

RAS NEOANTIGENS AND USES THEREOF

CROSS-REFERENCE

[0001] This application claims the benefit of U.S. Provisional Application No. 63/065,346, filed on August 13, 2020; which is incorporated herein by reference in its entirety.

BACKGROUND

[0002] Cancer immunotherapy focuses on enhancing one's body's immune response to fight and eradicate cancer cells. This is achieved by administering antigenic peptide therapy, where the peptides comprise cancer antigens, or administering nucleic acid encoding the antigenic peptides comprising the cancer antigens, or using adoptive immunotherapy targeted towards the cancer. Adoptive immunotherapy or adoptive cellular therapy with lymphocytes (ACT) is the transfer of gene modified T lymphocytes to a subject for the therapy of disease. Adoptive immunotherapy has yet to realize its potential for treating a wide variety of diseases including cancer, infectious disease, autoimmune disease, inflammatory disease, and immunodeficiency. However, most, if not all adoptive immunotherapy strategies require T cell activation and expansion steps to generate a clinically effective, therapeutic dose of T cells. Accurate identification of cancer antigenic epitopes, and their potential to produce immune activation in a patient is necessary. Additionally, existing strategies of obtaining patient cells, and ex vivo activation, expansion and recovery of effective number of cells for ACT is a prolonged, cumbersome and an inherently complex process - and poses a serious challenge. Accordingly, there remains a need for developing compositions and methods for generating antigen-specific immunotherapy directed to a single patient having a cancer.

SUMMARY

[0003] Provided herein is a method for treating cancer in a subject in need thereof, wherein the cancer contains a RAS mutation and the treatment is for a patient expressing a specific major histocompatibility complex (MHC) peptide encoded by a specific HLA allele. Also provided herein is an ex vivo method for preparing antigen-specific T cells, the method comprising contacting T cells with antigen presenting cells (APCs) comprising one or more peptides containing an epitope with a RAS mutation.

[0003a] In another aspect, provided herein is an ex vivo method for preparing antigen-specific T cells, the method comprising contacting T cells with antigen presenting cells (APCs) comprising one or more peptides containing an epitope with a sequence GACGVGKSA, wherein the APCs express a protein encoded by an HLA-C03:04 allele.

[0004] In some embodiments, the method for treating cancer described herein comprises administering a therapy, such as an immunotherapy, to a subject with a cancer comprising a RAS mutation. In some embodiments, the RAS mutation is a G12C mutation. In some embodiments, RAS mutation is a G12V mutation. In some embodiments, the method for treating cancer is for a subject that expresses an MHC protein encoded by HLA C03:04 allele. In some embodiments, the method for treating cancer is for a subject that expresses an MHC protein encoded by HLA C03:03 allele. In some embodiments, the therapy is a

peptide, a polynucleotide encoding the peptide, APCs comprising the peptide or the polynucleotide, or T cells stimulated with APCs comprising the peptide or the polynucleotide.

[0005] In some embodiments the method comprises generating an antigen therapy comprising one or more peptides, wherein the one or more peptides comprise at least one epitope with a sequence GACGVGKSA (SEQ ID NO: 1), that is capable of activating an anti-cancer immune response in a suitable subject. A suitable subject expresses an MHC protein encoded by HLA C03:04 allele. In some embodiments, the method comprises administering to a subject an antigen therapy, wherein the subject expresses an MHC protein encoded by HLA C03:04 allele and has a cancer cell with a KRAS G12C mutation, wherein the antigen therapy comprises one or more peptides containing an epitope with a sequence GACGVGKSA (SEQ ID NO: 1). In some embodiments, the subject expressing an MHC protein encoded by HLA C03:04 allele is administered an anti-cancer therapy that comprises one or more nucleic acids encoding the peptide, wherein the peptide comprises an epitope with a sequence GACGVGKSA (SEQ ID NO: 1).

[0006] In some embodiments, the method comprises administering antigen presenting cells expressing one or more peptides comprising an epitope with a sequence GACGVGKSA (SEQ ID NO: 1) or a polynucleotide sequence encoding the one or more peptides, and an MHC protein encoded by an HLA C03:04 allele to a subject who expresses the MHC protein encoded by the HLA C03:04 allele.

[0007] In some embodiments the method comprises generating T cell therapy for a subject that expresses an MHC protein encoded by HLA C03:04 allele and has a cancer cell with a KRAS G12C mutation, the method comprising, contacting allogeneic or autologous T cells with APCs comprising one or more peptides comprising an epitope with a sequence GACGVGKSA (SEQ ID NO: 1), expanding the T cells in culture under conditions that stimulate the T cells to be cytotoxic according to a cytotoxicity assay. In some embodiments, the method comprises administering the T cell therapy to the subject. In some embodiments, the method comprises preparing a T cell, wherein the T cell is responsive to an antigen comprising an amino acid sequence GACGVGKSA (SEQ ID NO: 1). In some embodiments, the method comprises preparing a T cell, the method comprising stimulating a T cell with a polypeptide comprising an amino acid sequence GACGVGKSA (SEQ ID NO: 1). In some embodiments, the method comprises administering to a subject in need thereof a T cell preparation comprising a T cell, wherein the T cell is responsive to an antigen comprising an amino acid sequence GACGVGKSA (SEQ ID NO: 1). In some embodiments, the subject is human. In some embodiments, the subject expresses an MHC protein encoded by HLA C03:04 allele.

[0008] In some embodiments, the method described herein targets a mutant RAS antigen comprising a G12V mutation. In some embodiments, the method is directed to a patient that expresses an MHC protein encoded by HLA C03:03 allele. In some embodiments, the method comprises generating an antigen therapy comprising one or more peptides, wherein the one or more peptides comprise at least one epitope with a sequence GAVGVGKSA (SEQ ID NO: 2) that can activate an anti-cancer immune response in a suitable patient. A suitable patient can express an MHC protein encoded by HLA C03:03 allele. In some embodiments, the method comprises administering to a patient the antigen therapy, wherein the patient an MHC protein encoded by HLA C03:03 allele and has a cancer cell with a KRAS G12V mutation, wherein the antigen therapy

comprises a one or more peptides containing an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2). In some embodiments, the patient expressing an MHC protein encoded by HLA C03:03 allele is administered an anti-cancer therapy that comprises one or more nucleic acids encoding the peptide, wherein the peptide comprises an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2).

[0009] In some embodiments, the method comprises administering antigen presenting cells expressing one or more peptides comprising an epitope with a sequence GACGVGKSA (SEQ ID NO: 1) or a polynucleotide sequence encoding the one or more peptides, and an MHC protein encoded by an HLA C03:04 allele to a subject who expresses the MHC protein encoded by the HLA C03:04 allele.

[0010] In some embodiments the method comprises generating T cell therapy for a patient that expresses an MHC protein encoded by HLA C03:03 allele and has a cancer cell with a KRAS G12V mutation, the method comprising, contacting allogeneic or an autologous T cells derived from the patient with APCs comprising one or more peptides containing an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2), expanding the T cells in culture under conditions that stimulate the T cells to be cytotoxic according to a cytotoxicity assay. In some embodiments, the method comprises administering the T cell therapy to the patient. In some embodiments, the method comprises preparing a T cell, wherein the T cell is responsive to an antigen comprising an amino acid sequence GAVGVGKSA (SEQ ID NO: 2). In some embodiments, the method comprises preparing a T cell, the method comprising stimulating a T cell with a polypeptide comprising an amino acid sequence GAVGVGKSA (SEQ ID NO: 2). In some embodiments, the method comprises administering to a subject in need thereof a T cell preparation comprising a T cell, wherein the T cell is responsive to an antigen comprising an amino acid sequence GAVGVGKSA (SEQ ID NO: 2). In some embodiments, the subject is human. In some embodiments, the subject expresses an MHC protein encoded by HLA C03:03 allele.

[0011] In one aspect, provided herein is an *ex vivo* method for preparing antigen-specific T cells, the method comprising contacting T cells with APCs comprising one or more peptides containing an epitope with a sequence selected from GACGVGKSA (SEQ ID NO: 1) and GAVGVGKSA (SEQ ID NO: 2), wherein the APCs express a protein encoded by an HLA-C03:04 allele and the epitope sequence is GACGVGKSA (SEQ ID NO: 1); and wherein the APCs express a protein encoded by an HLA-C03:03 allele and the epitope sequence is GAVGVGKSA (SEQ ID NO: 2).

[0012] In some embodiments, the T cells are from a subject with cancer. In some embodiments, the T cells are allogeneic T cells.

[0013] In some embodiments, the method further comprises administering the T cells to a subject in need thereof, wherein the subject expresses a protein encoded by an HLA-C03:04 allele, and the T cells have been contacted with APCs comprising one or more peptides containing the epitope GACGVGKSA (SEQ ID NO: 1).

[0014] In some embodiments, the method further comprises administering the T cells to a subject in need thereof, wherein the subject expresses one or more protein encoded by an HLA-C03:03 allele and

the T cells have been contacted with APCs comprising a peptide containing the epitope GAVGVGKSA (SEQ ID NO: 2).

[0015] In some embodiments, the APCs are from a subject with cancer. In some embodiments, the APCs are allogeneic APCs.

[0016] In some embodiments, the method comprises obtaining a biological sample comprising T cells and/or APCs from a subject. In some embodiments, the biological sample is peripheral blood mononuclear cell (PBMC) sample. In some embodiments, the method comprises depleting CD14⁺ cells from the biological sample comprising T cells and/or APCs. In some embodiments, the method comprises depleting CD25⁺ cells from the biological sample comprising T cells and/or APCs. In some embodiments, the method comprises incubating the T cells and APCs in the presence of FMS-like tyrosine kinase 3 receptor ligand (FLT3L).

[0017] In some embodiments, the method comprises stimulating or expanding the T cells in the presence of the APCs for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 or more days. In some embodiments, the method comprises expanding the T cells at least 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, 500-fold or 1,000-fold or more in the presence of the APCs. In some embodiments, the antigen-specific T cells are prepared in less than 28 days.

[0018] In some embodiments, the epitope binds to a protein encoded by an HLA allele of the subject, is immunogenic according to an immunogenicity assay, is presented by APCs according to a mass spectrometry assay, and/or stimulates T cells to be cytotoxic according to a cytotoxicity assay.

[0019] In one aspect, provided herein is a method of treating a subject with cancer comprising administering to the subject a peptide, a polynucleotide encoding the peptide, APCs comprising the peptide or the polynucleotide encoding the peptide, or T cells stimulated with APCs comprising the peptide or the polynucleotide encoding the peptide; wherein the peptide comprises an epitope with a sequence GACGVGKSA (SEQ ID NO: 1), and wherein the subject expresses a protein encoded by an HLA-C03:04 allele.

[0020] In one aspect, provided herein is a method of treating a subject with cancer comprising administering to the subject a peptide, a polynucleotide encoding the peptide, APCs comprising the peptide or the polynucleotide encoding the peptide, or T cells stimulated with APCs comprising the peptide or the polynucleotide encoding the peptide; wherein the peptide comprises an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2), and wherein the subject expresses a protein encoded by an HLA-C03:03 allele.

[0020a] In another aspect, provided here in is the use of a composition in the manufacture of a medicament for treating cancer in a subject, the composition comprising (a) a peptide, (b) a polynucleotide encoding the peptide, (c) antigen presenting cells (APCs) comprising (a) or (b), or (d) T cells stimulated with APCs comprising (a) or (b); wherein the peptide comprises an epitope with a sequence GACGVGKSA and the subject expresses a protein encoded by an HLA-C03:04 allele, wherein the epitope with the sequence GAVGVGKSA is capable of binding to the protein encoded by the HLA-C03:03 allele.

[0021] In some embodiments, the epitope with the sequence GACGVGKSA (SEQ ID NO: 1) binds to the protein encoded by the HLA-C03:04 allele. In one embodiment, said epitope is presented by the protein encoded by the HLA-C03:04 allele.

[0022] In some embodiments, the epitope with the sequence GAVGVGKSA (SEQ ID NO: 2) binds to the protein encoded by the HLA-C03:03 allele. In one embodiment, said epitope is presented by the protein encoded by the HLA-C03:03 allele.

[0023] In some embodiments, the cancer is selected from the group consisting of pancreatic ductal adenocarcinoma, non-small cell lung cancer, colorectal cancer and cholangiocarcinoma.

- [0024]** In some embodiments, the peptide comprises one or more additional epitopes.
- [0025]** In some embodiments, the method further comprises administering an additional anti-cancer therapy to the subject.
- [0026]** In some embodiments, the APCs are from the subject with cancer. In some embodiments of the method of treating described herein, the APCs are allogeneic APCs.
- [0027]** In some embodiments, the T cells are from the subject with cancer. In some embodiments, the T cells are allogeneic. In some embodiments, the T cells are stimulated with the APCs in vitro or ex vivo. In some embodiments, the T cells have been stimulated with the APCs for at least 3, 4, 5, 6, 17, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 or more days. In some embodiments, the T cells are expanded in the presence of the APCs in vitro or ex vivo. In some embodiments, the T cells have been expanded in the presence the APCs for at least 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 or more days. In some embodiments, the T cells have been expanded at least 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, 500-fold or 1,000-fold or more in the presence of the APCs.
- [0028]** In some embodiments, the T cells are assayed for expression of a T cell activation marker. In some embodiments, the T cells are assayed for cytokine production. In some embodiments, the T cell activation marker or cytokine is selected from the group consisting of cell surface expression of CD107a and/or CD107b, IL2, IFN- γ , TNF α , TNF β and any combination thereof.
- [0029]** In some embodiments, the T cells are antigen-specific T cells.
- [0030]** In one aspect, provided herein is a pharmaceutical composition comprising T cells comprising a population of T cells expressing a T cell receptor (TCR) that binds to a complex of an MHC protein encoded by an HLA-C03:04 allele and an epitope with a sequence GACGVGKSA (SEQ ID NO: 1).
- [0031]** In one aspect, provided herein is a pharmaceutical composition comprising T cells comprising a population of T cells expressing a T cell receptor (TCR) that binds to a complex of an MHC protein encoded by an HLA-C03:03 allele and an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2).
- [0032]** In one aspect, provided herein is a pharmaceutical composition comprising APCs expressing an MHC protein encoded by an HLA-C03:04 allele, wherein the APCs comprise a peptide having an epitope with a sequence GACGVGKSA (SEQ ID NO: 1) or a polynucleotide encoding the peptide.
- [0033]** In one aspect, provided herein is a pharmaceutical composition comprising APCs expressing an MHC protein encoded by an HLA-C03:03 allele, wherein the APCs comprise a peptide having an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2) or a polynucleotide encoding the peptide.
- [0033a]** In one aspect, provided herein is a pharmaceutical composition comprising (a) T cells comprising a population of T cells expressing a T cell receptor (TCR) that binds to a complex of (i) an MHC protein encoded by an HLA-C03:04 allele and (ii) an epitope with a sequence GACGVGKSA; or (b) antigen presenting cells (APCs) expressing an MHC protein encoded by an HLA-C03:04 allele, wherein the APCs comprise (i) a peptide having an epitope with a sequence GACGVGKSA or (ii) a polynucleotide encoding the peptide.

[0034] In some embodiments, the APCs are from a subject with cancer. In some embodiments, the APCs are allogeneic APCs.

[0035] In some embodiments, the T cells are from a subject with cancer.

[0036] In some embodiments, the T cells are allogeneic.

[0037] In some embodiments, the population of T cells comprises CD8⁺ T cells.

[0038] In some embodiments, at least 0.1% of the CD8⁺ T cells in the population of T cells are derived from naïve CD8⁺ T cells

[0039] In some embodiments, the population of T cells comprises CD4⁺ T cells.

[0040] In some embodiments, at least 0.1% of the CD4⁺ T cells in the population of T cells are derived from naïve CD4⁺ T cells.

[0041] In some embodiments, provided herein is a TCR comprising a TCR alpha chain and a TCR beta chain, wherein the TCR is capable of binding to a mutated RAS epitope comprising a GACGVGKSA (SEQ ID NO: 1) when presented in complex with an MHC encoded by C03:04 allele. In some embodiments, provided herein is a TCR comprising a TCR alpha chain and a TCR beta chain, wherein the TCR is capable of binding to a mutated RAS epitope comprising a GAVGVGKSA (SEQ ID NO: 2) when presented in complex with an MHC encoded by C03:03 allele.

[0041a] In one aspect, provided herein is a T cell receptor (TCR) comprising a TCR alpha chain and a TCR beta chain that binds to complex comprising a mutated RAS epitope with the sequence GACGVGKSA and an MHC encoded by C03:04 allele.

[0041b] In another aspect, provided herein is the composition comprising (a) a peptide, (b) a polynucleotide encoding the peptide, (c) antigen presenting cells (APCs) comprising (a) or (b), or (d) T cells stimulated with APCs comprising (a) or (b); wherein the peptide comprises an epitope with a sequence GACGVGKSA and the subject expresses a protein encoded by an HLA-C03:04 allele, wherein the epitope with the sequence GAVGVGKSA is capable of binding to the protein encoded by the HLA-C03:03 allele for use in therapy.

BRIEF DESCRIPTION OF THE DRAWINGS

[0042] **FIG. 1A** is schematic of an exemplary method provided herein to prime, activate and expand antigen-specific T cells.

[0043] **FIG. 1B** is schematic of an exemplary method provided herein to prime, activate and expand antigen-specific T cells.

[0044] **FIG. 2** is schematic of an exemplary method for offline characterization of shared epitopes.

[0045] **FIG. 3A** depicts data illustrating that in silico epitope prediction identified multiple neoantigens derived from RAS G12D mutations that are presented according to mass spectrometry. FIG. 3A discloses SEQ ID NOS 1275-1279, respectively, in order of appearance.

[0046] **FIG. 3B** depicts data illustrating that in silico epitope prediction identified multiple neoantigens derived from RAS G12V mutations that are presented according to mass spectrometry. FIG. 3B discloses SEQ ID NOS 1288, 1286, 97, 95, and 99, respectively, in order of appearance.

[0047] **FIG. 3C** depicts data illustrating that in silico epitope prediction identified multiple neoantigens derived from RAS G12C mutations that are presented according to mass spectrometry. FIG. 3C discloses SEQ ID NO: 1287.

[0048] FIG. 3D depicts data illustrating that in silico epitope prediction identified multiple neoantigens derived from RAS G12R mutations that are presented according to mass spectrometry FIG. 3D discloses SEQ ID NOS 1280-1283, respectively, in order of appearance.

[0049] FIG. 4 depicts data illustrating that presentation of shared neoantigen epitopes can be directly confirmed by mass spectrometry and that RAS neoantigens are targetable in defined patient populations.

[0050] FIG. 5 shows an exemplary head-to-toe plot of MS/MS spectra for the endogenously processed mutant RAS peptide epitope VVVGAVGVGK (SEQ ID NO: 3) (top) and its corresponding heavy isotopically labeled peptide (bottom). 293T cells were lentivirally transduced to make cells express RAS^{G12V} and HLA-A*03:01.

[0051] FIG. 6 depicts data illustrating that an exemplary method provided herein to prime, activate and expand antigen-specific T cells induces de novo CD8 T cell responses against RAS G12 neoantigens on HLA-A11:01 and HLA-A03:01.

[0059] FIG. 11A depicts a graph of IL2 concentration (pg/mL) released by Jurkat cells transduced with a TCR that binds to the underlined RAS-G12V epitope when bound to an MHC encoded by the HLA-A11:01 allele in the presence of FLT3L-treated PBMCs contacted with increasing amounts of the indicated RAS-G12V mutant peptides. Fig. 11A discloses SEQ ID NOS 94 and 1284-1285, respectively, in order of appearance.

[0060] FIG. 11B depicts an exemplary data illustrating the immunogenicity of the indicated RAS-G12V mutant peptides in vitro using PBMCs from healthy donors (top) and in vivo using HLA-A11:01 transgenic mice immunized with the peptides (bottom).

DETAILED DESCRIPTION

[0061] Although many epitopes have the potential to bind to an MHC molecule, few are capable of binding to an MHC molecule when tested experimentally. Although many epitopes also have the potential to be presented by an MHC molecule that can, for example, be detected by mass spectrometry, only a select number of these epitopes can be presented and detected by mass spectrometry. Although many epitopes also have the potential to be immunogenic, when tested experimentally many of these epitopes are not immunogenic, despite being demonstrated to be presented by antigen presenting cells. Many epitopes also have the potential to activate T cells to become cytotoxic; however, many epitopes that have been demonstrated to be presented by antigen presenting cells and/or to be immunogenic are still not capable of activating T cells to become cytotoxic.

[0062] Provided herein are antigens containing T cell epitopes that have been identified and validated as binding to one or more MHC molecules, presented by the one or more MHC molecules, being immunogenic and capable of activating T cells to become cytotoxic. The validated antigens and polynucleotides encoding these antigens can be used in preparing antigen specific T cells for therapeutic uses. In some embodiments, the validated antigens and polynucleotides encoding these antigens can be pre-manufactured and stored for use in a method of manufacturing T cells for therapeutic uses. For example, the validated antigens and polynucleotides encoding these antigens can be pre-manufactured or manufactured quickly to prepare therapeutic T cell compositions for patients quickly. Using validated antigens with T cell epitopes, immunogens such as peptides having HLA binding activity or RNA encoding such peptides can be manufactured. Multiple immunogens can be identified, validated and pre-manufactured in a library. In some embodiments, peptides can be manufactured in a scale suitable for storage, archiving and use for pharmacological intervention on a suitable patient at a suitable time.

[0063] Mutations in KRAS have been known for more than 60 years to cause various forms of cancer, but developing successful therapy against KRAS cancers remains largely elusive. Described herein are new immunotherapeutic agents and uses thereof based on the discovery of neoantigens arising from mutational events unique to an individual's tumor. Accordingly, the present disclosure described herein provides peptides, polynucleotides encoding the peptides, and peptide binding agents that can be used, for example,

[0118] Provided herein are KRAS epitopes each of which specifically can bind to the MHC protein encoded by the alleles indicated in right hand column in the same row of Table 1, that have been identified to bind to the MHC protein by mass spectrometry, and that each epitope is presented to T cells by association with the MHC protein in the respective right hand column for each row in Table 1. Provided herein are specific KRAS epitopes, each of which can specifically bind to a specific MHC encoded by an allele as indicated in Table 1, and is predetermined to be immunogenic by a suitable ex vivo validation assay. In one embodiment, the KRAS epitope has an amino acid sequence GACGVGKSA (SEQ ID NO: 1), and the epitope specifically binds to an MHC encoded by an HLA-C03:04 allele. In some embodiments, the KRAS epitope has an amino acid sequence GAVGVGKSA (SEQ ID NO: 2), and the epitope specifically binds to an MHC encoded by an HLA-C03:03 allele (Table 1).

Table 1

Epitope	MHC protein encoded by allele
GACGVGKSA (SEQ ID NO: 1)	C03:04
GAVGVGKSA (SEQ ID NO: 2)	C03:03

[0119] In some embodiments, provided herein is a method for preparing antigen-specific T cells, the method comprising contacting T cells from the subject or allogeneic T cells with APCs comprising one or more peptides containing an epitope with a sequence GACGVGKSA (SEQ ID NO: 1), wherein the APCs express a protein encoded by an HLA-C03:04 allele. In some embodiments, a method of treating a subject with cancer is provided herein, the method comprising administering to the subject, a therapy comprising: a peptide, a polynucleotide encoding the peptide, APCs comprising the peptide or polynucleotide, or T cells stimulated with the APCs; wherein the peptide comprises an epitope with a sequence GACGVGKSA (SEQ ID NO: 1); and wherein the subject expresses a protein encoded by an HLA-C03:04 allele.

[0120] In some embodiments, provided herein is a method for preparing antigen-specific T cells, the method comprising contacting T cells from the subject or allogeneic T cells with APCs comprising one or more peptides containing an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2), wherein the APCs express a protein encoded by an HLA-C03:03 allele. In some embodiments, a method of treating a subject with cancer is provided herein, the method comprising administering to the subject, a therapy comprising: a peptide, a polynucleotide encoding the peptide, APCs comprising the peptide or polynucleotide, or T cells stimulated with the APCs; wherein the peptide comprises an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2); and wherein the subject expresses a protein encoded by an HLA-C03:03 allele.

[0121] In some embodiments, the method described above comprising a peptide comprising an epitope of Table 1, or a polynucleotide encoding the peptide may be combined with 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more additional peptides comprising at least one epitope sequence selected from a library of epitope sequences, or polynucleotides encoding the same or APCs comprising

and approximately 25 percent of lung cancers. Mutation of glycine 12 (G12) causes RAS activation by interfering with GAP binding and GAP-stimulated GTP hydrolysis. There are currently no effective treatment for KRAS-positive cancers.

[0129] In one aspect, provided herein is a therapeutic composition for a subject having a cancer with a G12C KRAS mutation, wherein the subject express a protein encoded by an HLA-C03:04, and the therapeutic comprises of at least one peptide comprising an epitope having a sequence GACGVGKSA (SEQ ID NO: 1), or a polynucleotide encoding the at least one peptide. In some embodiments, provided herein is a method comprising, identifying whether a subject having a cancer related to a KRAS mutation comprises a KRAS G12C mutation by sequencing a biological sample from the subject; identifying the subject expresses a protein encoded by an HLA-C03:04 allele; and administering to the subject a composition comprising at least a peptide comprising an epitope GACGVGKSA (SEQ ID NO: 1).

[0130] In another aspect, provided herein is a therapeutic composition for a subject having a cancer with a G12V KRAS mutation, wherein the subject express a protein encoded by an HLA-C03:03, and the therapeutic comprises of at least one peptide comprising a the epitope having a sequence GAVGVGKSA (SEQ ID NO: 2), or a polynucleotide encoding the at least one peptide. In some embodiments, provided herein is a method comprising, identifying whether a subject having a cancer related to a KRAS mutation comprises a KRAS G12V mutation by sequencing a biological sample from the subject; identifying the subject expresses a protein encoded by an HLA-C03:03 allele; and administering to the subject a composition comprising at least one peptide comprising an epitope GAVGVGKSA (SEQ ID NO: 2).

