



(43) International Publication Date
12 November 2020 (12.11.2020)

(51) International Patent Classification:
G01N 33/68 (2006.01) *A61K 39/00* (2006.01)
A61P 35/00 (2006.01)

(21) International Application Number:
PCT/US2020/031357

(22) International Filing Date:
04 May 2020 (04.05.2020)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:

62/842,800	03 May 2019 (03.05.2019)	US
62/880,965	31 July 2019 (31.07.2019)	US
62/932,651	08 November 2019 (08.11.2019)	US
62/932,654	08 November 2019 (08.11.2019)	US

(72) Inventors; and
(71) Applicants: **RICHARD, Guilhem** [US/US]; c/o EpiVax Oncology, Inc., 180 Varick Street Suite 665, New York, NY 10014 (US). **SWEIS, Randy, F.** [US/US]; c/o The University of Chicago, 5801 South Ellis Avenue, Chicago, IL 60637 (US). **ARDITO, Matthew** [US/US]; c/o EpiVax, Inc., 188 Valley Street, Suite 44, Providence, RI 02909 (US). **GARCIA, Tzintzuni** [US/US]; c/o The University of Chicago, 5801 South Ellis Avenue, Chicago, IL 60637 (US). **MOISE, Leonard** [US/US]; c/o EpiVax, Inc., 188 Valley Street, Suite 44, Providence, RI 02909 (US). **PRINCIOTTA, Michael, F.** [US/US]; c/o EpiVax Oncology, Inc., 180 Varick Street Suite 665, New York, NY 10014 (US). **BRIDON, Dominique** [US/US]; c/o EpiVax Oncology, Inc., 180 Varick Street Suite 665, New York, NY 10014 (US). **MARTIN, William, D.** [US/US]; c/o EpiVax, Inc., 188 Valley Street, Suite 44, Providence, RI 02909 (US). **BERDUGO, Gad** [US/US]; c/o EpiVax Oncology, Inc.,

(54) Title: NEOANTIGENS IN CANCER

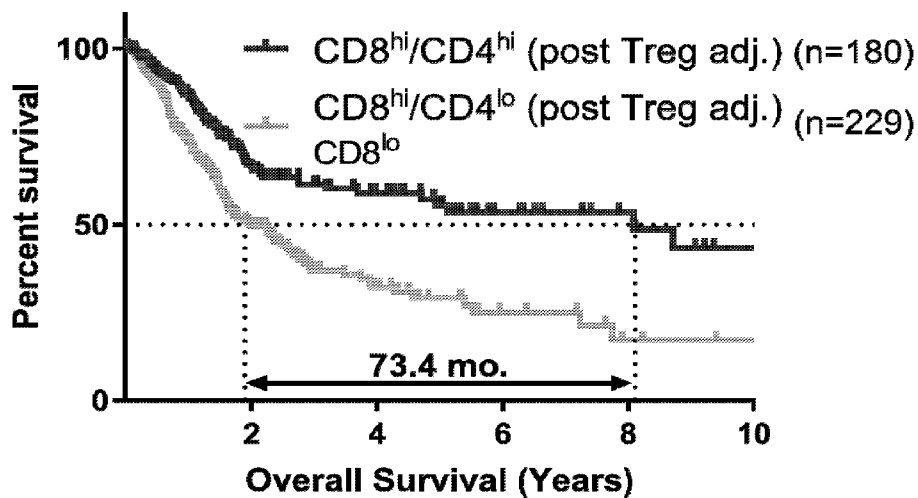


FIG. 6E

(57) Abstract: The invention provides improved strategies, prognostic indicators, compositions, and methods for producing personalized neoplasia vaccines. More particularly, embodiments of the present disclosure relate to the identification of neoplasia-specific neo-epitopes to predict survival and to identify and design subject-specific neo-epitopes, further assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined, or predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such neo-epitopes that are known, determined, or predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes that are to be used in personalized neoplasia vaccines. The present disclosure further relates to a novel ranking system for determining the optimal subject-specific neo-epitopes that are to



180 Varick Street Suite 665, New York, NY 10014 (US).
BALAR, Arjun [US/US]; c/o NYU Langone Health, 660
 1st Avenue, New York, NY 10016 (US). **STEINBERG,**
Gary, D. [US/US]; c/o NYU Langone Health, 660 1st Av-
 enue, New York, NY 10016 (US). **DE GROOT, Anne,**
S. [US/US]; c/o EpiVax, Inc., 188 Valley Street, Suite 44,
 Providence, RI 02909 (US).

(74) **Agent: KOWALSKI, Thomas, J.** et al.; Duane Morris
 LLP, 1540 Broadway, New York, NY 10036 (US).

(81) **Designated States** (*unless otherwise indicated, for every
 kind of national protection available*): AE, AG, AL, AM,
 AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ,
 CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO,
 DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN,
 HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP,
 KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME,
 MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ,
 OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA,
 SC, SD, SE, SG, SK, SL, ST, SV, SY, TH, TJ, TM, TN, TR,
 TT, TZ, UA, UG, US, UZ, VC, VN, WS, ZA, ZM, ZW.

(84) **Designated States** (*unless otherwise indicated, for every
 kind of regional protection available*): ARIPO (BW, GH,
 GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ,
 UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ,
 TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK,
 EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV,
 MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,
 TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW,
 KM, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished
 upon receipt of that report (Rule 48.2(g))*

NEOANTIGENS IN CANCER

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0001] This application claims priority to US provisional application Serial No. 62/842,800, filed May 3, 2019, US provisional application Serial No. 62/880,965, filed July 31, 2019, US provisional application Serial No. 62/932,651, filed November 8, 2019, US provisional application Serial No. 62/932,654, filed November 8, 2019, and US provisional application Serial No. 62/936,654, filed November 18, 2019, each incorporated by reference herein in its entirety.

[0002] Reference is made to international application Serial No. PCT/US2020/020089, filed February 27, 2020 and to US provisional application Serial No. 62/811,207, filed February 27, 2019, each incorporated by reference in its entirety..

[0003] The foregoing applications, and all documents cited therein or during their prosecution (“appln cited documents”) and all documents cited or referenced in the appln cited documents, and all documents cited or referenced herein (“herein cited documents”), and all documents cited or referenced in herein cited documents, together with any manufacturer’s instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

FIELD OF THE INVENTION

[0004] Embodiments of the present invention relate to improved strategies, prognostic indicators, compositions, and methods for producing and using personalized neoplasia vaccines. More particularly, embodiments of the present invention relate to the identification of neoplasia-specific neoantigens to identify and design subject-specific neo-epitopes, further assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host crossreactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or

other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), from the subject-specific neo-epitopes that are to be used in personalized neoplasia vaccines.

BACKGROUND OF THE INVENTION

[0005] There are many existing cancer therapies, including ablation techniques (e.g., surgical procedures, cryogenic/heat treatment, ultrasound, radiofrequency, and radiation) and chemical techniques (e.g., pharmaceutical agents, cytotoxic/chemotherapeutic agents, monoclonal antibodies, and various combinations thereof). However, these therapies are frequently associated with serious risk, toxic side effects, and extremely high costs, as well as uncertain efficacy. More recently, clinical studies have highlighted the potential of precision cancer immunotherapy to effectively control the cancer of patients by harnessing a patient's own immune system. Such precision cancer immunotherapies include the identification and use of a patient-specific pool of neoplasia-specific neoantigens in a personalized vaccine. However, while several different methodologies for preparing personalized neoplasia vaccines have been employed, recent studies showcase the difficulty of establishing robust CD8⁺ and CD4⁺ effector T cell responses to effectively treat the targeted neoplasia. This difficulty may be due to the inadvertent inclusion of suppressive T cell neo-epitopes in neoantigen-based vaccines that may be recognized by, and thus activate, regulatory T cells, which may abrogate effective immune responses against tumor cells. Further, T cells that recognize antigen-derived epitopes sharing TCR contacts with epitopes derived from self may be deleted or rendered anergic during thymic selection before they can be released to the periphery. As such, vaccine components targeting these T cells may be ineffective. On the other hand, vaccine-induced immune response targeting cross-reactive epitopes may induce unwanted autoimmune responses targeting the homologs of the cross-reactive epitopes identified by homology search. As a result, vaccine safety may be reduced. Thus, the inadvertent inclusion of other detrimental T cell-neo-epitopes in neoantigen-based vaccines that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells) may also lead to ineffective immune responses against tumor cells.

[0006] Immune tolerance is regulated by a complex interplay between antigen presenting cells (APC), T cells, B cells, cytokines, chemokines, and surface receptors. Initial self/non-self discrimination occurs in the thymus during neonatal development where medullary epithelial cells express specific self protein epitopes to immature T cells. T cells recognizing self antigens with

high affinity are deleted, but autoreactive T cells with moderate affinity sometimes avoid deletion and can be converted to so called ‘natural’ regulatory T cells. These natural regulatory T cells are exported to the periphery and help to control latent autoimmune response.

[0007] A second form of tolerance develops in the periphery. In this case activated T cells are converted to an ‘adaptive’ regulatory T cells phenotype through the action of certain immune suppressive cytokines and chemokines such as IL-10, TGF- β and CCL19. The possible roles for these ‘adaptive’ regulatory T cells include dampening immune response following the successful clearance of an invading pathogen, controlling excessive inflammation caused by an allergic reaction, controlling excessive inflammation caused by low level or chronic infection, or possibly controlling inflammatory response targeting beneficial symbiotic bacteria.

[0008] Naturally occurring regulatory T cells (including both natural regulatory T cells and adaptive regulatory T cells) are a critical component of immune regulation in the periphery. For example, upon activation of natural regulatory T cells through their TCR, natural regulatory T cells express immune modulating cytokines and chemokines. Activated natural regulatory T cells may suppress nearby effector T cells through contact dependent and independent mechanisms. In addition, the cytokines released by these cells including, but not limited to, IL-10 and TGF- β , are capable of inducing antigen-specific adaptive regulatory T cells. However, although regulatory T cells activity is essential for prevention of autoimmunity, excessive regulatory T cells function may abrogate effective immune responses against tumor cells (Nishikawa et al., “Regulatory T Cells in Tumor Immunity,” *Int. J. Cancer* 127:759-767 (2010)). Indeed, down-regulation of regulatory T cell activity has been used as an effective tool to improve anticancer therapies (Grauer et al., “Elimination of Regulatory T Cells is Essential for an Effective Vaccination with Tumor Lysate-Pulsed Dendritic Cells in a Murine Glioma Model,” *Int. J. Cancer* 122:1794-1802 (2008); Zhou et al., “Depletion of Endogenous Tumor-Associated Regulatory T Cells Improves the Efficacy of Adoptive Cytotoxic T-Cell Immunotherapy in Murine Acute Myeloid Leukemia,” *Blood* 114:3793-3802 (2009)). Thus, inadvertent inclusion of suppressive T cell neo-epitopes in neoantigen-based vaccines that may be recognized by, and thus activate, regulatory T cells, must be avoided to prevent the abrogation of an effective immune response against tumor cells.

[0009] As such, there is an ongoing need for improved strategies, compositions, and methods for producing personalized neoplasia vaccines. More particularly, there remains an ongoing need for strategies, compositions, and methods for producing personalized neoplasia vaccines that

include identifying neo-epitopes that are known or determined (e.g. predicted) to engage and/or induce regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes that are to be used in the personalized neoplasia vaccines. There also remains an ongoing need for improved ranking systems to determine the optimal subject-specific neo-epitopes that are to be used in personalized neoplasia vaccines.

[0010] Citation or identification of any document in this application is not an admission that such document is available as prior art to the present invention.

SUMMARY OF THE INVENTION

[0011] Accordingly, embodiments of the present invention provide novel strategies, prognostic indicators, compositions, and methods for producing and using personalized neoplasia vaccines.

[0012] In an aspect, the invention provides a prognostic method for determining risk of death of a human subject with a neoplasia, which comprises identifying neoplasia-specific mutations, assessing the neoplasia-specific neoantigens to identify and classify the neoantigens that promote effector T cell (Teff) function or regulatory T cell (Treg) function. In certain embodiments, the neoantigens are classified as simply as i) Class I and/or Class II MHC-binding neoantigens, and ii) immunogenic or tolerogenic. In certain embodiments, Class I and/or Class II binding is classified by strength of interaction of a neoantigen with Class I and/or Class II MHC, which can be calculated, measured, or by comparison to a database. In certain embodiments, the neoantigen are classified over a range of function, such as immunogenic, tolerable, or tolerogenic, or on a scale, such as a numeric scale, ranging from highly immunogenic to highly tolerogenic.

[0013] In an aspect, the prognostic method is used to distinguish subjects with neoplasias that are best suited to respond to a neoantigen vaccine. In another aspect, the prognostic method is used to identify subjects that would benefit improved outcomes by coadministration of a neoantigen vaccine and an agent that selectively inhibits Treg function.

[0014] Accordingly, the invention provides both prognostic method for determining risk of death, of a human subject with a neoplasia, as well as a diagnostic method and a method for selecting neoantigen vaccine components, which comprises identifying a population of neoplasia-specific mutations in a neoplasia specimen of a subject; assessing the neoplasia-specific mutations

identified to classify Class I and/or Class II neoantigens encoded by said mutations; analyzing the neoantigens encoded by said mutations to identify and classify neoantigens that engage effector T cells and neo-epitopes that engage regulatory T cells, and determining a prognostic score from the immunogenicity of the neoantigen population. In certain embodiments, the method is implemented on a computer.

[0015] The method of the invention is designed to classify, order, or otherwise recognize Class I and Class II neoantigens as effector neoantigens or tolerogenic antigens, or classify any neoantigen in between, for any given patient. The invention is further designed to recognize neoantigens that are crossreactive, for example having Class II effector and Class I tolerogenic activity, or Class I effector and Class II tolerogenic activity, or other combinations that are detrimental to prognosis or treatment outcomes.

[0016] Thus, in an embodiment of the invention, the method comprises classification of Class I neo-antigens of a subject as effector neoantigens or tolerogenic neoantigens. In another embodiment, the method comprises classification of the Class I neoantigens of a subject as effector neoantigens, tolerated neoantigens, or tolerogenic neoantigens. In another embodiment, the method comprises classification of the Class I neoantigens of a subject on a graded scale from a strong effector neoantigen to a strong tolerogenic neoantigen.

[0017] In an embodiment of the invention, the method comprises classification of the Class II neoantigens of a subject as effector neoantigens or tolerogenic neoantigens. In another embodiment, the method comprises classification of the Class II neoantigens of a subject as effector neoantigens, tolerated neoantigens, or tolerogenic neoantigens. In another embodiment, the method comprises classification of the Class II neoantigens of a subject on a graded scale from a strong effector neoantigen to a strong regulatory neoantigen.

[0018] In certain embodiments, the method comprises classification of the Class I neoantigens and classification of the Class II neoantigens of the subject, and can include identification of subject neoantigens that are cross-reactive between Class I and Class II.

[0019] Such embodiments of the invention may exclude neoantigens from prognostic or diagnostic methods if the neoantigen is a Class I effector neoantigen and a Class II tolerogenic neoantigen or an Class II effector neoantigen and a Class I tolerogenic neoantigen, or a tolerated Class I neoantigen and a tolerated Class II antigen, or an effector Class II neoantigen and a tolerated Class I neoantigen.

[0020] In certain embodiments, the prognostic score is calculated based on the top 50% of the effector neoantigens and the top 50% of the tolerogenic neoantigens, or the top 40% of effector neoantigens and the top 40% of the tolerogenic neoantigens, or the top 30% of effector neoantigens and the top 30% of the tolerogenic neoantigens, or the top 20% of the effector neoantigens and the top 20% of the tolerogenic neoantigens, or the top 10% of the effector neoantigens and the top 10% of the tolerogenic neoantigens, or the top 5% of the effector neoantigens and the top 5% of the tolerogenic neoantigens, or the top 2% of the effector neoantigens and the top 2% of the tolerogenic neoantigens, or the top 1% of the effector neoantigens and the top 1% of the tolerogenic neoantigens. In certain embodiments, the prognostic score is calculated based on at least the top 10 of the effector neoantigens and at least the top 10 of the tolerogenic neoantigens, or at least the top 25 of the effector neoantigens and at least the top 25 of the tolerogenic neoantigens, or at least on the top 50 of the effector neoantigens and at least the top 50 of the tolerogenic neoantigens, or at least on the top 100 of the effector neoantigens and at least the top 100 of the tolerogenic neoantigens.

[0021] In certain embodiments, the method comprises determining binding strength of a neoantigen to Teff and/or Treg cells. The strength of binding to Teff and/or Treg cells may be known, measured, predicted or calculated. In certain embodiments, the method comprises determining immunogenicity of a neoantigen by comparison to physicochemical methods and/or by comparison to a panel of antigens of known immunogenicity. In certain embodiments, the activity of a neoantigen in a subject is determined by its capacity to activate or inhibit an immune cell, such as, for example, to inhibit IFN γ production by itself or mixed with other antigens or neoantigens. In some embodiments, strength of binding to a Teff cell or a Treg cell is determined by comparison to a panel of neoantigens having predetermined Teff and/or Treg activity.

[0022] Accordingly, the invention provides prognostic and diagnostic biomarkers. The method involves identifying a plurality of neoplasia-specific mutations (neo-epitopes) in a subject and determining the extent to which a population of neoantigens containing the the neo-epitopes is immunogenic. Higher overall immunogenicity, i.e. higher capability to stimulate effector cells and lower capability to stimulate regulatory cells indicates a better prognosis.

[0023] In another aspect, the invention is directed to a method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, which includes: i) identifying neoplasia-specific mutations in a neoplasia specimen of a subject diagnosed as having a neoplasia; ii) to identify Class

I and Class II neo-epitopes encoded by said mutations for use in the personalized neoplasia vaccine, wherein said neo-epitopes are known, determined, or predicted to bind to a MHC protein of the subject; and iii) classifying the identified neo-epitopes encoded by said mutations from step (ii) to identify Class I and Class II neo-epitopes that are that are tolerated or tolerogenic, and excluding such Class II neo-epitopes that are tolerated or tolerogenic, and excluding such Class I neo-epitopes that are tolerogenic, from the subject-specific neo-epitopes for use in the personalized neoplasia vaccine.

[0024] Aspects of the invention include identifying sequence differences between the full or partial genome, exome, and/or transcriptome of a neoplasia specimen from the subject diagnosed as having a neoplasia and a non-neoplasia specimen. In aspects, a non-neoplasia specimen is derived from the subject diagnosed as having a neoplasia. In further aspects, identifying neoplasia-specific mutations or identifying sequence differences comprises Next Generation Sequencing (NGS). In aspects, identifying neoplasia-specific mutations in step (i) comprises selecting from the neoplasia a plurality of nucleic acid sequences, each comprising mutations not present in a non-neoplasia sample. In aspects, identifying neoplasia-specific mutations or identifying sequence differences comprises sequencing genomic DNA and/or RNA of the neoplasia specimen.

[0025] In aspects of the invention, the neoplasia-specific mutations are neoplasia-specific somatic mutations. In aspects, the neoplasia-specific mutations are single nucleotide variations (SNVs), insertions and deletions (which can generate both in-frame and frameshift mutations), and other large-scale rearrangements such as but not limited to chromosomal inversions, duplications, insertions, deletions, or translocations. In aspects, neoplasia specific mutations, including SNVs, insertions, and deletions, are non-synonymous mutations. In aspects, neoplasia-specific mutations, including SNVs, insertions and deletions (which can be non-synonymous mutations), and other large-scale rearrangements, are mutations of proteins encoded in the neoplasia specimen of the subject diagnosed as having a neoplasia. In aspects, neoplasia specific mutations, including SNVs, are non-synonymous mutations. In aspects, neoplasia-specific mutations, including SNVs (which can be non-synonymous mutations), indels, and frameshifts, are mutations of proteins expressed in the neoplasia specimen of the subject diagnosed as having a neoplasia.

[0026] In aspects of the invention, assessing the neoplasia-specific mutations in to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations includes: a) determining a binding score for a mutated peptide to one or more MHC molecules, wherein said

mutated peptide is encoded by at least one of said neoplasia-specific mutations; b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations; c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for a sufficiently large enough group randomly generated peptides (e.g., at least 10,000) using naturally observed amino acid frequencies; d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and e) identifying the mutated peptide as a neo-epitope when: 1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or 2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide and the non-mutated peptide. In further aspects, the one or more MHC molecules are MHC class I molecules and/or MHC class II molecules. In aspects, the mutated peptide and non-mutated peptide are both 9 amino acids in length or the mutated peptide and non-mutated peptide are both 10 amino acids in length. In aspects, the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, and wherein the TCR facing amino acid residues for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal. In further aspects, TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc.) as counted from the amino terminal. In aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal. In further aspects,

the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal. In aspects, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

[0027] In aspects of the invention, assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises *in silico* testing. In certain aspects, said *in silico* testing to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations in step (ii) comprises using an algorithm to screen protein sequences for putative T cell epitopes. In an embodiment, the algorithm comprises the EpiMatrix® algorithm.

[0028] In aspects of the invention, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises determining whether said identified neo-epitopes encoded by said mutations share TCR contacts with proteins derived from either the human proteome or the human microbiome, wherein said identified neo-epitopes encoded by said mutations that are determined to share TCR contacts with proteins derived from either the human proteome or the human microbiome are identified as neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope as counted from the amino terminal, wherein the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, and wherein the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2,

5, 7, and 8; positions 2, 3, 5, and 7, etc.) as counted from the amino terminal. In aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal. In aspects, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

[0029] In aspects of the invention, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises *in silico* testing. In aspects, *in silico* testing comprises analyzing whether the identified neo-epitopes are predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) using the JANUSMATRIX™ algorithm. In further aspects an identified neo-epitope is predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) if the JANUSMATRIX™ score for the neo-epitope is greater than or equal to 2 (and in further aspects, greater than or equal to 3). In aspects, the method further comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF-β production.

[0030] In aspects of the invention, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host

cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

[0031] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further includes: designing at least one subject-specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo-epitope encoded by said mutations, provided said neo-epitope is not identified as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, the method further includes providing the at least one peptide or polypeptide designed in step (iv) or a nucleic acid encoding said peptides or polypeptides. In even further aspects, the method further includes vi) providing a vaccine comprising the at least one peptide or polypeptide or nucleic acid provided in step (v).

[0032] In another aspect, the invention provides a pharmaceutical composition including a plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes or one or more nucleic acids encoding said plurality of selected peptides or polypeptides, wherein the one or more identified neo-epitopes induces a neoplasia-specific effector T cell response in a subject; and a pharmaceutically acceptable adjuvant and/or carrier. The plurality of selected peptides or polypeptides comprising the one or more identified neo-epitope or one or more nucleic acids encoding said plurality of selected peptides or polypeptides are selected by a process comprising: i) identifying neoplasia-specific mutations in a neoplasia specimen of a subject diagnosed as having a neoplasia; ii) assessing the neoplasia-specific mutations identified in step to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations for use in the pharmaceutical composition, wherein said neo-epitopes are known or determined (e.g. predicted) to bind to a MHC protein of the subject; iii) assessing the identified neo-epitopes encoded by said mutations from step (ii) to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes for use in the pharmaceutical composition; and iv) selecting the plurality of selected peptides or polypeptides comprising the one or more identified neo-epitopes

or selecting the one or more nucleic acids encoding said at least one peptide or polypeptide based on the assessments of step (ii) and step (iii), provided said neo-epitope is not identified in step (iii) as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells).

[0033] In aspects of the pharmaceutical composition, identifying neoplasia-specific mutations comprises identifying sequence differences between the full or partial genome, exome, and/or transcriptome of a neoplasia specimen from the subject diagnosed as having a neoplasia and a non-neoplasia specimen. In aspects, said non-neoplasia specimen is derived from the subject diagnosed as having a neoplasia. In further aspects, identifying neoplasia-specific mutations or identifying sequence differences comprises Next Generation Sequencing (NGS). In aspects, identifying neoplasia-specific mutations comprises selecting from the neoplasia a plurality of nucleic acid sequences, each comprising mutations not present in a non- neoplasia sample. In additional aspects, identifying neoplasia-specific mutations or identifying sequence differences comprises sequencing genomic DNA and/or RNA of the neoplasia specimen.

[0034] In aspects of the pharmaceutical composition, the neoplasia-specific mutations are neoplasia-specific somatic mutations. In aspects, the neoplasia-specific mutations are single nucleotide variations (SNVs), indels (which are also known as in-frame insertions or in-frame deletions), or frameshifts (which are also known as out-of-frame insertions or out-of-frame deletions). In aspects, neoplasia specific mutations, including SNVs, are non-synonymous mutations. In aspects, neoplasia-specific mutations, including SNVs (which can be non-synonymous mutations), indels, and frameshifts, are mutations of proteins encoded in the neoplasia specimen of the subject diagnosed as having a neoplasia

[0035] In aspects of the pharmaceutical composition, assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises: a) determining a binding score for a mutated peptide to one or more MHC molecules, wherein said mutated peptide is encoded by at least one of said neoplasia-specific mutations; b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations; c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for at least 10,000 randomly generated peptides using naturally

observed amino acid frequencies; d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and e) identifying the mutated peptide as a neo-epitope when: 1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or 2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide the non-mutated peptide. In further aspects, the mutated peptide and non- mutated peptide are both 9 amino acids in length or the mutated peptide and non-mutated peptide are both 10 amino acids in length. In aspects, the one or more MHC molecules are MHC class I molecules and/or MHC class II molecules. In aspects, the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, and wherein the TCR facing amino acid residues for a 10-mer mutated peptide and 10-mer non- mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal. In further aspects, TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc.) as counted from the amino terminal. In aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal. In aspects, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 10-mer identified neo-epitope

that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

[0036] In aspects of the pharmaceutical composition, assessing the neoplasia-specific mutations in step (ii) to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises *in silico* testing. In aspects, the *in silico* testing to identify known or predicted neo-epitopes encoded by said mutations in step (ii) comprises using an algorithm to screen protein sequences for putative T cell epitopes. In an embodiment, the algorithm comprises the EpiMatrix® algorithm.

[0037] In aspects of the pharmaceutical composition, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises determining whether said identified neo-epitopes encoded by said mutations share TCR contacts with proteins derived from either the human proteome or the human microbiome, wherein said identified neo-epitopes encoded by said mutations that are determined to share TCR contacts with proteins derived from either the human proteome or the human microbiome are identified as neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects of the pharmaceutical composition, TCR contacts for a 9-mer identified neo-epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope as counted from the amino terminal, wherein the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, and wherein the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc.) as counted from the amino terminal. In aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any

combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal. In aspects, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In further aspects, the TCR contacts for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

[0038] In aspects of the pharmaceutical composition, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises *in silico* testing. In aspects, *in silico* testing comprises analyzing whether the identified neo-epitopes are predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) using the JANUSMATRIX™ algorithm. In further aspects, an identified neo-epitope is predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) if the JANUSMATRIX™ score for the neo-epitope is greater than or equal to 2 (and in further aspects, greater than or equal to 3). In aspects, it is determined whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

[0039] In aspects of the pharmaceutical composition, assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

[0040] In aspects of the pharmaceutical composition the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13,

at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 peptides or polypeptides comprising one or more identified neo-epitopes. In aspects, the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes comprises from 3-20 selected peptides or polypeptides comprising one or more identified neo-epitopes.

[0041] In an aspect of the invention, vaccines comprising shared neo-epitopes are provided. About 99% of non-synonymous mutations (NSMs, e.g., missense, indel, and frameshift mutations) in TCGA bladder cancer mutanomes are private. However, thirty-nine shared NSMs are found in at least 1% of BLCA genomes, offering an opportunity for development of off-the-shelf vaccines. A panel of 10 shared neoantigens covers about 25% of the TCGA BLCA population, and expanding the panel to 20 shared neoantigens increases coverage to about one-third of BLCA patients.

[0042] In aspects of the pharmaceutical composition, each peptide or polypeptide of the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes has a length of from 9-100 amino acids. In aspects, each peptide or polypeptide of the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes has a length of from 9-40 amino acids, from 9-30 amino acids, from 9-25 amino acids, from 9-23 amino acids, from 9-20 amino acids, or from 9-15 amino acids.

[0043] In aspects of the pharmaceutical composition, the one or more nucleic acids encoding said plurality of selected peptides or polypeptides are DNA, RNA, or mRNA.

[0044] In aspects of the pharmaceutical composition, the pharmaceutical composition further comprises an anti-immunosuppressive agent. In aspects, the anti-immunosuppressive agent comprises a checkpoint blockage modulator, such as a checkpoint blockage inhibitor and immune checkpoint stimulators.

[0045] In aspects of the pharmaceutical composition, the adjuvant comprises poly-ICLC.

[0046] In aspects of the pharmaceutical composition, the neoplasia is a solid tumor. In aspects, the neoplasia is bladder cancer, breast cancer, brain cancer, colon cancer, gastric cancer, head and neck cancer, kidney cancer, liver cancer, lung cancer, melanoma, ovarian cancer, pancreatic cancer, prostate cancer, or testicular cancer. In aspects, the neoplasia is bladder cancer.

[0047] In another aspect, the invention provides a prognostic method for determining risk of death of a human subject with a neoplasia, which comprises identifying a population of neoplasia-specific mutations in a neoplasia specimen of a subject; assessing the neoplasia-specific mutations

identified in step (i) to identify Class I and Class II neo-epitopes encoded by said mutations, analyzing the neo-epitopes encoded by said mutations to identify and quantify neo-epitopes that engage effector T cells and neo-epitopes that engage regulatory T cells, and computing a prognostic score from the immunogenicity of the population

[0048] These and additional embodiments and features of the presently-disclosed subject matter will be clarified by reference to the figures and detailed description set forth herein.

[0049] Accordingly, it is an object of the invention not to encompass within the invention any previously known product, process of making the product, or method of using the product such that Applicants reserve the right and hereby disclose a disclaimer of any previously known product, process, or method. It is further noted that the invention does not intend to encompass within the scope of the invention any product, process, or making of the product or method of using the product, which does not meet the written description and enablement requirements of the USPTO (35 U.S.C. §112, first paragraph) or the EPO (Article 83 of the EPC), such that Applicants reserve the right and hereby disclose a disclaimer of any previously described product, process of making the product, or method of using the product. It may be advantageous in the practice of the invention to be in compliance with Art. 53(c) EPC and Rule 28(b) and (c) EPC. All rights to explicitly disclaim any embodiments that are the subject of any granted patent(s) of applicant in the lineage of this application or in any other lineage or in any prior filed application of any third party is explicitly reserved. Nothing herein is to be construed as a promise.

[0050] It is noted that in this disclosure and particularly in the claims and/or paragraphs, terms such as "comprises", "comprised", "comprising" and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean "includes", "included", "including", and the like; and that terms such as "consisting essentially of" and "consists essentially of" have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention.

[0051] It is understood that both the preceding summary and the following detailed description are exemplary and are intended to provide further explanation of the disclosure as claimed. Neither the summary nor the description that follows is intended to define or limit the scope of the disclosure to the particular features mentioned in the summary or description.

BRIEF DESCRIPTION OF THE DRAWINGS

[0052] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0053] The following detailed description, given by way of example, but not intended to limit the invention solely to the specific embodiments described, may best be understood in conjunction with the accompanying drawings.

[0054] Figure 1A-1C. - Prediction of neo-epitopes. (A) Bladder cancer 5-year survival predictions by three different analysis methods: tumor mutational burden (TMB); neo-epitope analysis of Class I and Class II neo-epitopes (NetMHCpan/NetMHCIIpan), and ANCER™ neoepitope analysis. and were compared using mutation data from The Cancer Genome Atlas (TCGA). (B) Accuracy analysis. (C) Predictive values of Class I and Class II epitopes and filtering out self-like neo-epitopes.

[0055] Figure 2. - Accurate and identification of CD4 and CD8 epitopes using EPIMATRIX®.

[0056] CD4 T cell epitopes - Class II predictions are 74% accurate when prospectively tested in in vitro HLA binding assays. IEDB predictions are 54-66% accurate when tested against the same set of peptides.

[0057] Figure 3. - Epitopes can be either effector or regulatory. JANUSMATRIX™ is an immunoinformatics tool developed to compare T cell epitopes and evaluate neo-epitope peptide sequences as self-like (immunosuppressive; Treg) and non-self. (Moise L. et al., Hum Vaccin Immunother. 2015;11(9):2312-21). As shown in the right panel, *in silico*- derived influenza (H7N9) Treg epitope reduces IFN γ responses to effector peptides similarly to a JANUSMATRIX™-derived Treg epitope (Liu R. et al., Hum Vaccin Immunother. 2015 11:9, 2241-2252).

[0058] Figure 4. - Immunosuppression of IFN γ responses by CT26 self-like neo-epitopes. ANCER™-derived Teff neo-epitopes induce an IFN γ response, while self-like neo-epitopes identified by JANUSMATRIX™ suppress the response 5-fold.

