CLAIMS

What is claimed is:

1. A truncated hepatitis B virus (HBV) polymerase polypeptide comprising an inactivated reverse transcriptase domain and an inactivated RNase H, wherein the polypeptide does not comprise all of the terminal protein (TP) domain and does not comprise all or part of the Spacer domain.

2. The truncated HBV polymerase polypeptide of claim 1, wherein the polypeptide is no longer than 600 amino acids in length, e.g., no longer than 595, 590, 585, 580, 575, 570, 565, 560, 555, 550, 545, 540 or 535 amino acids in length.3. The truncated HBV polymerase polypeptide of any one of claims 1 to 2, wherein the reverse transcriptase domain does not comprise a YMDD motif and the RNase H domain does not comprise an AELL motif.

4. The truncated HBV polymerase polypeptide of claim 3, wherein the YMDD motif in the reverse transcriptase domain is mutated to YMHD and wherein the AELL motif in the RNase H domain is mutated to AHLL.

5. The truncated HBV polymerase polypeptide of any one of claims 1 to 4, wherein the polypeptide is from an HBV genotype A, B, C or D.

6. The truncated HBV polymerase polypeptide of claim 5, wherein:

a) the polypeptide is from HBV genotype B and does not comprise a polypeptide sequence of SEQ ID NO: 50, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 50; or

b) the polypeptide is from HBV genotype D and does not comprise a polypeptide sequence of SEQ ID NO: 51, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 51.

7. The truncated HBV polymerase polypeptide of any one of claims 1 to 6, wherein the polypeptide comprises or consists of an amino acid sequence of any one of SEQ ID NOs: 13-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14.

8. The truncated HBV polymerase polypeptide of any one of claims 1 to 7, wherein the polypeptide does not comprise an amino sequence or fragment thereof from another HBV protein.

9. The truncated HBV polymerase polypeptide of any one of claims 1 to 8, wherein the polypeptide does not comprise an amino sequence or fragment thereof from an HBV protein selected from the group consisting of pre-core, core, X and envelope (e.g., small, medium or large surface antigen (sAg)).

10. An HBV polymerase deletion mutant polypeptide, comprising in sequential order from the N-terminus to the C-terminus, a terminal protein (TP) domain, an inactivated reverse transcriptase domain, and an inactivated RNase H, wherein the mutant polypeptide does not comprise all or part of a Spacer domain.

11. The HBV polymerase deletion mutant polypeptide of claim 1, wherein the polypeptide is no longer than 800 amino acids in length, e.g., no longer than 795, 790, 785, 780, 775, 770, 765, 760, 755, 750, 745, 740, 735, 730, 725, 720, 715, 710 or 705 amino acids in length.

12. The HBV polymerase deletion mutant polypeptide of any one of claims 10 to 11, wherein the reverse transcriptase domain does not comprise a YMDD motif and the RNase H domain does not comprise an AELL motif.

13. The HBV polymerase deletion mutant polypeptide of claim 12, wherein the YMDD motif in the reverse transcriptase domain is mutated to YMHD and wherein the AELL motif in the RNase H domain is mutated to AHLL.

15. The HBV polymerase deletion mutant polypeptide of claim 14, wherein:

a) the polypeptide is from HBV genotype A and does not comprise a polypeptide of SEQ ID NO: 42 or 46, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 42 or 46;

b) the polypeptide is from HBV genotype B and does not comprise a polypeptide of SEQ ID NO: 43 or 47, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 43 or 47;

c) the polypeptide is from HBV genotype C and does not comprise a polypeptide of SEQ ID NO: 44 or 48, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 44 or 48; or

d) the polypeptide is from HBV genotype D and does not comprise a polypeptide of SEQ ID NO: 45 or 49, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 45 or 49.

16. The HBV polymerase deletion mutant polypeptide of any one of claims 10 to 15, wherein the polypeptide comprises or consists of an amino acid sequence of any one of SEQ ID NOs: 5-12, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 5-12.

17. The HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, further comprising an HBV core polypeptide.

18. The HBV polymerase deletion mutant polypeptide of claim 17, comprising in sequential order from the N-terminus to the C-terminus, an HBV core polypeptide and the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16.

19. The HBV polymerase deletion mutant polypeptide of any one of claims 17 to 18, wherein the polypeptide comprises or consists of an amino acid sequence of any one of SEQ ID NOs: 19-26, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 19-26.

20. The HBV polymerase deletion mutant polypeptide of any one of claims 10 to 19, wherein the polypeptide does not comprise an amino sequence or fragment thereof from an HBV protein selected from the group consisting of X, pre-core, and envelope (e.g., small, medium or large surface antigen (sAg)).

21. A fusion protein comprising in sequential order from the N-terminus to the C-terminus, an HBV core polypeptide and an HBV small surface antigen (sAg) polypeptide, wherein:

a) the core polypeptide is from an HBV genotype B or C and the sAg polypeptide is from an HBV genotype C; or

b) the core polypeptide is from an HBV genotype D and the sAg polypeptide is from an HBV genotype D.

22. The fusion protein of claim 21, comprising

a) a core polypeptide comprising or consisting of an amino acid sequence of SEQ ID NO: 65, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 65, and a sAg polypeptide comprising or consisting of an amino acid sequence of SEQ ID NO: 3, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical SEQ ID NO: 3; or

b) a core polypeptide comprising or consisting of an amino acid sequence of SEQ ID NO: 66, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 66, and a sAg polypeptide comprising or consisting of an amino acid sequence of SEQ ID NO: 4, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical SEQ ID NO: 4.

23. The fusion protein of any one of claims 21 to 22, wherein the core polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, and an asparagine (N) residue at the amino acid position corresponding to position 67, wherein the position numbers are with reference to SEQ ID NO:65 or SEQ ID NO:66.

24. The fusion protein of any one of claims 21 to 23, wherein the sAg polypeptide comprises an isoleucine (I) residue at the amino acid position corresponding to position 68, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

25. The fusion protein of any one of claims 21 to 24, wherein the sAg polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 53, an isoleucine (I) residue at the amino acid position corresponding

to position 68, a threonine (T) residue at the amino acid position corresponding to position 125, a proline (P) residue at the amino acid position corresponding to position 127, an phenylalanine (F) residue at the amino acid position corresponding to position 161, a tyrosine (Y) residue at the amino acid position corresponding to position 200, a serine (S) residue at the amino acid position corresponding to position 210, and a leucine (L) residue at the amino acid position corresponding to position 213, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

26. The fusion protein of any one of claims 21 to 25, wherein the sAg polypeptide does not comprise a pre-S2 polypeptide.

27. The fusion protein of any one of claims 21 to 26, wherein the sAg polypeptide does not comprise an HBV pre-S2 polypeptide comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 79-83, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 79-83.

28. The fusion protein of any one of claims 21 to 27, wherein the sAg polypeptide does not comprise both of an HBV pre-S1 polypeptide and an HBV pre-S2 polypeptide.

29. The fusion protein of any one of claims 21 to 28, wherein the sAg polypeptide does not comprise an HBV pre-S1-pre-S2 polypeptide comprising or consisting of an amino acid sequence of any one of SEQ ID NO: 84-88, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 84-88.

30. The fusion protein of any one of claims 21 to 29, comprising a cleavable linker operably linked to and positioned between the HBV core polypeptide and the HBV sAg polypeptide.

31. The fusion protein of claim 30, wherein the cleavable linker is a 2A cleavable peptide.

32. The fusion protein of any one of claims 30 to 31, wherein the cleavable linker is a 2A cleavable peptide selected from the group consisting of foot-and-mouth disease

virus (F2A), equine rhinitis A virus (E2A), porcine teschovirus-1 (P2A) and Thosea asigna virus (T2A).

33. The fusion protein of any one of claims 30 to 32, wherein the cleavable linker comprises or consists of an amino acid sequence of ATNFSLLKQAGDVEENPGP (SEQ ID NO: 56), APVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 57), QCTNYALLKLAGDVESNPGP (SEQ ID NO: 58), or EGRGSLLTCGDVEENPGP (SEQ ID NO: 59), or an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% identical to ATNFSLLKQAGDVEENPGP (SEQ ID NO: 56), APVKQTLNFDLLKLAGDVESNPGP (SEQ ID NO: 57), QCTNYALLKLAGDVESNPGP (SEQ ID NO: 58), or EGRGSLLTCGDVEENPGP (SEQ ID NO: 59).

34. The fusion protein of any one of claims 30 to 33, wherein the cleavable linker is a porcine teschovirus-1 (P2A) linker.

35. The fusion protein of any one of claims 30 to 32, wherein the cleavable linker comprises or consists of an amino acid sequence of ATNFSLLKQAGDVEENPGP (SEQ ID NO: 56), or an amino acid sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or at least 99% identical to ATNFSLLKQAGDVEENPGP (SEQ ID NO: 56).

36. The fusion protein of any one of claims 30 to 35, further comprising a flexible linker and/or a furin recognition/cleavage site operably linked to and positioned N-terminal to the cleavable linker and C-terminal to the HBV core polypeptide.

37. The fusion protein of claim 36, wherein the furin recognition/cleavage site comprises or consists of an amino acid sequence selected from the group consisting of RAKR (SEQ ID NO: 60), REKR (SEQ ID NO: 61) and RRKR (SEQ ID NO: 62).

38. The fusion protein of any one of claims 36 to 37, wherein the flexible linker comprises a polyglycine or polyalanine sequence.

39. The fusion protein of any one of claims 36 to 38, wherein the flexible linker comprises or consists of a polyglycine or polyalanine sequence selected from the group consisting of AA, AAA, AAY, GG, GGG, GGS, GSG and GGGS (SEQ ID NO: 63).

40. The fusion protein of any one of claims 21 to 39, wherein the fusion protein is no longer than 450 amino acids in length, e.g., no longer than 445, 440, 435, 430, 425, 420, 415 or 410 amino acids in length.

41. The fusion protein of any one of claims 21 to 40, comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.

42. The fusion protein of any one of claims 21 to 41, comprising or consisting of an amino acid sequence of any one of SEQ ID NO: 41, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 41.

43. The fusion protein of any one of claims 41 to 42, wherein the fusion polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, an asparagine (N) residue at the amino acid position corresponding to position 67, a valine (V) residue at the amino acid position corresponding to position 74, a phenylalanine (F) residue at the amino acid position corresponding to position 97, a threonine (T) residue at the amino acid position corresponding to position 249, a threonine (T) residue at the amino acid position corresponding to position 250, a serine (S) residue at the amino acid position corresponding to position 317, a serine (S) residue at the amino acid position corresponding to position 318, an arginine (R) residue at the amino acid position corresponding to position 326, a tyrosine (Y) residue at the amino acid position corresponding to position 338, a glycine (G) residue at the amino acid position corresponding to position 363, and an alanine (A) residue at the amino acid position corresponding to position 372, wherein the position numbers are with reference to SEQ ID NO:41.