[0131] In some aspects, the present disclosure provides a composition comprising at least two peptides, a polynucleotide encoding the at least two peptides, APCs comprising the at least two peptides or the polynucleotide encoding the at least two peptides, or T cells stimulated with APCs comprising the at least two peptides or the polynucleotide encoding the at least two peptides. In some embodiments, the peptides comprise at least two distinct peptides. In some embodiments, the first peptide comprises a first epitope GACGVGKSA (SEQ ID NO: 1), and the second peptide comprises a second neoepitope, wherein the composition is administered to a subject that has a cancer with KRAS G12C mutation, and expresses a protein encoded by an HLA-C03:04 allele. In some embodiments, the first peptide comprises a first epitope GAVGVGKSA (SEQ ID NO: 2), and the second peptide comprises a second neoepitope, wherein the composition is administered to a subject that has a cancer with KRAS G12V mutation, and expresses a protein encoded by an HLA-C03:03 allele.

[0132] In some embodiments, the first and second peptides are derived from the same protein. The at least two distinct peptides may vary by length, amino acid sequence or both. The peptides can be derived from any protein known to or have been found to contain a tumor specific mutation. In some embodiments, the composition described herein comprises a first peptide or a polynucleotide encoding the first peptide, the first peptide comprising a first neoepitope of a protein and a second peptide or a polynucleotide

stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 2, a polynucleotide encoding a peptide comprising an epitope of Table 2, APCs comprising an epitope of Table 2 or a polynucleotide encoding a peptide comprising an epitope of Table 2, or T cells stimulated with APCs comprising an epitope of Table 2 or a polynucleotide encoding a peptide comprising an epitope of Table 2, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 2 and contains a cancer with a RAS Q61H mutation.

Table 2

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
ILDTAGHEEY	5	HLA-A36:01	1
ILDTAGHEEY	5	HLA-A01:01	2
DTAGHEEYSAM	6	HLA-A26:01	3
DTAGHEEYSAM	6	HLA-A25:01	4
GHEEYSAM	7	HLA-B15:09	4
DTAGHEEY	8	HLA-A26:01	5
ILDTAGHEE	9	HLA-C08:02	5
AGHEEYSAM	10	HLA-C01:02	6
AGHEEYSAM	10	HLA-B46:01	6
DTAGHEEY	8	HLA-A25:01	6
DTAGHEEY	8	HLA-A01:01	6
DTAGHEEY	8	HLA-B18:01	7
DTAGHEEY	8	HLA-A36:01	7
ILDTAGHEE	9	HLA-C05:01	7
ILDTAGHEE	9	HLA-A02:07	7
ILDTAGHEEY	5	HLA-A29:02	7
ILDTAGHEEY	5	HLA-C08:02	7
HEEYSAMRD	11	HLA-B49:01	8
TAGHEEYSA	12	HLA-B35:03	8
DTAGHEEYS	13	HLA-A68:02	9
DTAGHEEYSAMR	14	HLA-A68:01	9
GHEEYSAM	7	HLA-B39:01	9
ILDTAGHEE	9	HLA-A01:01	9
LDTAGHEEY	15	HLA-B53:01	9

HEEYSAMRD	11	HLA-B41:01	10
ILDTAGHEE	9	HLA-A36:01	10
DTAGHEEY	8	HLA-B58:01	11
LLDILDTAGH	16	HLA-A01:01	12
TAGHEEYSAM	17	HLA-B35:03	12
LDTAGHEEY	15	HLA-B35:01	13
DILDTAGHE	18	HLA-A26:01	14
DTAGHEEY	8	HLA-C12:03	14
ILDTAGHEEY	5	HLA-C05:01	14
AGHEEYSAM	10	HLA-A30:02	15
DILDTAGHEEY	19	HLA-A25:01	15
DTAGHEEY	8	HLA-C02:02	15
ILDTAGHEE	9	HLA-C04:01	15
DILDTAGH	20	HLA-A26:01	16
ILDTAGHEE	9	HLA-A02:01	16
LDTAGHEEY	15	HLA-A29:02	16
ILDTAGHE	21	HLA-A01:01	17
LDTAGHEEY	15	HLA-B18:01	17
AGHEEYSAM	10	HLA-C14:03	18
DILDTAGHEEY	19	HLA-A29:02	18
DTAGHEEYS	13	HLA-A26:01	18
ILDTAGHEEY	5	HLA-B15:01	18
DTAGHEEYSA	22	HLA-A68:02	19
ILDTAGHE	21	HLA-C05:01	19
ILDTAGHEEY	5	HLA-A02:07	19
ILDTAGHEEY	5	HLA-A30:02	19
LDTAGHEEY	15	HLA-A36:01	19
AGHEEYSAM	10	HLA-C14:02	20
AGHEEYSAM	10	HLA-B15:03	20
LLDILDTAGH	16	HLA-A02:07	20

[0136] Exemplary RAS epitope sequences comprising a Q61R mutation, corresponding HLA allele, and rank binding potential are listed in Table 3 below. In some embodiments, a peptide comprising an epitope of Table 1, a polynucleotide encoding a peptide comprising an epitope of Table 1, APCs comprising an

epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, or T cells stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 3, a polynucleotide encoding a peptide comprising an epitope of Table 3, APCs comprising an epitope of Table 3 or a polynucleotide encoding a peptide comprising an epitope of Table 3, or T cells stimulated with APCs comprising an epitope of Table 3 or a polynucleotide encoding a peptide comprising an epitope of Table 3, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 3 and contains a cancer with a RAS Q61R mutation.

Table 3

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
ILDTAGREEY	23	HLA-A36:01	1
ILDTAGREEY	23	HLA-A01:01	2
DTAGREEYSAM	24	HLA-A26:01	3
DILDTAGR	25	HLA-A33:03	4
DILDTAGR	25	HLA-A68:01	5
DTAGREEY	26	HLA-A26:01	6
DTAGREEYSAM	24	HLA-A25:01	6
CLLDILDTAGR	27	HLA-A74:01	7
DTAGREEY	26	HLA-A01:01	7
REEYSAMRD	28	HLA-B41:01	7
GREEYSAMR	29	HLA-B27:05	8
ILDTAGREE	30	HLA-C08:02	8
ILDTAGREEY	23	HLA-A29:02	8
REEYSAMRD	28	HLA-B49:01	8
AGREEYSAM	31	HLA-B46:01	9
DTAGREEY	26	HLA-B18:01	9
DTAGREEY	26	HLA-A25:01	9
DTAGREEY	26	HLA-A36:01	9
DILDTAGR	25	HLA-A74:01	10
DILDTAGRE	32	HLA-A26:01	10
ILDTAGREE	30	HLA-C05:01	10
DILDTAGR	25	HLA-A26:01	11
GREEYSAM	33	HLA-B39:01	11
AGREEYSAM	31	HLA-B15:03	12
GREEYSAM	33	HLA-C07:02	12
ILDTAGREE	30	HLA-A01:01	12
TAGREEYSA	34	HLA-B35:03	12
ILDTAGREEY	23	HLA-A30:02	13
DTAGREEYS	35	HLA-A68:02	14
ILDTAGRE	36	HLA-A01:01	14

CLLDILDTAGR	27	HLA-A31:01	15
DTAGREEYSAMR	37	HLA-A68:01	15
LLDILDTAGR	38	HLA-A01:01	15
DTAGREEY	26	HLA-B58:01	16
ILDTAGREEY	23	HLA-C08:02	16
DILDTAGR	25	HLA-A31:01	17
ILDTAGREE	30	HLA-C04:01	17
ILDTAGREEY	23	HLA-A32:01	17
LLDILDTAGR	38	HLA-A74:01	17
TAGREEYSAM	39	HLA-B35:03	17
DILDTAGREEY	40	HLA-A32:01	18
ILDTAGRE	36	HLA-C05:01	18
ILDTAGREE	30	HLA-A02:07	18
REEYSAMRD	28	HLA-B40:01	18
AGREEYSAM	31	HLA-B15:01	19
AGREEYSAMR	41	HLA-A31:01	19
ILDTAGRE	36	HLA-A36:01	19
LDILDTAGR	42	HLA-A68:01	19
LDTAGREEY	43	HLA-A29:02	19
LDTAGREEY	43	HLA-B35:01	19
REEYSAMRD	28	HLA-B45:01	19
REEYSAMRDQY	44	HLA-A36:01	19
DTAGREEY	26	HLA-C02:02	20

[0137] Exemplary RAS epitope sequences comprising a Q61K mutation, corresponding HLA allele, and rank binding potential are listed in Table 4 below. In some embodiments, a peptide comprising an epitope of Table 1, a polynucleotide encoding a peptide comprising an epitope of Table 1, APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, or T cells stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 4, a polynucleotide encoding a peptide comprising an epitope of Table 4, APCs comprising an epitope of Table 4 or a polynucleotide encoding a peptide comprising an epitope of Table 4, or T cells stimulated with APCs comprising an epitope of Table 4 or a polynucleotide encoding a peptide comprising an epitope of Table 4, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 4 and contains a cancer with a RAS Q61K mutation.

Table 4

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
ILDTAGKEEY	45	HLA-A36:01	1
ILDTAGKEEY	45	HLA-A01:01	2

DTAGKEEYSAM	46	HLA-A26:01	3
CLLDILDTAGK	47	HLA-A03:01	4
DTAGKEYEY	48	HLA-A01:01	5
DTAGKEYEY	48	HLA-A26:01	5
DTAGKEEYSAM	46	HLA-A25:01	5
AGKEEYSAM	49	HLA-B46:01	6
DILDTAGKE	50	HLA-A26:01	7
KEEYSAMRD	51	HLA-B41:01	7
DTAGKEYEY	48	HLA-B18:01	8
GKEEYSAM	52	HLA-B15:03	8
ILDTAGKEE	53	HLA-C08:02	8
ILDTAGKEYEY	45	HLA-A29:02	8
DTAGKEEYS	54	HLA-A68:02	9
LDTAGKEYEY	55	HLA-B53:01	9
TAGKEEYSAM	56	HLA-B35:03	9
DILDTAGK	57	HLA-A68:01	10
DTAGKEYEY	48	HLA-A36:01	10
KEEYSAMRD	51	HLA-B49:01	10
LDTAGKEYEY	55	HLA-C07:01	10
DTAGKEEYSAMR	58	HLA-A68:01	11
ILDTAGKEE	53	HLA-C05:01	11
ILDTAGKEYEY	45	HLA-C08:02	11
LLDILDTAGK	59	HLA-A01:01	12
AGKEEYSAM	49	HLA-A30:02	13
DTAGKEYEY	48	HLA-A25:01	13
DTAGKEEYS	54	HLA-A26:01	13
ILDTAGKE	60	HLA-C05:01	13
LDTAGKEYEY	55	HLA-B35:01	13
AGKEEYSAMR	61	HLA-A31:01	14
DILDTAGK	57	HLA-A33:03	14
ILDTAGKE	60	HLA-A01:01	14
ILDTAGKEE	53	HLA-A01:01	14
ILDTAGKEE	53	HLA-A02:07	14
TAGKEEYSAM	62	HLA-B35:03	14
AGKEEYSAM	49	HLA-B15:01	15
ILDTAGKEYEY	45	HLA-A30:02	15
LDTAGKEYEY	55	HLA-B46:01	15
DTAGKEYEY	48	HLA-B58:01	16
ILDTAGKEYEY	45	HLA-C05:01	17
AGKEEYSAM	49	HLA-A30:01	18
AGKEEYSAM	49	HLA-B15:03	18
DTAGKEYEY	48	HLA-C02:02	18
LDTAGKEYEY	55	HLA-A29:02	18

[0138] Exemplary RAS epitope sequences comprising a Q61L mutation, corresponding HLA allele, and rank binding potential are listed in Table 5 below. In some embodiments, a peptide comprising an epitope of Table 1, a polynucleotide encoding a peptide comprising an epitope of Table 1, APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, or T cells stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 5, a polynucleotide encoding a peptide comprising an epitope of Table 5, APCs comprising an epitope of Table 5 or a polynucleotide encoding a peptide comprising an epitope of Table 5, or T cells stimulated with APCs comprising an epitope of Table 5 or a polynucleotide encoding a peptide comprising an epitope of Table 5, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 5 and contains a cancer with a RAS Q61L mutation.

Table 5

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
ILDTAGLEEEY	63	HLA-A36:01	1
ILDTAGLEEEY	63	HLA-A01:01	2
LLDILDITAGL	64	HLA-A02:07	3
GLEEYSAMRDQY	65	HLA-A36:01	4
DTAGLEEEY	66	HLA-A25:01	5
DTAGLEEEY	66	HLA-A26:01	5
DTAGLEEEYSAM	67	HLA-A26:01	5
DTAGLEEEY	66	HLA-A01:01	6
ILDTAGLEE	68	HLA-C08:02	6
ILDTAGLEE	68	HLA-A01:01	6
CLLDILDITAGL	69	HLA-A02:04	7
ILDTAGLEE	68	HLA-A36:01	7
LLDILDITAGL	64	HLA-A01:01	7
DILDITAGL	70	HLA-B14:02	8
DILDITAGLEEEY	71	HLA-A25:01	8
DTAGLEEYS	72	HLA-A68:02	8
DTAGLEEYSAM	67	HLA-A25:01	8
GLEEYSAMR	73	HLA-A74:01	8
ILDTAGLE	74	HLA-A01:01	8
DILDITAGLEEEY	71	HLA-A26:01	9
DTAGLEEEY	66	HLA-A36:01	9
ILDTAGLEEEY	63	HLA-A29:02	9
DILDITAGL	70	HLA-B08:01	10
DTAGLEEEY	66	HLA-B18:01	10
ILDTAGLEE	68	HLA-A02:07	10
LDTAGLEEEY	75	HLA-B35:01	10

CLLDILDTAGL	69	HLA-A02:01	11
DTAGLECY	66	HLA-C02:02	11
ILDTAGLECY	68	HLA-C05:01	11
ILDTAGLECY	63	HLA-C08:02	11
ILDTAGLECY	63	HLA-A02:07	11
LLDILDTAGL	64	HLA-C08:02	11
DILDTAGL	70	HLA-A26:01	12
LDTAGLECY	75	HLA-B53:01	12
DTAGLECY	66	HLA-C03:02	13
DTAGLECY	66	HLA-B58:01	13
ILDTAGLECY	63	HLA-A30:02	13
LLDILDTAGL	64	HLA-C05:01	13
LLDILDTAGL	64	HLA-C04:01	13
DTAGLECYSAMR	76	HLA-A68:01	14
ILDTAGLE	74	HLA-A36:01	15
LLDILDTAGL	64	HLA-A02:01	15
AGLECYSAM	77	HLA-B15:03	16
DTAGLECYSA	78	HLA-A68:02	16
GLECYSAMRDQY	65	HLA-A01:01	16
ILDTAGLE	74	HLA-C04:01	16
ILDTAGLECY	63	HLA-B15:01	16
LDILDTAGL	79	HLA-B37:01	16
AGLECYSAM	77	HLA-A30:02	17
AGLECYSAM	77	HLA-B48:01	17
AGLECYSAMR	80	HLA-A31:01	17
ILDTAGLECY	68	HLA-C04:01	17
LDTAGLECY	75	HLA-C03:02	17
AGLECYSAM	77	HLA-C14:02	18
GLECYSAMR	73	HLA-A31:01	18
LECYSAMRD	81	HLA-B41:01	18
LLDILDTAGLE	82	HLA-A01:01	18
AGLECYSAM	77	HLA-C14:03	19
LDILDTAGL	79	HLA-B40:02	19
LDTAGLECY	75	HLA-A29:02	19
DILDTAGLE	83	HLA-A26:01	20
DTAGLECY	66	HLA-B15:01	20
ILDTAGLECY	63	HLA-A02:01	20
LDTAGLECY	75	HLA-A36:01	20
LDTAGLECY	75	HLA-B46:01	20
DTAGLECY	66	HLA-A68:02	21
DTAGLECY	66	HLA-C12:03	21
ILDTAGLE	74	HLA-C05:01	21
LDTAGLECY	75	HLA-B18:01	21
LECYSAMRD	81	HLA-B49:01	21

TAGLEEYSA	84	HLA-B54:01	21
DILDTAGLEYY	71	HLA-A29:02	22
GLEEYSAM	85	HLA-C05:01	22

[0139] Exemplary RAS epitope sequences comprising a G12C mutation, corresponding HLA allele, and rank binding potential are listed in Table 6 below. In some embodiments, a peptide comprising an epitope of Table 1, a polynucleotide encoding a peptide comprising an epitope of Table 1, APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, or T cells stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 6, a polynucleotide encoding a peptide comprising an epitope of Table 6, APCs comprising an epitope of Table 6 or a polynucleotide encoding a peptide comprising an epitope of Table 6, or T cells stimulated with APCs comprising an epitope of Table 6 or a polynucleotide encoding a peptide comprising an epitope of Table 6, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 6 and contains a cancer with a RAS G12C mutation.

Table 6

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
VVVGACGVGK	86	HLA-A11:01	1
VVGACGVGK	87	HLA-A03:01	2
VVGACGVGK	87	HLA-A11:01	3
VVVGACGVGK	86	HLA-A68:01	4
VVGACGVGK	87	HLA-A68:01	5
VVVGACGVGK	86	HLA-A03:01	5
VVGACGVGK	87	HLA-A30:01	6
ACGVGKSAL	88	HLA-B81:01	7
ACGVGKSAL	88	HLA-C01:02	7
ACGVGKSAL	88	HLA-C14:03	8
ACGVGKSAL	88	HLA-C03:04	9
VVVGACGVGK	86	HLA-A30:01	9
ACGVGKSAL	88	HLA-C14:02	10
CGVGKSAL	89	HLA-B08:01	10
KLVVVGACGV	90	HLA-A02:01	10
ACGVGKSAL	88	HLA-B07:02	11
GACGVGKSAL	91	HLA-B48:01	12
GACGVGKSAL	91	HLA-C03:03	13
ACGVGKSAL	88	HLA-B48:01	14
ACGVGKSAL	88	HLA-B40:01	14
YKLVVVGAC	92	HLA-B48:01	14
YKLVVVGAC	92	HLA-B15:03	14

GACGVGKSA	1	HLA-B46:01	15
GACGVGKSAL	91	HLA-C03:04	15
GACGVGKSAL	91	HLA-C01:02	15
LVVVGACGV	93	HLA-A68:02	15
CGVGKSAL	89	HLA-C03:04	16
GACGVGKSAL	91	HLA-C08:02	16
VVGACGVGK	87	HLA-A74:01	16

[0140] Exemplary RAS epitope sequences comprising a G12V mutation, corresponding HLA allele, and rank binding potential are listed in Table 7 below. In some embodiments, a peptide comprising an epitope of Table 1, a polynucleotide encoding a peptide comprising an epitope of Table 1, APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, or T cells stimulated with APCs comprising an epitope of Table 1 or a polynucleotide encoding a peptide comprising an epitope of Table 1, can be administered to a subject that expresses an MHC protein encoded by an HLA-C03:04 or HLA-C03:03 allele; and a peptide comprising an epitope of Table 7, a polynucleotide encoding a peptide comprising an epitope of Table 7, APCs comprising an epitope of Table 7 or a polynucleotide encoding a peptide comprising an epitope of Table 7, or T cells stimulated with APCs comprising an epitope of Table 7 or a polynucleotide encoding a peptide comprising an epitope of Table 7, can be administered to the subject, for example, if the subject expresses an MHC protein encoded by a corresponding HLA allele in Table 7 and contains a cancer with a RAS G12V mutation.

Table 7

Peptide	SEQ ID NO:	Allele	Rank of Binding Potential
VVGAVGVGK	94	HLA-A03:01	1
VVGAVGVGK	94	HLA-A11:01	2
VVVGAVGVGK	3	HLA-A11:01	2
VVVGAVGVGK	3	HLA-A68:01	3
VVGAVGVGK	94	HLA-A68:01	4
LVVVGAVGV	95	HLA-A68:02	5
VVGAVGVGK	94	HLA-A30:01	5
AVGVGKSAL	96	HLA-B81:01	6
KLVVVGAVGV	97	HLA-A02:01	6
AVGVGKSAL	96	HLA-B46:01	7
GAVGVGKSAL	98	HLA-C03:03	7
GAVGVGKSAL	98	HLA-B48:01	7
VVVGAVGVGK	3	HLA-A03:01	7
AVGVGKSAL	96	HLA-C03:04	8
GAVGVGKSAL	98	HLA-C03:04	8
KLVVVGAVGV	97	HLA-A02:07	9
VGVGKSAL	99	HLA-B08:01	9
VVVGAVGV	100	HLA-A68:02	9

AVGVGKSAL	96	HLA-C08:02	10
AVGVGKSAL	96	HLA-B07:02	10
GAVGVGKSAL	98	HLA-B35:03	10
AVGVGKSAL	96	HLA-C08:01	11
AVGVGKSAL	96	HLA-C01:02	11
GAVGVGKSA	2	HLA-B55:01	11
GAVGVGKSAL	98	HLA-B81:01	11
GAVGVGKSAL	98	HLA-C08:01	11
KLVVVGAVGV	97	HLA-B13:02	11
VGVGKSAL	99	HLA-C03:04	11
AVGVGKSAL	96	HLA-A32:01	12
GAVGVGKSA	2	HLA-B46:01	12
VGVGKSAL	99	HLA-C03:02	12
VGVGKSALTI	101	HLA-A23:01	12
GAVGVGKSA	2	HLA-B54:01	13
VGVGKSAL	99	HLA-C01:02	.3
AVGVGKSAL	96	HLA-B48:01	14
AVGVGKSAL	96	HLA-C03:03	14
AVGVGKSAL	96	HLA-B42:01	14
LVVVGAVGV	95	HLA-B55:01	14
VGVGKSAL	99	HLA-C08:01	14
VVGAVGVGK	94	HLA-A74:01	14
AVGVGKSAL	96	HLA-C05:01	15
AVGVGKSAL	96	HLA-C03:02	15
GAVGVGKSA	2	HLA-C03:04	15
KLVVVGAVGV	97	HLA-A02:04	15
LVVVGAVGV	95	HLA-A02:07	15
VGVGKSAL	99	HLA-B14:02	15
VVGAVGVGK	3	HLA-A30:01	15
VVGAVGVGK	94	HLA-B81:01	16
VVGAVGV	100	HLA-B55:01	16
AVGVGKSAL	96	HLA-C14:03	17
AVGVGKSAL	96	HLA-B15:01	17
LVVVGAVGV	95	HLA-B54:01	17
AVGVGKSA	102	HLA-B55:01	18
AVGVGKSAL	96	HLA-C17:01	18
GAVGVGKSA	2	HLA-B50:01	19
GAVGVGKSAL	98	HLA-C17:01	19
YKLVVVGAV	103	HLA-A02:04	19
GAVGVGKSAL	98	HLA-B35:01	20
VVGAVGVGK	94	HLA-A31:01	20
YKLVVVGAV	103	HLA-B51:01	20

[0256] In some aspects, provided herein is a composition comprising: (a) APCs expressing a protein encoded by an HLA-C03:04 allele, wherein the APCs comprise a peptide or a polynucleotide encoding the peptide; and (b) T cells stimulated with APCs of (a); wherein the peptide comprises an epitope with a sequence GACGVGKSA (SEQ ID NO: 1).

[0257] In some aspects, provided herein is a composition comprising: (a) APCs expressing a protein encoded by an HLA-C03:04 allele, wherein the APCs comprise a peptide or a polynucleotide encoding the peptide; and (b) T cells stimulated with APCs of (a); wherein the peptide comprises an epitope with a sequence GACGVGKSA (SEQ ID NO: 1), and further comprises (c) antigen presenting cells expressing a protein encoded by an HLA allele of a subject, wherein the APCs further comprise a peptide selected from Tables 1-12, that binds to the protein encoded by the HLA of the subject and (d) T cells stimulated with APCs of (c).

[0258] In some aspects, provided herein is a composition comprising: (a) APCs expressing a protein encoded by an HLA-C03:03 allele, wherein the APCs comprise a peptide or a polynucleotide encoding the peptide; (b) T cells stimulated with APCs of (a); wherein the peptide comprises an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2).

[0259] In some embodiments, provided herein is a composition comprising: (a) APCs expressing a protein encoded by an HLA-C03:03 allele, wherein the APCs comprise a peptide or a polynucleotide encoding the peptide; and (b) T cells stimulated with APCs of (a); wherein the peptide comprises an epitope with a sequence GAVGVGKSA (SEQ ID NO: 2), and further comprises (c) antigen presenting cells expressing a protein encoded by an HLA allele of a subject, wherein the APCs further comprise a peptide selected from Table 1-12, that binds to the protein encoded by the HLA of the subject and (d) T cells stimulated with APCs of (c).

[0260] Approximately 9% of US population show positive expression for a protein encoded by HLA-C03:03. Approximately, 15% of US population show positive expression for a protein encoded by HLA-C03:04. In some embodiments the compositions described herein are required for treating a KRAS mutation-related cancer. KRAS mutations are particularly prevalent in pancreatic and colorectal cancers. Approximate frequencies of G12C, D, V and R mutations in the different forms of cancer are indicated below: (PDAC, pancreatic ductal adenocarcinoma, NSCLC, non-small cell lung cancer; CRC, colorectal cancer).

