing titer is the reciprocal of the highest sample dilution that protects at least 50% of cells from cytopathic effects. A panel of 24 convalescent human serum samples were obtained from donors 18 to 70 years of age (mean age, 45.8 years) who had recovered from SARS-CoV-2 infection; samples were obtained at least 14 days after a polymerase chain reaction-confirmed diagnosis and after symptom resolution. The disease severities of these patients varied from non-symptomatic (n=3, 13%), mild (n=8, 33%), moderate (n=10, 42%), or severe (n=3, 13%).

Neutralizing geometric mean titers (GMTs) in subgroups of the donors were as follows: 40 for the 3 donors with non-symptomatic infections; 91.9 for the 8 donors with mild infection; 160 for those with moderate infection; and 226.3 in the 3 donors with severe infection. Each serum sample in the panel was from a different donor. Thus, most of the serum samples were obtained from persons with moderate Covid-19. The convalescent serum samples were tested side by side as comparators with the serum samples obtained from participants in this trial.

ELISA

We assessed binding antibody responses against the SARS-CoV-2 RBD and S1 by using the enzyme-linked immunosorbent assay (ELISA).

Microneutralization assay

We detected the SARS-CoV-2 specific neutralizing antibody in serum by microneutralization assay based on cytopathy observed in a biosafety level 3 laboratory (BSL-3) with SARS-CoV-2 virus strain BetaCoV/JS02/human/2020 (EPI_ISL_411952).

ELISpot

Specific T-cell responses against the peptides were assessed by using a commercial ex-vivo interferon-γ (INF-γ) enzyme-linked Immunospot (ELISpot) kit manufactured by Mabtech (Nacka Strand, Stockholm, Sweden)[22]. PBMCs were isolated from fresh blood samples, and stimulated with different overlapping peptide pools before the measurement. The S1 peptide pool, which covers the N-terminal half of SARS-CoV-2 spike, including the RBD, and the S2 peptide pool, which covers the C-terminal of SARS-CoV-2 spike, which does not include the RBD were used in this study[23]. A peptide pool consisting of 32 MHC class I restricted viral peptides from human Cytomegalovirus, Epstein-Barr virus and Influenza virus (CEF peptide pool), was used to stimulate CD8+ T cells to assess general T-cell reactivity (not specific to SARS-CoV-2[24].)

Outcomes

The primary and secondary objectives of this trial were to evaluate safety and immunogenicity of the candidate vaccine BNT162b1 in healthy Chinese adults. The primary endpoints for safety evaluation were the incidence of solicited local reactions at the injection site or systemic adverse reactions within 14 days post vaccination, and adverse events following the immunization until 28 days after receiving the boost dose. Any clinical laboratory abnormalities from baseline to 24 hours or 7 days after vaccination, and any serious adverse event (SAE) that occurred were also recorded.

The secondary endpoints for immunogenicity were geometric mean titer (GMT), seroconversion rates, and fold increase of virus-neutralizing antibody, and ELISA IgG antibodies binding to S1 or RBD measured at days 8, 22 after each vaccination. Seroconversion is defined as an increase by a factor of four or more in antibody titer over the baseline, or the lower limit value if the baseline titer is below the limit of detection. The serum dilution for ELISA started at 1:100, while that for microneutralization assay started at 1:10.

Cellular immune responses in terms of the number of positive cells with interferon gamma (IFN-γ) secretion among PBMCs at a concentration of 1×10^5/well at day 8 and 22 after the boost dose were explored as an exploratory endpoint.

Statistical analysis

The total sample size in this study was 144 participants, 24 participants of each age group was included in each treatment group. Based on an assumption of 8% of the adverse reaction occurrence post-vaccination, the probability of observation of at least one event in 24 participants in each dose group was 86.5%.

All randomized participants who received at least one dose of the investigational vaccine were included in the safety analysis. Safety endpoints were described as frequencies (%) with 95% confidence interval (CI) of the adverse reactions or events during the observation period. We compared the proportions of the participants with adverse reactions or events across the groups using Chi-square or Fisher exact. All participants who received at least one vaccination and had results of serologic measurements before or after vaccination were included in the immunogenicity analysis. The immunological endpoints were descriptively summarized at the specified time points, and compared across the groups, using ANOVA for log-transformed antibody titres, or Wilcoxon rank-sum test for non-normal data. The neutralising antibody responses of the participants in each dose group were compared with those of patients who had PCR-confirmed SARS-CoV-2 infection. Any serologic values below the lower limit of detection were set to half of the value (1:50 for ELISA and 1:5 for microneutralization assay), while the values above the highest dilution titer were

assigned values of the highest dilution for calculation. Pearson correlation analysis of the RBD or S1 specific ELISA antibody and neutralising antibody was performed to assess the relationship between responses on different assays.

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Table 24. Baseline characteristics of the participants, by age groups.

	Younger participants aged 18-55 years				Older participants aged 65-85 years		
Characteristic	**10 µg**	**30 µg**	**Placebo**		**10 µg**	**30 µg**	**Placebo**
No. of participants	24	24	24		24	24	24
Age, mean (SD), years	37.9 (9.6)	39.7 (9.0)	42.0 (8.7)		70.5 (5.0)	68.5 (3.0)	70.7 (4.4)
Sex (female)	12 (50%)	12 (50%)	12 (50%)		12 (50%)	12 (50%)	12 (50%)
Body-mass index, kg/m²	24.7 (3.2)	23.0 (2.7)	24.3 (3.4)		24.0 (3.0)	24.8 (2.9)	23.5 (2.5)
Medical history or existing disorder							
Cardiac ischemia	2 (8%)	2 (8%)	2 (8%)		0	0	0
Sinus bradycardia	0	2 (8%)	1 (4%)		0	0	0
Hyperuricemia	3 (13%)	1 (4%)	1 (4%)		3 (13%)	2 (8%)	2 (8%)
Nasopharyngitis	2 (8%)	0	0		0	0	0
Blood uric acid increased	2 (8%)	1 (4%)	1 (4%)		0	0	0
Hypertension	3 (13%)	0	1 (4%)		12 (50%)	9 (38%)	7 (29%)
Diabetes	0	0	0		1 (4%)	2 (8%)	1 (4%)
Gastric inflammation	0	0	0		0	0	2 (8%)
Others*	3 (13%)	5(21%)	1 (4%)		3 (13%)	3 (13%)	4 (17%)

Data are mean (SD) or n (%). *"Others" includes tonsillitis, helicobacter infection, human papilloma virus infection, periodontitis, electrocardiogram high voltage, lymphadenopathy, anemia, hepatic cyst, oropharyngeal discomfort, hyperthyroidism, noninfective gingivitis, hyperlipaemia, benign prostatic hyperplasia, prostatitis, blindness unilateral, cerebral infarct, limb injury, deformity of spine, calculus urinary and lymphadenopathy.

Table 25A Solicited adverse reactions within 14 days post-vaccination, and unsolicited adverse reactions till day 43, by age groups.

	Younger participants aged 18-55 years					Older participants aged 65-85 years			
Adverse reactions	**10 µg (n=24)**	**30 µg (n=24)**	**Placebo (n=24)**	**P value**		**10 µg (n=24)**	**30 µg (n=24)**	**Placebo (n=24)**	**P value**
Solicited adverse reactions within 14 days									
Any	21 (88%)	24 (100%)	4 (17%)	<0.0001		21 (88%)	23 (96%)	2 (8%)	<0.0001
Grade 3	3 (13%)	9 (38%)	0	0.0015		0	2 (8%)	0	0.3239
Injection-site adverse reactions									
Any	21 (88%)	24 (100%)	2 (8%)	<0.0001		18 (75%)	21 (88%)	0	<0.0001
Grade 3	0	0	0	-		0	0	0	-
Pain	21 (88%)	23 (96%)	2 (8%)	<0.0001		16 (67%)	21 (88%)	0	<0.0001
Redness	6 (25%)	8 (33%)	0	0.0059		3 (13%)	4 (17%)	0	0.1492
Swelling	5 (21%)	7 (29%)	0	0.0137		0	5 (21%)	0	0.0091
Induration	0	3 (13%)	0	0.1018		0	1 (4%)	0	1.0000
Systemic adverse reactions									
Any	17 (71%)	22 (92%)	3 (13%)	<0.0001		9 (38%)	19 (79%)	2 (8%)	<0.0001
Grade 3	3 (13%)	9 (38%)	0	0.0015		0	2 (8%)	0	0.3239
Fever*	14 (58%)	21 (88%)	1 (4%)	<0.0001		7 (29%)	19 (79%)	1 (4%)	<0.0001
Grade 3	3 (13%)	9 (38%)	0	0.0015		0	2 (8%)	0	0.3239
Headache	11 (46%)	19 (79%)	3 (13%)	<0.0001		1 (4%)	2 (8%)	0	0.7682
Fatigue	12 (50%)	16 (67%)	0	<0.0001		3 (13%)	8 (33%)	0	0.0045

Malaise	8 (33%)	9 (38%)	0	0.0013		2 (8%)	4 (17%)	1 (4%)	0.4858
Joint pain	4 (17%)	10 (42%)	1 (4%)	0.0067		0	1 (4%)	0	1.0000
Muscle pain	2 (8%)	10 (42%)	0	<0.0001		0	1 (4%)	0	1.0000
Chills	4 (17%)	7 (29%)	0	0.0118		1 (4%)	4 (17%)	0	0.1185
Nausea	3 (13%)	3 (13%)	0	0.2330		0	0	0	-
Anorexia	1 (4%)	4 (17%)	0	0.1185		0	3 (13%)	1 (4%)	0.3143
Diarrhea	2 (8%)	1 (4%)	1 (4%)	1.0000		0	0	0	1.0000
Vomiting	0	2 (8%)	0	0.3239		0	0	0	-

Table 25B (modified) Solicited adverse reactions within 14 days post-vaccination, and unsolicited adverse reactions until day 43, by age groups including "placebo-corrected" AE rates.

	Younger participants aged 18-55 years						Older participants aged 65-85 years					
Adverse reactions	10 µg (n=24)	10 µg (minus placebo-AEs)	30 µg (n=24)	30 µg (minus placebo-AEs)	Placebo (n=24)	P value	10 µg (n=24)	10 µg (minus placebo-AEs)	30 µg (n=24)	30 µg (minus placebo-AEs)	Placebo (n=24)	P value
Solicited adverse reactions within 14 days												
Any	21 (88%)	17 (71%)	24 (100%)	20 (83%)	4 (17%)	<0.0001	21 (88%)	19 (79%)	23 (96%)	21 (88%)	2 (8%)	<0.0001
Grade 3	3 (13%)	3 (13%)	9 (38%)	9 (38%)	0	0.0015	0	0	2 (8%)	2 (8%)	0	0.3239
Injection site adverse reactions												
Any	21 (88%)	19 (79%)	24 (100%)	22 (92%)	2 (8%)	<0.0001	18 (75%)	18 (75%)	21 (88%)	21 (88%)	0	<0.0001
Grade 3	0	0	0	0	0	-	0	0	0	0	0	-
Pain	21 (88%)	19 (79%)	23 (96%)	21 (88%)	2 (8%)	<0.0001	16 (67%)	16 (67%)	21 (88%)	21 (88%)	0	<0.0001
Redness	6 (25%)	6 (25%)	8 (33%)	8 (33%)	0	0.0059	3 (13%)	3 (13%)	4 (17%)	4 (17%)	0	0.1492

Swelling	5 (21%)	5 (21%)	7 (29%)	7 (29%)	0	0.0137	0	0	5 (21%)	5 (21%)	0	0.0091
Induration	0	0	3 (13%)	3 (13%)	0	0.1018	0	0	1 (4%)	1 (4%)	0	1.0000
Systemic adverse reactions												
Any	17 (71%)	14 (58%)	22 (92%)	19 (79%)	3 (13%)	<0.0001	9 (38%)	7 (29%)	19 (79%)	17 (71%)	2 (8%)	<0.0001
Grade 3	1 (4%)	1 (4%)	4 (17%)	4 (17%)	0	0.0015	0	0	2 (8%)	2 (8%)	0	0.3239
Fever*	14 (58%)	13 (54%)	21 (88%)	20 (83%)	1 (4%)	<0.0001	7 (29%)	6 (25%)	19 (79%)	18 (75%)	1 (4%)	<0.0001
Grade 3	1 (4%)	1 (4%)	4 (17%)	4 (17%)	0	0.0015	0	0	2 (8%)	2 (8%)	0	0.3239
Grade 3 by NMPA criteria	3 (13%)	3 (13%)	9 (38%)	9 (38%)	0	0.0015	0	0	2 (8%)	2 (8%)	0	0.3239
Headache	11 (46%)	8 (33%)	19 (79%)	16 (67%)	3 (13%)	<0.0001	1 (4%)	1 (4%)	2 (8%)	2 (8%)	0	0.7682
Fatigue	12 (50%)	12 (50%)	16 (67%)	16 (67%)	0	<0.0001	3 (13%)	3 (13%)	8 (33%)	8 (33%)	0	0.0045