44. The fusion protein of any one of claims 21 to 43, wherein the fusion polypeptide does not comprise an amino sequence or fragment thereof from an HBV protein selected from the group consisting of X, pre-core, pre-S1 and pre-S2.

45. The truncated HBV polymerase polypeptide of any one of claims 1 to 9, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 20, or the fusion protein of any one of claims 21 to 44, further comprising an N-terminal signal peptide or leader sequence.

~~46. The polypeptide or fusion protein of claim 45, wherein the signal peptide or leader sequence is from a source protein selected from a serum protein, a cytokine, a chemokine, a chaperone protein, an invariant protein, and a protein that directs proteins to the lysosomal compartment.~~

~~47. The polypeptide or fusion protein of any one of claims 45 to 46, wherein the signal peptide or leader sequence is from a source protein selected from the group consisting of colony stimulating factor 2 (CSF2, GM-CSF), tissue type plasminogen activator (PLAT, t-PA), C-C motif chemokine ligand 7 (CCL7, MCP-3), C-X-C motif chemokine ligand 10 (CXCL10, IP-10), catenin beta 1 (CTNNB1), CD74 (p33; DHLAG; HLADG; Ia-GAMMA, invariant chain), serum albumin (ALB), polyubiquitin B/C (UBB/UBC), calreticulin (CALR), vesicular stomatitis virus G protein (VSV-G), lysosomal associated membrane protein 1 (LAMP-1) and lysosomal associated membrane protein 2 (LAMP-2).~~

~~48. The polypeptide or fusion protein of any one of claims 45 to 47, wherein the signal peptide or leader sequence is selected from an amino acid sequence of any one of SEQ ID NOs: 67-78, or a sequence that is at least 95%, 96%, 97%, 98%, or 99% identical to any one of SEQ ID NOs: 67-78.~~

~~49. The truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, or the core-sAg fusion protein of any one of claims 21 to 44, wherein the polypeptide or fusion protein is recombinantly produced or chemically synthesized.~~

~~50. The truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, or the core-sAg fusion protein of any one of claims 21 to 44, wherein the polypeptide or fusion protein is capable of inducing, promoting or stimulating an immune response in a human.~~

~~51. The truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, or the core-sAg fusion protein of any one of claims 21 to 44, wherein the polypeptide or fusion protein is capable of inducing, promoting or stimulating an immune response against HBV in a human.~~

~~52. The truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, or the core-sAg~~

~~fusion protein of any one of claims 21 to 44, wherein the polypeptide or fusion protein is capable of inducing, promoting or stimulating proliferation and/or activation of one or more cell types selected from monocyte-derived dendritic cells (DCs), CD8+ T cells and CD4+ T cells.~~

~~53. A polynucleotide encoding the truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, or the core-sAg fusion protein of any one of claims 21 to 44.~~

~~54. The polynucleotide of claim 53, wherein the polynucleotide comprises cDNA, mRNA, self-amplifying RNA (SAM), self-replicating RNA, or self-amplifying replicon RNA (RepRNA).~~

~~55. The polynucleotide of claim 54, wherein the polynucleotide comprises self-replicating or self-amplifying alphavirus replicons.~~

~~56. The polynucleotide of any one of claims 53 to 55, comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 27-37 and 89-94, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 27-37 and 89-94.~~

~~57. A lipid nanoparticle (LNP) comprising one or more polynucleotides of any one of claims 53 to 56.~~

~~58. An expression cassette, comprising a polynucleotide of any one of claims 53 to 56 operably linked to one or more regulatory sequences.~~

~~59. The expression cassette of claim 58, wherein the polynucleotide is operably linked to and under the control of a constitutive promoter.~~

~~60. The expression cassette of any of claims 58 to 59, wherein the promoter is selected from cytomegalovirus major immediate-early (CMV), the CMV enhancer fused to the chicken beta-actin promoter (CAG), human elongation factor-1α (HEF-1α), mouse cytomegalovirus (mouse CMV), Chinese hamster elongation factor-1α (CHEF-1α), and phosphoglycerate kinase (PGK).~~

~~61. A vector comprising one or more polynucleotides of any one of claims 53 to 56, or an expression cassette of any one of claims 58 to 60.~~

~~62. The vector of claim 61, wherein the vector is a plasmid vector, a bacterial vector or a viral vector.~~

~~63. The vector of any one of claims 61 to 62, wherein the vector is a viral vector.~~

~~64. The vector of any one of claims 61 to 63, wherein the viral vector is a DNA virus or an RNA virus.~~

~~65. The vector of any one of claims 61 to 64, wherein the viral vector is from a virus selected from the group consisting of adenovirus, adeno-associated virus, arenavirus, alphavirus, poxvirus, cytomegalovirus, rhabdovirus, vesicular stomatitis virus, flavivirus, maraba virus and vaccinia virus.~~

~~66. The vector of any one of claims 61 to 65, wherein the viral vector is from a virus from a taxonomic family selected from Adenoviridae, Arenaviridae, Herpesviridae (*e.g.* Cytomegalovirus), Poxviridae (*e.g.* Vaccinia virus, *e.g.* modified vaccinia Ankara (MVA)), Flaviviridae (*e.g.* Yellow fever virus), Rhabdoviridae (*e.g.* Vesiculovirus, *e.g.* Maraba vesiculovirus), Togaviridae (*e.g.*, Alphavirus).~~

~~67. The vector of any one of claims 61 to 66, wherein the viral vector is an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV), Cali mammarenavirus (*a.k.a.*, Pichinde mammarenavirus or Pichinde arenavirus), Guanarito virus (GTOV), Junin virus (JUNV), Lassa virus (LASV), Lujo virus (LUJV), Machupo virus (MACV), Sabia virus (SABV), and Whitewater Arroyo virus (WWAV).~~

~~68. The vector of claim 67, wherein the viral vector is an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV) or Cali mammarenavirus.~~

~~69. The vector of any one of claims 61 to 66, wherein the viral vector is a human adenovirus or a simian adenovirus (*e.g.*, a chimpanzee adenovirus, a gorilla adenovirus or a rhesus adenovirus).~~

70. The vector of claim 69, wherein the viral vector is an adenovirus vector selected from adenovirus serotype 5 (Ad5), adenovirus serotype 26 (Ad26), adenovirus serotype 34 (Ad34), adenovirus serotype 35 (Ad35), adenovirus serotype 48 (Ad48), chimpanzee adenovirus (*e.g.* ChAdOx1, ChAdOx2, ChAd3 (AdC3), ChAd5 (AdC5), ChAd6 (AdC6), ChAd7 (AdC7), ChAd8 (AdC8), ChAd9 (AdC9), ChAd10 (AdC10), ChAd11 (AdC11), ChAd17 (AdC17), ChAd16 (AdC16), ChAd19 (AdC19), ChAd20 (AdC20), ChAd22 (AdC22), ChAd24 (AdC24), ChAdY25, ChAd26 (AdC26), ChAd28 (AdC28), ChAd30 (AdC30), ChAd31 (AdC31), ChAd37 (AdC37), ChAd38 (AdC38), ChAd43 (AdC43), ChAd44 (AdC44), ChAd55 (AdC55), ChAd63 (AdC63), ChAdV63, ChAd68 (AdC68), ChAd73 (AdC73), ChAd82 (AdC82), ChAd83 (AdC83), ChAd143 (AdC143), ChAd144 (AdC144), ChAd145 (AdC145), ChAd147 (AdC147)), gorilla adenovirus (*e.g.* GC44, GC45, GC46) and rhesus adenovirus (*e.g.*, RhAd51, RhAd52, RhAd53, RhAd54, RhAd55, RhAd56, RhAd57, RhAd58, RhAd59, RhAd60, RhAd61, RhAd62, RhAd63, RhAd64, RhAd65, RhAd66).

71. The vector of any one of claims 61 to 70, wherein the viral vector is replication-defective, replication-deficient, replication-attenuated or replication-competent.

72. The vector of any one of claims 61 to 68, wherein the viral vector is a replication-defective arenavirus having a bi-segmented genome.

73. The vector of any one of claims 61 to 68, wherein the viral vector is a replication-attenuated arenavirus having a tri-segmented genome.

74. An arenavirus vector comprising a polynucleotide encoding an HBV core-sAg fusion polypeptide comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41, and wherein the sAg polypeptide does not comprise an HBV pre-S1 polypeptide and/or an HBV pre-S2 polypeptide.

75. The arenavirus vector of claim 74, comprising a polynucleotide encoding an HBV core-sAg fusion polypeptide comprising or consisting of an amino acid sequence of any one of SEQ ID NO: 41, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 341, and wherein the sAg polypeptide does not comprise an HBV pre-S1 polypeptide and/or an HBV pre-S2 polypeptide.

~~76. The arenavirus vector of any one of claims 74 to 75, wherein the core polypeptide comprises a serine (S) residue at the amino acid position corresponding to position 12, and an asparagine (N) residue at the amino acid position corresponding to position 67, wherein the position numbers are with reference to SEQ ID NO:65 or SEQ ID NO:66.~~

~~77. The arenavirus vector of any one of claims 74 to 76, wherein the sAg polypeptide comprises an isoleucine (I) residue at the amino acid position corresponding to position 68, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.~~

~~78. The arenavirus vector of any one of claims 74 to 77, wherein the sAg polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 53, an isoleucine (I) residue at the amino acid position corresponding to position 68, a threonine (T) residue at the amino acid position corresponding to position 125, a proline (P) residue at the amino acid position corresponding to position 127, an phenylalanine (F) residue at the amino acid position corresponding to position 161, a tyrosine (Y) residue at the amino acid position corresponding to position 200, a serine (S) residue at the amino acid position corresponding to position 210, and a leucine (L) residue at the amino acid position corresponding to position 213, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.~~

~~79. The arenavirus vector of any one of claims 74 to 78, wherein the core-sAg fusion polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, an asparagine (N) residue at the amino acid position corresponding to position 67, a valine (V) residue at the amino acid position corresponding to position 74, a phenylalanine (F) residue at the amino acid position corresponding to position 97, a threonine (T) residue at the amino acid position corresponding to position 249, a threonine (T) residue at the amino acid position corresponding to position 250, a serine (S) residue at the amino acid position corresponding to position 317, a serine (S) residue at the amino acid position corresponding to position 318, an arginine (R) residue at the amino acid position corresponding to position 326, a tyrosine (Y) residue at the amino acid position corresponding to position 338, a glycine (G) residue at the amino acid position corresponding to position 363, and an alanine (A) residue at the amino acid position corresponding to position 372, wherein the position numbers are with reference to SEQ ID NO:41.~~