	PDAC	NSCLC	CRC
G12C	1.83%	12.71%	3.39%
G12D	38.83%	3.54%	12.08%
G12V	33.51%	4.65%	7.96%
G12R	16.30%	0.26%	0.55%

[0261] In some embodiments, the composition further comprises a peptide that comprises an epitope sequence according to any one of Tables 1-12, or an APC loaded with and expressing a peptide that comprises an epitope sequence according to any one of Tables 1-12 antigen presenting cells (APCs), or a T cell stimulated with an APC expressing a peptide that comprises an epitope sequence according to any one of Tables 1-12 antigen presenting cells (APCs). In some embodiments, a peptide comprises an epitope sequence according to Table 1. In some embodiments, a peptide comprises an epitope sequence according to Table 2. In some embodiments, a peptide comprises an epitope sequence according to Table 3. In some embodiments, a peptide comprises an epitope sequence according to Table 4. In some embodiments, a peptide comprises an epitope sequence according to Table 5. In some embodiments, a peptide comprises an epitope sequence according to Table 6. In some embodiments, a peptide comprises an epitope sequence according to Table 7. In some embodiments, a peptide comprises an epitope sequence according to Table 8. In some embodiments, a peptide comprises an epitope sequence according to Table 9. In some embodiments, a peptide comprises an epitope sequence according to Table 10. In some embodiments, a peptide comprises an epitope sequence according to Table 11. In some embodiments, a peptide comprises an epitope sequence according to Table 12.

Table 8

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (Binding HLA allele example(s))	Exemplary Diseases
KRAS	G12C	MTEYKLVVVGACGVGKSA LTIQLIQNHVFVDEYDPTIED SYRKQVVIDGETCLLDILD TAGQE (SEQ ID NO: 104)	KLVVVGACGV (A02.01) (SEQ ID NO: 250) LVVVVGACGV (A02.01) (SEQ ID NO: 251) VVGACGVGK (A03.01, A11.01) (SEQ ID NO: 252) VVVGACGVGK (A03.01) (SEQ ID NO: 253)	BRCA, CESC, CRC, HNSC, LUAD, PAAD, UCEC
KRAS	G12D	MTEYKLVVVGADGVGKSA LTIQLIQNHVFVDEYDPTIED SYRKQVVIDGETCLLDILD TAGQE (SEQ ID NO: 105)	VVGADGVGK (A11.01) (SEQ ID NO: 254) VVVGADGVGK (A11.01) (SEQ ID NO: 255) KLVVVGADGV (A02.01) (SEQ ID NO: 256) LVVVGADGV (A02.01) (SEQ ID NO: 257)	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRP, LIHC, LUAD, PAAD, SKCM, UCEC
KRAS	G12V	MTEYKLVVVGAVGVGKSA LTIQLIQNHVFVDEYDPTIED SYRKQVVIDGETCLLDILD TAGQE (SEQ ID NO: 106)	KLVVVGAVGV (A02.01) (SEQ ID NO: 258) LVVVGAVGV (A02.01) (SEQ ID NO: 259) VVGAVGVGK (A03.01, A11.01) (SEQ ID NO: 260) VVVGAVGVGK (A03.01, A11.01) (SEQ ID NO: 261)	BRCA, CESC, CRC, LUAD, PAAD, THCA, UCEC

KRAS	Q61H	AGGVGKSALTIQLIQNHFV DEYDPTIEDSYRKQVVIDG ETCLLDILD <u>T</u> AGH <u>E</u> EYSAM RDQYMRTGEGFLCVFAINN TKSFEDIHHYREQIKRVKD SEDVPM (SEQ ID NO: 107)	ILDTAGHEEY (A01.01) (SEQ ID NO: 262)	CRC, LUSC, PAAD, SKCM, UCEC
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KRAS	Q61L	AGGVGKSALTIQLIQNHFV DEYDPTIEDSYRKQVVIDG ETCLLDILDTAG <u>L</u> EEYSAM RDQYMRTGEGFLCVFAINN TKSFEDIHHYREQIKRVKD SEDVPM (SEQ ID NO: 108)	ILDTAGLEEEY (A01.01) (SEQ ID NO: 263) LLDILDTAGL (A02.01) (SEQ ID NO: 264)	CRC, GBM, HNSC, LUAD, SKCM, UCEC
NRAS	Q61K	AGGVGKSALTIQLIQNHFV DEYDPTIEDSYRKQVVIDG ETCLLDILDTAG <u>K</u> EEYSAM RDQYMRTGEGFLCVFAINN SKSFADINLYREQIKRVKDS DDVPM (SEQ ID NO: 109)	ILDTAGKEEY (A01.01) (SEQ ID NO: 265)	BLCA, CRC, LIHC, LUAD, LUSC, SKCM, THCA, UCEC
NRAS	Q61R	AGGVGKSALTIQLIQNHFV DEYDPTIEDSYRKQVVIDG ETCLLDILDTAG <u>R</u> EEYSAM RDQYMRTGEGFLCVFAINN SKSFADINLYREQIKRVKDS DDVPM (SEQ ID NO: 110)	ILDTAGREEY (A01.01) (SEQ ID NO: 266)	BLCA, CRC, LUSC, PAAD, PRAD, SKCM, THCA, UCEC
BTK	C481S	MIKEGSMSEDEFIEEAKV MMNLSHEKLVQLYGVCT KQRPIFIITEYMANG <u>S</u> LLN YLREMRHRFQTQQLEM CKDVCEAMEYLESKQFL HRDLAARNCLVND (SEQ ID NO: 111)	EYMANGSLL (A24.02) (SEQ ID NO: 267) MANGSLLNY (A01.01, A03.01, A11.01) (SEQ ID NO: 268) MANGSLLNYL (A02.01, B07.02, B08.01) (SEQ ID NO: 269) SLLNYLREM (A02.01, B07.02, B08.01) (SEQ ID NO: 270) YMANGSLLN (A02.01) (SEQ ID NO: 271) YMANGSLLNY (A01.01, A03.01, A11.01) (SEQ ID NO: 272)	CLL
EGFR	S492R	SLNITSLGLRSLKEISDGD VIISGNKNLCYANTINWK KLFGTSGQKTKI <u>R</u> NRGEN SCKATGQVCHALCSPEGC WGPEPRDCVSCRNVSRGR ECVDKCNLL (SEQ ID NO: 112)	IIRNRGENSCK (A03.01) (SEQ ID NO: 273)	CRC

EGFR	T790M	IPVAIKELREATSPKANKE ILDEAYVMASVDNPHVCR LLGICLTSTVQLIMQLMPF GCLLDYVREHKDNIGSQY LLNWCVQIAKGMNYLED RRLVHRDLAA (SEQ ID NO: 113)	CLTSTVQLIM (A01.01, A02.01) (SEQ ID NO: 274) IMQLMPFGC (A02.01) (SEQ ID NO: 275) IMQLMPFGCL (A02.01, A24.02, B08.01) (SEQ ID NO: 276) LIMQLMPFG (A02.01) (SEQ ID NO: 277) LIMQLMPFGC (A02.01) (SEQ ID NO: 278) LTSTVQLIM (A01.01) (SEQ ID NO: 279) MQLMPFGCL (A02.01, B07.02, B08.01) (SEQ ID NO: 280) MQLMPFGCLL (A02.01, A24.02, B08.01) (SEQ ID NO: 281) QLIMQLMPF (A02.01, A24.02, B08.01) (SEQ ID NO: 282) QLIMQLMPFG (A02.01) (SEQ ID NO: 283) STVQLIMQL (A02.01) (SEQ ID NO: 284) VQLIMQLMPF (A02.01, A24.02, B08.01) (SEQ ID NO: 285)	NSCLC, PRAD
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ABL1	E255K	VADGLITTLHYPAPKRNK PTVYGVSPNYDKWEMER TDITMKHKLGGGQY <u>GKV</u> YEGVWKKYSLTVAVKTL KEDTMEVEEFLKEAAVM KEIKHPNLVQLLGVC (SEQ ID NO: 114)	GQYGKVVYEG (A02.01) (SEQ ID NO: 286) GQYGKVVYEGV (A02.01) (SEQ ID NO: 287) KLGGGQYGGK (A03.01) (SEQ ID NO: 288) KLGGGQYGGKV (A02.01) (SEQ ID NO: 289) KVYEGVWKK (A02.01, A03.01) (SEQ ID NO: 290) KVYEGVWKKY (A03.01) (SEQ ID NO: 291) QYGGKVVYEGV (A24.02) (SEQ ID NO: 292) QYGGKVVYEGVW (A24.02) (SEQ ID NO: 293)	Chronic myeloid leukemia (CML), Acute lymphocytic leukemia (ALL), Gastrointestinal stromal tumors (GIST)
ABL1	E255V	VADGLITTLHYPAPKRNK PTVYGVSPNYDKWEMER TDITMKHKLGGGQY <u>G</u> V YEGVWKKYSLTVAVKTL KEDTMEVEEFLKEAAVM KEIKHPNLVQLLGVC (SEQ ID NO: 115)	GQYGVVYEG (A02.01) (SEQ ID NO: 294) GQYGVVYEGV (A02.01) (SEQ ID NO: 295) KLGGGQYGGV (A02.01) (SEQ ID NO: 296) KLGGGQYGGVV (A02.01) (SEQ ID NO: 297) QYGVVYEGV (A24.02) (SEQ ID NO: 298) QYGVVYEGVW (A24.02) (SEQ ID NO: 299) VVYEGVWKK (A02.01, A03.01) (SEQ ID NO: 300) VVYEGVWKKY (A03.01) (SEQ ID NO: 301)	Chronic myeloid leukemia (CML), Acute lymphocytic leukemia (ALL), Gastrointestinal stromal tumors (GIST)
ABL1	M351T	LLGVCTREPPFYIITEFMT YGNLLDYLRECNRQEVN AVLLYMATQISSA <u>T</u> EYL EKKNFIHRDLAARNCLVG ENHLVKVADFGLSRLMT GDTYTAHAGAKF (SEQ ID NO: 116)	ATQISSATEY (A01.01) (SEQ ID NO: 302) ISSATEYLEK (A03.01) (SEQ ID NO: 303) SSATEYLEK (A03.01) (SEQ ID NO: 304) TQISSATEYL (A02.01) (SEQ ID NO: 305) YMATQISSAT (A02.01) (SEQ ID NO: 306)	Chronic myeloid leukemia (CML), Acute lymphocytic leukemia (ALL), Gastrointestinal stromal tumors (GIST)
ABL1	T315I	SLTVAVKTLKEDTMEVEE FLKEAAVMKEIKHPNLVQ LLGVCTREPPFYII <u>I</u> EFMTY GNLLDYLRECNRQEVNA VLLYMATQISSA <u>M</u> EYLE KKNFIHRDLA (SEQ ID NO: 117)	FYIIIEFMTY (A24.02) (SEQ ID NO: 307) IIEFMTYGNL (A02.01) (SEQ ID NO: 308) IIIEFMTYG (A02.01) (SEQ ID NO: 309) IIIEFMTYGN (A02.01) (SEQ ID NO: 310) YIIIEFMTYG (A02.01) (SEQ ID NO: 311)	Chronic myeloid leukemia (CML), Acute lymphocytic leukemia (ALL), Gastrointestinal stromal tumors (GIST)

ABL1	Y253H	STVADGLITTLHYPAPKR NKPTVYGVSPNYDKWEM ERTDITMKHKLGGGQHG EVYEGVWKKYSLTVAVK TLKEDTMEVEEFLKEAAV MKEIKHPNLVQLLG (SEQ ID NO: 118)	GQHGEVYEGV (A02.01) (SEQ ID NO: 312) KLGGGQHGEV (A02.01) (SEQ ID NO: 313)	Chronic myeloid leukemia (CML), Acute lymphocytic leukemia (ALL), Gastrointestinal stromal tumors (GIST)
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ALK	G1269A	SSLAMLDLLHVARDIACG CQYLEENHFIHRDIAARN CLLTCPGPGRVAKIADFG MARDIYRASYYRKGGCA MLPVKWMPPEAFMEGIFT SKTDTWSFGVLL (SEQ ID NO: 119)	KIADFGMAR (A03.01) (SEQ ID NO: 314) RVAKIADFGM (A02.01, B07.02) (SEQ ID NO: 315)	NSCLC
ALK	L1196M	QVAVKTLPEVCSEQDELD FLMEALIISKFNHQNIVRCI GVSLQSLPRFILMELMAG GDLKSFLRETRPRPSQPSS LAMLDLLHVARDIACGC QYLEENHFI (SEQ ID NO: 120)	FILMELMAGG (A02.01) (SEQ ID NO: 316) ILMELMAGG (A02.01) (SEQ ID NO: 317) ILMELMAGGD (A02.01) (SEQ ID NO: 318) LMELMAGGDL (A02.01) (SEQ ID NO: 319) LPRFILMEL (B07.02, B08.01) (SEQ ID NO: 320) LPRFILMELM (B07.02) (SEQ ID NO: 321) LQSLPRFILM (A02.01, B08.01) (SEQ ID NO: 322) SLPRFILMEL (A02.01, A24.02, B07.02, B08.01) (SEQ ID NO: 323)	NSCLC
BRAF	V600E	MIKLIDIARQTAQGMDYL HAKSIIHRDLKSNINFLHE DLTVKIGDFGLATEKSRW SGSHQFEQLSGSILWMA EVIRMQDKNPYSFQSDVY AFGIVLYELM (SEQ ID NO: 121)	LATEKSRWS (A02.01, B08.01) (SEQ ID NO: 324) LATEKSRWSG (A02.01, B08.01) (SEQ ID NO: 325)	CRC, GBM, KIRP, LUAD, SKCM, THCA
EEF1B 2	S43G	MGFGDLKSPAGLQVLND YLADKSYIEGYVPSQADV AVFEAVSGPPPADLCHAL RWYNHIKSYEKEKASLPG VKKALGKYGPADVEDTT GSGAT (SEQ ID NO: 122)	GPPPADLCHAL (B07.02) (SEQ ID NO: 326)	BLCA, KIRP, PRAD, SKCM
ERBB3	V104M	ERCEVVMGNLEIVLTGHN ADLSFLQWIREVTGYVLV AMNEFSTLPLPNLRMVRG TQVYDGKFAIFVMLNYNT NSSHALRQLRLTQLTEILS GGVYIEKNDK (SEQ ID NO: 123)		CRC, Stomach Cancer

ESR1	D538G	HLMAGAGLTLQQQHQR AQLLLILSHIRHMSNKGM EHLYSMKCKNVVPLYGL LLEMLDAHRLHAPTSRGG ASVEETDQSHLATAGSTS SHSLQKYYITGEA (SEQ ID NO: 124)	GLLLEMLDA (A02.01) (SEQ ID NO: 327) LYGLLLEML (A24.02) (SEQ ID NO: 328) NVVPLYGLL (A02.01) (SEQ ID NO: 329) PLYGLLLEM (A02.01) (SEQ ID NO: 330) PLYGLLLEML (A02.01, A24.02) (SEQ ID NO: 331) VPLYGLLLEM (B07.02) (SEQ ID NO: 332) VVPLYGLLL (A02.01, A24.02) (SEQ ID NO: 333)	Breast Cancer
ESR1	S463P	NQGKCVEGMVEIFDMLL ATSSRFRMMNLQGEEFVC LKSILLNSGVYTFLPSTLK SLEEKDHIHRVLDKITDTL IHLMAKAGLTLQQQHQR LAQLLLILSH (SEQ ID NO: 125)	FLPSTLKSL (A02.01, A24.02, B08.01) (SEQ ID NO: 334) GVYTFLPST (A02.01) (SEQ ID NO: 335) GVYTFLPSTL (A02.01, A24.02) (SEQ ID NO: 336) TFLPSTLKSL (A24.02) (SEQ ID NO: 337) VYTFLPSTL (A24.02) (SEQ ID NO: 338) YTFLPSTLK (A03.01) (SEQ ID NO: 339)	Breast Cancer

ESR1	Y537C	IHLMAKAGLTLQQQHQR LAQLLLILSHIRHMSNKG MEHLYSMKCKNNVPLCD LLEMLDAHRLHAPTSRG GASVEETDQSHLATAGST SSHSLQKYYITGE (SEQ ID NO: 126)	NVVPLCDLL (A02.01) (SEQ ID NO: 340) NVVPLCDLLL (A02.01) (SEQ ID NO: 341) PLCDLLEML (A02.01) (SEQ ID NO: 342) PLCDLLEML (A02.01) (SEQ ID NO: 343) VPLCDLLEML (B07.02) (SEQ ID NO: 344) VVPLCDLLL (A02.01, A24.02) (SEQ ID NO: 345)	Breast Cancer
ESR1	Y537N	IHLMAKAGLTLQQQHQR LAQLLLILSHIRHMSNKG MEHLYSMKCKNNVPLND LLEMLDAHRLHAPTSRG GASVEETDQSHLATAGST SSHSLQKYYITGE (SEQ ID NO: 127)	NVVPLNDLL (A02.01) (SEQ ID NO: 346) NVVPLNDLLL (A02.01) (SEQ ID NO: 347) PLNDLLEML (A02.01) (SEQ ID NO: 348) PLNDLLEML (A02.01) (SEQ ID NO: 349) VPLNDLLEML (B07.02) (SEQ ID NO: 350)	Breast Cancer
ESR1	Y537S	IHLMAKAGLTLQQQHQR LAQLLLILSHIRHMSNKG MEHLYSMKCKNNVPLSD LLEMLDAHRLHAPTSRG GASVEETDQSHLATAGST SSHSLQKYYITGE (SEQ ID NO: 128)	NVVPLSDLL (A02.01) (SEQ ID NO: 351) NVVPLSDLLL (A02.01) (SEQ ID NO: 352) PLSDLLEML (A02.01) (SEQ ID NO: 353) PLSDLLEML (A02.01) (SEQ ID NO: 354) VPLSDLLEML (B07.02) (SEQ ID NO: 355) VVPLSDLLL (A02.01, A24.02) (SEQ ID NO: 356)	Breast Cancer
FGFR3	S249C	HRIGGIKLRHQQWSLVME SVVPSDRGNYTCVVENKF GSIRQTYTLDVLERCPHRP ILQAGLPANQTAVLGSDV EFHCKVYSDAQPHIQWLK HVEVNGSKVG (SEQ ID NO: 129)	VLERCPI (A02.01, B08.01) (SEQ ID NO: 357) YTLDVLERC (A02.01) (SEQ ID NO: 358)	BLCA, HNSC, KIRP, LUSC
FRG1B	L52S	AVKLSDSRIALKSGYGKY LGINSDELVGHSDAIGPRE QWEPVFQNGKMALSASN SCFIRCNEAGDIEAKSKTA GEEEMIKIRSCAEKETKK KDDIPEEDKG (SEQ ID NO: 130)	FQNGKMALS (A02.01) (SEQ ID NO: 359)	GBM, KIRP, PRAD, SKCM

HER2	V777L (Resistance)	GSGAFGTVYKGIWIPDGE NVKIPVAIKVLRENTSPKA NKEILDEAYVMAGLGSPY VSRLLGICLTSTVQLVTQL MPYGCLLDHVRNRGRL GSQDLLNWCM (SEQ ID NO: 131)	VMAGLGSPYV (A02.01, A03.01) (SEQ ID NO: 360)	BRCA
IDH1	R132H	RVEEFKLKQMWKSPNGTI RNILGGTVFREAIICKNIPR LVSGWVKPIIIGHHAYGD QYRATDFVVPGPVKVEIT YTPSDGTQKVITYLVHNFE EGGGVAMGM (SEQ ID NO: 132)	KPIIIGHHA (B07.02) (SEQ ID NO: 361)	BLCA, GBM, PRAD
IDH1	R132C	RVEEFKLKQMWKSPNGTI RNILGGTVFREAIICKNIPR LVSGWVKPIIGCHAYGD QYRATDFVVPGPVKVEIT YTPSDGTQKVITYLVHNFE EGGGVAMGM (SEQ ID NO: 133)	KPIIGCHA (B07.02) (SEQ ID NO: 362)	BLCA, GBM, PRAD

IDH1	R132G	RVEEFKLKQMWKSPNGTI RNILGGTVFREAIICKNIPR LVSGWVKPIIIGGHAYGD QYRATDFVVPGPVKVEIT YTPSDGTQKVTYLVHNFE EGGGVAMGM (SEQ ID NO: 134)	KPIIIGGHA (B07.02) (SEQ ID NO: 363)	BLCA, BRCA, CRC, GBM, HNSC, LUAD, PAAD, PRAD, UCEC
IDH1	R132S	RVEEFKLKQMWKSPNGTI RNILGGTVFREAIICKNIPR LVSGWVKPIIIGSHAYGDQ YRATDFVVPGPVKVEITY TPSDGTQKVTYLVHNFE GGGVAMGM (SEQ ID NO: 135)	KPIIIGSHA (B07.02) (SEQ ID NO: 364)	BLCA, BRCA, GBM, HNSC, LIHC, LUAD, LUSC, PAAD, SKCM, UCEC
KIT	T670I	VAVKMLKPSAHLTEREAL MSELKVLSYLG ^N NHMNIVN LLGACTIGGPTLVIIIEYCCY GDLLNFLRRKRDSFICKSQ EDHAEAAALYKNLLHSKES SCSDSTNE (SEQ ID NO: 136)	IIIEYCCYGDL (A02.01) (SEQ ID NO: 365) TIGGPTLVII (A02.01) (SEQ ID NO: 366) VIIIEYCCYG (A02.01) (SEQ ID NO: 367)	Gastrointestinal stromal tumors (GIST)
KIT	V654A	VEATAYGLIKSDAAMTVA VKMLKPSAHLTEREALMS ELKVLSYLG ^N NHMNIANLL GACTIGGPTLVITEYCCYG DLLNFLRRKRDSFICKSQE DHAEAAALYK (SEQ ID NO: 137)	HMNIANLLGA (A02.01) (SEQ ID NO: 368) IANLLGACTI (A02.01) (SEQ ID NO: 369) MNIANLLGA (A02.01) (SEQ ID NO: 370) YLG ^N NHMNIA (A02.01, B08.01) (SEQ ID NO: 371) YLG ^N NHMNIAN (A02.01) (SEQ ID NO: 372)	Gastrointestinal stromal tumors (GIST)
MEK	C121S	ISELGAGNGGVVFKVSHK PSGLVMARKLIHLEIKPAI RNQIIRELQVLHESNSPYIV GFYGA ^F YS ^D GEISICMEH MDGGS ^L DQVLKKAGRIPE QILGK ^V SI (SEQ ID NO: 138)	VLHESNSPY (A03.01) (SEQ ID NO: 373) VLHESNSPYI (A02.01) (SEQ ID NO: 374)	Melanoma
MEK	P124L	LGAGNGGVVFKVSHKPSG LVMARKLIHLEIKPAIRNQ IIRELQVLHECNSLYIVGFY GAFYSDGEISICMEHMDG GSLDQVLKKAGRIPEQILG KVSIAVI (SEQ ID NO: 139)	LQVLHECNSL (A02.01, B08.01) (SEQ ID NO: 375) LYIVGFYGA ^F (A24.02) (SEQ ID NO: 376) NSLYIVGFY (A01.01) (SEQ ID NO: 377) QVLHECNSL (A02.01, B08.01) (SEQ ID NO: 378) SLYIVGFYGA (A02.01) (SEQ ID NO: 379) SLYIVGFYGA (A02.01) (SEQ ID NO: 380) VLHECNSLY (A03.01) (SEQ ID NO: 381) VLHECNSLYI (A02.01, A03.01) (SEQ ID NO: 382)	Melanoma

MYC	E39D	MPLNVSFTNRNYDLDYDS VQPYFYCDEEENFYQQQQ QSD <u>L</u> QPPAPSEDIWKKFEL LTPPLSPSRRSGLCSPSY VAVTPFSLRGDNDGG (SEQ ID NO: 140)	FYQQQQQSDL (A24.02) (SEQ ID NO: 383) QQQSDLQPPA (A02.01) (SEQ ID NO: 384) QQSDLQPPA (A02.01) (SEQ ID NO: 385) YQQQQQSDL (A02.01, B08.01) (SEQ ID NO: 386)	Lymphoid Cancer; Burkitt Lymphoma
MYC	P57S	FTNRNYDLDYDSVQPYFY CDEEENFYQQQQQSELQP PAPSEDIWKKFELL <u>S</u> TPPL SPSRRSGLCSPSYVAVTPF SLRGDNDGGGGSFSTADQ LEMVTELLG (SEQ ID NO: 141)	FELLSTPPL (A02.01, B08.01) (SEQ ID NO: 387) LLSTPPLSPS (A02.01) (SEQ ID NO: 388)	Lymphoid Cancer

MYC	T58I	TNRNYDLDYDSVQPYFY CDEENFYQQQQQSELQP PAPSEDIWKKFELLPIPLS PSRRSGLCSPSYVAVTPFS LRGDNDGGGGSFSTADQL EMVTELLGG (SEQ ID NO: 142)	FELLPIPPL (A02.01) (SEQ ID NO: 389) IWKKFELLPI (A24.02) (SEQ ID NO: 390) LLPIPPLSPS (A02.01, B07.02) (SEQ ID NO: 391) LPIPPLSPS (B07.02) (SEQ ID NO: 392)	Neuroblastoma
PDGFR a	T674I	VAVKMLKPTARSSEKQA LMSELKIMTHLGPHLNIV NLLGACTKSGPIYIIIEYCF YGDLVNYLHKNRDSFLSH HPEKPKKELDIFGLNPADE STRSYVILS (SEQ ID NO: 143)	IIIEYCFYGDL (A02.01) (SEQ ID NO: 393) IIIEYCFYG (A02.01) (SEQ ID NO: 394) IYIIIEYCF (A24.02) (SEQ ID NO: 395) IYIIIEYCFY (A24.02) (SEQ ID NO: 396) YIIIEYCFYG (A02.01) (SEQ ID NO: 397)	Chronic Eosinophilic Leukemia
PIK3C A	E542K	IEEHANWSVSREAGFSYS HAGLSNRLARDNELREND KEQLKAISTRDPLSKITEQ EKDFLWSHRHYCVTIPEIL PKLLSVKWNRSRDEVAQ MYCLVKDWPP (SEQ ID NO: 144)	KITEQEKDFL (A02.01) (SEQ ID NO: 398)	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRC, KIRP, LIHC, LUAD, LUSC, PRAD, UCEC
PIK3C A	E545K	HANWSVSREAGFSYSHA GLSNRLARDNELRENDKE QLKAISTRDPLSEITKQEK DFLWSHRHYCVTIPEILPK LLSVKWNRSRDEVAQMY CLVKDWPPPIKP (SEQ ID NO: 145)	STRDPLSEITK (A03.01) (SEQ ID NO: 399) DPLSEITK (A03.01) (SEQ ID NO: 400)	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRC, KIRP, LIHC, LUAD, LUSC, PRAD, SKCM, UCEC
PIK3C A	H1047R	LFINLFSMMLGSGMPELQ SFDDIAYIRKTLALDKTEQ EALYFMKQMNDARHGG WTTKMDWIFHTIKQHAL N (SEQ ID NO: 146)		BRCA, CESC, CRC, GBM, HNSC, LIHC, LUAD, LUSC, PRAD, UCEC

