CLAIMS

1. A composition comprising at least two binding proteins, wherein i) at least one of the binding proteins is a T cell receptor (TCR) that is capable of binding to an immunogenic peptide derived from a target protein as an immunogenic peptide-MHC (pMHC) complex and ii) at least one of the binding proteins is a TCR that is capable of binding to a different immunogenic peptide from the same target protein or a different target protein than in i) as a pMHC complex, optionally wherein the composition comprises 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 or more binding proteins, optionally wherein:

1) the binding affinity of the TCR of i) and/or the TCR of ii) has a K_d less than or equal to about $5x10^{-4}$ M; and/or

2) the MHC of i) and the MHC of ii) are the same or different.

2. The composition of claim 1, wherein

the binding protein of i) comprises:

1) a) three T cell receptor (TCR) alpha chain CDR sequences: CDR1 having at least about 80% identity to residues 45-49 of SEQ ID NO: 12 (SVFSS), CDR2 having at least about 80% identity to residues 67-73 of SEQ ID NO: 12 (VVTGGEV), and CDR3 having at least about 80% identity to residues 107-120 of SEQ ID NO: 12 (CAGDESISYGKLTF); and

b) three TCR beta chain CDR sequences: CDR1 having at least about 80% identity to residues 46-50 of SEQ ID NO: 14 (SGHDY), CDR2 having at least about 80% identity to residues 68-73 of SEQ ID NO: 14 (FNNNVP), and CDR3 having at least about 80% identity to residues 111-124 of SEQ ID NO: 14 (CASSFLGWNEKLFF),

2) a) a TCR alpha chain CDR sequence with at least about 80% identity to a TCR alpha chain CDR sequence set forth in SEQ ID NO: 12; and/or

b) a TCR beta chain CDR sequence with at least about 80% identity to a TCR beta chain CDR sequence set forth in SEQ ID NO: 14,

3) a) a TCR alpha chain variable (V_α) domain sequence with at least about 80% identity to the TCR V_α domain sequence set forth in SEQ ID NO: 12; and/or

b) a TCR beta chain variable (V_β) domain sequence with at least about 80% identity to the TCR V_β domain sequence set forth in SEQ ID NO: 14, or

4) a) the TCR alpha chain sequence of SEQ ID NO: 12; and/or

b) the TCR beta chain sequence of SEQ ID NO: 14, and

the binding protein of ii) comprises:

1) a) three TCR alpha chain CDR sequences: CDR1 having at least about 80% identity to residues 47-53 of SEQ ID NO: 89 (TSESDYY), CDR2 having at least about 80% identity to residues 71-78 of SEQ ID NO: 89 (QEAYKQQN), and CDR3 having at least about 80% identity to residues 112-124 of SEQ ID NO: 89 (CAYRKTSYDKVIF); and

b) three TCR beta chain CDR sequences: CDR1 having at least about 80% identity to residues 56-60 of SEQ ID NO: 91 (PRHDT), CDR2 having at least about 80% identity to residues 78-83 of SEQ ID NO: 91 (FYEKMQ), and CDR3 having at least about 80% identity to residues 120-136 of SEQ ID NO: 91 (CASSFARLEGRDNEQFF),

2) a) a T cell receptor (TCR) alpha chain CDR sequence with at least about 80% identity to a TCR alpha chain CDR sequence set forth in SEQ ID NO: 89; and/or

b) a TCR beta chain CDR sequence with at least about 80% identity to a TCR beta chain CDR sequence set forth in SEQ ID NO: 91,

3) a) a TCR alpha chain variable (V_α) domain sequence with at least about 80% identity to the TCR V_α domain sequence set forth in SEQ ID NO: 89; and/or

b) a TCR beta chain variable (V_β) domain sequence with at least about 80% identity to the TCR V_β domain sequence set forth in SEQ ID NO: 91, or

4) a) the TCR alpha chain sequence of SEQ ID NO: 89; and/or

b) the TCR beta chain sequence of SEQ ID NO: 91.