~~80. The arenavirus vector of any one of claims 74 to 79, wherein the polynucleotide comprises or consists of a nucleic acid sequence of any one of SEQ ID NOs: 33-~~

~~37, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 33-37.~~

~~81. The arenavirus vector of any one of claims 74 to 80, wherein the polynucleotide comprises or consists of a nucleic acid sequence of SEQ ID NO: 37, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.~~

~~82. The arenavirus vector of any one of claims 74 to 81, wherein the vector has a bisegmented genome and further comprises a polynucleotide encoding a truncated HBV polymerase comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 13-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14, and wherein the truncated HBV polymerase does not comprise all of an HBV polymerase terminal protein (TP) domain and does not comprise all or part of an HBV polymerase Spacer domain.~~

~~83. The arenavirus vector of claim 82, wherein the truncated HBV polymerase does not comprise a polypeptide sequence of SEQ ID NO: 50 or SEQ ID NO:51, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 50 or SEQ ID NO: 51.~~

~~84. The arenavirus vector of any one of claims 82 to 83, wherein the polynucleotide comprises or consists of a nucleic acid sequence of any one of SEQ ID NOs: 29 and 89-94, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 29 and 89-94.~~

~~85. The arenavirus vector of any one of claims 82 to 84, wherein the arenavirus vector is a Lymphocytic choriomeningitis mammarenavirus (LCMV) vector and the polynucleotide comprises or consists of a nucleic acid sequence of SEQ ID NO: 29, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 29.~~

~~86. The arenavirus vector of any one of claims 82 to 84, wherein the arenavirus vector is a Cali mammarenavirus vector and the polynucleotide comprises or consists~~

of a nucleic acid sequence of SEQ ID NO: 90, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90.

87. An arenavirus vector comprising a polynucleotide encoding a truncated HBV polymerase comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 13-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14, and wherein the truncated HBV polymerase does not comprise all of an HBV polymerase terminal protein (TP) domain and does not comprise all or part of an HBV polymerase Spacer domain.

88. The arenavirus vector of claim 87, wherein the truncated HBV polymerase does not comprise a polypeptide sequence of SEQ ID NO: 50 or SEQ ID NO:51, or a sequence that is at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 50 or SEQ ID NO: 51.

89. The arenavirus vector of any one of claims 87 to 88, wherein the polynucleotide comprises or consists of a nucleic acid sequence of any one of SEQ ID NOs: 29 and 89-94, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 29 and 89-94.

90. The arenavirus vector of any one of claims 87 to 89, wherein the arenavirus vector is a Lymphocytic choriomeningitis mammarenavirus (LCMV) vector and the polynucleotide comprises or consists of a nucleic acid sequence of SEQ ID NO: 29, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 29.

91. The arenavirus vector of any one of claims 87 to 89, wherein the arenavirus vector is a Cali mammarenavirus vector and the polynucleotide comprises or consists of a nucleic acid sequence of SEQ ID NO: 90, or that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90.

92. The arenavirus vector of any one of claims 74 to 91, wherein the arenavirus vector is replication-defective, replication-deficient, or replication-incompetent.

93. A host cell comprising one or more polynucleotides of any one of claims 53 to 56, or one or more vectors of any one of claims 61 to 92.

94. The host cell of claim 93, wherein the one or more polynucleotides are not integrated into the host cell genome, e.g., are episomal.

95. The host cell of claim 93, wherein the one or more polynucleotides are integrated into the host cell genome.

96. The host cell of any one of claims 93 to 95, wherein the host cell is a mammalian cell, e.g., a human cell.

97. The host cell of any one of claims 93 to 96, wherein the host cell is in vitro.

98. The host cell of any one of claims 93 to 96, wherein the host cell is in vivo.

99. An immunogenic composition comprising one or more of the truncated HBV polymerase polypeptide of any one of claims 1 to 7, one or more of the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16, one or more of the core-sAg fusion protein of any one of claims 21 to 44, one or more polynucleotides of any one of claims 53 to 56, or one or more vectors of any one of claims 61 to 92; and a pharmaceutically acceptable carrier.

100. The immunogenic composition of claim 99, comprising two or more of the truncated HBV polymerase polypeptide of any one of claims 1 to 7, two or more of the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 19, two or more of the core-sAg fusion protein of any one of claims 21 to 44, two or more polynucleotides of any one of claims 53 to 56, or two or more vectors of any one of claims 61 to 92.

101. The immunogenic composition of any one of claims 99 to 100, wherein the one or more polynucleotides are DNA, cDNA, mRNA, or self-replicating RNA.

~~102. The immunogenic composition of any one of claims 99 to 100, comprising a first viral expression vector and a second viral expression vector, wherein:~~

~~a) the first viral expression vector comprises a polynucleotide encoding the truncated HBV polymerase polypeptide of any one of claims 1 to 7, or the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16; and~~

~~b) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein of any one of claims 21 to 44.~~

~~103. The immunogenic composition of claim 102, comprising a first viral expression vector and a second viral expression vector, wherein:~~

~~a) the first viral expression vector comprises a polynucleotide encoding an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 5-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 5-14; and~~

~~b) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.~~

1~~04~~. ~~The~~ An immunogenic composition ~~of any one of claims 102 to 103,~~ comprising a first viral expression vector and a second viral expression vector, wherein:

~~a)~~ the first viral expression vector comprises a polynucleotide encoding ~~an~~ a truncated HBV polymerase polypeptide mutant, wherein the polypeptide is no longer than 600 amino acids in length, does not comprise all of the terminal protein (TP) domain and does not comprise all or part of the Spacer domain, wherein the polypeptide ~~comprising~~ comprises or ~~consisting~~ consists of ~~an~~ the amino acid sequence of any one of SEQ ID NOs: 13-14~~, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14~~; and

~~b)~~ the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion comprising in sequential order from the N-terminus to the C terminus, an HBV core polypeptide and an HBV small surface antigen (sAg) polypeptide, wherein the fusion protein is no longer than 450 amino acids in length, and wherein the core polypeptide is from an HBV genotype D and the sAg polypeptide is from an HBV genotype D, wherein the fusion protein comprises or consists of~~protein comprising or consisting of~~ an amino acid sequence of any one of SEQ ID NOs: ~~38~~40-41, or an amino acid sequence that is at least ~~80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,~~ 97%, 98% or 99% identical to any one of SEQ ID NOs: ~~38~~40-41.

~~1052~~. The immunogenic composition of ~~any one of~~ claim~~s 102 to 104~~1, comprising a first viral expression vector and a second viral expression vector, wherein:

~~A.~~ the first viral expression vector comprises a polynucleotide encoding an HBV polymerase polypeptide mutant comprising or consisting of ~~an~~ the amino acid sequence of SEQ ID NO: 13~~, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 13~~; and

~~B.~~ the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein comprising or consisting of an amino acid sequence of SEQ ID NO: 41, or an amino acid sequence that is at least ~~80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%,~~ 97%, 98% or 99% identical to SEQ ID NO: 41.

~~106. The immunogenic composition of any one of claims 102 to 105, wherein the core polypeptide comprises a serine (S) residue at the amino acid position corresponding to position 12, and an asparagine (N) residue at the amino acid position corresponding to position 67, wherein the position numbers are with reference to SEQ ID NO:65 or SEQ ID NO:66.~~

~~107. The immunogenic composition of any one of claims 102 to 106, wherein the sAg polypeptide comprises an isoleucine (I) residue at the amino acid position corresponding to position 68, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.~~

~~108. The immunogenic composition of any one of claims 102 to 107, wherein the sAg polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 53, an isoleucine (I) residue at the amino acid position corresponding to position 68, a threonine (T) residue at the amino acid position corresponding to position 125, a proline (P) residue at the amino acid position corresponding to position 127, an phenylalanine (F) residue at the amino acid position corresponding to position 161, a tyrosine (Y) residue at the amino acid position corresponding to position 200, a serine (S) residue at the amino acid position corresponding to position 210, and a leucine (L) residue at the amino acid position corresponding to position 213, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.~~

~~109. The immunogenic composition of any one of claims 102 to 108, wherein the core-sAg fusion polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, an asparagine (N) residue at the amino acid position corresponding to position 67, a valine (V) residue at the amino acid position corresponding to position 74, a phenylalanine (F) residue at the amino acid position corresponding to position 97, a threonine (T) residue at the amino acid position corresponding to position 249, a threonine (T) residue at the amino acid position corresponding to position 250, a serine (S) residue at the amino acid position corresponding to position 317, a serine (S) residue at the amino acid position corresponding to position 318, an arginine (R) residue at the amino acid position corresponding to position 326, a tyrosine (Y) residue at the amino acid position corresponding to position 338, a glycine (G) residue at the amino acid position corresponding to position 363, and an alanine (A) residue at the amino acid position corresponding to position 372, wherein the position numbers are with reference to SEQ ID NO:41.~~

~~1103~~. The immunogenic composition of ~~any one of~~ claim~~s 102 to 109~~1 or 2, comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 29, 32, 89, 90, 91, 92, 93~~27-32~~ and ~~89-~~94, or a nucleic acid sequence that is at least ~~80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or~~ 99% identical to the full length of any one of SEQ ID NOs: 29, 32, 89, 90, 91, 92, 93~~27-32;~~ and ~~89-~~94;

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 33-37 or a sequence that is

at least ~~80%, 81%, 82%, 83%, 84%,~~ 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the full length of any one of SEQ ID NOs: 33-37.

~~111~~4. The immunogenic composition of any one of claims ~~102 to 110~~1 to 3, comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NOs: 29, 89, 90 or 92, or a sequence that is at least ~~80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or~~ 99% identical to the full length of SEQ ID NOs: 29, 89, 90 or 92; and

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37 or a nucleic acid sequence that is at least ~~80%, 81%, 82%, 83%, 84%,~~ 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to the full length of any one of SEQ ID NO: 37.

~~112~~5. The immunogenic composition of any one of claims ~~102 to 111~~1 to 4, wherein the first viral expression vector and the second viral expression vector are independently from a taxonomic family selected from Adenoviridae, Arenaviridae, Herpesviridae ~~(e.g. Cytomegalovirus)~~, Poxviridae ~~(e.g. Vaccinia virus, e.g. modified vaccinia Ankara (MVA))~~, Flaviviridae ~~(e.g. Yellow fever virus~~), Rhabdoviridae ~~(e.g. Vesiculovirus, e.g. Maraba vesiculovirus)~~, and Togaviridae ~~(e.g., Alphavirus)~~.