POLE	P286R	QRGGVITDEEETSKKIAD QLDNIVDMREYDVPYHIR LSIDIETTKLPLKFRDAET DQIMMISYMGQGYLIT NREIVSEDIEDFEFTPKPEY EGPFCVFN (SEQ ID NO: 147)	LPLKFRDAET (B07.02) (SEQ ID NO: 401)	Colorectal adenocarcinoma; Uterine/Endometrium Adenocarcinoma; Colorectal adenocarcinoma, MSI+; Uterine/Endometrium Adenocarcinoma, MSI+; Endometrioid carcinoma; Endometrium Serous carcinoma; Endometrium Carcinosarcoma-malignant mesodermal mixed tumor; Glioma; Astrocytoma; GBM
PTEN	R130Q	KFNCRVAQYPFEDHNPPQ LELIKPFCELDQWLSED DNHVAAIHCKAGKGQTG VMICAYLLHRGKFLKAQE ALDFYGEVTRDKKGVIT PSQRRYVYYYSY (SEQ ID NO: 148)	QTGVMICAYL (A02.01) (SEQ ID NO: 402)	BRCA, CESC, CRC, GBM, KIRC, LUSC, UCEC
RAC1	P29S	MQAICVVG DGAVGKT CLLISYTTNAFSGEYIPTVF DNYSANVMVDGKPVNLG LWDTAGQEDYDRLRPLS YPQTVGET (SEQ ID NO: 149)	AFSGEYIPTV (A02.01, A24.02) (SEQ ID NO: 403)	Melanoma
TP53	G245S	IRVEGNLRVEYLDDRNTF RHSVVVPYEPPEVGSDCT TIHYNMCMSSCMGSMN RRPILTIITLEDSSGNLLGR NSFEVRVCACPGRRRTE EENLRKKGEP (SEQ ID NO: 150)	SMNRRPILT (A02.01, B08.01) (SEQ ID NO: 404) YMCNSSCMGS (A02.01) (SEQ ID NO: 405)	BLCA, BRCA, CRC, GBM, HNSC, LUSC, PAAD, PRAD
TP53	R175H	TYSPALNKMFCQLAKTCP VQLWVDSTPPPGTRVRA MAIYKQSQHMTVVRRHC PHHERCSDSDGLAPPQHLLI RVEGNLRVEYLDDRNTFR HSVVVPYEPPEV (SEQ ID NO: 151)		BLCA, BRCA, CRC, GBM, HNSC, LUAD, PAAD, PRAD, UCEC

TP53	R248Q	EGNLRVEYLDDRNTFRHS VVVPYEPPEVGSDCTTIH YNYMCNSSCMGGMNQRP ILTIITLEDSSGNLLGRNSF EVRVCACPGRDRRTEEN LRKKGEPHHE (SEQ ID NO: 152)	GMNQRPILT (A02.01) (SEQ ID NO: 406)	BLCA, BRCA, CRC, GBM, HNSC, KIRC, LIHC, LUSC, PAAD, PRAD, UCEC
TP53	R248W	EGNLRVEYLDDRNTFRHS VVVPYEPPEVGSDCTTIH YNYMCNSSCMGGMNWR PILTIITLEDSSGNLLGRNS FEVRVCACPGRDRRTEEE NLRKKGEPHHE (SEQ ID NO: 153)	GMNWRPILT (A02.01) (SEQ ID NO: 407)	BLCA, BRCA, CRC, GBM, HNSC, LIHC, LUSC, PAAD, SKCM, UCEC
TP53	R273C	PEVGSDCTTIHYNYMCNS SCMGMNRRPILTIITLED SSGNLLGRNSFEVCVCAC PGRDRRTEENLRKKGEP HHELPPGSTKRALPNNTSS SPQPKKKPL (SEQ ID NO: 154)	LLGRNSFEVC (A02.01) (SEQ ID NO: 408)	BLCA, BRCA, CRC, GBM, HNSC, LUSC, PAAD, UCEC
ACVR2 A	D96fs; +1	GVEPCYGD ~~KDKRR~~ HCFA TWKNISGSIEIVKQGCWL DDINCYDRTDCVEKKRQP * (SEQ ID NO: 155)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

ACVR2 A	D96fs; - 1	GVEPCYGDKDKRRHCFA TWKNISGSIEIVKQGCWL DDINCYDRTDCVEKKTAL <u>KYIFVAVRAICVMKSFLIF</u> <u>RRWKSHSPLQIQLHLSHPI</u> <u>TTSCSIPWCHLC*</u> (SEQ ID NO: 156)	ALKYIFVAV (A02.01, B08.01) (SEQ ID NO: 409) ALKYIFVAVR (A03.01) (SEQ ID NO: 410) AVRAICVMK (A03.01) (SEQ ID NO: 411) AVRAICVMKS (A03.01) (SEQ ID NO: 412) CVEKKTALK (A03.01) (SEQ ID NO: 413) CVEKKTALKY (A01.01) (SEQ ID NO: 414) CVMKSFLIF (A24.02, B08.01) (SEQ ID NO: 415) CVMKSFLIFR (A03.01) (SEQ ID NO: 416) FLIFRRWKS (A02.01, B08.01) (SEQ ID NO: 417) FRRWKSHSPL (B08.01) (SEQ ID NO: 418) FVAVRAICV (A02.01, B08.01) (SEQ ID NO: 419) FVAVRAICVM (B08.01) (SEQ ID NO: 420) IQLHLSHPI (A02.01) (SEQ ID NO: 421) KSFLIFRRWK (A03.01) (SEQ ID NO: 422) KTALKYIFV (A02.01) (SEQ ID NO: 423) KYIFVAVRAI (A24.02) (SEQ ID NO: 424) RWKSHSPLQI (A24.02) (SEQ ID NO: 425) TALKYIFVAV (A02.01, B08.01) (SEQ ID NO: 426) VAVRAICVMK (A03.01) (SEQ ID NO: 427) VMKSFLIFR (A03.01) (SEQ ID NO: 428) VMKSFLIFRR (A03.01) (SEQ ID NO: 429) YIFVAVRAI (A02.01) (SEQ ID NO: 430)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
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C15OR F40	L132fs; +1	TAEAVNVAIAAPPSEGEA NAELCRYLSKVLELRKSD VVLDKVGLALFFFFFETK <u>SCSVAQAGVQWRSLSL</u> <u>QPPPGFKLFSCLSFLSSW</u> <u>DYRRMPPCLANFCIFNRD</u> <u>GVSPCWSGWS*</u> (SEQ ID NO: 157)	ALFFFFFFET (A02.01) (SEQ ID NO: 431) ALFFFFFFETK (A03.01) (SEQ ID NO: 432) AQAGVQWRS (A02.01) (SEQ ID NO: 433) CLANFCIFNR (A03.01) (SEQ ID NO: 434) CLSFLSSWDY (A01.01, A03.01) (SEQ ID NO: 435) FFETKSCSV (B08.01) (SEQ ID NO: 436) FFFETKSCSV (A02.01) (SEQ ID NO: 437) FKLFSCLSFL (A02.01) (SEQ ID NO: 438) FLSSWDYRRM (A02.01) (SEQ ID NO: 439) GFKLFSCLS (A24.02) (SEQ ID NO: 440) KLFCLSFL (A02.01, A03.01) (SEQ ID NO: 441) KLFCLSFLS (A02.01, A03.01) (SEQ ID NO: 442) LALFFFFFFET (A02.01) (SEQ ID NO: 443) LFFFFFFETK (A03.01) (SEQ ID NO: 444) LSFLSSWDY (A01.01) (SEQ ID NO: 445) LSFLSSWDYR (A03.01) (SEQ ID NO: 446) RMPPCLANF (A24.02) (SEQ ID NO: 447) RRMPPCLANF (A24.02) (SEQ ID NO: 448) SLQPPPGFK (A03.01) (SEQ ID NO: 449) VQWRSLSL (A02.01) (SEQ ID NO: 450)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
CNOT1	L1544fs ; +1	LSVIIFFFVYIHWALPLIL NNHHICLMSSIILDCNSVR QSIMSVCFFFSVIFSTRCL <u>TDSRYPNICWFK*</u> (SEQ ID NO: 158)	FFFSVIFST (A02.01) (SEQ ID NO: 451) MSVCFFFSV (A02.01) (SEQ ID NO: 452) SVCFFFSV (A02.01, B08.01) (SEQ ID NO: 453) SVCFFFSVI (A02.01) (SEQ ID NO: 454)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

CNOT1	L1544fs ; -1	LSVHFFVYIWHWALPLIL NNHHICLMSSIILDCNSVR QSIMSVCF ~~FFCYILNTMF~~ <u>DR*</u> (SEQ ID NO: 159)	FFCYILNTMF (A24.02) (SEQ ID NO: 455) MSVCFFFCY (A01.01) (SEQ ID NO: 456) SVCFFFCYI (A02.01) (SEQ ID NO: 457)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
EIF2B3	A151fs; -1	VLVLSCDLITDVALHEVV DLFRAYDASLAMLMRKG QDSIEPVPQGKGKKQWS <u>SVTSLEWTAQERGCSWL</u> <u>MKQTWKSWSLRDPYR</u> <u>SILEYVSTRVLWMPSTV*</u> (SEQ ID NO: 160)	KQWSSVTSL (A02.01) (SEQ ID NO: 458) VLWMPSTV (A02.01) (SEQ ID NO: 459)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
EPHB2	K1020fs ; -1	SIQVMRAQMNQIQSVEGQ PLARRPRATGRTRCQPR DVTKKTCNSNDGKK <u>REW</u> <u>EKRKQILGGGGKYKEYFL</u> <u>KRILIRKAMTVLAGDKKG</u> <u>LGRFMRCVQSETKAVSLQ</u> <u>LPLGR*</u> (SEQ ID NO: 161)	ILIRKAMTV (A02.01) (SEQ ID NO: 460)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

ESRP1	N512fs; +1	LDLGEFATDIRTHGVHM VLNHQGRPSGDAFIQMKS ADRAFMAAQKCHKK <u>KHE</u> <u>GQIC*</u> (SEQ ID NO: 162)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
ESRP1	N512fs; -1	LDLGEFATDIRTHGVHM VLNHQGRPSGDAFIQMKS ADRAFMAAQKCHKK <u>T*</u> (SEQ ID NO: 163)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
FAM11 1B	A273fs; -1	GALCKDGRFRSDIGEFEW KLKEGHKKIYGKQSMVD EVSGKVLEMDISKKK <u>HYN</u> <u>RKISIKKLNRMKVPLMKLI</u> <u>TRV*</u> (SEQ ID NO: 164)	RMKVPLMK (A03.01) (SEQ ID NO: 461)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
GBP3	T585fs; -1	RERAQLLEEQEKTLSKL QEQARVLKERCQGESTQL QNEIQKLQKTLKKK <u>PRDI</u> <u>CRIS*</u> (SEQ ID NO: 165)	TLKKKPRDI (B08.01) (SEQ ID NO: 462)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
JAK1	P861fs; +1	VNTLKEGKRLPCPPNCPD EVYQLMRKCWEFQPSNR TSFQNLIEGFEALLK <u>TSN*</u> (SEQ ID NO: 166)	LIEGFEALLK (A03.01) (SEQ ID NO: 463)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
JAK1	K860fs; -1	CRPVTPSCKEADLMTRC MNYDPNQRPFRAIMRDI NKLEEQNPDI ~~VE~~ SEK <u>NQQL</u> <u>KWTPHILKSAS*</u> (SEQ ID NO: 167)	QQLKWTPHI (A02.01) (SEQ ID NO: 464) QLKWTPHILK (A03.01) (SEQ ID NO: 465) IVSEKNQQLK (A03.01) (SEQ ID NO: 466) QLKWTPHILK (A03.01) (SEQ ID NO: 465) QQLKWTPHI (A24.02) (SEQ ID NO: 464) NQQLKWTPHIL (B08.01) (SEQ ID NO: 467) NQQLKWTPHI (B08.01) (SEQ ID NO: 468) QLKWTPHIL (B08.01) (SEQ ID NO: 469)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

LMAN 1	E305fs; +1	DDHDVLSFLTFLTEPGK EPPTPDKEISEKEKEYQE EFEHFQQELDKKKRGIPE <u>GPPRPPRAACGGNI*</u> (SEQ ID NO: 168)	GPPRPPRAAC (B07.02) (SEQ ID NO: 470) PPRPPRAAC (B07.02) (SEQ ID NO: 471)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
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LMAN 1	E305fs; -1	DDHDVLSFLTFQLTEPGK EPPTPDKEISEKEKEYQE EFEHFQQELDKKKRNSRR <u>ATPTSKGSLRRKYLRV*</u> (SEQ ID NO: 169)	SLRRKYLRV (B08.01) (SEQ ID NO: 472)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
MSH3	N385fs; +1	TKSTLIGEDVNPLIKLDDA VNVDEIMTDTSTSYLLCIS ENKENVRDKKKGQHFW <u>HCGSAACHRRGCV*</u> (SEQ ID NO: 170)	SAACHRRGCV (B08.01) (SEQ ID NO: 473)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
MSH3	K383fs; -1	LYTKSTLIGEDVNPLIKLD DAVNVDEIMTDTSTSYLL CISENKENVRDKKRATFL <u>LALWECSLPQARLCLIVS</u> <u>RTLLLVQS*</u> (SEQ ID NO: 171)	ALWECSLPQA (A02.01) (SEQ ID NO: 474) CLIVSRTL (B08.01) (SEQ ID NO: 475) CLIVSRTLLL (A02.01, B08.01) (SEQ ID NO: 476) FLLALWECS (A02.01) (SEQ ID NO: 477) FLLALWECSL (A02.01, B08.01) (SEQ ID NO: 478) IVSRTLLLV (A02.01) (SEQ ID NO: 479) LIVSRTLLL (A02.01, B08.01) (SEQ ID NO: 480) LIVSRTLLLV (A02.01) (SEQ ID NO: 481) LLALWECSL (A02.01, B08.01) (SEQ ID NO: 482) LPQARLCLI (B08.01, B07.02) (SEQ ID NO: 483) LPQARLCLIV (B08.01) (SEQ ID NO: 484) NVRDKKRATF (B08.01) (SEQ ID NO: 485) SLPQARLCLI (A02.01, B08.01) (SEQ ID NO: 486)	MSI+CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
NDUF C2	A70fs; +1	LPPPKLTDPRLLYIGFLGY CSGLIDNLIRRRPIATAGL HRQLLYITAFFFCWILSCK T* (SEQ ID NO: 172)	FFCWILSCK (A03.01) (SEQ ID NO: 487) FFFCWILSCK (A03.01) (SEQ ID NO: 488) ITAFFFCWI (A02.01) (SEQ ID NO: 489) LYITAFFFCW (A24.02) (SEQ ID NO: 490) YITAFFFCWI (A02.01) (SEQ ID NO: 491)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

NDUF C2	F69fs; -1	SLPPPKLTDPRLLYIGFLG YCSGLIDNLIRRRPIATAG LHRQLLYITAFFLLDIIL* (SEQ ID NO: 173)	ITAFFLLDI (A02.01) (SEQ ID NO: 492) LLYITAFFL (A02.01, B08.01) (SEQ ID NO: 493) LLYITAFFLL (A02.01, A24.02) (SEQ ID NO: 494) LYITAFFLL (A24.02) (SEQ ID NO: 495) LYITAFFLLD (A24.02) (SEQ ID NO: 496) YITAFFLLDI (A02.01) (SEQ ID NO: 497)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
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RBM27	Q817; +1	NQSGGAGEDCQIFSTPGH PKMIYSSSNLKTSPSKLCSG SKSHDVQEVLKKKTGSNE <u>VTTRYEEKKTGSVRKANR</u> <u>MPKDVNIQVRKKQKHET</u> <u>RRKSKYNEDFERAWRED</u> <u>LTIKR*</u> (SEQ ID NO: 174)	GSNEVTTRY (A01.01) (SEQ ID NO: 498) MPKDVNIQV (B07.02) (SEQ ID NO: 499) TGSNEVTTRY (A01.01) (SEQ ID NO: 500)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
RPL22	K16fs; +1	MAPVKKLVVKGGKKKEA <u>SSEVHS*</u> (SEQ ID NO: 175)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
RPL22	K15fs; - 1	MAPVKKLVVKGGKK <u>RSK</u> <u>F*</u> (SEQ ID NO: 176)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
SEC31 A	I462fs; +1	MPSHQGAEEQQQQHHVF ISQVVTEKEFLSRSDQLQQ AVQSQGFINYCQKK <u>N*</u> (SEQ ID NO: 177)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

SEC31 A	I462fs; - 1	MPSHQGAEEQQQQHHVF ISQVVTEKEFLSRSDQLQQ AVQSQGFINYCQKK <u>MLL</u> <u>RLNLRKMCGPF*</u> (SEQ ID NO: 178)	KKMLLRNL (A02.01) (SEQ ID NO: 501) KLMLLRNL (A02.01, A03.01, B07.02, B08.01) (SEQ ID NO: 502) KLMLLRNL (A03.01) (SEQ ID NO: 503) LLRLNLRKM (B08.01) (SEQ ID NO: 504) LMLLRNL (B08.01) (SEQ ID NO: 505) LMLLRNL (A03.01) (SEQ ID NO: 506) LNLKMCMPF (B08.01) (SEQ ID NO: 507) MLLRNL (A03.01) (SEQ ID NO: 508) MLLRNL (A02.01, A03.01, B08.01) (SEQ ID NO: 509) NLRKMCMPF (B08.01) (SEQ ID NO: 510) NYCQKKMLL (A24.02) (SEQ ID NO: 511) YCQKKMLL (B08.01) (SEQ ID NO: 512)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
SEC63	K530fs; +1	AEVFEKEQSICAAEEQPAE DGQGETNKNRTKGGWQQ KSKGPKKTAKSKKKETFK KKTYTCAITTVKATETKA GKWSRWE* (SEQ ID NO: 179)	FKKKTYTCAI (B08.01) (SEQ ID NO: 513) ITTVKATETK (A03.01) (SEQ ID NO: 514) KSKKKETFK (A03.01) (SEQ ID NO: 515) KSKKKETFK (A03.01) (SEQ ID NO: 516) KTYTCAITTV (A02.01, A24.02) (SEQ ID NO: 517) TFKKKTYTC (B08.01) (SEQ ID NO: 518) TYTCAITTV (A24.02) (SEQ ID NO: 519) TYTCAITTVK (A03.01) (SEQ ID NO: 520) YTCAITTVK (A03.01) (SEQ ID NO: 521)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

SEC63	K529fs; -1	MAEVFEKEQSICAAEEQP AEDGQGETNKNRTKGGW QQKSKGPKKTAKSKRN <u>L*</u> (SEQ ID NO: 180)	TAKSKRNL (B08.01) (SEQ ID NO: 522)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
SLC35 F5	C248fs; -1	NIMEIRQLPSSHALEAKLS RMSYPVKEQESILKTVGK LTATQVAKISFFF <u>FALCGF</u> <u>WQICHIKKHFQTHKLL*</u> (SEQ ID NO: 181)	FALCGFWQI (A02.01)(SEQ ID NO: 523)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
SMAP1	K172fs; +1	YEKKKYYDKNAIAITNISS SDAPLQPLVSSPSLQAAV DKNKLEKEKEKKKG <u>GREK</u> <u>ERKGARKAGKTTY*</u> (SEQ ID NO: 182)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
SMAP1	K171fs; -1	KYEKKKYYDKNAIAITNI SSSDAPLQPLVSSPSLQAA VDKNKLEKEKEKKRKRK <u>REKRSQKSRQNHQLKSC</u> <u>RRKISNWSLKKVPALKKL</u> <u>RSPLWIF*</u> (SEQ ID NO: 183)	LKKLRSP (B08.01) (SEQ ID NO: 524) SLKKVPAL (B08.01) (SEQ ID NO: 525) RKISNWSLKK (A03.01) (SEQ ID NO: 526) VPALKLRSP (B07.02) (SEQ ID NO: 527)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
TFAM	E148fs; +1	IYQDAYRAEWQVYKEEIS RFKEQLTPSQIMSLEKEIM DKHLKRKAMTKKKRVNT <u>AWTKKTSFSL*</u> (SEQ ID NO: 184)	KRVNTAWKTK (A03.01) (SEQ ID NO: 528) MTKKRVNTA (B08.01) (SEQ ID NO: 529) RVNTAWKTK (A03.01) (SEQ ID NO: 530) RVNTAWKTKK (A03.01) (SEQ ID NO: 531) TKKKRVNTA (B08.01) (SEQ ID NO: 532) WTKKTSFSL (B08.01) (SEQ ID NO: 533)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
TFAM	E148fs; -1	IYQDAYRAEWQVYKEEIS RFKEQLTPSQIMSLEKEIM DKHLKRKAMTKK <u>KS*</u> (SEQ ID NO: 185)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

TGFBR 2	P129fs; +1	KPQEVAVWRKNDENI TLETVCHDPKLPYHDFILE DAASPKCIMKEKKK <u>AW</u> * (SEQ ID NO: 186)		MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
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TGFBR 2	K128fs; -1	EKPQEVCAVWRKNDEN ITLETVCHDPKLPYHDFIL EDAASPKCIMKEKKSLVR <u>LSSCPVALMSAMTTSSS</u> <u>QKNITPAILTCC*</u> (SEQ ID NO: 187)	ALMSAMTTS (A02.01) (SEQ ID NO: 534) AMTTSSSQK (A03.01, A11.01) (SEQ ID NO: 535) AMTTSSSQKN (A03.01) (SEQ ID NO: 536) CIMKEKKSL (B08.01) (SEQ ID NO: 537) CIMKEKKSLV (B08.01) (SEQ ID NO: 538) IMKEKKSL (B08.01) (SEQ ID NO: 539) IMKEKKSLV (B08.01) (SEQ ID NO: 540) KSLVRLSSCV (A02.01) (SEQ ID NO: 541) LVRLSSCPV (A02.01) (SEQ ID NO: 542) RLSSCPVA (A02.01, A03.01) (SEQ ID NO: 543) RLSSCPVAL (A02.01) (SEQ ID NO: 544) SAMTTSSSQK (A03.01, A11.01) (SEQ ID NO: 545) SLVRLSSCV (A02.01) (SEQ ID NO: 546) VPVALMSAM (B07.02) (SEQ ID NO: 547) VRLSSCPVA (A02.01) (SEQ ID NO: 548)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
THAP5	K99fs; - 1	VPSKYQFLCSDHFTPDSL DIRWGIRYLKQTAVPTIFS LPEDNQGKDPSKKNPRRK <u>TWKMRKKYAQKPSQKN</u> <u>HL*</u> (SEQ ID NO: 188)	KMRKKYAQK (A03.01) (SEQ ID NO: 549)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
TTK	R854fs; -1	GTTEEMKYVLGQLVGLN SPNSILKAAKTLYEYSG GESHNSSSKTFEKKGEK <u>NDLQLFVMSDTTYKIYWT</u> <u>VILLNPCGNLHLKTTSL*</u> (SEQ ID NO: 189)	FVMSDTTYK (A03.01) (SEQ ID NO: 550) FVMSDTTYKI (A02.01) (SEQ ID NO: 551) KTFEKKGEK (A03.01) (SEQ ID NO: 552) LFVMSDTTYK (A03.01) (SEQ ID NO: 553) MSDTTYKIY (A01.01) (SEQ ID NO: 554) VMSDTTYKI (A02.01) (SEQ ID NO: 555) VMSDTTYKIY (A01.01) (SEQ ID NO: 556)	MSI+ CRC, MSI+ Uterine/Endom etrium Cancer, MSI+ Stomach Cancer, Lynch syndrome

XPOT	F126fs; -1	QQLIRETLISWLQAQMLN PQPEKTFIRNKAAQVFAL L FVTEYLTKWPKFFL <u>TFS</u> <u>Q*</u> (SEQ ID NO: 190)	YLTkWPKFFL (A02.01) (SEQ ID NO: 557)	MSI+ CRC, MSI+ Uterine/Endometrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
APC	V1352fs F1354fs Q1378fs S1398fs	<u>AKFQQCHSTLEPNPADCR</u> <u>VLVYLQNQPGTKLLNFLO</u> <u>ERNLPPKVVL RHPKVHLN</u> <u>TMFRRPHSCLADVLLSVH</u> <u>LIVLRVVRLPAPFRVNHA</u> <u>VEW*</u> (SEQ ID NO: 191)	FLQERNLPP (A02.01) (SEQ ID NO: 558) FRRPHSCLA (B08.01) (SEQ ID NO: 559) LIVLRVVRL (B08.01) (SEQ ID NO: 560) LLSVHLIVL (A02.01, B08.01) (SEQ ID NO: 561)	CRC, LUAD, UCEC, STAD