3. The composition of claim 1, wherein the binding protein of i) and/or ii) comprises:

1) a) a T cell receptor (TCR) alpha chain CDR sequence with at least about 80% identity to a TCR alpha chain CDR sequence selected from the group consisting of TCR alpha chain CDR sequences listed in Table 1, Table 4, or Table 6; and/or

b) a TCR beta chain CDR sequence with at least about 80% identity to a TCR beta chain CDR sequence selected from the group consisting of TCR beta chain CDR sequences listed in Table 1, Table 4, or Table 6;

2) a) a TCR alpha chain variable (V_α) domain sequence with at least about 80% identity to a TCR V_α domain sequence selected from the group consisting of TCR V_α domain sequences listed in Table 1, Table 4, or Table 6; and/or

b) a TCR beta chain variable (V_β) domain sequence with at least about 80% identity to a TCR V_β domain sequence selected from the group consisting of TCR V_β domain sequences listed in Table 1, Table 4, or Table 6; and/or

3) a) a TCR alpha chain sequence selected from the group consisting of TCR alpha chain sequences listed in Table 1, Table 4, or Table 6; and/or

b) a TCR beta chain sequence selected from the group consisting of TCR beta chain sequences listed in Table 1, Table 4, or Table 6.

4. The composition of claim 2 or 3, wherein 1) the TCR alpha chain CDR, TCR V_α domain, and/or TCR alpha chain of the binding protein of i) and/or ii) is encoded by a TRAV, TRAJ, and/or TRAC gene or fragment thereof selected from the group of TRAV, TRAJ, and TRAC genes listed in Table 1, Table 2, Table 4, and/or Table 6, and/or 2) the TCR beta chain CDR, TCR V_β domain, and/or TCR beta chain of the binding protein of i) and/or ii) is encoded by a TRBV, TRBJ, and/or TRBC gene or fragment thereof selected from the group of TRBV, TRBJ, and TRBC genes listed in Table 1, Table 2, Table 4, and/or Table 6, and/or 3) each CDR of the binding protein of i) and/or ii) has up to five amino acid substitutions, insertions, deletions, or a combination thereof as compared to the cognate reference CDR sequence listed in Table 1, Table 4, or Table 6.

5. The composition of any one of claims 1-4, wherein the immunogenic peptide comprises an amino acid sequence shown in Table 3.

6. The composition of any one of claims 1-5, wherein the binding protein of i) and/or ii) has one or more of the following properties:

1) is chimeric, humanized, or human;

2) is a TCR, an antigen-binding fragment of a TCR, a single chain TCR (scTCR), a chimeric antigen receptor (CAR), or a fusion protein comprising a TCR and an effector domain,

optionally wherein the binding domain comprises a transmembrane domain and an effector domain that is intracellular;

3) binds to the pMHC complex on a cell surface;

4) has a higher binding affinity to the peptide-MHC (pMHC) than does a known T-cell receptor;

5) has at least 1.05-fold higher binding affinity to the peptide-MHC (pMHC) than does a known T-cell receptor;

6) induces higher T cell expansion, cytokine release, and/or cytotoxic killing than does a known T-cell receptor when contacted with target cells with a heterozygous expression of the target, optionally wherein the target cell is: i) SK-MEL-5, DEL, THP-1, or TF-1 cell line, ii) a cancer cell, optionally wherein the cancer is a hematological malignancy or a solid tumor, further optionally wherein the cancer is a melanoma, head and neck cancer, or lung cancer; and/or

7) induces at least 1.05-fold increase in T cell expansion, cytokine release, and/or cytotoxic killing than does a known T-cell receptor when contacted with target cells with a heterozygous expression of the target, optionally wherein the target cell is: i) SK-MEL-5, DEL, THP-1, or TF-1 cell line, ii) a cancer cell, optionally wherein the cancer is a hematological malignancy or a solid tumor, further optionally wherein the cancer is a melanoma, head and neck cancer, or lung cancer.