~~113~~6. The immunogenic composition of any one of claims ~~102 to 112~~1 to 5, wherein the first viral expression vector and the second viral expression vector are from the same taxonomic family.

~~114~~7. The immunogenic composition of claim ~~113~~6, wherein the first viral expression vector and the second viral expression vector are from Arenaviridae.

~~115~~8. The immunogenic composition of ~~any one of~~ claim~~s 113 to 114~~6 or 7, wherein the first viral expression vector and the second viral expression vector are independently from an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV), Pichinde mammarenavirus (PICV)~~Cali mammarenavirus~~, Guanarito virus (GTOV), Junin virus (JUNV), Lassa virus (LASV), Lujo virus (LUJV), Machupo virus (MACV), Sabia virus (SABV), and Whitewater Arroyo virus (WWAV).

~~1169~~. The immunogenic composition of any one of claims ~~113 to 1156~~ to 8, wherein the first viral expression vector and the second viral expression vector are from an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV) or Pichinde mammarenavirus (PICV)~~Cali mammarenavirus~~.

~~11710~~. The immunogenic composition of any one of claims ~~113 to 1166~~ to 9, wherein the first viral expression vector and the second viral expression vector are replication-defective or replication-deficient.

11~~8~~. The immunogenic composition of any one of claims ~~113 to 1166~~ to 9, wherein the first viral expression vector and the second viral expression vector are replication-attenuated.

~~119. The immunogenic composition of any one of claims 102 to 104, wherein the first viral expression vector and the second viral expression vector are from different taxonomic families.~~

~~120. An immunogenic composition, comprising a first LCMV arenavirus expression vector and a second LCMV arenavirus expression vector, wherein:~~

~~a) the first LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 29, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 29; and~~

~~b) the second LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37 or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 37.~~

~~121. An immunogenic composition, comprising a first Pichinde arenavirus expression vector and a second Pichinde arenavirus expression vector, wherein:~~

~~a) the first Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 90, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%,~~

88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90; and

b) the second Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37 or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NO: 37.

122. The immunogenic composition of any one of claims 102 to 1211 to 11, wherein the first viral expression vector and the second viral expression vector are provided in a ratio in the range of from 1:10 to 10:1, *e.g.*, 1:9 to 9:1, 1:8 to 8:1, 1:7 to 7:1, 1:6 to 6:1, 1:5 to 5:1, 1:4 to 4:1, 1:3 to 3:1, 1:2 to 2:1 or 1:1.

123. The immunogenic composition of any one of claims 102 to 1221 to 12, comprising in the range of about 10^3 to about 10^{12} viral focus forming units (FFUffu) or plaque forming units (PFUpfu) or infectious units (IUiu) or viral particles (vp) per milliliter, *e.g.* from about 10^4 to about 10^7 viral FFU or PFU or IU or vp per milliliter, *e.g.* from about 10^3 to about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} or 10^{12} viral FFU or PFU or IU or vp per milliliter, of each of the first viral expression vector and the second viral expression vector.

124. The immunogenic composition of any one of claims 99 to 1231 to 13, further comprising one or more of an adjuvant, a detergent, a micelle-forming agent, and an oil.

125. The immunogenic composition of any one of claims 99 to 1241 to 14, formulated for administration via a route selected from the group consisting of intravenous, intramuscular, intradermal, subcutaneous and mucosal (e.g. buccal, intranasal, intrarectal, intravaginal).

126. The immunogenic composition of any one of claims 99 1 to 125, formulated as a liquid, e.g., as an aqueous solution or suspension.

127. The immunogenic composition of any one of claims 99 1 to 125, wherein the composition is lyophilized.

128. A kit comprising one or more unitary doses of one or more of the truncated HBV polymerase polypeptide of any one of claims 1 to 7, one or more of the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 19, one or more of the core

sAg fusion protein of any one of claims 21 to 44, one or more polynucleotides of any one of claims 53 to 56, one or more vectors of any one of claims 61 to 92, or one or morethe immunogenic compositions of any one of claims 99 1 to 127.

129. The kit of claim 128, comprising one or more unitary doses of two or more of the truncated HBV polymerase polypeptide of any one of claims 1 to 7, the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 19, the core-sAg fusion protein of any one of claims 21 to 44, the polynucleotides of any one of claims 53 to 56, the vectors of any one of claims 61 to 92, or the immunogenic compositions of any one of claims 99 to 127.

130. The kit of claim 128, wherein the one or more unitary doses are in a single container.

131. The kit of claim 128, wherein the one or more unitary doses are in two or more separate containers.

132. The kit of any one of claims 128 to 131, comprising one or more containers selected from the group consisting of vials, ampules and pre-loaded syringes. 133. The kit of any one of claims 128 to 132, comprising one or more containers comprising the one or more polypeptides, one or more polynucleotides, one or more vectors or one or more immunogenic compositions in an aqueous solution or suspension.

134. The kit of any one of claims 128 to 132, comprising one or more containers comprising the one or more polypeptides, one or more polynucleotides, one or more vectors or one or more immunogenic compositions as a lyophilized preparation.

135. The kit of any one of claims 128 to 134, wherein the one or more unitary doses are the same.

136. The kit of any one of claims 128 to 134, wherein the one or more unitary doses are the different.

137. The kit of any one of claims 128 to 136, comprising one or more unitary doses of one or more viral vectors of any one of claims 61 to 92, wherein the unitary doses are in the range of about 10^3 to about 10^{12} viral focus forming units (FFU) or plaque forming units (PFU) or infectious units (IU) or viral particles (vp), *e.g.* from about 10^4 to about 10^7 viral FFU

~~or PFU or IU or vp, *e.g.* from about 10^3 to about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} or 10^{12} viral FFU or PFU or IU or vp.~~

~~138. The kit of any one of claims 128 to 137, comprising one or more polynucleotides encoding, or one or more vectors expressing, or an immunogenic composition comprising, two immunogenic polypeptides, the immunogenic polypeptides comprising:~~

~~a) an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 5-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 5-14; and~~

~~b) an HBV core-sAg fusion protein comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.~~

~~139. The kit of any one of claims 128 to 138 comprising one or more polynucleotides encoding, or one or more vectors expressing, or an immunogenic composition comprising, two immunogenic polypeptides, the immunogenic polypeptides comprising:~~

~~a) an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 13-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14; and~~

~~b) an HBV core-sAg fusion protein comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.~~

~~140. The kit of any one of claims 128 to 139, comprising one or more polynucleotides encoding, or one or more vectors expressing, or an immunogenic composition comprising, two immunogenic polypeptides, the immunogenic polypeptides comprising:~~

a) an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of SEQ ID NO: 13, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 13; and

b) an HBV core-sAg fusion protein comprising or consisting of an amino acid sequence of SEQ ID NO: 41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 41.

141. The kit of any one of claims 128 to 140, comprising first and second vectors encoding first and second immunogenic polypeptides, respectively, the first and second immunogenic polypeptides comprising, respectively:

a) an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of SEQ ID NO: 13, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 13; and

b) an HBV core-sAg fusion protein comprising or consisting of an amino acid sequence of SEQ ID NO: 41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 41.

142. The kit of any one of claims 128 to 141, wherein the core polypeptide comprises a serine (S) residue at the amino acid position corresponding to position 12, and an asparagine (N) residue at the amino acid position corresponding to position 67, wherein the position numbers are with reference to SEQ ID NO:65 or SEQ ID NO:66.

143. The kit of any one of claims 128 to 142, wherein the sAg polypeptide comprises an isoleucine (I) residue at the amino acid position corresponding to position 68, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

144. The kit of any one of claims 128 to 143, wherein the sAg polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 53, an isoleucine (I) residue at the amino acid position corresponding to position 68, a threonine (T) residue at the amino acid position corresponding to position 125, a proline (P)

residue at the amino acid position corresponding to position 127, an phenylalanine (F) residue at the amino acid position corresponding to position 161, a tyrosine (Y) residue at the amino acid position corresponding to position 200, a serine (S) residue at the amino acid position corresponding to position 210, and a leucine (L) residue at the amino acid position corresponding to position 213, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

145. The kit of any one of claims 128 to 144, wherein the core-sAg fusion polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, an asparagine (N) residue at the amino acid position corresponding to position 67, a valine (V) residue at the amino acid position corresponding to position 74, a phenylalanine (F) residue at the amino acid position corresponding to position 97, a threonine (T) residue at the amino acid position corresponding to position 249, a threonine (T) residue at the amino acid position corresponding to position 250, a serine (S) residue at the amino acid position corresponding to position 317, a serine (S) residue at the amino acid position corresponding to position 318, an arginine (R) residue at the amino acid position corresponding to position 326, a tyrosine (Y) residue at the amino acid position corresponding to position 338, a glycine (G) residue at the amino acid position corresponding to position 363, and an alanine (A) residue at the amino acid position corresponding to position 372, wherein the position numbers are with reference to SEQ ID NO:41.

146. The kit of any one of claims 128 to 145, comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 27-32 and 89-94, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 27-32 and 89-94; and

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 33-37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 33-37.

147. The kit of any one of claims 128 to 139, comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NOs: 29, 89, 90 or 92, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NOs: 29, 89, 90 or 92; and

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

148. The kit of any one of claims 128 to 147, comprising:

a) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors comprise a replication-deficient or replication-defective Cali mammarenavirus; and

b) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors comprise a replication-deficient or replication-defective Lymphocytic choriomeningitis mammarenavirus (LCMV).

149. The kit of any one of claims 128 to 147, comprising:

a) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors are from Adenoviridae; and

b) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors are from Poxviridae (*e.g.*, Vaccinia virus, *e.g.*, modified vaccinia Ankara (MVA)).

150. The kit of any one of claims 128 to 147, comprising:

a) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors are from Arenaviridae; and

b) one or more unitary doses of an immunogenic composition of any one of claims 102 to 111, wherein the first and second viral expression vectors are from Adenoviridae.

151. A kit, comprising a first LCMV arenavirus expression vector and a second LCMV arenavirus expression vector, wherein:

a) the first LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 29, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 29; and

b) the second LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

152. The kit of claim 151, further comprising a first Pichinde arenavirus expression vector and a second Pichinde arenavirus expression vector, wherein:

a) the first Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 90, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90; and

b) the second Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

153. A kit, comprising a first Pichinde arenavirus expression vector and a second Pichinde arenavirus expression vector, wherein:

the first Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 90, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90; and

the second Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

154. The kit of any one of claims 128 to 153, further comprising one or more unitary doses of one or more additional therapeutic agents.

