[0023] In some embodiments, the PI3K recruitment domain comprises a sequence with at least 90% sequence identity to YEDMRGILYAAPQLRSIRGQPGPNHEEDADSYENM (SEQ ID NO: 41).

[0024] In some embodiments, the intracellular domain comprises an intracellular domain from CD39, CD56, CD57, CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, DAP10, NKG2C, NKG2D, NKG2E, Ly49D, Ly49D, NKp46, NKp30 or NKp44.

[0025] In some embodiments, the intracellular domain comprises an intracellular domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, or DAP10.

[026] Provided herein is a recombinant polynucleic acid composition comprising a recombinant polynucleic acid sequence encoding a chimeric fusion protein (CFP) comprising a transmembrane domain that specifically integrates within a membrane protein complex of a B cell, wherein the B cell is characterized as naturally expressing the membrane protein complex; wherein, when the recombinant polynucleic acid composition comprising the recombinant polynucleic acid sequence is contacted to any cell of a heterogenous cell population, at least greater than 50% of cells within the heterogenous cell population that are characterized as naturally expressing the membrane protein complex, e.g., B cells, expresses the CFP, and a cell within the heterogenous cell population that lacks the membrane protein complex, e.g., non-B cells, fails to express the CFP. In some embodiments, the naturally expressing the membrane protein complex of a B cell may be a CD19 or CD20 TM domain and intracellular domain. In some embodiments, it comprises an extracellular domain that comprises a sequence from the CD19, and an scFv that binds to a cancer antigen.

[027] In some embodiments, the recombinant polynucleic acid composition is expressed in at least greater than 60%, 70%, 80% or 90% B cells within the heterogenous cell population. In some embodiments, the CFR is expressed in at least 50% of B cells in a heterogenous population PBMC, e.g. obtained from peripheral blood drawn at 1, 2, or 3 days after introduction of the polynucleic acid in the system of the subject. In some embodiments, the recombinant polynucleic acid composition less than 10% cells within the heterogenous cell population that lacks a CD20 or CD19 express the CFP. In some embodiments, the CFP is expressed in less than 10% T cells in a population of cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the CFP is expressed in less than 10% of myeloid cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the CFP is expressed in less than 10% of epithelial cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the recombinant polynucleic acid is expressed at greater than 50% of B cells, e.g., greater than 60%, 70%, 80% or 90% of B cells within the heterogenous cell population tested ex vivo. In some embodiments, the recombinant polynucleic acid is expressed at less than 10% of B cells, e.g.,

[0061] In some embodiments, the transmembrane domain is a transmembrane domain from a cell surface receptor selected from a group consisting of CD3, CD4, CD5, CD7, CD8, CD28, CD48, CD3ε, CD3δ, CD3γ, CD3ζ, TCRα chain, TCRβ chain, TCRγ chain and TCRδ chain. In some embodiments, the transmembrane domain is a transmembrane domain from a cell surface receptor selected from a group consisting of CD3, CD4, CD5, CD7, CD8, CD28 and CD48. In some embodiments, in the extracellular domain is an extracellular domain from CD3, CD4, CD5, CD7, CD8, CD28, CD48, CD3ε, CD3δ, CD3γ, CD3ζ, TCRα chain, TCRβ chain, TCRγ chain and TCRδ chain. In some embodiments, the extracellular domain is an extracellular domain from CD3, CD4, CD5, CD7, CD8, CD28 or CD48. In some embodiments, the extracellular domain comprises a hinge domain from CD8, wherein the hinge domain is operatively linked to the transmembrane domain. In some embodiments, the CFP is preferentially or specifically expressed in T cells of the human subject. In some embodiments, the antigen binding domain comprises a Fab fragment, an scFv domain or an sdAb domain. In some embodiments, the CFP further comprises an intracellular domain. In some embodiments, the intracellular domain comprises an intracellular signaling domain from FcγR, FcαR, FcεR, CD40 or CD3ζ. In some embodiments, the intracellular domain further comprises a phosphoinositide 3-kinase (PI3K) recruitment domain. In some embodiments, the PI3K recruitment domain comprises a sequence with at least 90% sequence identity to the sequence YEDMRGILYAAPQLRSIRGQPGPNHEEDADSYENM (SEQ ID NO: 41). In some embodiments, the intracellular domain comprises an intracellular domain from CD3, CD4, CD5, CD7, CD8, CD28, CD48, CD3ε, CD3δ, CD3γ or CD3ζ. In some embodiments, the intracellular domain comprises an intracellular domain from CD3, CD4, CD5, CD7, CD8, CD28 or CD48. In some embodiments, the recombinant polynucleic acid is an mRNA. In some embodiments, the nanoparticle delivery vehicle comprises a lipid nanoparticle. In some embodiments, the lipid nanoparticle comprises a polar lipid. In some embodiments, the lipid nanoparticle comprises a non-polar lipid. In some embodiments, the lipid nanoparticle is from 100 to 300 nm in diameter. In some embodiments, the lipid nanoparticle comprises (6Z,9Z,28Z,31Z)-heptatriaconta-6,9,28,31-tetraen-19-yl 4-(dimethylamino) butanoate (DLin-MC3-DMA; MC3). In some embodiments, the lipid nanoparticle comprises (a) a nucleic acid; (b) a cationic lipid; (c) a non-cationic lipid; and (d) a conjugated lipid that inhibits aggregation of particles. In some embodiments, the nucleic acid comprises a charged polyanioinc nucleic acid.

[0062] Provided herein is a pharmaceutical composition comprising the composition comprising the CFP comprising: (a) an extracellular domain comprising an antigen binding domain, and (b) a transmembrane domain operatively linked to the extracellular domain; wherein the transmembrane domain is a transmembrane domain from a protein that multimerizes with a cell surface receptor expressed by T cells; and a pharmaceutically acceptable excipient.

and intracellular domain. In some embodiments, it comprises an extracellular domain that comprises a sequence from the CD19, and an scFv that binds to a cancer antigen.

[0066] In some embodiments, the recombinant polynucleic acid composition is expressed in at least greater than 60%, 70%, 80% or 90% B cells within the heterogenous cell population. In some embodiments, the CFR is expressed in at least 50% of B cells in a heterogenous population PBMC, e.g. obtained from peripheral blood drawn at 1, 2, or 3 days after introduction of the polynucleic acid in the system of the subject. In some embodiments, the recombinant polynucleic acid composition less than 10% cells within the heterogenous cell population that lacks a CD20 or CD19 express the CFP. In some embodiments, the CFP is expressed in less than 10% T cells in a population of cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the CFP is expressed in less than 10% of myeloid cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the CFP is expressed in less than 10% of epithelial cells in a biological sample from the subject at 1, 2, or 3 days after administration of a composition comprising the recombinant polynucleic acid. In some embodiments, the recombinant polynucleic acid is expressed at greater than 50% of B cells, e.g., greater than 60%, 70%, 80% or 90% of B cells within the heterogenous cell population tested ex vivo. In some embodiments, the recombinant polynucleic acid is expressed at less than 10% of B cells, e.g., less than 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% 1% or less in cells other than B cells, e.g. epithelial cells or myeloid cells within the heterogenous cell population tested ex vivo.

[0067] In one aspect, provided herein is a composition comprising a nucleic acid encoding a sequence having at least 80% sequence identity to any one of sequences of SEQ ID NOs: 20-40. In some embodiments, the composition comprises a nucleic acid encoding a sequence having at least 90% sequence identity to any one of sequences of SEQ ID NOs: 20-40. In some embodiments, the composition comprises a nucleic acid encoding a sequence having at least 95% sequence identity to any one of sequences of SEQ ID NOs: 20-40.