7. The composition of any one of claims 2-6, wherein

1) the TCR alpha chain and the TCR beta chain are covalently linked, optionally wherein the TCR alpha chain and the TCR beta chain are covalently linked through a linker peptide; and/or

2) the TCR alpha chain and/or the TCR beta chain of the binding protein of i) and/or ii) are covalently linked to a moiety, optionally wherein the covalently linked moiety:

a) comprises an affinity tag or a label, optionally wherein the affinity tag is selected from the group consisting of CD34 enrichment tag, Glutathione-S-Transferase (GST), calmodulin binding protein (CBP), protein C tag, Myc tag, HaloTag, HA tag, Flag tag, His tag, biotin tag, and V5 tag, and/or wherein the label is a fluorescent protein; and/or

b) is selected from the group consisting of an inflammatory agent, cytokine, toxin, cytotoxic molecule, radioactive isotope, or antibody or antigen-binding fragment thereof.

8. The composition of any one of claims 1-7, wherein the MHC of i) and/or the MHC of ii):

1) is a MHC multimer, optionally wherein the MHC multimer is a tetramer;

2) is a MHC class I molecule;

3) comprises an MHC alpha chain that is an HLA serotype HLA-A*02; and/or

4) comprises an HLA allele selected from the group consisting of HLA-A*02, HLA-A*03, HLA-A*01, HLA-A*11, HLA-A*24, HLA-B*07, HLA-C*07, HLA-C*01, HLA-C*02, HLA-C*03, HLA-C*04, HLA-C*05, HLA-C*06, HLA-C*08, HLA-C*12, HLA-C*14, HLA-C*15, HLA-C*16, HLA-C*17, and HLA-C*18, optionally wherein the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0204, HLA-A*0205, HLA-A*0206, HLA-A*0207, HLA-A*0210, HLA-A*0211, HLA-A*0212, HLA-A*0213, HLA-A*0214, HLA-A*0216, HLA-A*0217, HLA-A*0219, HLA-A*0220, HLA-A*0222, HLA-A*0224, HLA-A*0230, HLA-A*0242, HLA-A*0253, HLA-A*0260, HLA-A*0274 allele, HLA-A*0301, HLA-A*0302, HLA-A*0305, HLA-A*0307, HLA-A*0101, HLA-A*0102, HLA-A*0103, HLA-A*0116 allele, HLA-A*1101, HLA-A*1102, HLA-A*1103, HLA-A*1104, HLA-A*1105, HLA-A*1119 allele, HLA-A*2402, HLA-A*2403, HLA-A*2405, HLA-A*2407, HLA-A*2408, HLA-A*2410, HLA-A*2414, HLA-A*2417, HLA-A*2420, HLA-A*2422, HLA-A*2425, HLA-A*2426, HLA-A*2458 allele, HLA-B*0702, HLA-B*0704, HLA-B*0705, HLA-B*0709, HLA-B*0710, HLA-B*0715, HLA-B*0721, HLA-C*0702, HLA-C*0701 , HLA-C*0401, HLA-C*0602, HLA-C*0304, HLA-C*0501, HLA-C*1601, HLA-C*0202, HLA-C*0303, HLA-C*1203, HLA-C*0802, HLA-C*0102, HLA-C*1701, HLA-C*1502, HLA-C*1402, HLA-C*1202, HLA-C*0704, HLA-C*0801, HLA-C*0302, HLA-C*1801, HLA-C*1505, HLA-C*1602, HLA-C*0804, HLA-C*0305, and HLA-C*1403 allele.

9. The composition of any one of claims 1-8, wherein:

1) binding of the composition to the pMHC complexes elicits an immune response that is greater than either TCR alone, optionally wherein the immune response is a T cell response and/or a synergistic response, further optionally wherein the T cell response is selected from the group consisting of T cell expansion, cytokine release, and/or cytotoxic killing; and/or

2) is capable of specifically binding to the immunogenic peptide-MHC (pMHC) complex with a K_d less than or equal to about $1x10^{-4}$ M, less than or equal to about $5x10^{-5}$ M, less than or equal to about $1x10^{-5}$ M, less than or equal to about $5x10^{-6}$ M, less than or equal to about $1x10^{-6}$ M, less than or equal to about $5x10^{-7}$ M, less than or equal to about $1x10^{-7}$ M, less than or equal to about $5x10^{-8}$ M, less than or equal to about $1x10^{-8}$ M, less than or equal to about $5x10^{-9}$ M, less than or equal to about $1x10^{-9}$ M, less than or equal to about $5x10^{-10}$ M, less than or equal to about $1x10^{-10}$ M, less than or equal to about $5x10^{-11}$ M, less than or equal to about $1x10^{-11}$ M, less than or equal to about $5x10^{-12}$ M, or less than or equal to about $1x10^{-12}$ M.