Malaise	8 (33%)	8 (33%)	9 (38%)	9 (38%)	0	0.0013		2 (8%)	1 (4%)	4 (17%)	3 (13%)	1 (4%)	0.4858
Joint pain	4 (17%)	3 (13%)	10 (42%)	9 (38%)	1 (4%)	0.0067		0	0	1 (4%)	1 (4%)	0	1.0000
Muscle pain	2 (8%)	2 (8%)	10 (42%)	10 (42%)	0	<0.0001		0	0	1 (4%)	1 (4%)	0	1.0000
Chills	4 (17%)	4 (17%)	7 (29%)	7 (29%)	0	0.0118		1 (4%)	1 (4%)	4 (17%)	4 (17%)	0	0.1185
Nausea	3 (13%)	3 (13%)	3 (13%)	3 (13%)	0	0.2330		0	0	0	0	0	-
Anorexia	1 (4%)	1 (4%)	4 (17%)	4 (17%)	0	0.1185		0	-1	3 (13%)	2 (8%)	1 (4%)	0.3143
Diarrhea	2 (8%)	1 (4%)	1 (4%)	0	1 (4%)	1.0000		0	0	0	0	0	1.0000
Vomiting	0	0	2 (8%)	2 (8%)	0	0.3239		0	0	0	0	0	-
Unsolicited adverse reactions within 28 days													
Any	9 (38%)	8 (33%)	10 (42%)	9 (38%)	1 (4%)	0.0046		4(17%)	2 (8%)	9 (38%)	7 (29%)	2(8%)	0.0590
Fever†	0	0	0	0	0	-		0	0	1 (4%)	1 (4%)	0	1.0000
Temperature intolerance	2(8%)	2 (8%)	6(25%)	6 (25%)	0	0.0230		0	0	4(17%)	4 (17%)	0	-

Injection site discomfort	3(13%)	3 (13%)	4(17%)	4 (17%)	0	0.1492		2(8%)	2 (8%)	3(13%)	3 (13%)	0	0.3580
Injection site pruritus	2(8%)	2 (8%)	3(13%)	3 (13%)	0	0.3580		0	0	1 (4%)	1 (4%)	0	1.0000
Pain not at injection site	1(4%)	1 (4%)	1(4%)	1 (4%)	0	1.0000		0	0	0	0	0	-
Dizziness	3(13%)	3 (13%)	1(4%)	1 (4%)	0	0.3142		0	0	3(13%)	3 (13%)	0	0.1018
Blood uric acid increased	1(4%)	1 (4%)	1(4%)	1 (4%)	0	1.0000		2(8%)	0	1(4%)	-1	2(8%)	1.0000

Data are shown as number of participants with event (%). Grade 3 was severe reaction (i.e., prevented activity). SAEs= Serious adverse events. A participant was only counted once in the specific reaction category, also with more than one episode of the adverse reaction. Only unsolicited adverse reactions reported by two or more participants were listed. * Those febrile participants were graded according to the guidelines of Food and Drug Administration (FDA), the United States. Fever was also graded according to the grading guidelines for adverse events in vaccine clinical trials, issued by the National Medical Products Administration (NMPA), China, which defines grade 3 fever as axillary temperature ≥38.5℃. †One participant experienced grade 3 fever accompanied with pain, itching and pruritus at the injection site after the prime dose, and electively withdrew from the boost vaccination.

Example 33: Neutralization of SARS-CoV-2 lineage B.1.1.7 pseudovirus by BNT162b2 vaccine-elicited sera

In September 2020, the SARS-CoV-2 variant B.1.1.7 was detected in the United Kingdom, and it subsequently increased in prevalence, showed enhanced transmissibility, and spread to other countries and continents. B1.1.7 has a series of mutations in its spike protein: ΔH69/V70, ΔY144, N501Y, A570D, D614G, P681H, T716I, S982A, and D1118H. One of these, N501Y, was of particular concern because it is located in the receptor binding site; the spike with this mutation binds more tightly to its cellular receptor, ACE-2; and virus with this mutation has increased host range that includes mice. 19 pseudoviruses, each bearing a SARS-CoV-2 S with a different mutation found in circulating strains, were neutralized as efficiently as non-mutant pseudoviruses by BNT162b2-immune sera. The following study demonstrates that a virus with the full set of mutations in the UK variant spike is also neutralized efficiently by BNT162b2-immune sera.

We generated VSV-SARS-CoV-2-S pseudoviruses bearing the Wuhan reference strain or lineage B.1.1.7 strain spike protein. Sera of 16 participants in the previously reported trial (Sahin U. et al., medRxiv 2020.12.09.20245175; doi: https://doi.org/10.1101/2020.12.09.20245175), drawn from eight younger (18-55 yrs) and eight older adults (56-85 yrs) 21 days after the booster immunization with 30 μg BNT162b2, were tested for neutralization of SARS-CoV-2 Wuhan and lineage B.1.1.7 spike-pseudotyped VSV by a 50% pseudovirus neutralization assay ($pVNT_{50}$; Figure 122). The ratio of the 50% neutralization GMT of the sera against the SARS-CoV-2 lineage B.1.1.7 spike-pseudotyped VSV to that against the Wuhan reference spike-pseudotyped VSV was 0.79, indicating no biologically significant difference in neutralization activity against the two pseudoviruses.

The preserved neutralization of pseudoviruses bearing the B.1.1.7 spike by BNT162b2-immune sera suggests that the UK variant viruses will not escape BNT162b2-mediated protection. Furthermore, since there is good concordance between pseudotype neutralization and SARS-CoV-2 neutralization assays, the use of a non-replicating pseudovirus system is not expected to be a potential limitation of the work.

Materials and Methods

VSV-SARS-CoV-2 S variant pseudovirus generation

A recombinant replication-deficient vesicular stomatitis virus (VSV) vector that encodes green fluorescent protein (GFP) and luciferase instead of the VSV-glycoprotein (VSV-G) was pseudotyped with SARS-CoV-2 spike (S) derived from either the Wuhan reference strain (NCBI Ref: 43740568) or the variant of concern (VOC)-202012/01 (also known as SARS-CoV-2 lineage B.1.1.7) according to published pseudotyping protocols (Fig. 123) (PMID: 21998709). In brief, HEK293T/17 monolayers transfected to express SARS-CoV-2 S were inoculated with VSV-G complemented VSVΔG vector. After incubation for 1 h at 37 °C, the inoculum was removed. Cells were washed with PBS before medium supplemented with anti-VSV-G antibody (clone 8G5F11, Kerafast Inc.) was added to neutralize residual VSV-G complemented input virus. VSV-SARS-CoV-2-S pseudotype-containing medium was harvested 20 h after inoculation, 0.2 µm filtered and stored at -80 °C. Prior to use in the neutralization test, the pseudovirus batches were titrated on Vero 76 cells, and the percent infected cells determined by flow cytometry (Fig. 124). Individual titers were calculated in transducing units (TU) per mL. Production of the VSV-SARS-CoV-2-S pseudoviruses bearing the Wuhan reference strain or lineage B.1.1.7 strain spike protein yielded similar titers (Table 26).

Table 26. Titers of SARS-CoV-2 Wuhan reference strain and lineage B.1.1.7 spike-pseudotyped VSV in transducing units (TU) per mL.

VSV pseudovirus bearing	Titer [TU/mL]
Wuhan strain SARS-CoV-2 S	$1.59x10^5$
Lineage B.1.1.7 SARS-CoV-2 S	$1.30 x10^5$

Serum specimens and neutralization assay

The immunization and serum collection regimen is illustrated schematically in Fig. 125. For measuring neutralization titers, each serum was 2-fold serially diluted in culture medium with the first dilution of 1:20 (dilution range of 1:20 to 1:2560). VSV-SARS-CoV-2-S particles were diluted in culture medium to obtain 100 TU in the assay. Serum dilutions were mixed 1:1 with pseudovirus for 30 minutes at room temperature prior to addition to Vero 76 cell monolayers

in 96-well plates and incubation at 37 °C for 24 hours. Supernatants were removed, and the cells were lysed with luciferase reagent (Promega). Luminescence was recorded, and neutralization titers were calculated in GraphPad Prism version 9 by generating a 4-parameter logistical (4PL) fit of the percent neutralization at each serial serum dilution. The 50% pseudovirus neutralisation titre ($pVNT_{50}$) was reported as the interpolated reciprocal of the dilution yielding a 50% reduction in luminescence. A table of the neutralization titers is provided (Table 27). The ratio for each serum of the $pVNT_{50}$ against SARS-CoV-2 lineage B.1.1.7 and the Wuhan reference strain spike-pseudotyped VSV is plotted in Fig. 126.

Table 27. $pVNT_{50}$ values of 16 BNT162b2 post-immunization sera against SARS-CoV-2 Wuhan reference strain spike-pseudotype and lineage B.1.1.7 spike-pseudotyped VSV.

Serum ID	$pVNT_{50}$		$pVNT_{50}$ ratio
	Wuhan ref.	B.1.1.7	(B.1.1.7/Wuhan ref.)
1	160	161.2	1.01
2	114.1	85.8	0.75
3	223.2	128.6	0.58
4	193	268.4	1.39
5	111.9	64.3	0.57
6	128	99.1	0.77
7	278.1	226.8	0.82
8	203.6	185	0.91
9	94.9	58.4	0.62
10	209.7	126.8	0.60
11	50.8	41.7	0.82
12	241.3	486.1	2.01
13	174	84.8	0.49
14	292.5	136.7	0.47
15	186.7	121.6	0.65
16	86.3	116.2	1.35

Example 34: Exemplary regimen for administration of a SARS-CoV-2 RNA Vaccine in Pregnant Women

The present Example describes an exemplary regimen for administration of a SARS-CoV-2 RNA vaccine described herein (specifically, in this Example, BNT162b2) in pregnant women (*e.g.*, in healthy pregnant women 18 years of age and older).

Pregnant women are at risk for acquiring SARS-CoV-2 infection and COVID-19. Pregnancy may confer increased risk of severe COVID-19 because of physiological changes during pregnancy that can increase susceptibility to respiratory infections and subsequent rapid progression to respiratory failure. Additionally, pregnant women with COVID-19 have been reported to have higher rates of preterm birth, cesarean delivery, fetal distress, and infants requiring neonatal intensive care.

The present Example describes certain protocols in accordance with which BNT162b2 may be administered to pregnant women and/or to infants born from such pregnant women, and also describes certain assessments that may be performed and/or results that may be achieved. For example, this Example describes a study that will assess safety of BNT162b2 in pregnant women and their infants; it will also assess the immunogenicity of BNT162b2 in pregnant women, the transfer of antibody to their infants, and the kinetics of antibody transfer in the infant.

Among other things, the present Example describes a study that will assess the safety and tolerability of prophylactic BNT162b2 when administered to maternal participants 18 years of age or older vaccinated at 24 to 34 weeks' gestation. Without wishing to be bound by any particular theory, the present Example proposes that vaccination beginning within this time period may provide particular advantages. Recognizing that proposals ranging from vaccination at any time during pregnancy (see, for example, "Israel Recommends COVID Vaccination in All Stages of Pregnancy, Updating Guidelines" *Haaretz* February 1, 2021) and others have proposed refraining from vaccinating during pregnancy (see, for example, WHO Strategic Advisory Group recommendation), the present Example describes a particular regimen in which pregnant mothers receive a first dose of vaccine between about 24 to about 34, or in some embodiments between about 27 to about 34 weeks of gestation, and a second dose about 21 days later, ideally prior to delivery of the baby.

Without wishing to be bound by any particular theory, the present Example proposes that vaccination according to this regimen may, for example, reduce risk to the fetus as may result, for example, from exposure to an immunized maternal immune response early in pregnancy. Furthermore, still without wishing to be bound by any particular theory, the present Example proposes that the provided vaccination schedule may provide particular benefits when at least two doses are administered prior to delivery of the baby. Among other things, the present Example proposes that a provided regimen may provide a particularly beneficial risk/benefit balance. Among other things, the present disclosure teaches that benefits that may be provided by immunization of pregnant mothers, and particularly by such immunization in accordance with a regimen described in the present Example, may impart immunity to the baby that, in some embodiments, may carry past delivery, this reducing need for immunization of the baby, at least for a period of days weeks, months, or years (e.g., 1, 2, 3, 4, 5, 6, 7, 8 weeks or more, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24 or more months, or 1, 2, 3, 4, or 5 years) post-delivery. Thus, in some embodiments, as noted herein, infants born of mothers vaccinated during pregnancy, e.g, according to a particular regimen as described herein, may not need further vaccination, or may need reduced vaccination (e.g., lower doses and/or smaller numbers of administrations – e.g., boosters –, and/or lower overall exposure over a given period of time), for a period of time (e.g., as noted herein) after birth.

For example, in maternal participants receiving at least 1 dose of study intervention from each vaccine group, the percentage of maternal participants reporting: (i) Local reactions for up to 7 days following each dose; (ii) Systemic events for up to 7 days following each dose (iii) AEs from Dose 1 through 1 month after Dose 2 (iv) SAEs from Dose 1 through 1 month after delivery will be assessed. Alternatively or additionally, in maternal participants complying with certain key protocol criteria (evaluable maternal participants) and no serological or virological evidence (up to 1 month after receipt of the second dose) of past SARS-CoV-2 infection: (v) GMR, estimated by the ratio of the geometric mean of SARS-CoV-2 neutralizing titers in pregnant women to those in nonpregnant women 1 month after Dose 2 may be assessed.

Still further alternatively or additionally, in maternal participants complying with the key

protocol criteria (evaluable participants) and/or with without or without (e.g., separately for those with and those without, or independent of) serological or virological evidence (prior to 7 days after receipt of Dose 2) of past SARS-CoV-2 infection: (vi) 100 × (1 – IRR) [ratio of active vaccine to placebo] may be assessed.