[0068] In one aspect, provided herein is a composition comprising a nucleic acid encoding a sequence having at 80% identical to any one the sequences of SEQ ID NO: 1-19; further comprising a lipid molecule.

[0069] In some embodiments, the composition comprises a nucleic acid encoding a sequence having a polynucleic acid molecule having a sequence that is at least 90% identical to any one the sequences of SEQ ID NO: 1-19. In some embodiments, the composition comprises a nucleic acid encoding a sequence having composition comprises a polynucleic acid comprising a sequence having at least 80% sequence identity to any one of sequences of SEQ ID NOs: 1-19, further comprising a sequence encoding an anti-TROP2 binding domain. In some embodiments, the anti-TROP2 binding domain comprises a HC CDR3 sequence, GGFGSSYWYFDV (SEQ ID NO: 42) and a LC CDR3 sequence, QQHYITPLT (SEQ ID NO: 43).

[0069a] In one aspect, provided herein is a composition comprising a nucleic acid comprising a sequence encoding a chimeric fusion protein (CFP), wherein the CFP comprises:

(a) an extracellular domain comprising an antigen binding domain,

(b) a transmembrane domain that specifically integrates within a membrane protein complex of a cell, the cell being characterized as naturally expressing the membrane protein complex; and

(c) an intracellular domain; and

wherein the cell that is characterized as naturally expressing the membrane protein complex is a NK cell or a B cell.

[0069b] In another aspect, provided herein is a composition comprising a nucleic acid comprising a sequence encoding a chimeric fusion protein (CFP), wherein the CFP comprises (a) an extracellular domain comprising an antigen binding domain, (b) a transmembrane domain operatively linked to the extracellular domain and that specifically integrates within a membrane protein complex of a cell, the cell being characterized as naturally expressing the membrane protein complex and (c) an intracellular domain; wherein, when the composition comprising the recombinant nucleic acid is contacted to a heterogenous cell population, greater than 50% cells in the heterogenous cell population that naturally express the membrane protein complex expresses the CFP, and greater than 10% cells within the heterogenous cell population that lack the membrane protein complex fail to express the CFP.

[0069c] In another aspect, provided herein is a pharmaceutical composition, comprising the composition as described herein and a pharmaceutically acceptable excipient, wherein the pharmaceutical composition is formulated for in vivo delivery in a subject in need thereof.

[0069d] In yet another aspect, provided herein is a use of the composition as described herein in the manufacture of a medicament for treating a disease in a subject, wherein the disease is a cancer, an autoimmune disease, a fibrotic disease, or an infectious disease.

[0069e] In yet another aspect, provided herein is the composition as described herein for use in therapy.

known as apyrase conserved regions (ACR) 1–5, which are pivotal for the catabolic activity of the enzyme. Expression of CD39 is upregulated in tumor cells and infections. For example CD159 (NKG2) is a receptor specific to NK cells. CD159 (NKG2) has 7 known subtypes, A, B, C, D, E and F. The NKG2 receptors can dimerize with other receptors, e.g.CD94 and induce activating or inhibitory function for the cell.

[00162] In some embodiments, the transmembrane domain is a transmembrane domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, or DAP10. In some embodiments, the extracellular domain is an extracellular domain from CD39, CD56, CD57, CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, DAP10, NKG2C, NKG2D, NKG2E, Ly49D, Ly49D, NKp46, NKp30 or NKp44.

[00163] In some embodiments, the antigen binding domain comprises a Fab fragment, an scFv domain or an sdAb domain. In some embodiments, the extracellular domain is an extracellular domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12 or DAP10.

[00164] In some embodiments, the extracellular domain further a hinge domain from CD8, wherein the hinge domain is operatively linked to the transmembrane domain.

[00165] In some embodiments, the antigen binding domain comprises a sequence of an antigen binding domain provided herein, such as a sequence of an antigen binding domain in a Table 1 provided herein.

[00166] In some embodiments, the target protein is CD5. In some embodiments, the antigen binding domain comprises an anti-CD5 antibody or binding fragment thereof, e.g., an scFv that comprises a heavy chain complementarity determining region 3 (HC CDR3) that is the HC CDR3 RGYDWYFDV (SEQ ID NO: 294). In some embodiments, the extracellular domain comprising an anti-CD5 antibody or binding fragment thereof comprises an Anti-CD5 heavy chain variable domain having a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to EIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGLEWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGTTVTVSS (SEQ ID NO: 44). In some embodiments, the extracellular domain comprising an anti-CD5 antibody or binding fragment thereof comprises an anti-CD5 scFv having a sequence, that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to EIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGLEWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGTTVTV*SSGGGGSGGGGSGGGGS*DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPSRFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK (SEQ ID NO: 45), where the CDR regions are underlined.

[00167] In one embodiment, the chimeric fusion protein comprises an extracellular domain having a CD5 binding domain, according to the paragraphs above, and comprises a domain that allows NK cell

specific expression of the CFP. For example, the CFP having a CD5 binding domain according to the paragraphs above comprises a domain that exhibits a dependency on an ITAM motif containing co-receptor for specific expression in an NK cell, and can express predominantly or only in an NK cell, and not express substantively in non-NK cells. In some embodiments, for example, a CD5 binding CFP is designed that comprises a domain from a NKG2D immune receptor, wherein the domain from a NKG2D immune receptor can dimerize with an ITAM motif containing receptor, DAP10 or a DAP12. In another exemplary embodiment, the CD5 binding CFP comprises a domain from a NKG2C or an NKG2E immune receptor, that can heterodimerize with CD94, which bind to DAP12. In yet another exemplary embodiment, the CD5 binding CFP comprises a domain from a Ly49D or a Ly49H immune receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the CD5 binding CFP comprises a domain from a KIR receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the CD5 binding CFP comprises a domain from an NKp46 immune receptor, or an NKp44 receptor or an NKp30 receptor that can associate with CD3zeta or Fcgamma chain. The construct designs described herein are then tested for NK cell specific expression and or functionality. In some embodiments, any one or more of the chimeric fusion protein designs described above exhibit an NK cell-specific expression. In some embodiments, the chimeric fusion protein is tested for NK cell specific function. In some embodiments, the NK cell-specific chimeric fusion protein is used for therapeutic application.

[00168] In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 binding domain, having an HC CDR3 sequence WGGDGFYAMDV (SEQ ID NO: 46).

[00169] In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 heavy chain variable domain having a sequence, that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYA DSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTVSS (SEQ ID NO: 47). In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 heavy chain variable domain having a sequence, that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to LVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS ADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTV (SEQ ID NO: 48).

[00170] In some embodiments, the extracellular domain comprising an anti HER2 antibody or binding fragment comprises a LC CDR3 QQHYTTPPT (SEQ ID NO: 49). In some embodiments, the extracellular domain comprising an anti HER2 antibody or binding fragment comprises an anti-HER2 light chain variable domain having a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to

DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF SGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSE VQLVE (SEQ ID NO: 50).

[00171] In some embodiments, the extracellular domain comprising an anti HER2 antibody or binding fragment comprises an anti-HER2 light chain variable domain having a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF SGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK (SEQ ID NO: 51).

[00172] In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 scFv having a sequence, that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRF SGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSE VQLVE*SSGGGGSGGGGSGGGGS*LVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWV ARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMD VWGQGTLVTV (SEQ ID NO: 52).

[00173] In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 scFv having a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGS RSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVES GGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS ADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTVSS (SEQ ID NO: 53).

[00174] In some embodiments, the extracellular domain comprising an anti-HER2 antibody or binding fragment thereof comprises an anti-HER2 scFv having a 70-100% sequence identity to a sequence, that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGS RSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVES GGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTIS ADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTVSS (SEQ ID NO: 53).