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10. An isolated nucleic acid molecule that hybridizes, under stringent conditions, with the complement of a nucleic acid encoding a polypeptide selected from the group consisting of polypeptide sequences listed in Table 1, Table 4, or Table 6, or a binding protein of the composition of any one of claims 1-9, or a sequence with at least about 80% homology to a nucleic acid encoding a polypeptide selected from the group consisting of the polypeptide sequences listed in Table 1, , Table 4, or Table 6, optionally wherein the isolated nucleic acid molecule comprises 1) a TRAV, TRAJ, and/or TRAC gene or fragment thereof selected from the group of TRAV, TRAJ, and TRAC genes listed in Table 1, Table 2, Table 4, and/or Table 6 and/or 2) a TRBV, TRBJ, and/or TRBC gene or fragment thereof selected from the group of TRBV, TRBJ, and TRBC genes listed in Table 1, Table 2, Table 4, and/or Table 6, or a binding protein of the composition of any one of claims 1-9, optionally wherein the nucleic acid is codon optimized for expression in a host cell.

11. A vector comprising the isolated nucleic acid of claim 10, optionally wherein:

1) the vector is a cloning vector, expression vector, or viral vector;

2) the vector further comprises nucleic acid sequence encoding CD8α, CD8β, a dominant negative TGFβ receptor II (DN-TGFβRII), selectable protein marker,

optionally wherein:

a) the selectable protein marker is dihydrofolate reductase (DHFR); and/or

b) the nucleic acid sequence encoding CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker is operably linked to a nucleic acid encoding a tag,

optionally wherein

i) the nucleic acid encoding a tag is at the 5’ upstream of the nucleic acid sequence encoding CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker such that the tag is fused to the N-terminus of CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker; and/or

ii) the tag is a CD34 enrichment tag; and/or

3) the isolated nucleic acid of claim 10, and/or the nucleic acid sequence encoding TCRα, TCRβ, CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker are interconnected with an internal ribosome entry site or a nucleic acid sequence encoding a self-cleaving peptide, optionally wherein the self-cleaving peptide is P2A, E2A, F2A or T2A.

12. A host cell which comprises the isolated nucleic acid of claim 10, comprises the vector of claim 11, and/or expresses the binding protein composition of any one of claims 1-9, optionally wherein the cell is genetically engineered, further optionally wherein the host cells is a collection of host cells each comprising an isolated nucleic acid of claim 10, comprises the vector of claim 11, and/or expresses the binding protein composition of any one of claims 1-9.

13. The host cell of claim 12, wherein the host cell:

1) comprises a chromosomal gene knockout of a TCR gene, an HLA gene, or both;

2) comprises a knockout of an HLA gene selected from anα1 macroglobulin gene, α2 macroglobulin gene, α3 macroglobulin gene, β1 microglobulin gene, β2 microglobulin gene, and combinations thereof;

3) comprises a knockout of a TCR gene selected from a TCR α variable region gene, TCR β variable region gene, TCR constant region gene, and combinations thereof;

4) expresses CD8α, CD8β, a DN-TGFβRII, and/or a selectable protein marker, optionally wherein the selectable protein marker is DHFR, further optionally wherein the CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker is fused to a CD34 enrichment tag, optionally wherein host cells are enriched using the CD34 enrichment tag;

5) is a hematopoietic progenitor cell, peripheral blood mononuclear cell (PBMC), cord blood cell, or immune cell,

optionally wherein the immune cell is a T cell, cytotoxic lymphocyte, cytotoxic lymphocyte precursor cell, cytotoxic lymphocyte progenitor cell, cytotoxic lymphocyte stem cell, $CD4^+$ T cell, $CD8^+$ T cell, CD4/CD8 double negative T cell, gamma delta (γδ) T cell, natural killer (NK) cell, NK-T cell, dendritic cell, or a combination thereof,

further optionally wherein the T cell is

a) a naive T cell, central memory T cell, effector memory T cell, or a combination thereof;

b) a primary T cell or a cell of a T cell line; and/or

c) does not express or has a lower surface expression of an endogenous TCR; and/or