[0059] Figure 5A-5B. - Analysis of Class I and Class II neo-epitopes in 13 GVAX-treated pancreatic patients. (A) Neo-epitope composition. Number and frequency of Class I and Class II neo-epitopes with low, average, and high cross-reactivity (XR) potential across pancreatic cancer patients. (B) The ratio of MHC Class II effector (Teff) vs. regulatory (Treg) neo-epitopes found

in tumor is associated with tumor outcomes. Patients that are (Teff/Treg)^{hi} have a higher disease free survival (DFS) time than (Teff/Treg)^{lo} patients and the ratio is a more sensitive predictor than tumor mutational burden.

[0060] Figure 6A-6E. - TCGA marker analysis. (A) Patients separated on the basis of total mutational burden. (B) Patients separated on the basis of raw CD8 neo-epitope content. (C) Patients separated on basis of CD8 neo-epitope content with “tolerated” neo-epitopes removed. (D) Patients separated on basis of CD8 neo-epitope content with “tolerated” CD8 neo-epitopes removed and raw CD4 neo-epitope content. (E) Patients separated on basis of CD8 neo-epitope content with “tolerated” CD8 neo-epitopes removed and CD4 neo-epitope content with “tolerated” CD4 neo-epitopes removed, using higher cutoff for CD4 tolerated epitope removal.

[0061] Figure 7A-7B. Patient stratification. (A) Patient TMB significantly stratifies short- and long-term survivors. (B) Evaluating CD8 neo-epitope burden with ANCER™ helps stratify bladder cancer patients. (C) Inclusion of CD4 neo-epitope burden helps ANCER™ further stratify cancer patients. (E) Patient stratification is further enhanced when evaluating the phenotype of CD4 neo-epitopes.

[0062] The following detailed description, given by way of example, but not intended to limit the invention solely to the specific embodiments described, may best be understood in conjunction with the accompanying drawings.

DETAILED DESCRIPTION OF THE INVENTION

[0063] Particular details of various embodiments of the invention are set forth to illustrate certain aspects and not to limit the scope of the invention. It will be apparent to one of ordinary skill in the art that modifications and variations are possible without departing from the scope of the embodiments defined in the appended claims. More specifically, although some aspects of embodiments of the present invention may be identified herein as preferred or particularly advantageous, it is contemplated that the embodiments of the present invention are not limited to these preferred aspects.

[0064] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which the presently-disclosed subject matter belongs.

[0065] While clinical studies have highlighted the potential of personalized cancer immunotherapy to effectively control the cancer of patients across cancer indications, recent studies showcase the difficulty of establishing robust CD8⁺ and CD4⁺ T cell responses against the patient's cancer. We hypothesized that poor cancer vaccine performance may be due in large part to the inadvertent inclusion of suppressive T cell neo-epitopes in neoantigen vaccines that may be recognized by, and thus activate, regulatory T cells (Tregs), and/or the inadvertent inclusion of other detrimental T cell-neo-epitopes in neoantigen-based vaccines that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells). To test this hypothesis, we used the instantly-disclosed strategies, compositions, and methods for producing personalized neoplasia vaccines to identify and select neo-epitopes from the CT26 syngeneic mouse model. Distinctive features of the instantly-disclosed strategies, compositions, and methods for producing personalized neoplasia vaccines over other personalized vaccine pipelines are the ability to predict CD4⁺ and CD8⁺ T cell neo-epitopes and to identify, and subsequently remove, neo-epitopes that may be recognized by and activate regulatory T cells, and/or the inadvertent inclusion of other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells).

[0066] In a first set of experiments, optimally selected CT26 neo-epitope vaccine candidates encoding CD4⁺ and CD8⁺ neo-epitopes were designed and ranked with the instantly-disclosed strategies and methods. Self-like, putative regulatory T cell epitopes and epitopes that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells) were removed in this process.

[0067] To gain further insight into the role of Treg cells and components of neo-epitope vaccine candidates, a retrospective analysis was performed to identify correlations between cancer patient treatment outcomes and repertoires of neo-epitopes in the cancer patients. An initial analysis focused on Class II neo-epitopes and was extended to include Class I neo-epitopes.

[0068] Thus, the Class I and Class II neo-epitopes are now more precisely classified as to immunogenic activity. Class I and Class II neo-epitopes are advantageously ranked as immunogenic, tolerated, or tolerogenic. Further, a retrospective analysis of Class I and Class II neoepitopes in bladder cancer patients comparing proportions of immunogenic, tolerated, or

tolerogenic neoepitopes with overall survival reveals distinctions between Class I and Class II that provide for more effective neoantigen vaccines.

[0069] Neo-epitopes may be recognized by regulatory T cells due to their high degree of similarity with self. Previously, co-administration of the CT26 self-like neo-epitopes (e.g. which were predicted to be recognized by and activate regulatory T cells) with our optimally designed neo-epitope vaccine in naïve Balb/c mice were shown to diminish IFN γ ELISpot responses by 5-fold compared to vaccination without the self-like neo-epitopes ($p = 0.003$). Thus, it was indicated that poor cancer vaccine performance may be due in large part to the inadvertent inclusion of suppressive T cell neo-epitopes in neo-epitope vaccines that may be recognized by, and thus activate, regulatory T cells, and/or the inadvertent inclusion of other detrimental T cell- neo-epitopes in neoantigen-based vaccines that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells).

[0070] While it has been well known that regulatory T cells are present in tumors, these results suggest the possibility that tumor-derived neo-epitopes may be recruiting regulatory T cells to the tumor. More importantly, the inadvertent inclusion of regulatory T cell-driving neo-epitopes, and/or the inadvertent inclusion of other detrimental T cell-neo-epitopes that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells), in vaccine formulations may hinder efforts to induce strong T cell-mediated tumor control while also leading to possible autoimmune responses. Screening of neoantigen sequences to identify and remove potential regulatory T cell inducing neo-epitopes and/or other detrimental T cell-neo-epitopes that may be recognized by, and thus activate, other detrimental T cells (including T cells with potential host cross-reactivity that may lead to autoimmune responses, as well as anergic T cells) (e.g., using specialized tools, including *in silico* screening tools) offers the possibility of enriching and designing new vaccines with higher quality candidates while minimizing costs and turnaround times.

[0071] We now show by classification of neoantigens and retrospective analysis of bladder cancer patients the advantages and improved effects of combinations of Class I and Class II neoantigens. Further, cross-reactive neoantigens that bind to both Class I and Class II MHC may have immunogenicity with respect to one while tolerated or tolerogenic with respect to the other.

Our results allow improved discrimination of Class I and Class II neoantigens that cross-react. Thus the invention provides improvements in effectiveness of neoantigen vaccines, as well as a being a prognostic indicator.

[0072] Accordingly, the instant invention is directed to improved strategies, compositions, and methods for producing and administering personalized neoplasia vaccines. The instant invention also provides a prognostic method for example to assess risk of death, or to adjust treatment. More particularly, embodiments of the present disclosure relate to the identification of neoplasia-specific neoantigens to identify and design subject-specific neo-epitopes, further assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes that are to be used in personalized neoplasia vaccines. Further, the instant disclosure relates to a novel ranking system for determining the optimal peptides or polypeptides comprising subject-specific neo-epitopes that are to be used in personalized neoplasia vaccines.

[0073] One embodiment is directed to a method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, which includes: i) identifying neoplasia-specific mutations in a neoplasia specimen of a subject diagnosed as having a neoplasia; ii) assessing the neoplasia-specific mutations identified in step (i) to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations for use in the personalized neoplasia vaccine, wherein said neo-epitopes are known or determined (e.g. predicted) to bind to a MHC protein of the subject; and iii) assessing the identified neo-epitopes encoded by said mutations from step (ii) to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes for use in the personalized neoplasia vaccine. In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further includes: iv) designing at least one subject-

specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo-epitope encoded by said mutations, provided said neo-epitope is not identified in step (iii) as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, the method further includes: v) providing the at least one peptide or polypeptide designed in step (iv) or a nucleic acid encoding said peptides or polypeptides. In even further aspects, the method further includes vi) providing a vaccine comprising the at least one peptide or polypeptide or nucleic acid provided in step (v).

[0074] In aspects, a method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine includes: i) assessing identified neoplasia-specific mutations from a neoplasia specimen of a subject diagnosed as having a neoplasia identified to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations for use in the personalized neoplasia vaccine, wherein said neo-epitopes are known or determined (e.g. predicted) to bind to a MHC protein of the subject; and ii) assessing the identified neo-epitopes encoded by said mutations from step (i) to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), and excluding such identified neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) from the subject-specific neo-epitopes for use in the personalized neoplasia vaccine. In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further includes: iii) designing at least one subject-specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo-epitope encoded by said mutations, provided said neo-epitope is not identified in step (ii) as being known or determined (e.g. predicted) engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, the method further includes: iv) providing the at least one peptide or polypeptide designed in step (iii) or a nucleic acid encoding said peptides or polypeptides. In even further aspects, the method further includes v) providing a vaccine comprising the at least one peptide or polypeptide or nucleic acid provided in step (iv).

Definitions

[0075] As used herein, the singular forms “a,” “an,” and “the” are intended to include the plural forms, including “at least one,” unless the content clearly indicates otherwise. “Or” means “and/or.” As used herein, the term “and/or” and “one or more” includes any and all combinations of the associated listed items.

[0076] As used herein, the term “about” is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein are modified by the term about.

[0077] As used herein, the term “antigen” refers to any substance that will elicit an immune response. In aspects, an antigen relates to any substance, preferably a peptide or protein, that reacts specifically with antibodies or T-lymphocytes (T cells). According to the present invention, the term “antigen” comprises any molecule which comprises at least one epitope. Preferably, an antigen is a molecule which, optionally after processing, induces an immune reaction, which is preferably specific for the antigen (including cells expressing the antigen). An antigen is preferably presented by a cell, preferably by an antigen presenting cell which includes a diseased cell, in particular a cancer cell, in the context of MHC molecules, which results in an immune reaction against the antigen. An antigen is preferably a product which corresponds to or is derived from a naturally occurring antigen. Such naturally occurring antigens include tumor antigens, *e.g.*, a part of a tumor cell such as a protein or peptide expressed in a tumor cell which may be derived from the cytoplasm, the cell surface or the cell nucleus, in particular those which primarily occur intracellularly or as surface antigens of tumor cells.

[0078] As used herein, the term “biological sample” as refers to any sample of tissue, cells, or secretions from an organism.

[0079] As used herein, the terms “comprises,” “comprising,” “containing” and “having” and the like can have the meaning ascribed to them in U.S. Patent law and can mean “includes,” “including,” and the like; “consisting essentially of” or “consists essentially” likewise has the meaning ascribed in U.S. Patent law and the term is open-ended, allowing for the presence of more than that which is recited so long as basic or novel characteristics of that which is recited is not changed by the presence of more than that which is recited, but excludes prior art embodiments.

[0080] As used herein, the term “control” is meant a standard or reference condition.

[0081] As used herein, the term “disease” is meant any condition or disorder that damages or interferes with the normal function of a cell, tissue, or organ.

[0082] As used herein, the term “effective amount” is meant the amount required to ameliorate the symptoms of a disease (e.g., a neoplasia/tumor) relative to an untreated patient. The effective amount of active compound(s) used to practice the present invention for therapeutic treatment of a disease varies depending upon the manner of administration, the age, body weight, and general health of the subject. Ultimately, the attending physician or veterinarian will decide the appropriate amount and dosage regimen. Such amount is referred to as an “effective” amount.

[0083] As used herein, “fragment” refers to a portion of a polypeptide or nucleic acid molecule. This portion contains, preferably, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90% of the entire length of the reference nucleic acid molecule or polypeptide. A fragment may contain 5, 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100, 200, 300, 400, 500, 600, 700, 800, 900, 1000 or more nucleotides or amino acids.

[0084] As used herein, the term “immune response” refers to the concerted action of lymphocytes, antigen presenting cells, phagocytic cells, granulocytes, and soluble macromolecules produced by the above cells or the liver (including antibodies, cytokines, and complement) that results in selective damage to, destruction of, or elimination from the human body of cancerous cells, metastatic tumor cells, malignant melanoma, invading pathogens, cells or tissues infected with pathogens, or, in cases of autoimmunity or pathological inflammation, normal human cells or tissues.

[0085] As used herein, the term “immune synapse” means the protein complex formed by the simultaneous engagement of a given T cell epitope to both a cell surface MHC complex and TCR.

[0086] As used herein, the term “isolated” means that the polynucleotide or polypeptide or fragment, variant, or derivative thereof has been essentially removed from other biological materials with which it is naturally associated, or essentially free from other biological materials derived, e.g., from a recombinant host cell that has been genetically engineered to express the polypeptide of the invention.

[0087] As used herein, the terms “the major histocompatibility complex (MHC)”, “MHC molecules”, “MHC proteins” or “HLA proteins” are to be understood as meaning, in particular, proteins capable of binding peptides resulting from the proteolytic cleavage of protein antigens and representing potential T-cell epitopes, transporting them to the cell surface and presenting

them there to specific cells, in particular cytotoxic T-lymphocytes or T-helper cells. The major histocompatibility complex in the genome comprises the genetic region whose gene products expressed on the cell surface are important for binding and presenting endogenous and/or foreign antigens and thus for regulating immunological processes. The major histocompatibility complex is classified into two gene groups coding for different proteins, namely molecules of MHC class I and molecules of MHC class II. The molecules of the two MHC classes are specialized for different antigen sources. The molecules of MHC class I present endogenously synthesized antigens, for example viral proteins and tumor antigens. The molecules of MHC class II present protein antigens originating from exogenous sources, for example bacterial products. The cellular biology and the expression patterns of the two MHC classes are adapted to these different roles. MHC molecules of class I consist of a heavy chain and a light chain and are capable of binding a peptide of about 8 to 11 amino acids, but usually 9 or 10 amino acids, if this peptide has suitable binding motifs, and presenting it to cytotoxic T-lymphocytes. The peptide bound by the MHC molecules of class I originates from an endogenous protein antigen. The heavy chain of the MHC molecules of class I is preferably an HLA-A, HLA-B or HLA-C monomer, and the light chain is β -2-microglobulin. MHC molecules of class II consist of an α -chain and a β -chain and are capable of binding a peptide of about 15 to 24 amino acids if this peptide has suitable binding motifs, and presenting it to T-helper cells. The peptide bound by the MHC molecules of class II usually originates from an extracellular of exogenous protein antigen. The α -chain and the β -chain are in particular HLA-DR, HLA-DQ and HLA-DP monomers.

[0088] As used herein, the term “MHC Binding Motif” refers to a pattern of amino acids in a protein sequence that predicts binding to a particular MHC allele.

[0089] As used herein, the term “MHC Ligand” means a polypeptide capable of binding to one or more specific MHC alleles. The term “HLA ligand” is interchangeable with the term “MHC Ligand”. Cells expressing MHC/Ligand complexes on their surface are referred to as “Antigen Presenting Cells” (APCs). Similarly, as used herein, the term “MHC binding peptide” relates to a peptide which binds to an MHC class I and/or an MHC class II molecule. In the case of MHC class I/peptide complexes, the binding peptides are typically 8-10 amino acids long although longer or shorter peptides may be effective. In the case of MHC class II/peptide complexes, the binding peptides are typically 10-25 amino acids long and are in particular 13-18 amino acids long, whereas longer and shorter peptides may also be effective.

[0090] As used herein, the term “epitope” refers to an antigenic determinant in a molecule such as an antigen, i.e., to a part in or fragment of the molecule that is recognized by the immune system, for example, that is recognized by a T cell, in particular when presented in the context of MHC molecules. An epitope of a protein such as a tumor antigen preferably comprises a continuous or discontinuous portion of said protein and is preferably between 5 and 100, preferably between 5 and 50, more preferably between 8 and 30, most preferably between 10 and 25 amino acids in length, for example, the epitope may be preferably 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25 amino acids in length. It is particularly preferred that the epitope in the context of the present invention is a T cell epitope.

[0091] As used herein, the term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide of the present disclosure, however, can be joined to, linked to, or inserted into another polypeptide (e.g., a heterologous polypeptide) with which it is not normally associated in a cell and still be "isolated" or "purified." When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, for example, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation.

[0092] As used herein the term “neo-epitope” refers to a T cell epitope that is not present in a reference such as a normal non-cancerous or germline cell but is found in cancer cells. This includes, in particular, situations wherein in a normal non-cancerous or germline cell a corresponding epitope is found, however, due to one or more mutations in a cancer cell the sequence of the epitope is changed so as to result in the neo-epitope. This also includes situations wherein in a normal non-cancerous or germline cell no T cell epitope is found, however, due to one or more mutations in a cancer cell the sequence is changed so as to create a new neo-epitope. In aspects, a “neo-epitope” of the present disclosure may be encoded by a neoplasia-specific mutation that is unique to the neoplasia patient/subject (e.g., epitope that is specific to both the cancer cell and subject from which it is found), and may be referred to herein as a “subject-specific neo-epitope.” In aspects, a “neo-epitope” of the present disclosure may be encoded by a neoplasia-specific mutation that is present in a neoplasia (e.g., cancer) cell in at least 1%, 2%, 3%, 4%, 5%,

or more than 5% of subjects in a population of subjects suffering from the neoplasia (e.g., bladder cancer), and may be referred to herein as a “shared neo-epitope.” In aspects, a “shared neo-epitope” may be present in two or more, three or more, four or more, five or more, etc. subjects in a population of subjects suffering from the neoplasia (e.g., bladder cancer).

[0093] As used herein, the terms “neoantigen” or “neo-antigenic” means a class of tumor antigens that arises from a neoplasia-specific mutation(s) which alters the amino acid sequence of genome encoded proteins. “Neoantigens” can include one or more neo-epitopes, including subject-specific or shared neo-epitopes. A “subject-specific neo-epitope” means a neoplasia-specific mutation that is unique to the neoplasia patient/subject (e.g., a mutation that is specific to both the cancer cell and subject from which it is found). A “shared neoplasia-specific mutation” means a neoplasia-specific mutation that is present in a neoplasia (e.g., cancer) cell in at least 1%, 2%, 3%, 4%, 5%, or more than 5% of subjects in a population of subjects suffering from the neoplasia, e.g., the specific type of neoplasia, such as bladder cancer. In aspects, a “shared neoplasia-specific mutation” means a neoplasia-specific mutation that is present in a neoplasia (e.g., cancer) cell in two or more, three or more, four or more, five or more, etc. subjects in a population of subjects suffering from the neoplasia, e.g., the specific type of neoplasia, such as bladder cancer.

[0094] As used herein, the term “neoplasia” refers to any disease that is caused by or results in the abnormal proliferation of cells, inappropriately low levels of apoptosis, or both. Neoplasia can be benign, pre-malignant, or malignant. Cancer is an example of a neoplasia. Non-limiting examples of cancer include leukemia (e.g., acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic myelocytic leukemia, chronic lymphocytic leukemia), polycythemia vera, lymphoma (e.g., Hodgkin's disease, non-Hodgkin's disease), Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors such as sarcomas and carcinomas (e.g., fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma,

hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, uterine cancer, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, schwannoma, meningioma, melanoma, neuroblastoma, and retinoblastoma). Lymphoproliferative disorders are also considered to be proliferative diseases.

[0095] As used herein, the term “pharmaceutically acceptable” refers to approved or approvable by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, including humans.

[0096] As used herein, the term “pharmaceutically acceptable excipient, carrier or diluent” or the like refer to an excipient, carrier or diluent that can be administered to a subject, together with an agent, and which does not destroy the pharmacological activity thereof and is nontoxic when administered in doses sufficient to deliver a therapeutic amount of the agent.

[0097] Ranges provided herein are understood to be shorthand for all of the values within the range. For example, a range of 1 to 25 is understood to include any number, combination of numbers, or sub-range from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or 25, as well as all intervening decimal values between the aforementioned integers such as, for example, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. With respect to sub-ranges, “nested sub-ranges” that extend from either end point of the range are specifically contemplated. For example, a nested sub-range of an exemplary range of 1 to 25 may comprise 1 to 5, 1 to 10, 1 to 15, and 1 to 20 in one direction, or 25 to 20, 25 to 15, 25 to 10, and 25 to 5 in the other direction.

[0098] As used herein, the term “regulatory T cell”, “Treg” or the like, means a subpopulation of T cells that suppress immune effector function, including the suppression or down regulation of CD4⁺ and/or CD8⁺ effector T cell (Teff) induction, proliferation, and/or cytokine production, through a variety of different mechanisms including cell-cell contact and suppressive cytokine production. In aspects, CD4⁺ Tregs are characterized by the presence of certain cell surface markers including but not limited to CD4, CD25, and FoxP3. In aspects, upon activation, CD4⁺ regulatory T cells secrete immune suppressive cytokines and chemokines including but not limited to IL-10 and/or TGF β . CD4⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules

including but not limited to granzyme B and perforin. In aspects, CD8⁺ Tregs are characterized by the presence of certain cell surface markers including but not limited to CD8, CD25, and, upon activation, FoxP3. In aspects, upon activation, regulatory CD8⁺ T cells secrete immune suppressive cytokines and chemokines including but not limited to IFN γ , IL-10, and/or TGF β . In aspects, CD8⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and/or perforin.

[0099] As used herein, the term “regulatory T cell epitope” (“Tregitope”) refers to a “T cell epitope” that causes a tolerogenic response (Weber CA et al., (2009), *Adv Drug Deliv*, 61(11):965-76) and is capable of binding to MHC molecules and engaging (i.e. interacting with and activating) circulating naturally occurring Tregs (in aspects, including natural Tregs and/or adaptive Tregs). In aspects, upon activation, CD4⁺ regulatory T cells secrete immune suppressive cytokines and chemokines including but not limited to IL-10 and/or TGF β . CD4⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and perforin. In aspects, CD8⁺ Tregs are characterized by the presence of certain cell surface markers including but not limited to CD8, CD25, and, upon activation, FoxP3. In aspects, upon activation, regulatory CD8⁺ T cells secrete immune suppressive cytokines and chemokines including but not limited to IFN γ , IL-10, and/or TGF β . In aspects, CD8⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and/or perforin.

[00100] As used herein, the term “T cell epitope” means an MHC ligand or protein determinant, 7 to 30 amino acids in length, and capable of specific binding to MHC molecules (e.g. human leukocyte antigen (HLA) molecules) and interacting with specific T cell receptors (TCRs). As used herein, in the context of a T cell epitope (e.g., a neo-epitope, Tregitope, etc.) that is known or determined (e.g. predicted) to engage a T cell (e.g., regulatory T cells and/or other detrimental T cells, such as T cells with potential host cross-reactivity and/or anergic T cells), the terms “engage”, “engagement” or the like means that when bound to a MHC molecule (e.g. human leukocyte antigen (HLA) molecules), the T cell epitope is capable of interacting with the TCR of the T cell and activating the T cell (which in the case of an anergic T cell, includes functional

inactivation). Generally, T cell epitopes are linear and do not express specific three-dimensional characteristics. T cell epitopes are not affected by the presence of denaturing solvents. The ability to interact with T cell epitopes can be predicted by *in silico* methods (De Groot AS et al., (1997), *AIDS Res Hum Retroviruses*, 13(7):539-41; Schafer JR et al., (1998), *Vaccine*, 16(19):1880-4; De Groot AS et al., (2001), *Vaccine*, 19(31):4385-95; De Groot AR et al.,(2003), *Vaccine*, 21(27-30):4486-504, all of which are herein incorporated by reference in their entirety.

[00101] As used herein, the term “T Cell Receptor” or “TCR” refers to a protein complex expressed by T cells that is capable of engaging a specific repertoire of MHC/Ligand complexes as presented on the surface of APCs.

[00102] As used herein, the term “vaccine” refers to a pharmaceutical preparation (pharmaceutical composition) or product that upon administration induces an immune response, in particular a cellular immune response, which recognizes and attacks a pathogen or a diseased cell such as a neoplasia (e.g., a cancer cell). A vaccine may be used for the prevention or treatment of a disease. Accordingly, vaccines are medicaments which include antigens and are used in humans or animals for generating specific defense and protective substance by vaccination. The term “personalized neoplasia vaccine” or the like concerns a particular neoplasia patient and means that a neoplasia (e.g. cancer) vaccine is adapted to the needs or special circumstances of an individual neoplasia patient.

HLA/MHC binding

[00103] In aspects of the invention, neoantigens and self antigens are evaluated for immune presentation. The major histocompatibility complex (MHC) is a large locus on vertebrate's DNA containing a set of closely linked polymorphic genes that code for cell surface proteins essential for the adaptive immune system. The human MHC is also called the HLA (human leukocyte antigen) HLA. Neoantigens may be individually evaluated for binding *in vitro* or to panels of mono-allelic cells. MHC binding can be determined by identifying peptides associated with MHC by liquid chromatography-tandem mass spectrometry (LC MS/MS) which allows identification of a large number of sequences that have undergone the entire peptide presentation pathway. (Crech et al., 2018, *The Role of Mass Spectrometry and Proteogenomics in the Advancement of HLA Epitope Prediction*. *Proteomics* 18(12):e1700259). The LC MS/MS dataset published by Abelin et al. represents over 26,000 Class I peptides eluted across 16 HLA-A or HLA-B monoallelic cell lines. (Abelin et al., 2017, *Mass Spectrometry Profiling of HLA-Associated Peptidomes in Mono-*

allelic Cells Enables More Accurate Epitope Prediction. *Immunity* 46(2):315-326). Such eluted peptides databases are useful to identify peptides that bind to MHC, to evaluate *in silico* predictions, to screen or rank peptides identified by *in silico* predictions, and to improve *in silico* prediction methods. binding to HLA/MHC may be evaluated.

[00104] Several public *in silico* tools have been developed to predict MHC binding. NetMHCpan-2.0 is an *in silico* tool that generates quantitative predictions of the affinity of any peptide-MHC class I interaction. NetMHCpan-2.0 was trained on a large set of quantitative MHC binding data, covering human HLA-A and HLA-B. (Hoof I, Peters B, Sidney J, et al. NetMHCpan, a method for MHC class I binding prediction beyond humans. *Immunogenetics*. 2009;61:1–13). NetMHCpan-3.0 captures differences in the length profile of binders to different MHC molecules leading to improved accuracy for ligand identification due to more uniform sampling of the MHC. (Nielsen M, Andreatta M. NetMHCpan-3.0; improved prediction of binding to MHC class I molecules integrating information from multiple receptor and peptide length datasets. *Genome Med*. 2016;8:33). NetMHCpan-4.0 is further iteration of the *in silico* tool and is trained on binding affinity and eluted ligand data. (Jurtz V, Paul S, Andreatta M, et al. NetMHCpan-4.0: Improved Peptide–MHC Class I Interaction Predictions Integrating Eluted Ligand and Peptide Binding Affinity Data. *J. Immunol*. 2017;199:3360 LP-3368).

T cells

[00105] T-cells are the most important effector cell types that mediate various immune responses and therefore, have been preferred targets for immunomodulation. T cells can be broadly classified as T-effector (Teff) cells and T-regulatory (Treg) cells based on the paradoxical nature of their function. (Kumar, P. et al., 2018, A Comprehensive Review on the Role of Co-signaling Receptors and Treg Homeostasis in Autoimmunity and Tumor Immunity. *J. Autoimmun*. 95:77). Foxp3 is the lineage-specific transcription factor exclusively expressed in Tregs and not in Teff cells (Josefowicz, S.Z. et al., 2012, Regulatory T cells: mechanisms of differentiation and function. *Annu Rev Immunol* 30:531). The major discriminating factor between Treg and Teff cells is their affinity for self-antigens. (Jordan, M.S. et al., 2001, Thymic selection of CD4(+)CD25(+) regulatory T cells induced by an agonist self-peptide. *Nat Immunol* 2:468). During thymic selection, T-cell clones expressing high-affinity T-cell receptors (TCRs) for self-antigens are either deleted by negative selection or rendered anergic. However, thymic negative selection is imperfect in that self-reactive T-cell clones often escape negative selection, migrate to the periphery and

contribute to autoimmunity. However, T-cells expressing TCRs with an intermediate affinity for self-antigens gain Foxp3 expression and become Tregs are positively selected and migrate to the periphery where they help maintain peripheral self-tolerance (Jordan, 2001).

T cell receptor (TCR) repertoire

[00106] The T cell receptor repertoire is diverse and differs according to T cell function. Bentzen describes a method for determining interactions that govern TCR recognition of peptide-major histocompatibility complex (pMHC) by measuring relative affinities of TCRs to libraries of barcoded peptide-MHC variants and develop a TCR fingerprint. (Bentzen et al., 2018, T cell receptor fingerprinting enables in-depth characterization of the interactions governing recognition of peptide-MHC complexes. *Nature Biotechnology* 36:1191). Jurtz et al. developed a method to predict T cell receptor fingerprinting enables in-depth characterization of the interactions governing recognition of peptide-MHC complexes (Jurtz et al., 2018, NetTCR: sequence-based prediction of TCR binding to peptide-MHC complexes using convolutional neural networks. doi:10.1101/433706). In another example, a machine learning approach, called NetTCR, has been developed and was trained on 8,920 TCR β CDR3 sequences and 91 cognate peptide targets obtained from IEDB and from immune assay data. (Klinger et al., 2015, Multiplex identification of antigen-specific T cell receptors using a combination of immune assays and immune receptor sequencing. *PloS One* 10, e0141561). Ogishi and Yotsuyanagi have taken advantage of immunodominant epitopes, which would be expected to exhibit some prominent features that make them especially prone to be recognized by T cells to model repertoire-wide TCR-epitope contact potential (Ogishi and Yotsuyanagi, 2019, Quantitative prediction of the landscape of T cell epitope immunogenicity in sequence space. *Front. Immunol.* 10, 827).

Identifying Neoplasia-Specific Mutations

[00107] In aspects, the step of identifying neoplasia-specific mutations (e.g., cancer-specific mutations) comprises sequencing genomic DNA and/or RNA of a neoplasia specimen (e.g., a neoplasia specimen of the patient). In aspects, a neoplasia specimen relates to any sample, such as a bodily sample derived from a patient, containing or being expected of containing neoplasia cells (e.g. tumor or cancer cells). In aspects, the bodily sample may be any tissue sample such as blood, a tissue sample obtained from a neoplasia sample (e.g., a primary tumor or from tumor

metastases/circulating tumor cells), or any other sample containing neoplasia cells (e.g., tumor or cancer cells).

[00108] In aspects, the step of identifying of neoplasia-specific mutations comprises comparing the sequence information obtained from the neoplasia specimen with a reference sample, such as sequence information obtained from sequencing nucleic acid (e.g., such as DNA or RNA) of normal, non-neoplasia cells (e.g., non-cancerous cells) cells, such as somatic or germline tissue/cells. In aspects, a reference sample may be obtained from the neoplasia patient or a different individual. In aspects, a reference sample may be any tissue sample such as blood or a sample from a non-neoplasia tissue. In aspects, normal genomic germline DNA may be obtained from peripheral blood mononuclear cells (PBMCs).

[00109] In aspects, neoplasia-specific mutations may include all neoplasia-specific (e.g. cancer-specific) mutations present in one or more neoplasia cells (e.g., cancer or tumor cells) of a patient, or it may refer to only a portion of the neoplasia-specific mutations present in one or more neoplasia cells of a patient. Accordingly, the present disclosure may involve the identification of all neoplasia-specific mutations present in one or more neoplasia cells of a patient, or it may involve the identification of only a portion of the neoplasia-specific mutations present in one or more neoplasia cells of a patient. In aspects, the methods of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine of the present disclosure provide for the identification of a number of neoplasia-specific mutations which will provide a sufficient number of neo-epitopes to be included in the instantly-disclosed strategies, methods, and compositions.

[00110] In aspects, the mutations are neoplasia-specific mutations (e.g., somatic mutations) in a neoplasia specimen (e.g. a tumor specimen) of a neoplasia patient (e.g. a cancer patient), which may be determined by identifying sequence differences between the genome, exome and/or transcriptome of a neoplasia specimen and the genome, exome and/or transcriptome of a non-neoplasia specimen. In aspects, neoplasia-specific mutations, including somatic mutations, are determined in the genome, preferably the entire genome, of a neoplasia specimen. As such, the instant disclosure may include identifying all or a portion of neoplasia-specific mutations of the genome, preferably the entire genome, of one or more neoplasia cells. In aspects, neoplasia-specific mutations, including somatic mutations, are determined in the exome, preferably the entire exome, of a neoplasia specimen. As such, the instant disclosure may include identifying all or a portion of neoplasia-specific mutations of the exome, preferably the entire exome of one or more

neoplasia cells. In aspects, optionally, neoplasia-specific mutations, including somatic mutations, are determined in the transcriptome, preferably the entire transcriptome, of a neoplasia specimen. As such, the instant disclosure may include identifying all or a portion of the neoplasia-specific transcriptome, preferably the entire transcriptome, of one or more neoplasia cells.