In one embodiment, the chimeric fusion protein comprises an extracellular domain having a HER2 binding domain, according to the paragraphs above, and comprises a domain that allows NK cell specific expression of the CFP. For example, the CFP having a HER2 binding domain according to the paragraphs above comprises a domain that exhibits a dependency on an ITAM motif containing co-receptor for specific expression in an NK cell, and can express predominantly or only in an NK

cell, and not express substantively in non-NK cells. In some embodiments, for example, a HER2 binding CFP is designed that comprises a domain from a NKG2D immune receptor, wherein the domain from a NKG2D immune receptor can dimerize with an ITAM motif containing receptor, DAP10 or a DAP12. In another exemplary embodiment, the HER2 binding CFP comprises a domain from a NKG2C or an NKG2E immune receptor, that can heterodimerize with CD94, which bind to DAP12. In yet another exemplary embodiment, the HER2 binding CFP comprises a domain from a Ly49D or a Ly49H immune receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the HER2 binding CFP comprises a domain from a KIR receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the HER2 binding CFP comprises a domain from an NKp46 immune receptor, or an NKp44 receptor or an NKp30 receptor that can associate with CD3zeta or Fcgamma chain. In some embodiments, any one or more of the chimeric fusion protein designs described above exhibit an NK cell-specific expression. In some embodiments, the chimeric fusion protein is tested for NK cell specific expression. In some embodiments, the NK cell-specific chimeric fusion protein is used for therapeutic application.

[00175] In some embodiments, the target protein is CD70. In some embodiments, the antigen binding domain comprises an anti-CD70 antibody or binding fragment thereof, wherein the antigen binding domain comprises a heavy chain variable domain (VH) comprising a heavy chain complementarity determining region 3 (HC CDR3) that is the HC CDR3 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYAD SVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 54) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHY ADSVKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVS S (SEQ ID NO: 55), or a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to any one of the above sequences. In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 1 (HC CDR1) that is the HC CDR1 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYAD SVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 54) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADS VKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 55). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof further

comprises a heavy chain complementarity determining region 2 (HC CDR2) that is the HC CDR2 of any one of the VH sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYAD SVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 54) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHY ADSVKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVS S (SEQ ID NO: 55). In some embodiments, the VH of the anti-CD70 antibody or binding fragment thereof comprises with 70-100% sequence identity to any one of the sequences selected from the group consisting of QVQLQESGGGLVQAGGSLRLSCAAPRSIFSINAMGWYRQAPGKQRELVAAITSGGSPTYAD SVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYCATGPYGLDNALDAWGQGTQVTVSS (SEQ ID NO: 54) and QVQLQESGGGLVQTGGSLRLACTASGFTFDDYAIAWFRQAPGKEREFVAAISWSGGTTHYADS VKGRFTISRDNAKNTLYLQMSSLKPEDTAVYFCAKSLRSSPSSRWFGSRGQGTQVTVSS (SEQ ID NO: 55) In some embodiments, the VH is a single domain antibody domain. In some embodiments, the VH is a VHH.

[00176] In one embodiment, the chimeric fusion protein comprises an extracellular domain having a CD70 binding domain, according to the paragraphs above, and comprises a domain that allows NK cell specific expression of the CFP. For example, the CFP having a CD70 binding domain according to the paragraphs above comprises a domain that exhibits a dependency on an ITAM motif containing co-receptor for specific expression in an NK cell, and can express predominantly or only in an NK cell, and not express substantively in non-NK cells. In some embodiments, for example, a CD70 binding CFP is designed that comprises a domain from a NKG2D immune receptor, wherein the domain from a NKG2D immune receptor can dimerize with an ITAM motif containing receptor, DAP10 or a DAP12. In another exemplary embodiment, the CD70 binding CFP comprises a domain from a NKG2C or an NKG2E immune receptor, that can heterodimerize with CD94, which bind to DAP12. In yet another exemplary embodiment, the CD70 binding CFP comprises a domain from a Ly49D or a Ly49H immune receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the CD70 binding CFP comprises a domain from a KIR receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the CD70 binding CFP comprises a domain from an NKp46 immune receptor, or an NKp44 receptor or an NKp30 receptor that can associate with CD3zeta or Fcgamma chain. In some embodiments, any one or more of the chimeric fusion protein designs described above exhibit an NK cell-specific expression. In some embodiments, the chimeric fusion protein is tested for NK cell specific expression. In some embodiments, the NK cell-specific chimeric fusion protein is used for therapeutic application.

[00177] In some embodiments the target protein is GPC3. In some embodiments, the antigen binding domain comprises an anti-GPC3 antibody or binding fragment thereof, wherein the antigen binding domain comprises a heavy chain variable domain (VH) comprising a heavy chain complementarity determining region 3 (HC CDR3) of any one of the sequences selected from the group consisting of ATACADTTQYAYDY (SEQ ID NO: 56), ATACADTTLYEYDY (SEQ ID NO: 57), ATACVDTTQYEYDY (SEQ ID NO: 58), ATACADATQHEYDY (SEQ ID NO: 59), ATACADTTQYDYDY (SEQ ID NO: 60), ATACADTTQYEYDY (SEQ ID NO: 61), ATACADTTHYEYDY (SEQ ID NO: 62), ATACVITTLYEYDY (SEQ ID NO: 63), ATACAETTLYEYDY (SEQ ID NO: 64), ATACADTTQHEYDY (SEQ ID NO: 65), ATACVDTTHYEYDY (SEQ ID NO: 66), ATACASTTLYEYDY (SEQ ID NO: 67), ATACVVTTLYEYDY (SEQ ID NO: 68), ATACGGATGPYDY (SEQ ID NO: 69), ATACAGAIGPYDY (SEQ ID NO: 70), ATACVVVGDQNDY (SEQ ID NO: 71), ATACVVVGDRNDY (SEQ ID NO: 72), ATDCAGGTSTPYDY (SEQ ID NO: 73), ATDCAGGTATPYDY (SEQ ID NO: 74), ATACVVADRNEYDY (SEQ ID NO: 75), ATSCVVVTKNEYDY (SEQ ID NO: 76), ATACSGLTHEYDY (SEQ ID NO: 77), ATTCSGLTHEYDY (SEQ ID NO: 78), ATACANWSSLGPYDY (SEQ ID NO: 79), ATACANWSTLGPYDY (SEQ ID NO: 80), ATACSDPRVYEYDY (SEQ ID NO: 81), ATTCASPEKYEYDY (SEQ ID NO: 82), ATHCGGTSWGTSYDY (SEQ ID NO: 83), ATHCGGSSWSNEYDY (SEQ ID NO: 84), YARYSGRTY (SEQ ID NO: 85), ASSAWPAGPKHQVEYDY (SEQ ID NO: 86), ATACGSLVGMYDY (SEQ ID NO: 87), ATACGSAVHEYDY (SEQ ID NO: 88), ATDCVGFGSNWFDY (SEQ ID NO: 89), ATACASPVIYEYDY (SEQ ID NO: 90), ATDCAGGVGHEYDY (SEQ ID NO: 91), ATDCSLHGSDYPYDY (SEQ ID NO: 92) and AVRIYSGSFDNTLAYDY (SEQ ID NO: 93). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 1 (HC CDR1) of any one of the sequences selected from the group consisting of sequences: GFPLAYYA (SEQ ID NO: 94), GFSLDYYA (SEQ ID NO: 95), GFPLDYYA (SEQ ID NO: 96), GFTLDYYA (SEQ ID NO: 97), GFSLNYYA (SEQ ID NO: 98), GFTLAYYA (SEQ ID NO: 99), GFTLGYYA (SEQ ID NO: 100), GFPLNYYA (SEQ ID NO: 101), GFPLHYYA (SEQ ID NO: 102), GFSLGYYA (SEQ ID NO: 103), GFPLGYYA (SEQ ID NO: 104), GFPLEYYA (SEQ ID NO: 105), GSDFRADA (SEQ ID NO: 106), GRTFSSYG (SEQ ID NO: 107), GFSLAYYA (SEQ ID NO: 108) and GLTFRSVG (SEQ ID NO: 109). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof further comprises a heavy chain complementarity determining region 2 (HC CDR2) of any one of the sequences selected from the group consisting of sequences: ISNSDGST (SEQ ID NO: 110), ISASDGST (SEQ ID NO: 111), ISSSDGST (SEQ ID NO: 112), ISSSDGNT (SEQ ID NO: 113), ISSADGST (SEQ ID NO: 114), ISSSGGST (SEQ ID NO: 115), ISSGDGST (SEQ ID NO:

116), ISAGDGNT (SEQ ID NO: 117), ISSSDDST (SEQ ID NO: 118), ISSNDGST (SEQ ID NO: 119), ISSPDGST (SEQ ID NO: 120), ISSRTGGT (SEQ ID NO: 121), ISAGDGSST (SEQ ID NO: 122), ISSSDGSSSDGNT (SEQ ID NO: 123), ISSGDGNT (SEQ ID NO: 124), ISSGDGKT (SEQ ID NO: 125), ISSSDGGT (SEQ ID NO: 126), ISSRTGST (SEQ ID NO: 127), ISSRTGNT (SEQ ID NO: 128), ISSSDGHSST (SEQ ID NO: 129), ISSSSDGNT (SEQ ID NO: 130), ISASNGNT (SEQ ID NO: 131), ISSGSDGNT (SEQ ID NO: 132), ISASDGNT (SEQ ID NO: 133), IDSITSI (SEQ ID NO: 134), ISWSGGSTIAASVGST (SEQ ID NO: 135), ISSSDGSDGNT (SEQ ID NO: 136) and ASPSGVIT (SEQ ID NO: 137). In some embodiments, the VH of the anti-GPC3 antibody or binding fragment thereof comprises with 70-100% sequence identity to any one of the sequences selected from the group consisting of QVQLQESGGGLVHSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ ID NO: 138), QVQLQESGGGLVHSGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSVKGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 139), QVQLQESGGGLVHSGGSLRLSCAASGFTLDYYAIGWFRRAPGKEREGVSCISSGDGKTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAGAIGPYDYWGQGTQVTVSS (SEQ ID NO: 140),
QVQLQESGGGLVPPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV KGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 141),
QVQLQESGGGLVQAGGSLRLSCAASGFSLGYYAIGWFRQAPGKEREGVSCISSSDGHSSTYYAD SVKGRFTISRDNAKNTVYLQMNNLKPEDTAVYYCATDCAGGTATPYDYWGQGTQVTVSS (SEQ ID NO: 142),
QVQLQESGGGLVQAGGSLRLSCAASGRTFSSYGMGWFRQAPGKEREFVAAISWSGGSTYYADS VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCASSAWPAGPKHQVEYDYWGQGTQVTVSS (SEQ ID NO: 143),
QVQLQESGGGLVQAGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVACISSRTGSTYYADSV KGRFTISRDNAKNTVALQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 144),
QVQLQESGGGLVQDGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAETTLYEYDYWGQGTQVTVSS (SEQ ID NO: 145),
QVQLQESGGGLVQPGESLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACANWSTLGPYDYWGQGTQVTVSS (SEQ ID NO: 146),
QVQLQESGGGLVQPGESLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADSV KGRFTISRDNAKNTVYLQMNRLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 147),
QVQLQESGGGLVQPGGSLKLSCAASGSDFRADAMGWYRQAPGKEREPVAIDSITSIYYVDSVEG RFTISRDNTKNTVYLQMTSLKPEDTAVYYCYARYSGRTYWGRGTQVTVSS (SEQ ID NO: 148),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLRPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID NO: 149),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV KGRFAISRDNAKNTVYLQMNSLKPEDTAVYYCATACSDPRVYEYDYWGQGTQVTVSS (SEQ ID NO: 150),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ ID NO: 151),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTHYEYDYWGQGTQVTVSS (SEQ ID NO: 152),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVSS (SEQ ID NO: 153),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 154),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 155),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 156),
QVQLQESGGGLVQPGGSLRLSCAASGFPLAYYAIGWFRRAPGKEREGVSCISSSDGNTYYADAV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ ID NO: 157),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISAGDGSSTYYADS VKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACASTTLYEYDYWGQGTQVTVSS (SEQ ID NO: 158),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV KGRFTISRDNAKNAVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 159),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV KGRFTISRDNAKNTVYLQMNSLGPEDTAVYYCATACADTTQYDYDYWGQGTQVTVSS (SEQ ID NO: 160),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSADGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 161),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSPDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 162),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSDGNTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCSLHGSDYPYDYWGQGTQVTVSS (SEQ ID NO: 163),
QVQLQESGGGLVQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVSS (SEQ ID NO: 164),
QVQLQESGGGLVQPGGSLRLSCAASGFPLEYYAIGWFRQAPGKEREGVSCISSSDGSTYYADSV KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACSDPRVYEYDYWGQGTQVTVSS (SEQ ID NO: 165)

,
QVQLQESGGGLVQPGGSLRLSCAASGFPLGYYAIGWFRQAPGKEREGVSCISSSDDSTYYA
DSVKGRFTISRDNDKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS
(SEQ ID NO: 166),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSGDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATSCVVVTKNEYDYWGQGTQVTVS
S (SEQ ID NO: 167),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 168),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVVADRNEYDYWGQGTQVTVS
S (SEQ ID NO: 169),
QVQLQESGGGLVQPGGSLRLSCAASGFPLHYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLRPEDTAVYYCATACVVADRNEYDYWGQGTQVTVS
S (SEQ ID NO: 170),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISASDGNTYYA
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(SEQ ID NO: 171),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFIISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 172),
QVQLQESGGGLVQPGGSLRLSCAASGFPLNYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGSAVHEYDYWGQGTQVTVSS
(SEQ ID NO: 173),
QVQLQESGGGLVQPGGSLRLSCAASGFSLAYYAIGWFRQAPGKEREGVSCIAASVGSTYYA
DSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATDCAGGVGHEYDYWGQGTQVTVS
S (SEQ ID NO: 174),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 175),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVS
S (SEQ ID NO: 176),
QVQLQESGGGLVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS

(SEQ ID NO: 177),
QVQLQESGGGLVQPGGSLRLSCAASGFSLNYYAIGWFRQAPGKEREGVSCISAGDGNTYYA
DSVKGRFTISRDNAANTVSLQMDSLKPEDTAVYYCATACVITTLYEYDYWGQGTQVTVSS
(SEQ ID NO: 178),
QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVS
S (SEQ ID NO: 179),
QVQLQESGGGLVQPGGSLRLSCAASGFTLAYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVS
S (SEQ ID NO: 180),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 181),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVACISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPQDTAVYYCATACGSLVGMYDYWGQGTQVTVSP
(SEQ ID NO: 182),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISASDGNTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATTCASPEKYEYDYWGQGTQVTVSS
(SEQ ID NO: 183),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISASNGNTYYA
DSVKGRFTISRDSAKNTVYLQMNSLKPEDTAVYYCATTCSGLTHEYDYWGQGTQVTVSS
(SEQ ID NO: 184),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGNTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 185),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATHCGGSSWSNEYDYWGQGTQVTV
SS (SEQ ID NO: 186),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSNDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVS
S (SEQ ID NO: 187),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGGTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS
(SEQ ID NO: 188),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSSSDGN
TYYADSVKGRFTISRDNAKNTVYLQMNNLKPEDTAVYYCATACVVTTLYEYDYWGQGTQ
VTVSS (SEQ ID NO: 189),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA
DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVS
P (SEQ ID NO: 190),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 191),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYA DSVKGRFTISRDNAKNTVYLQMNMLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVS S (SEQ ID NO: 192),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACASPVIYEYDYWGQGTQVTVSS (SEQ ID NO: 193),
QVQLQESGGGLVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSGGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCAGGTSTPYDYWGQGTQVTVSS (SEQ ID NO: 194),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVS S (SEQ ID NO: 195),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACANWSSLGPYDYWGQGTQVTV SS (SEQ ID NO: 196),
QVQLQESGGGLVQPGGSLRLSCAASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTGVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 197),
QVQLQESGGGLVQPGGSLRLSCEGSGFSLDYYAIGWFRQAPGKEREGVSCISSGDGNTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATDCVGFGSNWFDYWGQGTQVTVS S (SEQ ID NO: 198),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVACISSRTGSTYYA DSVKGRFTISRDNAKNTVALQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 199),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYA DSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDRNDYWGQGTQVTVSS (SEQ ID NO: 200),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVDTTQYEYDYWGQGTQVTVS S (SEQ ID NO: 201),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGGTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 202),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGNTYYA DSVKGRFTISRDDAKNMVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVS S (SEQ ID NO: 203),
QVQLQESGGGLVQPGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGSTYYA DSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 204),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQALGKEREGVSCISSRTGSTYYA

DSVKGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVS
S (SEQ ID NO: 205),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYA
DSVKGRFAISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS
(SEQ ID NO: 206),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYA

DSVKGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID NO: 207),
QVQLQESGGGLVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYA DSVKGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVS S (SEQ ID NO: 208),
QVQLQESGGGLVQPGGSLRLSCVASGFPLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 209),
QVQLQESGGGLVQPGGSLRLSCVASGFSLDYYAIGWFRQAPGKEREGVSCISNSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYAYDYWGQGTQVTVS S (SEQ ID NO: 210),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSGSDGNTYY ADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACSGLTHEYDYWGQGTQVTVSS (SEQ ID NO: 211),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSSDDSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYEYDYWGQGTQVTVS S (SEQ ID NO: 212),
QVQLQESGGGLVQPGGSLRLSCVASGFTLDYYAIGWFRQAPGKEREGVSCISSSSDGNTYY ADSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATTCSGLTHEYDYWGQGTQVTVSS (SEQ ID NO: 213),
QVQLQESGGGLVQPGGSLRLSCVASGFTLGYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTQYDYDYWGQGTQVTVS S (SEQ ID NO: 214),
QVQLQESGGGLVQPGGSLRLSCVGSGFTLDYYAIGWFRQAPGKEREGVSCISSNDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 215),
QVQLQESGGGLVQSGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISASDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACAETTLYEYDYWGQGTQVTVSS (SEQ ID NO: 216),
QVQLQESGGGLVQTGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSSDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACGGATGPYDYWGQGTQVTVSS (SEQ ID NO: 217),
QVQLQESGGGMVQAGESLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADATQHEYDYWGQGTQVTVS S (SEQ ID NO: 218),
QVQLQESGGGSVQPGESLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISASDGSTYYA

DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID NO: 219),
QVQLQESGGGSVQPGGSLRLSCAASGFTLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYA DSVKGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTHYEYDYWGQGTQVTVS

S (SEQ ID NO: 220),
QVQLQESGGGSVQSGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV
KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ
ID NO: 221),
QVQLQESGGGSVRPGGSLRLSCAASGFPLAYYAIGWFRQAPGKEREGVSCISSSDGNTYYADAV
KGRFTISRDNAKNAVYLQMNSLKPEDTAVYYCATACADTTQHEYDYWGQGTQVTVSS (SEQ
ID NO: 222),
QVQLQESGGGVAQPGGSLRLSCAASGFPLDYYAIGWFRQAPGKEREGVSCISASDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATACADTTLYEYDYWGQGTQVTVSS (SEQ ID
NO: 223),
QVQLQESGGGVVQAGGSLKLSCAASGSDFRADAMGWYRQAPGKEREPVAIDSITSIYYVDSVE
GRFTISRDNTKNTVYLQMTSLKPEDTAVYYCYARYSGRTYWGRGTQVTVSS (SEQ ID NO: 224),
QVQLQESGGGVVQPGGSLRLSCAASGFSLDYYAIGWFRQAPGKEREGVSCISSGDGSTYYADSV
KGRFTISRDNAKNTVYLQMNSLKPEDTAVYYCATHCGGTSWGTSYDYWGQGTQVTVSS (SEQ
ID NO: 225),
QVQLQESGGGVVQPGGSLRLSCAASGLTFRSVGMGWFRRAPGKEREFVATASPSGVITYYADS
VKGRFTISRDNAKNTVYLEMNSLKPEDTAVYYCAVRIYSGSFDNTLAYDYWGQGTQVTVSS
(SEQ ID NO: 226),
QVQLQESGGGVVQPGGSLRLSCTASGFSLGYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV
KGRFTVSRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ
ID NO: 227), and
QVQLQESGGGVVQSGGSLRLSCTASGFSLDYYAIGWFRQAPGKEREGVSCISSRTGSTYYADSV
KGRFTISRDDAKNTVYLQMNSLKPEDTAVYYCATACVVVGDQNDYWGQGTQVTVSS (SEQ ID
NO: 228). In some embodiments, the VH is a single domain antibody domain. In some embodiments, the VH is a VHH.

[00178] In some embodiments, the extracellular domain of a CFP comprises an anti-GPC3 variable heavy chain (VH) domain, having a 70-100% sequence identity to
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWMGALDPKTGDT
AYSQKFKGKATLTADKSTSTAYMELSSLTSEDTAVYYCTRFYSYTYWGQGTLVTVSS (SEQ
ID NO: 229).

[00179] In some embodiments, the extracellular domain of a CFP comprises an anti-GPC3 variable light chain (VL) domain, having a 70-100% sequence identity to
DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWYLQKPGQSPQLLIYKVSNRFSG
VPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQNTHVPPTFGQGTKLEIK (SEQ ID NO: 230).
In some embodiments, the extracellular domain of a CFP comprises an anti-GPC3 scFv, comprising a sequence that has 70%-100% sequence identity to the sequence,
QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQGLEWMGALDPKTGDT
AYSQKFKGKATLTADKSTSTAYMELSSLTSEDTAVYYCTRFYSYTYWGQGTLVTVSSGGG

GSGGGGSGGGGSDVVMTQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWYLQKPGQSP QLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQNTHVPPTFGQGTKLEIK (SEQ ID NO: 231).