6) is capable of producing a cytokine or a cytotoxic molecule when contacted with a target cell that comprises a peptide-MHC (pMHC) complex comprising the HA-2 peptide epitope in the context of an MHC molecule,

optionally wherein

a) the host cell is contacted with the target cell in vitro, ex vivo, or in vivo;

b) the cytokine is TNF-α, IL-2, and/or IFN-γ;

c) the cytotoxic molecule is perforins and/or granzymes, optionally wherein the cytotoxic molecule is granzyme B;

d) the host cell is capable of producing a higher level of cytokine or a cytotoxic molecule when contacted with a target cell with a heterozygous expression of the target, optionally wherein the host cell is capable of producing an at least 1.05-fold higher level of cytokine or a cytotoxic molecule;

e) is capable of killing a target cell that comprises a peptide-MHC (pMHC) complex comprising the target peptide epitope in the context of an MHC molecule,

optionally wherein

i) the killing is determined by a killing assay;

ii) the ratio of the host cell and the target cell in the killing assay is from 20:1 to 0.625:1, optionally wherein

iii) the target cell is a T2 cell pulsed with 1 μg/mL to 50 pg/mL of immunogenic peptide;

iv) the host cell is capable of killing a higher number of target cells when contacted with target cells with a heterozygous expression of the target, optionally wherein the host cell is capable of killing an at least 1.05-fold higher number of target cells; and/or

v) the target cell is a SK-MEL-5, DEL, THP-1, or TF-1 cell line;

f) the immunogenic peptide comprises an amino acid sequence shown in Table 3;

g) the MHC molecule is a MHC class I molecule;

h) the MHC molecule comprises an MHC alpha chain that is an HLA serotype HLA-A*02, HLA-A*03, HLA-A*01, HLA-A*11, HLA-A*24, HLA-B*07, HLA-C*07, HLA-C*01, HLA-C*02, HLA-C*03, HLA-C*04, HLA-C*05, HLA-C*06, HLA-C*08, HLA-C*12, HLA-C*14, HLA-C*15, HLA-C*16, HLA-C*17, or HLA-C*18;

i) the HLA allele is selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0204, HLA-A*0205, HLA-A*0206, HLA-A*0207, HLA-A*0210, HLA-A*0211, HLA-A*0212, HLA-A*0213, HLA-A*0214, HLA-A*0216, HLA-A*0217, HLA-A*0219, HLA-A*0220, HLA-A*0222, HLA-A*0224, HLA-A*0230, HLA-A*0242, HLA-A*0253, HLA-A*0260, HLA-A*0274 allele, HLA-A*0301, HLA-A*0302, HLA-A*0305, HLA-A*0307, HLA-A*0101, HLA-A*0102, HLA-A*0103, HLA-A*0116 allele, HLA-A*1101, HLA-A*1102, HLA-A*1103, HLA-A*1104, HLA-A*1105, HLA-A*1119 allele, HLA-A*2402, HLA-A*2403, HLA-A*2405, HLA-A*2407, HLA-A*2408, HLA-A*2410, HLA-A*2414, HLA-A*2417, HLA-A*2420, HLA-A*2422, HLA-A*2425, HLA-A*2426, HLA-A*2458 allele, HLA-B*0702, HLA-B*0704, HLA-B*0705, HLA-B*0709, HLA-B*0710, HLA-B*0715, HLA-B*0721, HLA-C*0702, HLA-C*0701 , HLA-C*0401, HLA-C*0602, HLA-C*0304, HLA-C*0501, HLA-C*1601, HLA-C*0202, HLA-C*0303, HLA-C*1203, HLA-C*0802, HLA-C*0102, HLA-C*1701, HLA-C*1502, HLA-C*1402, HLA-C*1202, HLA-C*0704, HLA-C*0801, HLA-C*0302, HLA-C*1801, HLA-C*1505, HLA-C*1602, HLA-C*0804, HLA-C*0305, and HLA-C*1403 allele; and/or

j) the target cell is a cell line selected from the group consisting of SK-MEL-5, Del, THP-1, and TF-1 cell lines, or is a cancer cell expressing the immunogenic peptide, optionally wherein the cancer cell is of a hematological malignancy or a solid tumor; and/or

k) the host cell does not express the immunogenic peptide, is not recognized by a binding protein of any one of claims 1-9, is not of serotype list in (h), and/or does not express an HLA allele listed in (i).