[00111] In aspects, any suitable sequencing method as is known in the art can be used according to the instant disclosure for determining neoplasia-specific mutations is step (i), including but not limited to “conventional” sequencing methodology and Next Generation Sequencing (NGS) technologies. “Next Generation Sequencing” or “NGS” refers to all high throughput sequencing technologies which, in contrast to the “conventional” sequencing methodology known as Sanger chemistry, read nucleic acid templates randomly in parallel along the entire genome by breaking the entire genome into small pieces. As is known in the art, such NGS technologies (also known as massively parallel sequencing technologies) are able to deliver nucleic acid sequence information of a whole genome, exome, transcriptome (all transcribed sequences of a genome) or methylome (all methylated sequences of a genome) in very short time periods, e.g. within 1-2 weeks, preferably within 1-7 days or most preferably within less than 24 hours and allow, in principle, single cell sequencing approaches. Multiple NGS platforms which are commercially available or which are known in the art can be used. Non-limiting examples of such NGS technologies/platforms include, but are not limited to sequencing-by-ligation approaches, ion semiconductor sequencing, pyrosequencing, single-molecule sequencing technologies, nano-technologies for single-molecule sequencing, and electron microscopy based technologies for single-molecule sequencing. Further, in aspects, “Third Generation Sequencing” methods, as are known in the art, could be used for determining neoplasia-specific mutations. In aspects, neoplasia-specific mutations may be determined by direct protein sequencing techniques, as are known in the art. Further, in aspects, neoplasia-specific mutations can be determined by using MHC multimers, as is known in the art.

[00112] As such, in aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the step of identifying neoplasia-specific mutations includes identifying sequence differences between the full or partial genome, exome, and/or transcriptome of a neoplasia specimen from the subject diagnosed as having a neoplasia and a non-neoplasia specimen. In aspects, a non-neoplasia specimen is derived from the subject diagnosed as having a neoplasia. In further aspects, identifying neoplasia-specific mutations or identifying sequence

differences comprises Next Generation Sequencing (NGS). In aspects, the step of identifying neoplasia-specific mutations comprises selecting from the neoplasia a plurality of nucleic acid sequences, each comprising mutations not present in a non-neoplasia sample. In aspects, identifying neoplasia-specific mutations comprises sequencing genomic DNA and/or RNA of the neoplasia specimen.

[00113] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the neoplasia-specific mutations are neoplasia-specific somatic mutations. In aspects, the neoplasia-specific mutations are single nucleotide variations (SNVs), insertions and deletions (which can generate both in-frame and frameshift mutations), and other large-scale rearrangements such as but not limited to chromosomal inversions, duplications, insertions, deletions, or translocations. In aspects, neoplasia specific mutations, including SNVs, insertions, and deletions, are non-synonymous mutations. In aspects, neoplasia-specific mutations, including SNVs, insertions and deletions (which can be non-synonymous mutations), and other large-scale rearrangements, are mutations of proteins encoded in the neoplasia specimen of the subject diagnosed as having a neoplasia. In aspects, neoplasia specific mutations, including SNVs, are non-synonymous mutations. In aspects, neoplasia-specific mutations, including SNVs (which can be non-synonymous mutations), indels, and frameshifts, are mutations of proteins encoded in the neoplasia specimen of the subject diagnosed as having a neoplasia.

Identifying Subject-Specific Neo-Epitopes

[00114] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the step of assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises *in silico* testing. In aspects, *in silico* testing includes using validated algorithms (e.g., but not limited to, EpiMatrix[®], netMHCpan, NetMHC, netMHCcons, SYFPEITHI, HLA_BIND) to predict which neoplasia-specific mutations create neo-epitopes, particularly neo-epitopes that can bind to the MHC allotypes of the patient. For example, using validated algorithms, bioinformatic analysis of the identified neoplasia-specific mutations and their respective cognate native antigens can be performed to predict which identified neoplasia-specific mutations create neo-epitopes that can bind to the patient's MHC allotype, and in aspects to predict which identified neoplasia-specific mutations create neo-epitopes that could bind to the patient's MHC allotype more effectively than the cognate native antigen. Thus, in aspects, assessing identified neoplasia-specific mutations from

a neoplasia specimen of a subject diagnosed as having a neoplasia identified to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations for use in the personalized neoplasia vaccine, wherein said neo-epitopes are known or determined (e.g. predicted) to bind to a MHC protein of the subject comprises the use of well-validated algorithms.

[00115] In aspects, said *in silico* testing to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises using the EpiMatrix[®] algorithm. EpiMatrix[®] is a proprietary computer algorithm developed by EpiVax, which is used to screen protein sequences for the presence of putative T cell epitopes. The algorithm uses matrices for prediction of 9- and 10-mer peptides binding to MHC molecules. Each matrix is based on position-specific coefficients related to amino acid binding affinities that are elucidated by a method similar to, but not identical to, the pocket profile method (Sturniolo, T. et al., *Nat. Biotechnol.*, 17:555-561, 1999). Input sequences are parsed into overlapping 9-mer or 10-mer frames where each frame overlaps the last by 8 or 9 amino acids, respectively. Thus, in aspects, input sequences of the mutated peptide from step (a) and the non-mutated peptide from step (b) are parsed into overlapping 9-mer or 10-mer frames where each frame overlaps the last by 8 or 9 amino acids. Each of the resulting frames from the mutated peptide from step (a) and the non-mutated peptide from step (b) are then scored for predicted binding affinity with respect to MHC class I alleles (e.g., but not limited to, HLA-A and HLA-B alleles) and MHC class II alleles (e.g., but not limited to HLA-DRB1 alleles). EpiMatrix[®] raw scores are normalized against the scores of a large sample of randomly generated peptides (e.g., but not limited to 10,000 randomly generated peptides). The resulting “Z” scores are normally distributed and directly comparable across alleles. The resulting “Z” score is reported. In aspects, any 9-mer or 10-mer peptide with an allele-specific EpiMatrix[®] Z-score that is theoretically the top 5% of any given sample (e.g., having an EpiMatrix[®] Z-score above 1.64), is considered a putative T cell epitope. In aspects, EpiMatrix[®] identifies the mutated peptide as a neo-epitope when: 1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non- mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or 2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide the non-mutated peptide.

Previous studies have also demonstrated that EpiMatrix[®] accurately predicts published MHC ligands and T cell epitopes.

[00116] In aspects of the prognostic methods and methods of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations includes one or more of the following steps:

a) determining a binding score for a mutated peptide to one or more MHC molecules, wherein said mutated peptide is encoded by at least one of said neoplasia-specific mutations;

b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations;

c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for sufficiently large enough set (e.g., at least 10,000) randomly generated peptides using naturally observed amino acid frequencies;

d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and

e) identifying the mutated peptide as a neo-epitope when: 1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or 2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide the non-mutated peptide. In further aspects, the one or more MHC molecules are MHC class I molecules and/or MHC class II molecules.

[00117] In aspects of the invention, the step of assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes encoded by said mutations comprises *in vitro* testing. More particularly, determining the binding score of both the mutated peptide of step (a) and the non-mutated peptide of step (b) may comprise *in vitro* MHC binding assays (as are known in the art) to determine a binding score for the mutated peptide to one or more MHC molecules and to determine a binding score for the non-mutated peptide to the one or more MHC

molecules. In aspects, and similar to an *in silico* analysis, input sequences are parsed into overlapping 9-mer or 10-mer frames where each frame overlaps the last by 8 or 9 amino acids, respectively. Thus, in aspects, input sequences of the mutated peptide from step (a) and the non-mutated peptide from step (b) are parsed into overlapping 9-mer or 10-mer frames where each frame overlaps the last by 8 or 9 amino acids. Each of the resulting frames from the mutated peptide from step (a) and the non-mutated peptide from step (b) are then scored for binding affinity with respect to MHC class I alleles (e.g., but not limited to, HLA-A and HLA-B alleles) in *in vitro* binding assays, with such binding assays as are known in the art. In the case of testing for epitopes that bind MHC class II alleles (e.g., but not limited to HLA-DRB1 alleles) in *in vitro* binding assays, input sequences are parsed into overlapping 15-mer or 20-mer frames where each frame overlaps the last by 5 or 10 amino acids, respectively. Thus, in aspects, input sequences of the mutated peptide from step (a) and the non-mutated peptide from step (b) are parsed into overlapping 15-mer or 20-mer frames where each frame overlaps the last by 5 or 10 amino acids. Each of the resulting frames from the mutated peptide from step (a) and the non-mutated peptide from step (b) are then scored for binding affinity with respect to MHC class II alleles (e.g., but not limited to HLA-DRB1 alleles) in *in vitro* binding assays, with such binding assays as are known in the art.

[00118] In aspects of the invention, the step of determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for a sufficiently large enough set (e.g., at least 10,000) randomly generated peptides using naturally observed amino acid frequencies, the raw binding scores, whether determined by *in silico* methods or *in vitro* methods, are adjusted to fit a normal, or Z-distribution. Raw binding scores are normalized based on the average (μ) binding score and standard deviation (σ) of a set of a large number (e.g., 10,000) random 9- or 10-mer amino acid sequences, following the naturally observed amino acid frequencies from UniProtKB/Swiss-Prot, as follows:

$$\text{Normalized binding score} = \frac{\text{Raw binding score} - \mu}{\sigma}$$

[00119] Normalized binding scores, which may be referred to as binding scores or likelihood of binding, within the top 5% of this normal distribution are defined as “hits”; which are potentially immunogenic and worthy of further consideration. These peptides have a significant chance of binding to MHC molecules with moderate to high affinity and, therefore, have a significant chance

of being presented on the surface of both professional antigen presenting cells (APC) such as dendritic cells or macrophages, as well as non-professional APC, where they may be interrogated and potentially bound by passing CD8⁺ and CD4⁺ T cells.

[00120] In aspects, the mutated peptide and non-mutated peptide are both 9 amino acids in length or the mutated peptide and non-mutated peptide are both 10 amino acids in length. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule comprises identifying the amino acid residues which are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule comprises identifying the amino acid residues which are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule comprises identifying the amino acid residues which are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule comprises identifying the amino acid residues which are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc. of the mutated and non-mutated peptide as counted from the amino terminal). In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule comprises identifying the amino acid residues which are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule comprises identifying the amino

acid residues which are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal.

[00121] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, particularly assessing the neoplasia-specific mutations to identify known or determined (e.g. predicted) neo-epitopes, the identified neo-epitopes may be optionally further confirmed by experimental validation for peptide-MHC binding, activation of CD8⁺ and/or CD4⁺ T cells, and/or by confirmation of gene expression at the RNA level. Such experimental validation may comprise *in vitro* and/or *in vivo* techniques, as are known in the art.

Identification and Removal of Neo-Epitopes that are Known or Determined (e.g. Predicted) to Engage Regulatory T cells and/or Other Detrimental T cells

[00122] As previously described, the instantly-disclosed data suggest the possibility that tumor-derived neo-epitopes may be recruiting regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) to the tumor. As such, the inadvertent inclusion of regulatory T cell-driving neo-epitopes and/or other detrimental T cell-driving neo-epitopes (including T cells with potential host cross-reactivity and/or anergic T cells) in vaccine formulations may hinder efforts to induce strong T cell-mediated tumor control. Screening of neoantigen sequences to identify and remove potential regulatory T cell inducing neo-epitopes and/or other detrimental T cell inducing neo-epitopes (e.g., using specialized tools, including *in silico* screening tools) may be critical to designing new vaccines with higher quality candidates.

[00123] As such, in aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the step of assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises determining whether said identified neo-epitopes encoded by said mutations share TCR contacts with proteins derived from either the human proteome or the human microbiome, wherein said identified neo-epitopes encoded by said mutations that are determined to share TCR contacts with proteins derived from either the human proteome or the human microbiome are identified as neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, TCR contacts for a 9-mer

identified neo-epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope as counted from the amino terminal, wherein the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, and wherein the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule comprises identifying the amino acid residues which are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc. of the mutated and non-mutated peptide as counted from the amino terminal). In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 9-mer mutated peptide and a 9-mer non- mutated peptide that bind to a MHC class I molecule comprises identifying the amino acid residues which are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal. In aspects, the step of determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule comprises identifying the amino acid residues which are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal.

[00124] In aspects, the step of assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells comprises conducting a homology screen on each identified neo-epitope or epitope sequence presenting a high likelihood of binding to MHC in order to characterize the degree of similarity with self of each of the encoded MHC class I- and MHC class II-restricted identified neo- epitopes and their corresponding non-mutated epitopes. MHC class I or MHC class II neo- epitopes and MHC class I or MHC class II corresponding non-mutated epitopes with two or more (and in further aspects, three or more) cross-reactive matches in the reference proteome are categorized as exhibiting a high degree of similarity with self and are considered to have a higher likelihood of

being tolerated or to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells).

[00125] In aspects, a homology screen is used to remove epitopes containing combinations of TCR-facing residues that are commonly found in a reference proteome. In aspects, a homology screen comprises analysis of all the predicted epitopes contained within a given protein sequence and dividing each predicted epitope into its constituent amino acid content of both the MHC-binding epitope and the TCR-binding epitope. In aspects, the TCR-binding epitope (which can be referred to as TCR binding residues, TCR facing epitope, TCR facing residues, or TCR contacts) for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope, while the MHC-binding epitope (which can be referred to as MHC contacts, MHC facing residues, MHC-binding residues, or MHC-binding face) for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at position 1, 4, 6, and 9, both as counted from the amino terminal. In aspects, the TCR binding epitope for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at position 1, 2, 3, and 9, both as counted from the amino terminal. In aspects, the TCR binding epitope for a 10-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope, while the MHC binding epitope for a 10-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at position 1, 2, 3, 9, and 10, both as counted from the amino terminal. In aspects, the TCR-binding epitope for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc.) of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the amino terminal. In aspects, the TCR binding epitope for 9-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the amino terminal. In aspects, the TCR-binding epitope for a 10-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at any combination

of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope or epitope, while the MHC binding agretope for a 10-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the aminoterminal.

[00126] Each sequence is then screened against a database of proteins (e.g., a database of human proteins derived from the UniProt database (UniProt Proteome ID UP000005640, Reviewed/Swiss-Prot set)). Cross-conserved epitopes, or peptides derived from the reference proteome with a compatible MHC binding agretope (i.e. the agretopes of both the input (mutated) peptide and its reference non-mutated counterpart are predicted to bind to the same MHC allele) and exactly the same TCR facing epitope, are returned. The Homology Score of an epitope corresponds to the number of matching cross-conserved MHC binding peptides within the reference proteome. In other words, the Homology Score H_e of an epitope e is calculated as follows:

$$H_e = |X_e|$$

where:

X_e corresponds to the set of MHC binding peptides derived from the reference proteome that are restricted to the same MHC class I or MHC class II as epitope e and presenting a TCR facing epitope identical to the epitope e .

[00127] By extension, the Homology Score of a given peptide or protein corresponds to the average Homology Score of each individual epitope contained with the peptide or protein. In other words, the Homology Score H_p of a peptide p is calculated as follows:

$$H_p = \frac{\sum_{e \in E} H_e}{|E|} \text{ where:}$$

- E corresponds to the set of MHC class I- or MHC class II-restricted epitopes within peptide p ;
- H_e corresponds to the Homology Score of epitope e as defined above.

[00128] In aspects, an analysis procedure is then run on each mutated sequence to determine if a substring within the amino acid sequence can be found, such that:

- at least one MHC class I- or MHC class II-restricted epitope is encoded in the substring, and;
- all MHC class I- or MHC class II-restricted neo-epitopes encoded in the substring have no more than two cross-reactive matches in the reference proteome, and;

- all MHC class I- or MHC class II-restricted epitopes encoded in the substring have no more than two cross-reactive matches in the reference proteome.

[00129] This analysis procedure has the effect of removing amino acid substrings containing putative epitopes that engage regulatory T cells other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) and other highly cross-conserved epitopes from the identified neo-epitope sequences. The resulting sequences will only contain epitopes or neo-epitopes that exhibit low degree of similarity with self-sequences. Neo-epitope sequences are discarded from consideration for use in a personalized neoplasia-specific vaccine if no substring matching the above criteria can be found. Conversely, the same homology analysis can be performed against a set of known infectious disease-derived epitopes known to be immunogenic, extracted for example from the IEDB database, or against a set of other known immunogenic sequences or common pathogen-derived sequences. This analysis has the purpose of identifying neo-epitope candidates that share a high degree of homology with other known or putative effector T cell epitopes. Neoantigens containing such neo-epitopes can be prioritized in vaccine formulations.

[00130] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the step of assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises *in silico* testing. In aspects, *in silico* testing comprises analyzing whether the identified neo-epitopes are predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) using the JANUSMATRIX™ algorithm. JANUSMATRIX™ is a homology analysis tool that compares putative T cell epitopes and their TCR-facing residues across genome sequences rather than linear peptide fragments, and thus considers aspects of antigen recognition that are not captured by raw sequence alignment. In aspects, JANUSMATRIX™ parses the epitopes into 9-mer frames and/or 10-mer frames and divides each 9-mer or 10-mer into the MHC-binding epitope and the TCR-binding epitope. In aspects, the TCR-binding epitope (which can be referred to as TCR binding residues, TCR facing epitope, TCR facing residues, or TCR contacts) for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope, while the MHC-binding epitope (which can be referred to

as MHC contacts, MHC facing residues, MHC-binding residues, or MHC-binding face) for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at position 1, 4, 6, and 9, both as counted from the amino terminal. In aspects, the TCR binding epitope for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at position 1, 2, 3, and 9, both as counted from the amino terminal. In aspects, the TCR binding epitope for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope, while the MHC binding epitope for a 10-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at position 1, 2, 3, 9, and 10, both as counted from the amino terminal. In aspects, the TCR-binding epitope for a 9-mer identified neo-epitope or epitope that bind to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 (e.g., but not limited to, positions 3, 5, 7 and 8; positions 2, 5, 7, and 8; positions 2, 3, 5, and 7, etc.) of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the amino terminal. In aspects, the TCR binding epitope for 9-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope or epitope, while the MHC binding epitope for a 9-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the amino terminal. In aspects, the TCR-binding epitope for a 10-mer identified neo-epitope or epitope that bind to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope or epitope, while the MHC binding epitope for a 10-mer identified neo-epitope or epitope is the complementary face to the TCR facing residues, both as counted from the amino terminal. JANUSMATRIX™ then searches for potentially cross-reactive TCR-facing epitopes across any number of large sequence databases that have been pre-loaded into the tool, including the protein sequences from bacterial and viral organisms that make up the gut microbiome (e.g., the human gut microbiome), autologous proteins from the genome (e.g., the human genome), and viral and bacterial pathogens (e.g., human viral and human bacterial pathogens). JANUSMATRIX™ focuses in 9-mer and/or 10-mer searches because although peptides of different lengths interact with the MHC, most T cell epitopes can be mapped to a minimum of nine or ten amino acids in any given peptide, even if the peptide is longer.

In further aspects an identified neo-epitope is predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) if the output JANUSMATRIX™ score for the neo-epitope is greater than or equal to 2 (and in further aspects, greater than or equal to 3).

[00131] In aspects, the method further comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production. As described previously, in aspects, upon activation, CD4⁺ regulatory T cells secrete immune suppressive cytokines and chemokines including but not limited to IL-10 and/or TGF β . CD4⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and perforin. In aspects, CD8⁺ Tregs are characterized by the presence of certain cell surface markers including but not limited to CD8, CD25, and, upon activation, FoxP3. In aspects, upon activation, regulatory CD8⁺ T cells secrete immune suppressive cytokines and chemokines including but not limited to IFN γ , IL-10, and/or TGF β . In aspects, upon activation, CD8⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and/or perforin.

[00132] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the step of assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*. In aspects, a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production. As described previously, in aspects, upon activation, CD4⁺ regulatory T cells secrete immune suppressive cytokines and chemokines including but not limited to IL-10 and/or TGF β . CD4⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to

granzyme B and perforin. In aspects, CD8⁺ Tregs are characterized by the presence of certain cell surface markers including but not limited to CD8, CD25, and, upon activation, FoxP3. In aspects, upon activation, regulatory CD8⁺ T cells secrete immune suppressive cytokines and chemokines including but not limited to IFN γ , IL-10, and/or TGF β . In aspects, upon activation, CD8⁺ Tregs may also exert immune suppressive effects through direct killing of target cells, characterized by the expression upon activation of effector molecules including but not limited to granzyme B and/or perforin. In aspects, cross-reactive or auto-reactive T cell responses will be tested by *in vitro* priming of T cells using neoepitope peptides containing non-synonymous amino acid substitutions and presented by autologous pAPC. This *in vitro* immunogenicity protocol may follow the methodology established by Wullner et al. (Wullner D, Zhou L, Bramhall E, Kuck A, Goletz TJ, Swanson S, Chirmule N, Jawa V. Considerations for Optimization and Validation of an In vitro PBMC Derived T cell Assay for Immunogenicity Prediction of Biotherapeutics. *Clin Immunol* 2010 Oct; 137(1): 5-14, incorporated by reference in its entirety). T cells that expand following *in vitro* priming to the neoepitope peptides will then be tested for reactivity to the corresponding native or wild type (non-mutated) peptide epitopes. Reactivity to native peptide sequences will be determined by measuring cytokine production including, but not limited to, IFN γ , TNF α , IL-2 and/or markers of T cell effector function including, but not limited to, CD107a and granzyme B.

Ranking Polypeptides Comprising Subject-Specific Neo-Epitopes Encoded by Said Identified Neoplasia-Specific Mutations

[00133] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further comprises ranking peptides or polypeptides comprising said identified subject-specific neo-epitopes, provided said neo-epitope is not identified as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), for their usability in an immunogenic composition, such as a personalized neoplasia vaccine. As such, in aspects, the identified subject-specific peptides or polypeptides comprise at least one identified neo-epitope encoded by said identified neoplasia-specific mutations, provided said neo-epitope is not identified as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells), are ranked for their usability as epitopes in an immunogenic composition, such as a personalized neoplasia

vaccine. In aspects, the methods comprise a manual or computer-based analytical process in which peptides or polypeptides comprising the identified subject-specific neo-epitopes are analyzed and selected for their usability in the respective vaccine to be provided. In aspects, said analytical process is a computational algorithm-based process. Preferably, said analytical process comprises determining and/or ranking peptides or polypeptides comprising subject-specific neo-epitopes according to a determination (e.g., prediction) of their capacity of being immunogenic.

[00134] In aspects, comprises ranking peptides or polypeptides comprising said identified subject-specific neo-epitopes for their usability as epitopes in an immunogenic composition, such as a personalized neoplasia vaccine comprises determining (e.g., predicting) one or more characteristics associated with the peptides or polypeptides comprising identified subject-specific neo-epitopes, the characteristics including immunogenicity-related features, sequencing-related features, and/or physiochemical-related features.

[00135] In aspects, determined immunogenicity-related features of the peptides or polypeptides comprising identified subject-specific neo-epitopes may include one of more of: count of MHC class I neo-epitopes; percentile ranks of the MHC class I neo-epitopes; MHC class I-restricted regulatory T cell and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); Count of MHC class II neo-epitopes; percentile ranks of the MHC class II neo-epitopes; MHC class II-restricted regulatory T cell and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); and/or whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains both MHC class I and II neo-epitopes.

[00136] In aspects, determined sequencing-related features of the peptides or polypeptides comprising identified subject-specific neo-epitopes may include one of more of: expression level of the associated transcript; coverage of the mutation in the tumor DNA, *i.e.*, the number of unique sequencing reads that overlap the genomic position of the mutation; variant allele fraction (VAF) of the mutation in the tumor DNA, *i.e.*, the relative frequency, from 0 to 1, of the observed mutation across sequencing reads; and/or other sequencing metadata, as may be needed.

[00137] In aspects, determined physiochemical-related features of the peptides or polypeptides comprising identified subject-specific neo-epitopes may include one of more of: net charge of the

optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one charged residue; the count of cysteines (C) within the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one cysteine (C) and is negatively charged; whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a poly-proline motif ('PP'); whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one methionine (M); whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains an N-terminal glutamine (Q); whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a glycine (G) and/or proline (P) in the last or second to last positions; whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a 'DG', 'DS', 'DA', or 'DN' motif; and/or the hydropathy index of the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes).

[00138] In aspects, the method further comprises ranking, based on the determined characteristics, each of the peptides or polypeptides comprising identified subject-specific neo-epitopes. In aspects, the top 5-30, including every value and range therein, ranked peptides or polypeptides comprising identified subject-specific neo-epitopes are included in the personalized neoplasia vaccine. In aspects, the peptides or polypeptides comprising identified subject-specific neo-epitopes are scored and ranked according to the ranking scheme disclosed in Example 1.

Effect of Inhibitory CD8+ cells

Suppressor (Treg) CD8+ T cells appear to develop in the periphery and have not been well characterized. CD8+ T cells with suppressive phenotype have been described in human tumors, but data directly correlating control of tumor growth cell phenotype is limited and generation of CD8+ T cells with suppressive phenotype can result from multiple mechanisms. The inventors have characterized CD8+ suppressive effects and developed a score of overall immunogenic activity of variant alleles of a CT26 neoantigen vaccine.

$$\text{Score} = \text{Immunogenicity} \times \text{VAF}$$

where

Immunogenicity

$$= (\text{Class I neo-epitope content} - \text{Class I cross-reactive potential}) \\ + (\text{Class II neo-epitope content} - \text{Class II cross-reactive potential})$$

and:

VAF is the Variant Allele Frequency as it is observed within a tumor sample.

Class I and Class II immunogenicity have also been observed to coincide with effector and regulatory activity, measured for example by cytokine release, or by a predictive algorithm as follows:

$$\text{Class I Immunogenicity} = \beta \max \left(\sum Z - \left(\sum Z + \frac{JMX}{2} \right) \right)$$

and

$$\text{Class II Immunogenicity} = \alpha \left(0, \sum Z - \left(\sum Z + \frac{JMX}{2} \right) \right)$$

where Z = Neo-epitope Z score (class I or II)

and

JMX = JANUSMATRIX™ score (class I or II)

[00139] JANUSMATRIX™ examines cross-reactive T cell epitopes from both HLA binding and TCR-facing sides to allow comparison across large genome sequence databases including common human pathogens. JANUSMATRIX™ score is representative of predicted engagement of regulatory T cells and/or other detrimental T cells.

[00140] In general, peptides with more Class II neo-epitopes will have higher Class II immunogenicity scores, and immunogenic potentials can be negated by cross-reactivity potential. Peptides with Class I JMX scores below 3 will retain positive Class II immunogenicity scores, peptides with JMX scores of 3 will have null immunogenicity scores, while peptides with Class II JMX scores of 3 or more will have negative Class II Immunogenicity scores.

[00141] In general, peptides with more Class I neo-epitopes will have higher Class I immunogenicity scores, and immunogenic potentials can be negated by cross-reactivity potential. Peptides with Class I JMX scores below 3 will retain positive Class I Immunogenicity scores,

while peptides with Class I JMX scores of 3 or more will have null Class I Immunogenicity scores. Said another way, for Class I, high JMX scores had a neutral impact on immunogenicity.

Analysis of Class II and Class I neo-epitopes in tumors

[00142] Class II and Class I neo-epitopes in tumors were analyzed and correlated with patient outcomes. Neo-epitope expression is a substantially better predictor of disease free survival (DFS) than mutation burden. Subjects displaying relatively high levels of Teff neo-epitopes compared to Treg epitopes demonstrate longer DFS and the association is improved when both Class II and Class I neo-epitopes are accounted for.

[00143] For vaccine design and prognostic applications, analysis of neoepitopes includes consideration of one or more of the following:

[00144] Immunogenicity-related features: Count of MHC class I neo-epitopes; Minimal percentile rank of a MHC class I neo-epitope; MHC class I-restricted Treg induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); Count of MHC class II neo-epitopes (in aspects, which may include one or more of); Minimal percentile rank of a MHC class II neo-epitope; MHC class II-restricted Treg induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains both MHC class I and II neo-epitopes.

[00145] Sequencing-related features (in aspects, which may include one or more of): Expression level of the associated transcript; Coverage of the mutation in the tumor DNA, i.e. the number of unique sequencing reads that overlap the genomic position of the mutation; Variant allele fraction (VAF) of the mutation in the tumor DNA, i.e. the relative frequency, from 0 to 1, of the observed mutation across sequencing reads; Other sequencing metadata, as needed.

[00146] Physicochemical-related features (in aspects, which may include one or more of): Net charge of the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one charged residue; The count of cysteines (C) within the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one cysteine (C) and is negatively charged; Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-

epitopes) contains a poly-proline motif('PP'); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one methionine(M); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains an N-terminal glutamine (Q); Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a glycine (G) and/or proline (P) in the last or second to last positions; Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a 'DG', 'DS', 'DA', or 'DN' motif; The hydropathy index of the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes).

[00147] Scores can be assigned to features of neoantigens. One exemplary scheme follows, including points, percentages, and penalizing steps that may be varied or optimized.

[00148] Count of MHC class I neo-epitopes (maximum of *20 points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing one or less MHC class I neo-epitopes are assigned *0%* of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing two MHC class I neo-epitopes are assigned *80%* of the points (i.e. 16 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing three or more MHC class I neo-epitopes are assigned *100%* of the points (i.e. 20 points)

[00149] Minimal percentile rank of a MHC class I neo-epitope (maximum of *20 points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls between *5%* (inclusive) and *2.5%* (exclusive) are assigned *0%* of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls between *1%* (exclusive) and *2.5%* (inclusive) are assigned *50%* of the points (i.e. 10 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls within *1%* (inclusive) are assigned *100%* of the points (i.e. 20 points)

[00150] Count of MHC class II neo-epitopes (maximum of *10 points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing one or less MHC class II neo-epitopes are assigned *0%* of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing 2 MHC class II neo-

epitopes are assigned 80% of the points (i.e. 8 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) containing three or more MHC class II neo-epitopes are assigned 100% of the points (i.e. 10 points)

[00151] Minimal percentile rank of a MHC class II neo-epitope (maximum of 5 *points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls between 5% (inclusive) and 2.5 (exclusive) are assigned 0% of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls between 1% (exclusive) and 2.5% (inclusive) are assigned 50% of the points (i.e. 2.5 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls within 1% (inclusive) are assigned 100% of the points (i.e. 5 points)

[00152] Presence of both MHC class I and II neo-epitopes (maximum of 20 *points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing MHC class I neo-epitopes only or MHC class II neo- epitopes only are assigned 0% of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing at least one MHC class I neo-epitope and at least one MHC class II neo-epitope are assigned 100% of the points (i.e. 20 points)

[00153] MHC class I-restricted Treg induction potential (maximum of 5 *points*): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score (as calculated above), between 0 (inclusive) and 0.25 (exclusive) are assigned 100% of the points (i.e. 5 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score, between 0.25 (inclusive) and 0.5 (exclusive) are assigned 50% of the points (i.e. 2.5 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score, between 0.5 (inclusive) and 1 (exclusive) are assigned 10% of the points (i.e. 0.5 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted

average depth of coverage within the reference proteome, or MHC class I Homology Score, above 1 (inclusive) are assigned 0% of the points (i.e. 0 point)

[00154] MHC class II-restricted Treg induction potential (maximum of 20 points): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between 0 (inclusive) and 0.25 (exclusive) are assigned 100% of the points (i.e. 20 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between 0.25 (inclusive) and 0.5 (exclusive) are assigned 50% of the points (i.e. 10 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between 0.5 (inclusive) and 1 (exclusive) are assigned 10% of the points (i.e. 2 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, above 1 (inclusive) are assigned 0% of the points (i.e. 0 point)

[00155] Transcript expression (in e.g. Transcript Per Million, TPM, which is calculated as is known in the art) (maximum of 30 points): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies in the top 10% of the TPMs are assigned 100% of the points (i.e. 30 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies below the top 25% of the TPMs are assigned 0% of the points (i.e. 0 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies between the top 25% and 10% of the TPMs are assigned a linearly distributed percent of points.

[00156] Coverage, calculated as is known in the art (maximum of 1 point): Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a depth of coverage in the tumor DNA of less than 20 are assigned 0% of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a coverage in the tumor DNA of between 20 and 50 (strictly below) are assigned 50% of the points (i.e. 0.5 point); Neoantigens (e.g. peptide or polypeptide comprising

one or more identified neo-epitopes) containing a mutation with a coverage in the tumor DNA of 50 or more are assigned 100% of the points (i.e. 1 point).

[00157] Variant allele fraction (VAF), calculated as is known in the art (maximum of 20 points):

[00158] For neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from the mutanome of syngeneic models: Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF below 0.5 are assigned 0% of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF between 0.5 and 0.75 (strictly below) are assigned 50% of the points (i.e. 10 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF equal to or more than 0.75 are assigned 100% of the points (i.e. 20 points)

[00159] For neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from the mutanome of patients: Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF below 0.1 are assigned 0% of the points (i.e. 0 point); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF between 0.1 and 0.25 (strictly below) are assigned 50% of the points (i.e. 10 points); Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF equal to or more than 0.25 are assigned 100% of the points (i.e. 20 points).