Yet further alternatively or additionally, one or more of the following may be assessed:

- In maternal participants complying with the key protocol criteria (evaluable maternal participants) from each vaccine group: (a) GMCs/GMTs, at baseline (before Dose 1), 2 weeks after Dose 2, 1 month after Dose 2, and 6 months after delivery (b) GMFRs from baseline through 2 weeks after Dose 2, 1 month after Dose 2, and 6 months after delivery;

- In infants born to maternal participants receiving at least 1 dose of study intervention from each vaccine group, the percentage of infants with: (a) Specific birth outcomes (b) AEs from birth through 1 month of age (c) SAEs and AESIs (major congenital anomalies, developmental delay) through 6 months of age;

- In infants born to evaluable maternal participants from each vaccine group: (a) GMCs and GMFRs, at birth and 6 months after delivery;

- In maternal participants who received BNT162b2 (at initial randomization and at 1 month after delivery): (a) Incidence per 1000 person-years of follow-up;

- In maternal participants who received BNT162b2 at initial randomization and without evidence of prior SARS-CoV-2 infection: (a) Incidence per 1000 person-years of follow-up

- In each subset of evaluable maternal participants from each vaccine group with: (a) Confirmed COVID-19 (b) Confirmed severe COVID-19 (c) SARS-CoV-2 infection but no confirmed COVID-19 (d) GMCs/GMTs and GMFRs at baseline, 1 month after Dose 2, and 6 months after delivery;

- In evaluable maternal participants: (a) GMCs/GMTs at baseline and before Dose 2 (b) GMFRs from baseline to before Dose 2;

- In infants born to maternal participants from each vaccine group, based on the breastfeeding status: (a) GMCs and GMFRs, at birth and 6 months after delivery;

- In infants born to maternal participants receiving at least 1 dose of study intervention from each vaccine group, based on the breastfeeding status, the percentage of infants with:

(a) AEs from birth through 1 month of age (b) SAEs and AESIs (major congenital anomalies, developmental delay) through 6 months of age;

- In infants born to maternal participants from each vaccine group: (a) Incidence rate of infant participants with confirmed COVID-19;

- In infants born to maternal participants from each vaccine group: (a) Incidence rate of MIS-C.

In some embodiments, a first dose will be administered to pregnant women during their 27 to 34 weeks of gestation, followed by a second dose approximately 21 days later. In some embodiments, a first dose will be administered to pregnant women during their 24 to 34 weeks of gestation, followed by a second dose approximately 21 days later. In some embodiments, participant mothers are assessed for a period of time up to about 6, 7, 8, 9, 10, 12, 13, 14, 15, 16, 17, 18 months or more (e.g., after initiation of the study, after administration of the first dose, after administration of the second dose, and/or after birth of the infant).

Is some embodiments, an infant born to a mother to whom one or more (e.g., two) vaccine doses have been administered (e.g., to whom two doses were administered during gestation) is assessed for a period of time up to about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 months or more (e.g., after initiation of the study, after administration of the first dose, after administration of the second dose, and/or after birth of the infant).

In some embodiments, a dose will be 30 ug of BNT162b2 as described herein.

In some embodiments, assessment of vaccine performance are made in populations of pregnant women of any age, or within a particular age range (e.g., equal to or above 18 years of age). In some embodiments, assessment of vaccine performance are made in populations of women carrying singleton pregnancies.

In some embodiments, gestational age is assessed by one or more of last menstrual period, ultrasound examiniation, physical examination, and/or combinations thereof. In some embodiments, gestational age is determined by ultrasound. In some embodiments, gestational age is determined by consideration of two or more assessments (e.g., two or more ultrasounds performed at different times, such as in different trimesters, of the pregnancy).

In some embodiments, assessment of vaccine performance is made in populations characterized by one or more of: ultrasound examination performed at at least 18 weeks of pregnancy with no significant fetal abnormalities observed (e.g., upon assessment by a licensed investigator); documented negative HIV, syphilis, and/or HBV tests or combinations thereof; prepregnancy BMI of ≤40 kg/m^2.

In some embodiments, assessment of vaccine performance is made in populations that do not include subjects characterized by one or more of: suffering from a medical or psychiatric condition that may increase the risk of vaccination or otherwise, in the reasonable judgement of a licensed investigator make the subject inappropriate for receipt of the vaccine; prevopis clinical or micobiological diagnosis of COVID-19; history of severe adverse reaction associated with a vaccine and/or sever allergic reaction (e.g., anaphylaxis) to any component of the vaccine; known or suspected immunodeficiency; bleeding diathesis or condition associated with prolonged bleeding, gestational hypertension or preeclampsia-eclampsia, placental abnormality, polyhydramnios or oligohydramnios, significant bleeding or blood clotting disorder, gestational diabetes, one or more signs of premature labor with the current pregnancy or having ongoing intervention (medical/surgical) in the current pregnancy to prevent preterm birth, prior stillbirth or neonatal death, prior low birth weight or preterm delivery, prior history of at least 3 miscarriages, prior pregnancies numbering greater than 5, or previous infant with a known genetic disorder or major congenital anomaly, previous vaccination with any coronavirus vaccine, receipt of medications intended to prevent COVID-19, receipt of blood/plasma products or immunoglobulin from 60 days before administration of study intervention or planned receipt through delivery (with 1 exception, anti-D immunoglobulin (eg, RhoGAM), which can be given at any time), current alcohol abuse or illicit drug use, participants who receive treatment with immunosuppressive therapy (including cytotoxic agents or systemic corticosteroids, eg, for cancer or an autoimmune disease, or planned receipt through the postvaccination blood draw), participation in other studies involving study intervention within 28 days prior to study entry and/or during study participation, previous participation in other studies involving study intervention containing LNPs, current febrile illness, current symptoms of COVID-19 infection, Receipt of any seasonal or pandemic influenza vaccine in the previous 14 days, anticipated receipt of any seasonal or

pandemic influenza vaccine in the 7 days after study intervention administration, receipt of a tetanus-, diphtheria-, and/or pertussis-containing vaccine in the previous 14 days, anticipated receipt of a tetanus-, diphtheria-, and/or pertussis-containing vaccine in the 7 days after study intervention administration, receipt of short-term (<14 days) systemic corticosteroids less than 28 days prior to dosing (inhaled/nebulized, intra-articular, intrabursal, or topical (skin or eyes) corticosteroids are permitted).

In some embodiments, a mother vaccinated as described herein may be taking or may begin taking, for example, an antipyretic or other pain medication to treat symptoms associated with the vaccination. Alternatively or additionally, in some embodiments, a mother may be taking or may begin taking a medication required for treatment of a preexisting stable condition and/or an inhaled, topical or localized injection of corticosteroids.

In some embodiments, a mother vaccinated as described herein may be given one or more antenatal corticosteroids, in particular if the pregnancy is at risk for preterm delivery. In some embodiments, the corticosteroid is a glucocorticoid. In some embodiments, the corticosteroid is betamethasone or progesterone, or a mixture thereof.

In some embodiments, vaccination as described in this Example reduces incidence of COVID-19 disease (and/or documented SARS-CoV-2 infection), or of severe COVID-19 disease, in mothers and/or infants born to them, for example relative to that observed in a comparable unvaccinated (e.g., having received placebo) population. In some embodiments, a mother is considered to have COVID-19 disease if least 1 of symptom of COVID-19 disease (fever; new or increased cough; new or increased shortness of breath; new or increased muscle pain; new loss of taste or smell; sore throat; diarrhea; vomiting; and/or in some embodiments fatigue, headache, nasal congestion or runny nose, nausea) is present and a SARS-CoV-2 NAAT-positive test is obtained during, or within 4 days before or after, the symptomatic period, either at the central laboratory or at a local testing facility (using an acceptable test). In some embodiments, a mother is considered to have severe COVID-19 disease if she has confirmed COVID-19 and one or more of the following is present:

- Clinical signs at rest indicative of severe systemic illness (RR ≥30 breaths/min, HR ≥125 beats/min, SpO2 ≤93% on room air at sea level, or PaO2/FiO2 <300 mm Hg);
- Respiratory failure (defined as needing high-flow oxygen, noninvasive ventilation,

mechanical ventilation, or ECMO);

- Evidence of shock (SBP <90 mm Hg, DBP <60 mm Hg, or requiring vasopressors);
- Significant acute renal, hepatic, or neurologic dysfunction*;
- Admission to an ICU;
- Death.

In some embodiments, an infant is considered to have COVID-19 disease if at least one symptom (fever, new or increased cough, new or increased shortness of breath, diarrhea, vomiting; and/or in some embodiments one or more of nasal congestion or runny nose, poor appetite or poor feeding, abdominal pain/colic) is present and a SARS-COV-2 NAAT-positive test result is obtained during, or within 4 days before or adter, the symptomatic period, either at the central laboratory or at a local testing facility (using an acceptable test). In some embodiments, an infant is considered to have severe COVID-19 disease if she has confirmed COVID-19 and one or more of the following is present:

(i) Clinical signs at rest indicative of severe systemic illness:

- RR (breaths/min): >50 from birth to 1 week of age, ≥40 from 1 week to 1 month of age, ≥34 from 1 month to 6 months of age;
- HR (beats/min): >180;
- SpO2 ≤92% on room air or >50% FiO2 to maintain ≥92%, or PaO2/FiO2 <300 mm Hg24;

(ii) Respiratory failure (defined as needing high-flow oxygen including nasal CPaP/BiPaP, noninvasive ventilation, mechanical ventilation, or ECMO);

(iii) Evidence of shock or cardiac failure:

- SBP (mm Hg) (<5th percentile for age):
  + <65 from birth to 1 week of age, <75 from 1 week to 1 month of age, <100 from 1 month to 6 months of age;

OR

- Requiring vasoactive drugs to maintain BP in the normal range;

(iv) Significant acute renal failure: serum creatinine >2 times ULN for age or 2-fold increase in baseline creatinine;

(v) Significant GI/hepatic failure: total bilirubin >4 mg/dL or ALT 2 times ULN for age;

(vi) Significant neurologic dysfunction: Glasgow Coma Scale score <11 or acute change in mental status with a decrease in Glasgow Coma Scale score ≥3 points from abnormal baseline;

(vii) Admission to an ICU;

(viii) Death.

In some embodiments, incidence of multisystem inflammatory syndrome is not significantly increased (e.g., relative to a comparable population whose mothers were not vaccinated, and/or who were not vaccinated according to a protocol as described herein) in infants whose mothers were vaccinated as described herein. In some embodiments, an infant is considered to have multisystem inflammatory syndrome if:

- the infant presents with fever (≥38.0°C for ≥24 hours or report of subjective fever lasting ≥24 hours); AND

- there is laboratory evidence of inflammation (based on local laboratory ranges) including, but not limited to, 1 or more of the following: an elevated CRP, ESR, fibrinogen, procalcitonin, D-dimer, ferritin, LDH, or IL-6, elevated neutrophils, reduced lymphocytes, and low albumin; AND

- there is evidence of clinically severe illness requiring hospitalization (definition as noted above for severe disease), with multisystem (≥2) organ involvement:

  o Cardiac (eg, shock, elevated troponin, elevated BNP, abnormal echocardiogram, arrhythmia);

  o Renal (eg, acute kidney injury or renal failure);

  o Respiratory (eg, pneumonia, ARDS, pulmonary embolism);

  o Hematologic (eg, elevated D-dimers, thrombophilia, or thrombocytopenia);

  o GI/hepatic (eg, elevated bilirubin, elevated liver enzymes, or diarrhea);

  o Dermatologic (eg, rash, mucocutaneous lesions);

  o Neurological (eg, CVA, aseptic meningitis, encephalopathy); AND

- there is no alternative plausible diagnoses; AND

- the infant is determined to be positive for current or recent SARS-CoV-2 infection by RT-PCR, serology, or antigen test; OR

- the infant has had COVID-19 exposure within the 4 weeks prior to the onset of symptoms.

In some embodiments, vaccination of mothers as described herein does not materially increase incidence of preterm delivery of infany morbidity.

In some embodiments, incidence of COVID-19 disease (and/or documented SARS-CoV-2 infection) in infants whose mothers were vaccinated as described herein is reduced relative to that of infacts whose mothers were not so vaccinated. In some embodiments, incidence of COVID-19 disease (and/or documented SARS-CoV-2 infection) in infants whose mothers were vaccinated as described herein is comparable to that of infants who were directly vaccinated after their delivery.

In some embodiments, vaccination as described herein achieves one or more of the following Primary or Secondary Outcome measures:

Primary Outcome Measures:

1. Percentage of maternal participants reporting: Local reactions

Pain at the injection site, redness, and swelling as self-reported on electronic diaries

[Time Frame: For 7 Days after Dose 1 and Dose 2]

2. Percentage of maternal participants reporting systemic events

Fever, fatigue, headache, chills, vomiting, diarrhea, new or worsened muscle pain, and new or worsened joint pain as

self-reported on electronic diaries.

[Time Frame: For 7 days after Dose 1 and Dose 2]

3. Percentage of maternal participants reporting adverse events

As elicited by investigational site staff

[Time Frame: From Dose 1 through 1 month after Dose 2]

4. Percentage of maternal participants reporting serious adverse events

As elicited by investigational site staff

[Time Frame: From Dose 1 through 6 months after delivery]

5. Demonstrate non inferiority of immune response in pregnant women compared to nonpregnant female participants

from the C4591001 study without evidence of past SARS-CoV-2 infection.