[00180] In one embodiment, the chimeric fusion protein comprises an extracellular domain having a GPC3 binding domain, according to the paragraphs above, and comprises a domain that allows NK cell specific expression of the CFP. For example, the CFP having a GPC3 binding domain according to the paragraphs above comprises a domain that exhibits a dependency on an ITAM motif containing co-receptor for specific expression in an NK cell, and can express predominantly or only in an NK cell, and not express substantively in non-NK cells. In some embodiments, for example, a GPC3 binding CFP is designed that comprises a domain from a NKG2D immune receptor, wherein the domain from a NKG2D immune receptor can dimerize with an ITAM motif containing receptor, DAP10 or a DAP12. In another exemplary embodiment, the GPC3 binding CFP comprises a domain from a NKG2C or an NKG2E immune receptor, that can heterodimerize with CD94, which bind to DAP12. In yet another exemplary embodiment, the GPC3 binding CFP comprises a domain from a Ly49D or a Ly49H immune receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the GPC3 binding CFP comprises a domain from a KIR receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the GPC3 binding CFP comprises a domain from an NKp46 immune receptor, or an NKp44 receptor or an NKp30 receptor that can associate with CD3zeta or Fcgamma chain. In some embodiments, any one or more of the chimeric fusion protein designs described above exhibit an NK cell-specific expression. In some embodiments, the chimeric fusion protein is tested for NK cell specific expression. In some embodiments, the NK cell-specific chimeric fusion protein is used for therapeutic application.

[00181] In some embodiments, the extracellular domain of a CFP comprises an anti-TROP2 binding domain that comprises a HC CDR3 sequence, GGFGSSYWYFDV (SEQ ID NO: 42). In some embodiments, the extracellular domain of a CFP comprises an anti-TROP2 binding domain that comprises a LC CDR3 sequence, QQHYITPLT (SEQ ID NO: 43).

[00182] In some embodiments, the extracellular domain of a CFP comprises an anti-TROP2 binding domain that has 70-100% sequence identity to the scFv, DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKLLIYSASYRYTGVPDRF SGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEIKRGGGGSGGGGSGGGGSQ VQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPT YTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYWYFDVWGQGSLVTVS S (SEQ ID NO: 232). In some embodiments, the extracellular domain of a CFP comprises an anti-TROP2 binding domain that has 70-100% sequence identity to the scFv, QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEP

TYTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSYWYFDVWGQGSLVT VSSGGGGSGGGGSGGGGSDIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKA PKLLIYSASYRYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYITPLTFGAGTKVEIK R (SEQ ID NO: 233).

[00183] In one embodiment, the chimeric fusion protein comprises an extracellular domain having a TROP2 binding domain, according to the paragraphs above, and comprises a domain that allows NK cell specific expression of the CFP. For example, the CFP having a TROP2 binding domain according to the paragraphs above comprises a domain that exhibits a dependency on an ITAM motif containing co-receptor for specific expression in an NK cell, and can express predominantly or only in an NK cell, and not express substantively in non-NK cells. In some embodiments, for example, a TROP2 binding CFP is designed that comprises a domain from a NKG2D immune receptor, wherein the domain from a NKG2D immune receptor can dimerize with an ITAM motif containing receptor, DAP10 or a DAP12. In another exemplary embodiment, the TROP2 binding CFP comprises a domain from a NKG2C or an NKG2E immune receptor, that can heterodimerize with CD94, which bind to DAP12. In yet another exemplary embodiment, the TROP2 binding CFP comprises a domain from a Ly49D or a Ly49H immune receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the TROP2 binding CFP comprises a domain from a KIR receptor, that can associate with or bind to the ITAM containing co-receptor DAP12. In some embodiments, the TROP2 binding CFP comprises a domain from an NKp46 immune receptor, or an NKp44 receptor or an NKp30 receptor that can associate with CD3zeta or Fcgamma chain. The construct designs described herein are then tested for NK cell specific expression and or functionality. In some embodiments, any one or more of the chimeric fusion protein designs described above exhibit an NK cell-specific expression. In some embodiments, the chimeric fusion protein is tested for NK cell specific function. In some embodiments, the NK cell-specific chimeric fusion protein is used for therapeutic application.

[00184] In some embodiments, the extracellular domain of a CFP comprises an Ig binding domain. In some embodiments, the extracellular domain comprises an IgA, IgD, IgE, IgG, IgM, FcRγI, FcRγIIA, FcRγIIB, FcRγIIC, FcRγIIIA, FcRγIIIB, FcRn, TRIM21, FcRL5 binding domain. In some embodiments, the extracellular domain of a CFP comprises an FcR extracellular domain. In some embodiments, the extracellular domain of a CFP comprises an FcRα, FcRβ, FcRε or FcRγ extracellular domain. In some embodiments, the extracellular domain comprises an FcRα (FCAR) extracellular domain. In some embodiments, the extracellular domain comprises an FcRβ extracellular domain. In some embodiments, the extracellular domain comprises an FCER1A extracellular domain. In some embodiments, the extracellular domain comprises an FDGR1A, FCGR2A, FCGR2B, FCGR2C, FCGR3A, or FCGR3B extracellular domain. In some embodiments, the extracellular domain comprises an integrin domain or an integrin receptor domain. In some embodiments, the extracellular

Factor Receptor vIII (EGFRvIII), Mesothelin, Human Epidermal Growth Factor Receptor 2 (HER2), EBNA-1, LEMD1, Phosphatidyl Serine, Carcinoembryonic Antigen (CEA), B-Cell Maturation Antigen (BCMA), Glypican 3 (GPC3), Follicular Stimulating Hormone receptor, Fibroblast Activation Protein (FAP), Erythropoietin-Producing Hepatocellular Carcinoma A2 (EphA2), EphB2, a Natural Killer Group 2D (NKG2D) ligand, Disialoganglioside 2 (GD2), CD2, CD3, CD4, CD5, CD7, CD8, CD19, CD20, CD22, CD24, CD30, CD33, CD38, CD44v6, CD45, CD56CD79b, CD97, CD117, CD123, CD133, CD138, CD171, CD179a, CD213A2, CD248, CD276, PSCA, CS-1, CLECL1, GD3, PSMA, FLT3, TAG72, EPCAM, IL-1, an integrin receptor, PRSS21, VEGFR2, PDGFRβ, SSEA-4, EGFR, NCAM, prostase, PAP, ELF2M, GM3, TEM7R, CLDN6, TSHR, GPRC5D, ALK, Dsg1, Dsg3, IGLL1 and combinations thereof. In some embodiments, the antigen is an antigen of a protein selected from the group consisting of CD2, CD3, CD4, CD5, CD7, CCR4, CD8, CD30, CD45, and CD56. In some embodiments, the antigen is an ovarian cancer antigen or a T lymphoma antigen. In some embodiments, the antigen is an antigen of an integrin receptor. In some embodiments, the antigen is an antigen of an integrin receptor or integrin selected from the group consisting of α1, α2, αIIb, α3, α4, α5, α6, α7, α8, α9, α10, α11, αD, αE, αL, αM, αV, αX, β 1, β 2, β 3, β 4, β 5, β 6, β 7, and β8. In some embodiment, the antigen is an antigen of an integrin receptor ligand. In some embodiments, the antigen is an antigen of fibronectin, vitronectin, collagen, or laminin. In some embodiments, the antigen binding domain can bind to two or more different antigens.

[00187] In some embodiments, the antigen binding domain comprises an autoantigen or fragment thereof, such as Dsg1 or Dsg3. In some embodiments, the extracellular antigen binding domain comprises a receptor domain or an antibody domain wherein the antibody domain binds to an auto antigen, such as Dsg1 or Dsg3.

[00188] Table 1. Provided herein are exemplary extracellular antigen binding domain sequences. The present disclosure encompasses any one of the sequences provide in Table 1, as well as a sequence that is at least 80%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to any of the sequences disclosed. Underlines denote the CDR sequences in sequential order of CDR1, CDR2 and CDR3 for the respective heavy and light chains in accordance to the Kabat numbering system.