[00160] Penalties can be assigned to a candidate neoantigen.

[00161] Severe penalties (e.g. set to a deduction of 100 points, which may be assigned before or after the 100-point normalization) if: the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) has no charged residues, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) has a null net charge, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains at least two cysteines, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains at least one cysteine and is negatively charged, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains an N-terminal glutamine, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains a poly-proline motif, or the neoantigen (e.g. peptide or

polypeptide comprising one or more identified neo- epitopes) has an hydropathy index greater or equal to 2.

[00162] Moderate penalties (e.g. set to a deduction of 10 points) can be assigned to a candidate neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) if: the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains one cysteine

[00163] Minor penalties (e.g. set to a deduction of 1 point) can be assigned to a candidate neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) if: the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) is negatively charged, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains at least one methionine, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains a glycine and/or proline in the last or second to last positions, or the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) contains a 'DG', 'DS', 'DA', or 'DN' motif.

Designing of Subject-Specific Peptides Comprising at Least One Identified Neo-Epitope Encoded by Said Identified Neoplasia-Specific Mutations

[00164] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further comprises designing at least one subject-specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo-epitope encoded by said mutations, provided said neo-epitope is not identified in as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells).

[00165] In aspects of the method of identifying subject-specific neo-epitopes for a personalized neoplasia vaccine, the method further includes: iv) designing at least one subject-specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo- epitope encoded by said mutations, provided said neo-epitope is not identified in step (iii) as being known or determined (e.g. predicted) to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). In aspects, the method further includes providing the at least one peptide or polypeptide designed in step (iv) or a nucleic acid encoding said peptides or polypeptides. In even further aspects, the method further includes vi)

providing a vaccine comprising the at least one peptide or polypeptide or nucleic acid provided in step (v).

[00166] In aspects, the subject-specific peptides or polypeptides comprising the at least one identified neo-epitope can be of a variety of lengths. In aspects, such subject-specific peptides or polypeptides will at least contain an identified neo-epitope that is determined (e.g. predicted) to bind to the MHC molecule of the patient. In aspects, the subject-specific peptides or polypeptides comprise additional adjacent amino acids extending in the N- and/or C-terminal directions. In aspects, the subject-specific peptides or polypeptides comprising the at least one identified neo-epitope comprising, consisting, or consisting essentially of an amino acid sequence of the at least one identified neo-epitope (e.g., a 9-mer identified neo-epitope that bind to a MHC class II molecule and/or a 9-mer or 10-mer identified neo-epitope that bind to a MHC Class I molecule, and/or fragments or variants thereof), and optionally 1 to 12 additional amino acids distributed in any ratio on the N terminus and/or C-terminus of the the at least one identified neo-epitope. In aspects, the instant disclosure is directed to a peptide or polypeptide have a core amino acid sequence comprising, consisting of, or consisting essentially of the at least one identified neo-epitope, and optionally having extensions of 1 to 12 amino acids on the C-terminal and/or the N-terminal of the core amino acid sequence, wherein the overall number of these flanking amino acids is 1 to 12, 1 to 3, 2 to 4, 3 to 6, 1 to 10, 1 to 8, 1 to 6, 2 to 12, 2 to 10, 2 to 8, 2 to 6, 3 to 12, 3 to 10, 3 to 8, 3 to 6, 4 to 12, 4 to 10, 4 to 8, 4 to 6, 5 to 12, 5 to 10, 5 to 8, 5 to 6, 6 to 12, 6 to 10, 6 to 8, 7 to 12, 7 to 10, 7 to 8, 8 to 12, 8 to 10, 9 to 12, 9 to 10, or 10 to 12, wherein the flanking amino acids can be distributed in any ratio to the C-terminus and the N-terminus (for example all flanking amino acids can be added to one terminus, or the amino acids can be added equally to both termini or in any other ratio). In aspects, the instant disclosure is directed to a peptide or polypeptide have a core sequence comprising, consisting of, or consisting essentially of the at least one identified neo-epitope (and/or fragments and variants thereof), optionally with extensions of 1 to 12 amino acids on the C-terminal and/or the N-terminal, wherein the overall number of these flanking amino acids is 1 to 12, 1 to 3, 2 to 4, 3 to 6, 1 to 10, 1 to 8, 1 to 6, 2 to 12, 2 to 10, 2 to 8, 2 to 6, 3 to 12, 3 to 10, 3 to 8, 3 to 6, 4 to 12, 4 to 10, 4 to 8, 4 to 6, 5 to 12, 5 to 10, 5 to 8, 5 to 6, 6 to 12, 6 to 10, 6 to 8, 7 to 12, 7 to 10, 7 to 8, 8 to 12, 8 to 10, 9 to 12, 9 to 10, or 10 to 12, wherein the flanking amino acids can be distributed in any ratio to the C-terminus and the N-terminus (for example all flanking amino acids can be added to one terminus, or the amino acids can be added equally to both

termini or in any other ratio), provided that the polypeptide with the flanking amino acids is still able to bind to the same HLA molecule (i.e., retain MHC binding propensity) as said polypeptide core sequence without said flanking amino acids. In aspects, said polypeptide with the flanking amino acids is still able to bind to the same HLA molecule (i.e., retain MHC binding propensity) and retain the same TCR specificity as said polypeptide core sequence without said flanking amino acids. In aspects, said flanking amino acid sequences are those that also flank the the at least one identified neo-epitope in the naturally occurring protein.

[00167] In aspects, the subject-specific peptides or polypeptides can be capped with an N-terminal acetyl and C-terminal amino group. In aspects, the subject-specific peptides or polypeptides can be either in neutral (uncharged) or salt forms, and may be either free of or include modifications such as glycosylation, side chain oxidation, or phosphorylation.

[00168] In aspects, a subject-specific peptide or polypeptide can be "isolated" or "purified", which means that it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A subject-specific peptide or polypeptide of the present disclosure, however, can be joined to, linked to, or inserted into another polypeptide (e.g., a heterologous polypeptide) with which it is not normally associated in a cell and still be "isolated" or "purified."

[00169] In aspects, a subject-specific peptide or polypeptide may comprise, but is not limited to, about 9 to about 100 amino acid residues, including any value or range therein. In aspects, a subject-specific peptide or polypeptide may comprise greater than 100 amino acid residues. In aspects, each subject-specific peptide or polypeptide comprising one or more identified neo-epitopes has a length of from 9-40 amino acids, from 9-30 amino acids, from 9-25 amino acids, from 9-23 amino acids, from 9-20 amino acids, or from 9-15 amino acids. In aspects, a subject-specific peptide or polypeptide may comprise at least one identified neo-epitope that is determined (e.g. predicted) to bind to the MHC molecule of the patient, with each at least one neo-epitope including an extension of amino acids (e.g., of a length of 1-12 amino acids, as described above), the extension possibly serving to improve the biochemical properties of the subject-specific peptides or polypeptides (e.g., but not limited to solubility or stability) or to improve the likelihood for efficient proteasomal processing of the peptide.

[00170] In aspects a subject-specific peptide or polypeptide may comprise one or more identified neo-epitopes, wherein each one or more identified neo-epitopes may be spaced by

linkers, in particular neutral linkers. The term “linker” refers to a peptide added between two peptide domains such as epitopes or vaccine sequences to connect said peptide domains. In aspects, a linker sequence is used to reduce steric hindrance between each one or more identified neo-epitopes, is well translated, and supports or allows processing of the each one or more identified neo-epitopes. The linker should have little or no immunogenic sequence elements. For example, in aspects, the present disclosure is directed to a concatemeric polypeptide or peptide that comprises one or more of the instantly-disclosed subject-specific peptides or polypeptides linked, fused, or joined together (e.g., fused in-frame, chemically-linked, or otherwise bound) to an additional peptide or polypeptide. Such additional peptide or polypeptide may be one or more of the instantly-disclosed subject-specific peptides or polypeptides, or may be an additional peptide or polypeptide of interest, such as traditional tumor-associated antigens (TAAs). In aspects a concatemeric peptide is composed of 2 or more, 3 or more, 4 or more, 5 or more 6 or more 7 or more, 8 or more, 9 or more of the instantly-disclosed subject-specific peptides or polypeptides. In other aspects, the concatemeric peptides or polypeptides include 1000 or more, 1000 or less, 900 or less, 500 or less, 100 or less, 75 or less, 50 or less, 40 or less, 30 or less, 20 or less or 100 or less subject-specific peptides or polypeptides. In yet other embodiments, a concatemeric peptide has 3-100, 5-100, 10-100, 15-100, 20-100, 25-100, 30- 100, 35-100, 40-100, 45-100, 50-100, 55-100, 60-100, 65-100, 70-100, 75-100, 80-100, 90-100, 5-50, 10-50, 15-50, 20-50, 25-50, 30-50, 35-50, 40-50, 45-50, 100-150, 100-200, 100-300, 100-400, 100-500, 50-500, 50-800, 50-1,000, or 100-1,000 of the instantly-disclosed subject-specific peptides or polypeptides linked, fused, or joined together. Each peptide or polypeptide of the concatemeric polypeptide may optionally have one or more linkers, which may optionally be cleavage sensitive sites, adjacent to their N and/or C terminal end. In such a concatemeric peptide, two or more of the peptides (including subject-specific peptides or polypeptides as disclosed herein) may have a cleavage sensitive site between them. Alternatively two or more of the peptides (including subject-specific peptides or polypeptides as disclosed herein) may be connected directly to one another or through a linker that is not a cleavage sensitive site.

[00171] As used herein, two peptide or polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, more typically greater than about 90%, and more typically greater than 95% or more homologous or identical. To determine

the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (e.g., percent homology equals the number of identical positions/total number of positions \times 100).

[00172] In aspects, the present disclosure also encompasses a subject-specific peptides or polypeptides comprising at least one identified neo-epitope, with the at least one identified neo-epitope having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu, Met, and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln, exchange of the basic residues His, Lys and Arg and replacements among the aromatic residues Trp, Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found (Bowie JU *et al.*, (1990), *Science*, 247(4948):130610, which is herein incorporated by reference in its entirety).

[00173] In aspects, a variant of the at the least one identified neo-epitope of the subject specific peptides of polypeptides can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a combination of any of these. In aspects, variant of the at least one identified neo-epitope of the subject specific peptides of polypeptides can be fully functional (e.g., retain MHC binding propensity and TCR specificity) or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions; in this case, typically MHC contact

residues provided MHC binding is preserved. In aspects, functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function (e.g., retain MHC binding propensity and TCR specificity). Alternatively, such substitutions can positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region; in this case, typically TCR contact residues.

[00174] In aspects, the present disclosure also includes fragments of the instantly-disclosed at the least one identified neo-epitope of the subject specific peptides of polypeptides. In aspects, the present disclosure also encompasses fragments of the variants of the identified neo-epitopes described herein. In aspects, as used herein, a fragment comprises at least about nine contiguous amino acids. Useful fragments (and fragments of the variants of the identified neo-epitopes described herein) include those that retain one or more of the biological activities of the identified neo-epitope, particularly MHC binding propensity and TCR specificity. Biologically active fragments are, for example, about 9, 12, 15, 16, 20 or 30 or more amino acids in length, including any value or range therebetween. In aspects, fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. In aspects, several fragments can be comprised within a single larger polypeptide. In aspects, a fragment designed for expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

[00175] In aspects, the at the least one identified neo-epitope of the subject specific peptides of polypeptides can include allelic or sequence variants (“mutants”) or analogs thereof. In aspects, the subject-specific peptides or polypeptides comprising the at least one identified neo-epitope can include chemical modifications (e.g., pegylation, glycosylation). In aspects, a mutant retains the same functions performed by a polypeptide encoded by a nucleic acid molecule of the present disclosure, particularly MHC binding propensity and TCR specificity. In aspects, a mutant can provide for enhanced binding to MHC molecules. In aspects, a mutant can lead to enhanced binding to TCRs. In another instance, a mutant can lead to a decrease in binding to MHC molecules and/or TCRs. Also contemplated is a mutant that binds, but does not allow signaling via the TCR.

[00176] In aspects, a subject-specific peptide or polypeptide comprising at least one identified neo-epitope can include a pharmaceutically acceptable salt thereof. “Pharmaceutically acceptable

salt” of a peptide or polypeptide means a salt that is pharmaceutically acceptable and that possesses the desired pharmacological activity of the parent peptide or polypeptide. As used herein, “pharmaceutically acceptable salt” refers to derivative of the instantly-disclosed peptides or polypeptides, wherein such compounds are modified by making acid or base salts thereof. Examples of pharmaceutically acceptable salts include, but are not limited to, mineral or organic acid salts of basic residues such as amines, alkali or organic salts of acidic residues such as carboxylic acids, and the like. The pharmaceutically acceptable salts include the conventional non-toxic salts or the quaternary ammonium salts of the parent compound formed, for example, from non-toxic inorganic or organic acids. For example, such conventional non-toxic salts include, but are not limited to, those derived from inorganic and organic acids selected from 2- acetoxybenzoic, 2-hydroxyethane sulfonic, acetic, ascorbic, benzene sulfonic, benzoic, bicarbonic, carbonic, citric, edetic, ethane disulfonic, 1,2-ethane sulfonic, fumaric, glucoheptonic, gluconic, glutamic, glycolic, glycollyarsanilic, hexylresorcinic, hydrabamic, hydrobromic, hydrochloric, hydroiodic, hydroxymaleic, hydroxynaphthoic, isethionic, lactic, lactobionic, lauryl sulfonic, maleic, malic, mandelic, methane sulfonic, napsylic, nitric, oxalic, pamoic, pantothenic, phenylacetic, phosphoric, polygalacturonic, propionic, salicylic, stearic, subacetic, succinic, sulfamic, sulfanilic, sulfuric, tannic, tartaric, toluene sulfonic, and the commonly occurring amine acids, e.g., glycine, alanine, phenylalanine, arginine, etc.

[00177] The subject-specific peptides or polypeptides comprising the at least one identified neo-epitope may be produced by any known methods of producing peptides or polypeptides, including known *in vitro* and *in vivo* methods. *In vitro* production may be done by variety of methods known in the art, which include peptide or polypeptide chemical synthesis techniques, the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteins or peptides from natural sources, *in vitro* translation, followed by any necessary purification of the expressed peptide/polypeptide. Alternatively, the subject-specific peptides or polypeptides comprising the at least one identified neo-epitope may be produced *in vivo* by introducing molecules (e.g., DNA, RNA, viral expression systems, and the like) that encode tumor specific neoantigens into a subject, whereupon the encoded tumor specific neoantigens are expressed.

[00178] In aspects, the present disclosure also provides for nucleic acids (e.g., DNA, RNA, vectors, viruses, or hybrids) that encode in whole or in part one or more peptides or polypeptides

or concatemeric peptides of the present disclosure. In aspects, a nucleic acid (e.g., a polynucleotide) encoding a subject-specific peptides or polypeptides or concatemeric peptides comprising the at least one identified neo-epitope may be used to produce the neo-epitope *in vitro* or *in vivo*. The polynucleotide may be, e.g., DNA, cDNA, PNA, CNA, RNA, either single- and/or double-stranded, or native or stabilized forms of polynucleotides as are known in the art. An expression vector capable of expressing a polypeptide can also be prepared. Expression vectors for different cell types are well known in the art and can be selected without undue experimentation. Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host (e.g., bacteria), although such controls are generally available in the expression vector. The vector is then introduced into the host bacteria for cloning using standard techniques (see, e.g., Sambrook et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[00179] In aspects, the present disclosure is directed to expression vectors comprising the subject-specific peptides or polypeptides or concatemeric peptides comprising the at least one identified neo-epitope, as well as host cells containing the expression vectors, are also contemplated. The subject-specific peptides or polypeptides or concatemeric peptides comprising the at least one identified neo-epitope may be provided in the form of RNA or cDNA molecules encoding the desired neo-epitopes. One or more peptides or polypeptides or concatemeric peptides of the present disclosure may be encoded by a single expression vector. Such nucleic acid molecules may act as vehicles for delivering neoantigenic peptides/polypeptides/concatemeric peptides to the subject in need thereof, *in vivo*, in the form of, e.g., DNA/RNA vaccines.

[00180] In aspects, the subject-specific peptides or polypeptides (including concatemeric peptides) comprising at least one identified neo-epitope can be purified to homogeneity or partially purified. It is understood, however, that preparations in which the subject-specific peptides or polypeptides comprising at least one identified neo-epitope are not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the at least one neo-epitope, even in the presence of considerable amounts of other components. Thus, the present disclosure encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the subject-specific peptides or polypeptides

comprising at least one identified neo-epitope having less than about 30% (by dry weight) other proteins (*e.g.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, less than about 5% other proteins, less than about 4% other proteins, less than about 3% other proteins, less than about 2% other proteins, less than about 1% other proteins, or any value or range therein. In aspects, when a subject-specific peptide or polypeptide comprising at least one identified neo-epitope of the present disclosure is recombinantly produced, said peptide or polypeptide can also be substantially free of culture medium, for example, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the peptide or polypeptide or nucleic acid preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the peptide or polypeptide or nucleic acid is separated from chemical precursors or other chemicals that are involved in its synthesis. The language "substantially free of chemical precursors or other chemicals" can include, for example, preparations of the peptide or polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, less than about 5% chemical precursors or other chemicals, less than about 4% chemical precursors or other chemicals, less than about 3% chemical precursors or other chemicals, less than about 2% chemical precursors or other chemicals, or less than about 1% chemical precursors or other chemicals.

Pharmaceutical Compositions

[00181] In aspects, a produced subject-specific peptide or polypeptide (including concatemeric peptides) comprising one or more identified neo-epitopes as described herein may subsequently be formulated into a pharmaceutical composition, such as a personalized neoplasia vaccine, and administered to a subject to treat the subject's neoplasia.

[00182] Thus, a further embodiment is directed to a pharmaceutical composition including a plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes or one or more nucleic acids encoding said plurality of selected peptides or polypeptides, wherein the one or more identified neo-epitopes induces a neoplasia-specific effector T cell response in a subject. In aspects, plurality of selected peptides or polypeptides comprising the one or more identified neo-epitopes or one or more nucleic acids encoding said plurality of selected peptides or polypeptides are selected and produced by the methods as disclosed herein.

[00183] In aspects, a pharmaceutical composition may further comprise a pharmaceutically acceptable excipient. A “pharmaceutically acceptable excipient” means an excipient that is useful in preparing a pharmaceutical composition that is generally safe, non-toxic and neither biologically nor otherwise undesirable, and includes excipient that is acceptable for veterinary use as well as human pharmaceutical use. Thus, the term “pharmaceutical excipient” is used herein to describe any ingredient other than the compound(s) of the invention. Examples of pharmaceutical excipients include one or more substances which may act as diluents, flavoring agents, solubilisers, lubricants, suspending agents, binders, preservatives, wetting agents, tablet disintegrating agents, or an encapsulating material. The choice of excipient will to a large extent depend on factors such as the particular mode of administration, the effect of the excipient on solubility and stability, and the nature of the dosage form. A “pharmaceutical excipient” includes both one and more than one such excipient.

[00184] In aspects, a pharmaceutical composition may comprise a pharmaceutically acceptable carrier for administration to a human or an animal. As such, the pharmaceutical compositions can be administered orally as a solid or as a liquid, or can be administered intramuscularly or intravenously as a solution, suspension, or emulsion. Alternatively, the pharmaceutical compositions can be administered by inhalation, intravenously, or intramuscularly as a liposomal suspension. In some embodiments, the pharmaceutical composition is formulated for oral administration. In other embodiments, the pharmaceutical composition is formulated for intravenous administration. In aspects, a pharmaceutical composition may comprise a pharmaceutically acceptable adjuvant. Such adjuvants may include, but are not limited to, poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS 15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRITX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PEPTEL, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon. In aspects of the pharmaceutical composition, the adjuvant comprises poly-ICLC. The TLR9 agonist CpG and the synthetic double-stranded RNA (dsRNA) TLR3 ligand poly-ICLC are two of the most promising neoplasia vaccine adjuvants currently in clinical development. In preclinical studies, poly-ICLC appears to be the most potent TLR adjuvant when compared to LPS and CpG. This appears due to

its induction of pro-inflammatory cytokines and lack of stimulation of IL-10, as well as maintenance of high levels of co-stimulatory molecules in DCs. Poly-ICLC is a synthetically prepared double-stranded RNA consisting of polyI and polyC strands of average length of about 5000 nucleotides, which has been stabilized to thermal denaturation and hydrolysis by serum nucleases by the addition of polylysine and carboxymethylcellulose. The compound activates TLR3 and the RNA helicase-domain of MDA5, both members of the PAMP family, leading to DC and natural killer (NK) cell activation and mixed production of type I interferons, cytokines, and chemokines.

[00185] In aspects of the pharmaceutical composition the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 peptides or polypeptides, each comprising one or more identified neo-epitopes. In aspects, the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes comprises from 3-20 selected peptides or polypeptides, each comprising one or more identified neo-epitopes.

[00186] In aspects of the pharmaceutical composition, the one or more nucleic acids encoding said plurality of selected peptides or polypeptides are DNA, RNA, or mRNA. In aspects of the pharmaceutical composition, the pharmaceutical composition further comprises an anti-immunosuppressive agent. In aspects, the anti-immunosuppressive agent comprises a checkpoint blockage modulator, such as a checkpoint blockage inhibitor and immune checkpoint stimulators or other additional therapeutic adjuvants as described below.

Methods of Treatment

[00187] One embodiment is directed to a method of treating neoplasia (e.g. cancer or a tumor) in a subject in need of treatment thereof, the method comprising administering an effective amount of the instantly-disclosed subject-specific peptides or polypeptides (including concatemeric peptides) comprising one or more identified neo-epitopes or instantly-disclosed pharmaceutical compositions. It will be appreciated that the administration to a subject of an effective amount of the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can provide therapy for a wide variety of cancers including, but not limited to solid tumors, such as lung, breast, colon, ovarian, brain, liver, pancreas, prostate, malignant melanoma, non-melanoma skin cancers, as well as hematologic

tumors and/or malignancies, such as childhood leukemia and lymphomas, multiple myeloma, Hodgkin's disease, lymphomas of lymphocytic and cutaneous origin, acute and chronic leukemia such as acute lymphoblastic, acute myelocytic or chronic myelocytic leukemia, plasma cell neoplasm, lymphoid neoplasm and cancers associated with AIDS. In certain embodiments of a method of treating cancer in a subject in need of treatment thereof, the method comprises administering to the subject an effective amount of the instantly-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or instantly-disclosed pharmaceutical compositions, the cancer is bladder cancer.

[00188] As used herein, the term “treating” relates to any treatment of a neoplasia (e.g. cancer or a solid tumor), including but not limited to prophylactic treatment and therapeutic treatment. “Treating” includes any effect, e.g., preventing, lessening, reducing, modulating, or eliminating, that results in the improvement of the neoplasia. For example, “treating” or “treatment” of a cancer state includes: inhibiting the cancer, i.e., arresting the development of the cancer or its clinical symptoms; or relieving the cancer, i.e., causing temporary or permanent regression of the cancer or its clinical symptoms. “Prevent,” “preventing,” “prevention,” “prophylactic treatment,” and the like, refer to reducing the probability of developing a disease or condition in a subject, who does not have, but is at risk of or susceptible to developing a disease or condition.

[00189] A “subject” includes mammals, e.g., humans, companion animals (e.g., dogs, cats, birds, and the like), farm animals (e.g., cows, sheep, pigs, horses, fowl, and the like) and laboratory animals (e.g., rats, mice, guinea pigs, birds, and the like). In certain embodiments of a method of treating neoplasia in a subject in need of treatment thereof comprising administering to the subject an effective amount of the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions, the subject that is administered an effective amount is a mammal, and more particularly a human.

[00190] An “effective amount” is defined herein in relation to the treatment of neoplasia (e.g., a cancer or a solid tumor) is an amount that will decrease, reduce, inhibit, or otherwise abrogate the growth of a neoplasia (e.g. a cancer cell or tumor). The “effective amount” will vary depending on the neoplasia and its severity and the age, weight, etc., of the mammal to be treated. The amount, as well as timing and dosing schedule, of a composition of the present disclosure administered to the subject will depend on the type and severity of the disease and on the characteristics of the individual, such as general health, age, sex, body weight and tolerance to drugs. It will also depend

on the degree, severity and type of neoplasia disease. The skilled artisan will be able to determine appropriate dosages and dosage scheduling depending on these and other factors.

[00191] In some aspects, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can be delivered regionally to a particular affected region or regions of the subject's body. In some embodiments, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can be administered systemically. For example, in some embodiments of a method treating cancer in a subject in need of treatment thereof, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions are administered orally. In accordance with the presently disclosed methods, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can be administered orally as a solid or as a liquid. In other embodiments of treating cancer in a subject in need of treatment, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions are administered intravenously. In accordance with the presently disclosed methods, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can be administered intravenously as a solution, suspension, or emulsion. Alternatively, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions also can be administered by inhalation, intravenously, or intramuscularly as a liposomal suspension.

[00192] The compositions of the present invention can also be administered in combination with one or more additional therapeutic compounds. Thus, in some aspects of a method of treating neoplasia (e.g. a cancer or a solid tumor) in a subject in need of treatment thereof comprising administering to the subject an effective amount of the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions, the method further comprises administering to the subject one or more additional therapeutic compounds. It will be appreciated that therapeutic benefits for the treatment of cancer can be realized by combining treatment with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions with one or more additional therapeutic compounds. The term “additional therapeutic compounds”

includes other anti-cancer agents or treatments. The choice of such combinations will depend on various factors including, but not limited to, the type of disease, the age and general health of the subject, the aggressiveness of disease progression, and the ability of the subject to tolerate the agents that comprise the combination. For example, the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions can be combined with other agents and therapeutic regimens that are effective at reducing tumor size (e.g., radiation, surgery, chemotherapy, hormonal treatments, and or gene therapy). Further, in some embodiments, it can be desirable to combine the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions with one or more agents that treat the side effects of a disease or the side effects of one of the additional therapeutic agents, e.g., providing the subject with an analgesic.

[00193] Thus, the term “additional therapeutic compounds” includes a variety of include anti-cancer agents or treatments, such as chemical compounds that are also known as anti-neoplastic agents or chemotherapeutic agents. The agents can be used in combination with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions. Such compounds include, but are not limited to, alkylating agents, DNA intercalators, protein synthesis inhibitors, inhibitors of DNA or RNA synthesis, DNA base analogs, topoisomerase inhibitors, anti-angiogenesis agents, and telomerase inhibitors or telomeric DNA binding compounds. For example, suitable alkylating agents include alkyl sulfonates, such as busulfan, improsulfan, and piposulfan; aziridines, such as a benzodizepa, carboquone, meturedopa, and uredepa; ethylenimines and methylmelamines, such as altretamine, triethylenemelamine, triethylenephosphoramidate, triethylenethiophosphoramidate, and trimethylolmelamine; nitrogen mustards such as chlorambucil, chlornaphazine, cyclophosphamide, estramustine, iphosphamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichine, phenesterine, prednimustine, trofosfamide, and uracil mustard; nitroso ureas, such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, and ranimustine.

[00194] Chemotherapeutic protein synthesis inhibitors can also be combined with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions for the treatment of cancer. Such inhibitors include abrin, aurintricarboxylic acid, chloramphenicol, colicin E3, cycloheximide, diphtheria toxin, edeine A,

emetine, erythromycin, ethionine, fluoride, 5-fluorotryptophan, fusidic acid, guanylyl methylene diphosphonate and guanylyl imidodiphosphate, kanamycin, kasugamycin, kirromycin, and O-methyl threonine.

[00195] Additionally, protein synthesis inhibitors can also be combined with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions for the treatment of cancer. Such inhibitors include modeccin, neomycin, norvaline, pactamycin, paromomycine, puromycin, ricin, shiga toxin, showdomycin, sparsomycin, spectinomycin, streptomycin, tetracycline, thiostrepton, and trimethoprim. Furthermore, inhibitors of DNA synthesis can be combined with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions for the treatment of cancer. Such inhibitors include alkylating agents such as dimethyl sulfate, mitomycin C, nitrogen and sulfur mustards, intercalating agents, such as acridine dyes, actinomycins, adriamycin, anthracenes, benzopyrene, ethidium bromide, propidium diiodide-intertwining, and agents, such as distamycin and netropsin. Topoisomerase inhibitors, such as coumermycin, nalidixic acid, novobiocin, and oxolinic acid, inhibitors of cell division, including colcemide, colchicine, vinblastine, and vincristine; and RNA synthesis inhibitors including actinomycin D, α -amanitine and other fungal amatoxins, cordycepin (3'-deoxyadenosine), dichlororibofuranosyl benzimidazole, rifampicine, streptovaricin, and streptolydigin also can be combined with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions to provide a suitable cancer treatment.

[00196] Thus, current chemotherapeutic agents that can be used in a combination treatment with the presently-disclosed subject-specific peptides or polypeptides comprising one or more identified neo-epitopes or pharmaceutical compositions include, but are not limited to, adrimycin, 5-fluorouracil (5FU), etoposide, camptothecin, actinomycin-D, mitomycin, cisplatin, hydrogen peroxide, carboplatin, procarbazine, mechlorethamine, cyclophosphamide, ifosfamide, melphalan, chjlorambucil, bisulfan, nitrosurea, dactinomycin, duanorubicin, doxorubicin, bleomycin, plicomycin, tamoxifen, taxol, transplatin, vinblastin, and methotrexate, and the like.

[00197] The additional therapeutic agents can be administered by the same route or by different routes. For example, a first therapeutic agent of the combination selected may be administered by intravenous injection while the other therapeutic agents of the combination may be administered

orally. Alternatively, for example, all therapeutic agents may be administered orally or all therapeutic agents may be administered by intravenous injection. The sequence in which the therapeutic agents are administered is not narrowly critical.

[00198] Although the present invention and its advantages have been described in detail, it should be understood that various changes, substitutions and alterations can be made herein without departing from the spirit and scope of the invention as defined in the appended claims.

[00199] The present invention will be further illustrated in the following Examples which are given for illustration purposes only and are not intended to limit the invention in any way.

Examples

Example 1

[00200] Tumor growth inhibition post vaccination with a Tregitope-depleted personalized cancer vaccine.

[00201] Clinical studies have highlighted the potential of precision cancer immunotherapy to effectively control the tumor of patients across cancer indications. However, recent studies showcase the difficulty of establishing robust CD8⁺ and CD4⁺ T cell responses. Poor cancer vaccine performance is due in part to the inadvertent inclusion of suppressive T cell neo-epitopes in neoantigen vaccines that may be recognized by regulatory T cells (Tregs).

[00202] To test this hypothesis, we identify and select neo-epitopes and exclude such identified neo-epitopes that are predicted to engage regulatory T cells from the subject-specific neo-epitopes for use in the personalized neoplasia vaccine). State-of-the-art predictive algorithms have been extensively validated in prospective vaccine studies for infectious diseases (Moise et al., Hum. Vaccines Immunother 2015; Wada et al., Sci. Rep. 2017). Distinctive features of the procedure over other *in silico* pipelines include the ability to accurately predict CD4⁺ and CD8⁺T cell epitopes and to identify tolerated or Treg epitopes.

[00203] Bioinformatics design of a Tregitope-depleted vaccine

[00204] Each peptide is first parsed into overlapping 9- and 10-mer frames and evaluated frame for its likelihood to bind to Balb/c MHC class I (H2-Dd and H2-Kd) and MHC class II (I-Ad, I-Ed) alleles. For human analyses, each frame is evaluated for its likelihood to bind to the patient's MHC class I (HLA-A, HLA-B) and MHC class II (HLA-DRB1) alleles. In the event that a patient

expresses an MHC allele for which predictions are not readily available, a homology analysis can be performed between the patient allele and our reference alleles. For this analysis, we extract the amino acid sequences from the MHC binding pockets of the patient allele and compare them to the binding pockets from alleles we reliably model. Any non-supported patient allele whose MHC binding pockets are at least 90% homologous with the MHC binding pockets of a reference allele can be included in our analysis, where the model for the homologous reference allele is used to assess a frame's likelihood of binding to the patient allele.

[00205] Each frame-by-allele “assessment” is a statement about (i.e., determination of) predicted MHC binding affinity. Raw binding scores are adjusted to fit a normal, or Z-distribution. Raw binding scores are normalized based on the average (μ) binding score and standard deviation (σ) of a set of 10,000 random 9- or 10-mer amino acid sequences, following the naturally observed amino acid frequencies from UniProtKB/Swiss-Prot (web.expasy.org/docs/relnotes/relstat.html), as follows:

$$\text{Normalized binding score} = \frac{\text{Raw binding score} - \mu}{\sigma}$$

Normalized binding scores, herein referred to as binding scores or likelihood of binding, within the top 5% of this normal distribution are defined as “hits”; that is to say, potentially immunogenic and worthy of further consideration. These peptides have a significant chance of binding to MHC molecules with moderate to high affinity and, therefore, have a significant chance of being presented on the surface of both professional antigen presenting cells (APC) such as dendritic cells or macrophages, as well as non-professional APC, where they may be interrogated by passing T cells.