APC	S1421fs R1435fs T1438fs P1442fs P1443fs V1452fs P1453fs K1462fs E1464fs	<u>APVIFQIALDKPCHQAEV</u> <u>KHLHHLLKQLKPSEKYLK</u> <u>IKHLLKRRERVDLSKLQ*</u> (SEQ ID NO: 192)	EVKHLHHLL (B08.01) (SEQ ID NO: 562) HLHHLLKQLK (A03.01) (SEQ ID NO: 563) HLLKRRERV (B08.01) (SEQ ID NO: 564) KIKHLLLR (A03.01) (SEQ ID NO: 565) KPSEKYLKI (B07.02) (SEQ ID NO: 566) KYLKIKHLL (A24.02) (SEQ ID NO: 567) KYLKIKHLL (A24.02) (SEQ ID NO: 568) LLKQLKPSEK (A03.01) (SEQ ID NO: 569) LLKRRERVDL (B08.01) (SEQ ID NO: 570) LLKRRERVDL (B08.01) (SEQ ID NO: 571) QLKPSEKYLK (A03.01) (SEQ ID NO: 572) YLKIKHLL (A02.01, B08.01) (SEQ ID NO: 573) YLKIKHLLK (A03.01) (SEQ ID NO: 574)	CRC, LUAD, UCEC, STAD
APC	T1487fs H1490fs L1488fs	<u>MLQFRGSRFFQMLILYYIL</u> <u>PRKVLQMDFLVHPA*</u> (SEQ ID NO: 193)	ILPRKVLQM (B08.01) (SEQ ID NO: 575) KVLQMDFLV (A02.01, A24.02) (SEQ ID NO: 576) LPRKVLQMD (B07.02, B08.01) (SEQ ID NO: 577) LQMDFLVHPA (A02.01) (SEQ ID NO: 578) QMDFLVHPA (A02.01) (SEQ ID NO: 579) YILPRKVLQM (A02.01, B08.01) (SEQ ID NO: 580)	CRC, LUAD, UCEC, STAD

ARID1 A	Q1306fs S1316fs Y1324fs T1348fs G1351fs G1378fs P1467fs	<u>ALGPHSRISCLPTQTRGCI</u> <u>LLAATPRSSSSSSSNDMIP</u> <u>MAISSPPKAPLLAAPSPAS</u> <u>RLQCINSNSRITSGQWMA</u> <u>HMALLPSGTKGRCTACTH</u> <u>ALGRGSLSSSSCPQPSPSL</u> <u>PASNKLPSLPLSKMYTTS</u> <u>MAMPILPLPQLLLSADQQ</u> <u>AAPRTNFHSSLAETVSLHP</u> <u>LAPMPSKTCHHK*</u> (SEQ ID NO: 194)	APSPASRLQC (B07.02) (SEQ ID NO: 581) HPLAPMPSKT (B07.02) (SEQ ID NO: 582) ILPLPQLLL (A02.01) (SEQ ID NO: 583) LLSADQQA (A02.01) (SEQ ID NO: 584) LPTQTRGCI (B07.02) (SEQ ID NO: 585) LPTQTRGCIL (B07.02) (SEQ ID NO: 586) RISCLPTQTR (A03.01) (SEQ ID NO: 587) SLAETVSLH (A03.01) (SEQ ID NO: 588) TPRSSSSSS (B07.02) (SEQ ID NO: 589) TPRSSSSSS (B07.02) (SEQ ID NO: 590)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
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ARID1 A	S674fs P725fs R727fs I736fs	<u>AHQGFPAAKESRVIQLSL</u> <u>LSLLIPPLTCLASEALPRPL</u> <u>LALPPVLLSLAQDHSRL</u> <u>QCQATRCHLGHPVASRTA</u> <u>SCILP*</u> (SEQ ID NO: 195)	ALPPVLLSL (A02.01) (SEQ ID NO: 591) ALPPVLLSLA (A02.01) (SEQ ID NO: 592) ALPRPLLAL (A02.01) (SEQ ID NO: 593) ASRTASCIL (B07.02) (SEQ ID NO: 594) EALPRPLLAL (B08.01) (SEQ ID NO: 595) HLGHPVASR (A03.01) (SEQ ID NO: 596) HPVASRTAS (B07.02) (SEQ ID NO: 597) HPVASRTASC (B07.02) (SEQ ID NO: 598) IIQLSLLSLL (A02.01) (SEQ ID NO: 599) IQLSLLSLL (A02.01) (SEQ ID NO: 600) IQLSLLSLLI (A02.01, A24.02) (SEQ ID NO: 601) LLALPPVLL (A02.01) (SEQ ID NO: 602) LLIPPLTCL (A02.01) (SEQ ID NO: 603) LLIPPLTCLA (A02.01) (SEQ ID NO: 604) LLSLLIPPL (A02.01) (SEQ ID NO: 605) LLSLLIPPLT (A02.01) (SEQ ID NO: 606) LPRPLLALPP (B07.02) (SEQ ID NO: 607) QLSLLSLLI (A02.01) (SEQ ID NO: 608) RLLQCQATR (A03.01) (SEQ ID NO: 609) RPLLALPPV (B07.02) (SEQ ID NO: 610) RPLLALPPVL (B07.02) (SEQ ID NO: 611) SLAQDHSRL (A02.01) (SEQ ID NO: 612) SLAQDHSRLL (A02.01) (SEQ ID NO: 613) SLLIPPLTCL (A02.01) (SEQ ID NO: 614) SLLSLLIPP (A02.01) (SEQ ID NO: 615) SLLSLLIPPL (A02.01, B08.01) (SEQ ID NO: 616)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
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ARID1 A	G414fs Q473fs H477fs S499fs P504fs Q548fs P549fs	<u>PILAATGTSVRTAARTWV</u> <u>PRAAIRVPDPAAVPDDHA</u> <u>GPGAEGHGRPLLYTADSS</u> <u>LWTRPQRVWSTGPDSIL</u> <u>QPAKSSPSAAAATLLPAT</u> <u>TVPDPSCPTFVSAAATVST</u> <u>TTAPVLSASILPAAIPASTS</u> <u>AVPGSIPLPAVDDTAAPPE</u> <u>PAPLLTATGSVSLPAAATS</u> <u>AASTLDALPAGCVSSAPV</u> <u>SAVPANCLFPAALPSTAG</u> <u>AISRFIWVSGILSPLNDLQ*</u> (SEQ ID NO: 196)	AAATSAASTL (B07.02) (SEQ ID NO: 617) AAIPASTSAV (B07.02) (SEQ ID NO: 618) AIPASTSAV (A02.01) (SEQ ID NO: 619) ALPAGCVSSA (A02.01) (SEQ ID NO: 620) APLLTATGSV (B07.02) (SEQ ID NO: 621) APVLSASIL (B07.02) (SEQ ID NO: 622) ATLLPATTV (A02.01) (SEQ ID NO: 623) ATVSTTTAPV (A02.01) (SEQ ID NO: 624) AVPANCLFPA (A02.01) (SEQ ID NO: 625) CLFPAALPST (A02.01) (SEQ ID NO: 626) CPTFVSAAA (B07.02) (SEQ ID NO: 627) FPAALPSTA (B07.02) (SEQ ID NO: 628) FPAALPSTAG (B07.02) (SEQ ID NO: 629) GAECHGRPL (B07.02) (SEQ ID NO: 630) GAISRFIWV (A02.01) (SEQ ID NO: 631) ILPAAIPAST (A02.01) (SEQ ID NO: 632) IWVSGILSPL (A24.02) (SEQ ID NO: 633) LLTATGSVSL (A02.01) (SEQ ID NO: 634) LLYTADSSL (A02.01) (SEQ ID NO: 635) LPAAATSAA (B07.02) (SEQ ID NO: 636) LPAAATSAAS (B07.02) (SEQ ID NO: 637) LPAAIPAST (B07.02) (SEQ ID NO: 638) LPAGCVSSA (B07.02) (SEQ ID NO: 639) LPAGCVSSAP (B07.02) (SEQ ID NO: 640) LYTADSSLW (A24.02) (SEQ ID NO: 641) QPAKSSPSA (B07.02) (SEQ ID NO: 642)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
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			QPAKSSPSAA (B07.02) (SEQ ID NO: 643) RFIWVSGIL (A24.02) (SEQ ID NO: 644) RPQRVWSTG (B07.02) (SEQ ID NO: 645) RVWSTGPDSI (A02.01) (SEQ ID NO: 646) SAVPGSIPL (B07.02) (SEQ ID NO: 647) SILPAAIPA (A02.01) (SEQ ID NO: 648) SLPAAATSA (A02.01) (SEQ ID NO: 649) SLPAAATSAA (A02.01) (SEQ ID NO: 650) SLWTTRPQR (A03.01) (SEQ ID NO: 651) SLWTTRPQRV (A02.01) (SEQ ID NO: 652) SPSAAAATL (B07.02) (SEQ ID NO: 653) SPSAAAATLL (B07.02) (SEQ ID NO: 654) TLDALPAGCV (A02.01) (SEQ ID NO: 655) TVSTTTAPV (A02.01) (SEQ ID NO: 656) VLSASILPA (A02.01) (SEQ ID NO: 657) VLSASILPAA (A02.01) (SEQ ID NO: 658) VPANCLFPA (B07.02) (SEQ ID NO: 659) VPANCLFPAA (B07.02) (SEQ ID NO: 660) VPDPSCPTF (B07.02) (SEQ ID NO: 661) VPGSIPLPA (B07.02) (SEQ ID NO: 662) VPGSIPLPAV (B07.02) (SEQ ID NO: 663) WVSGILSPL (A02.01) (SEQ ID NO: 664) YTADSSLWTT (A02.01) (SEQ ID NO: 665)	
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ARID1 A	T433fs A441fs Y447fs P483fs P484fs P504fs S519fs H544fs P549fs P554fs Q563fs	<u>PCRAGRRVPWAASLIHSR</u> <u>FLLMDNKAPAGMVNRAR</u> <u>LHITTSKVLTLSSSSHPTPS</u> <u>NHRPRPLMPNLRISSSHSL</u> <u>NHHSSSPLSLHTPSSHPSL</u> <u>HISSPRLHTPPSSRRHSSTP</u> <u>RASPPTHSHRLSLLTSSSN</u> <u>LSSQHPRRSPSRLRILSPSL</u> <u>SSPSKLPIPSSASLHRRSYL</u> <u>KIHLGLRHPQPPQ*</u> (SEQ ID NO: 197)	APAGMVNRA (B07.02) (SEQ ID NO: 666) ASLHRRSYL (B08.01) (SEQ ID NO: 667) ASLHRRSYLK (A03.01) (SEQ ID NO: 668) FLLMDNKAPA (A02.01) (SEQ ID NO: 669) HPRRSPSRL (B07.02, B08.01) (SEQ ID NO: 670) HPSLHISSP (B07.02) (SEQ ID NO: 671) HRRSYLKIHL (B08.01) (SEQ ID NO: 672) HSRFLMDNK (A03.01) (SEQ ID NO: 673) KLPISSASL (A02.01) (SEQ ID NO: 674) KVLTLSSSSH (A03.01) (SEQ ID NO: 675) LIHSRFLM (B08.01) (SEQ ID NO: 676) LLMDNKAPA (A02.01) (SEQ ID NO: 677) LMDNKAPAGM (A02.01) (SEQ ID NO: 678) LPISSASL (B07.02) (SEQ ID NO: 679) MPNLRISSS (B07.02, B08.01) (SEQ ID NO: 680) MPNLRISSSH (B07.02) (SEQ ID NO: 681) NLRISSSHSL (B07.02, B08.01) (SEQ ID NO: 682) PPTHSHRLSL (B07.02) (SEQ ID NO: 683) RAGRRVPWAA (B08.01) (SEQ ID NO: 684) RARLHITTSK (A03.01) (SEQ ID NO: 685) RISSSHSLNH (A03.01) (SEQ ID NO: 686) RLHTPPSSR (A03.01) (SEQ ID NO: 687) RLHTPPSSRR (A03.01) (SEQ ID NO: 688) RLRILSPSL (A02.01, B07.02, B08.01) (SEQ ID NO: 689) RPLMPNLRI (B07.02) (SEQ ID NO: 690) RPRPLMPNL (B07.02) (SEQ ID NO: 691)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
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			SASLHRRSYL (B07.02, B08.01) (SEQ ID NO: 692) SLHISSPRL (A02.01) (SEQ ID NO: 693) SLHRRSYLK (A03.01) (SEQ ID NO: 694) SLHRRSYLKI (B08.01) (SEQ ID NO: 695) SLIHSRFL (A02.01) (SEQ ID NO: 696) SLIHSRFLM (A02.01, B08.01) (SEQ ID NO: 697) SLLTSSSNL (A02.01) (SEQ ID NO: 698) SLNHHSSSPL (A02.01, B07.02, B08.01) (SEQ ID NO: 699) SLSSPSKLPI (A02.01) (SEQ ID NO: 700) SPLSLHTPS (B07.02) (SEQ ID NO: 701) SPLSLHTPPS (B07.02) (SEQ ID NO: 702) SPPTHSHRL (B07.02) (SEQ ID NO: 703) SPRLHTPPS (B07.02) (SEQ ID NO: 704) SPRLHTPPSS (B07.02) (SEQ ID NO: 705) SPSLSSPSKL (B07.02) (SEQ ID NO: 706) SYLKIHLGL (A24.02) (SEQ ID NO: 707) TPSNHRPRPL (B07.02, B08.01) (SEQ ID NO: 708) TPSSHPSLHI (B07.02) (SEQ ID NO: 709)	
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ARID1 A	A2137fs P2139fs L1970fs V1994fs	<u>RTNPTVRMRPHCVPFWT</u> <u>GRILLPSAASVCPIPF</u> <u>HLQAMTLRCPNTQGC</u> <u>CSSWAS*</u> (SEQ ID NO: 198)	CVPFWTGRIL (B07.02) (SEQ ID NO: 710) HCVPFWTGRIL (B07.02) (SEQ ID NO: 711) ILLPSAASV (A02.01) (SEQ ID NO: 712) ILLPSAASVC (A02.01) (SEQ ID NO: 713) LLPSAASVCPI (A02.01) (SEQ ID NO: 714) LPSAASVCPI (B07.02) (SEQ ID NO: 715) MRPHCVPF (B08.01) (SEQ ID NO: 716) RILLPSAASV (A02.01) (SEQ ID NO: 717) RMRPHCVPF (A24.02, B07.02, B08.01) (SEQ ID NO: 718) RMRPHCVPF (A24.02) (SEQ ID NO: 719) RTNPTVRMR (A03.01) (SEQ ID NO: 720) SVCPIFEA (A02.01) (SEQ ID NO: 721) TVRMRPHCV (B08.01) (SEQ ID NO: 722) TVRMRPHCVPF (B08.01) (SEQ ID NO: 723) VPFWTGRIL (B07.02) (SEQ ID NO: 724) VPFWTGRILL (B07.02) (SEQ ID NO: 725) VRMRPHCVPF (B08.01) (SEQ ID NO: 726)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
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ARID1 A	N756fs S764fs T783fs Q799fs A817fs	<u>TNQALPKIEVICRGTPRCP</u> <u>STVPPSPAQPYLRLVSLPED</u> <u>RYTQAWAPTSRTPWGAM</u> <u>VPRGVSM AHKVATPGSQ</u> <u>TIMPCPMPTTPVQAWLEA</u> <u>*</u> (SEQ ID NO: 199)	AMVPRGVSM (B07.02, B08.01) (SEQ ID NO: 727) AMVPRGV SMA (A02.01) (SEQ ID NO: 728) AWAPTSRTPW (A24.02) (SEQ ID NO: 729) CPMPTTPVQA (B07.02) (SEQ ID NO: 730) CPSTVPPSPA (B07.02) (SEQ ID NO: 731) GAMVPRGVSM (B07.02, B08.01) (SEQ ID NO: 732) MPCPMPTTPV (B07.02) (SEQ ID NO: 733) MPTTPVQAW (B07.02) (SEQ ID NO: 734) MPTTPVQAWL (B07.02) (SEQ ID NO: 735) SLPEDRYTQA (A02.01) (SEQ ID NO: 736) SPAQP YLRV (B07.02) (SEQ ID NO: 737) SPAQP YLRVS (B07.02) (SEQ ID NO: 738) TIMPCPMPT (A02.01) (SEQ ID NO: 739) TPVQAWLEA (B07.02) (SEQ ID NO: 740) TSRTPWGAM (B07.02) (SEQ ID NO: 741) VPPSPAQP YL (B07.02) (SEQ ID NO: 742) VPRGV SMAH (B07.02) (SEQ ID NO: 743)	STAD, UCEC, BLCA, BRCA, LUSC, CESC, KIRC, UCS
β2M	N62fs E67fs L74fs F82fs T91fs E94fs	<u>RMERELKKWSIQTCLSAR</u> <u>TGLSISCTTLNSPPLKKMS</u> <u>MPAV*</u> (SEQ ID NO: 200)	CLSARTGLSI (B08.01) (SEQ ID NO: 744) CTTLNSPPLK (A03.01) (SEQ ID NO: 745) GLSISCTTL (A02.01) (SEQ ID NO: 746) SPPLKKMSM (B07.02, B08.01) (SEQ ID NO: 747) TLNSPPLKK (A03.01) (SEQ ID NO: 748) TTLNSPPLK (A03.01) (SEQ ID NO: 749) TTLNSPPLKK (A03.01) (SEQ ID NO: 750)	CRC, STAD, SKCM, HNSC

β2M	L13fs S14fs	<u>LCSRYSLFLAWRLSSVLQ</u> <u>RFREFTHVQQRMESQIS*</u> (SEQ ID NO: 201)	LQRFRFTHV (B08.01) (SEQ ID NO: 751) LQRFRFTHVI (B08.01) (SEQ ID NO: 752) RLSSVLQRF (A24.02) (SEQ ID NO: 753) RLSSVLQRF (A03.01) (SEQ ID NO: 754) VLQRFRFTHV (A02.01, B08.01) (SEQ ID NO: 755)	CRC, STAD, SKCM, HNSC
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CDH1	A691fs P708fs L711fs	<u>RSACVTVKGPLASVGRHS</u> <u>LSKQDCKFLPFWGFLEEF</u> <u>LLC*</u> (SEQ ID NO: 202)	ASVGRHSLSK (A03.01) (SEQ ID NO: 756) KFLPFWGFL (A24.02) (SEQ ID NO: 757) LASVGRHSL (B07.02) (SEQ ID NO: 758) LPFWGFLEEF (B07.02) (SEQ ID NO: 759) PFWGFLEEF (A24.02) (SEQ ID NO: 760) SVGRHSLSK (A03.01) (SEQ ID NO: 761)	ILC LumA Breast Cancer
CDH1	H121fs P126fs H128fs N144fs V157fs P159fs N166fs N181fs F189fs P201fs F205fs	<u>IQWGTTTAPRPIRPPFLES</u> <u>KQNCSEHPTPLLAEDRR</u> <u>ETGLFLPSAAQKMKAHF</u> <u>LKTWFRSNPTKTKKARFS</u> <u>TASLAKELTHPLLVSLLK</u> <u>EKQDG*</u> (SEQ ID NO: 203)	APRPIRPPF (B07.02) (SEQ ID NO: 762) APRPIRPPFL (B07.02) (SEQ ID NO: 763) AQKMKAHFL (B08.01) (SEQ ID NO: 764) FLPSAAQKM (A02.01) (SEQ ID NO: 765) GLFLPSAAQK (A03.01) (SEQ ID NO: 766) HPLLVSLLL (B07.02) (SEQ ID NO: 767) KAHFLKTWFR (A03.01) (SEQ ID NO: 768) KARFSTASL (B07.02) (SEQ ID NO: 769) KMKAHFLK (A03.01) (SEQ ID NO: 770) KTWFRSNPTK (A03.01) (SEQ ID NO: 771) LAKELTHPL (B07.02, B08.01) (SEQ ID NO: 772) LAKELTHPLL (B08.01) (SEQ ID NO: 773) NPTKTKKARF (B07.02) (SEQ ID NO: 774) QKMKAHFL (B08.01) (SEQ ID NO: 775) RFSTASLAK (A03.01) (SEQ ID NO: 776) RPIRPPFLES (B07.02) (SEQ ID NO: 777) RSNPTKTKK (A03.01) (SEQ ID NO: 778) SLAKELTHPL (A02.01, B08.01) (SEQ ID NO: 779) TKKARFSTA (B08.01) (SEQ ID NO: 780)	ILC LumA Breast Cancer

CDH1	V114fs P127fs V132fs P160fs	<u>PTDPFLGLRLGLHLQKVF</u> <u>HQSHAEYSGAPPPPPAPSG</u> <u>LRFWNPSRIAHISQLLSWP</u> <u>QKTEERLGYSSHQLPRK*</u> (SEQ ID NO: 204)	GLRFWNPSR (A03.01) (SEQ ID NO: 781) ISQLLSWPQK (A03.01) (SEQ ID NO: 782) RIAHISQLL (A02.01) (SEQ ID NO: 783) RLGYSSHQL (A02.01) (SEQ ID NO: 784) SQLLSWPQK (A03.01) (SEQ ID NO: 785) SRIAHISQL (B08.01) (SEQ ID NO: 786) WPQKTEERL (B07.02) (SEQ ID NO: 787) YSSHQLPRK (A03.01) (SEQ ID NO: 788)	ILC LumA Breast Cancer
CDH1	L731fs R749fs E757fs G759fs	<u>FCCSCCFFGGERWSKSPY</u> <u>CPQRMTPGTTFITMMKKE</u> <u>AEKRTRTLT*</u> (SEQ ID NO: 205)	CPQRMTPGTT (B07.02) (SEQ ID NO: 789) EAEKRTRTL (B08.01) (SEQ ID NO: 790) GTTFITMMK (A03.01) (SEQ ID NO: 791) GTTFITMMKK (A03.01) (SEQ ID NO: 792) ITMMKKEAEK (A03.01) (SEQ ID NO: 793) RMTPGTTFI (A02.01) (SEQ ID NO: 794) SPYCPQRM (B07.02) (SEQ ID NO: 795) TMMKKEAEK (A03.01) (SEQ ID NO: 796) TPGTTFITM (B07.02) (SEQ ID NO: 797) TPGTTFITMM (B07.02) (SEQ ID NO: 798) TTFITMMKK (A03.01) (SEQ ID NO: 799)	ILC LumA Breast Cancer
CDH1	S19fs E24fs S36fs	<u>WRRNCKAPVSLRKSVQTP</u> <u>ARSSPARPDTRRLPSLGV</u> <u>PGQPWALGAAASRRCCC</u> <u>CCRSPLGSARSRSPATLAL</u> <u>TPRATRSRCPGATWREAA</u> <u>SWAE*</u> (SEQ ID NO: 206)	CPGATWREA (B07.02) (SEQ ID NO: 800) CPGATWREAA (B07.02) (SEQ ID NO: 801) RSRCPGATWR (A03.01) (SEQ ID NO: 802) TPRATRSRC (B07.02) (SEQ ID NO: 803)	ILC LumA Breast Cancer

GATA3	P394fs P387fs S398fs H400fs M401fs S408fs P409fs S408fs P409fs T419fs H424fs P425fs S427fs F431fs S430fs H434fs H435fs S438fs M443fs G444fs *445fs	<u>PGRPLQTHVLPEPHLALQ</u> <u>PLQPHADHAHADAPAIQP</u> <u>VLWTTTPPLQHGHRHGLEP</u> <u>CSMLTGPPARVPAVPFDL</u> <u>HFCRSSIMKPKRDGYMFL</u> <u>KAESKIMFATLQRSSLWC</u> <u>LCSNH*</u> (SEQ ID NO: 207)	HVLPEPHLAL (B07.02) (SEQ ID NO: 804) RPLQTHVLPE (B07.02) (SEQ ID NO: 805) VLWTTTPPLQH (A03.01) (SEQ ID NO: 806)	Breast Cancer
GATA3	P426fs H434fs P433fs T441fs	<u>PRPRRCTRHPACPLDHTTP</u> <u>PAWSPPWVRALLDAHRA</u> <u>PSESPCSPFRLAFLQEQYH</u> <u>EA*</u> (SEQ ID NO: 208)	APSESPCSPF (B07.02) (SEQ ID NO: 807) CPLDHTTPPA (B07.02) (SEQ ID NO: 808) FLQEQYHEA (A02.01, B08.01) (SEQ ID NO: 809) RLAFLQEQYH (A03.01) (SEQ ID NO: 810) SPCSPFRLAF (B07.02) (SEQ ID NO: 811) SPPWVRALL (B07.02) (SEQ ID NO: 812) YPACPLDHTT (B07.02) (SEQ ID NO: 813)	Breast Cancer