CFP/ Domain	**Sequence**
GMCSF Signal peptide	MWLQSLLLLGTVACSIS (SEQ ID NO: 234)
Anti-CD5 heavy chain variable domain	EIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGL EWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDT AVYFCTRRGYDWYFDVWGQGTTVTV (SEQ ID NO: 235)
Anti-CD5 heavy chain variable domain	EIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGL EWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDT AVYFCTRRGYDWYFDVWGQGTTVTVSS (SEQ ID NO: 44)

Anti-CD5 light chain variable domain	DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPSRFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK (SEQ ID NO: 236)
Anti-CD5 scFv	EIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGLEWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGTTVTV*SSGGGGSGGGGSGGGGS*DIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPSRFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK (SEQ ID NO: 45)
Anti-CD5 scFv with leader sequence	MWLQSLLLLGTVACSISEIQLVQSGGGLVKPGGSVRISCAASGYTFTNYGMNWVRQAPGKGLEWMGWINTHTGEPTYADSFKGRFTFSLDDSKNTAYLQINSLRAEDTAVYFCTRRGYDWYFDVWGQGTTVTVSSGGGGSGGGGSGGGGSDIQMTQSPSSLSASVGDRVTITCRASQDINSYLSWFQQKPGKAPKTLIYRANRLESGVPSRFSGSGSGTDYTLTISSLQYEDFGIYYCQQYDESPWTFGGGTKLEIK (SEQ ID NO: 237)
Anti-HER2 light chain variable domain	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVE (SEQ ID NO: 50)
Anti-HER2 light chain variable domain	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIK (SEQ ID NO: 51)
Anti-HER2 heavy chain variable domain	LVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTV (SEQ ID NO: 48)
Anti-HER2 heavy chain variable domain	EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTVSS (SEQ ID NO: 47)
Anti-HER2 scFv	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVE*SSGGGGSGGGGSGGGGS*LVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRYADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFYAMDVWGQGTLVTV (SEQ ID NO: 52)
Anti-HER2 scFv	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPKLLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYTTPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVESGGGLVQPG

	GSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFY AMDVWGQGTLVTVSS (SEQ ID NO: 53)
Anti-HER2 scFv	DIQMTQSPSSLSASVGDRVTITCRASQDVNTAVAWYQQKPGKAPK LLIYSASFLYSGVPSRFSGSRSGTDFTLTISSLQPEDFATYYCQQHYT TPPTFGQGTKVEIKRTGSTSGSGKPGSGEGSEVQLVESGGGLVQPG GSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSRWGGDGFY AMDVWGQGTLVTVSS (SEQ ID NO: 53)
Anti-CD137 binding domain	MEFGLSWLFLVAILKGVQCGLLDLRQGMFAQLVAQNVLLIDGPLS WYSDPGLAGVSLTGGLSYKEDTKELVVAKAGVYYVFFQLELRRV VAGEGSGSVSLALHLQPLRSAAGAAALALTVDLPPASSEARNSAFG FQGRLLHLSAGQRLGVHLHTEARARHAWQLTQGATVLGLFRVTPE IPAGLPSPRSE (SEQ ID NO: 238)
Anti-CD70 binding domain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTNYGMNWVRQAPGQ GLEWMGWINTYTGEPTYADAFKGRVTMTTDTSTSTAYMELRSLRS DDTAVYYCARDYGDYGMDYWGQGTTVTVSSGSTSGSGKPGSSEG STKGDIVMTQSPDSLAVSLGERATINCRASKSVSTSGYSFMHWYQQ KPGQPPKLLIYLASNLESGVPDRFSGSGSGTDFTLTISSLQAEDVAV YYCQHSREVPWTFGQGTKVEIK (SEQ ID NO: 239)
Anti-Claudin18.2 binding domain (scFv)	QVQLQESGPGLVKPSQTLSLTCTVSGGSISSGYNWHWIRQPPGKGL EWIGYIHYTGSTNYNPALRSRVTISVDTSKNQFSLKLSSVTAADTAV YYCARIYNGNSFPYWGQGTTVTVSSGGGGSGGGGSGGGGSDIVMT QSPDSLAYSLGERATINCKSSQSLFNSGNQKNYLTWYQQKPGQPPK LLIYWASTRESGVPDRFSGSGSGTDIFITISSLQAEDVAVYYCQNAY SFPYTFGGGTKLEIKR (SEQ ID NO: 240)
Anti-Trop-2 binding domain (scFv)	DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKL LIYSASYRYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYIT PLTFGAGTKVEIKRGGGGSGGGGSGGGGSQVQLQQSGSELKKPGA SVKVSCKASGYTFTNYGMNWVKQAPGQGLKWMGWINTYTGEPT YTDDFKGRFAFSLDTSVSTAYLQISSLKADDTAVYFCARGGFGSSY WYFDVWGQGSLVTVSS (SEQ ID NO: 232)
Anti-Trop-2 binding domain (scFv)	QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQG LKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADD TAVYFCARGGFGSSYWYFDVWGQGSLVTVSSGGGGSGGGGSGGG GSDIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAP

	KLLIYSASYRYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQH YITPLTFGAGTKVEIKR (SEQ ID NO: 233)
Anti-Trop-2 VH domain	QVQLQQSGSELKKPGASVKVSCKASGYTFTNYGMNWVKQAPGQG LKWMGWINTYTGEPTYTDDFKGRFAFSLDTSVSTAYLQISSLKADD TAVYFCARGGFGSSYWYFDVWGQGSLVTVSS (SEQ ID NO: 241)
Anti-TROP2 VL domain	DIQLTQSPSSLSASVGDRVSITCKASQDVSIAVAWYQQKPGKAPKL LIYSASYRYTGVPDRFSGSGSGTDFTLTISSLQPEDFAVYYCQQHYIT PLTFGAGTKVEIKR (SEQ ID NO: 242)
Anti-GPC3 binding domain variable heavy chain	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQG LEWMGALDPKTGDTAYSQKFKGKATLTADKSTSTAYMELSSLTSE DTAVYYCTRFYSYTYWGQGTLVTVSS (SEQ ID NO: 229)
Anti-GPC3 binding domain variable light chain	DVVMTQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWYLQKPG QSPQLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC SQNTHVPPTFGQGTKLEIK (SEQ ID NO: 230)
Anti-GPC3 binding domain (scFv)	QVQLVQSGAEVKKPGASVKVSCKASGYTFTDYEMHWVRQAPGQG LEWMGALDPKTGDTAYSQKFKGKATLTADKSTSTAYMELSSLTSE DTAVYYCTRFYSYTYWGQGTLVTVSSGGGGSGGGGSGGGGSDVV MTQSPLSLPVTPGEPASISCRSSQSLVHSNRNTYLHWYLQKPGQSPQ LLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCSQNT HVPPTFGQGTKLEIK (SEQ ID NO: 231)

[00189] In some embodiments, the transmembrane domain of a CFP expressed in a NK cell is a transmembrane domain from a cell surface receptor selected from a group consisting of CD39, CD56, CD57, CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, DAP10, NKG2C, NKG2D, NKG2E, Ly49D, Ly49D, NKp46, NKp30 and NKp44. In some embodiments, the transmembrane domain is a transmembrane domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, or DAP10. In some embodiments, the extracellular domain is an extracellular domain from CD39, CD56, CD57, CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, DAP10, NKG2C, NKG2D, NKG2E, Ly49D, Ly49D, NKp46, NKp30 or NKp44. In some embodiments, the extracellular domain is an extracellular domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12 or DAP10. In some embodiments, the extracellular domain further comprises a hinge domain from CD8, wherein the hinge domain is operatively linked to the transmembrane domain. In some embodiments, the CFP is preferentially or specifically expressed in

[00212] In some embodiments, the CFP further comprises an intracellular domain. In some embodiments, the intracellular domain comprises an intracellular signaling domain from FcγR, FcαR, FcεR, CD40 or CD3ζ. In some embodiments, the intracellular domains further comprises a phosphoinositide 3-kinase (PI3K) recruitment domain. In some embodiments, the PI3K recruitment domain comprises a sequence with at least 90% sequence identity to YEDMRGILYAAPQLRSIRGQPGPNHEEDADSYENM (SEQ ID NO: 41). In some embodiments, the intracellular domain comprises an intracellular domain from CD39, CD56, CD57, CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, DAP10, NKG2C, NKG2D, NKG2E, Ly49D, Ly49D, NKp46, NKp30 or NKp44. In some embodiments, the intracellular domain comprises an intracellular domain from CD94, CD159a, CD159c, CD314, CD335, CD336, CD337, DAP12, or DAP10.