[00206] T cell epitopes predicted in mutated sequences are compared to normal matched sequences in order to identify neo-epitopes. T cell epitopes from mutated sequences are labeled as neo-epitopes if:

- Their likelihood of binding to MHC falls within the top 5 percentile of our expected distribution and the likelihood of binding to MHC of the normal matched sequence falls below the top 10 percentile of the expected distribution, or;
- Their likelihood of binding to MHC falls within the top 5 percentile of our expected distribution and the likelihood of binding to MHC of the normal matched

sequence falls within the top 10 percentile of the expected distribution, and there is a least one mismatched TCR-facing amino acid between the mutated and non-mutated peptides.

[00207] TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, and wherein the TCR facing amino acid residues for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal.

[00208] Additionally, sequences presenting a high likelihood of binding to MHC are screened using a customized homology search to remove epitopes containing combinations of TCR-facing residues that are commonly found in a reference proteome. This homology screen first considers all the predicted epitopes contained within a given protein sequence and divides each predicted epitope into its constituent agretope and epitope. Each sequence is then screened against a database of murine proteins derived from the UniProt database (UniProt Proteome ID UP000000589, Reviewed/Swiss-Prot set). For human analyses, each sequence would be then screened against a database of human proteins derived from the UniProt database (UniProt Proteome ID UP000005640, Reviewed/Swiss-Prot set).

[00209] Cross-conserved epitopes, or peptides derived from the reference proteome with a compatible MHC binding agretope (i.e. the agretopes of both the input (mutated) peptide and its reference non-mutated counterpart are predicted to bind to the same MHC allele) and exactly the same TCR facing epitope, are returned. The Homology Score of an epitope corresponds to the number of matching cross-conserved MHC binding peptides within the reference proteome. In other words, the Homology Score H_e of an epitope e is calculated as follows:

$$H_e = |X_e|$$

where:

X_e corresponds to the set of MHC binding peptides derived from the reference proteome that are restricted to the same MHC class I or MHC class II as epitope e and presenting a TCR facing epitope identical to the epitope e .

[00210] By extension, the Homology Score of a given peptide or protein corresponds to the average Homology Score of each individual epitope contained with the peptide or protein. In other words, the Homology Score H_p of a peptide p is calculated as follows

$$H_p = \frac{\sum_{e \in E} H_e}{|E|}$$

where:

- E corresponds to the set of MHC class I- or MHC class II-restricted epitopes within peptide p ;
- H_e corresponds to the Homology Score of epitope e as defined above.

[00211] T cells that recognize antigen-derived epitopes sharing TCR contacts with epitopes derived from self may be deleted or rendered anergic during thymic selection before they can be released to the periphery. As such, vaccine components targeting these T cells may be ineffective. On the other hand, vaccine-induced immune response targeting cross-reactive epitopes may induce unwanted autoimmune responses targeting the homologues of the cross-reactive epitopes identified by our homology search. As a result, vaccine safety may be reduced. A review of MHC class II-restricted T cell epitopes contained in the IEDB database (iedb.org) indicates that there is a statistically significant relationship between high Homology Scores and observed production of IL-10 and a statistically significant inverse relationship between high Homology Scores and observed production of IL-4 (see, e.g., Moise et al. *iVax: An integrated toolkit for the selection and optimization of antigens and the design of epitope-driven vaccines*. *Human Vaccin Immunother.* 2015; 11(9):2312-21, herein incorporated by reference in its entirety). Conversely, the same homology analysis can be performed against a set of known infectious disease-derived epitopes known to be immunogenic, extracted for example from the IEDB database, or against a set of other known immunogenic sequences or common pathogen-derived sequences. This analysis has the purpose of identifying neo-epitope candidates that share a high degree of homology with other known or putative effector T cell epitopes. Peptides or polypeptides containing such neo-

epitopes (or nucleic acid encoding said peptides or polypeptides) can be prioritized in vaccine formulations.

[00212] Each mutated sequence undergoes the homology screen described above in order to characterize the degree of similarity with self of each of the encoded MHC class I- and MHC class II-restricted epitopes and neo-epitopes. MHC class I or MHC class II epitopes and MHC class I or MHC class II neo-epitopes with two or more cross-reactive matches in the reference proteome are categorized as exhibiting a high degree of similarity with self and are considered to have a higher likelihood of being tolerated or to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells). An optimization procedure is then run on each mutated sequence to determine if a substring within the amino acid sequence can be found, such that:

- At least one MHC class I- or MHC class II-restricted epitope is encoded in the substring, and;
- All MHC class I- or MHC class II-restricted neo-epitopes encoded in the substring have no more than two cross-reactive matches in the reference proteome, and;
- All MHC class I- or MHC class II-restricted epitopes encoded in the substring have no more than two cross-reactive matches in the reference proteome.

[00213] This procedure has the effect of removing amino acid substrings containing putative Tregitopes and/or other putative detrimental T cell epitopes (including epitopes that engage T cells with potential host cross-reactivity and/or anergic T cells) and other highly cross-conserved epitopes from mutated sequences. The resulting optimized sequences will only contain epitopes or neo-epitopes that exhibit low degree of similarity with self-sequences. Mutated sequences are discarded from consideration if no substring matching the above criteria can be found.

[00214] One hundred thirty-five of the 378 analyzed mutated sequences could be optimized to yield amino acid sequences that contained MHC class I and/or MHC class II restricted neo-epitopes displaying a low degree of self-similarity. These 135 sequences (peptides or polypeptides comprising one or more identified neo-epitopes) were then ranked according to one or more of the following features:

- Immunogenicity-related features:
 - o Count of MHC class I neo-epitopes;
 - o Minimal percentile rank of a MHC class I neo-epitope;

- MHC class I-restricted Treg induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes);
- Count of MHC class II neo-epitopes (in aspects, which may include one or more of);
- Minimal percentile rank of a MHC class II neo-epitope;
- MHC class II-restricted Treg induction potential of the neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes);
- Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains both MHC class I and II neo-epitopes.
- Sequencing-related features (in aspects, which may include one or more of):
 - Expression level of the associated transcript;
 - Coverage of the mutation in the tumor DNA, i.e. the number of unique sequencing reads that overlap the genomic position of the mutation;
 - Variant allele fraction (VAF) of the mutation in the tumor DNA, i.e. the relative frequency, from 0 to 1, of the observed mutation across sequencing reads;
 - Other sequencing metadata, as needed.
- Physicochemical-related features (in aspects, which may include one or more of):
 - Net charge of the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes);
 - Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one charged residue;
 - The count of cysteines (C) within the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes);
 - Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one cysteine (C) and is negatively charged;
 - Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a poly-proline motif ('PP');
 - Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one methionine (M);
 - Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or

- more identified neo-epitopes) contains an N-terminal glutamine (Q);
- Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a glycine (G) and/or proline (P) in the last or second to last positions;
- Whether the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a 'DG', 'DS', 'DA', or 'DN' motif;
- The hydrophathy index of the optimized neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes).

[00215] Scores can be assigned to neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) according to the following scoring scheme (in aspects, scores (e.g., points and/or percentages) that are italicized and bolded may be subject to adjustment; in aspects, the scoring scheme may include one of more of the following scoring steps/penalizing steps:).

- Count of MHC class I neo-epitopes (maximum of *20 points*):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing one or less MHC class I neo-epitopes are assigned *0%* of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing two MHC class I neo-epitopes are assigned *80%* of the points (i.e. 16 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing three or more MHC class I neo-epitopes are assigned *100%* of the points (i.e. 20 points)
- Minimal percentile rank of a MHC class I neo-epitope (maximum of *20 points*):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls between *5%* (inclusive) and *2.5%* (exclusive) are assigned *0%* of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls between *1%* (exclusive) and *2.5%* (inclusive) are assigned *50%* of the points (i.e. 10 points)

- Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class I neo-epitope falls within 1% (inclusive) are assigned 100% of the points (i.e. 20 points)
- Count of MHC class II neo-epitopes (maximum of 10 points):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing one or less MHC class II neo-epitopes are assigned 0% of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing 2 MHC class II neo-epitopes are assigned 80% of the points (i.e. 8 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing three or more MHC class II neo-epitopes are assigned 100% of the points (i.e. 10 points)
- Minimal percentile rank of a MHC class II neo-epitope (maximum of 5 points):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls between 5% (inclusive) and 2.5 (exclusive) are assigned 0% of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls between 1% (exclusive) and 2.5% (inclusive) are assigned 50% of the points (i.e. 2.5 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) where the minimal percentile rank of a MHC class II neo-epitope falls within 1% (inclusive) are assigned 100% of the points (i.e. 5 points)
- Presence of both MHC class I and II neo-epitopes (maximum of 20 points):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing MHC class I neo-epitopes only or MHC class II neo-epitopes only are assigned 0% of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing at least one MHC class I neo-epitope and at least one MHC

- class II neo-epitope are assigned *100%* of the points (i.e. 20 points)
- MHC class I-restricted Treg induction potential (maximum of *5 points*):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score (as calculated above), between *0* (inclusive) and *0.25* (exclusive) are assigned *100%* of the points (i.e. 5 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score, between *0.25* (inclusive) and *0.5* (exclusive) are assigned *50%* of the points (i.e. 2.5 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score, between *0.5* (inclusive) and *1* (exclusive) are assigned *10%* of the points (i.e. 0.5 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class I-restricted average depth of coverage within the reference proteome, or MHC class I Homology Score, above *1* (inclusive) are assigned *0%* of the points (i.e. 0 point)
 - MHC class II-restricted Treg induction potential (maximum of *20 points*):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between *0* (inclusive) and *0.25* (exclusive) are assigned *100%* of the points (i.e. 20 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between *0.25* (inclusive) and *0.5* (exclusive) are assigned *50%* of the points (i.e. 10 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, between *0.5* (inclusive)

- and 1 (exclusive) are assigned 10% of the points (i.e. 2 points)
- Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) with a MHC class II-restricted average depth of coverage within the reference proteome, or MHC class II Homology Score, above 1 (inclusive) are assigned 0% of the points (i.e. 0 point)
 - Transcript expression (in e.g. Transcript Per Million, TPM, which is calculated as is known in the art) (maximum of 30 points):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies in the top 10% of the TPMs are assigned 100% of the points (i.e. 30 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies below the top 25% of the TPMs are assigned 0% of the points (i.e. 0 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from a transcript whose expression lies between the top 25% and 10% of the TPMs are assigned a linearly distributed percent of points.
 - Coverage, calculated as is known in the art (maximum of 1 point):
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a depth of coverage in the tumor DNA of less than 20 are assigned 0% of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a coverage in the tumor DNA of between 20 and 50 (strictly below) are assigned 50% of the points (i.e. 0.5 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a coverage in the tumor DNA of 50 or more are assigned 100% of the points (i.e. 1 point)
 - Variant allele fraction (VAF), calculated as is known in the art (maximum of 20 points):
 - For neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from the mutanome of syngeneic models:
 - Neoantigens (e.g. peptide or polypeptide comprising one or more

identified neo-epitopes) containing a mutation with a VAF below 0.5 are assigned 0% of the points (i.e. 0 point)

- Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF between 0.5 and 0.75 (strictly below) are assigned 50% of the points (i.e. 10 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF equal to or more than 0.75 are assigned 100% of the points (i.e. 20 points)
- For neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) derived from the mutanome of patients:
- Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF below 0.1 are assigned 0% of the points (i.e. 0 point)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF between 0.1 and 0.25 (strictly below) are assigned 50% of the points (i.e. 10 points)
 - Neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) containing a mutation with a VAF equal to or more than 0.25 are assigned 100% of the points (i.e. 20 points)

[00216] Points are then summed and normalized to a 100-point scale, where a perfect neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes), in other words, a neoantigen that is assigned the maximum number of points, would score 100.

[00217] Severe penalties (currently set to a deduction of 100 points, which may be assigned before or after the 100-point normalization) can be assigned to a candidate neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) if:

- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) has no charged residues, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) has a null net charge, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least two cysteines, or

- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one cysteine and is negatively charged, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains an N-terminal glutamine, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a poly-proline motif, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) has an hydropathy index greater or equal to 2.

[00218] Moderate penalties (currently set to a deduction of 10 points) can be assigned to a candidate neoantigen (e.g. peptide or polypeptide comprising one or more identified neo- epitopes) if:

- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains one cysteine

[00219] Minor penalties (currently set to a deduction of 1 point) can be assigned to a candidate neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) if:

- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) is negatively charged, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains at least one methionine, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a glycine and/or proline in the last or second to last positions, or
- The neoantigen (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) contains a 'DG', 'DS', 'DA', or 'DN' motif.

[00220] Alternatively, scores can be assigned according to following scoring scheme:

$$S_p = (C1_p + C2_p) \times F_p \times E_p$$

or

$$S_p = (C1_p + C2_p) \times F_p$$

where:

- S_p corresponds to the score of peptide p ;
- $C1_p$ corresponds to the MHC class I-restricted immunogenic potential of peptide p ;

- $C2_p$ corresponds to the MHC class II-restricted immunogenic potential of peptide p ;
- F_p corresponds to the observed frequency of the mutation encoded by peptide p in the tumor biopsy;
- E_p corresponds to expression of the mutation encoded by peptide p in the tumor biopsy (which in aspects is expression of the gene containing the mutation), expressed as a percentile rank of the observed expression distribution.

[00221] The MHC class I-restricted immunogenic potential $C1_p$ of peptide p is calculated as follows:

$$C1_p = \alpha_1 \left(Z1_p - \left(Z1_p \times \frac{H1_p}{\beta_1} \right) \right)$$

or as

$$C1_p = \alpha_1 \sum_{e \in E1_p} \left(Z1_e - \left(Z1_e \times \frac{H1_e}{\beta_1} \right) \right)$$

where:

- α_1 (e.g., usually set to 1) and β_1 (e.g., usually set to 2, which corresponds to situations in the above-defined methods wherein “epitopes with two or more cross-reactive matches in the reference proteome are categorized as exhibiting a high degree of similarity with self”) are predefined constants;
- $E1_p$ corresponds to the set of MHC class I-restricted neo-epitopes within peptide p ;
- $Z1_p$ corresponds to the sum of the percentile ranks of each MHC class I-restricted neo-epitope within peptide p , expressed using standard Z-Scores;
- $Z1_e$ corresponds to the percentile rank of the MHC class I-restricted neo-epitope e , expressed using standard Z-Scores;
- $H1_p$ is the MHC class I-restricted Homology Score of peptide p , as defined above;
- $H1_e$ is the MHC class I-restricted Homology Score of neo-epitope e , as defined above.

[00222] The MHC class II-restricted immunogenic potential $C2_p$ of peptide p is calculated as follows:

$$C2_p = \alpha_2 \left(Z2_p - \left(Z2_p \times \frac{H2_p}{\beta_2} \right) \right)$$

or as

$$C2_p = \alpha_2 \sum_{e \in E2_p} \left(Z2_e - \left(Z2_e \times \frac{H2_e}{\beta_2} \right) \right)$$

where:

- α_2 (e.g., usually set to 1) and β_2 (e.g., usually set to 2, which corresponds to situations in the above-defined methods wherein “epitopes with two or more cross-reactive matches in the reference proteome are categorized as exhibiting a high degree of similarity with self”) are predefined constants;
- $E2_p$ corresponds to the set of MHC class II-restricted neo-epitopes within peptide p ;
- $Z2_p$ corresponds to the sum of the percentile ranks of each MHC class II-restricted neo-epitope within peptide p , expressed using standard Z-Scores;
- $Z2_e$ corresponds to the percentile rank of the MHC class II-restricted neo-epitope e , expressed using standard Z-Scores;
- $H2_p$ is the MHC class II-restricted Homology Score of peptide p , as defined above;
- $H2_e$ is the MHC class II-restricted Homology Score of neo-epitope e , as defined above.

[00223] Candidate neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) are then ranked according to their score, from high to low. The highest ranking neoantigens (e.g. peptide or polypeptide comprising one or more identified neo-epitopes) are selected.

[00224] The following tables provide exemplary peptides from a CL-26 cancer model.

Table 1: Neoantigens comprising one or more identified neo-epitopes							
Pep ID	Locus	Sequence <i>MHC class I neo-epitopes</i> (restriction) <u>MHC class II neo-epitopes</u> (restriction)	Gene	Ref AA	AA Pos	Alt AA	SEQ ID NO:
EO_CT26_01	CHR4:86583172	Ac-LQARLTSYETLK-NH2	Haus6	Ala	821	Thr	1
		<u>ARLTSYETL</u> (Dd)					2
		<u>ARLTSYETL</u> (Kd)					3
		<u>ARLTSYETL</u> (Ad)					4
EO_CT26_02	CHR11:69649178	Ac-ETPEACRQARNYLEFSE-NH2	Fxr2	Ser	287	Asn	5
		<u>EACRQARNY</u> (Ad)					6
		<u>ACRQARNYL</u> (Kd)					7
		<u>RQARNYLEF</u> (Ad)					8

EO_CT26_03	CHR2:128676212	Ac-SSRVQYVVNPAVKIVF-NH2	Anapc1	Asp	241	Asn	9
		<u>RVQYVVNPA</u> (Ad)					10
		<u>QYVVNPAVKI</u> (Kd)					11
EO_CT26_04	CHR2:158851764	Ac-TSKYYMRDVIAIESA-NH2	Dhx35	Thr	646	Ile	12
		<i>SKYYMRDVI</i> (Kd)					13
		<i>KYYMRDVIAI</i> (Kd)					14
		<i>YYMRDVIAI</i> (Dd)					15
		<i>YYMRDVIAI</i> (Kd)					16
		<u>YYMRDVIAI</u> (Ad)					17
EO_CT26_05	CHR6:3377051	Ac-PALLIKHMYNKLIS-NH2	Samd9l	Arg	70	His	18
		<u>PALLIKHMY</u> (Ad)					19
		<u>LLIKHMYNK</u> (Ed)					20
		<i>LIKHMYNKL</i> (Kd)					21
		<i>KHMYNKLIS</i> (Ad)					22
EO_CT26_06	CHR5:100037938	Ac-LSWDTSKKNLTEYLSRF-NH2	Hnrmpd1	Asp	163	Asn	23
		<i>SWDTSKKNL</i> (Kd)					24
		<i>TSKKNLTEYL</i> (Kd)					25
		<i>SKKNLTEYL</i> (Kd)					26
EO_CT26_07	CHR12:98815985	NNVHYLNDGDIIYHTAS-NH2	Eml5	Asp	1396	Ala	27
		<i>HYLNDGDAI</i> (Kd)					28
		<i>HYLNDGDAAI</i> (Kd)					29
		<u>GDAIIYHTA</u> (Ad)					30
EO_CT26_08	CHRX:60293650	Ac-PQPDLYRFVRRISI-NH2	Atp11c	Gly	223	Arg	31
		<u>DLYRFVRRI</u> (Ed)					32
		<i>LYRFVRRISI</i> (Kd)					33
EO_CT26_09	CHR12:98785005	Ac-DTKCTKADCLFTHMSR-NH2	Zc3h14	Pro	653	Leu	34
		<u>TKCTKADCL</u> (Ad)					35
		<i>KADCLFTHM</i> (Kd)					36
EO_CT26_10	CHR15:3275728	EEDGIAVWTLNGN-NH2	Sepp1	Asp	122	Ala	37
		<i>DGIAVWTL</i> (Dd)					38
		<i>DGIAVWTL</i> (Kd)					39
EO_CT26_11	CHR7:55873449	Ac-ATVHSSMNKMLEE-NH2	Cyfip1	Glu	71	Lys	40
		<i>TVHSSMNKM</i> (Kd)					41
		<u>VHSSMNKML</u> (Ed)					42
EO_CT26_12	CHR12:91825363	ILGYRYWTGIGVLQSC-NH2	Sel1l	Ala	299	Thr	43
		<i>GYRYWTGIGV</i> (Kd)					44
		<i>RYWTGIGVL</i> (Dd)					45
		<i>RYWTGIGVL</i> (Kd)					46
		<i>RYWTGIGVLQ</i> (Kd)					47
EO_CT26_13	CHR6:52729334	Ac-FCYVTYKGEIRGAS-NH2	Tax1bp1	His	107	Tyr	48
		<i>CYVTYKGEI</i> (Kd)					49
EO_CT26_14	CHR2:109298148	Ac-VKICNMQKAAIL-NH2	Kif18a	Glu	383	Ala	50
		<u>KICNMQKAA</u> (Ad)					51

		<i>KICNMQKAAI</i> (Kd)					52
EO_CT26_15	CHR10:122089020	Ac-RQFPVVEANWTMLHDE-NH2	Tmem5	Ser	259	Asn	53
		<i>VVEANWTML</i> (Dd)					54
EO_CT26_16	CHR2:180713221	Ac-MSYAEKSDEITKD-NH2	Gid8	Pro	7	Ser	55
		<i>SYAEKSDEI</i> (Kd)					56
EO_CT26_17	CHR7:45442527	Ac-RIQEFVRSIFY-NH2	Gys1	Gly	310	Ser	57
		<i>RIQEFVRSI</i> (Kd)					58
EO_CT26_18	CHR5:129697821	Ac-KVGLTVKTYEFLERNIP-NH2	Sept14	Leu	97	Phe	59
		<i>LTVKTYEFL</i> (Kd)					60
		<i>KTYEFLERN</i> (Ed)					61
		<i>KTYEFLERNI</i> (Kd)					62
		<i>TYEFLERNI</i> (Dd)					63
		<i>TYEFLERNI</i> (Kd)					64
EO_CT26_19	CHR7:65663891	Ac-NSSTYWKGNPETLQ-NH2	Tarsl2	Glu	353	Lys	65
		<i>TYWKGNPEM</i> (Kd)					66
		<i>TYWKGNPEME</i> (Kd)					67
		<i>KGNPEMETL</i> (Kd)					68
EO_CT26_20	CHR11:58188928	Ac-RKSYMQKYFLDTV	Gm122 50	Asn	390	Lys	69
		<i>KSYMQKYFL</i> (Kd)					70
		<i>SYMQKYFL</i> (Kd)					71
		<i>SYMQKYFLD</i> (Kd)					72
		<i>YMQKYFLDT</i> (Kd)					73

Table 2: Highly cross-conserved MHC class II-restricted neo-epitopes

Pep ID	Locus	Sequence MHC class II tolerated/tolerogenic epitopes (restriction)	Gene	Ref AA	AA Pos	Alt AA	SEQ ID NO
EO_CT26_Treg_01	CHR2:109894549	Ac-PQKLQALQRALQSE-NH2	Lin7	Val	41	Ala	74
		<i>KLQALQRAL</i> (Ad)					75
EO_CT26_Treg_02	CHR2:156167568	Ac-PHSIKLSRRRSRSKNPFRKDKSPVR-NH2	Rbm39	Ser	129	Asn	76
		<i>IKLSRRRSR</i> (Ed)					77
		<i>KLRRRSRS</i> (Ed)					78
		<i>LSRRRSRSK</i> (Ed)					79
		<i>SRRRSRSKN</i> (Ed)					80
		<i>SKNPFRKDK</i> (Ed)					81
EO_CT26_Treg_03	CHR2:76712742	Ac-HPWLKQRIDKVSTK-NH2	Ttn	Arg	31554	Lys	82
		<i>WLKQRIDKV</i> (Ed)					83
EO_CT26_Treg_04	CHR3:40805884	Ac-HSVEMLLKPRRSLDEN-NH2	Plk4	Ser	405	Leu	84
		<i>MLLKPRRSL</i> (Ad, Ed)					85
EO_CT26_Treg_05	CHR3:90025194	Ac-KTPSSLENDSSNLD-NH2	Ubap21	Met	295	Leu	87
		<i>SSELENDSSN</i> (Ed)					87
EO_CT26_Treg_06	CHR5:106983158	Ac-SRVQAAQAQHSKDSL YKRDND-NH2	Cdc7	Glu	500	Lys	88
		<i>QAAQAQHSK</i> (Ad)					89
		<i>HSKDSL YKR</i> (Ed)					90

EO_CT26_Treg_07	CHR9:85719917	Ac-LEGVRLENEKSNVIAKKTGNK-NH2	Ibtk	Ile	747	Ser	91
		<u>VRLENEKSN</u> (Ed)					92
		<u>EKSNVIAKK</u> (Ed)					93
		<u>KSNVIAKKT</u> (Ed)					94
EO_CT26_Treg_08	CHR11:40728456	Ac-DTTLLASTKKAKKSVSKK-NH2	Hmnr	Ala	66	Thr	95
		<u>LLASTKKAK</u> (Ed)					96
		<u>STKKAKKSV</u> (Ed)					97
EO_CT26_Treg_09	CHR12:98794154	Ac-LLVSSLKIWRKKRDRRC ^{AIH} -NH2	Eml5	Gly	44	Arg	98
		<u>SSLKIWRKK</u> (Ed)					99
		<u>SLKIWRKKR</u> (Ed)					100
		<u>LKIWRKKRD</u> (Ed)					101
		<u>WRKKRDRRC</u> (Ed)					102
EO_CT26_Treg_10	CHR16:57513281	Ac-PMNELDKVVKHKES-NH2	Filip11	Glu	146	Lys	103
		<u>ELDKVVKKH</u> (Ed)					104

Table 3: Highly cross-conserved MHC class I-restricted neo-epitopes

Pep ID	Locus	Sequence	Gene	Ref AA	AA Pos	Alt AA	SEQ ID NO
		MHC class I tolerated/tolerogenic epitopes (restriction)					
EO_CT26_Treg_MHCI_01	CHR1:163996661	Ac-VLDFGCGSGLLGITA-NH2	Mettl18	Leu	184	Phe	105
		<u>FGCGSGLLG</u> (Dd)					106
		<u>CGSGLLGIT</u> (Dd)					107
		<u>GSGLLGITA</u> (Dd)					108
EO_CT26_Treg_MHCI_02	CHR2:109894549	Ac-PQKLQALQRALQSE-NH2	Lin7c	Val	41	Ala	74
		<u>KLQALQRAL</u> (Dd)					75
EO_CT26_Treg_MHCI_03	CHR3:29979653	Ac-NMDTRPSSDSSLQHA-NH2	Mecom	Gly	301	Ser	109
		<u>TRPSSDSSL</u> (Dd)					110
EO_CT26_Treg_MHCI_04	CHR3:138148475	Ac-RRDVARSSLRLI ^{IDC} -NH2	Trmt10a	Val	105	Ile	111
		<u>VARSSLRLI</u> (Dd)					112
EO_CT26_Treg_MHCI_05	CHR5:44192134	Ac-MSNNFVEIKESVFKK-NH2	Tapt1	Gly	285	Glu	113
		<u>NFVEIKESV</u> (Kd)					114
EO_CT26_Treg_MHCI_06	CHR5:137327443	Ac-PSRAIPLGIIIAVAY-NH2	Slc12a9	Thr	302	Ile	115
		<u>RAIPLGIII</u> (Dd)					116
		<u>AIPLGIIIA</u> (Dd)					117
EO_CT26_Treg_MHCI_07	CHR7_55873449	Ac-VHSSMNKMLEEGQEY-NH2	Cyfip1	Glu	71	Lys	118
		<u>SMNKMLEEG</u> (Kd)					119
EO_CT26_Treg_MHCI_08	CHR13_12409236	Ac-QHFGVEKTVSSLLN-NH2	Heatr1	Glu	552	Lys	120
		<u>GVEKTVSSL</u> (Kd)					121
EO_CT26_Treg_MHCI_09	CHR17_84429178	Ac-IKCLMENLKDEISQA-NH2	Thada	Glu	892	Lys	122
		<u>LMENLKDEI</u> (Kd)					123
EO_CT26_Treg_MHCI_10	CHR19_53635752	Ac-QQRKFKASRASILSEM-NH2	Smc3	Asp	733	Ala	124
		<u>KFKASRASIL</u> (Kd)					125
		<u>FKASRASIL</u> (Dd)					126

[00225] *In vivo Study Design*

[00226] The effectiveness of the vaccine was tested in Balb/c mice. Mice are separated into three groups: 1) PBS control; 2) poly-ICLC (vehicle); 3) selected Neoantigen Peptides + poly-ICLC.

- Group 1: PBS, sc injections at days 5, 8, 12, 15, 19, 22, and 26.
- Group 2: poly-ICLC, 50 µg, sc injections at days 5, 8, 12, 15, 19, 22, and 26.
- Group 3: 5 µg / selected Neoantigen Peptide (100 µg total selected Neoantigen Peptides) + 50 µg poly-ICLC, sc injections at days 5, 8, 12, 15, 19, 22, and 26.

[00227] All mice (N=10 mice per group) were injected 3×10^5 tumor cells in 0% Matrigel at day 0. Mice are sacrificed once the tumor volume reached 2,000 mm³ or at day 45, whichever comes first.

[00228] Poly-ICLC Fails to Control Tumor Burden

[00229] Group 2 (mice immunized with poly-ICLC) showed no reduction in tumor burden compared to Group 1 (mice immunized with PBS). These results are consistent with previously reported experiments by Charles River. Less than 50% of mice from Group 1 survived past day 28, with seven out of ten mice (70%) reaching a tumor volume of at least 2,000 mm³ by that day.

[00230] Selected Neoantigen Peptide Vaccine Reduces Tumor Burden

[00231] Group 3 (mice immunized with the selected Neoantigen Peptide vaccine + poly-ICLC) showed a prolonged survival compared to Group 1. In contrast with Group 1 fewer mice from Group 3 reached endpoint by that day.

Example 2

[00232] Suppression of IFN γ Responses When Co-Administering Self-Like Neo-Epitopes Along With a Peptide Vaccine

[00233] Using the Ancer™ platform, CT26 variants were identified and ranked as potential vaccine candidate peptides. From this list, 20 neoantigens were selected to be utilized in the development of a peptide-based vaccine developed for the CT26 colorectal cancer syngeneic mouse model (see above).

[00234] To demonstrate the importance to identify and eliminate putative “self-like” neo-epitopes due to their potential to dampen immunogenicity responses to vaccine candidates, we have identified CT26 neo-epitopes exhibiting high degree of self-similarity based on

JANUSMATRIX™ and tested how their inclusion in vaccine formulations alter their immunogenicity.

[00235] Selection of CT26 Self-like Sequences

[00236] The 378 variants extracted from the private and public CT26 mutantomes were screened with the JANUSMATRIX™ algorithm to identify neoantigen sequences that displayed a high degree of similarity with murine sequences. Thirty-five and 24 out of these 378 SNVs generated putative “self-like” regulatory T cell neo-epitopes restricted to MHC class II and MHC class I, respectively. Ten of these MHC class-II-restricted sequences were filtered out due to potential manufacturability issues or due to the presence of putative Treg neo-epitopes with limited potential of binding to MHC.

[00237] The remaining 25 MHC class II-restricted sequences were manually reviewed to prioritize neoantigens containing the most highly cross-conserved neo-epitopes. In other words, neoantigens encoding MHC class II-restricted neo-epitopes with the highest number of homologous matches with compatible TCR faces within the reference murine proteome were prioritized over the remaining neoantigens. Ten MHC class II “self-like” neoantigens were selected from this list to be used in *in vivo* immunogenicity studies.

[00238] In addition, ten MHC class I “self-like” neoantigens were selected to be used in follow-up *in vivo* studies.

[00239] Study Design

[00240] Balb/c mice were separated into three groups: A) Vehicle control; B) Ancer™-selected CT26 Neoantigen Peptides + adjuvant; C) Ancer™-selected CT26 Neoantigen Peptides + JANUSMATRIX™ MHC class II selected peptides + adjuvant. All vaccines were formulated with the addition of the adjuvant Poly-ICLC. Poly-ICLC, also known as Hiltonol, is a synthetic double-stranded RNA (dsRNA) agonist for pattern recognition receptors (PRRs), and TLR3 agonist. Groups A, B, and C received an initial vaccination with subsequent boosts of vaccine at 2- and 4-weeks post initial vaccination. All mice are sacrificed at 7-10 days after the final boost and spleens were harvested for splenocyte isolation and IFN γ ELISpot assay.