GMR, estimated by the ratio of the geometric mean of SARS CoV 2 neutralizing titers in pregnant women to those in
nonpregnant female participants
[Time Frame: 1 month after Dose 2]
6. Demonstrate non inferiority of immune response in pregnant women compared to nonpregnant female participants
from the C4591001 study with and without evidence of prior SARS-CoV-2 infection
GMR, estimated by the ratio of the geometric mean of SARS CoV 2 neutralizing titers in pregnant women to those in
nonpregnant female participants
[Time Frame: 1 month after Dose 2]

Secondary Outcome Measures:

7. Evaluate efficacy against confirmed COVID 19 in participants without evidence of infection prior to vaccination
1000 person years of follow-up
[Time Frame: 7 days after Dose 2]
8. Evaluate efficacy against confirmed COVID 19 in participants without evidence of prior infection.
1000 person years of follow-up
[Time Frame: 7 days after Dose 2]

Example 35: Neutralization of SARS-CoV-2 lineage B.1.1.298 (Danish strain; a.k.a., SARS-CoV-2/hu/DK/CL-5/1 (Cluster 5)) and B.1.351 (South African strain; a.k.a., 20H/501Y.V2 (501.V2)) pseudovirus by BNT162b2 vaccine-elicited human sera

Sera of 12 younger adult participants in the previously reported German phase 1/2 trial drawn at 7 or 21 days after the booster immunization with 30 µg BNT162b2, were tested for neutralization of SARS-CoV-2 Wuhan Hu-1 (reference), South African lineage B.1.351 (SA-strain), and Danish mink-related lineage B.1.1.298 (DNK-strain) spike protein pseudotyped VSV by a 50% neutralization assay (pVNT50). The SA-strain spike protein carries the following amino acid changes compared to the Wuhan reference: L18F, D80A, D215G, ΔL242-244,

R246I, K417N, E484K, N501Y, D614G, A701V. The DNK-strain spike protein carries the following amino acid changes compared to the Wuhan reference: Y453F, D614G, I692V, M1229I.

BNT162b2-immune sera neutralized the DNK-strain pseudovirus almost as efficiently as the SARS-CoV-2 Wuhan Hu-1 pseudotyped reference. A decrease (5-fold) in neutralizing titers was measured against the SARS-CoV-2 lineage B.1.351 pseudovirus when comparing the titers to the Wuhan Hu-1 pseudotyped reference. Importantly, all tested BNT162b2-immune sera were still able to neutralize with no complete escape being noted (Fig. 127).

Materials and Methods:

A recombinant replication-deficient VSV vector that encodes green fluorescent protein (GFP) and luciferase (Luc) instead of the VSV-glycoprotein (VSV-G) was pseudotyped with Wuhan-Hu-1 isolate SARS-CoV-2 spike (S) (GenBank: QHD43416.1), a variant harbouring four mutations found in the S protein of the Danish mink-related lineage B.1.1.298 (Y453F, D614G, I692V, M1229I), or variants harbouring ten mutations (L18F, D80A, D215G, R246I, Δ242/243/244, K417N, E484K, N501Y, D614G, A701V) found in the South African lineage B.1.351 S protein according to published pseudotyping protocols. In brief, HEK293T/17 monolayers transfected to express the respective SARS-CoV-2 S truncated of the C-terminal cytoplasmic 19 amino acids (SARS-CoV-2-S(CΔ19)) were inoculated with VSVΔG-GFP/Luc vector. After incubation for 1 h at 37 °C, the inoculum was removed, and cells were washed with PBS before medium supplemented with anti-VSV-G antibody (clone 8G5F11, Kerafast) was added to neutralise residual input virus. VSV-SARS-CoV-2 pseudovirus-containing medium was collected 20 h after inoculation, 0.2-µm-filtered and stored at −80 °C.

For pseudovirus neutralisation assays, 40,000 Vero 76 cells were seeded per 96-well. Sera were serially diluted 1:2 in culture medium starting with a 1:10 dilution (dilution range of 1:10 to 1:2,560). VSV-SARS-CoV-2-S pseudoparticles were diluted in culture medium for a fluorescent focus unit (ffu) count in the assay of ~1,000 TU in the assay. Serum dilutions were mixed 1:1 with pseudovirus for 30 minutes at room temperature prior to addition to Vero 76 cell monolayers in 96-well plates and incubation at 37 °C for 24 hours. Supernatants were removed, and the cells were lysed with luciferase reagent (Promega). Luminescence was

recorded, and neutralisation titers were calculated in GraphPad Prism version 9 by generating a 4-parameter logistical (4PL) fit of the percent neutralisation at each serial serum dilution. The 50% pseudovirus neutralisation titre (pVNT50) was reported as the interpolated reciprocal of the dilution yielding a 50% reduction in luminescence.

Example 36: Neutralization of N501Y mutant SARS-CoV-2 by BNT162b2 vaccine-elicited sera

Rapidly spreading variants of SARS-CoV-2 have arisen in the United Kingdom and South Africa (Volz E. et al. Report 42 - Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data. https://www.imperial.ac.uk/mrc-global-infectious-disease-analysis/covid-19/report-42-sars-cov-2-variant/; Tegally H. et al. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Afric. medRxiv 2020. https://doi.org/10.1101/2020.12.21.20248640). These variants have multiple mutations in their S glycoproteins, which are key targets of virus neutralizing antibodies. These rapidly spreading variants share the spike N501Y substitution. This mutation is of particular concern because it is located in the viral receptor binding site for cell entry, increases binding to the receptor (angiotensin converting enzyme 2), and enables the virus to expand its host range to infect mice (Gu H. et al. Adaptation of SARS-CoV-2 in BALB/c mice for testing vaccine efficacy. Science 2020;369:1603-7; Chan K.K. et al. An engineered decoy receptor for SARS-CoV-2 broadly binds protein S sequence variants. Cold Spring Harbor Laboratory 2020.doi: 10.1101/2020.10.18.344622).

We generated an isogenic Y501 SARS-CoV-2 on the genetic background of the N501 clinical strain USA-WA1/2020, which also provided the genetic background of the BNT162b2-encoded spike antigen. Sera of 20 participants in the previously reported trial (Walsh E.E. et al. Safety and Immunogenicity of Two RNA-Based Covid-19 Vaccine Candidates. N Engl J Med 2020; Polack F.P. et al. Safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine. N Eng. J Med 2020. DOI: 10.1056/NEJMoa2034577), drawn 2 or 4 weeks after immunization with two 30-µg doses of BNT162b2 spaced three weeks apart, were tested for neutralization of N501 and Y501 viruses by a 50% plaque reduction neutralization assay ($PRNT_{50}$; Figure 128). The ratio of the 50% neutralization GMT of the sera against the Y501 virus to that against the N501 virus

was 1.46, indicating no reduction in neutralization activity against the virus bearing the Y501 spike.

Materials and Methods

Construction of isogenic viruses

We prepared an isogenic pair of SARS-CoV-2 containing the N501 or Y501 spike protein (Figure 129). The N501Y mutation was generated by an A-to-T substitution at nucleotide 23,063 of the viral genome using an infectious cDNA clone of clinical strain WA1 (2019-nCoV/USA_WA1/2020) (Xie X. et al. An Infectious cDNA Clone of SARS-CoV-2. Cell Host Microbe 2020;27:841-8 e3). Following a previously reported mutagenesis protocol (Plante J.A. et al. Spike mutation D614G alters SARS-CoV-2 fitness. Nature 2020), we recovered N501 and Y501 viruses with titers of $>10^7$ plaque-forming units (PFU) per ml. The two viruses developed similar plaque morphologies on Vero E6 cells (Fig. 130).

Serum specimens and neutralization assay

The immunization and serum collection regimen is illustrated schematically in Fig. 131. For measuring neutralization titers, each serum was 2-fold serially diluted in culture medium with the first dilution of 1:40 (dilution range of 1:40 to 1:1280). The diluted serum was incubated with 100 PFU of N501 or Y501 virus at 37 °C for 1 h, after which the serum-virus mixtures were inoculated onto Vero E6 cell monolayer in 6-well plates. A conventional (non-fluorescent) plaque reduction neutralization assay was performed to quantify the serum-mediated virus suppression as previously reported (Muruato A.E. et al. A high-throughput neutralizing antibody assay for COVID-19 diagnosis and vaccine evaluation. Nat Commun 2020;11:4059). A minimal serum dilution that suppressed >50% of viral plaques is defined as $PRNT_{50}$. A table of the neutralization titers is provided (Table 28). The ratio for each serum of the $PRNT_{50}$ against N501 and Y501 virus is plotted in Fig. 132.

Table 28. $PRNT_{50}$ values of 20 BNT162b2 post-immunization sera against N501 and Y501 SARS-CoV-2.

Serum ID	$PRNT_{50}$		$PRNT_{50}$ ratio
	N501	Y501	(Y501/N501)
1	160	640	4
2	160	320	2
3	320	640	2
4	80	160	2
5	160	160	1
6	320	320	1
7	640	640	1
8	160	160	1
9	640	640	1
10	640	1280	2
11	160	640	4
12	320	320	1
13	640	1280	2
14	640	320	0.5
15	320	640	2
16	320	640	2
17	640	640	1
18	640	1280	2
19	640	640	1
20	640	640	1

Example 37: Neutralization of spike 69/70 deletion, E484K, and N501Y SARS-CoV-2 by BNT162b2 vaccine-elicited sera

Rapidly spreading variants of SARS-CoV-2 have arisen in the United Kingdom (UK), South Africa (SA), and other regions (Volz E. et al. CMe. Report 42 - Transmission of SARS-CoV-2 Lineage B.1.1.7 in England: Insights from linking epidemiological and genetic data. https://wwwimperialacuk/mrc-global-infectious-disease-analysis/covid-19/report-42-sars-cov-2-variant/ 2021; Tegally H. et al. e. Emergence and rapid spread of a new severe acute respiratory syndrome-related coronavirus 2 (SARS-CoV-2) lineage with multiple spike mutations in South Africa medRxiv 2020. :https://doi.org/10.1101/2020.12.21.20248640). These variants have multiple mutations in their spike glycoproteins, which are key targets of virus neutralizing antibodies. The emerged spike mutations have raised concerns of vaccine

efficacy against these new strains. The goal of this study is to examine the effect of several key spike mutations from the UK and SA strains on BNT162b2 vaccine-elicited neutralization. We engineered three SARS-CoV-2s containing key spike mutations from the newly emerged United Kingdom (UK) and South African (SA) variants: N501Y from UK and SA; 69/70-deletion+N501Y+D614G from UK; and E484K+N501Y+D614G from SA. Neutralization geometric mean titers (GMTs) of twenty BTN162b2-vaccinated human sera against the three mutant viruses were 0.81- to 1.46-fold of the GMTs against parental virus, indicating small mutational effects on neutralization by sera elicited by two BNT162b2 doses.

Using an infectious cDNA clone of SARS-CoV-2 (Xie X. et al. An Infectious cDNA Clone of SARS-CoV-2. Cell Host Microbe 2020;27:841-8 e3), we engineered three spike mutant viruses on the genetic background of clinical strain USA-WA1/2020 (Fig. 133). (i) Mutant N501Y virus contains the N501Y mutation that is shared by both the UK and SA variants. This mutation is located in the viral receptor binding domain (RBD) for cell entry, increases binding to the receptor (angiotensin converting enzyme 2), and enables the virus to expand its host range to infect mice (Xie X. et al. An Infectious cDNA Clone of SARS-CoV-2. Cell Host Microbe 2020;27:841-8 e3; Wrapp D. et al. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science 2020;367:1260-3). (ii) Mutant Δ69/70+N501Y+D614G virus contains two additional changes from the UK variants: amino acid 69 and 70 deletion (Δ69/70) and D614G substitution. Amino acids 69 and 70 are located in the N-terminal domain of the spike S1 fragment; deletion of these residues may allosterically change the conformation of spike (Wrapp D. et al. Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. Science 2020;367:1260-3). The D614G mutation is dominant in circulating strains around the world (Plante JA et al. Spike mutation D614G alters SARS-CoV-2 fitness. Nature 2020; Korber B. et al. Tracking Changes in SARS-CoV-2 Spike: Evidence that D614G Increases Infectivity of the COVID-19 Virus. Cell 2020). (iii) Mutant E484K+N501Y+D614G virus contains the E484K substitution, which is also located in the viral RBD. The E484K substitution alone confers resistance to several monoclonal antibodies (Ku Z. et al. Molecular determinants and mechanism for antibody cocktail preventing SARS-CoV-2 escape. Nat Commun 2021;12:469; Baum A. et al. Antibody cocktail to SARS-CoV-2 spike protein prevents rapid mutational escape seen with individual antibodies. Science 2020;369:1014-8). Compared with the wild-type USA-

WA1/2020 strain, the three mutant viruses showed similar plaque morphologies on Vero E6 cells (Fig. 134).

We tested a panel of human sera from twenty participants in the previously reported clinical trial (Walsh EE et al. Safety and Immunogenicity of Two RNA-Based Covid-19 Vaccine Candidates. N Engl J Med 2020; Polack FP et al. Safety and Efficacy of the BNT162b2 mRNA Covid-19 Vaccine. N Engl J Med 2020), drawn 2 or 4 weeks after immunization with two 30-µg doses of BNT162b2 spaced three weeks apart (Fig. 135). Each serum was tested for neutralization of wild-type USA-WA1/2020 strain and the three mutant viruses by a 50% plaque reduction neutralization assay ($PRNT_{50}$; Tables 29 and 30).