14. A population of host cells of claim 12 or 13.

15. Use of a combination of a composition of any one of claims 1-14, or a combination of binding proteins, nucleic acids, vectors, and/or host cells according to any one of claims 1-14, in the manufacture of a medicament for preventing and/or treating a non-malignant disorder, a hyperproliferative disorder or a relapse of a hyperproliferative disorder characterized by expression of an immunogenic peptide antigen in a subject, optionally wherein:

1) the composition comprises cells, optionally wherein the cell is an allogeneic cell, syngeneic cell, or autologous cell;

2) the cell is genetically modified;

3) the cell comprises a chromosomal gene knockout of a TCR gene, an HLA gene, or both a TCR gene and an HLA gene;

4) the cell comprises a knockout of an HLA gene selected from an αl macroglobulin gene, α2 macroglobulin gene, α3 macroglobulin gene, β1 microglobulin gene, β2 microglobulin gene, and a combination thereof;

5) the cell comprises a knockout of a TCR gene selected from a TCR α variable region gene, TCR β variable region gene, TCR constant region gene, and combinations thereof;

6) the cell expresses CD8α, CD8β, a DN-TGFβRII, and/or a selectable protein marker, optionally wherein the selectable protein marker is DHFR and further optionally wherein the CD8α, CD8β, the DN-TGFβRII, and/or the selectable protein marker is fused to a CD34 enrichment tag, optionally wherein cells are enriched using the CD34 enrichment tag;

7) the cell is a hematopoietic progenitor cell, peripheral blood mononuclear cell (PBMC), cord blood cell, or immune cell;

8) the immune cell is a cytotoxic lymphocyte, cytotoxic lymphocyte precursor cell, cytotoxic lymphocyte progenitor cell, cytotoxic lymphocyte stem cell, $CD4^+$ T cell, $CD8^+$ T cell, CD4/CD8 double negative T cell, gamma delta (γδ) T cell, natural killer (NK) cell, NK-T cell, dendritic cell, or combination thereof;

9) the T cell is a naive T cell, central memory T cell, effector memory T cell, or combination thereof;

10) the T cell is a primary T cell or a cell of a T cell line;

11) the T cell does not express or has a lower surface expression of an endogenous TCR;

12) the cell is capable of producing a cytokine or a cytotoxic molecule when contacted with a target cell that comprises a peptide-MHC (pMHC) complex comprising the immunogenic peptide in the context of an MHC molecule;

13) the cytokine is TNF-α, IL-2, and/or IFN-γ;

14) the cytotoxic molecule is perforins and/or granzymes, optionally wherein the cytotoxic molecule is granzyme B;

15) the cell is capable of producing a higher level of cytokine or a cytotoxic molecule when contacted with a target cell with a heterozygous expression of the target, optionally wherein the cell is capable of producing an at least 1.05-fold higher level of cytokine or a cytotoxic molecule;

16) the host cell is capable of killing a target cell that comprises a peptide–MHC (pMHC) complex comprising the target in the context of an MHC molecule, optionally wherein the host cell is capable of killing an at least 1.05-fold higher number of target cells; and/or

17) the immunogenic peptide comprises an amino acid sequence shown in Table 3.