[00241] Group A: 50ug Poly-ICLC in 200 uL

[00242] Group B: 20 Ancer™-selected CT26 Neoantigen Peptides at 5 ug/peptide, 100 ug total peptide, 50ug Poly-ICLC, 200 uL

[00243] Group C: 20 Ancer™-selected CT26 Neoantigen Peptides + 10 JANUSMATRIX™ MHC class II self-like peptides at 5 ug/peptide, 150 ug total peptide, 50ug Poly-ICLC, 200 uL

[00244] Isolated splenocytes were plated and stimulated with Ancer™-selected CT26 Neoantigen Peptides (CT26_pool), JANUSMATRIX™ selected peptides (CT26-Treg_pool), class I peptide pool, as well as individual Ancer™-selected CT26 Neoantigen peptide CT26-1 (CT26_peptide 1) and CT26-20 (CT26_peptide 1). Plates were incubated overnight and then read. A positive result was defined as spot forming cells >50 SFC/million splenocytes over background, and a Stimulation index >2-fold over background. Statistical significance was determined by Student's T-test; per mouse – antigen vs. no antigen stimulus, as well as group comparisons (p<0.05).

[00245] Ancer™-selected CT26 Neoantigen Peptides are Immunogenic

[00246] CT26 neoantigen peptide pool, Class I only pool, and individual peptide CT26-1 elicited a significant epitope-specific IFN γ response in mice who were vaccinated with CT26 peptides. JanuxMatrix selected peptides were not recognized and no positive results were measured in this stimulation condition. Ancer™-selected CT26 Neoantigen Peptides were determined to be immunogenic in mice that were vaccinated with Ancer™-selected CT26 Neoantigen Peptides + Poly-ICLC. Recall responses to the CT26_pool stimulated a significantly increased epitope-specific IFN γ response compared to cells stimulated with media only. No IFN γ response was measured in the cells stimulated with the CT26-Treg peptide pool demonstrating that irrelevant peptides are not recognized in mice vaccinated with only CT26 peptides. In addition, the CT26 neoantigens were able to stimulate a CD8+ specific T cell response as demonstrated by the positive response to the class I pool. Responses to individual epitopes varied. While CT26-1 (class I and II) epitope appears immunogenic, CT26-20 (Class I) was not.

[00247] Ancer™-selected CT26 MHC class II “Self-like” Treg Neoantigen Peptides Suppress Neoantigen Immune Responses

[00248] The Ancer™-selected CT26 Neoantigen Peptide pool elicited a strong IFN γ response in group B vaccinated mice that was not seen in group A demonstrating epitope specific responses. The CT26 peptide pool and Class I pool were also able to stimulate strong epitope specific IFN γ responses in group B mice when compared to group A, but the addition of JANUSMATRIX™ selected MHC class II epitopes in the vaccines administered to group C significantly reduces IFN γ responses.

[00249] Ancer™-selected CT26 Neoantigen Peptide responses are suppressed in group C mice who were immunized with both Ancer™-selected CT26 Neoantigen Peptides and JANUSMATRIX™ selected neoantigens compared to group B who only received Ancer™-selected CT26 Neoantigen Peptides.

Example 3

[00250] *In vitro* HLA peptide binding assay

[00251] HLA binding of individual tumor-specific mutated peptides (e.g., a peptide or polypeptide comprising one or more identified neo-epitopes, as disclosed herein) identified from patient whole exome sequencing data are validated by testing in an *in vitro* competitive binding assay. In this assay, binding affinity of the test peptide is established by measuring inhibition of HLA binding by a control peptide of known binding affinity. Test peptides are incubated at several concentrations with control peptide at a set concentration along with the corresponding HLA molecule. The level of inhibition of control peptide binding to the HLA molecule is measured at each test peptide concentration and these data are used to establish the binding affinity of the test peptide for the specific HLA molecule evaluated in the assay.

[00252] An exemplary Class II HLA Binding Assay is adapted from Steere AC et al., 2006, Antibiotic-Refractory Lyme Arthritis is Associated with HLA-DR Molecules that Bind a *Borrelia burgdorferi* Peptide. *J Exp Med* 203(4): 961-71. The assay yields an indirect measure of peptide-MHC affinity. In the binding assay, a biotinylated, HLA-specific high binding control peptide, and soluble HLA molecules are incubated along with an unlabeled experimental peptide. The experimental peptide is mixed with the binding reagents in an aqueous buffering solution at a pH of 5.4, yielding a final range of eight concentrations from 102,500 nM to 0 nM. The mixture is incubated for 24 hours at 37°C to reach equilibrium. The temperature and pH conditions used for the binding reaction were chosen to represent the physiological conditions found in the endosome during peptide processing and loading onto the HLA molecule. The following day the binding reaction is neutralized, and the HLA-peptide complexes are captured on an enzyme-linked immunosorbent assay (ELISA) plate coated with a pan anti-human HLA-DR antibody (clone L243) for 24 hours at 4°C. After wash and incubation with Europium-labeled Streptavidin for one hour at ambient temperature, time-resolved fluorescence measuring bound labeled control peptide is assessed by a SpectraMax M5 plate reader. All assays are performed in triplicate

Example 4

[00253] *In vitro* immunogenicity protocol

[00254] Upon verification of peptide binding to patient-specific HLA molecules, the ability of patient's T cells to recognize and respond to tumor-specific mutated peptides (e.g., the subject-specific peptides or polypeptides comprising the at least one identified neo-epitope comprising, consisting, or consisting essentially of an amino acid sequence of the at least one identified neo-epitope (and/or fragments or variants thereof) is determined, and optionally 1 to 12 additional amino acids distributed in any ratio on the N terminus and/or C-terminus of the the at least one identified neo-epitope). Mutated peptides that have been confirmed to bind patient HLA molecules are synthesized and used to pulse patient-derived professional antigen presenting cells (pAPC), such as autologous dendritic cells or CD40L-expanded autologous B cells. Weekly *in vitro* restimulations with peptide-pulsed autologous pAPC in the presence of IL-2 and IL-7 are used to expand patient-derived T cells. After several weeks of culture, expanded T cells are tested for peptide-HLA specific reactivity by ELISpot assay to measure IFN γ release. Further characterization of peptide-specific T cell responses may be performed using *in vitro* killing assays such as chromium release assays or comparable methods using patient T cell clones. T cell clones are generated by *in vitro* stimulation using peptide-pulsed autologous pAPC and including the additional step of cloning by limiting dilution following standard protocols.

Example 5

[00255] Evaluation of inhibitory Treg peptide sequences

[00256] The ability of peptide sequences to activate inhibitory regulatory T cell (Treg) responses capable of suppressing effector T cell function can be evaluated using an *in vitro* assay referred to as the tetanus toxoid bystander suppression assay (TTBSA). This assay is based on the ability of Tregs to suppress the function of memory T cells specific to tetanus toxoid. Incubation of peripheral blood mononuclear cells (PBMCs) from patients with a history of immunization with tetanus toxoid results in expansion of tetanus toxoid specific CD4⁺ effector T cells. When peptides recognized by Tregs are added *in vitro* along with tetanus toxoid, activation and proliferation of the tetanus toxoid specific CD4⁺ effector T cells is inhibited by the Tregs in a dose dependent manner. This inhibition of effector T cell activation and proliferation is used as a measure of peptide-specific Treg activity.

Example 6

[00257] Evaluation of inhibitory Treg peptide sequences

[00258] Cross-reactive or auto-reactive T cell responses are tested by *in vitro* priming of T cells using neoepitope peptides containing non-synonymous amino acid substitutions and presented by autologous pAPC. This *in vitro* immunogenicity protocol may follow the methodology established by Wullner et al. (Wullner D, Zhou L, Bramhall E, Kuck A, Goletz TJ, Swanson S, Chirmule N, Jawa V. Considerations for Optimization and Validation of an In vitro PBMC Derived T cell Assay for Immunogenicity Prediction of Biotherapeutics. *Clin Immunol* 2010 Oct; 137(1): 5-14, incorporated by reference in its entirety). T cells that expand following *in vitro* priming to the neoepitope peptides are then tested for reactivity to the corresponding native or wild type (non-mutated) peptide epitopes. Reactivity to native peptide sequences is determined by measuring cytokine production including, but not limited to, IFN γ , TNF α , IL-2 and/or markers of T cell effector function including, but not limited to, CD107a and granzyme B.

Example 7

[00259] Retrospective survival analysis of TCGA bladder cancer patients

[00260] Genomic data derived from the muscle-invasive bladder cancer (BLCA) cohort of The Cancer Genome Atlas (TCGA) was analyzed independently by three pipelines (Fig. 1A) to determine whether an advanced *in silico* T cell epitope screening system (ANCER™) would improve prognostic stratification compared to tumor mutational burden (TMB) or T cell epitope analyses performed with publicly available tools (NetMHCpan/NetMHCIIpan).

[00261] Methods:

[00262] BLCA patient mutanomes (n=412) were retrieved from the TCGA and evaluated with NetMHCpan/NetMHCIIpan or with ANCER™, a screening platform that combines machine learning-based HLA I and HLA II neo-epitope identification tools with removal of inhibitory regulatory T cell epitopes. BLCA patients were stratified based on median TMB (including silent and non-silent mutations) or median neo-epitope burdens based on NetMHCpan/NetMHCIIpan or ANCER™.

[00263] A) For each pipeline, overall survival (OS) between patients with "high" and "low" mutational or neo-epitope burden was analyzed using the Kaplan-Meier method and differences analyzed by log-rank testing. The effect of integrating both CD8 and CD4 neo-epitope burdens was investigated as most mutanome pipelines exclusively focus on CD8 neo-epitopes.

[00264] B) In addition, we examined the positive (PPV) and negative predictive values (NPV) of 5-year survival predictors based on median mutational or neo-epitope burdens. For each pipeline, patients with "high" or "low" mutational or neo-epitope burden were predicted to survive more than 5 years. Predicted survival status was compared to observed OS. Patients lost to follow-up before the 5-year cutoff were removed from the analysis. Differences between the models were evaluated using McNemar's Test.

[00265] Results:

[00266] A) Compared to low TMB, high TMB was significantly associated with improved survival (median OS increased by 39 mo., $p = 0.0001$, Fig. 6A, Fig. 7A). Improved differentiation of median OS was obtained when separating patients based on their total CD8 neo-epitope content, as estimated by ANCER™ (median OS increased by 60 mo., $p < 0.0001$, Fig. 6B). Removal of CD8 neo-epitopes thought to be "tolerated" did not significantly change differences between median OS (Fig. 6C). However, improved patient stratification was observed when also considering patient total CD4 neo-epitope content in addition to their CD8 neo-epitopes (median OS increased by 70 mo., $p = 0.0001$, Fig 6D). We further evaluated whether the screening of "tolerated" CD4 sequences could improve our analysis. Upon identifying CD4 neo-epitopes likely to induce T effector (Teff) responses, it was found that the median survival of patients with high CD8 and high CD4 Teff contents was extended to 73.4 months compared to the remainder of the cohort ($p < 0.0001$, Fig. 6E, 7C). CD8 and CD4 neo-epitope analyses performed with NetMHCpan and NetMHCIIpan did not enhance patient stratification compared to analyses using the TMB or neo-epitopes identified with ANCER™ (median OS increased by 34 mo., $p = 0.0020$, Fig. 7A, 7B).

[00267] B) Predictive accuracy of 5-year survival status using ANCER™ (median CD8 and CD4 neo-epitope burdens, filtered for "tolerated" neo-epitopes) were significantly more accurate (65% accuracy, Fig. 1B) compared to predictions using median TMB (59% accuracy, ANCER™ vs TMB $p = 0.0125$) or median neo-epitopes identified by NetMHCpan/NetMHCIIpan (61% accuracy, ANCER™ vs NetMHCpan/NetMHCIIpan $p = 0.0192$). Improved predictions were also observed when determining the positive and negative predictive value (PPV and NPV) of each model (Fig. 1C, left panel), with increased PPV and NPV obtained for ANCER™ (PPV = 34.1%, NPV = 87.6%) compared to TMB- (PPV = 29.5%, NPV = 86.1%) or NetMHCpan/NetMHCIIpan-based predictors (PPV = 29.5%, NPV = 84.8%). Results also showcased the importance of

predicting both Class I and Class II neo-epitopes (Fig. 1C, center panel) and of filtering self-like (including potential inhibitory or cross-reactive) neo-epitopes (Fig. 1C, right panel) when predicting 5-year survival.

[00268] Conclusions:

[00269] Our analysis suggests that optimal host-immune recognition of CD8, CD4, and Treg epitopes plays a key role in cancer survival. While defining CD8 neo-epitope burden enhanced associations with OS, the inclusion of CD4 Teff neo-epitope burden substantially helped identify long-term survivors. These results suggest that defining the number of true neo-epitopes using ANCER™ represents a novel and useful prognostic or predictive biomarker.

[00270] Improved stratification of patients over the TMB analysis was obtained when separating patients based on their Class I neo-epitope content, as estimated by ANCER™ (Fig. 7A, 7B). No improvement over the TMB analysis was obtained when estimating Class I neo-epitope content with public tools. (Fig. 7B) Incremental improvements were obtained when considering tumor “raw” Class II neo-epitope content (i.e. not filtered by JANUSMATRIX™) in addition to the Class I content, as estimated by ANCER™ (Fig. 7C). An analysis with Class II public prediction tools was unsuccessful to improve patient stratification (Fig. 7C). Refining the Class II neo-epitope content with JANUSMATRIX™ (i.e. excluding putative Treg neoepitopes from the analysis) further improved patient stratification. (Fig. 7D). ANCER™ predicts patient 5-year survival status at a higher accuracy, PPV, and NPV than other predictors (Fig. 1B, 1C).

Example 8

[00271] Association of MHC Class II effector (Teff) vs. regulatory (Treg) neo-epitopes with outcomes in pancreatic cancer patients.

[00272] Pancreatic cancer remains one of the deadliest cancers despite immunotherapy breakthroughs. Patients with poor outcomes may have tumors enriched in neo-epitopes activating regulatory T cells (Tregs).

[00273] Whole exome sequencing data derived from 13 pancreatic cancer patients with available HLA I and II typing and treated with GVAX, an autologous cancer vaccine engineered to secrete the stimulatory GM-CSF cytokine, was analyzed with ANCER™, an in silico neo-epitope identification platform. Distinctive features of ANCER™ are its ability to accurately predict HLA II ligands and to identify tolerated or Treg epitopes. Using ANCER™, we estimated the ratio of effector versus regulatory neo-epitope content for each patient. Fig. 5A shows the number and

frequency of Class I and Class II neo-epitopes classified as having low, average, or high cross-reactivity (XR) potential.

[00274] The ratio of Class II effector (Teff) to regulatory (Treg) neo-epitopes was then analyzed to determine whether there is a correlation with disease-free survival. Median disease-free survival (DFS) time of patients with high effector content (25 months) was over four times greater than in patients whose ratio shifted towards high regulatory content (6 months). Analysis of the same patients using their tumor mutational burden (TMB) did not yield conclusive results. In contrast, patients with high TMB had a similar median DFS time (17 months) than patients with low TMB (14 months). Fig. 5B shows patients with higher ratios of Teff/Treg (Teff/Treg)^{hi} neo-epitopes had better outcomes than patients with lower ratios of Teff/Treg (Teff/Treg)^{lo} neo-epitopes. The ratio of Teff/Treg neo-epitopes was also a better predictor of disease free survival than tumor mutational burden.

[00275] The results indicate that higher numbers of neo-epitopes that may activate Treg in the tumors are in a trend associated with shorter DFS.

* * *

[00276] Having thus described in detail preferred embodiments of the present invention, it is to be understood that the invention defined by the above paragraphs is not to be limited to particular details set forth in the above description as many apparent variations thereof are possible without departing from the spirit or scope of the present invention.

WHAT IS CLAIMED IS:

1. A prognostic method for determining risk of death, of a human subject with a neoplasia, which comprises identifying a population of neoplasia-specific mutations in a neoplasia specimen of a subject; assessing the neoplasia-specific mutations identified to classify Class I and/or Class II neoantigens encoded by said mutations; analyzing the neoantigens encoded by said mutations to identify and classify neoantigens that engage effector T cells and neo-epitopes that engage regulatory T cells, and computing a prognostic score from the immunogenicity of the population.
2. The method of claim 1, which comprises classification of the Class I neo-epitopes as effector neoantigens or tolerogenic neoantigens.
3. The method of claim 1, which comprises classification of the Class I neo-epitopes as effector neoantigens, tolerated neoantigens, or tolerogenic neoantigens.
4. The method of claim 1, which comprises classification of the Class I neoantigens on a graded scale from a strong effector neoantigen to a strong tolerogenic neoantigen.
5. The method of claim 1, which comprises classification of the Class II neoantigens as effector neoantigens or tolerogenic neoantigens.
6. The method of claim 1, which comprises classification of the Class II neoantigens as effector neoantigens, tolerated neoantigens, or tolerogenic neoantigens.
7. The method of claim 1, which comprises classification of the Class II neoantigens on a graded scale from a strong effector neoantigen to a strong regulatory neoantigen.
8. The method of any one of claim 1 to 7, which comprises classification of the Class I neoantigens and classification of the Class II neoantigens.
9. The method of any one of the previous claims, which comprises identification of neoantigens that are cross-reactive between Class I and Class II.
10. The method of any one of the previous claims, which comprises exclusion of the

neoantigen from the computation if it is an effector Class I neoantigen and a tolerogenic Class II neoantigen or an effector Class II neoantigen and a tolerogenic Class I neoantigen, or a tolerated Class I neoantigen and a tolerated Class II antigen, or an effector Class II neoantigen and a tolerated Class I neoantigen.

11. The method of any one of the previous claims, wherein the prognostic score is calculated based on the top 50% of the effector neoantigens and the top 50% of the tolerogenic neoantigens.

12. The method of any one of the previous claims, wherein the prognostic score is calculated based on the top 20% of the effector neoantigens and the top 20% of the tolerogenic neoantigens.

13. The method of any one of the previous claims, wherein the prognostic score is calculated based on the top 5% of the effector neoantigens and the top 5% of the tolerogenic neoantigens.

14. The method of any one of the previous claims, wherein the prognostic score is calculated based at least on the top 100 of the effector neoantigens and at least the top 100 of the tolerogenic neoantigens.

15. The method of any one of the previous claims, which comprises determining strength of binding to Teff and/or Treg cells.

16. The method of claim 15, wherein the strength of binding to Teff and/or Treg cells is known, measured, predicted or calculated.

17. The method of claim 15, wherein strength of binding to a Treg cell is determined by its capacity to inhibit IFN γ production.

18. The method of claim 15, wherein strength of binding to a Teff cell or a Treg cell is determined by comparison to a panel of neoantigens having predetermined Teff and/or Treg activity.

19. The method of any one of claims 1 to 15, wherein assessing neoplasia-specific mutations comprises:

a) determining a binding score for a mutated peptide to one or more MHC molecules, wherein said mutated peptide is encoded by at least one of said neoplasia-specific

mutations;

b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations;

c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for at least 10,000 randomly generated peptides using naturally observed amino acid frequencies;

d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and

e) using it to calculate a prognostic score when:

1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or

2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide the non-mutated peptide.

20. A method of identifying subject-specific neoantigens for a personalized neoplasia vaccine, said method comprising:

i) identifying neoplasia-specific mutations in a neoplasia specimen of a subject;

ii) assessing the neoplasia-specific mutations identified in step (i) to identify Class I and Class II neo-epitopes encoded by said mutations for use in the personalized neoplasia vaccine, wherein said neo-epitopes are known, determined, or predicted to bind to a MHC protein of the subject; and

iii) classifying the neo-epitopes that engage regulatory T cells as tolerated or tolerogenic, and excluding such Class II neo-epitopes that are tolerated or tolerogenic, and excluding such Class I neo-epitopes that are tolerogenic.

21. The method of claim 20, wherein identifying neoplasia-specific mutations in step (i) comprises identifying sequence differences between the full or partial genome, exome, and/or

transcriptome of a neoplasia specimen from the subject diagnosed as having a neoplasia and a non-neoplasia specimen.

22. The method of claim 20 or 21, wherein identifying neoplasia-specific mutations or identifying sequence differences comprises Next Generation Sequencing (NGS).

23. The method of claim 20 or 21, wherein identifying neoplasia-specific mutations in step (i) comprises selecting from the neoplasia a plurality of nucleic acid sequences, each comprising mutations not present in a non-neoplasia sample.

24. The method of claim 20 or 21, wherein identifying neoplasia-specific mutations or identifying sequence differences comprises sequencing genomic DNA and/or RNA of the neoplasia specimen.

25. The method of claim 21, wherein said non-neoplasia specimen is derived from the subject diagnosed as having a neoplasia.

26. The method of any one of claims 20-25, wherein said neoplasia-specific mutations are neoplasia-specific somatic mutations.

27. The method of any one of claims 20-25, wherein said neoplasia-specific somatic mutations are single nucleotide variations (SNVs), in-frame insertions, in-frame deletions, out-of-frame insertions, and out-of-frame deletions.

28. The method of claim 26-27, wherein said neoplasia-specific somatic mutations are mutations of proteins encoded in the neoplasia specimen of the subject diagnosed as having a neoplasia.

29. The method of any one of claims 20 to 28, wherein assessing the neoplasia-specific mutations in step (ii) to identify known or determined neo-epitopes encoded by said mutations comprises:

a) determining a binding score for a mutated peptide to one or more MHC molecules, wherein said mutated peptide is encoded by at least one of said neoplasia-specific mutations;

b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations;

c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for at least 10,000 randomly generated peptides using naturally observed amino acid frequencies;

d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and

e) identifying the mutated peptide as a neo-epitope when:

1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or

2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide the non-mutated peptide.

30. The method of claim 29, wherein the mutated peptide and non-mutated peptide are both 9 amino acids in length or the mutated peptide and non-mutated peptide are both 10 amino acids in length.

31. The method of claim 29, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, and wherein the TCR facing amino acid residues for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the aminoterminal.

32. The method of any one of claims 1-31, wherein assessing the neoplasia-specific mutations in step (ii) to identify known or determined neo-epitopes encoded by said mutations comprises *in silico* testing.

33. The method of claim 32, wherein said *in silico* testing to identify known or determined neo-epitopes encoded by said mutations in step (ii) comprises using an algorithm to screen protein sequences for putative T cell epitopes.

34. The method of any one of claims 1-33, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises determining whether said identified neo-epitopes encoded by said mutations share TCR contacts with proteins derived from either the human proteome or the human microbiome, wherein said identified neo-epitopes encoded by said mutations that are determined to share TCR contacts with proteins derived from either the human proteome or the human microbiome are identified as neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells).

35. The method of claim 34, wherein TCR contacts for a 9-mer identified neo-epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope as counted from the amino terminal, wherein the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, and wherein the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the aminoterminal.

36. The method of any one of claims 1-35, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises *in silico* testing.

37. The method of claim 36, wherein said *in silico* testing comprises analyzing whether the

identified neo-epitopes are predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) using an algorithm that predicts cross reactivity with regulatory cells.

38. The method of claim 37, wherein an identified neo-epitope is predicted to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) if the score for the neo-epitope is greater than a predetermined cutoff.

39. The method of any one of claims 1-35, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*.

40. The method of claim 39, wherein a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

41. The method of any one of claims 36-38, further comprising determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*.

42. The method of claim 41, wherein a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

43. The method of any one of claims 1-42, further comprising:

iv) designing at least one subject-specific peptide or polypeptide, said peptide or polypeptide comprising at least one identified neo-epitope encoded by said mutations, provided said neo-epitope is not identified in step (iii) as being known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or

anergic T cells).

44. The method of claim 43, further comprising:

v) providing the at least one peptide or polypeptide designed in step (iv) or a nucleic acid encoding said peptides or polypeptides.

45. The method of claim 44, further comprising:

vi) providing a vaccine comprising the at least one peptide or polypeptide or nucleic acid provided in step (v).

46. A pharmaceutical composition comprising:

a plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes or one or more nucleic acids encoding said plurality of selected peptides or polypeptides, wherein the one or more identified neo-epitopes induces a neoplasia-specific effector T cell response in a subject; and

a pharmaceutically acceptable adjuvant and/or carrier;

wherein the plurality of selected peptides or polypeptides comprising the one or more identified neo-epitopes or one or more nucleic acids encoding said plurality of selected peptides or polypeptides are selected by a process comprising:

i) identifying neoplasia-specific mutations in a neoplasia specimen of a subject diagnosed as having a neoplasia;

ii) assessing the neoplasia-specific mutations identified in step (i) to identify known or determined neo-epitopes encoded by said mutations for use in the pharmaceutical composition, wherein said neo-epitopes are known or determined to bind to a MHC protein of the subject;

iii) classifying the neoplasia-specific mutations identified in step (ii) to identify Class I and Class II neo-epitopes encoded by said mutations that are tolerated or tolerogenic, and excluding such Class II neo-epitopes that are tolerated or tolerogenic, and excluding such Class I neo-epitopes that are tolerogenic ; and

iv) selecting the plurality of selected peptides or polypeptides comprising the one or more identified neo-epitopes or selecting the one or more nucleic acids encoding said at least one peptide or polypeptide based on the assessments of step (ii) and step (iii).

47. The pharmaceutical composition of claim 46, wherein identifying neoplasia-specific

mutations in step (i) comprises identifying sequence differences between the full or partial genome, exome, and/or transcriptome of a neoplasia specimen from the subject diagnosed as having a neoplasia and a non-neoplasia specimen.

48. The pharmaceutical composition of any one of claims 46 or 47, wherein identifying neoplasia-specific mutations or identifying sequence differences comprises Next Generation Sequencing (NGS).

49. The pharmaceutical composition of any one of claims 46 or 47, wherein identifying neoplasia-specific mutations in step (i) comprises selecting from the neoplasia a plurality of nucleic acid sequences, each comprising mutations not present in a non-neoplasia sample.

50. The pharmaceutical composition of any one of claims 46 or 47, wherein identifying neoplasia-specific mutations or identifying sequence differences comprises sequencing genomic DNA and/or RNA of the neoplasia specimen.

51. The pharmaceutical composition of claim 47, wherein said non-neoplasia specimen is derived from the subject diagnosed as having a neoplasia.

52. The pharmaceutical composition of any one of claims 46-51, wherein said neoplasia-specific mutations are neoplasia-specific somatic mutations.

53. The pharmaceutical composition of any one of claims 46-51, wherein said neoplasia-specific mutations are single nucleotide variations (SNVs), in-frame insertions, in-frame deletions, out-of-frame insertions, and out-of-frame deletions.

54. The pharmaceutical composition of any one of claims 52 or 53, wherein said neoplasia-specific somatic mutations are mutations of proteins expressed in the neoplasia specimen of the subject diagnosed as having a neoplasia.

55. The pharmaceutical composition of any one of claims 46-54, wherein assessing the neoplasia-specific mutations in step (ii) to identify known or determined neo-epitopes encoded by said mutations comprises:

- a) determining a binding score for a mutated peptide to one or more MHC molecules,

wherein said mutated peptide is encoded by at least one of said neoplasia-specific mutations;

b) determining a binding score for a non-mutated peptide to the one or more MHC molecules, wherein the non-mutated peptide is identical to the mutated peptide except for the encoded at least one of said neoplasia-specific mutations;

c) determining the percentile rank of the binding scores of both the mutated peptide of step (a) and the non-mutated peptide of step (b) as compared to an expected distribution of binding scores for at least 10,000 randomly generated peptides using naturally observed amino acid frequencies;

d) determining the TCR facing amino acid residues of said mutated peptide and said non-mutated peptide; and

e) identifying the mutated peptide as a neo-epitope when:

1) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution and the non-mutated peptide has a determined binding score below the top 10 percentile of the expected distribution; or

2) the mutated peptide has a determined binding score in the top 5 percentile of the expected distribution, the non-mutated peptide has a determined binding score in the top 10 percentile of the expected distribution, and there is at least one mismatched TCR facing amino acid between the mutated peptide and the non-mutated peptide.

56. The pharmaceutical composition of claim 55, wherein the mutated peptide and non-mutated peptide are both 9 amino acids in length or the mutated peptide and non-mutated peptide are both 10 amino acids in length.

57. The pharmaceutical composition of claim 55, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, wherein the TCR facing amino acid residues for a 9-mer mutated peptide and a 9-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the mutated and non-mutated peptide as counted from the amino terminal, and wherein the TCR facing amino acid residues for a 10-mer mutated peptide and 10-mer non-mutated peptide that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the mutated and non-mutated peptide as counted from the amino terminal.

58. The pharmaceutical composition of any one of claims 47-57, wherein assessing the neoplasia-specific mutations in step (ii) to identify known or determined neo-epitopes encoded by said mutations comprises *in silico* testing.

59. The pharmaceutical composition of claims 58, wherein said *in silico* testing to identify known or determined neo-epitopes encoded by said mutations in step (ii) comprises using an algorithm to screen protein sequences for putative T cell epitopes.

60. The pharmaceutical composition of any one of claims 47-59, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells in step (iii) comprises determining whether said identified neo-epitopes encoded by said mutations share TCR contacts with proteins derived from either the proteome or the microbiome, wherein said identified neo-epitopes encoded by said mutations that are determined to share TCR contacts with proteins derived from either the human proteome or the human microbiome are identified as neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells).

61. The pharmaceutical composition of claim 60, wherein TCR contacts for a 9-mer identified neo-epitope that bind to a MHC class II molecule are at position 2, 3, 5, 7, and 8 of the identified neo-epitope as counted from the amino terminal, wherein the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at position 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, and wherein the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal.

62. The pharmaceutical composition of any one of claims 47-61, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells in step (iii) comprises *in silico* testing.

63. The pharmaceutical composition of claim 62, wherein said *in silico* testing comprises analyzing whether the identified neo-epitopes are predicted to engage regulatory T cells and/or

other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) using an algorithm that predicts cross reactivity with regulatory cells.

64. The pharmaceutical composition of claim 45, wherein an identified neo-epitope is predicted to engage regulatory T cells if the score for the neo-epitope is greater than a predetermined cutoff.

65. The pharmaceutical composition of any one of claims 47-61, wherein assessing the identified neo-epitopes encoded by said mutations to identify neo-epitopes that are known or determined to engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) in step (iii) comprises determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*.

66. The pharmaceutical composition of claim 65, wherein a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

67. The pharmaceutical composition of any one of claims 62-64, further comprising determining whether the identified neo-epitopes engage regulatory T cells and/or other detrimental T cells (including T cells with potential host cross-reactivity and/or anergic T cells) *in vitro*.

68. The pharmaceutical composition of claim 67, wherein a neo-epitope is determined to engage regulatory T cells when said neo-epitope results in regulatory T cell activation, proliferation, and/or IL-10 or TGF- β production.

69. The pharmaceutical composition of any one of claims 47-68, wherein the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes comprises at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 peptides or polypeptides comprising one or more identified neo-epitopes.

70. The pharmaceutical of any one of claims 47-69, wherein the plurality of selected peptides

or polypeptides comprising one or more identified neo-epitopes comprises from 3-20 selected peptides or polypeptides comprising one or more identified neo-epitopes.

71. The pharmaceutical of any one of claims 47-70, wherein each peptide or polypeptide of the plurality of selected peptides or polypeptides comprising one or more identified neo-epitopes has a length of from 9-100 aminoacids.

72. The pharmaceutical composition of any one of claims 47-71, wherein the one or more nucleic acids encoding said plurality of selected peptides or polypeptides are DNA, RNA, or mRNA.

73. The pharmaceutical composition of any one of claims 47-72, wherein n the pharmaceutical composition further comprises an anti-immunosuppressive agent.

74. The pharmaceutical composition of claim 73, wherein the anti-immunosuppressive agent comprises a checkpoint blockage modulator.

75. The pharmaceutical composition of any one of claims 47-74, wherein the adjuvant comprises poly-ICLC.

76. The pharmaceutical composition of any one of claims 47-75, wherein the neoplasia is a solid tumor.

77. The pharmaceutical composition of any one of claims 47-76, wherein the neoplasia is bladder cancer, breast cancer, brain cancer, colon cancer, gastric cancer, head and neck cancer, kidney cancer, liver cancer, lung cancer, melanoma, ovarian cancer, pancreatic cancer, prostate cancer, or testicular cancer.

78. The pharmaceutical composition of any one of claims 47-77, wherein the neoplasia is bladder cancer.

79. The method of claim 29, wherein TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 as counted from the amino terminal, the TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8;

1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, the TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal, the TCR facing amino acid residues for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal, the TCR facing amino acid residues for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

80. The method of claim 34, wherein TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 as counted from the amino terminal, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal, the TCR contacts for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

81. The pharmaceutical composition of claim 57, wherein the TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 as counted from the amino terminal, the TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, the TCR facing amino acid residues for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal, the TCR facing amino acid residues for a 10-mer identified neo-epitope that bind to a MHC class I molecule are

at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal, the TCR facing amino acid residues for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

82. The pharmaceutical composition of claim 60, wherein TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class II molecule are at any combination of residues at positions 2, 3, 5, 7, and 8 as counted from the amino terminal, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at positions 4, 5, 6, 7, and 8; 1, 4, 5, 6, 7 and 8; or 1, 3, 4, 5, 6, 7, and 8 of the identified neo-epitope as counted from the amino terminal, the TCR contacts for a 9-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, and 8 as counted from the amino terminal, the TCR contacts for a 10-mer identified neo-epitope that bind to a MHC class I molecule are at position 4, 5, 6, 7, 8, and 9; 1, 4, 5, 6, 7, 8, and 9; or 1, 3, 4, 5, 6, 7, 8, and 9 of the identified neo-epitope as counted from the amino terminal, the TCR contacts for a 10-mer identified neo-epitope that binds to a MHC class I molecule are at any combination of residues at positions 1, 3, 4, 5, 6, 7, 8, and 9 as counted from the amino terminal.