Table 29. $PRNT_{50}$s of twenty BNT162b2 post-immunization sera against wild-type (USA-WA1/2020) and mutant N501Y SARS-CoV-2s

Serum ID	$PRNT_{50}$		$PRNT_{50}$ ratio
	WT	N501Y	(N501Y/WT)
1	160	640	4
2	160	320	2
3	320	640	2
4	80	160	2
5	160	160	1
6	320	320	1
7	640	640	1
8	160	160	1
9	640	640	1
10	640	1280	2
11	160	640	4
12	320	320	1
13	640	1280	2
14	640	320	0.5
15	320	640	2
16	320	640	2
17	640	640	1
18	640	1280	2
19	640	640	1
20	640	640	1

Table 30. $PRNT_{50}$s of twenty BNT162b2 post-immunization sera against wild-type (USA-WA1/2020), Δ69/70+N501Y+D614G, and E484K+N501Y+D614G SARS-CoV-2s

	$PRNT_{50}$		$PRNT_{50}$ ratio

Serum ID	WT	Δ69/70+N501Y +D614G	E484K+N501Y+D 614G	Δ69/70+N501Y+ D614G/WT	E484K+N501Y+D 614G/WT
1	320	640	320	2	1
2	160	160	80	1	0.5
3	640	1280	640	2	1
4	160	160	80	1	0.5
5	320	320	320	1	1
6	640	640	640	1	1
7	640	1280	320	2	0.5
8	320	320	160	1	0.5
9	1280	1280	1280	1	1
10	640	1280	640	2	1
11	320	320	320	1	1
12	640	1280	320	2	0.5
13	1280	2560	1280	2	1
14	320	320	320	1	1
15	320	640	320	2	1
16	640	640	640	1	1
17	640	1280	640	2	1
18	320	640	320	2	1
19	640	640	320	1	0.5
20	640	1280	640	2	1

All sera showed equivalent neutralization titers between the wild-type and mutant viruses, with differences of ≤ 4 fold (Fig. 136). Notably, ten out of the twenty sera had neutralization titers against mutant Δ69/70+N501Y+D614G virus that were twice their titers against the wild-type virus (Fig. 136b), whereas six out of the twenty sera had neutralization titers against mutant E484K+N501Y+D614G virus that were half their titers against the wild-type virus (Fig. 136c). The ratios of the neutralization GMTs of the sera against the N501Y, Δ69/70+N501Y+D614G, and E484K+N501Y+D614G viruses to their GMTs against the USA-WA1/2020 virus were 1.46, 1.41, and 0.81, respectively (Fig. 137).

Consistent with other recent reports of the neutralization of variant SARS-CoV-2 or corresponding pseudoviruses by convalescent or post-immunization sera (Wibmer CK et al. SARS-CoV-2 501Y.V2 escapes neutralization by South African COVID-19 donor plasma. bioRxiv 2021:doi: https://doi.org/10.1101/2021.01.18.427166; Wang Z. et al. mRNA vaccine-elicited antibodies to SARS-CoV-2 and circulating variants. bioRxiv 2021:doi: https://doi.org/10.1101/2021.01.15.426911), the neutralization GMT of the serum panel

against the virus with three mutations from the SA variant (E484K+N501Y+D614G) was slightly lower than the neutralization GMTs against the N501Y virus or the virus with three mutations from the UK variant (Δ69/70+N501Y+D614G). However, the magnitude of the differences in neutralization GMTs against any of the viruses in this study was small, as compared to the 4-fold differences in hemagglutination-inhibition titers that have been used to signal potential need for a strain change in influenza vaccines (Smith DJ et al. Mapping the antigenic and genetic evolution of influenza virus. Science 2004;305:371-6).

Methods

Construction of isogenic viruses. Three recombinant SARS-CoV-2 mutants (N501Y, Δ69/70-N501Y+D614G, E484K+N501Y+D614G in spike protein) were prepared on the genetic background of an infectious cDNA clone derived from clinical strain WA1 (2019-nCoV/USA_WA1/2020) (Xie X. et al. An Infectious cDNA Clone of SARS-CoV-2. Cell Host Microbe 2020;27:841-8 e3) by following the PCR-based mutagenesis protocol as reported previously (Plante JA et al. Spike mutation D614G alters SARS-CoV-2 fitness. Nature 2020). The full-length infectious cDNAs were in vitro ligated and used as templates to transcribe full-length viral RNA. Mutant viruses (P0) were recovered on day 2 from Vero E6 cells after electroporation of the in vitro RNA transcripts. P1 viruses were harvested as stocks by passaging the P0 virus once on Vero E6 cells. The titers of P1 viruses were determined by plaque assay on Vero E6 cells. The genome sequences of the P1 viruses were validated by Sanger sequencing. The detailed protocol was recently reported (Xie X. et al. Engineering SARS-CoV-2 using a reverse genetic system. Nature Protocols 2021:https://doi.org/10.1038/s41596-021-00491-8).

Serum specimens and neutralization assay. The immunization and serum collection regimen are illustrated schematically in Fig. 135. A conventional (non-fluorescent) plaque reduction neutralization assay was performed to quantify the serum-mediated virus suppression as previously reported (Muruato AE et al. A high-throughput neutralizing antibody assay for COVID-19 diagnosis and vaccine evaluation. Nat Commun 2020;11:4059). Briefly, each serum was 2-fold serially diluted in culture medium with the first dilution of 1:40 (dilution range of 1:40 to 1:1280). The diluted sera were incubated with 100 plaque-forming units of wild-type

or mutant viruses at 37°C for 1 h, after which the serum-virus mixtures were inoculated onto Vero E6 cell monolayer in 6-well plates. After 1 h of infection at 37°C, 2 ml of 2% Seaplaque agar (Lonza) in Dulbecco's modified Eagle medium (DMEM) containing 2% fetal bovine serum (FBS) and 1% penicillin/streptomycin (P/S) was added to the cells. After 2 days of incubation, 2 ml of 2% Seaplaque agar (Lonza) in DMEM containing 2% FBS, 1% P/S and 0.01% neutral red (Sigma) were added on top of the first layer. After another 16 h of incubation at 37°C, plaque numbers were counted. The minimal serum dilution that inhibits 50% of plaque counts is defined as the 50% plaque reduction neutralization titer ($PRNT_{50}$). Each serum was tested in duplicates. The $PRNT_{50}$ assay was performed at the biosafety level-3 facility at the University of Texas Medical Branch.

Example 38: Neutralizing Activity of BNT162b2-Elicited Serum

New, highly transmissible SARS-CoV-2 variants that were first detected in the United Kingdom (B.1.1.7 lineage), South Africa (B.1.351 lineage), and Brazil (P.1 lineage) with mutations in the S gene are spreading globally. To analyze effects on neutralization elicited by BNT162b2, we engineered *S* mutations from each of the three new lineages into USA-WA1/2020, a relatively early isolate of the virus from January 2020 (Fig. 138). We subsequently produced five recombinant viruses. The first had all the mutations found in the S gene in the B.1.1.7 lineage (B.1.1.7-spike), the second had all the mutations found in the S gene in the P.1 lineage (P.1-spike), the third had all the mutations found in the S gene in the B.1.351 lineage (B.1.351-spike), the fourth had an N-terminal domain deletion found in the B.1.351 lineage and the globally dominant D614G substitution (B.1.351-Δ242-244+D614G), and the fifth had the three mutations from the B.1.351 lineage at the receptor-binding site (K417N, E484K, and N501Y) and a D614G substitution (B.1.351-RBD+D614G). The amino acid residues mutated in the B.1.351-RBD+D614G virus are also among those mutated in the P.1 lineage virus, though in the P.1 lineage virus, K417 is mutated to threonine rather than asparagine. All the mutant viruses yielded infectious viral titers exceeding 10^7 plaque-forming units per milliliter. The B.1.1.7-spike and B.1.351-spike virus formed plaques that were smaller than those of the other viruses (Fig. 139).

We performed 50% plaque reduction neutralization testing ($PRNT_{50}$) using 20 serum samples that had been obtained from 15 participants in the pivotal trial (Polack FP et al. Safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine. N Engl J Med 2020; 383: 2603-15; Walsh EE et al. Safety and immunogenicity of two RNA-based Covid-19 vaccine candidates. N Engl J Med 2020; 383: 2439-50) 2 or 4 weeks after the administration of the second dose of 30 μg of BNT162b2 (which occurred 3 weeks after the first immunization) (Fig. 140). All the serum samples efficiently neutralized USA-WA1/2020 with almost all of them having titers higher than 1:40. Geometric mean neutralizing titers against USA-WA1/2020, B.1.1.7-spike, P.1-spike, B.1.351-spike, B.1.351-Δ242-244+D614G, and B.1.351-RBD+D614G viruses were 532, 663, 437, 194, 485, and 331, respectively (Fig. 141 and Table 31). Thus, as compared with neutralization of USA-WA1/2020, neutralization of B.1.1.7-spike and P.1-spike viruses was roughly equivalent, and neutralization of B.1.351-spike virus was still robust but ~2.7-fold lower. Our data are also consistent with lower neutralization titers against the virus with the full set of B.1.351-spike mutations than virus with either subset of mutations and suggest that mutations in the receptor-binding site (K417N, E484K, and N501Y) affect neutralization more than the 242-244 deletion in the N-terminal domain of the spike protein.

Because neutralization of the B.1.1.7-spike and P.1-spike viruses by BNT162b2-elicited sera is roughly equivalent to neutralization of USA-WA1/2020, the neutralization data provide strong support that BNT162b2 will continue to protect against the variants first detected in the UK or Brazil. Protection against B.1.351 lineage virus is also anticipated, given that, although neutralization titers against this variant are somewhat lower, they are still robust and much higher than the barely detectable titers observed after one dose of BNT162b2, when strong efficacy was already observed in the pivotal C4591001 efficacy trial (Polack FP et al. Safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine. N Engl J Med 2020;383:2603-15; Walsh EE et al. Safety and immunogenicity of two RNA-based Covid-19 vaccine candidates. N Engl J Med 2020;383:2439-50; Sahin U et al. BNT162b2 induces SARS-CoV-2-neutralising antibodies and T cells in humans. December 11, 2020 (https://www.-medrxiv.-org/-content/-10.-1101/-2020.-12.-09.-20245175v1). preprint.). In addition, T cell immunity may also be involved in protection (Liao M et al. Single-cell landscape of bronchoalveolar immune cells in patients with COVID-19. Nature Medicine 2020/), and BNT162b2 immunization elicits CD8+ T-cell responses

that recognize multiple variants (Skelly DT et al. Vaccine-induced immunity provides more robust heterotypic immunity than natural infection to emerging SARS-CoV-2 variants of concern. Research Square 2021).

Materials and Methods

Construction of isogenic viruses. All recombinant SARS-CoV-2s with spike mutations (**Figure 138**) were prepared on the genetic background of an infectious cDNA clone derived from clinical strain USA-WA1/2020 (Xie X et al. An Infectious cDNA Clone of SARS-CoV-2. Cell Host Microbe 2020;27:841-8 e3). The mutations were introduced into the spike gene using a PCR-based mutagenesis protocol as reported previously (Plante JA et al. Spike mutation D614G alters SARS-CoV-2 fitness. Nature 2020. doi: 10.1038/s41586-020-2895-3; Xie X et al. Neutralization of SARS-CoV-2 spike 69/70 deletion, E484K and N501Y variants by BNT162b2 vaccine-elicited sera. Nat Med 2021. doi: 10.1038/s41591-021-01270-4). The full-length infectious cDNAs were ligated and used as templates to *in vitro* transcribe full-length viral RNAs. The original viral stocks (P0) were recovered from Vero E6 cells on day 2 post electroporation of the *in vitro* transcribed RNAs. The P0 viruses were propagated on Vero E6 cells for another round to produce P1 viruses for the neutralization assays. The titers of P1 viruses were measured by plaque assay on Vero E6 cells (**Figure 139**). The complete spike sequences of the P1 viruses were confirmed by Sanger sequencing to have only the intended nucleotide changes from the USA-WA1/2020 sequence. A detailed protocol of the above experiments was recently reported (Xie X et al. Engineering SARS-CoV-2 using a reverse genetic system. Nature Protocols 2021:https://doi.org/10.1038/s41596-021-00491-8).

Serum specimens and neutralization assay. Figure 140 illustrates the immunization and serum collection scheme. A conventional 50% plaque-reduction neutralization test ($PRNT_{50}$) was performed to quantify the serum-mediated virus suppression as previously reported (Muruato AE et al. A high-throughput neutralizing antibody assay for COVID-19 diagnosis and vaccine evaluation. Nat Commun 2020;11:4059). Briefly, individual sera were 2-fold serially diluted in culture medium with a starting dilution of 1:40 (dilution range of 1:40 to 1:1280). The diluted sera were incubated with 100 PFU of USA-WA1/2020 or mutant SARS-CoV-2. After 1 h incubation at 37 °C, the serum-virus mixtures were inoculated onto a monolayer of Vero

E6 cells pre-seeded on 6-well plates on the previous day. A minimal serum dilution that suppressed >50% of viral plaques is defined as $PRNT_{50}$. The neutralization titers are presented in **Table 31**.