MLL2	P519fs E524fs P647fs S654fs L656fs R755fs L761fs Q773fs	<u>TRRCHCCPHLRSHPCPHH</u> <u>LRNHPRPHHLRHHACHH</u> <u>HLRNCPPHFLRHCTCPG</u> <u>RWRNRPSLRRLRSLCLP</u> <u>HLNHHFLHWRSRPCLHR</u> <u>KSHPHLLHLRRLYPHHLK</u> <u>HRPCPHHLKNLLCPRHLR</u> <u>NCPLPRHLKHLACLHHLR</u> <u>SHPCPLHLKSHPCPLHHR</u> <u>HLVCSHHLKSLLCPLHLR</u> <u>SLPFPHHLRHHACPHHLR</u> <u>TRLCPHHLKNHLCPPHLR</u> <u>YRAYPPCLWCHACLHRL</u> <u>RNLPCPHRLRSLPRPLHLR</u> <u>LHASPHHLRTPPHPHHLR</u> <u>THLLPHHRRTRSCPCRWR</u> <u>SHPCCHYLRSRNSAPGPR</u> <u>GRTCHPGLRSRTCPPGLRS</u> <u>HTYLRRRLRSHTCPPSLRSH</u> <u>AYALCLRSHTCPPRLRDHI</u> <u>CPLSLRNCTCPPRLRSRTC</u> <u>LLCLRSACPPNLRNHTC</u> <u>PPSLRSHACPPGLRNRICP</u> <u>LSLRSHPCPLGLKSPLRSQ</u> <u>ANALHLRSCPCSLPLGNH</u> <u>PYLPCLSQPCLSLGNHLC</u> <u>PLCPRSCRCPHLGSHPCRL</u> <u>S*</u> (SEQ ID NO: 209)	ALHLRSCPC (B08.01) (SEQ ID NO: 814) CLHHRRHLV (B08.01) (SEQ ID NO: 815) CLHHRRHLVC (B08.01) (SEQ ID NO: 816) CLHRKSHPHL (B08.01) (SEQ ID NO: 817) CLRSACPP (B08.01) (SEQ ID NO: 818) CLRSHTCPP (B08.01) (SEQ ID NO: 819) CLWCHACLH (A03.01) (SEQ ID NO: 820) CPHHLKNHL (B07.02) (SEQ ID NO: 821) CPHHLKNLL (B07.02) (SEQ ID NO: 822) CPHHLRTRL (B07.02, B08.01) (SEQ ID NO: 823) CPLHLRSLPF (B07.02, B08.01) (SEQ ID NO: 824) CPLPRHLKHL (B07.02, B08.01) (SEQ ID NO: 825) CPLSLRSHPC (B07.02) (SEQ ID NO: 826) CPRHLRNCPL (B07.02, B08.01) (SEQ ID NO: 827) FPHHLRHHA (B07.02, B08.01) (SEQ ID NO: 828) FPHHLRHHAC (B07.02, B08.01) (SEQ ID NO: 829) GLRSRTCPL (B08.01) (SEQ ID NO: 830) HACLHRLRNL (B08.01) (SEQ ID NO: 831) HLACLHHLR (A03.01) (SEQ ID NO: 832) HLCPPHLRY (A03.01) (SEQ ID NO: 833) HLCPPHLRYR (A03.01) (SEQ ID NO: 834) HLKHLACLH (A03.01) (SEQ ID NO: 835) HLKHRPCPH (B08.01) (SEQ ID NO: 836) HLKNHLCPP (B08.01) (SEQ ID NO: 837) HLKSHPCPLH (A03.01) (SEQ ID NO: 838) HLKSLLCPL (A02.01, B08.01) (SEQ ID NO: 839)	STAD, BLCA, CRC, HNSC, BRCA
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			HLLHLRRLY (A03.01) (SEQ ID NO: 840) HLRNCPLPR (A03.01) (SEQ ID NO: 841) HLRNCPLPRH (A03.01) (SEQ ID NO: 842) HLRRLYPHHL (B08.01) (SEQ ID NO: 843) HLRSHPCPL (B07.02, B08.01) (SEQ ID NO: 844) HLRSHPCPLH (A03.01) (SEQ ID NO: 845) HLRSLPFP (A03.01) (SEQ ID NO: 846) HLRTRLCPH (A03.01, B08.01) (SEQ ID NO: 847) HLVCSHHLK (A03.01) (SEQ ID NO: 848) HPCLHRRHL (B07.02, B08.01) (SEQ ID NO: 849) HPGLRSRTC (B07.02) (SEQ ID NO: 850) HPLLHLRRL (B07.02, B08.01) (SEQ ID NO: 851) HRKSHPLL (B08.01) (SEQ ID NO: 852) HRRTRSCPC (B08.01) (SEQ ID NO: 853) KSHPHLLHLR (A03.01) (SEQ ID NO: 854)	
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			KSLLCPLHLR (A03.01) (SEQ ID NO: 855) LLCPLHLRSL (A02.01, B08.01) (SEQ ID NO: 856) LLHLRRLYPH (B08.01) (SEQ ID NO: 857) LPRHLKHLA (B07.02) (SEQ ID NO: 858) LPRHLKHLAC (B07.02, B08.01) (SEQ ID NO: 859) LRRLRSHTC (B08.01) (SEQ ID NO: 860) LRRLYPHHL (B08.01) (SEQ ID NO: 861) LVCSHHLKSL (B08.01) (SEQ ID NO: 862) NLRNHTCPPS (B08.01) (SEQ ID NO: 863) PLHLRSLPF (B08.01) (SEQ ID NO: 864) RLCPHHLKNH (A03.01) (SEQ ID NO: 865) RLYPHHLKH (A03.01) (SEQ ID NO: 866) RLYPHHLKHR (A03.01) (SEQ ID NO: 867) RPCPHHLKNL (B07.02) (SEQ ID NO: 868) RSHPCPLHLK (A03.01) (SEQ ID NO: 869) RSLPFPHLR (A03.01) (SEQ ID NO: 870) RTRLCPHHL (B07.02) (SEQ ID NO: 871) RTRLCPHHLK (A03.01) (SEQ ID NO: 872) SLLCPLHLR (A03.01) (SEQ ID NO: 873) SLRSHACPP (B08.01) (SEQ ID NO: 874) SPLRSQANA (B07.02) (SEQ ID NO: 875) YLRRLRSHT (B08.01) (SEQ ID NO: 876) YPHHLKHRPC (B07.02, B08.01) (SEQ ID NO: 877)	
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PTEN	I122fs I135fs A148fs L152fs D162fs I168fs	<u>SWKGTNWCNDMCIFITSG</u> <u>QIFKGTRGPRFLWGSKDQ</u> <u>RQKGSNYSQSEALCVLL*</u> (SEQ ID NO: 210)	FITSGQIFK (A03.01) (SEQ ID NO: 878) IFITSGQIF (A24.02) (SEQ ID NO: 879) SQSEALCVL (A02.01) (SEQ ID NO: 880) SQSEALCVLL (A02.01) (SEQ ID NO: 881)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM
PTEN	L265fs K266fs	<u>KRTKCFTEFG*</u> (SEQ ID NO: 211)		UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM
PTEN	A39fs E40fs V45fs R47fs N48fs	<u>PIFIQTLLLWDFLQKDLKA</u> <u>YTGILMM*</u> (SEQ ID NO: 212)	AYTGILMM (A24.02) (SEQ ID NO: 882) DLKAYTGIL (B08.01) (SEQ ID NO: 883)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM
PTEN	T319fs T321fs K327fs A328fs A333fs	<u>QKMILTKQIKTKPTDTFLQ</u> <u>ILR*</u> (SEQ ID NO: 213)	ILTKQIKTK (A03.01) (SEQ ID NO: 884) KMILTKQIK (A03.01) (SEQ ID NO: 885) KPTDTFLQI (B07.02) (SEQ ID NO: 886) KPTDTFLQIL (B07.02) (SEQ ID NO: 887) MILTKQIKTK (A03.01) (SEQ ID NO: 888)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM

PTEN	N63fs E73fs A86fs N94fs	<u>GFWIQSIKTITRYTIFVLKD</u> <u>IMTPPNLIAELHNILLKTIT</u> <u>HHS*</u> (SEQ ID NO: 214)	ITRYTIFVLK (A03.01) (SEQ ID NO: 889) LIAELHNIL (A02.01) (SEQ ID NO: 890) LIAELHNILL (A02.01) (SEQ ID NO: 891) MTPPNLIAEL (A02.01) (SEQ ID NO: 892) NLIAELHNI (A02.01) (SEQ ID NO: 893) NLIAELHNIL (A02.01) (SEQ ID NO: 894) RYTIFVLKDI (A24.02) (SEQ ID NO: 895) TITRYTIFVL (A02.01) (SEQ ID NO: 896) TPPNLIAEL (B07.02) (SEQ ID NO: 897)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM
PTEN	T202fs G209fs C211fs I224fs G230fs P231fs R233fs D236fs	<u>NYSNVQWRNLQSSVCGL</u> <u>PAKGEDIFLQFRTHTTGR</u> <u>QVHVL*</u> (SEQ ID NO: 215)	FLQFRTHTT (A02.01, B08.01) (SEQ ID NO: 898) LPAKGEDIFL (B07.02) (SEQ ID NO: 899) LQFRTHTTGR (A03.01) (SEQ ID NO: 900) NLQSSVCGL (A02.01) (SEQ ID NO: 901) SSVCGLPAK (A03.01) (SEQ ID NO: 902) VQWRNLQSSV (A02.01) (SEQ ID NO: 903)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM
PTEN	G251fs E256fs K260fs Q261fs L265fs M270fs H272fs T286fs E288fs	<u>YQSRVLPQTEQDAKKGO</u> <u>NVSLGKYILHTRTRGNL</u> <u>RKSRKWKSM*</u> (SEQ ID NO: 216)	GQNVSLLGK (A03.01) (SEQ ID NO: 904) HTRTRGNLRK (A03.01) (SEQ ID NO: 905) ILHTRTRGNL (B08.01) (SEQ ID NO: 906) KGQNVSLLGK (A03.01) (SEQ ID NO: 907) LLGKYILHT (A02.01) (SEQ ID NO: 908) LRKSRKWKSM (B08.01) (SEQ ID NO: 909) SLLGKYILH (A03.01) (SEQ ID NO: 910) SLLGKYILHT (A02.01) (SEQ ID NO: 911)	UCEC, PRAD, SKCM, STAD, BRCA, LUSC, KIRC, LIHC, KIRP, GBM

TP53	A70fs P72fs A76fs A79fs P89fs W91fs S96fs V97fs V97fs G108fs G117fs S121fs V122fs C124fs K139fs V143fs	<u>SSQNARGCSPRGPCTSSSY</u> <u>TGGPCTSPLLAPVIFCPFPE</u> <u>NLPGQLRFPSGLLAFWDS</u> <u>QVCDLHVLPCPQQDVLPT</u> <u>GQDLPCA AVG*</u> (SEQ ID NO: 217)	CTSPLLAPV (A02.01) (SEQ ID NO: 912) FPENLPGQL (B07.02) (SEQ ID NO: 913) GLLAFWDSQV (A02.01) (SEQ ID NO: 914) IFCPFPENL (A24.02) (SEQ ID NO: 915) LLAFWDSQV (A02.01) (SEQ ID NO: 916) LLAPVIFCP (A02.01) (SEQ ID NO: 917) LLAPVIFCPF (A02.01, A24.02) (SEQ ID NO: 918) LPCPQQDVL (B07.02) (SEQ ID NO: 919) RFPSGLLAF (A24.02) (SEQ ID NO: 920) RFPSGLLAFW (A24.02) (SEQ ID NO: 921) SPLLAPVIF (B07.02) (SEQ ID NO: 922) SPRGPCTSS (B07.02) (SEQ ID NO: 923) SPRGPCTSSS (B07.02) (SEQ ID NO: 924) SQVCDLHVL (A02.01) (SEQ ID NO: 925) VIFCPFPENL (A02.01) (SEQ ID NO: 926)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC
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TP53	V173fs H178fs D186fs H193fs L194fs E198fs V203fs E204fs L206fs D207fs N210fs T211fs F212fs V225fs S241fs	<u>GAAPTMSAAQIAMVWPL</u> <u>LSILSEWKEICVWSIWM</u> <u>ETLFDIVWWCPMSRLRLA</u> <u>LTVPPSTTTTCVTVPAWA</u> <u>A*</u> (SEQ ID NO: 218)	AMVWPLLSI (A02.01) (SEQ ID NO: 927) AMVWPLLSIL (A02.01) (SEQ ID NO: 928) AQIAMVWPL (A02.01, A24.02) (SEQ ID NO: 929) AQIAMVWPLL (A02.01) (SEQ ID NO: 930) CPMSRLRLA (B07.02, B08.01) (SEQ ID NO: 931) CPMSRLRLAL (B07.02, B08.01) (SEQ ID NO: 932) IAMVWPLLSI (A02.01, A24.02, B08.01) (SEQ ID NO: 933) ILSEWKEICV (A02.01) (SEQ ID NO: 934) IVWWCPMSR (A03.01) (SEQ ID NO: 935) IVWWCPMSRL (A02.01) (SEQ ID NO: 936) IWMETLFDI (A24.02) (SEQ ID NO: 937) LLSILSEWK (A03.01) (SEQ ID NO: 938) MSAAQIAMV (A02.01) (SEQ ID NO: 939) MSRLRLALT (B08.01) (SEQ ID NO: 940) MSRLRLALTV (B08.01) (SEQ ID NO: 941) MVWPLLSIL (A02.01) (SEQ ID NO: 942) RLALTVPST (A02.01) (SEQ ID NO: 943) TLFDIVWWC (A02.01) (SEQ ID NO: 944) TLFDIVWWCP (A02.01) (SEQ ID NO: 945) TMSAAQIAMV (A02.01) (SEQ ID NO: 946) VWSIWMETL (A24.02) (SEQ ID NO: 947) WMTETLFDI (A02.01, A24.02) (SEQ ID NO: 948) WMTETLFDIV (A01.01, A02.01) (SEQ ID NO: 949)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC
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TP53	R248fs P250fs S260fs N263fs G266fs N268fs V272fs V274fs P278fs D281fs R282fs T284fs E285fs L289fs K292fs P301fs S303fs T312fs S314fs K319fs K320fs P322fs Y327fs F328fs L330fs R333fs R335fs R337fs E339fs	<u>TGGPSSPSSHWKTPVVIY</u> <u>WDGTALRCVFVPVLGET</u> <u>GAQRKRISARKGSLTTSCP</u> <u>QGALSEHCPTTPAPLPSQR</u> <u>RNHWMENISPFERSVGVS</u> <u>SRCSES*</u> (SEQ ID NO: 219)	ALRCVFVPV (A02.01, B08.01) (SEQ ID NO: 950) ALRCVFVPVL (A02.01, B08.01) (SEQ ID NO: 951) ALSEHCPTT (A02.01) (SEQ ID NO: 952) AQRKRISARK (A03.01) (SEQ ID NO: 953) GAQRKRISA (B08.01) (SEQ ID NO: 954) HWMENISPF (A24.02) (SEQ ID NO: 955) LPSQRRNHW (B07.02) (SEQ ID NO: 956) LPSQRRNHW (B07.02, B08.01) (SEQ ID NO: 957) NISPFERSVG (A02.01) (SEQ ID NO: 958) RISARKGSL (B07.02, B08.01) (SEQ ID NO: 959) SPERSVGVS (B07.02) (SEQ ID NO: 960) SPSSHWKTPV (B07.02, B08.01) (SEQ ID NO: 961) TALRCVFVPV (A02.01) (SEQ ID NO: 962) VIYWDGTAL (A02.01) (SEQ ID NO: 963) VIYWDGTALR (A03.01) (SEQ ID NO: 964) VLGETGAQRK (A03.01) (SEQ ID NO: 965)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC
TP53	S149fs P151fs P152fs V157fs Q165fs S166fs H168fs V173fs	<u>FHTPARHPRPRHGHQLQAV</u> <u>TAHDGGCEALPPP*</u> (SEQ ID NO: 220)	HPRPRHGH (B07.02, B08.01) (SEQ ID NO: 966) HPRPRHGHQL (B07.02) (SEQ ID NO: 967) RPRHGHQLA (B07.02) (SEQ ID NO: 968) RPRHGHQLQAV (B07.02, B08.01) (SEQ ID NO: 969)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC

TP53	P47fs D48fs D49fs Q52fs F54fs E56fs P58fs P60fs E62fs M66fs P72fs V73fs P75fs A78fs P82fs P85fs S96fs P98fs T102fs Y103fs G108fs F109fs R110fs G117fs	<u>CCPRTILNNGSLKTQVQM</u> <u>KLPECQRLLPWPLHQQL</u> <u>LHRRPLHQPPGpchllsl</u> <u>PRKPTRAATVSVWASCIL</u> <u>GQPSL*</u> (SEQ ID NO: 221)	GSLKTQVQMK (A03.01) (SEQ ID NO: 970) PPGPCHLLSL (B07.02) (SEQ ID NO: 971) RTILNNGSLK (A03.01) (SEQ ID NO: 972) SLKTQVQMK (A03.01) (SEQ ID NO: 973) SLKTQVQMKL (B08.01) (SEQ ID NO: 974) TILNNGSLK (A03.01) (SEQ ID NO: 975)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC
TP53	L26fs P27fs P34fs P36fs A39fs Q38fs	<u>VRKHFQTYGNYFLKTTFC</u> <u>PPCRPKQWMI*</u> (SEQ ID NO: 222)	CPPCRPKQWM (B07.02) (SEQ ID NO: 976) TTFCPPCRPK (A03.01) (SEQ ID NO: 977)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC

TP53	C124fs L130fs N131fs C135fs K139fs A138fs T140fs V143fs Q144fs V147fs T150fs P151fs P152fs G154fs R156fs R158fs A161fs	<u>LARTPLPSTRCFANWPRP</u> <u>ALCSCGLIPHRPAPASAP</u> <u>WPSTSSHST*</u> (SEQ ID NO: 223)	CFANWPRPAL (A24.02) (SEQ ID NO: 978) FANWPRPAL (B07.02, B08.01) (SEQ ID NO: 979) GLIPHRPA (A02.01) (SEQ ID NO: 980) HPRPAPASA (B07.02, B08.01) (SEQ ID NO: 981) HPRPAPASAP (B07.02) (SEQ ID NO: 982) IPHRPAPA (B07.02, B08.01) (SEQ ID NO: 983) IPHRPAPAS (B07.02) (SEQ ID NO: 984) RPALCSCGL (B07.02) (SEQ ID NO: 985) RPALCSCGLI (B07.02) (SEQ ID NO: 986) TPLPSTRCF (B07.02) (SEQ ID NO: 987) WPRPALCSC (B07.02) (SEQ ID NO: 988) WPRPALCSCG (B07.02) (SEQ ID NO: 989)	BRCA, CRC, LUAD, PRAD, HNSC, LUSC, PAAD, STAD, BLCA, OV, LIHC, SKCM, UCEC, LAML, UCS, KICH, GBM, ACC
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VHL	L178fs D179fs L184fs T202fs R205fs D213fs G212fs	<u>ELQETGHRQVALRRSGRP</u> <u>PKCAERPGAADTGAHCTS</u> <u>TDGRLKISVETYTVSSQLL</u> <u>MVLMsLDLDTGLVPSLVS</u> <u>KCLILRVK*</u> (SEQ ID NO: 224)	ALRRSGRPPK (A03.01) (SEQ ID NO: 990) GLVPSLVSK (A03.01) (SEQ ID NO: 991) KISVETYTV (A02.01) (SEQ ID NO: 992) LLMVLMsLDL (A02.01, B08.01) (SEQ ID NO: 993) LMSLDLDTGL (A02.01) (SEQ ID NO: 994) LMVLMsLDL (A02.01) (SEQ ID NO: 995) LVSKCLILRV (A02.01) (SEQ ID NO: 996) QLLMVLMsL (A02.01, B08.01) (SEQ ID NO: 997) RPGAADTGA (B07.02) (SEQ ID NO: 998) RPGAADTGAH (B07.02) (SEQ ID NO: 999) SLDLDTGLV (A02.01) (SEQ ID NO: 1000) SLVSKCLIL (A02.01, B08.01) (SEQ ID NO: 1001) SQLLMVLMsL (A02.01) (SEQ ID NO: 1002) TVSSQLLMV (A02.01) (SEQ ID NO: 1003) TYTVSSQLL (A24.02) (SEQ ID NO: 1004) TYTVSSQLLM (A24.02) (SEQ ID NO: 1005) VLMSLDLDT (A02.01) (SEQ ID NO: 1006) VPSLVSKCL (B07.02) (SEQ ID NO: 1007) VSKCLILRVK (A03.01) (SEQ ID NO: 1008) YTVSSQLLM (A01.01) (SEQ ID NO: 1009) YTVSSQLLMV (A02.01) (SEQ ID NO: 1010)	KIRC, KIRP
VHL	L158fs K159fs R161fs Q164fs	<u>KSDASRLSGA*</u> (SEQ ID NO: 225)		KIRC, KIRP
VHL	P146fs I147fs F148fs L158fs	<u>RTAYFCQYHTASVYSERA</u> <u>MPPGCPEPSQA*</u> (SEQ ID NO: 226)	FCQYHTASV (B08.01) (SEQ ID NO: 1011)	KIRC, KIRP

VHL	S68fs S72fs I75fs S80fs P86fs P97fs I109fs H115fs L116fs G123fs T124fs N131fs L135fs V137fs G144fs D143fs I147fs	<u>TRASPPRSSSAIAVRASCC</u> <u>PYGSTSTASRSPTQRCRLA</u> <u>RAAASTATEVTFGSSEMQ</u> <u>GHTMGFWLTKLNYLCHL</u> <u>SMLTDSLFLPISHCQCIL*</u> (SAQ ID NO: 227)	CPYGSTSTA (B07.02) (SEQ ID NO: 1012) CPYGSTSTAS (B07.02) (SEQ ID NO: 1013) LAAAAASTAT (B07.02) (SEQ ID NO: 1014) MLTDSLFLP (A02.01) (SEQ ID NO: 1015) PPRSSSAIAV (B07.02) (SEQ ID NO: 1016) RAAASTATEV (B07.02) (SEQ ID NO: 1017) SPPRSSSAI (B07.02) (SEQ ID NO: 1018) SPPRSSSAIA (B07.02) (SEQ ID NO: 1019) SPTQRCRLA (B07.02) (SEQ ID NO: 1020) TQRCRLARA (B08.01) (SEQ ID NO: 1021) TQRCRLARAA (B08.01) (SEQ ID NO: 1022)	KIRC, KIRP
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VHL	K171fs P172fs N174fs L178fs D179fs L188fs	<u>SSLRITGDWTSSGRSTKIW</u> <u>KTQMCRKKTWSG*</u> (SEQ ID NO: 228)	KIWKTQMCR (A03.01) (SEQ ID NO: 1023) WTSSGRSTK (A03.01) (SEQ ID NO: 1024)	KIRC, KIRP
VHL	V62fs V66fs Q73fs V84fs F91fs T100fs P103fs S111fs L116fs H115fs D126fs	<u>RRRRGGVGRRGVRPGRV</u> <u>RPGGTGRRGGDGGRAAA</u> <u>ARAALGELARALPGHLLQ</u> <u>SQSARRAARMAQLRRRA</u> <u>AALPNAAAWHGPPHPQL</u> <u>PRSPLALQRCRDTRWASG</u> * (SEQ ID NO: 229)	ALGELARAL (A02.01) (SEQ ID NO: 1025) AQLRRRAAA (B08.01) (SEQ ID NO: 1026) AQLRRRAAAL (B08.01) (SEQ ID NO: 1027) ARRAARMAQL (B08.01) (SEQ ID NO: 1028) HPQLPRSPL (B07.02, B08.01) (SEQ ID NO: 1029) HPQLPRSPLA (B07.02) (SEQ ID NO: 1030) LARALPGHL (B07.02) (SEQ ID NO: 1031) LARALPGHLL (B07.02) (SEQ ID NO: 1032) MAQLRRRAA (B07.02, B08.01) (SEQ ID NO: 1033) MAQLRRRAAA (B07.02, B08.01) (SEQ ID NO: 1034) QLRRRAAAL (B07.02, B08.01) (SEQ ID NO: 1035) RAAALPNAAA (B07.02) (SEQ ID NO: 1036) RMAQLRRRAA (B07.02, B08.01) (SEQ ID NO: 1037) SQSARRAARM (B08.01) (SEQ ID NO: 1038)	KIRC, KIRP
AR-v7	cryptic final exon	SCKVFFKRAAEGKQKLYLC ASRNDCTIDKFRKNCPS CRLRKCYEAGMTLGE <u>KF</u> <u>RVGNCKHLKMTRP*</u> (SEQ ID NO: 230)	GMTLGEKFRV (A02.01) (SEQ ID NO: 1039) RVGNCKHLK (A03.01) (SEQ ID NO: 1040)	Prostate Cancer, Castration-resistant Prostate Cancer
AC011 997.1:L RRC69	AC0119 97.1:LR RC69 *out-of-frame	MAGAPPPASLPPCSLISDC CASNQRDVGVPSEP: <u>G</u> : <u>NNIKICNESASRK*</u> (SEQ ID NO: 231)	GPSEPGNNI (B07.02) (SEQ ID NO: 1041) KICNESASRK (A03.01) (SEQ ID NO: 1042)	LUSC, Breast Cancer, Head and Neck Cancer, LUAD

EEF1D P3	EEF1DP 3:FRY *out-of- frame	HGWRPFLPVRARSRWN RLDVTVANGR:S: <u>WKYG</u> <u>WSLLRVPOVNGIQVLNV</u> <u>SLKSSSNVISYE*</u> (SEQ ID NO: 232)	GIQVLNVSLK (A03.01) (SEQ ID NO: 1043) IQVLNVSLK (A03.01) (SEQ ID NO: 1044) KSSSNVISY (A01.01, A03.01) (SEQ ID NO: 1045) KYGWSLLRV (A24.02) (SEQ ID NO: 1046) RSWKYGWSL (A02.01) (SEQ ID NO: 1047) SLKSSSNVI (B08.01) (SEQ ID NO: 1048) SWKYGWSLL (A24.02) (SEQ ID NO: 1049) TVANGRSWK (A03.01) (SEQ ID NO: 1050) VPQVNGIQV (B07.02) (SEQ ID NO: 1051) VPQVNGIQVL (B07.02) (SEQ ID NO: 1052) VTVANGRSWK (A03.01) (SEQ ID NO: 1053) WSLLRVQV (B08.01) (SEQ ID NO: 1054)	Breast Cancer
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MAD1 L1:MA FK	MAD1L 1:MAF K	RLKEVFQTKIQEFRKACY TLTGYQIDITTENQYRLTS LYAEHPGDCLIFK:: <u>LRVP</u> <u>GSSVLVTVPGL*</u> (SEQ ID NO: 233)	HPGDCLIFKL (B07.02) (SEQ ID NO: 1055) KLRVPGSSV (B07.02) (SEQ ID NO: 1056) KLRVPGSSVL (B07.02) (SEQ ID NO: 1057) RVPGSSVLV (A02.01) (SEQ ID NO: 1058) SVLVTVPGL (A02.01) (SEQ ID NO: 1059) VPGSSVLVTV (B07.02) (SEQ ID NO: 1060)	CLL
PPP1R1 B:STA RD3	PPP1R1 B:STAR D3	AEVLKVIRQSAGQKTTCCG QGLEGPOWERPPPLDESER DGGSEDQVEDPALS:A: <u>LL</u> <u>LRPRPPRPEVGAHQDEQ</u> <u>AAQGADPRLGAQPACR</u> <u>GLPGLLTVPQPEPLLAPP</u> <u>SAA*</u> (SEQ ID NO: 234)	ALLLRPRPPR (A03.01) (SEQ ID NO: 1061) ALSALLLRPR (A03.01) (SEQ ID NO: 1062)	Breast Cancer
BCR:A BL	BCR:A BL	ERAEWRENIREQQKKCFR SFSLTVELQMLTNSCVK LQTVHSIPLTINKE:: <u>EALQ</u> <u>RPVASDFEPQGLSEAAR</u> <u>WNSKENLLAGPSENDPN</u> <u>LFVALYDFVASG</u> (SEQ ID NO: 235)	LTINKEEAL (A02.01, B08.01) (SEQ ID NO: 1063)	CML, AML
BCR:A BL	BCR:A BL	ELQMLTNSCVKLQTVHSI PLTINKEDDESPGLYGFLN VIVHSATGFKQSS:K: <u>ALQ</u> <u>RPVASDFEPQGLSEAAR</u> <u>WNSKENLLAGPSENDPN</u> <u>LFVALYDFVASGD</u> (SEQ ID NO: 236)	IVHSATGFK (A03.01) (SEQ ID NO: 1064) ATGFKQSSK (A03.01) (SEQ ID NO: 1065)	CML, AML
C11orf9 5:REL A	C11orf9 5:RELA	ISNSWDAHLGLGACGEAE GLGVQGAEEEEEEEEEE EEGAGVPACPPKGP:E: <u>LF</u> <u>PLIFPAEPAQASGPYVEII</u> <u>EQPKQRGMRFRYKCEG</u> <u>RSAGSIPGERSTD</u> (SEQ ID NO: 237)	ELFPLIFPA (A02.01, B08.01) (SEQ ID NO: 1066) KGPELFPLI (A02.01, A24.02) (SEQ ID NO: 1067) KGPELFPLIF (A24.02) (SEQ ID NO: 1068)	Supretentorial ependyomas
CBFB: MYH11	(variant “type a”)	LQRLDGMGCLEFDEERA QQEDALAQQAFEEARRRT REFEDRDRSHREEME:: <u>VH</u> <u>ELEKSKRALETQMEEM</u> <u>KTQLEEELEDELQATEDA</u> <u>KLRLEVNMQALKGQF</u> (SEQ ID NO: 238)		AML