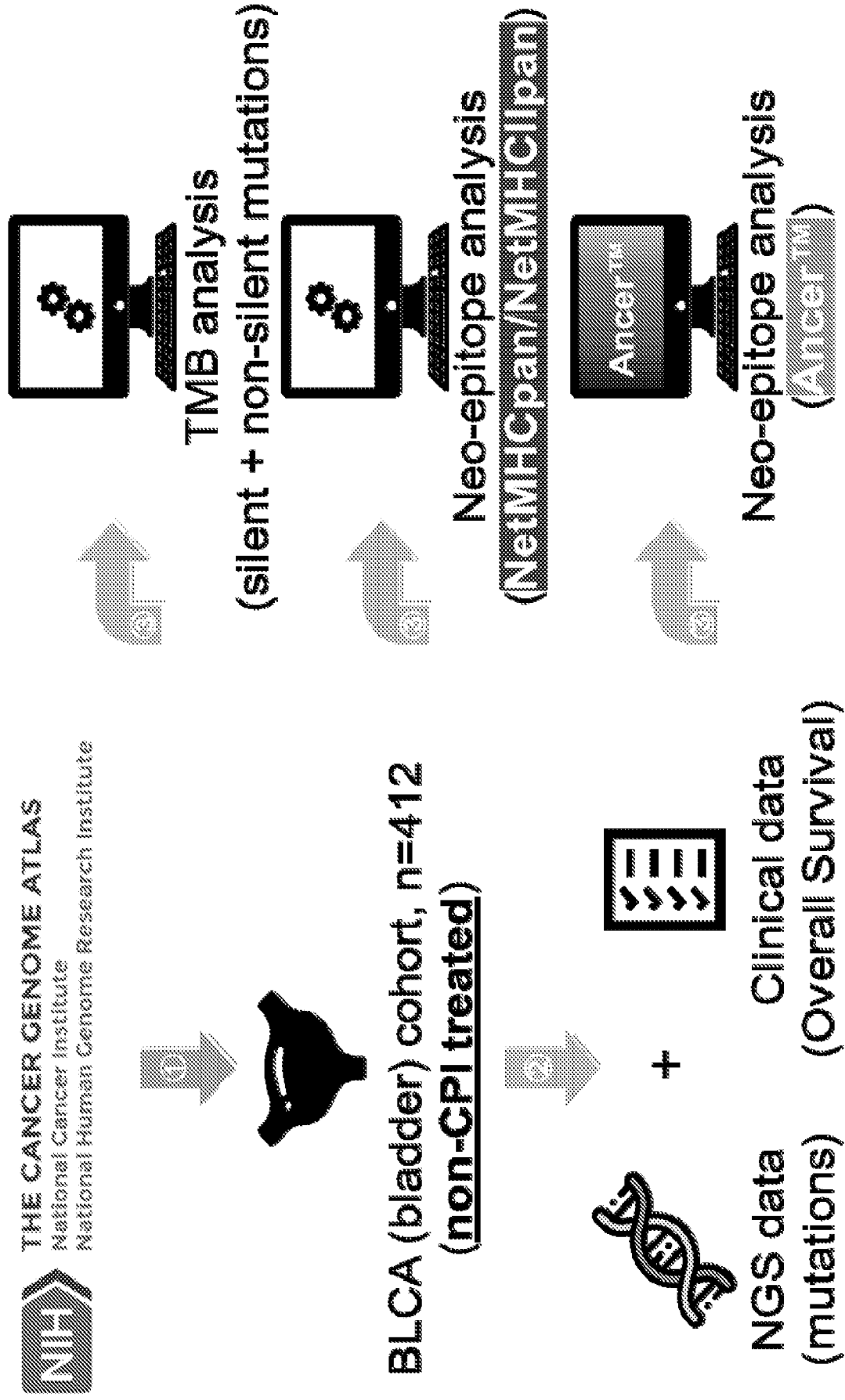


FIG. 1A

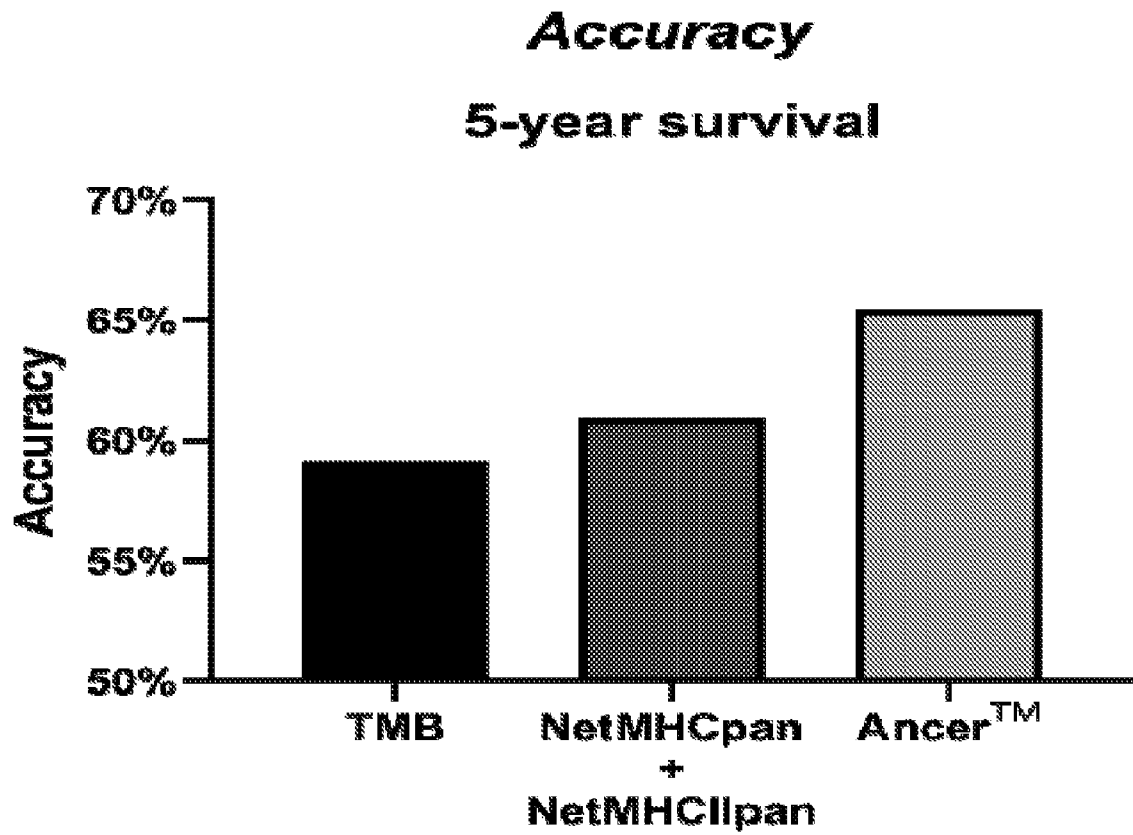


FIG. 1B

5-year survival PPV/NPV plots

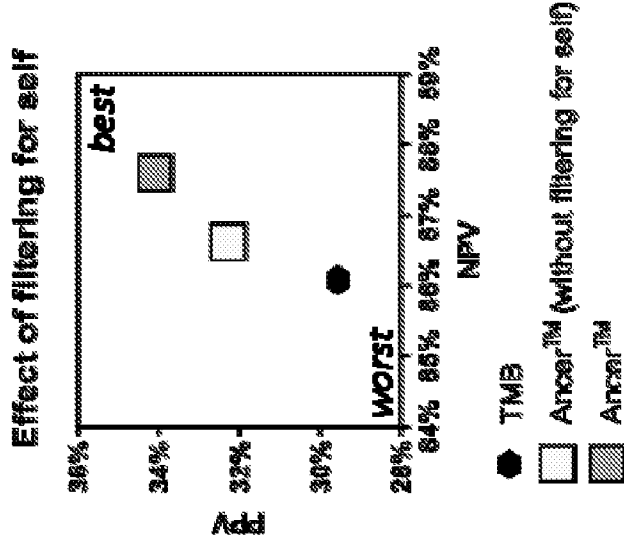
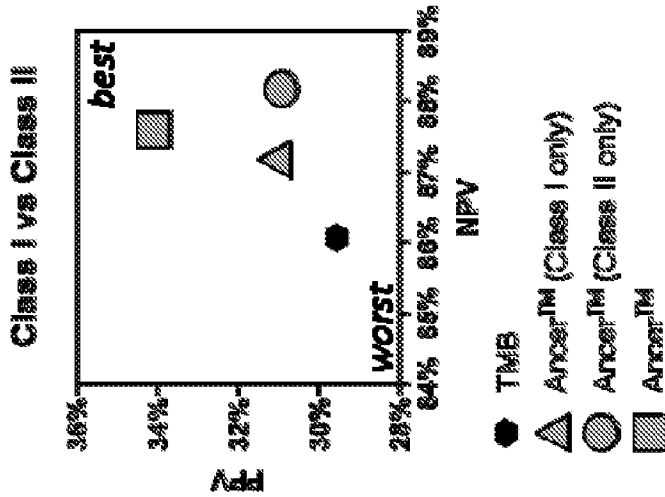
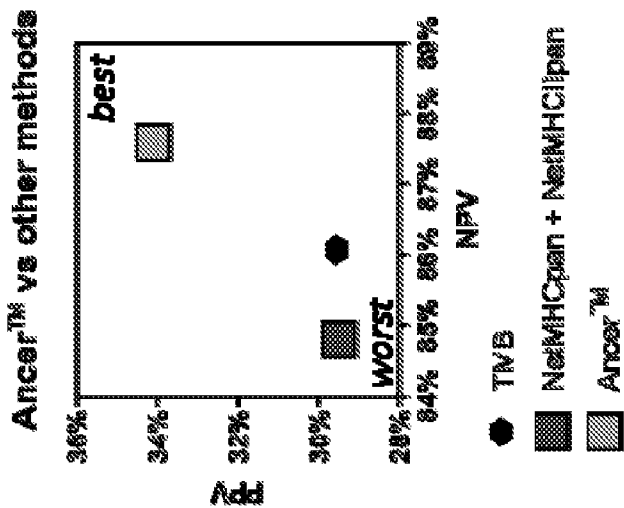


FIG. 1C

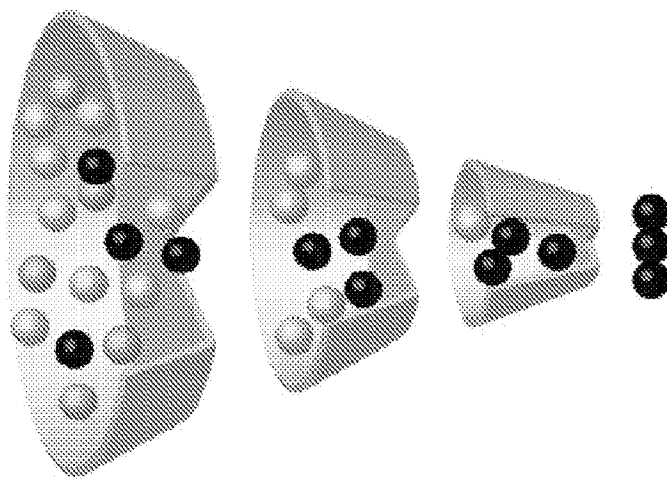
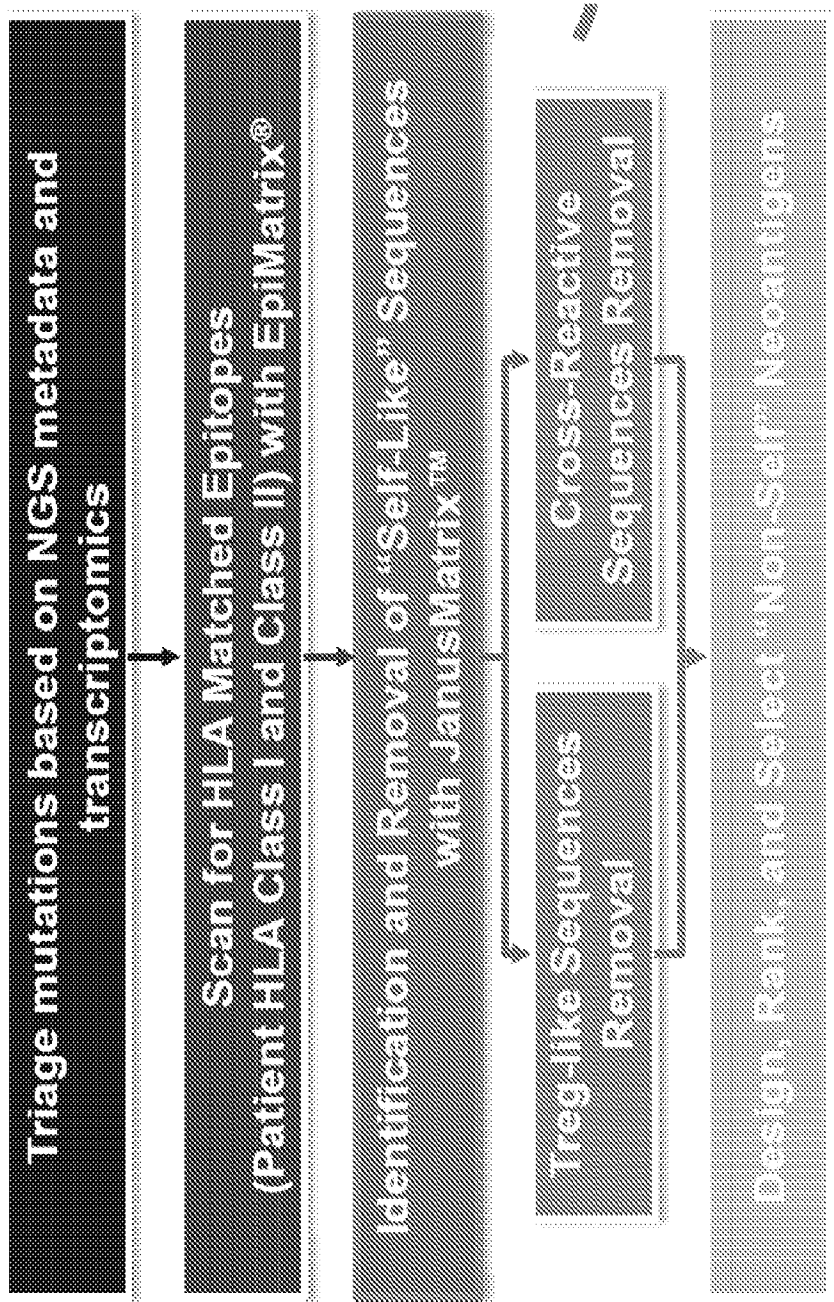


FIG. 2

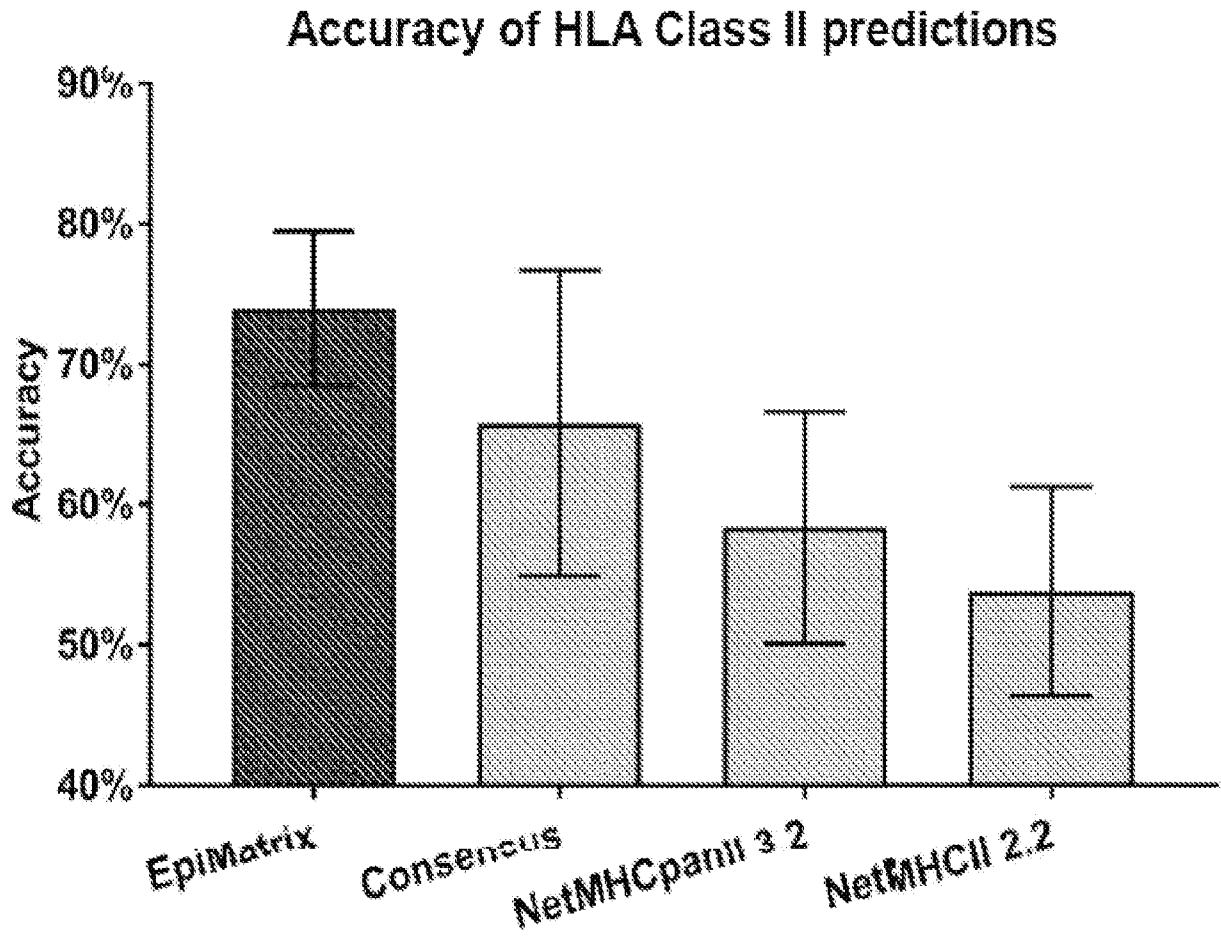


Fig. 2 CONT'D

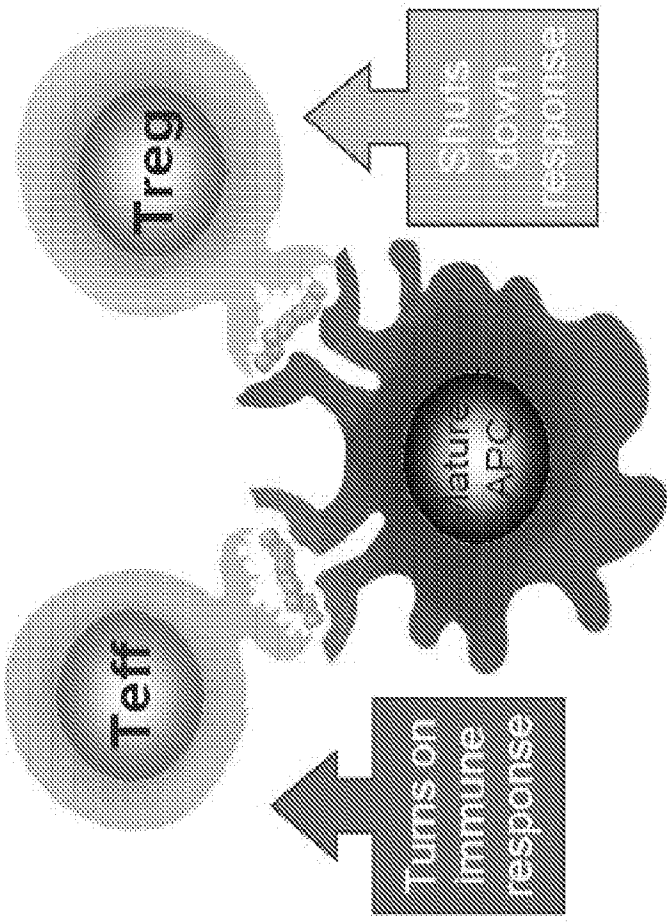
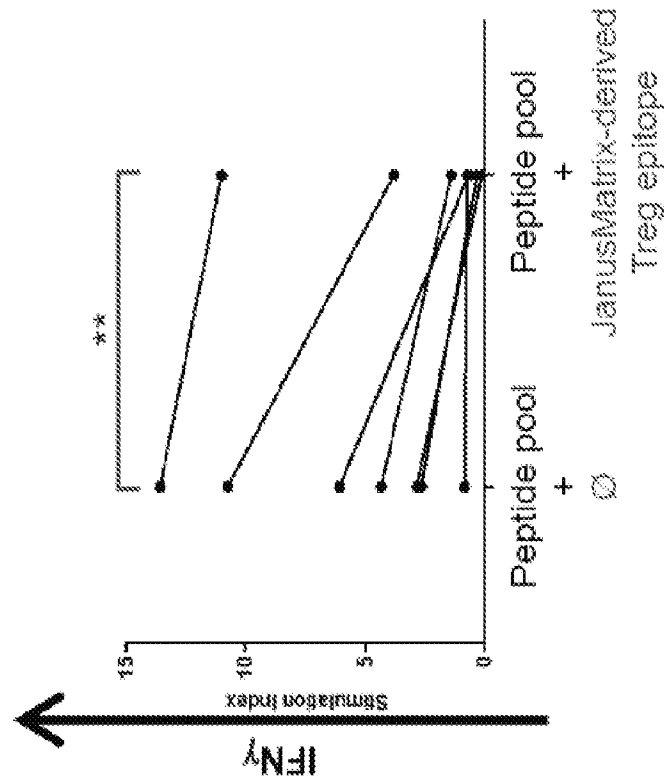
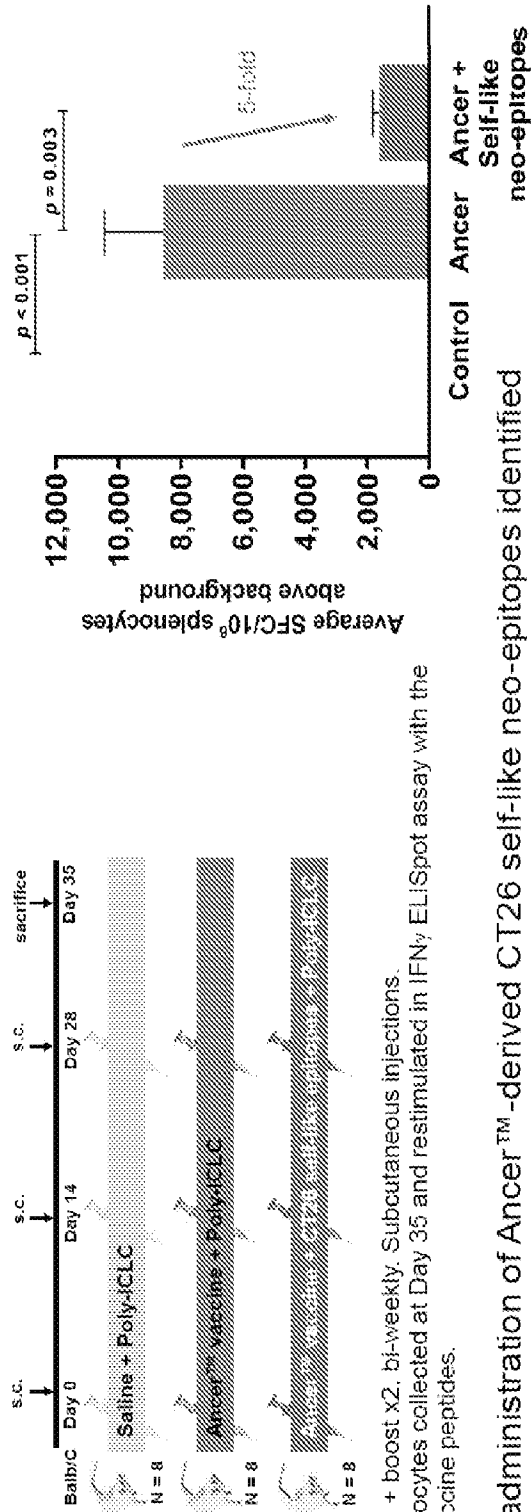
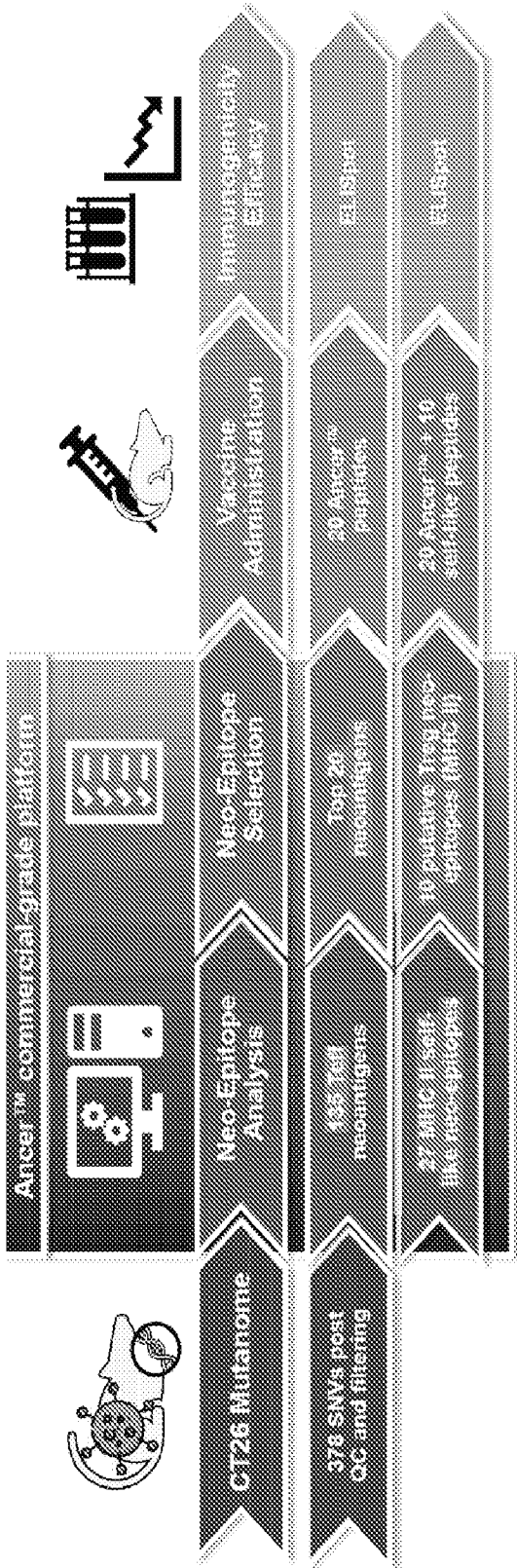


Fig. 3



Prime + boost x2, bi-weekly. Subcutaneous injections. Splenocytes collected at Day 35 and restimulated in IFN γ ELISpot assay with the 20 vaccine peptides.

Co-administration of Ancer™-derived CT26 self-like neo-epitopes identified with JanusMatrix™ significantly reduces IFN γ responses by 5-fold.

FIG. 4

Neo-epitope composition:

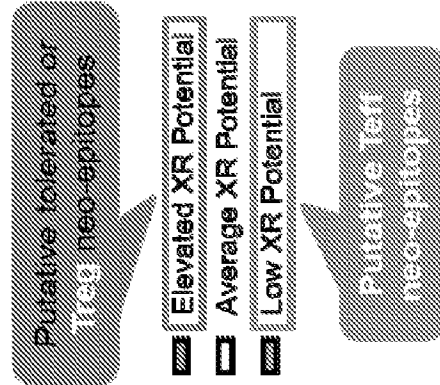
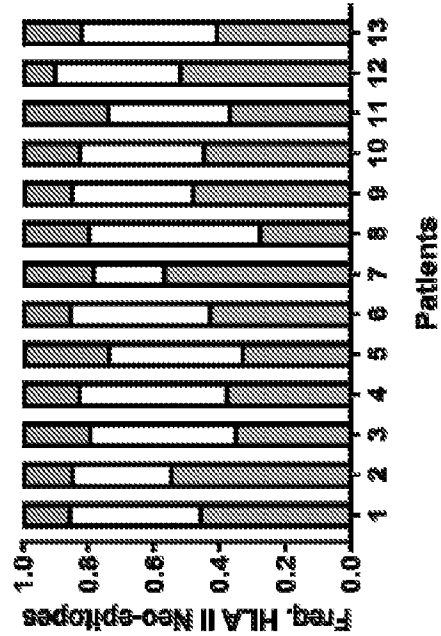
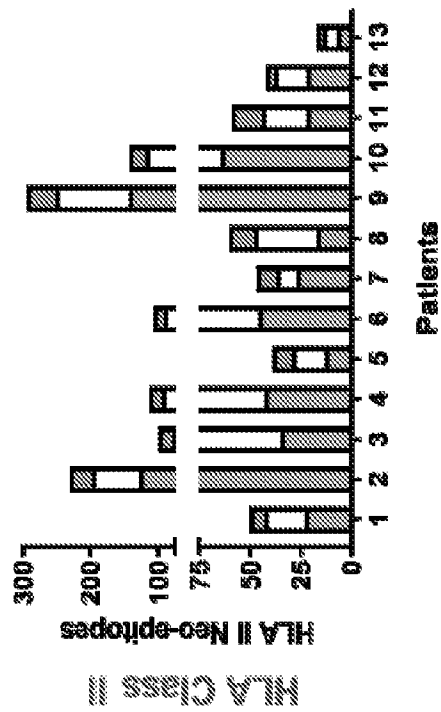
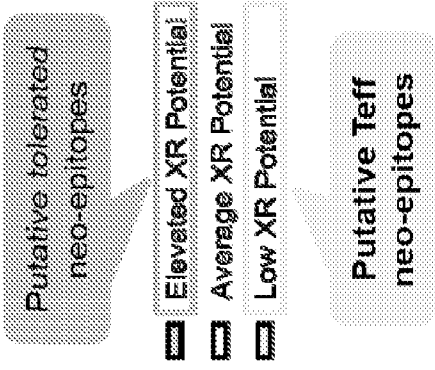
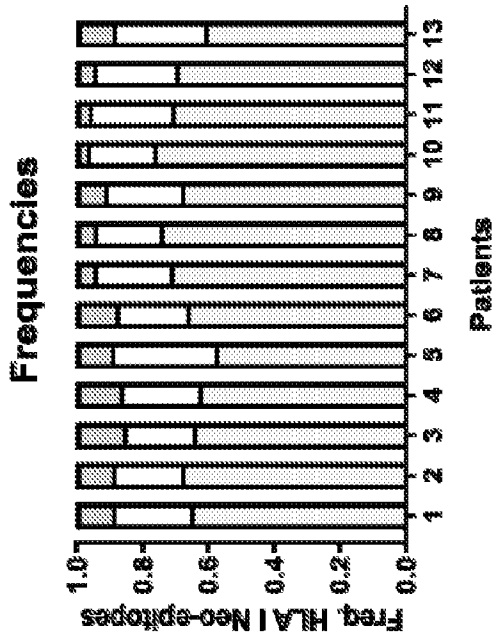
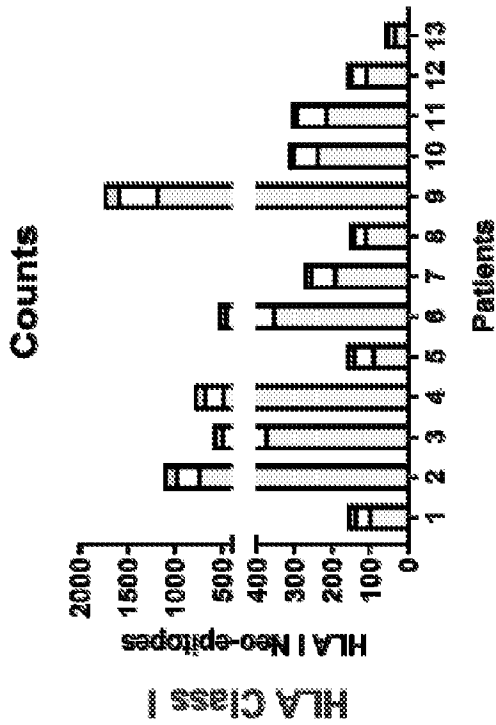
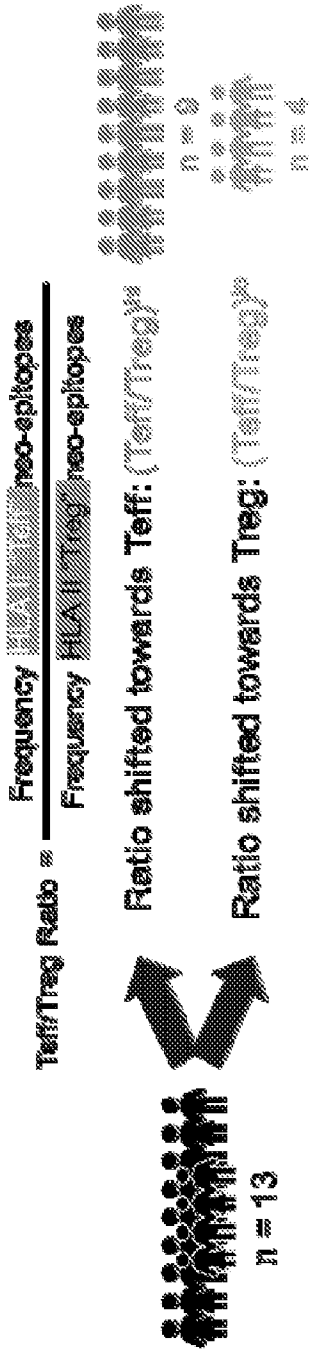


FIG 5A



- Do (Teff/Treg)⁺ patients have a higher disease free survival (DFS) time than (Teff/Treg)⁻ patients?
- How does the ratio of Teff/Treg neo-epitopes compare to a TMB predictor?