Table 31. $PRNT_{50}$'s of twenty BNT162b2 post-immunization sera against USA-WA1/2020 and mutant SARS-CoV-2.

Serum ID	*$PRNT_{50}$												
	USA-WA1/2020				B.1.1.7 -spike	P.1-spike			B.1.315-spike			B.1.351-Δ242-244 +D614G	B.1.351-RBD +D614G
	Exp1	Exp2	Exp3	GMT		Exp1	Exp2	GMT	Exp1	Exp2	GMT		
1	320	320	320	320	640	320	320	320	160	160	160	320	320
2	160	160	160	160	160	80	80	80	40	40	40	160	80
3	640	640	640	640	640	640	640	640	320	320	320	640	640
4	160	320	320	254	320	320	320	320	80	160	113	160	80
5	320	320	320	320	640	320	320	320	160	160	160	320	320
6	320	640	640	508	320	640	320	453	160	160	160	320	160
7	1280	640	640	806	1280	640	1280	905	320	320	320	1280	1280
8	320	320	320	320	320	160	160	160	80	80	80	160	160
9	1280	1280	1280	1280	1280	1280	640	905	640	640	640	1280	1280
10	640	640	1280	806	1280	640	320	453	640	320	453	1280	640
11	320	320	320	320	640	320	320	320	80	160	113	320	160
12	640	640	640	640	640	640	320	453	160	160	160	320	320
13	1280	1280	1280	1280	1280	640	640	640	160	320	226	1280	640
14	320	320	640	403	320	320	160	226	160	80	113	320	160
15	640	640	640	640	640	1280	640	905	320	320	320	640	320
16	320	320	640	403	1280	640	320	453	160	320	226	640	320
17	1280	1280	1280	1280	1280	1280	640	905	320	320	320	1280	640
18	640	640	640	640	640	640	320	453	160	320	226	320	320
19	640	640	640	640	640	1280	640	905	320	320	320	640	640
20	640	640	640	640	1280	640	320	453	160	160	160	640	320
†GMT	502	520	577	532	663	520	368	437	184	204	194	485	331
#95% CI	371-680	401-674	443-751	409-693	497-884	372-726	275-491	325-589	133-255	151-276	144-261	345-681	228-480

*The data for USA-WA1/2020 are from three experiments; the data for B.1.1.7-spike, B.1.351-Δ242-244+D614G, and B.1.351-RBD-D614G viruses are from one experiment each; and the data for P.1-spike and B.1.351-spike viruses are from two experiments. For each independent experiment, individual $PRNT_{50}$ value is the geometric mean of duplicate plaque assay results; no differences were observed between the duplicate assays.

[†]Geometric mean neutralizing titers.

[#]95% confidence interval (95% CI) for the GMT.

Example 39: Durability of BNT162b2-induced CD4+ and CD8+ T-cell responses

In a subset of 24 subjects across dose levels 10 to 30 µg, samples collected at Day 85 and Day 184 (nine and 23 weeks post-boost, respectively) were analyzed in order to determine the durability of T-cell responses induced by BNT162b2. On Day 184 and after an initial contraction, both $CD4^+$ and $CD8^+$ T-cell responses were detectable in the majority of individuals, across the three dose levels tested. Kinetics of $CD4^+$ and $CD8^+$ responses observed in four older adult subjects vaccinated with 10 µg BNT162b2 were comparable to younger adult subjects, with S protein-specific $CD4^+$ T cells still detectable in all four subjects 23 weeks after boost vaccination. BNT162b2 induced $CD4^+$ and $CD8^+$ responses were either higher than or in the range of recall antigen memory responses (**Fehler! Verweisquelle konnte nicht gefunden werden.**42).

Example 40: MHC-I binding epitopes recognized by CD8 T-cells induced by BNT162b2

Using MHC-class I multimer technology, several epitopes spread across the whole length of the S Protein and presented by a combination of common HLA-A and HLA-B alleles were identified to be recognized by CD8+ T-cells induced by BNT162-b2 (measured 7 days after the boost vaccination). Some peptide/HLA combinations were found in more than one subject.

Table 32. MHC-I binding epitopes recognized by CD8 T-cells induced by BNT162b2

HLA	Epitope	Position in S Protein	Identified in No. Subjects
B35:01	LPFNDGVYF	84-92	1
A03:01	GVYFASTEK	89-97	1
A02:01	YLQPRTFLL	269-277	3
B35:01	QPTESIVRF	321-329	1
A26:01	CVADYSVLY	361-369	1
B15:01	CVADYSVLY	361-369	1
A03:01	KCYGVSPTK	378-386	2
A24:02	NYNYLYRLF	448-456	3
B15:01	FQPTNGVGY	497-505	1
B35:01	IPFAMQMAY	896-904	1
A02:01	RLQSLQTYV	1000-1008	2
A68:01	GTHWFVTQR	1099-1108	1

C04:01	VYDPLQPEL	1137-1145	1
A24:02	QYIKWPWYI	1208-1216	3
A24:02	KWPWYIWLGF	1211-1220	1

Example 41: Histological findings following administration of BNT162b2

Classical chromogenic immunohistochemistry (IHC) and chromogenic dual IHC-ISH (*in situ* hybridization) experiments were performed to investigate biodistribution of BNT162b2 in mouse tissues 6h and 6d post-injection.

Protocol

After harvesting, tissue is fixed in 4% RotiHistofix overnight at 4°C and embedded in paraffin wax after dehydration in Leica Tissue Processor. Chromogenic IHC is performed. Spike protein is detected with anti-Spike2 mouse monoclonal antibody (Genetex). Dual IHC-ISH assay is conducted according to a self-established protocol based on Document MK 51-149 from Advanced Cell Diagnostics using the company kits and reagents. BNT162b2 probe (modV9) for ISH is custom designed by Advanced Cell Diagnostics based on the sequence provided by TRON. IHC protocol for the immune cell markers CD11c (Cell Signaling), CD19 (Cell Signaling), CD169 (Thermo Fisher) and F4/80 (Cell Signaling) were in place at TRON and they are adapted to dual IHC-ISH assay for the project. Images are acquired using Vectra Polaris Multispectral Slide Scanner microscope (Akoya Bioscience) and analysed with PhenoChart software (Akoya Bioscience).

Results

As can be seen in Figure 143, a specific vaccine mRNA signal (red) is detected in the lymph nodes (LN) 6h post injection using modV9 probe in dual IHC-ISH assay. Vaccine is mostly localized to subcapsular sinus (LN in 9 and 5 positions) and B cell follicles (LN in 12 and 1 positions). Dendritic cells are visualized by CD11c staining (turquoise, upper images) and only some of them uptake the vaccine. Majority of CD169+ macrophages (subcapsular sinus macrophages, turquoise, middle images) are positive for the vaccine. B cells (CD19+, turquoise, lower images) are the second major population showing vaccine signal.

A specific vaccine mRNA signal is still detectable in the LN 6d post injection using modV9 probe in dual IHC-ISH assay, albeit in very less amount (data not shown). Some CD11c+ DCs and subcapsular sinus macrophages are positive for the vaccine. Most of the vaccine signal detected is in the B cells (CD19+).

As can be seen in Figure 144, a specific vaccine mRNA signal (red) is detected in the spleen 6h post injection using modV9 probe in dual IHC-ISH assay. Majority of the vaccine signal is detected in the white pulp. Dendritic cells are visualized by CD11c staining (turquoise, upper images) and only some of them uptake the vaccine. A small portion of F4/80+ macrophages (turquoise, middle images) uptake the vaccine. B cells (CD19+, turquoise, lower images) are the major population showing the vaccine signal.

A specific vaccine mRNA signal is still detectable in the spleen 6d post injection using modV9 probe in dual IHC-ISH assay, albeit in very less amount (data not shown). The vaccine signal detected is solely in the B cells (CD19+). No DCs and macrophages show vaccine signal 6d post-injection.

After 6h, using mouse anti-S2 mouse monoclonal antibody, we detected a signal in the muscle, especially in some muscle fibers and in the connective tissue perimysium. In the LNs, we detected cells expressing Spike protein in the T cell zone (data not shown).

After 6d, using mouse anti-S2 mouse monoclonal antibody, no Spike expression is detectable in the muscle. On the contrary, LNs are full of cells expressing the vaccine (data not shown).

No nonspecific staining is detected with the S2 mouse monoclonal antibody in the chromogenic IHC experiments.

Summary

A very strong vaccine signal is visible in the draining LNs and spleen 6h post-injection. In the LN, vaccine is mostly detected in B cell follicles and subcapsular sinus, with some signal also in the T cell zone. By dual IHC-ISH, we showed that indeed the B cells (CD19+) and subcapsular sinus macrophages (CD169+) are the major cells that uptake the vaccine. Dendritic cells (CD11c+) in the T cell zone and intermediary sinus also uptake the vaccine. After 6d, some vaccine mRNA is still visible in the draining LNs. The signal observed in the T-cell zone after 6d is in the dendritic cells (CD11c+). Some B cells and LN macrophages also still have some vaccine at that stage.

Analysis of the spleen harvested 6h post-injection showed that vaccine already reaches spleen within 6h, most probably via blood circulation. The signal is located white pulp, where B cells and T cells form the major population and antigen presentation to T cells occur in the white pulp. With dual IHC-ISH assay, we showed that majority of B cells uptake the vaccine. Many DCs (CD11c+) surrounding the B cells are also positive. After 6d, signal is restricted to B cells.

IHC protocol is established to detect spike protein expression using anti-Spike S2 mouse monoclonal antibody on the cell pellets treated with/without the vaccine. A specific signal is detected only in the cells treated with BNT162b2. No nonspecific staining was visible in the naïve tissues tested. In the muscle, Spike expression is detected 6h post injection in the muscle fibers and in the connective tissue perimysium. After 6d, no staining is detectable in the muscle. On the contrary, the massive Spike expression is visible 6d post injection in LN, in particular in the T-cell zone.

Example 42: Stability studies.

Stability assessments of BNT162b2 formulations at various concentrations (e.g., 0.5 mg/mL, 1 mg/mL, and 2 mg/mL) have been performed, and have included assessments of compositions, stored at various temperatures (e.g., –70°C [e.g., -70 ± 10 °C], -20°C [e.g., -20 ± 5 °C], +5°C [e.g., 5 ± 3 °C], or +25°C [e.g., 25 ± 2 °C]) and/or for various periods of time (e.g., 0.5 months, 1 month, 2 months, 3 months, 4 months, and in certain cases one or more intervening time points (e.g., 1.5 months, 2.5 months, etc).

In exemplary studies, mice were injected (single leg) at day 0 with 20 uL of a relevant formulation. Blood was collected and serum generated at days 14, 21, and 28 after the administration; spleen were isolated at day 28.

ELISAs were performed to detect presence of antibodies in serum that bind to S1 protein, or specifically to the RBD domain. Figure 145 presents exemplary S1 ELISA results obtained with 28-day serum from mice injected with indicated formulations that had been stored under indicated temperature conditions for indicated periods of time. As can be seen with reference to Figure 145, all stored samples performed well, and reasonably comparably, after one (1) month of storage. After two (2) or three (3) months of storage, some decreased activity was observed for samples stored at +25°C, but samples stored at –70°C, -20°C, +5°C maintained significant performance.

At some time points, one or more parameters such as appearance, RNA content, RNA integrity, RNA encapsulation, lipid content (overall and/or of individual components and/or ratios thereof), particle size, particle polydispersity index, *in vitro* expressability, *etc*) were assessed; additional or alternative parameters may be or have been assessed.

Exemplary observations include that storage at +25°C is not recommended for periods of time longer than about 2 weeks, and preferably not more than about 1 week as, among other things, RNA integrity was observed to decrease significantly. It was also observed that, in at least some cases, significant ability to induce antibodies was maintained even when *in vitro* expressability was materially reduced. Change in polydispersity index, particularly after about 3 months of storage, or after about 4 months of storage, were observed to be greater for formulations stored at +5°C or above than for those stored at lower temperatures.

Example 43: Storage and shipping

This example illustrates storage, shipping and dose preparation of a multi-dose vial of a vaccine concentrate for injection. As shown in Figure 146, at the stage of primary packing, 2 mL type 1 glass, preservative-free, multi-dose vial (MDV) is used, wherein the MDV has 0.45 mL frozen liquid drug product and there are 5 doses per vial. At the stage of secondary packing, a single tray holds 195 vials, such as 975 doses per tray. The tray (white box) dimensions are 229 X 229 x 40 mm. At the stage of tertiary packing, a minimum of 1 tray (975

doses) (or up to 5 trays (max 4875 doses)) is stacked in a payload carton. The payload carton is submerged in 23 Kg of dry ice pellets (10 mm - 16 mm pellets). The thermal shipper dimensions are as follows: internal dimensions: 245mm X 245mm X 241mm; external dimensions: 400mm X 400mm X 560mm. The total weight of the thermal shipper is ~ 35 Kg. Different sizes of Ultra-Low Temperature (ULT) freezers are available in the market. Figure 147 shows an example for a small volume storage (about 90 litres; about 30K doses (left)) and for a large volume storage (about 500 litres; about 200K doses (right)). The thermal shipper keeps ULT up to 10 days if stored at 15°C to 25°C temperatures without opening. Upon receipt and after opening, the box should be replenished with dry ice within 24 hours (23 Kg of dry ice pellets (10 mm - 16 mm pellets)). The thermal shipper should be re-iced every 5 days. It is recommended that the thermal shipper is opened not more than twice a day. The thermal shipper should be closed within 1 minute (or less) after opening. The vaccine can be stored at 2°C to 8°C up to 2 days or at room temperature for no more than 2 hours after thawing. Post-dilution in use period is 6 hours.