CD74:R OS1	(exon6:exon32)	KGSFPENLRHLKNTMETI DWKVFESWMHHWLLFE MSRHSLEQKPTDAPPK::A GVPNKPGIPKLLEGSKN SIQWEKAEDNGCRITYYI LEIRKSTSNLQNN (SEQ ID NO: 239)	KPTDAPPKAGV (B07.02) (SEQ ID NO: 1069)	NSCLC, Crizotinib resistance
EGFR	EGFRvII (internal deletion)	MRPSGTAGAALLALLAAL CPASRALEEEKK:G:NYVVT DHGSCVRACGADSYEME EDGVRKCKKCEGPCRKV CNGIGIGEFKD (SEQ ID NO: 240)	ALEEKKGNYV (A02.01) (SEQ ID NO: 1070)	GBM

EGFR: SEPT14	EGFR:S EPT14	LPQPPICTIDVYMIMVKC WMIDADSRPKFRELHIEFS KMARDPQRYLVIQ::LQD KFEHLKMIQQEEIRKLE EEKKQLEGEIIDFYKMK AASEALQTQLSTD (SEQ ID NO: 241)	IQLQDKFEHL (A02.01, B08.01) (SEQ ID NO: 1071) QLQDKFEHL (A02.01, B08.01) (SEQ ID NO: 1072) QLQDKFEHLK (A03.01) (SEQ ID NO: 1073) YLVIQLQDKF (A02.01, A24.02) (SEQ ID NO: 1074)	GBM, Glioma, Head and Neck Cancer
EML4: ALK	EML4: ALK	SWENSDDSRNKLSKIPSTP KLIPKVTKTADKHKDVIN QAKMSTREKNSQ:V:YRR KHQELQAMQMELQSPE YKLSKLRTSTIMTDYNP NYCFAGKTSSISDL (SEQ ID NO: 242)	QVYRRKHQEL (B08.01) (SEQ ID NO: 1075) STREKNSQV (B08.01) (SEQ ID NO: 1076) VYRRKHQEL (A24.02, B08.01) (SEQ ID NO: 1077)	NSCLC
FGFR3: TACC3	FGFR3: TACC3	EGHRMDKPANCTHDLYM IMRECWAAPSQRPTFKQ LVEDLDRVLTVTSTD::VK ATQEENRELRSRCEELH GKNLELGKIMDRFEEVV YQAMEEVQKQKELS (SEQ ID NO: 243)	VLTVTSTDV (A02.01) (SEQ ID NO: 1078) VLTVTSTDVK (A03.01) (SEQ ID NO: 1079)	Bladder Cancer, LUSC
NAB:S TAT6	NAB:ST AT6 “”	RDNTLLRRVELFSLSRQ VARESTYLSSLKGSRLHPE ELGGPPLKCLKQE::ATSK SQIMSLWGLVSKMPPEK VQRLYVDFPQHLRHLLG DWLESQPWEFLVGSDAF CC (SEQ ID NO: 244)	IMSLWGLVS (A02.01) (SEQ ID NO: 1080) IMSLWGLVSK (A03.01) (SEQ ID NO: 1081) KLKQEATSK (A03.01) (SEQ ID NO: 1082) QIMSLWGLV (A02.01) (SEQ ID NO: 1083) SQIMSLWGL (A02.01, A24.02, B08.01) (SEQ ID NO: 1084) SQIMSLWGLV (A02.01) (SEQ ID NO: 1085) TSKSQIMSL (B08.01) (SEQ ID NO: 1086)	Solitary fibrous tumors
NDRG1 :ERG	NDRG1 :ERG	MSREMQDVDLAEVKPLV EKGETITGLLQEFDVQ::EA LSVVSEDQSLFECAYGTP HLAKTEMTASSSDYGQT SKMSPRVPQQDW (SEQ ID NO: 245)	LLQEFDVQEA (A02.01) (SEQ ID NO: 1087) LQEFDVQEAL (A02.01) (SEQ ID NO: 1088)	Prostate Cancer
PML:R ARA	PML:R ARA (exon3:e xon3)	VLDMHGFLRQALCRLRQ EEPQSLQAAVRTDGFDEF KVRLQDLSSCITQGK:A:IE TQSSSSEEIVSPSPPLPR IYKPCFVCQDKSSGYHYG VSACEGCKG (SEQ ID NO: 246)		Acute promyelocytic leukemia

PML:R ARA	PML:R ARA (exon6:exon3)	RSSPEQPRPSTSKAVSPPH LDGPPSPRSPVIGSEVFLP NSNHVASGAGEA: A:IETQ SSSSEEIVSPSPSPPLPRI YKPCFVCQDKSSGYHYG VSACEGCKG (SEQ ID NO: 247)		Acute promyelocytic leukemia
RUNX1	RUNX1 (ex5)- RUNX1 T1(ex2)	VARENDLRFVGRSGRGKS FTLTITVFTNPPQVATYHR AIKITVDGPREPR: N:RTEK HSTMPDSPVDVKTQSRL TPPTMPPPPPTTQGAPRTS SFTPTTLTNGT (SEQ ID NO: 248)	GPREFRNRT (B07.02) (SEQ ID NO: 1089) RNRTEKHSTM (B08.01) (SEQ ID NO: 1090)	AML

TMPRS S2:ERG	TMPRS S2:ERG	MALNS::EALSVVSEDQSL FECAYGTPHLAKTEMTAS SSSDYGQTSKMSRPVPPQ DW (SEQ ID NO: 249)	ALNSEALSV (A02.01) (SEQ ID NO: 1091) ALNSEALSVV (A02.01) (SEQ ID NO: 1092) MALNSEALSV (A02.01, B08.01) (SEQ ID NO: 1093)	Prostate Cancer
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Table 9

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
AKT1	E17K	MSDVAIVKEGWLH KRGK <u>Y</u> IKTWRPRYF LLKNDGTFIGYKERP QDVDQREAPLNNFS VAQCQLMKTER (SEQ ID NO: 1094)	KYIKTWRPRY (A24.02) (SEQ ID NO: 1104) WLHKRGKYI (A02.01, B07.02, B08.01) (SEQ ID NO: 1105) WLHKRGKYIK (A03.01) (SEQ ID NO: 1106)	BRCA, CESC, HNSC, LUSC, PRAD, SKCM, THCA
ANAPC1	T537A	TMLVLEGSGNLVLY TGVVRVGKVFIPGLP APSLTMSNTMPRPST PLDGVSAPKPLSKLL GSLDEVVLLSPVPEL RDSSKLHDSLYNED CTFQQLGTYIHSI (SEQ ID NO: 1095)	APKPLSKLL (B07.02) (SEQ ID NO: 1107) GVSAPKPLSK (A03.01) (SEQ ID NO: 1108) VSAPKPLSK (A03.01) (SEQ ID NO: 1109)	GBM, LUSC, PAAD, PRAD, SKCM
FGFR3	S249C	HRIGGIKLRHQQWS LVMESVVPSPDRGNY TCVVENKFGSIRQTY TLDVLER <u>C</u> PHRPILQ AGLPANQTAVLGSD VEFHCKVYSDAQPH IQWLKHVEVNGSKV G (SEQ ID NO: 129)	CPHRPILQA (B07.02) (SEQ ID NO: 1110)	BLCA, HNSC, KIRP, LUSC
FRG1B	I10T	MREPIYMHSTMVFL PWELHTKKGSPPE QFMAVKLSDSRTAL KSGYGKYLGINSE LVGHSDAIGPREQW EPVFQNGKMALLAS NSCFIR (SEQ ID NO: 1096)	KLSDSRTAL (A02.01, B07.02, B08.01) (SEQ ID NO: 1111) KLSDSRTALK (A03.01) (SEQ ID NO: 1112) LSDSRTALK (A01.01, A03.01) (SEQ ID NO: 1113) RTALKSGYGK (A03.01) (SEQ ID NO: 1114) TALKSGYGK (A03.01) (SEQ ID NO: 1115)	KIRP, PRAD, SKCM
FRG1B	L52S	AVKLSDSRIALKSGY GKYLGINSELDVGH SDAIGPREQWEPVF QNGKMAL <u>S</u> ASNSCF IRCNEAGDIEAKSKT AGEEEMIKIRSCAEK ETKKKDDIPEEDKG (SEQ ID NO: 130)	ALSASNSCF (A02.01, A24.02, B07.02) (SEQ ID NO: 1116) ALSASNSCFI (A02.01) (SEQ ID NO: 1117) FQNGKMALSA (A02.01, B08.01) (SEQ ID NO: 1118)	GBM, KIRP, PRAD, SKCM

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
HER2	L755S (Resistance)	AMPNQAQMRLKET ELRKVKVLGSGAFG TVYKGIWIPDGENV KIPVAIKV <u>S</u> RENTSP KANKEILDEAYVMA GVGSPYVSRLLGICL TSTVQLVTQLMPYG C (SEQ ID NO: 1097)	KVSRENTSPK (A03.01) (SEQ ID NO: 1119)	BRCA
IDH1	R132G	RVEEFKLKQMWKSP NGTIRNILGGTVFRE AIICKNIPRLVSGWV KPIIIGG <u>H</u> AYGDQYR ATDFVVPGPVKVEIT YTPSDGTQKVTYLV HNFEEGGGVAMGM (SEQ ID NO: 134)	KPIIIGGHAY (B07.02) (SEQ ID NO: 1120)	BLCA, BRCA, CRC, GBM, HNSC, LUAD, PAAD, PRAD, UCEC
KRAS	G12C	MTEYKLVVVGAC <u>G</u> VGKSALTILQIQLNHF VDEYDPTIEDSYRK QVVIDGETCLLDILD TAGQE (SEQ ID NO: 104)	KLVVVGACGV (A02.01) (SEQ ID NO: 250) LVVVVGACGV (A02.01) (SEQ ID NO: 251) VVGACGVGK (A03.01, A11.01) (SEQ ID NO: 252) VVVGACGVGK (A03.01) (SEQ ID NO: 253)	BRCA, CESC, CRC, HNSC, LUAD, PAAD, UCEC
KRAS	G12D	MTEYKLVVVGAD <u>G</u> VGKSALTILQIQLNHF VDEYDPTIEDSYRK QVVIDGETCLLDILD TAGQE (SEQ ID NO: 105)	VVGADGVGK (A11.01) (SEQ ID NO: 254) VVVGADGVGK (A11.01) (SEQ ID NO: 255) KLVVVGADGV (A02.01) (SEQ ID NO: 256) LVVVVGADGV (A02.01) (SEQ ID NO: 257)	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRP, LIHC, LUAD, PAAD, SKCM, UCEC
KRAS	G12V	MTEYKLVVVGAV <u>G</u> VGKSALTILQIQLNHF VDEYDPTIEDSYRK QVVIDGETCLLDILD TAGQE (SEQ ID NO: 106)	KLVVVGAVGV (A02.01) (SEQ ID NO: 258) LVVVGAVGV (A02.01) (SEQ ID NO: 259) VVGAVGVGK (A03.01, A11.01) (SEQ ID NO: 260) VVVGAVGVGK (A03.01, A11.01) (SEQ ID NO: 261)	BRCA, CESC, CRC, LUAD, PAAD, THCA, UCEC
KRAS	Q61H	AGGVGKSALTILQIQLNHFVDEYDPTIEDSYRKQVVIDGETCLLDILDTAG <u>H</u> EEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIKRVKDSDEVPM (SEQ ID NO: 107)	ILDTAGHEEY (A01.01) (SEQ ID NO: 262)	CRC, LUSC, PAAD, SKCM, UCEC

KRAS	Q61L	AGGVGKSALTIQLIQ NHFVDEYDPTIEDSY RKQVVIDGETCLLDI LDTAGL <u>E</u> EYSAMRD QYMRTGEGFLCVFA INNTKSFEDIHHYRE QIKRVKDSEDVPM (SEQ ID NO: 108)	ILDTAGLEEY (A01.01) (SEQ ID NO: 263) LLDILDTAGL (A02.01) (SEQ ID NO: 264)	CRC, GBM, HNSC, LUAD, SKCM, UCEC
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Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
NRAS	Q61K	AGGVGKSALTIQLIQ NHFVDEYDPTIEDSY RKQVVIDGETCLLDI LDTAGKEEYSAMRD QYMRTGEGFLCVFA INNSKSFADINLYRE QIKRVKDSDDVPM (SEQ ID NO: 109)	ILDTAGKEEY (A01.01) (SEQ ID NO: 265)	BLCA, CRC, LIHC, LUAD, LUSC, SKCM, THCA, UCEC
NRAS	Q61R	AGGVGKSALTIQLIQ NHFVDEYDPTIEDSY RKQVVIDGETCLLDI LDTAGREEYSAMRD QYMRTGEGFLCVFA INNSKSFADINLYRE QIKRVKDSDDVPM (SEQ ID NO: 110)	ILDTAGREEY (A01.01) (SEQ ID NO: 266)	BLCA, CRC, LUSC, PAAD, PRAD, SKCM, THCA, UCEC
PIK3CA	E542K	IEEHANWSVSREAG FSYSHAGLSNRLAR DNELRENDKEQLKA ISTRDPLSKITEQEKD FLWSHRHYCVTIPEI LPKLLLSVKWNSRD EVAQMYCLVKDWP P (SEQ ID NO: 144)	AISTRDPLSK (A03.01) (SEQ ID NO: 1121)	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRC, KIRP, LIHC, LUAD, LUSC, PRAD, UCEC
PTEN	R130Q	KFNCRVAQYPFEDH NPPQLELIKPFCEDL DQWLSEDDNHVAAI HCKAGKGQTGVMIC AYLLHRGKFLKAQE ALDFYGEVRTRDKK GVTIPSQRRYVYYY SY (SEQ ID NO: 148)	QTGVMICAY (A01.01) (SEQ ID NO: 1122)	BRCA, CESC, CRC, GBM, KIRC, LUSC, UCEC
RAC1	P29S	MQAICVVGVDGA VGKTCLLISYTTNAF SGEYIPTVFDNYSAN VMVDGKPVNLGLW DTAGQEDYDRLRPL SYPQTVGET (SEQ ID NO: 149)	FSGEYIPTV (A02.01) (SEQ ID NO: 1123) TTNAFSGEY (A01.01) (SEQ ID NO: 1124) YTTNAFSGEY (A01.01) (SEQ ID NO: 1125)	Melanoma

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
SF3B1	K700E	AVCKSKKSWQARH TGIKIVQQIAILMGC AILPHLRSLVEIIEHG LVDEQQEVRTISALA IAALAEAATPYGIES FDSVLKPLWKGIRQ HRGKGLAAFLKAI (SEQ ID NO: 1098)	GLVDEQQEV (A02.01) (SEQ ID NO: 1126)	AML associated with MDS; Chronic lymphocytic leukaemia-small lymphocytic lymphoma; Myelodysplastic syndrome; AML; Luminal NS carcinoma of breast; Chronic myeloid leukaemia; Ductal carcinoma of pancreas; Chronic myelomonocytic leukaemia; Chronic lymphocytic leukaemia-small lymphocytic lymphoma; Myelofibrosis; Myelodysplastic syndrome; PRAD; Essential thrombocythaemia ; Medullomyoblastoma
SPOP	F133L	YLSLYLLLVSCPKSE VRAKFKFSILNAKGE ETKAMESQRAYRFV QGKDWGLKKFIRRD FLLDEANGLLPDDK LTLFCEVSVVQDSV NISGQNTMNMVKVP E (SEQ ID NO: 1099)	FVQGKDWGL (A02.01, B08.01) (SEQ ID NO: 1127)	PRAD
SPOP	F133V	YLSLYLLLVSCPKSE VRAKFKFSILNAKGE ETKAMESQRAYRFV QGKDWGVKKFIRRD FLLDEANGLLPDDK LTLFCEVSVVQDSV NISGQNTMNMVKVP E (SEQ ID NO: 1100)	FVQGKDWGV (A02.01) (SEQ ID NO: 1128)	PRAD

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
TP53	G245S	IRVEGNLRVEYLDD RNTFRHSVVVPYEP EVGSDCTTIHYNM CNSSCMGSMNRRPI LTIITLEDSSGNLLGR NSFEVRVCACPGRD RRTEENLRKKGEP (SEQ ID NO: 150)	CMGSMNRRPI (A02.01, B08.01) (SEQ ID NO: 1129) GSMNRRPIL (B08.01) (SEQ ID NO: 1130) MGSMNRRPI (B08.01) (SEQ ID NO: 1131) MGSMNRRPIL (B08.01) (SEQ ID NO: 1132) SMNRRPILTI (A02.01, A24.02, B08.01) (SEQ ID NO: 1133)	BLCA, BRCA, CRC, GBM, HNSC, LUSC, PAAD, PRAD
TP53	R248Q	EGNLRVEYLDDRNT FRHSVVVPYEPPEV GSDCTTIHYNMCMN SSCMGGMNQRPI ITLEDSSGNLLGRNS FEVRVCACPGRRR TEENLRKKGEP HHE (SEQ ID NO: 152)	CMGGMNQRPI (A02.01, B08.01) (SEQ ID NO: 1134) GMNQRPI (A02.01, B08.01) (SEQ ID NO: 1135) NQRPI (A02.01, B08.01) (SEQ ID NO: 1136)	BLCA, BRCA, CRC, GBM, HNSC, KIRC, LIHC, LUSC, PAAD, PRAD, UCEC
TP53	R248W	EGNLRVEYLDDRNT FRHSVVVPYEPPEV GSDCTTIHYNMCMN SSCMGGMNWRPI IITLEDSSGNLLGRNS FEVRVCACPGRRR TEENLRKKGEP HHE (SEQ ID NO: 153)	CMGGMNWRPI (A02.01, A24.02, B08.01) (SEQ ID NO: 1137) GMNWRPI (A02.01, B08.01) (SEQ ID NO: 1138) MNWRPI (A02.01, A24.02, B08.01) (SEQ ID NO: 1139) MNWRPI (A02.01, A24.02) (SEQ ID NO: 1140)	BLCA, BRCA, CRC, GBM, HNSC, LIHC, LUSC, PAAD, SKCM, UCEC
TP53	R273C	PEVGSDCTTIHYNM MCNSSCMGGMNRR PILTIITLEDSSGNLL GRNSFEVVCACPG RDRRTEENLRKKG EPHHELPPGSTRAL PNNTSSSPQPKKPL (SEQ ID NO: 154)	NSFEVVCAC (A02.01) (SEQ ID NO: 1141)	BLCA, BRCA, CRC, GBM, HNSC, LUSC, PAAD, UCEC
TP53	R273H	PEVGSDCTTIHYNM MCNSSCMGGMNRR PILTIITLEDSSGNLL GRNSFEVHVCACPG RDRRTEENLRKKG EPHHELPPGSTRAL PNNTSSSPQPKKPL (SEQ ID NO: 1101)	NSFEVHVCAC (A02.01) (SEQ ID NO: 1142)	BRCA, CRC, GBM, HNSC, LIHC, LUSC, PAAD, UCEC
TP53	Y220C	TEVVRRCPPHERCS DSDGLAPPQHILRVE GNLRVEYLDDRNTF RHSVVVPCEPPEVGS DCTTIHYNMCMNSS CMGGMNRRPILTIIT LEDSSGNLLGRNSF (SEQ ID NO: 1102)	VVPCEPPEV (A02.01) (SEQ ID NO: 1143) VVVPCEPPEV (A02.01) (SEQ ID NO: 1144)	BLCA, BRCA, GBM, HNSC, LIHC, LUAD, LUSC, PAAD, SKCM, UCEC

Gene	Amino Acid Alteration	Mutation Sequence Context	Peptides (HLA allele example(s))	Exemplary Diseases
MSH6	F1088fs; +1	YNFDKNYKDWQSA VECIAVLDVLLCLA NYSRGGDGPMCRPV ILLPEDTPPLLRA (SEQ ID NO: 1103)	ILLPEDTPPL (A02.01) (SEQ ID NO: 1145) LLPEDTPPL (A02.01) (SEQ ID NO: 1146)	MSI+ CRC, MSI+ Uterine/Endometrium Cancer, MSI+ Stomach Cancer, Lynch syndrome
APC	F1354fs	<u>AKFQQCHSTLEPNP</u> <u>ADCRVLVYLQNQPG</u> <u>TKLLNFLQERNLPPK</u> <u>VVLRHPKVHLNTMF</u> <u>RRPHSCLADVLLSV</u> <u>HLIVLRVVRLPAPFR</u> <u>VNHAVEW*</u> (SEQ ID NO: 191)	APFRVNHAV (B07.02) (SEQ ID NO: 1147) CLADVLLSV (A02.01) (SEQ ID NO: 1148) FLQERNLPPK (A03.01) (SEQ ID NO: 1149) HLIVLRVVRL (A02.01, B08.01) (SEQ ID NO: 1150) HPKVHLNTM (B07.02, B08.01) (SEQ ID NO: 1151) HPKVHLNTMF (B07.02, B08.01) (SEQ ID NO: 1152) KVHLNTMFR (A03.01) (SEQ ID NO: 1153) KVHLNTMFRR (A03.01) (SEQ ID NO: 1154) LPAPFRVNHA (B07.02) (SEQ ID NO: 1155) MFRRPHSCL (B07.02, B08.01) (SEQ ID NO: 1156) MFRRPHSCLA (B08.01) (SEQ ID NO: 1157) NTMFRRPHSC (B08.01) (SEQ ID NO: 1158) RPHSCLADV (B07.02) (SEQ ID NO: 1159) RPHSCLADV (B07.02) (SEQ ID NO: 1160) RVVRLPAPFR (A03.01) (SEQ ID NO: 1161) SVHLIVLRV (A02.01) (SEQ ID NO: 1162) TMFRRPHSC (B08.01) (SEQ ID NO: 1163) TMFRRPHSCL (A02.01, B08.01) (SEQ ID NO: 1164) VLLSVHLIV (A02.01) (SEQ ID NO: 1165) VLLSVHLIVL (A02.01) (SEQ ID NO: 1166) VLRVVRLPA (B08.01) (SEQ ID NO: 1167) VVRLPAPFR (A03.01) (SEQ ID NO: 1168)	CRC, LUAD, UCEC, STAD

[0262] Table 10 shows HLA affinity and stability of selected BTK peptides:

Table 10

Gene	HLA Allele	Peptide Sequence	SEQ ID NO:	Affinity (nM)	Stability (half-life (hr.))
BTK, C481S	A01.01	YMANGSLLNY	1169	13.24495	0.866167
BTK, C481S	A01.01	MANGSLLNY	1170	439.029	0.216408
BTK, C481S	A03.01	MANGSLLNY	1170	35.62463	0.237963
BTK, C481S	A03.01	YMANGSLLNY	1169	95.93212	0.279088
BTK, C481S	A11.01	MANGSLLNY	1170	535.6333	NB
BTK, C481S	A11.01	YMANGSLLNY	1169	974.2881	NB
BTK, C481S	A24.02	EYMANGSLL	1171	4.961145	5.716141
BTK_C481S	A02.01	SLLNYLREM	1172	67.69132	3.043604
BTK_C481S	A02.01	MANGSLLNYL	1173	1006.566	0

BTK_C481S	A02.01	YMANGSLLN	1174	3999.442	0
BTK_C481S	B07.02	SLLNYLREM	1172	865.8805	0
BTK_C481S	B07.02	MANGSLLNYL	1173	16474.59	0
BTK_C481S	B08.01	SLLNYLREM	1172	959.6542	0
BTK_C481S	B08.01	MANGSLLNYL	1173	18463.09	0

[0263] Table 11 shows HLA affinity and stability of selected EGFR peptides:

Table 11

Gene	HLA Allele	Peptide Sequence	SEQ ID NO:	Affinity (nM)	Stability (half-life (hr.))
EGFR, T790M	A01.01	LTSTVQLIM	1175	2891.111	0.103721
EGFR_T790M	A01.01	CLTSTVQLIM	1176	8276.876	0
EGFR_T790M	A02.01	MQLMPFGCLL	1177	16.26147	0.381118
EGFR_T790M	A02.01	MQLMPFGCL	1178	116.3352	0.368273
EGFR_T790M	A02.01	LIMQLMPFGC	1179	132.4766	0.381284
EGFR_T790M	A02.01	QLIMQLMPF	1180	192.8406	0.34067
EGFR_T790M	A02.01	CLTSTVQLIM	1176	537.1391	0
EGFR_T790M	A02.01	IMQLMPFGCL	1181	653.1065	0.515559
EGFR_T790M	A02.01	IMQLMPFGC	1182	1205.368	0.370112
EGFR_T790M	A02.01	LIMQLMPFG	1183	3337.708	0
EGFR_T790M	A02.01	VQLIMQLMPF	1184	4942.892	0
EGFR_T790M	A02.01	QLIMQLMPFG	1185	5214.668	0
EGFR_T790M	A02.01	STVQLIMQL	1186	7256.773	0
EGFR_T790M	A24.02	QLIMQLMPF	1180	2030.807	0.368673
EGFR_T790M	A24.02	VQLIMQLMPF	1184	4103.131	0
EGFR_T790M	A24.02	IMQLMPFGCL	1181	14119.38	0
EGFR_T790M	A24.02	MQLMPFGCLL	1177	18857.47	0
EGFR_T790M	B07.02	MQLMPFGCL	1178	1589.188	0
EGFR_T790M	B08.01	QLIMQLMPF	1180	330.1933	0
EGFR_T790M	B08.01	IMQLMPFGCL	1181	427.3913	0
EGFR_T790M	B08.01	MQLMPFGCL	1178	4931.727	0
EGFR_T790M	B08.01	MQLMPFGCLL	1177	11244.9	0
EGFR_T790M	B08.01	VQLIMQLMPF	1184	16108.18	0
EGFR_T790M	B08.02	QLIMQLMPF	1180	5590.3	ND

as pancreatic adenocarcinoma (PDACs). CAFs express Col10a1 antigen. CAFs are cells that may help perpetuate a tumor. Col10A1 often confers negative prognosis for the tumor. In some embodiments Col10A1 may be considered as a biomarker for tumor sustenance and progression. It is a 680 amino acid long heterodimer protein associated with poor prognosis in breast cancer and colorectal cancers.