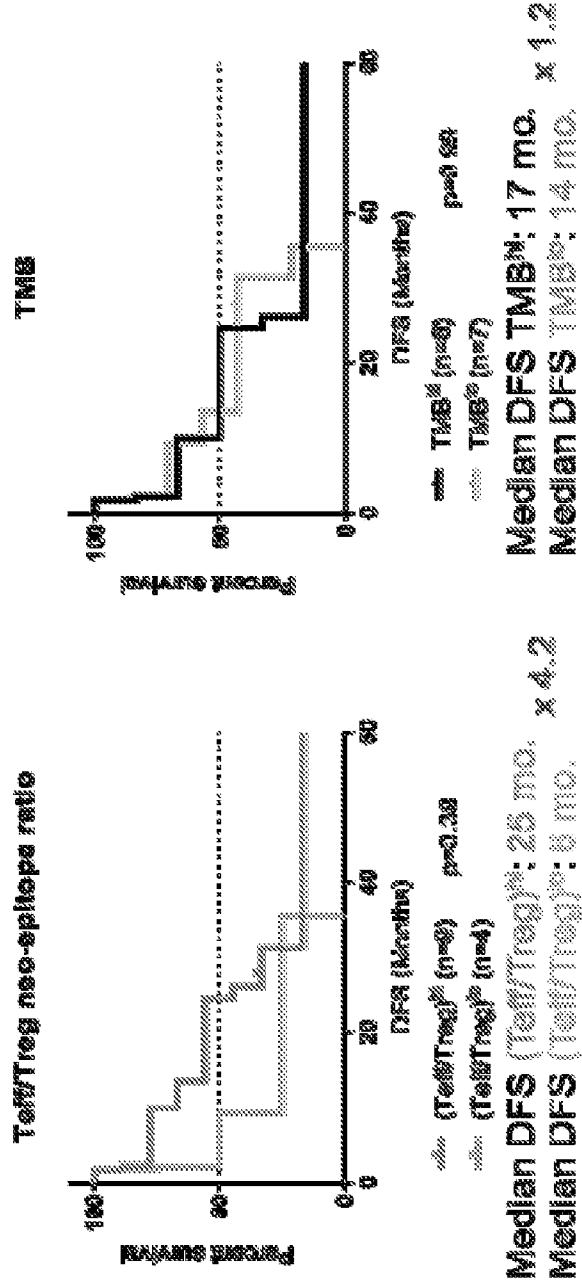


FIG. 5B

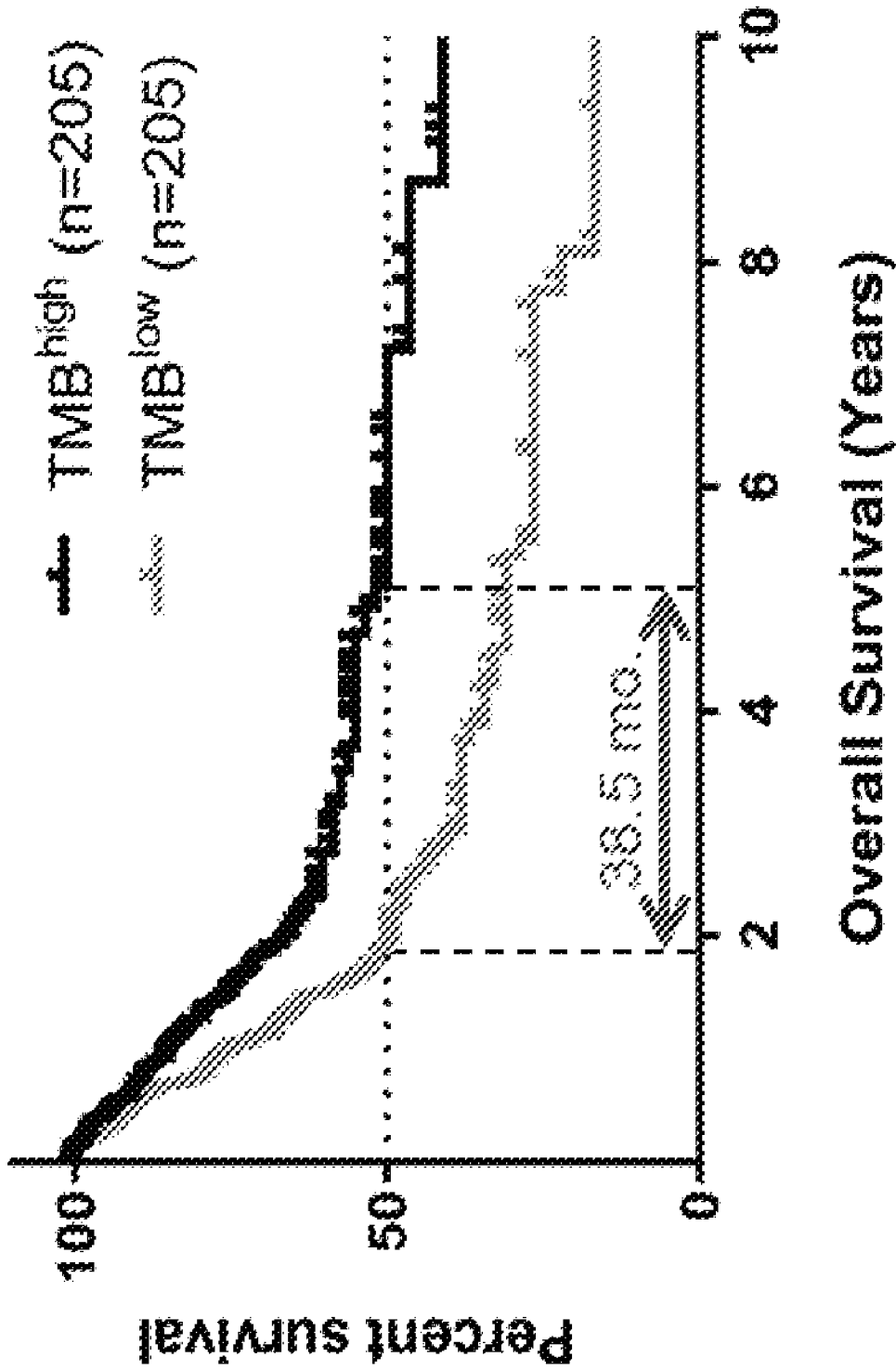


FIG. 6A

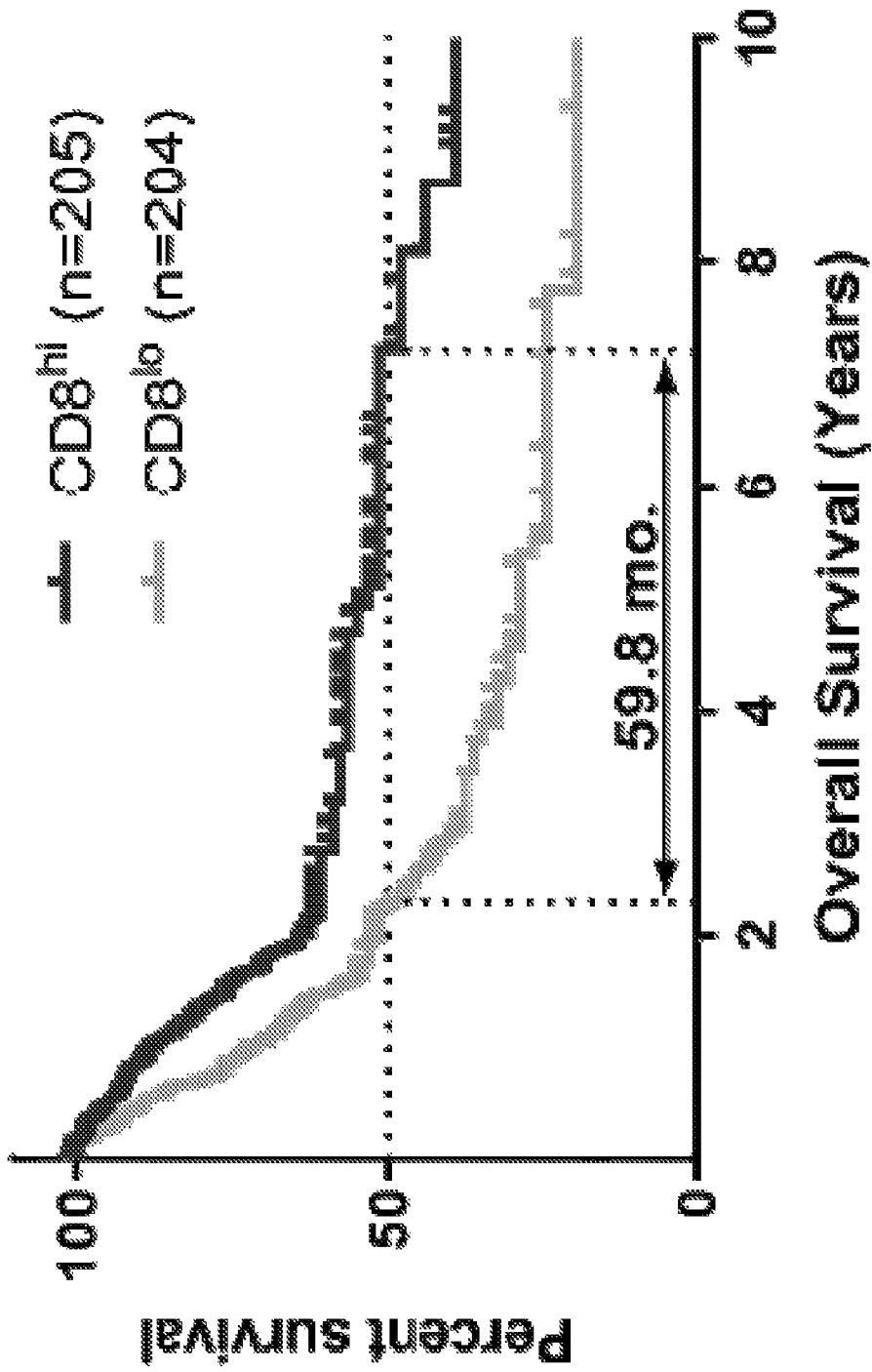


FIG. 6B

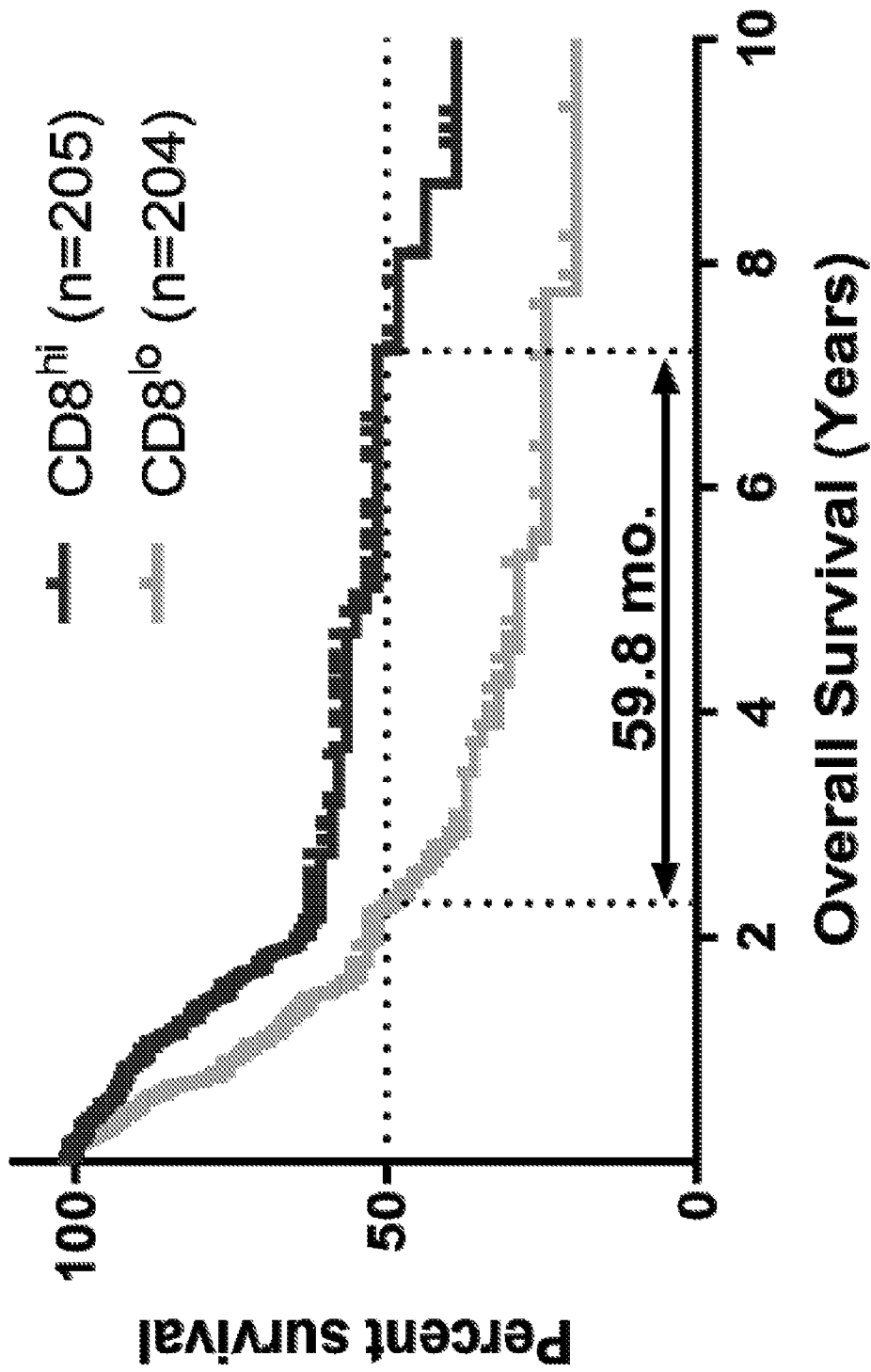


FIG. 6C

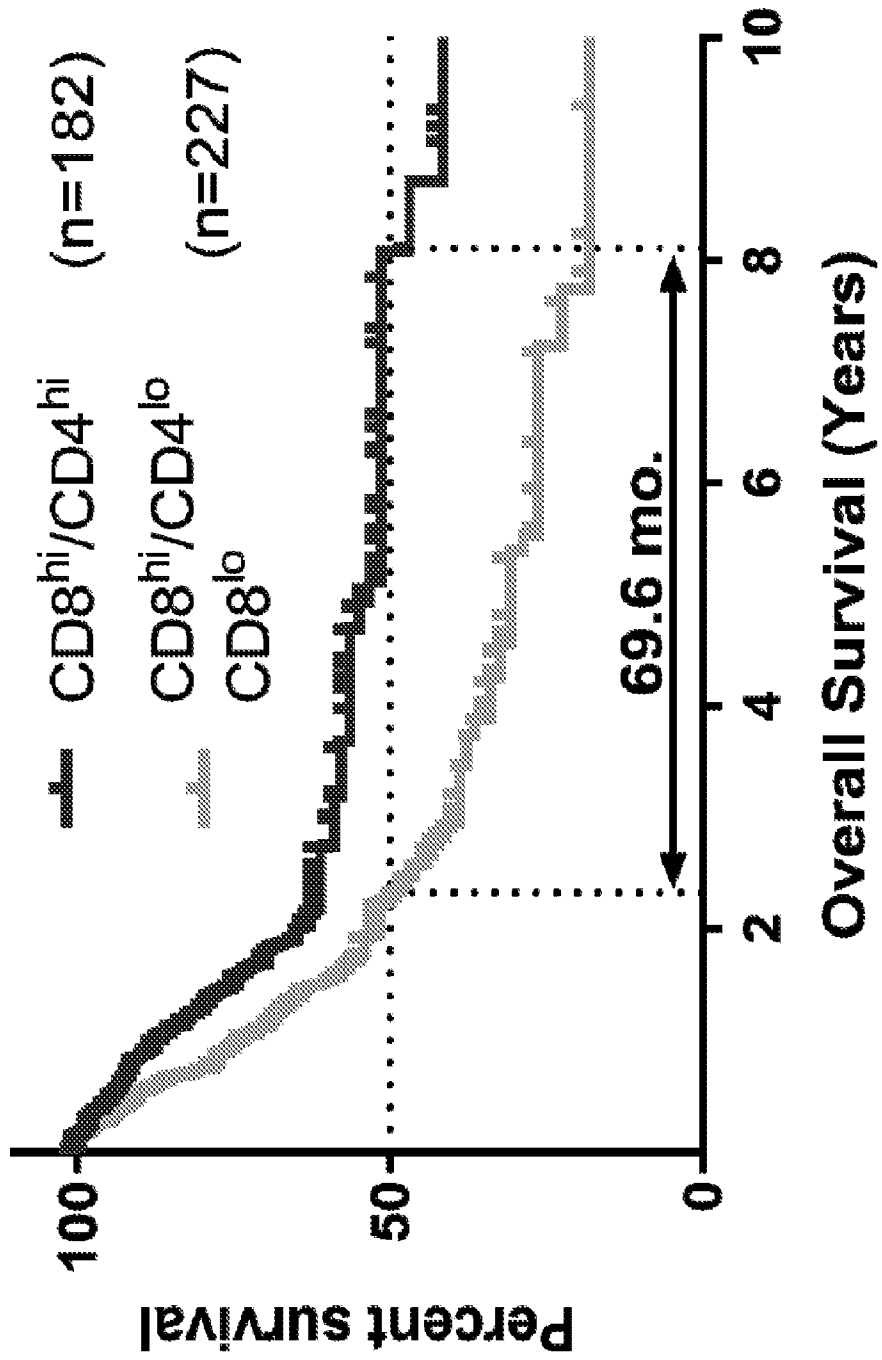


FIG. 6D

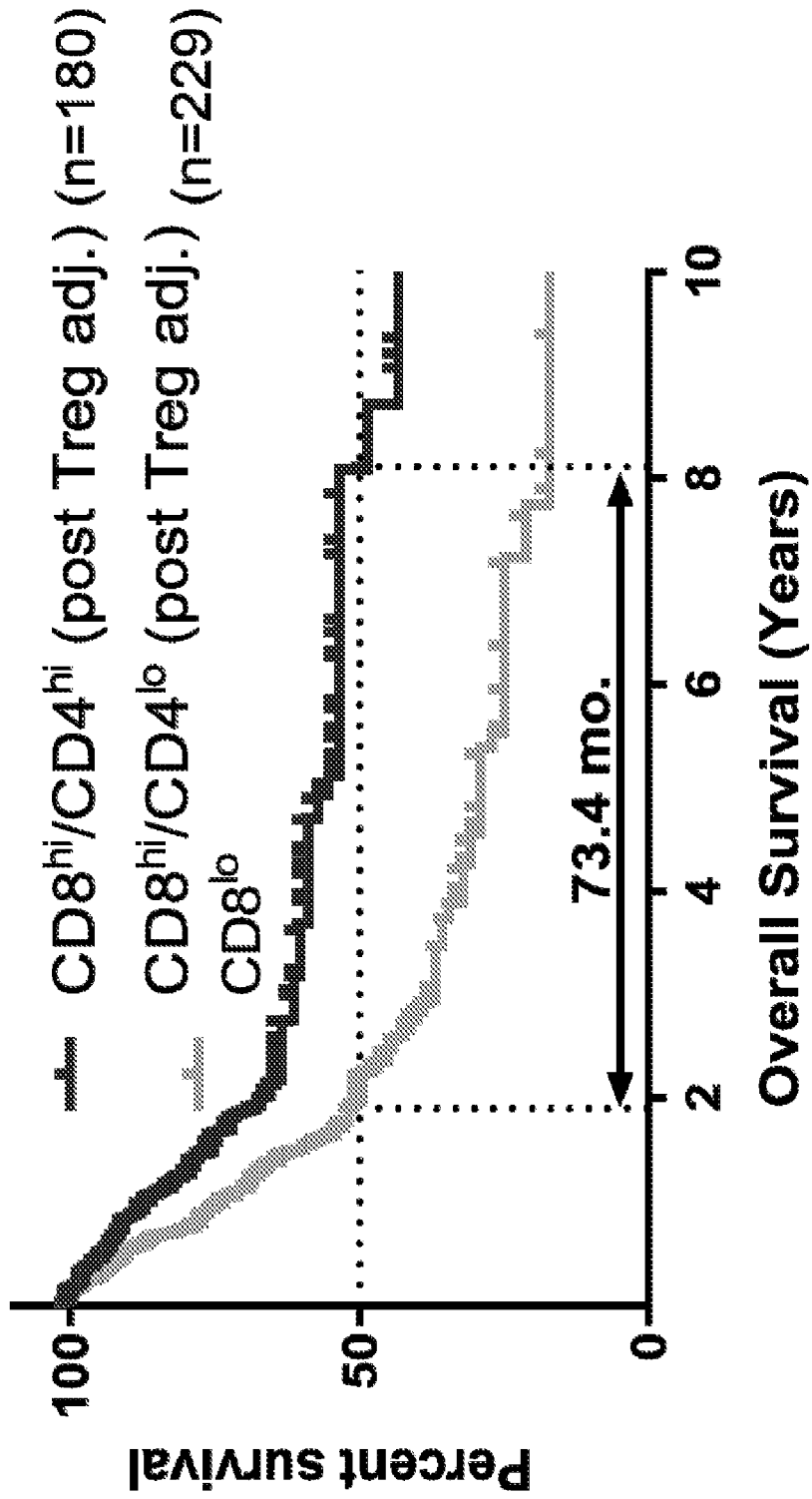


FIG. 6E

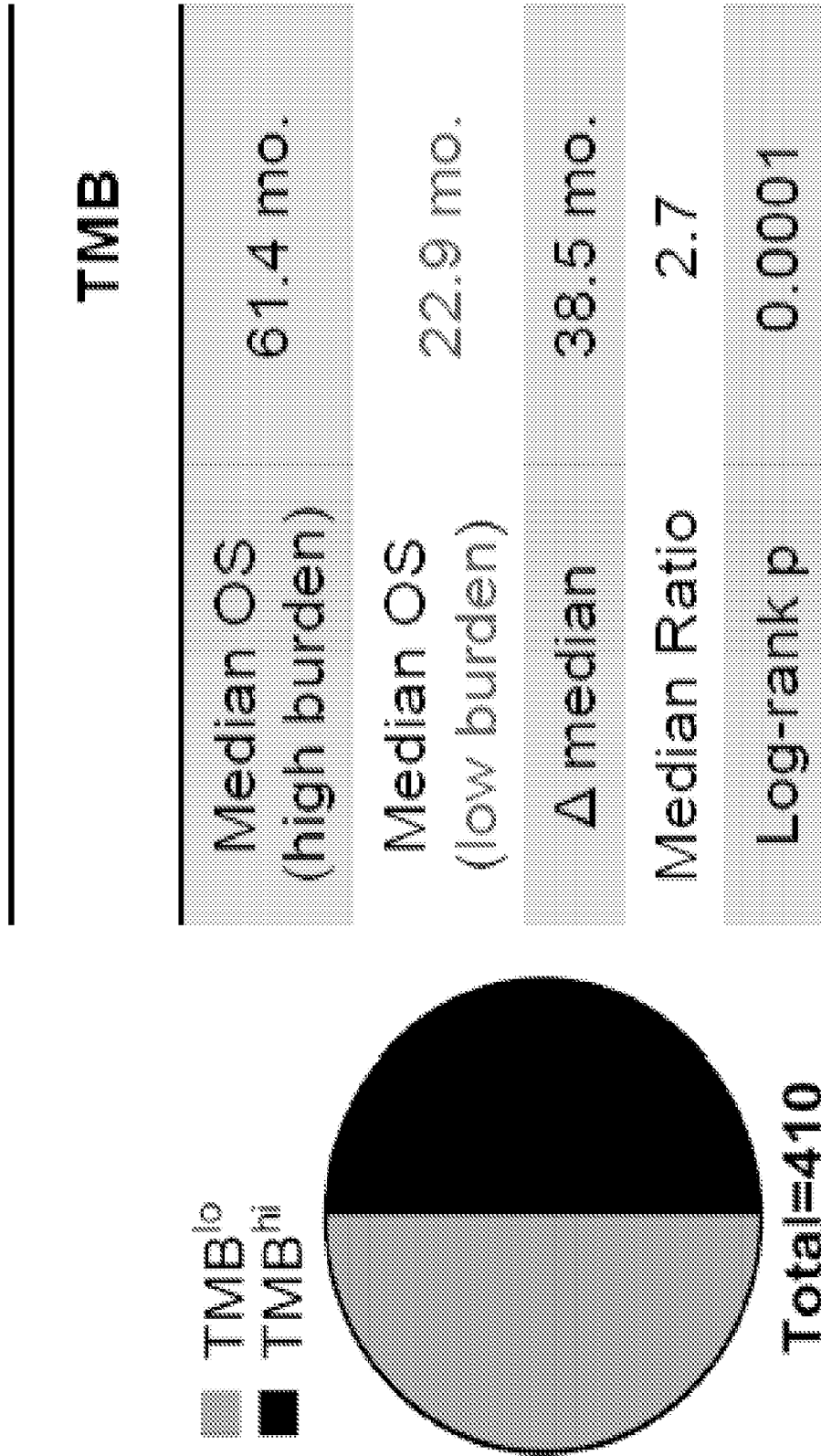


FIG. 7A

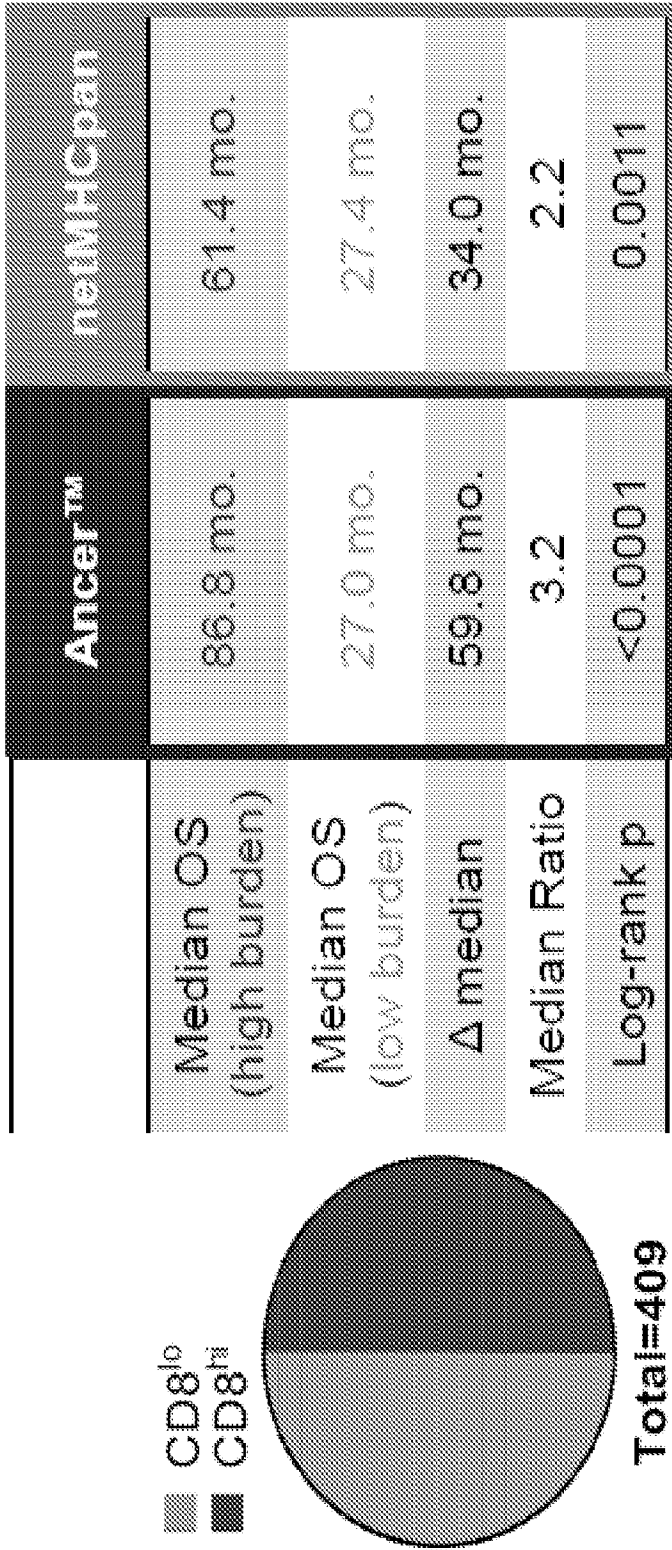


FIG. 7B

	Ancer™	netMHCpan netMHCIIpan
Median OS (high burden)	97.0 mo.	61.4 mo.
Median OS (low burden)	27.4 mo.	27.4 mo.
Δ median	69.6 mo.	34.0 mo.
Median Ratio	3.5	2.2
Log-rank p	0.0001	0.0020

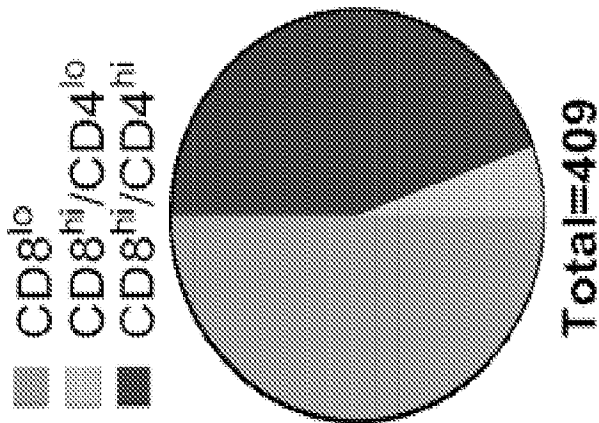


FIG. 7C

	Ancer™	netMHCpan netMHCclipan
Median OS (high burden)	97.0 mo.	N/A
Median OS (low burden)	23.6 mo.	N/A
Δ median	73.4 mo.	N/A
Median Ratio	4.1	N/A
Log-rank p	<0.0001	N/A

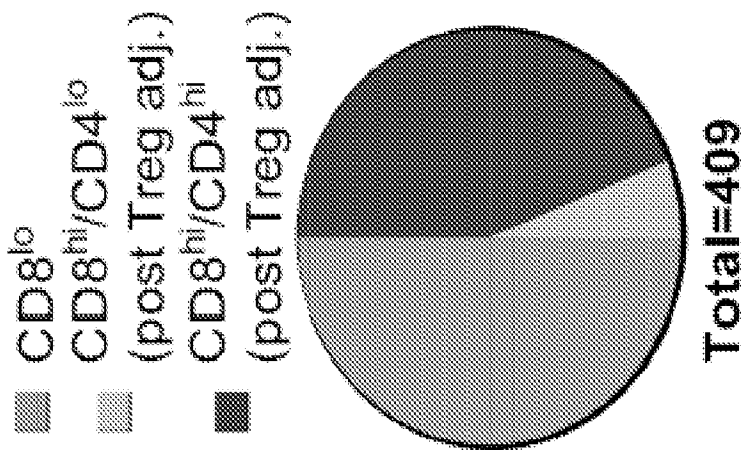


FIG. 7D