16. The use of claim 15, wherein the MHC molecule:

1) is an MHC class I molecule;

2) comprises an MHC alpha chain that is an HLA serotype HLA-A*02, HLA-A*03, HLA-A*01, HLA-A*11, HLA-A*24, HLA-B*07, HLA-C*07, HLA-C*01, HLA-C*02, HLA-C*03, HLA-C*04, HLA-C*05, HLA-C*06, HLA-C*08, HLA-C*12, HLA-C*14, HLA-C*15, HLA-C*16, HLA-C*17, or HLA-C*18; and/or

3) comprises an HLA allele selected from the group consisting of HLA-A*0201, HLA-A*0202, HLA-A*0203, HLA-A*0204, HLA-A*0205, HLA-A*0206, HLA-A*0207, HLA-A*0210, HLA-A*0211, HLA-A*0212, HLA-A*0213, HLA-A*0214, HLA-A*0216, HLA-A*0217, HLA-A*0219, HLA-A*0220, HLA-A*0222, HLA-A*0224, HLA-A*0230, HLA-A*0242, HLA-A*0253, HLA-A*0260, HLA-A*0274 allele, HLA-A*0301, HLA-A*0302, HLA-A*0305, HLA-A*0307, HLA-A*0101, HLA-A*0102, HLA-A*0103, HLA-A*0116 allele,

HLA-A*1101, HLA-A*1102, HLA-A*1103, HLA-A*1104, HLA-A*1105, HLA-A*1119 allele, HLA-A*2402, HLA-A*2403, HLA-A*2405, HLA-A*2407, HLA-A*2408, HLA-A*2410, HLA-A*2414, HLA-A*2417, HLA-A*2420, HLA-A*2422, HLA-A*2425, HLA-A*2426, HLA-A*2458 allele, HLA-B*0702, HLA-B*0704, HLA-B*0705, HLA-B*0709, HLA-B*0710, HLA-B*0715, HLA-B*0721, HLA-C*0702, HLA-C*0701 , HLA-C*0401, HLA-C*0602, HLA-C*0304, HLA-C*0501, HLA-C*1601, HLA-C*0202, HLA-C*0303, HLA-C*1203, HLA-C*0802, HLA-C*0102, HLA-C*1701, HLA-C*1502, HLA-C*1402, HLA-C*1202, HLA-C*0704, HLA-C*0801, HLA-C*0302, HLA-C*1801, HLA-C*1505, HLA-C*1602, HLA-C*0804, HLA-C*0305, and HLA-C*1403 allele.

17. The use of claim 15 or 16, wherein:

1) the target cell is a non-malignant cell or a hyperproliferating cell expressing the antigen in the subject;

2) the composition further comprises a pharmaceutically acceptable carrier;

3) the composition induces an immune response against the non-malignant cells or the hyperproliferating cells expressing the antigen in the subject that is greater than either TCR alone, optionally wherein the immune response is a synergistic response;

4) the composition induces an antigen-specific T cell immune response against the non-malignant cells or the hyperproliferating cells expressing the antigen in the subject;

5) the antigen-specific T cell immune response comprises at least one of a $CD4^+$ helper T lymphocyte (Th) response and a CD8+ cytotoxic T lymphocyte (CTL) response;

6) a) the hyperproliferative disorder comprises a hematological malignancy or a solid tumor, or b) the non-malignant disorder is an autoimmune disorder, optionally wherein the autoimmune disorder is systemic sclerosis or multiple sclerosis;

7) the subject is receiving or previously received a hematopoietic cell transplant (HCT), optionally wherein the HCT comprises cells that do not express the immunogenic antigen, are not recognized by a binding protein of any one of claims 1-9, are not of serotype listed in claim 16 (2), and/or do not express an HLA allele listed in claim 16 (3); and/or

8) the HCT comprises a donor hematopoietic cell comprising a chromosomal knockout of a gene that encodes an HLA component, a chromosomal knockout of a gene that encodes a TCR component, or both.

18. The use of any one of claims 15-17, wherein

1) the use further comprises at least one additional treatment for the non-malignant disorder, the hyperproliferative disorder or the relapse of a hyperproliferative disorder to be administered to the subject;

2) the at least one additional treatment for the non-malignant disorder, the hyperproliferative disorder or the relapse of a hyperproliferative disorder is to be administered concurrently or sequentially with the composition; and/or

3) the subject is an animal model of disorder characterized by the immunogenic antigen expression and/or a mammal, optionally wherein the mammal is a human, a primate, or a rodent.

19. A combination of a composition of any one of claims 1-14, or a combination of binding proteins, nucleic acids, vectors, and/or host cells according to any one of claims 1-14, for use in therapy.