155. The kit of claim 154, comprising one or more agonists or activators of one or more toll-like receptors (TLRs).

156. The kit of claim 155, wherein the TLR agonist or activator is selected from the group consisting of a TLR2 agonist, a TLR3 agonist, a TLR4 agonist, a TLR5 agonist, a TLR7 agonist, a TLR8 agonist and a TLR9 agonist.

157. The kit of any one of claims 155 to 156, wherein the TLR7 agonist is selected from the group consisting of GS-9620 (vesatolimod), R848 (Resiquimod), DS-0509, LHC-165 and TMX-101 (imiquimod), and/or wherein the TLR8 agonist is selected from the group consisting of GS-9688, R848 (Resiquimod) and NKTR-262 (dual TLR7/TLR8 agonist).

158. The kit of any one of claims 154 to 157, comprising one or more interleukin receptor agonists of an interleukin receptor selected from IL-2, IL-7, IL-12 and IL-15.

159. The kit of claim 158, comprising one or more cytokines selected from the group consisting of IL-2, IL-7, IL-12, IL-15, and variants thereof.

160. The kit of any one of claims 154 to 159, comprising one or more innate immune activators.

161. The kit of claim 160, wherein the one or more innate immune activators comprises an agonist of a receptor selected from the group consisting of fms related tyrosine

kinase 3 (FLT3), stimulator of interferon genes (STING) receptor, DExD/H-box helicase 58 (DDX58; a.k.a., RIG-I), nucleotide binding oligomerization domain containing 2 (NOD2).

162. The kit of any one of claims 160 to 161, comprising one or more unitary doses of GS-3583 and/or GS-9992.

163. The kit of any one of claims 154 to 162, comprising one or more antagonists or inhibitors of an inhibitory immune checkpoint protein or receptor and/or one or more activators or agonists of a stimulatory immune checkpoint protein or receptor.

164. The kit of claim 163, wherein the one or more immune checkpoint proteins or receptors are selected from the group consisting of: CD27, CD70; CD40, CD40LG; CD47, CD48 (SLAMF2), transmembrane and immunoglobulin domain containing 2 (TMIGD2, CD28H), CD84 (LY9B, SLAMF5), CD96, CD160, MS4A1 (CD20), CD244 (SLAMF4); CD276 (B7H3); V-set domain containing T cell activation inhibitor 1 (VTCN1, B7H4); V-set immunoregulatory receptor (VSIR, B7H5, VISTA); immunoglobulin superfamily member 11 (IGSF11, VSIG3); natural killer cell cytotoxicity receptor 3 ligand 1 (NCR3LG1, B7H6); HERV-H LTR-associating 2 (HHLA2, B7H7); inducible T cell co-stimulator (ICOS, CD278); inducible T cell co-stimulator ligand (ICOSLG, B7H2); TNF receptor superfamily member 4 (TNFRSF4, OX40); TNF superfamily member 4 (TNFSF4, OX40L); TNFRSF8 (CD30), TNFSF8 (CD30L); TNFRSF10A (CD261, DR4, TRAILR1), TNFRSF9 (CD137), TNFSF9 (CD137L); TNFRSF10B (CD262, DR5, TRAILR2), TNFRSF10 (TRAIL); TNFRSF14 (HVEM, CD270), TNFSF14 (HVEML); CD272 (B and T lymphocyte associated (BTLA)); TNFRSF17 (BCMA, CD269), TNFSF13B (BAFF); TNFRSF18 (GITR), TNFSF18 (GITRL); MHC class I polypeptide-related sequence A (MICA); MHC class I polypeptide-related sequence B (MICB); CD274 (CD274, PDL1, PD-L1); programmed cell death 1 (PDCD1, PD1, PD-1); cytotoxic T-lymphocyte associated protein 4 (CTLA4, CD152); CD80 (B7-1), CD28; nectin cell adhesion molecule 2 (NECTIN2, CD112); CD226 (DNAM-1); Poliovirus receptor (PVR) cell adhesion molecule (PVR, CD155); PVR related immunoglobulin domain containing (PVRIG, CD112R); T cell immunoreceptor with Ig and ITIM domains (TIGIT); T cell immunoglobulin and mucin domain containing 4 (TIMD4; TIM4); hepatitis A virus cellular receptor 2 (HAVCR2, TIMD3, TIM3); galectin 9 (LGALS9); lymphocyte activating 3 (LAG3, CD223); signaling lymphocytic activation molecule family member 1 (SLAMF1, SLAM, CD150); lymphocyte antigen 9 (LY9, CD229, SLAMF3); SLAM family member 6 (SLAMF6, CD352); SLAM family member 7 (SLAMF7, CD319); UL16 binding protein 1 (ULBP1); UL16

~~binding protein 2 (ULBP2); UL16 binding protein 3 (ULBP3); retinoic acid early transcript 1E (RAET1E; ULBP4); retinoic acid early transcript 1G (RAET1G; ULBP5); retinoic acid early transcript 1L (RAET1L; ULBP6); lymphocyte activating 3 (CD223); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer cell lectin like receptor C1 (KLRC1, NKG2A, CD159A); killer cell lectin like receptor K1 (KLRK1, NKG2D, CD314); killer cell lectin like receptor C2 (KLRC2, CD159c, NKG2C); killer cell lectin like receptor C3 (KLRC3, NKG2E); killer cell lectin like receptor C4 (KLRC4, NKG2F); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR3DL1); killer cell lectin like receptor D1 (KLRD1); and SLAM family member 7 (SLAMF7).~~

~~165. The kit of any one of claims 163 to 164, comprising one or more blockers or inhibitors of one or more T cell inhibitory immune checkpoint proteins or receptors.~~

~~166. The kit of claim 165, wherein the T cell inhibitory immune checkpoint proteins or receptors are selected from the group consisting of CD274 (CD274, PDL1, PD L1); programmed cell death 1 ligand 2 (PDCD1LG2, PD L2, CD273); programmed cell death 1 (PDCD1, PD1, PD 1); cytotoxic T lymphocyte associated protein 4 (CTLA4, CD152); CD276 (B7H3); V set domain containing T cell activation inhibitor 1 (VTCN1, B7H4); V set immunoregulatory receptor (VSIR, B7H5, VISTA); immunoglobulin superfamily member 11 (IGSF11, VSIG3); TNFRSF14 (HVEM, CD270), TNFSF14 (HVEML); CD272 (B and T lymphocyte associated (BTLA)); PVR related immunoglobulin domain containing (PVRIG, CD112R); T cell immunoreceptor with Ig and ITIM domains (TIGIT); lymphocyte activating 3 (LAG3, CD223); hepatitis A virus cellular receptor 2 (HAVCR2, TIMD3, TIM3); galectin 9 (LGALS9); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); and killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR3DL1).~~

~~167. The kit of any one of claims 163 to 166, comprising one or more agonists or activators of one or more T-cell stimulatory immune checkpoint proteins or receptors.~~

~~168. The kit of claim 167, wherein the T-cell stimulatory immune checkpoint proteins or receptors are selected from the group consisting of CD27, CD70; CD40, CD40LG; inducible T-cell co-stimulator (ICOS, CD278); inducible T-cell co-stimulator ligand (ICOSLG, B7H2); TNF receptor superfamily member 4 (TNFRSF4, OX40); TNF superfamily member 4 (TNFSF4, OX40L); TNFRSF9 (CD137), TNFSF9 (CD137L); TNFRSF18 (GITR), TNFSF18 (GITRL); CD80 (B7-1), CD28; nectin cell adhesion molecule 2 (NECTIN2, CD112); CD226 (DNAM-1); Poliovirus receptor (PVR) cell adhesion molecule (PVR, CD155).~~

~~169. The kit of any one of claims 167 to 168, comprising one or more unitary doses of AGEN-2373 and/or AGEN-1223.~~

~~170. The kit of any one of claims 163 to 169, comprising one or more blockers or inhibitors of one or more NK-cell inhibitory immune checkpoint proteins or receptors.~~

~~171. The kit claim 170, wherein the NK-cell inhibitory immune checkpoint proteins or receptors are selected from the group consisting of killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR3DL1); killer cell lectin like receptor C1 (KLRC1, NKG2A, CD159A); and killer cell lectin like receptor D1 (KLRD1, CD94).~~

~~172. The kit of any one of claims 163 to 171, comprising one or more agonists or activators of one or more NK-cell stimulatory immune checkpoint proteins or receptors.~~

~~173. The kit of claim 172, wherein the NK-cell stimulatory immune checkpoint proteins or receptors are selected from CD16, CD226 (DNAM-1); killer cell lectin like receptor K1 (KLRK1, NKG2D, CD314); and SLAM family member 7 (SLAMF7).~~

~~174. The kit of any one of claims 163 to 173, wherein the one or more immune checkpoint inhibitors comprises a proteinaceous inhibitor of PD-L1 (CD274), PD-1 (PDCD1) or CTLA4.~~

~~175. The kit of claim 174, wherein the proteinaceous inhibitor of CTLA4 is selected from the group consisting of ipilimumab, tremelimumab, BMS-986218, AGEN1181, AGEN1884, BMS-986249, MK-1308, REGN-4659, ADU-1604, CS-1002, BCD-145, APL-509, JS-007, BA-3071, ONC-392, AGEN-2041, JHL-1155, KN-044, CG-0161, ATOR-1144, PBI-5D3H5, FPT-155 (CTLA4/PD-L1/CD28), PF-06936308 (PD-1/ CTLA4), MGD-019 (PD-1/CTLA4), KN-046 (PD-1/CTLA4), MEDI-5752 (CTLA4/PD-1), XmAb-20717 (PD-1/CTLA4) and AK-104 (CTLA4/PD-1).~~