Example 44: Shipping and Handling

This example illustrates shipping and handling procedures for a vaccine in a multi-dose vial. The nature of this vaccine requires it to be kept at extremely low temperatures during shipment and storage after it arrives. To achieve this, multiple dose vials of the frozen vaccine are shipped in insulated thermal shipping containers containing dry ice. This allows the vaccine to remain frozen at this low temperature.

Dry ice is the frozen form of carbon dioxide. When heated, most frozen solids melt to a liquid form, but dry ice transforms directly into a gas (sublimation). Dry ice sublimes at temperatures at or above -109°F (-78°C). The main hazards of dry ice include asphyxiation and burns. Use of dry ice in confined spaces (small rooms or walk-in coolers) and/or poorly ventilated areas can result in depletion of oxygen, causing asphyxiation. Exposed skin should be protected from contact with dry ice.

When the thermal shipping container is received, it should be visually inspected to confirm that all ordered quantities, including vial trays and vials, were received in good standing with all vials intact. Use caution when lifting the shipping container, as it may be heavy. Depending

on the amount of vaccine ordered, the shipping container can weigh approximately 36.5 kg (81 lbs). Before opening the thermal shipping container, make sure the area in which you are working has proper ventilation. Use of dry ice in confined spaces, such as small rooms, walk-in coolers, and/or poorly ventilated areas, can result in depletion of oxygen, causing asphyxiation. Make sure to wear safety glasses with side shields or safety goggles and waterproof insulated gloves when handling dry ice. General safety guidance for dry ice includes the following:

Do not touch - avoid eye contact

Use waterproof insulated gloves when removing or adding dry ice to prevent cold burns and frostbite. Avoid contact with face and eyes. Wear safety glasses with side shields or safety goggles.

Do not eat

Dry ice is harmful if eaten or swallowed. If ingested, seek immediate medical care.

Do not store in confined spaces

Dry ice changes to a gas very rapidly at room temperature, displacing oxygen. Only use dry ice in open or well-ventilated areas.

Do not place in airtight containers

Airtight containers may explode as dry ice rapidly expands to a gas when exposed to temperatures above -109°F (-78°C).

Ventilation

At room temperature (including most cold storage temperatures), dry ice becomes carbon dioxide gas, which may cause difficulty breathing or suffocation. If dry ice has been in a closed area, trailer, or container, open doors and allow adequate ventilation before entering. If you feel short of breath or develop a headache, these may be signs that you have inhaled too much carbon dioxide. Leave the area immediately. Carbon dioxide is heavier than air and accumulates in low, poorly ventilated spaces. Operational practices for accessing a closed area where dry ice is present should be reviewed and agreed upon with your Occupational Health and Safety officer.

Burn Treatment

Dry ice may cause cold burns to the skin. Use waterproof insulated gloves when handling dry ice. Seek medical care as directed by the Dry Ice Safety Data Sheet.

Disposal

Once dry ice is no longer needed, open the container and leave it at room temperature in a well-ventilated area. It will readily sublime from a solid to a gas. DO NOT leave dry ice in an unsecured area. DO NOT place in drain or flush in toilet. DO NOT dispose in trash. DO NOT place in a closed area such as an airtight container or walk-in cooler.

Dry Ice Replenishment

The thermal shipping container can be used as a temporary storage device. Dry ice may need to be replenished during this time.

Contents and Packaging

There are several types of thermal shipping containers that can be used. Do not discard the original thermal shipping container or any of its components. Two types of thermal shipper are shown in Figures 151 and 152.

Unpacking thermal shipping containers: For either of the thermal shippers shown in Figures 151 and 152, the first step is to break open the seal of the outer box. When you open the thermal shipping container, you will see a temperature-monitoring device embedded in the foam lid. In the thermal shipping container shown in Figure 151, this lid will be attached to the thermal shipping container. Take caution when opening the lid as you'll notice one flap of the thermal shipping container is permanently affixed to the lid. Do not pull this flap. When opening the lid, use the three finger holes in the foam lid, which will then allow the lid to swing open. When opening the foam lid associated with the thermal shipper shown in Figure 152, gently remove the entire lid (with the temperature-monitoring device still attached) and place to the side.

The temperature-monitoring device continuously tracks the temperature during shipment to ensure the frozen vaccine product has been maintained at the required temperature during transport to vaccination centers. Upon receipt, press and hold the stop button for 5 seconds. Sites are responsible for continuing to monitor the product storage temperature.

Make sure that you are now wearing waterproof insulated gloves and safety glasses with side shields or safety goggles as you prepare to handle layers of the container that have dry ice. Beneath the foam lid is the dry ice pod, which holds a layer of dry ice to help maintain the temperature of the multiple dose vials. There will also be dry ice in compartments in the container that surround the box that holds the vial trays. If using the thermal shipping container as temporary storage, both of those areas will need to be filled when re-icing. Using your waterproof insulated gloves, remove the dry ice pod.

You will now see a lid for the box that holds the vial trays. Open the box and you will see the vial trays. There will be up to 5 vial trays inside. Remove the box that holds the vial trays from the thermal shipping container in order to access and remove the vial trays. Inspect vials for damage. In the event of vial breakage, damage or leakage, to prevent cuts and exposure to the vaccine, do not handle the vial with bare hands. Wear protective gloves and dispose the vial pieces in a medical sharps container using forceps, tongs or other appropriate tools. After removing the vial trays from the thermal shipping container, you must immediately store the vaccine product in the ultra-low temperature (ULT) freezer. If a ULT freezer is not available, the thermal shipping container may be used as temporary storage. If using the thermal shipping container as temporary storage, it must be opened, inspected, and replenished within 24 hours of receipt. After the thermal shipping container is no longer needed to store the vaccine, you can discard the dry ice. Take necessary precautions by reviewing the Dry Ice Safety Data Sheet, and consult with your Occupational Health Department. To discard, open the thermal shipping container and leave it at room temperature in a well ventilated area. It will sublime from a solid to a gas. DO NOT leave dry ice in an unsecured area. DO NOT place in drain or flush in toilet. DO NOT dispose in trash. DO NOT place in a closed area such as an airtight container or walk-in cooler.

Example 45: Vial Trays

This example illustrates trays that are useful for storage of vials containing temperature-sensitive materials. The trays are made of corrugated translucent or white polypropylene (e.g. Akylux®, Biplex®, or equivalent thereof), which provides protection against

static dust. An important consideration for the tray material is that it should avoid becoming brittle at ultra-low temperatures, such as -80°C, and should also keep its strength after thawing (and wetting due to condensation). Several possible specifications of such trays are noted in the table below:

Table 33: Tray Specifications

Tray	Inside (folded): AxBxH (mm)	Outside (folded): AxBxH (mm)	Thickness in mm (±0.25)	Weight (g/m^2)	Type FEFCO	Color
1	580 x 380 x 148.5	586 x 386 x 160.5	3.0	550	0201	Translucent
2	580 x 380 x 148.5	586 x 386 x 152.5	3.0	550	0201	Translucent
3	580 x 380 x 166.5	586 x 386 x 178.5	3.0	550	0201	Translucent
4	383 x 253 x 337.5	390 x 260 x 351.5	3.5	800	0201	Translucent
5	393 x 270 x 291	401 x 278 x 307	4.0	800	0204	Translucent
6	394 x 394 x 262	400 x 400 x 274	3.0	550	0201	Translucent
7	224 x 216 x 36	232 x 232 x 40	2.2	350	0426	White

a. Explanation for calculation of height: (for FEFCO 0210, 0204)

e.g. Tray 4: distance between the score lines for the long flaps: 346 mm; distance between the score lines for the short flaps: 343 mm

Mean height = (346 +343) / 2 = 344.5 mm

Inside dimension: mean height – 2 x thickness = 337.5 mm

Outside dimension: mean height + 2 x thickness = 351.5 mm

b. Design

According to the FEFCO type mentioned in the table above - manufacturer joint tightly sealed.
Joint: Welded. No joint for FEFCO 0426

c. Tolerance

- Dimensions: ± 1 mm on plano, cutted moded
- Dimensions: ± 2 mm, caused by joint
- Height of folded box: - 1 mm / + 3 mm; For FEFCO 0426 tolerance is -1/+1 mm
- Weight: ± 7.5 %
- Thickness: ± 0.25 mm

d. Identification

Each pack is identified with: item number; purchase order number; and quantity per pack.

e. Drawings

Detailed drawings for several example trays are shown in Figures 148, 149, and 150.

Example 46: Dynamic Thawing Simulation

The Covid-19 vaccine is a lipid nanoparticle (LNP) intended to give relief for the global Covid-19 Pandemic that occurred in early 2020. Due to the medical necessity of this product an urgent market introduction of this vaccine is desirable. Recommended storage temperatures at this stage are between -60°C and -90°C. In order to overcome potential temperature limitations of this product, a production process is envisioned where the secondary packaging will happen in line or immediately after the manufacturing steps and secondary packaging will be followed immediately by a freezing step to a temperature between −60°C and −90°C. This is to avoid rethawing between primary and secondary packaging. This study has been performed to support short transfers of the product at room temperature (RT). In previous studies it was proven that the product quality is not impacted by three short temperature excursions from −60°C to −90°C up to −10°C and one excursion up to −5°C. The goal of this study is to investigate the impact of a simulated transportation at RT of 5, 10 and 15 minutes

on the product temperature in order to confirm that the temperature on the worst case positions will stay < −10°C within these transport time intervals. The impact is determined on the actual fill of 0.45mL. As the real product consists largely of water, which has a high heat capacity compared to other chemicals, water will be used as an alternative for the product to follow up the temperature profile. The vials used for this product are 2 mL vials (PPU5A0049) with a 0.45mL fill. The vials were filled, stoppered, crimped and labeled at a filling line. The vials were packed before freezing in Akylux trays. Stacks of 5 trays have been tested during this study.

MATERIALS AND METHODS

Material, Equipment & Instruments

The following is a list of equipment, and instruments used for the execution of the formulation, filling, freezing drying and capping. The list includes, but is not limited to:

Material

- 2mL vials (PPU5A0049): 0.45mL fill, stoppered, crimped, labeled and packed in correct secondary packaging.

Equipment

- Phcbi MDF-DU702VH freezer set at -75°C
- Perforated shelves
- Four Testo 176 temperature loggers with twelve type T thermocouples in total

Thermocouple placement

The heating rate is expected to be different for center vials compared to edge vials. Edge vials are expected to heat faster as they are in closer contact with the surrounding air at RT during transport. RT transport is intended to happen in stacks of five vial trays. Thermocouples (TC) are used to monitor the temperature. Three vial trays are probed in each stack with two thermocouples each (center or edge vials) for a total of twelve thermocouples in the study. TC locations are shown in Figure 153.

Transportation simulation and Temperature read-out

The stacks are placed inside the storage freezer for a sufficient time (>12h) to allow the product to freeze down to the target freezing temperature. Before initiating the transportation simulation, it is confirmed that all product temperatures are between -70°C and -80°C. The stacks are taken out of the freezer and placed on a trolley with a plastic surface. As the temperature difference between the product and the surroundings is very high (90 to 100°C), the thawing study was done under dynamic conditions. As such the continuous supply of air at RT was mimicked. The transportation is simulated by walking around in the laboratory environment for 5, 10 and 15 minutes. Finally, the stacks were placed back in the freezer again and left for at least four hours before reading out the sensors.

Results and Discussion

Figures 154, 155 and 156 show the graph of the temperatures obtained during the dynamic thawing experiment. During the simulations of the RT transport, temperatures on the worst case positions increase rapidly, while the vials in the center of the stack maintain a stable temperature. Once the product is placed back in the freezer, temperatures of the edge positions decrease rapidly.

Table 34 below summarizes the results obtained for each dynamic test duration. It shows that the maximum temperature reached for the 5-minute test was −31.6°C, for the 10 minute test −18.2°C and for the 15 minute test −17°C. Once the temperature of the product is greater than −20°C, the slope at which the product temperature increases starts to decrease. All product temperatures stayed well below −10°C. Based on this data, a maximum of 15 minutes room transportation time can be allowed for a stack of five vial trays.

Table 34: Tabulated results for thawing time and recover time for 0.45 mL fill

	Maximum temperature during thawing		
	5 min test	**10 min test**	**15 min test**
Thawing time (min)	**Maximum product temperature (°C)**		
3	**-39.8**	**-40.7**	**-51.8**
5	**-31.6**	**-32.1**	**-40.9**
7	**N/A**	**-26.1**	**-33.8**

10	**N/A**	**-18.2**	**-25.9**
15	**N/A**	**N/A**	**-18.0**

Based on Figures 154, 155, and 156 it is also noted that the product which is in contact with the surface of the trolley has a slightly faster temperature increase compared to the product in the top vial tray. It is expected that the heat conduction properties of the surface on which a frozen vial tray is placed might play an important role in the thawing speed.