[0268] Activation of Col10a1 specific CD8+ T cells and CD4+ T cells may help attack and destruction of Col10A1 specific fibroblasts and help break down the tissue matrix of solid tumors.

[0269] T cells can be generated ex vivo using the method described herein, so that the T cells are activated against cancer-associated fibroblasts (CAFs). For this, Col10a1 peptides comprising epitopes that can specifically activate T cells were generated, and the HLA binding partner determined, using the highly reliable data generated from the in-house generated machine learning epitope presentation software described previously as described in Table 12.

Table 12

Peptide	SEQ ID NO:	HLA Allele	Rank on HLA allele
FTCQIPGIYY	1187	HLA-A01:01	1
GSDGKPGY	1188	HLA-A01:01	2
NAESNGLY	1189	HLA-A01:01	3
LTENDQVWL	1190	HLA-A01:01	4
GTHVWVGLY	1191	HLA-A01:01	5
TYDEYTKGY	1192	HLA-A01:01	6
YTYDEYTKGY	1193	HLA-A01:01	7
FTCQIPGIY	1194	HLA-A01:01	8
NAESNGLYSSEY	1195	HLA-A01:01	9
YLDQASGSA	1196	HLA-A01:01	10
FLLLVSLNL	1197	HLA-A02:01	1
FLLLVSLNLV	1198	HLA-A02:01	2
GLYKNGTPV	1199	HLA-A02:01	3
GLDGPKGNPGL	1200	HLA-A02:01	4
LLLVSLNLV	1201	HLA-A02:01	5
SLSGTPLVSA	1202	HLA-A02:01	6
GLYSSEYV	1203	HLA-A02:01	7
SLSGTPLV	1204	HLA-A02:01	8
MLPQIPFLL	1205	HLA-A02:01	9
GLPGPPGPSA	1206	HLA-A02:01	10
SAFTVILSK	1207	HLA-A03:01	1

AVMPEGFIK	1208	HLA-A03:01	2
GLYKNGTPVMY	1209	HLA-A03:01	3
AIGTPIPFDK	1210	HLA-A03:01	4
GLPGGPGAK	1211	HLA-A03:01	5
ILYNRQQHY	1212	HLA-A03:01	6
AGPPGPPGFGK	1213	HLA-A03:01	7
GIPGFPGSK	1214	HLA-A03:01	8
GTHVWVGLYK	1215	HLA-A03:01	9
GVPGQPGIK	1216	HLA-A03:01	10
AVMPEGFIK	1208	HLA-A11:01	1
SAFTVILSK	1207	HLA-A11:01	2
VSAFTVILSK	1217	HLA-A11:01	3
GTHVWVGLYK	1215	HLA-A11:01	4
AIGTPIPFDK	1210	HLA-A11:01	5
AVMPEGFIKA	1218	HLA-A11:01	6
SSFSGFLVA	1219	HLA-A11:01	7
PVSAFTVILSK	1220	HLA-A11:01	8
GIPGFPGSK	1214	HLA-A11:01	9
GVPGMNGQK	1221	HLA-A11:01	10
AYPAIGTPIPF	1222	HLA-A24:02	1
IGPPGIPGF	1223	HLA-A24:02	2
HYDPRTGIF	1224	HLA-A24:02	3
EYVHSSFSGF	1225	HLA-A24:02	4
AGPPGPPGF	1226	HLA-A24:02	5
YYFSYHVHV	1227	HLA-A24:02	6
AYPAIGTPI	1228	HLA-A24:02	7
PLPNTKTQF	1229	HLA-A24:02	8
MLPQIPFLL	1205	HLA-A24:02	9
CQIPGIYYF	1230	HLA-A24:02	10
RPSLSGTPL	1231	HLA-B07:02	1
LPQIPFLLL	1232	HLA-B07:02	2
IPFLLL VSL	1233	HLA-B07:02	3
LPGPPGPSAV	1234	HLA-B07:02	4
GPIGPPGIPGF	1235	HLA-B07:02	5

IPGPAGISV	1236	HLA-B07:02	6
YPAIGTPIPF	1237	HLA-B07:02	7
SPGPPGPAGI	1238	HLA-B07:02	8
LPGPPGPSA	1239	HLA-B07:02	9
SPGPPGPAG	1240	HLA-B07:02	10
TIKSKGIAV	1241	HLA-B08:01	1
IPFLLLVSL	1233	HLA-B08:01	2
HVHVKGTHV	1242	HLA-B08:01	3
LPNTKTQF	1243	HLA-B08:01	4
LPQIPFLL	1244	HLA-B08:01	5
PFLLLVSL	1245	HLA-B08:01	6
SLNLVHGV	1246	HLA-B08:01	7
LPQIPFLLL	1232	HLA-B08:01	8
TGMPVSAF	1247	HLA-B08:01	9
TPIPFDKIL	1248	HLA-B08:01	10

[0270] Neoantigenic peptides provided herein are prevalidated for HLA binding immunogenicity (Tables 1-12). In some embodiments the neoantigenic peptides, prepared and stored earlier, are used to contact an antigen presenting cell (APC) to then allow presentation to a T cell in vitro for preparation of neoantigen-specific activated T cell. In some embodiments, between 2-80 or more neoantigenic peptides are used to stimulate T cells from a patient at a time.

[0271] In some embodiments the APC is an autologous APC. In some embodiments the APC is a non-autologous APC. In some embodiments the APC is a synthetic cell designed to function as an APC. In some embodiments the T cell is an autologous cell. In some embodiments, an antigen presenting cell is a cell that expresses an antigen. For example, an antigen presenting cell may be a phagocytic cell such as a dendritic cell or myeloid cell, which process an antigen after cellular uptake and presents the antigen in association with an MHC for T cell activation. For certain purposes, an APC as used herein is a cell that normally presents an antigen on its surface. In a non-binding or non-limiting example, relevant to certain cytotoxicity assays as described herein, a tumor cell is an antigen presenting cell, that the T cell can recognize an antigen presenting cell (tumor cell). Similarly, a cell or cell line expressing an antigen can be, for certain purposes as used herein, an antigen presenting cell.

[0272] In some embodiments, one or more polynucleotides encoding one or more neoantigenic peptides may be used to express in a cell to present to a T cell for activation in vitro. The one or more polynucleotides encoding one or more of the neoantigenic peptides are encoded in a vector. In some embodiments, the composition comprises from about 2 to about 80 neoantigenic polynucleotides. In some embodiments, at least

the antigen presenting cells are non-infected cells. In embodiments, the antigen presenting cells are autologous. In embodiments, the antigen presenting cells have been treated to strip endogenous MHC-associated peptides from their surface. In embodiments, the treatment to strip the endogenous MHC-associated peptides comprises culturing the cells at about 26°C. In embodiments, the treatment to strip the endogenous MHC-associated peptides comprises treating the cells with a mild acid solution. In embodiments, the antigen presenting cells have been pulsed with at least one neoantigenic peptide described herein. In embodiments, pulsing comprises incubating the antigen presenting cells in the presence of at least about 2 µg/ml of each of at least one neoantigenic peptide described herein. In embodiments, ratio of isolated T cells to antigen presenting cells is between about 30:1 and 300:1. In embodiments, the incubating the isolated population of T cells is in the presence of IL2 and IL-7. In embodiments, the MHC of the MHC-peptide is MHC class I or class II.

[0278] Provided herein is a composition comprising activated tumor specific T cells produced by a method described herein.

[0279] Provided herein is a method of treating cancer in a subject comprising administering to the subject a therapeutically effective amount of activated tumor specific T cell described herein, or produced by a method described herein. In embodiments, the administering comprises administering from about 10^6 to 10^{12} , from about 10^8 to 10^{11} , or from about 10^9 to 10^{10} of the activated tumor specific T cells.

[0280] Provided herein is a nucleic acid comprising a promoter operably linked to a polynucleotide encoding the T cell receptor described herein. In embodiments, the TCR is capable of binding the at least one neoantigenic peptide in the context of major histocompatibility complex (MHC) class I or class II. In some embodiments, provided herein is a TCR comprising a TCR alpha chain and a TCR beta chain capable of binding to a mutated RAS epitope in complex with an MHC encoded by a C03:04 or a 03:03 HLA molecule. A TCR can be identified that specifically binds to an epitope, e.g., a mutant RAS epitope as described herein, for example, by isolating and sequencing TCRs from T cells that can bind to and are activated by the antigen-MHC complex. In some embodiments, provided herein are TCRs that can bind to an antigen comprising a GACGVGKSA epitope (SEQ ID NO: 1) in complex with a protein encoded by an HLA-C03:04 allele. In some embodiments, provided herein are TCRs that can bind to an antigen comprising a GAVGVGKSA epitope (SEQ ID NO: 2) in complex with a protein encoded by the HLA-C03:03 allele. In some embodiments, the TCR is modified. Also provided herein is a nucleic acid molecule comprising a sequence encoding a TCR alpha chain and/or a TCR beta chain that can bind to an antigen comprising a GACGVGKSA epitope (SEQ ID NO: 1) in complex with a protein encoded by an HLA-C03:04 allele. Also provided herein is a nucleic acid molecule comprising a sequence encoding a TCR alpha chain and/or a TCR beta chain that can bind to an antigen comprising a GAVGVGKSA epitope (SEQ ID NO: 2) in complex with a protein encoded by the HLA-C03:03 allele.

monitor complex formation. Dissociation is initiated by addition of higher concentrations of unlabeled light-chain and incubation at 37°C. Stability is defined as the length of time in hours it takes for half of the complexes to dissociate, as measured by scintillation counts.

[0312] To assess whether antigens could be processed and presented from the larger polypeptide context, peptides eluted from HLA molecules isolated from cells expressing the genes of interest were analyzed by tandem mass spectrometry (MS/MS).

[0313] For analysis of presentation of RAS neoantigens, cell lines were utilized that have RAS mutations naturally or were lentivirally transduced to express the mutated RAS gene. HLA molecules were either isolated based on the natural expression of the cell lines or the cell lines were lentivirally transduced or transiently transfected to express the HLA of interest. 293T cells were transduced with a lentiviral vector encoding various regions of a mutant RAS peptide. Greater than 50 million cells expressing peptides encoded by a mutant RAS peptide were cultured and peptides were eluted from HLA-peptide complexes using an acid wash. Eluted peptides were then analyzed by targeted MS/MS with parallel reaction monitoring (PRM). For 293T cells lentivirally transduced with both a RAS^{G12V} mutation and an HLA-A*03:01 gene, the peptide with amino acid sequence vvvgaVgvgk (SEQ ID NO: 3) was detected by mass spectrometry. Spectral comparison to its corresponding stable heavy-isotopically labeled synthetic peptide (**FIG. 5**) showed mass accuracy of the detected peptide to be less than 5 parts per million (ppm). Endogenous peptide spectrum is shown in the top panel and the corresponding stable heavy-isotopically labeled spectrum is shown in the bottom panel. For SW620 cells naturally expressing a RAS^{G12V} mutation and lentivirally transduced with the HLA-A*03:01 gene, the peptide with amino sequence vvvgaVgvgk (SEQ ID NO: 3) was detected by mass spectrometry.

HLA Class I Binding and Stability

[0314] A subset of the peptides used for affinity measurements were also used for stability measurements using the assay described (n=275). These data are shown in Table 3. Less than 50 nM was considered by the field as a strong binder, 50-150 nM was considered an intermediate binder, 150-500 nM was considered a weak binder, and greater than 500 nM was considered a very weak binder. The connection between the observed stability and observed affinity was evident by the decreasing median stability across these binned stability intervals. However, there is considerable overlap between the bins, and importantly there are epitopes in all bins with observed stability in the multiple hour range, including the very weak binders.

[0315] Immunogenicity assays are used to test the ability of each test peptide to expand T cells. Mature professional APCs are prepared for these assays in the following way. Monocytes are enriched from healthy human donor PBMCs using a bead-based kit (Miltenyi). Enriched cells are plated in GM-CSF and IL-4 to induce immature DCs. After 5 days, immature DCs are incubated at 37°C with each peptide for 1 hour before addition of a cytokine maturation cocktail (GM-CSF, IL-1 β , IL-4, IL-6, TNF α , PGE1 β). Cells are

of cytokines by CD4⁺ T cells (e.g., IFN γ and TNF α) are assessed by intracellular staining. These cytokines, especially IFN γ , used to identify stimulated cells.

[0324] In some embodiments the immunogenicity is measured by measuring a protein or peptide expressed by the T cell, using ELISpot assay. Peptide-specific T cells are functionally enumerated using the ELISpot assay (BD Biosciences), which measures the release of IFN γ from T cells on a single cell basis. Target cells (T2 or HLA-A0201 transfected C1Rs) were pulsed with 10 μ M peptide for one hour at 37 degrees C, and washed three times. 1×10^5 peptide-pulsed targets are co-cultured in the ELISPOT plate wells with varying concentrations of T cells (5×10^2 to 2×10^3) taken from the immunogenicity culture. Plates are developed according to the manufacturer's protocol, and analyzed on an ELISPOT reader (Cellular Technology Ltd.) with accompanying software. Spots corresponding to the number of IFN gamma-producing T cells are reported as the absolute number of spots per number of T cells plated. T cells expanded on modified peptides are tested not only for their ability to recognize targets pulsed with the modified peptide, but also for their ability to recognize targets pulsed with the parent peptide. Some exemplary data are shown below in Table 13.

Table 13

Peptide	SEQ ID NO:	Allele	Gene	Predicted Affinity (nM)	RECON Percent Rank	Immunogenicity (# donors/2)
SLQCVSLHL	1249	HLA-A02:01	KLK2	39.4	0.4	
LVLSIALSV	1250	HLA-A02:01	KLK2	54.9	1.1	
VILGVHLSV	1251	HLA-A02:01	KLK2	62.1	0.4	
VLAPQESSV	1252	HLA-A02:01	KLK2	65.7	0.08	
SLQCVSLHLL	1253	HLA-A02:01	KLK2	90.3	0.4	
MLLRLSEPA	1254	HLA-A02:01	KLK2;KLK3	56	2.5	
LTMPALPMV	1255	HLA-A02:01	KLK3	14.3	1.1	
FLTLSVTWIA	1256	HLA-A02:01	KLK3	16.9	3.5	
KLQCVDLHV	1257	HLA-A02:01	KLK3	21.2	0.3	
*FLTPKKLQCV	1258	HLA-A02:01	KLK3	126.4	0.17	1
FLRPGDDSTL	1259	HLA-A02:01	KLK3	982.7	0.4	
*FLGYLILGV	1260	HLA-A02:01	KLK4	6.3	0.05	1
*LLANDLMLI	1261	HLA-A02:01	KLK4	10.7	0.4	2
*FQNSYTIGL	1262	HLA-A02:01	KLK4	15.1	1.6	2
MLIKLDESV	1263	HLA-A02:01	KLK4	17.6	0.25	
VLQCVNVSV	1264	HLA-A02:01	KLK4	19.2	0.1	

*LLANGRMPTV	1265	HLA-A02:01	KLK4	25.9	0.25	2
*ILNDTGCHYV	1266	HLA-A02:01	TGM4	17.2	0.1	1
*FQYPEFSIEL	1267	HLA-A02:01	TGM4	21.2	1	1
ILGKYQLNV	1268	HLA-A02:01	TGM4	22	0.3	
LLGNSVNFTV	1269	HLA-A02:01	TGM4	27.8	0.7	
*VLDCCISLL	1270	HLA-A02:01	TGM4	30.6	0.4	1
ILGSFELQL	1271	HLA-A02:01	TGM4	31.2	0.25	
*RLIWLVKMV	1272	HLA-A02:01	TGM4	64.4	0.17	1
VLLGNSVNFTV	1273	HLA-A02:01	TGM4	83.7	0.6	
TLAIPLTDV	1274	HLA-A02:01	TGM4	149.2	0.25	

[0325] CD107a and CD107b are expressed on the cell surface of CD8⁺ T cells following activation with cognate peptide. The lytic granules of T cells have a lipid bilayer that contains lysosomal-associated membrane glycoproteins (“LAMPs”), which include the molecules CD107a and b. When cytotoxic T cells are activated through the T cell receptor, the membranes of these lytic granules mobilize and fuse with the plasma membrane of the T cell. The granule contents are released, and this leads to the death of the target cell. As the granule membrane fuses with the plasma membrane, CD107a and b are exposed on the cell surface, and therefore are markers of degranulation. Because degranulation as measured by CD107a and b staining is reported on a single cell basis, the assay is used to functionally enumerate peptide-specific T cells. To perform the assay, peptide is added to HLA-A0201-transfected cells C1R to a final concentration of 20 μ M, the cells were incubated for 1 hour at 37 degrees C, and washed three times. 1×10^5 of the peptide-pulsed C1R cells were aliquoted into tubes, and antibodies specific for CD107a and b are added to a final concentration suggested by the manufacturer (Becton Dickinson). Antibodies are added prior to the addition of T cells in order to “capture” the CD107 molecules as they transiently appear on the surface during the course of the assay. 1×10^5 T cells from the immunogenicity culture are added next, and the samples were incubated for 4 hours at 37 degrees C. The T cells are further stained for additional cell surface molecules such as CD8 and acquired on a FACS Calibur instrument (Becton Dickinson). Data is analyzed using the accompanying Cellquest software, and results were reported as the percentage of CD8⁺ CD107 a and b⁺ cells.

[0326] Cytotoxic activity is measured using a chromium release assay. Target T2 cells are labeled for 1 hour at 37 degrees C with Na⁵¹Cr and washed. 5×10^3 target T2 cells were then added to varying numbers of T cells from the immunogenicity culture. Chromium release is measured in supernatant harvested after 4 hours of incubation at 37 degrees C. The percentage of specific lysis is calculated as:

Experimental release-spontaneous release/Total release-spontaneous release x 100

[0327] Immunogenicity assays were carried out to assess whether each peptide can elicit a T cell response by antigen-specific expansion. Though current methods are imperfect, and therefore negative results do not imply a peptide is incapable of inducing a response, a positive result demonstrates that a peptide can induce a T cell response. Several peptides from Table 3 were tested for their capacity to elicit CD8⁺ T cell responses with multimer readouts as described. Each positive result was measured with a second multimer preparation to avoid any preparation biases. In an exemplary assay, HLA-A02:01⁺ T cells were co-cultured with monocyte-derived dendritic cells loaded with TMPRSS2::ERG fusion neoepitope (ALNSEALSV (SEQ ID NO: 4); HLA-A02:01) for 10 days. CD8⁺ T cells were analyzed for antigen-specificity for TMPRSS2::ERG fusion neoepitope using multimers (initial: BV421 and PE; validation: APC and BUV396).

[0328] While antigen-specific CD8⁺ T cell responses are readily assessed using well-established HLA Class I multimer technology, CD4⁺ T cell responses require a separate assay to evaluate because HLA Class II multimer technology is not well-established. In order to assess CD4⁺ T cell responses, T cells were re-stimulated with the peptide of interest and compared to a control. In the case of a completely novel sequence (e.g., arising from a frame-shift or fusion), the control was no peptide. In the case of a point-mutation, the control was the WT peptide. After stimulation, production of cytokines by CD4⁺ T cells (e.g., IFN γ and TNF α) were assessed by intracellular staining. These cytokines, especially IFN γ , used to identify stimulated cells. Antigen-specific CD4⁺ T cell responses showed increased cytokine production relative to control.

Example 7. Cell Expansion and Preparation

[0329] To prepare APCs, the following method was employed (a) obtain of autologous immune cells from the peripheral blood of the patient; enrich monocytes and dendritic cells in culture; load peptides and mature DCs.

T cell Induction (Protocol 1)

[0330] First induction: (a) Obtaining autologous T cells from an apheresis bag; (b) Depleting CD25⁺ cells and CD14⁺ cells, alternatively, depleting only CD25⁺ cells; (c) Washing the peptide loaded and mature DC cells, resuspending in the T cell culture media; (d) Incubating T cells with the matured DC.

[0331] Second induction: (a) Washing T cells, and resuspending in T cell media, and optionally evaluating a small aliquot from the cell culture to determine the cell growth, comparative growth and induction of T cell subtypes and antigen specificity and monitoring loss of cell population; (b) Incubating T cells with mature DC.

[0332] Third induction: (a) Washing T cells, and resuspending in T cell media, and optionally evaluating a small aliquot from the cell culture to determine the cell growth, comparative growth and induction of T cell subtypes and antigen specificity and monitoring loss of cell population; (b) Incubating T cells with mature DC.

[0344] The cytotoxic capacity of the induced CD8⁺ responses from said patient was also assessed. Both SRSF1E>K and ARAP1Y>H responses showed a significant upregulation of CD107a on the CD8⁺ T cells and active Caspase3 on the tumor cells transduced with the mutant construct after co-culture.

[0345] Using the stimulation protocol, predicted patient-specific neoantigens, as well as model neoantigens, were confirmed to be immunogenic by the induction of multiple neoantigen-specific CD8⁺ and CD4⁺ T cell responses in patient material. The ability to induce polyfunctional and mutant-specific CD8⁺ and CD4⁺ T cell responses proves the capability of predicting high-quality neoantigens and generating potent T cell responses. The presence of multiple enriched neoantigen-specific T cell populations (memory and de novo) at the end of the stimulation process demonstrates the ability to raise new T cell responses and generate effective cancer immunotherapies to treat cancer patients.

[0346] Exemplary materials for T cell culture are provided below:

[0347] Materials: AIM V media (Invitrogen) Human FLT3L; preclinical CellGenix #1415-050 Stock 50 ng/μL TNFα; preclinical CellGenix #1406-050 Stock 10 ng/μL; IL-1β, preclinical CellGenix #1411-050 Stock 10 ng/μL; PGE1 or Alprostadil – Cayman from Czech republic Stock 0.5 μg/μL; R10 media- RPMI 1640 glutamax + 10% Human serum+ 1% PenStrep; 20/80 Media- 18% AIM V + 72% RPMI 1640 glutamax + 10% Human Serum + 1% PenStrep; IL7 Stock 5 ng/μL; IL15 Stock 5 ng/μL; DC media (Cellgenix); CD14 microbeads, human, Miltenyi #130-050-201, Cytokines and/or growth factors, T cell media (AIM V + RPMI 1640 glutamax + serum + PenStrep), Peptide stocks - 1 mM per peptide (HIV A02 – 5-10 peptides, HIV B07- 5-10 peptides, DOM - 4-8 peptides, PIN - 6-12 peptides).

Example 9. Exemplary KRAS mutations

[0348] Exemplary KRAS mutations, sequences comprising the mutated residue and exemplary diseases are listed below (Table 16).

Table 16

Gene	Exemplary Protein Change	Mutation Sequence Context (Mutated non-native residue underlined)	SEQ ID NO:	Exemplary Diseases
KRAS	G12C	MTEYKLVVVGAC <u>G</u> VGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE	104	BRCA, CESC, CRC, HNSC, LUAD, PAAD, UCEC
KRAS	G12D	MTEYKLVVVGAD <u>G</u> VGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE	105	BLCA, BRCA, CESC, CRC, GBM, HNSC, KIRP, LIHC, LUAD, PAAD, SKCM, UCEC

KRAS	G12V	MTEYKLVVVGA <u>V</u> GVGKSALTIQLIQNHFVD EYDPTIEDSYRKQVVIDGETCLLDILDTAGQE	106	BRCA, CRC, PAAD, UCEC	CESC, LUAD, THCA,
KRAS	Q61H	AGGVGKSALTIQLIQNHFVDEYDPTIEDSYRK QVVIDGETCLLDILDTAG <u>H</u> EEYSAMRDQYMR	107	CRC, PAAD, UCEC	LUSC, SKCM,

		TGEGFLCVFAINNTKSFEDIHHYREQIKRVKD SEDVPM		
KRAS	Q61L	AGGVGKSALTIQLIQNHVDEYDPTIEDSYRK QVVIDGETCLLDILDTAGLEEEYSAMRDQYMR TGEGFLCVFAINNTKSFEDIHHYREQIKRVKD SEDVPM	108	CRC, GBM, HNSC, LUAD, SKCM, UCEC