~~176. The kit of claim 174, wherein the proteinaceous inhibitor of PD-L1 (CD274) or PD-1 (PDCD1) is selected from the group consisting of zimberelimab (AB122), pembrolizumab, nivolumab, cemiplimab, pidilizumab, AMP-224, MEDI0680 (AMP-514), spartalizumab, atezolizumab, avelumab, ASC22, durvalumab, BMS-936559, CK-301, PF-06801591, BGB-A317 (tislelizumab), GLS-010 (WBP-3055), AK-103 (HX-008), AK-105, CS-1003, HLX-10, MGA-012, BI-754091, AGEN-2034, JS-001 (toripalimab), JNJ-63723283, genolimzumab (CBT-501), LZM-009, BCD-100, LY-3300054, SHR-1201, SHR-1210 (camrelizumab), Sym-021, ABBV-181, PD1-PIK, BAT-1306, (MSB0010718C), CX-072, CBT-502, TSR-042 (dostarlimab), MSB-2311, JTX-4014, BGB-A333, SHR-1316, CS-1001 (WBP-3155, KN-035, IBI-308 (sintilimab), HLX-20, KL-A167, STI-A1014, STI-A1015 (IMC-001), BCD-135, FAZ-053, TQB-2450, MDX1105-01, FPT-155 (CTLA4/PD-L1/CD28), PF-06936308 (PD-1/ CTLA4), MGD-013 (PD-1/LAG-3), FS-118 (LAG-3/PD-L1) MGD-019 (PD-1/CTLA4), KN-046 (PD-1/CTLA4), MEDI-5752 (CTLA4/PD-1), RO-7121661 (PD-1/TIM-3), XmAb-20717 (PD-1/CTLA4), AK-104 (CTLA4/PD-1), M7824 (PD-L1/TGFβ-EC domain), CA-170 (PD-L1/VISTA), CDX-527 (CD27/PD-L1), LY-3415244 (TIM3/PDL1), and INBRX-105 (4-1BB/PDL1).~~

~~177. The kit of any one of claims 163 to 176, wherein the one or more immune checkpoint inhibitors comprises a small molecule inhibitor of CD274 (PDL1, PD-L1), programmed cell death 1 (PDCD1, PD1, PD-1) or CTLA4.~~

~~178. The kit of claim 177, wherein the small molecule inhibitor of CD274 or PDCD1 is selected from the group consisting of GS-4224, GS-4416, INCB086550 and MAX10181.~~

~~179. The kit of claim 177, wherein the small molecule inhibitor of CTLA4 comprises BPI-002.~~

~~180. The kit of any one of claims 154 to 179, further comprising one or more anti-viral agents.~~

~~181. The kit of 180, wherein the one or more antiviral agents are selected from the group consisting of lamivudine (LAM), adefovir dipivoxil (ADV), entecavir (ETV), telbivudine (LdT), tenofovir disoproxil fumarate (TDF), tenofovir alafenamide (TAF or VEMLIDY®) and ledipasvir + sofosbuvir (HARVONI®).~~

~~182. The kit of any one of claims 154 to 181, further comprising one or more therapeutic agents selected from the group consisting of HBV antigen inhibitors (e.g., HBV core antigen (HBcAg) inhibitors, HBV surface antigen (HBsAg) inhibitors, HBx inhibitors, HBV E antigen inhibitors), anti-HBV antigen antibodies, inhibitory nucleic acids targeting HBV (e.g., antisense oligonucleotide, short interfering RNA (siRNA), DNA-directed RNA interference (ddRNAi)), gene editors targeting HBV (e.g., CRISPR-Cas (e.g., Cas9, Cas12, Cascade, Cas13), zinc finger nucleases, homing endonucleases, homing meganucleases (e.g., ARCUS), synthetic nucleases, TALENs), covalently closed circular DNA (cccDNA) inhibitors and HBsAg secretion or assembly inhibitors and HBV viral entry inhibitors.~~

~~183. A method for eliciting an immune response to human hepatitis B virus (HBV) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more immunogenic compositions of any one of claims 99 to 127.~~

~~184. A method of treating or preventing human hepatitis B virus (HBV) in a subject in need thereof, comprising administering to the subject a therapeutically effective amount of one or more immunogenic compositions of any one of claims 99 to 127.~~

~~185. Use of the one or more immunogenic compositions of any one of claims 99 to 127 in a method of eliciting an immune response to human hepatitis B virus (HBV) or in a method of treating or preventing human hepatitis B virus (HBV).~~

~~186. The one or more immunogenic compositions of any one of claims 99 to 127 for use in a method of eliciting an immune response to human hepatitis B virus (HBV) or in a method of treating or preventing human hepatitis B virus (HBV).~~

~~187. The method or use of any one of claims 183 to 186, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:~~

a) the first viral expression vector comprises a polynucleotide encoding the truncated HBV polymerase polypeptide of any one of claims 1 to 7, or the HBV polymerase deletion mutant polypeptide of any one of claims 10 to 16; and

b) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein of any one of claims 21 to 44.

188. The method or use of any one of claims 183 to 187, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide encoding an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 5-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 5-14; and

b) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.

189. The method or use of any one of claims 183 to 188, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide encoding an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 13-14, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 13-14; and

b) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein comprising or consisting of an amino acid sequence of any one of SEQ ID NOs: 38-41, or a sequence that is at least

80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 38-41.

190. The method or use of any one of claims 183 to 189, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:

c) the first viral expression vector comprises a polynucleotide encoding an HBV polymerase polypeptide mutant comprising or consisting of an amino acid sequence of SEQ ID NO: 13, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 13; and

d) the second viral expression vector comprises a polynucleotide encoding the core-sAg fusion protein comprising or consisting of an amino acid sequence of SEQ ID NO: 41, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 41.

e) 191. The method or use of any one of claims 183 to 190, wherein the core polypeptide comprises a serine (S) residue at the amino acid position corresponding to position 12, and an asparagine (N) residue at the amino acid position corresponding to position 67, wherein the position numbers are with reference to SEQ ID NO:65 or SEQ ID NO:66.

192. The method or use of any one of claims 183 to 191, wherein the sAg polypeptide comprises an isoleucine (I) residue at the amino acid position corresponding to position 68, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

193. The method or use of any one of claims 183 to 192, wherein the sAg polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 53, an isoleucine (I) residue at the amino acid position corresponding to position 68, a threonine (T) residue at the amino acid position corresponding to position 125, a proline (P) residue at the amino acid position corresponding to position 127, an phenylalanine (F) residue at the amino acid position corresponding to position 161, a tyrosine (Y) residue at the amino acid position corresponding to position 200, a serine (S) residue at the amino acid

position corresponding to position 210, and a leucine (L) residue at the amino acid position corresponding to position 213, wherein the position numbers are with reference to SEQ ID NO:3 or SEQ ID NO:4.

194. The method or use of any one of claims 183 to 193, wherein the core-sAg fusion polypeptide comprises one or more of a serine (S) residue at the amino acid position corresponding to position 12, an asparagine (N) residue at the amino acid position corresponding to position 67, a valine (V) residue at the amino acid position corresponding to position 74, a phenylalanine (F) residue at the amino acid position corresponding to position 97, a threonine (T) residue at the amino acid position corresponding to position 249, a threonine (T) residue at the amino acid position corresponding to position 250, a serine (S) residue at the amino acid position corresponding to position 317, a serine (S) residue at the amino acid position corresponding to position 318, an arginine (R) residue at the amino acid position corresponding to position 326, a tyrosine (Y) residue at the amino acid position corresponding to position 338, a glycine (G) residue at the amino acid position corresponding to position 363, and an alanine (A) residue at the amino acid position corresponding to position 372, wherein the position numbers are with reference to SEQ ID NO:41.

195. The method or use of any one of claims 183 to 194, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic sequence of any one of SEQ ID NOs: 27-32 and 89-94, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 27-32 and 89-94; and

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of any one of SEQ ID NOs: 33-37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to any one of SEQ ID NOs: 33-37.

196. The method or use of any one of claims 183 to 195, the one or more immunogenic compositions comprising a mixture comprising a first viral expression vector and a second viral expression vector, wherein:

a) the first viral expression vector comprises a polynucleotide comprising or consisting of a nucleic sequence of SEQ ID NOs: 29, 89, 90 or 92, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NOs: 29, 89, 90 or 92; and

b) the second viral expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

197. The method or use of any one of claims 187 to 196, wherein the first viral expression vector and the second viral expression vector are from Arenaviridae.

198. The method or use of any one of claims 187 to 197, wherein the first viral expression vector and the second viral expression vector are from an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV), Cali mammarenavirus, Guanarito virus (GTOV), Junin virus (JUNV), Lassa virus (LASV), Lujo virus (LUJV), Machupo virus (MACV), Sabia virus (SABV), and Whitewater Arroyo virus (WWAV).

199. The method or use of any one of claims 187 to 198, wherein the first viral expression vector and the second viral expression vector are from an arenavirus vector selected from Lymphocytic choriomeningitis mammarenavirus (LCMV) or Cali mammarenavirus.

200. The method or use of any one of claims 187 to 199, wherein the first viral expression vector and the second viral expression vector are replication-defective or replication-deficient.

201. The method or use of any one of claims 187 to 199, wherein the first viral expression vector and the second viral expression vector are replication-attenuated.

202. The method or use of any one of claims 183 to 201, wherein the one or more immunogenic compositions comprises a mixture comprising a first LCMV arenavirus expression vector and a second LCMV arenavirus expression vector, wherein:

a) the first LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic sequence of SEQ ID NO: 29, or a

sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 29; and

b) the second LCMV arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

203. The method or use of any one of claims 183 to 202, wherein the one or more immunogenic compositions comprises or further comprises a mixture comprising a first Pichinde arenavirus expression vector and a second Pichinde arenavirus expression vector, wherein:

a) the first Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic sequence of SEQ ID NO: 90, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 90; and

b) the second Pichinde arenavirus expression vector comprises a polynucleotide comprising or consisting of a nucleic acid sequence of SEQ ID NO: 37, or a sequence that is at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identical to SEQ ID NO: 37.

204. The method or use of any one of claims 183 to 203, wherein the subject is infected with HBV, is suspected of being infected with HBV, or is at risk of being infected with HBV.

205. The method or use of any one of claims 183 to 204, wherein the subject is asymptomatic.

206. The method or use of any one of claims 183 to 204, wherein the subject is chronically infected with HBV.

207. The method or use of claim 206, wherein the subject is exhibiting or experiencing one or more symptoms selected from hepatic failure, hepatic cancer, hepatic fibrosis and hepatic cirrhosis.

208. The method or use of any one of claims 183 to 204, wherein the subject is acutely infected with HBV.

209. The method or use of claim 206 to 208, wherein the subject is exhibiting or experiencing one or more symptoms selected from jaundice, visible webs of swollen blood vessels in the skin, dark-colored (e.g., orange or brown) urine, light-colored feces, fever, persistent fatigue, malaise, abdominal pain, abdominal fluid, loss of appetite, nausea, and vomiting.

210. The method or use of any one of claims 183 to 209, wherein the subject is co-infected with hepatitis D virus (HDV).

211. The method or use of any one of claims 183 to 210, wherein the composition is administered via a route selected from intravenous, intramuscular, intradermal, subcutaneous and mucosal (e.g. buccal, intranasal, intrarectal, intravaginal).