Conclusions

Stacks of five vial trays each filled with vials with a fill volume 0.45 mL were tested towards temperature increase during transportation at RT. In order to do so, the stacks were placed on separate trolleys which were transported for 5, 10 and 15 minutes, respectively. The results show that RT transport times up to 15 minutes can be tolerated. During these short times product temperature will not increase above -10°C. Product data is available showing that multiple excursions to −10°C and single excursions to −5°C will not impact the product quality.

Example 47: Arrangement of Vials in Trays

This example illustrates how vials can be placed in a tray in order to maximize the payload that can effectively be kept at sufficiently cold temperature (e.g. -80°C) given the space constraints of a thermal shipper, and vial tray as described in Examples 43, 44 and 45.

With the payload space defined by the thermal shipper (see Examples 43 and 44) as about 229 x 229 x 229 mm, several configurations were tried that included different vial tray sizes, as well as how the vials were placed inside the vial trays. Table 35 below summarizes the configurations that were explored for optimum payload given the size constraints, and the requirement that the payload be kept at a sufficiently cold temperature.

Table 35: Proposed Vial Configurations in Thermal Shipper in Fixed Payload Space

Configuration	A*	B*	H*	#vials/tray	#trays/layer	#layers/box	#vials/box
A	179	92	43	(10 x 5) 50	2	4	400

B	91.3	92	43	(5 x 5) 25	4	4	400
C	86	87	41	(5 x 5) 25	4	5	500
D	86	86	41	(5 x 5) 25	4	5	500
E	102	102	41	(6 x 6) 36	4	5	720
F	211	211	41	(12 x 12) 144	1	5	720
G	211	211	41	(11x7)+(12x7) 161	1	5	805
H	229	229	44	(13 x 13) 169	1	5	845
I	229	229	44	(13x8)+(12x7) 188	1	5	940
J	229	229	44	(13 x 15) 195	1	5	975
K	195	105	41	(11 x 6) 66	2	5	660
L	200	105	41	(12 x 6) 72	2	5	720

*A, B, and H are the dimensions (in mm) of the vial tray used, and as further illustrated in Figures 157 to 167

As can be seen further in Figures 157 to 167, configurations A to L demonstrate a variety of options that were considered in order to maximize the number of vials that could be placed in a fixed volume (about 229 x 229 x 229 mm), as constrained by the thermal shipper that was designed to keep the material in the vial at an ultra-low temperature (e.g. -80°C). As shown

in Table 35, Configuration J resulted in the maximum number of vials (975) that can be accommodated in this space.

We Claim:

1. A kit comprising: a) a primary container; b) a payload container; c) at least one tray placed within the payload container; and d) a dry ice container; wherein the at least one tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

2. The kit according to claim 1, wherein the payload container has the dimensions of about 229 mm x 229 mm x 229 mm.

3. The kit according to any of claims 1-2, wherein the at least one tray contains a temperature-sensitive material.

4. The kit according to claim 3, wherein the kit is capable of maintaining the temperature of the material within the tray at −50°C or lower for at least 10 days.

5. The kit according to any of claims 3-4, wherein the kit is capable of maintaining the temperature of the material within the tray at −70°C or lower for at least 10 days.

6. The kit according to any of claims 3-5, wherein the kit is capable of maintaining the temperature of the material within the tray at −80°C for at least 10 days.

7. The kit according to any of claims 1-6, further comprising a temperature monitoring system.

8. The kit according to any of claims 1-7, further comprising a light sensor.

9. The kit according to any of claims 3-8, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein the temperature monitoring system is capable of displaying or warning when the temperature inside the payload container is greater than about −80° C.

10. The kit according to any of claims 1-9, wherein the primary container comprises a top portion and a bottom portion, and the primary container is configured

to receive the payload container in the bottom portion and to receive the dry ice container in the top portion.

11. The kit according to any of claims 1-10, wherein the payload container is configured to receive the at least one tray.

12. The kit according to any of claims 1-11, wherein the payload container is capable of containing one or more trays within the payload container simultaneously.

13. The kit according to any of claims 1-12, wherein the payload container is capable of containing 1, 2, 3, 4, or 5 trays within the payload container simultaneously.

14. The kit according to any of claim 3-13, wherein the temperature-sensitive material is contained within at least one glass vial, and wherein the at least one glass vial is placed within the tray.

15. The kit according to claim 14, where the at least one glass vial is a multi-dose vial.

16. The kit according to any of claims 1-15, wherein each tray is configured to contain at least 25 vials, or wherein at least one tray contains at least 25 vials.

17. The kit according to any of claims 1-16, wherein each tray is configured to contain at least 50 vials, or wherein at least one tray contains at least 50 vials.

18. The kit according to any of claims 1-17, wherein each tray is configured to contain at least 75 vials, or wherein at least one tray containst at least 75 vials.

19. The kit according to any of claims 1-18, wherein each tray is configured to contain at least 125 vials, or wherein at least one tray contains at least 125 vials.

20. The kit according to any of claims 1-19, wherein each tray is configured to contain at least 150 vials, or wherein at least one tray contains at least 150 vials.

21. The kit according to any of claims 1-20, wherein each tray is configured to contain at least 195 vials, or wherein at least one tray contains at least 195 vials.

22. A container system comprising: a) a primary container; b) a payload container that is configured to receive at least one tray; and c) a dry ice container; wherein the at least one tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

23. The container system according to claim 19, wherein the payload container has the dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 228 to about 233 mm.

24. The container system according to claim 20, wherein the payload container has the dimensions of about 229 mm x 229 mm x 229 mm.

25. The container system according to any of claims 22-24, wherein the at least one tray contains a temperature-sensitive material.

26. The container system according to any of claims 22-25, further comprising a temperature monitoring system.

27. The container system according to any of claims 22-25, further comprising a light sensor.

28. The container system according to any of claims 25-27, wherein the system is capable of maintaining the temperature of the material within the tray at −50°C or lower for at least 10 days.

29. The container system according to any of claims 25-28, wherein the system is capable of maintaining the temperature of the material within the tray at −70°C or lower for at least 10 days.

30. The container system according to any of claims 25-29, wherein the system is capable of maintaining the temperature of the material within the tray at −80°C or lower for at least 10 days.

31. The container system according to any of claims 22-30, wherein the primary container comprises a top portion and a bottom portion, and the primary container is

configured to receive the payload container in the bottom portion and to receive the dry ice container in the top portion.

32. The container system according to any of claims 22-31, wherein the payload container is configured to receive the at least one tray.

33. The container system according to any of claims 22-32, wherein the payload container is capable of containing one or more trays within the payload container simultaneously.

34. The container system according to any of claims 22-33, wherein the payload container is capable of containing 1, 2, 3, 4, or 5 trays within the payload container simultaneously.

35. The container system according to any of claims 25-34, wherein the temperature-sensitive material is contained within at least one glass vial, and wherein the at least one glass vial is placed within the tray.

36. The container system according to claim 35, wherein the at least one glass vial is a multi-dose vial.

37. The container system according to any of claims 22-36, wherein each tray is configured to contain at least 25 vials, or wherein at least one tray contains at least 25 vials.

38. The container system according to any of claims 22-37, wherein each tray is configured to contain at least 100 vials, or wherein at least one tray contains at least 100 vials.

39. The container system according to any of claims 22-38, wherein each tray is configured to contain at least 195 vials, or wherein at least one tray contains at least 195 vials.

40. A method of transporting a temperature-sensitive material comprising the steps of: a) placing the material in a kit according to any of claims 1-21, or in a

container system according to any of claims 23-39; and b) transporting the kit or container system.

41. The method according to claim 40, wherein the temperature inside the payload container is continuously monitored throughout the duration of the transporting .

42. The method according to any of claims 40-41, where the transporting is carried out on land, air, and/or water.

43. The method according to any of claims claim 40-42, where the transporting is carried out via land vehicle, airplane, and/or boat.

44. The method according to any of claims 40-43, wherein the temperature inside the payload container is maintained at −70°C or lower throughout the duration of the transporting.

45. The method according to any of claims 40-44, wherein the temperature inside the payload container is maintained at −80°C or lower throughout the duration of the transporting.

46. The method according to any of claims 40-45, wherein there are at least 150 vials in each tray.

47. The method according to any of claims 40-46, wherein there are 195 vials in each tray.

48. The method according to any of claims 40-47, wherein there are at least 5 trays within the payload container.

49. The method according to any of claims 40-48, wherein the location of the kit or container system is at least periodically monitored through use of a global positioning system (GPS).

50. A payload container having dimensions of about 229 mm x 229 mm x 229 mm, and is configured to receive at least five trays within the payload container, and

wherein each tray is configured to hold at least 100 vials of temperature-sensitive material.

51. A payload container having dimensions of about 229 mm x 229 mm x 229 mm, wherein at least 5 trays are placed within the payload container, and wherein each tray contains at least 100 vials of temperature-sensitive material.

52. The payload container according to any of claims 50-51, wherein each tray contains at least 150 vials of temperature-sensitive material.

53. The payload container according to any of claims 50-52, wherein each tray contains 195 vials of temperature-sensitive material.

54. A tray configured for carrying temperature-sensitive material, wherein the tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm.

55. The tray according to claim 54, configured to hold at least 150 vials within the tray.

56. The tray according to any of claims 54-55, configured to hold 195 vials within the tray.

57. A tray configured for carrying temperature-sensitive material, wherein the tray has dimensions A x B x H, where A is about 228 to about 233 mm, B is about 228 to about 233 mm, and H is about 38 to about 46 mm, and wherein the tray contains at least 150 vials.

58. The tray according to claim 57, wherein the tray contains 195 vials.

59. A multi-dose formulation comprising a lipid nanoparticle encapsulated mRNA, wherein the multi-dose formulation is capable of remaining stable for a specified time with multiple or repeated withdraws of at least a portfion of the formulation from a container for the multi-dose formulation.

60. The formulation according to claim 59, comprising at least 2 doses per container.

61. The formulation according to any one of claims 59-60, comprising a total of 5 doses per container.

62. The formulation according to any one of claims 59-61, comprising a total of 6 doses per container.

63. The formulation according to any one of claims 59-60, comprising a total of 2 to 12 doses per container.

64. The formulation according to any one of claims 59-63, wherein each dose is equal in volume.

65. The formulation according to any one of claims 59-64, wherein the formulation has a total volume of 1-3 mL.

66. The formulation according to any one of claims 59-65, wherein the formulation is frozen.

67. The formulation according to any one of claims 59-66, wherein the formulation comprises RNA encoding:

an amino acid sequence comprising a SARS-CoV-2 S protein and/or an immunogenic variant thereof; and/or

an immunogenic fragment of the SARS-CoV-2 S protein and/or an immunogenic variant thereof.

68. A composition comprising RNA encoding:

an amino acid sequence comprising a SARS-CoV-2 S protein and/or an immunogenic variant thereof; and/or

an immunogenic fragment of the SARS-CoV-2 S protein and/or an immunogenic variant thereof,

wherein the composition or medical preparation has been stored at a temperature below -20 °C and protected from light, and wherein the RNA is stable.

69. The composition according to claim 68, wherein the composition further comprises one or more lipid nanoparticle encapsulating the RNA.

70. The composition according to any one of claims 68- 69, wherein the lipid nanoparticle is stable.

71. The composition according to any one of claims 68- 70, wherein the composition is a medical preparation suitable for administration to a subject.

72. A kit comprising (a) a composition comprising a lipid nanoparticle encapsulated mRNA; and (b) a temperature monitoring system.

73. The kit according to claim 72, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein the temperature monitoring system is capable of displaying and/or warning when the temperature of the kit attains a temperature above about −80° C.

74. The kit according to claim 72, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein the temperature monitoring system is capable of displaying or warning when the temperature of the kit attains a temperature above about −60° C.

75. The kit according to claim 72, wherein the temperature monitoring system comprises a temperature sensor and a display, wherein the temperature monitoring system is capable of displaying or warning when the temperature of the kit attains a temperature above about −20° C.

76. A kit comprising (a) a composition comprising a lipid nanoparticle encapsulated mRNA; and (b) a light sensor.

77. The kit according to claim 76, wherein the composition is protected from light.

78. The kit according to any one of claims 76-77, wherein the light sensor comprises a photosensitive element configured to react to exposure to light, resulting in a change in a material and/or electrical property of the photosensitive element.

79. The kit according to any one of claims 76-78, wherein the composition does not contain more than 0.1% by weight of degradation products produced by exposure of the mRNA to light during some or all of the preparation, storage, transport, characterization, and/or use of the composition.

80. A kit comprising (a) a composition comprising a lipid nanoparticle encapsulated mRNA; and (b) a real-time monitoring of temperature, light, and/or location logging device.

81. A method of shipping and/or storing a composition comprising shipping and/or storing a lipid nanoparticle encapsulated mRNA wherein the composition is filled into a glass vial or syringe; wherein the glass vial or syringe comprises at least one dose.

82. The method according to claim 81, wherein the glass vial or syringe comprises multiple doses.

83. The method according to any one of claims 81-82, wherein the glass vial or syringe comprises 2-6 doses.

84. The method according to any one of claims 81-83, wherein the composition is shipped or stored at a temperature at or below 4°C.

85. The method according to any one of claims 81-84, wherein the composition is shipped or stored at a temperature at or below 0°C.

86. The method according to any one of claims 81-85, wherein the composition is shipped or stored at a temperature at or below -20°C.

87. The method according to any one of claims 81-86, wherein the composition is shipped or stored at a temperature at or below -60°C.

88. The method according to any one of claims 81-87, wherein the composition is shipped or stored at a temperature at or below -80°C.