212. The method or use of any one of claims 183 to 211, comprising administering from about 10^3 to about 10^{12} viral focus forming units (FFU) or plaque forming units (PFU) or infectious units (IU) or viral particles (vp), *e.g.* from about 10^4 to about 10^7 viral FFU or PFU or IU or vp, *e.g.* from about 10^3 to about 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, 10^{10}, 10^{11} or 10^{12} viral FFU or PFU or IU or vp, per administration.

213. The method or use of any one of claims 183 to 212, wherein one or more compositions are administered multiple times.

214. The method or use of any one of claims 183 to 213, comprising administering intravenously or intramuscularly from about 10^6 to about 10^8 viral FFU or PFU or IU or vp per administration every other week (Q2W) or monthly (Q4W).

215. The method or use of any one of claims 183 to 214, comprising multiple administrations of the one or more compositions over a time period of at least about 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 13 months, 14 months, 15 months, 16 months, 17

~~months, 18 months, 19 months, 20 months, 21 months, 22 months, 23 months, 24 months, or longer, or until sAg is not detectable in the serum or plasma of the subject.~~

~~216. The method or use of any one of claims 183 to 215, comprising a prime-boost regimen comprising administering a priming composition at a first time point and administering one or more boosting compositions at one or more subsequent time points.~~

~~217. The method or use of claim 216, comprising repeating the prime-boost regimen one or more iterations.~~

~~218. The method or use of any one of claims 216 to 217, wherein the administrations of the priming composition and the one or more boosting compositions are spaced at least 1 week and up to at least 2 weeks, 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months or 6 months apart.~~

~~219. The method or use of any one of claims 216 to 218, wherein the priming composition and the boosting composition comprise the same immunogenic composition.~~

~~220. The method or use of any one of claims 216 to 218, wherein the priming composition and the boosting composition comprise different immunogenic compositions.~~

~~221. The method or use of any one of claims 216 to 218, wherein the priming composition and the boosting composition comprise the same one or more polypeptides and same viral expression vector.~~

~~222. The method or use of any one of claims 216 to 218, wherein the priming composition and the boosting composition comprise different polypeptides and/or different viral expression vectors.~~

~~223. The method or use of claim 222, comprising priming with a priming composition comprising one or more viral expression vectors, and boosting with a boosting composition comprising one or more viral expression vectors.~~

~~224. The method or use of any one of claims 216 to 223, wherein the prime-boost regimen comprises:~~

~~a) Priming with a priming composition comprising one or more viral expression vectors and boosting with a boosting composition comprising one or more polynucleotides, wherein the one or more polynucleotides comprise DNA, cDNA, mRNA or self-~~

replicating RNA;

b) Priming with a priming composition comprising one or more polynucleotides, wherein the one or more polynucleotides comprise DNA, cDNA, mRNA or self-replicating RNA, and boosting with a boosting composition comprising one or more viral expression vectors;

c) Priming with a priming composition comprising one or more viral expression vectors, and boosting with a boosting composition comprising one or more viral expression vectors, wherein the one or more viral expression vectors in the priming composition and the one or more viral expression vectors in the boosting composition are from identical, related or unrelated taxonomical families;

d) Priming with a priming composition comprising one or more replication-deficient viral expression vectors and boosting with a boosting composition comprising one or more replication-deficient viral expression vectors, wherein the one or more replication-deficient viral expression vectors in the priming composition and the one or more replication-deficient viral expression vectors in the boosting composition are from identical, related or unrelated taxonomical families;

e) Priming with a priming composition comprising one or more replication-attenuated viral expression vectors and boosting with a boosting composition comprising one or more replication-attenuated viral expression vectors, wherein the one or more replication-attenuated viral expression vectors in the priming composition and the one or more replication-attenuated viral expression vectors in the boosting composition are from identical, related or unrelated taxonomical families;

f) Priming with a priming composition comprising one or more replication-deficient viral expression vectors and boosting with a boosting composition comprising one or more replication-attenuated viral expression vectors;

g) Priming with a priming composition comprising one or more replication-attenuated viral expression vectors and boosting with a boosting composition comprising one or more replication-deficient viral expression vectors;

h) Priming with a priming composition comprising one or more Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors and boosting with a boosting composition comprising one or more Pichinde mammarenavirus viral expression vectors;

i) Priming with a priming composition comprising one or more Pichinde mammarenavirus viral expression vectors and boosting with a boosting composition

comprising one or more Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors;

j) Priming with a priming composition comprising one or more replication deficient Pichinde mammarenavirus viral expression vectors and boosting with a boosting composition comprising one or more replication deficient Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors;

k) Priming with a priming composition comprising one or more replication deficient Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors and boosting with a boosting composition comprising one or more replication deficient Pichinde mammarenavirus viral expression vectors;

l) Priming with a priming composition comprising one or more arenavirus viral expression vectors and boosting with a boosting composition comprising one or more adenovirus viral expression vectors;

m) Priming with a priming composition comprising one or more adenovirus viral expression vectors and boosting with boosting composition comprising one or more arenavirus viral expression vectors;

n) Priming with a priming composition comprising one or more poxvirus viral expression vectors and boosting with a boosting composition comprising one or more arenavirus viral expression vectors;

o) Priming with a priming composition comprising one or more arenavirus viral expression vectors and boosting with boosting composition comprising one or more poxvirus viral expression vectors;

p) Priming with a priming composition comprising one or more poxvirus viral expression vectors and boosting with a boosting composition comprising one or more adenovirus viral expression vectors; or

q) Priming with a priming composition comprising one or more adenovirus viral expression vectors and boosting with boosting composition comprising one or more poxvirus viral expression vectors.

225. The method or use of any one of claims 216 to 223, wherein the prime-boost regimen comprises:

a) Priming with a priming composition comprising one or more Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors and boosting

with a boosting composition comprising one or more Pichinde mammarenavirus viral expression vectors;

b) Priming with a priming composition comprising one or more Pichinde mammarenavirus viral expression vectors and boosting with a boosting composition comprising one or more Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors;

c) Priming with a priming composition comprising one or more replication deficient Pichinde mammarenavirus viral expression vectors and boosting with a boosting composition comprising one or more replication deficient Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors; or

d) Priming with a priming composition comprising one or more replication deficient Lymphocytic choriomeningitis mammarenavirus (LCMV) viral expression vectors and boosting with a boosting composition comprising one or more replication deficient Pichinde mammarenavirus viral expression vectors.

226. The method or use of any one of claims 216 to 225, wherein the priming composition and the boosting composition comprise an immunogenic composition of any one of claims 102 to 111.

227. The method or use of any one of claims 183 to 226, wherein the subject is not receiving antiviral therapy or antiviral therapy is discontinued prior to administration of the one or more immunogenic compositions.

228. The method or use of any one of claims 183 to 227, wherein antiviral therapy is discontinued after one or more administrations of the one or more immunogenic compositions.

229. The method or use of any one of claims 183 to 228, further comprising administering to the subject one or more additional therapeutic agents, e.g. two, three, four, or more additional therapeutic agents.

230. The method or use of claim 229, comprising co-administering one or more agonists or activators of one or more toll-like receptors (TLRs).

~~231. The method or use of claim 230, wherein the TLR agonist or activator is selected from the group consisting of a TLR2 agonist, a TLR3 agonist, a TLR4 agonist, a TLR5 agonist, a TLR7 agonist, a TLR8 agonist and a TLR9 agonist.~~

~~232. The method or use of any one of claims 230 to 231, wherein the TLR7 agonist is selected from the group consisting of GS-9620 (vesatolimod), R848 (Resiquimod), DS-0509, LHC-165 and TMX-101 (imiquimod), and/or wherein the TLR8 agonist is selected from the group consisting of GS-9688, R848 (Resiquimod) and NKTR-262 (dual TLR7/TLR8 agonist).~~

~~233. The method or use of any one of claims 229 to 232, comprising co-administering one or more interleukin receptor agonists of an interleukin receptor selected from IL-2, IL-7, IL-12 and IL-15.~~

~~234. The method or use of claim 233, comprising co-administering one or more cytokines selected from the group consisting of IL-2, IL-7, IL-12, IL-15, and variants thereof.~~

~~235. The method or use of any one of claims 229 to 234, comprising co-administering one or more innate immune activators.~~

~~236. The method or use of claim 235, wherein the one or more innate immune activators comprises an agonist of a receptor selected from the group consisting of fms related tyrosine kinase 3 (FLT3), stimulator of interferon genes (STING) receptor, DExD/H-box helicase 58 (DDX58; a.k.a., RIG-I), nucleotide binding oligomerization domain containing 2 (NOD2).~~

~~237. The method or use of any one of claims 235 to 236, comprising co-administering GS-3583 and/or GS-9992.~~

~~238. The method or use of any one of claims 229 to 237, comprising co-administering one or more antagonists or inhibitors of an inhibitory immune checkpoint protein or receptor and/or one or more activators or agonists of a stimulatory immune checkpoint protein or receptor.~~

~~239. The method or use of claim 238, wherein the one or more immune checkpoint proteins or receptors are selected from the group consisting of: CD27, CD70; CD40,~~

CD40LG; CD47, CD48 (SLAMF2), transmembrane and immunoglobulin domain containing 2 (TMIGD2, CD28H), CD84 (LY9B, SLAMF5), CD96, CD160, MS4A1 (CD20), CD244 (SLAMF4); CD276 (B7H3); V-set domain containing T cell activation inhibitor 1 (VTCN1, B7H4); V-set immunoregulatory receptor (VSIR, B7H5, VISTA); immunoglobulin superfamily member 11 (IGSF11, VSIG3); natural killer cell cytotoxicity receptor 3 ligand 1 (NCR3LG1, B7H6); HERV-H LTR-associating 2 (HHLA2, B7H7); inducible T-cell co-stimulator (ICOS, CD278); inducible T-cell co-stimulator ligand (ICOSLG, B7H2); TNF receptor superfamily member 4 (TNFRSF4, OX40); TNF superfamily member 4 (TNFSF4, OX40L); TNFRSF8 (CD30), TNFSF8 (CD30L); TNFRSF10A (CD261, DR4, TRAILR1), TNFRSF9 (CD137), TNFSF9 (CD137L); TNFRSF10B (CD262, DR5, TRAILR2), TNFRSF10 (TRAIL); TNFRSF14 (HVEM, CD270), TNFSF14 (HVEML); CD272 (B- and T-lymphocyte associated (BTLA)); TNFRSF17 (BCMA, CD269), TNFSF13B (BAFF); TNFRSF18 (GITR), TNFSF18 (GITRL); MHC class I polypeptide-related sequence A (MICA); MHC class I polypeptide-related sequence B (MICB); CD274 (CD274, PDL1, PD-L1); programmed cell death 1 (PDCD1, PD1, PD-1); cytotoxic T-lymphocyte associated protein 4 (CTLA4, CD152); CD80 (B7-1), CD28; nectin cell adhesion molecule 2 (NECTIN2, CD112); CD226 (DNAM-1); Poliovirus receptor (PVR) cell adhesion molecule (PVR, CD155); PVR related immunoglobulin domain containing (PVRIG, CD112R); T cell immunoreceptor with Ig and ITIM domains (TIGIT); T cell immunoglobulin and mucin domain containing 4 (TIMD4; TIM4); hepatitis A virus cellular receptor 2 (HAVCR2, TIMD3, TIM3); galectin 9 (LGALS9); lymphocyte activating 3 (LAG3, CD223); signaling lymphocytic activation molecule family member 1 (SLAMF1, SLAM, CD150); lymphocyte antigen 9 (LY9, CD229, SLAMF3); SLAM family member 6 (SLAMF6, CD352); SLAM family member 7 (SLAMF7, CD319); UL16 binding protein 1 (ULBP1); UL16 binding protein 2 (ULBP2); UL16 binding protein 3 (ULBP3); retinoic acid early transcript 1E (RAET1E; ULBP4); retinoic acid early transcript 1G (RAET1G; ULBP5); retinoic acid early transcript 1L (RAET1L; ULBP6); lymphocyte activating 3 (CD223); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer cell lectin like receptor C1 (KLRC1, NKG2A, CD159A); killer cell lectin like receptor K1 (KLRK1, NKG2D, CD314); killer cell lectin like receptor C2 (KLRC2, CD159c, NKG2C); killer cell lectin like receptor C3 (KLRC3, NKG2E); killer cell lectin like receptor C4 (KLRC4, NKG2F); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); killer cell immunoglobulin like receptor, three Ig domains and long

~~cytoplasmic tail 1 (KIR3DL1); killer cell lectin like receptor D1 (KLRD1); and SLAM family member 7 (SLAMF7).~~

~~240. The method or use of any one of claims 238 of 239, comprising co-administering one or more blockers or inhibitors of one or more T-cell inhibitory immune checkpoint proteins or receptors.~~

~~241. The method or use of claim 240, wherein the T-cell inhibitory immune checkpoint proteins or receptors are selected from the group consisting of CD274 (CD274, PDL1, PD-L1); programmed cell death 1 ligand 2 (PDCD1LG2, PD-L2, CD273); programmed cell death 1 (PDCD1, PD1, PD-1); cytotoxic T-lymphocyte associated protein 4 (CTLA4, CD152); CD276 (B7H3); V-set domain containing T-cell activation inhibitor 1 (VTCN1, B7H4); V-set immunoregulatory receptor (VSIR, B7H5, VISTA); immunoglobulin superfamily member 11 (IGSF11, VSIG3); TNFRSF14 (HVEM, CD270), TNFSF14 (HVEML); CD272 (B and T lymphocyte associated (BTLA)); PVR related immunoglobulin domain containing (PVRIG, CD112R); T-cell immunoreceptor with Ig and ITIM domains (TIGIT); lymphocyte activating 3 (LAG3, CD223); hepatitis A virus cellular receptor 2 (HAVCR2, TIMD3, TIM3); galectin 9 (LGALS9); killer-cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer-cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer-cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer-cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); and killer-cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR3DL1).~~

~~242. The method or use of any one of claims 238 of 239, comprising co-administering one or more agonists or activators of one or more T-cell stimulatory immune checkpoint proteins or receptors.~~

~~243. The method or use of claim 242, wherein the T-cell stimulatory immune checkpoint proteins or receptors are selected from the group consisting of CD27, CD70; CD40, CD40LG; inducible T-cell co-stimulator (ICOS, CD278); inducible T-cell co-stimulator ligand (ICOSLG, B7H2); TNF receptor superfamily member 4 (TNFRSF4, OX40); TNF superfamily member 4 (TNFSF4, OX40L); TNFRSF9 (CD137), TNFSF9 (CD137L); TNFRSF18 (GITR), TNFSF18 (GITRL); CD80 (B7-1), CD28; nectin cell adhesion molecule 2 (NECTIN2, CD112); CD226 (DNAM-1); Poliovirus receptor (PVR) cell adhesion molecule (PVR, CD155).~~

244. The method or use of any one of 242 to 243, comprising co-administering AGEN-2373 and/or AGEN-1223.

245. The method or use of any one of claims 238 of 244, comprising co-administering one or more blockers or inhibitors of one or more NK-cell inhibitory immune checkpoint proteins or receptors.

246. The method or use of claim 245, wherein the NK-cell inhibitory immune checkpoint proteins or receptors are selected from the group consisting of killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR, CD158E1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 1 (KIR2DL1); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 2 (KIR2DL2); killer cell immunoglobulin like receptor, two Ig domains and long cytoplasmic tail 3 (KIR2DL3); killer cell immunoglobulin like receptor, three Ig domains and long cytoplasmic tail 1 (KIR3DL1); killer cell lectin like receptor C1 (KLRC1, NKG2A, CD159A); and killer cell lectin like receptor D1 (KLRD1, CD94).

247. The method or use of any one of claims 238 to 239, comprising co-administering one or more agonists or activators of one or more NK-cell stimulatory immune checkpoint proteins or receptors.

248. The method or use of claim 247, wherein the NK-cell stimulatory immune checkpoint proteins or receptors are selected from CD16, CD226 (DNAM-1); killer cell lectin like receptor K1 (KLRK1, NKG2D, CD314); and SLAM family member 7 (SLAMF7).

249. The method or use of any one of claims 238 to 241, wherein the one or more immune checkpoint inhibitors comprises a proteinaceous inhibitor of PD-L1 (CD274), PD-1 (PDCD1) or CTLA4.

250. The method or use of claim 249, wherein the proteinaceous inhibitor of CTLA4 is selected from the group consisting of ipilimumab, tremelimumab, BMS-986218, AGEN1181, AGEN1884, BMS-986249, MK-1308, REGN-4659, ADU-1604, CS-1002, BCD-145, APL-509, JS-007, BA-3071, ONC-392, AGEN-2041, JHL-1155, KN-044, CG-0161, ATOR-1144, PBI-5D3H5, FPT-155 (CTLA4/PD-L1/CD28), PF-06936308 (PD-1/ CTLA4), MGD-019 (PD-1/CTLA4), KN-046 (PD-1/CTLA4), MEDI-5752 (CTLA4/PD-1), XmAb-20717 (PD-1/CTLA4) and AK-104 (CTLA4/PD-1).

~~251. The method or use of claim 249, wherein the proteinaceous inhibitor of PD-L1 (CD274) or PD-1 (PDCD1) is selected from the group consisting of zimberelimab (AB122), pembrolizumab, nivolumab, cemiplimab, pidilizumab, AMP-224, MEDI0680 (AMP-514), spartalizumab, atezolizumab, avelumab, ASC22, durvalumab, BMS-936559, CK-301, PF-06801591, BGB-A317 (tislelizumab), GLS-010 (WBP-3055), AK-103 (HX-008), AK-105, CS-1003, HLX-10, MGA-012, BI-754091, AGEN-2034, JS-001 (toripalimab), JNJ-63723283, genolimzumab (CBT-501), LZM-009, BCD-100, LY-3300054, SHR-1201, SHR-1210 (camrelizumab), Sym-021, ABBV-181, PD1-PIK, BAT-1306, (MSB0010718C), CX-072, CBT-502, TSR-042 (dostarlimab), MSB-2311, JTX-4014, BGB-A333, SHR-1316, CS-1001 (WBP-3155, KN-035, IBI-308 (sintilimab), HLX-20, KL-A167, STI-A1014, STI-A1015 (IMC-001), BCD-135, FAZ-053, TQB-2450, MDX1105-01, FPT-155 (CTLA4/PD-L1/CD28), PF-06936308 (PD-1/ CTLA4), MGD-013 (PD-1/LAG-3), FS-118 (LAG-3/PD-L1) MGD-019 (PD-1/CTLA4), KN-046 (PD-1/CTLA4), MEDI-5752 (CTLA4/PD-1), RO-7121661 (PD-1/TIM-3), XmAb-20717 (PD-1/CTLA4), AK-104 (CTLA4/PD-1), M7824 (PD-L1/TGFβ-EC domain), CA-170 (PD-L1/VISTA), CDX-527 (CD27/PD-L1), LY-3415244 (TIM3/PDL1), and INBRX-105 (4-1BB/PDL1).~~

~~252. The method or use of any one of claims 238 to 241, wherein the one or more immune checkpoint inhibitors comprises a small molecule inhibitor of CD274 (PDL1, PD-L1), programmed cell death 1 (PDCD1, PD1, PD-1) or CTLA4.~~

~~253. The method or use of claim 252, wherein the small molecule inhibitor of CD274 or PDCD1 is selected from the group consisting of GS-4224, GS-4416, INCB086550 and MAX10181.~~

~~254. The method or use of claim 252, wherein the small molecule inhibitor of CTLA4 comprises BPI-002.~~

~~255. The method or use of any one of claims 229 to 254, further comprising co-administering to the subject one or more antiviral agents.~~

~~256. The method or use of 255, wherein the one or more antiviral agents are selected from the group consisting of lamivudine (LAM), adefovir dipivoxil (ADV), entecavir (ETV), telbivudine (LdT), tenofovir disoproxil fumarate (TDF), tenofovir alafenamide (TAF or VEMLIDY®) and ledipasvir + sofosbuvir (HARVONI®).~~

~~257. The method or use of any one of claims 229 to 256, further comprising co-administering to the subject one or more therapeutic agents selected from the group consisting of HBV antigen inhibitors (e.g., HBV core antigen (HBcAg) inhibitors, HBV surface antigen (HBsAg) inhibitors, HBx inhibitors, HBV E antigen inhibitors), anti-HBV antigen antibodies, inhibitory nucleic acids targeting HBV (e.g., antisense oligonucleotide, short interfering RNA (siRNA), DNA-directed RNA interference (ddRNAi)), gene editors targeting HBV (e.g., CRISPR-Cas (e.g., Cas9, Cas12, Cascade, Cas13), zinc finger nucleases, homing endonucleases, homing meganucleases (e.g., ARCUS), synthetic nucleases, TALENs), covalently closed circular DNA (cccDNA) inhibitors and HBsAg secretion or assembly inhibitors and HBV viral entry inhibitors.~~

~~258. The method or use of any one of claims 229 to 257, wherein the method activates in the subject CD8+ T cells and/or CD4+ T cells targeting one or more HBV polypeptide epitopes.~~

~~259. The method or use of any one of claims 229 to 258, wherein the method elicits in the subject production of antibodies that bind one or more HBV polypeptides.~~