[00213] Table 2. Exemplary intracellular domains may be considered from any one of the domains.

CFP/ Domain	**Sequence**
FcRγ-chain intracellular signaling domain	LYCRRLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKP PQ (SEQ ID NO: 243)
FcRγ-chain intracellular signaling domain	LYCRLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPP Q (SEQ ID NO: 244)
FcRγ-chain intracellular signaling domain	RLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 245)
FcRγ-chain intracellular signaling domain	RRLKIQVRKAAITSYEKSDGVYTGLSTRNQETYETLKHEKPPQ (SEQ ID NO: 246)
PI3K recruitment domain	YEDMRGILYAAPQLRSIRGQPGPNHEEDADSYENM (SEQ ID NO: 41)
CD40 intracellular domain	KKVAKKPTNKAPHPKQEPQEINFPDDLPGSNTAAPVQETLHGC QPVTQEDGKESRISVQERQ (SEQ ID NO: 247)
TNFR1 intracellular domain	QRWKSKLYSIVCGKSTPEKEGELEGTTTKPLAPNPSFSPTPGFTPTLGFS PVPSSTFTSSSTYTPGDCPNFAAPRREVAPPYQGADPILATALASDPIPN PLQKWEDSAHKPQSLDTDDPATLYAVVENVPPLRWKEFVRRLGLSDH EIDRLELQNGRCLREAQYSMLATWRRRTPRREATLELLGRVLRDMDL LGCLEDIEEALCGPAALPPAPSLLR (SEQ ID NO: 248)
TNFR2 intracellular domain	PLCLQREAKVPHLPADKARGTQGPEQQHLLITAPSSSSSSLESSA SALDRRAPTRNQPQAPGVEASGAGEARASTGSSDSSPGGHGTQ

	VNVTCIVNVCSSSDHSSQCSSQASSTMGDTDSSPSESPKDEQVPFSKEE CAFRSQLETPETLLGSTEEKPLPLGVPDAGMKPS (SEQ ID NO: 249)
CLEC9A (1-35) intracellular signaling domain	MHEEEIYTSLQWDSPAPDTYQKCLSSNKCSGACCL (SEQ ID NO: 250)

[00214] The inhibitory receptors expressed on a NK cell include among others, KIR-L, that can bind to HLA A, or HLA-B, or HLA-c; LAIR-1 that can bind collagen; SIGLEC 3, 7, 9 that can bind to sialic acid, CD94-NKG2A that can bind to HLA-E; KLRG1, that can bind to cadherins, NKR-P1A that can bind to LLT-1.

[00215] In one embodiment, specific recombinant molecules may be designed, and generated that can inhibit or block NK cell deactivation upon engagement of the receptors described above in this paragraph to their respective ligands.

[00216] In some embodiments, upon binding of the CFP to the antigen of the target cell, the killing activity of a cell expressing the CFP is increased by at least greater than 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 100%, 150%, 200%, 250%, 300%, 350%, 400%, 450%, 500%, 550%, 600%, 650%, 700%, 750%, 800%, 850%, 900%, 950%, or 1000% compared to a cell not expressing the CFP. In some embodiments, the CFP functionally incorporates into a cell membrane of a cell when the CFP is expressed in the cell. In some embodiments, upon binding of the CFP to the antigen of the target cell, the killing activity of a cell expressing the CFP is increased by at least 1.1-fold, 1.5-fold, 2-fold, 2.5-fold, 3-fold, 3.5-fold, 4-fold, 4.5-fold, 5-fold, 5.5-fold, 6-fold, 6.5-fold, 7-fold, 7.5-fold, 8-fold, 8.5-fold, 9-fold, 9.5-fold, 10-fold, 11-fold, 12-fold, 13-fold, 14-fold, 15-fold, 16-fold,-fold, 17-fold, 18-fold, 19-fold, 20-fold, 25-fold, 30-fold, 40-fold, 50-fold, 75-fold, or 100-fold compared to a cell not expressing the CFP.

[00217] In some embodiments, the target cell expressing the antigen is a cancer cell. In some embodiments, the target cell expressing the antigen is at least 0.8 microns in diameter.

[00218] In some embodiments, a cell expressing the CFP exhibits an increase in lysis of a target cell expressing the antigen compared to a cell not expressing the CFP when tested in vitro. In some embodiments, a cell expressing the CFP exhibits at least a 1.1-fold increase in phagocytosis of a target cell expressing the antigen compared to a cell not expressing the CFP. In some embodiments, a cell expressing the CFP exhibits at least a 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold or 50-fold increase in phagocytosis of a target cell expressing the antigen compared to a cell not expressing the CFP. In some embodiments, a cell expressing the CFP exhibits an increase in production of a cytokine compared to a cell not expressing the CFP. In some embodiments, the cytokine is selected from the group consisting of IL-1, IL3, IL-6, IL-12, IL-13, IL-

cell. In some embodiments, the nucleic acid, e.g. an IVT mRNA comprises a 3'UTR and a 5'UTR. In some embodiments, the 3' UTR sequence is followed by a poly A sequence. In some embodiments, the poly A sequence is at least 100 nucleotides long (SEQ ID NO: 288). In some embodiments, the poly A sequence is at least about 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190 or 200 nucleotides long. In some embodiments, the poly A sequence is greater than 200 nucleotides long (SEQ ID NO: 295). In some embodiments, within the 5' UTR, a translation start site is at least 15 nucleotides downstream of the 5' end of the mRNA. In some embodiments, a translation start site is at least 20 nucleotides downstream of the 5' end of the mRNA. In some embodiments, the translation start site is at least 25 nucleotides downstream of the ribosome binding site. In some embodiments, the translation start site is at least 30 nucleotides downstream of the ribosome binding site. In some embodiments, the 5' end of the nucleic acid comprises a methyl guanylate cap. In some embodiments, the nucleic acid comprises a single translational start site. In some embodiments, the mRNA coding sequence is 100-10,000 nucleotides long. In some embodiments, the recombinant polynucleic acid comprises a sequence encoding a homeostatic regulator of inflammation. In some embodiments, the homeostatic regulator of inflammation is a sequence in an untranslated region (UTR) of an mRNA. In some embodiments, the sequence in the UTR is a sequence that binds to an RNA binding protein. In some embodiments, translation is inhibited or prevented upon binding of the RNA binding protein to the sequence in an untranslated region (UTR). In some embodiments, the sequence in the UTR comprises a consensus sequence of WWWU(AUUUA)UUUW (SEQ ID NO: 285), wherein W is A or U. In some embodiments, the recombinant polynucleic acid is expressed on a bicistronic vector.

[0292] In some embodiments, the mRNA comprises one or more modified nucleotides for increased stability and nuclease resistance, such as is well known in the art. In some embodiments, the mRNA is modified at the termini for enhanced and/or prolonged expression in a cell, e.g., an NK cell. In some embodiments, the nucleic acid comprises one or more modified nucleotide bases, wherein a fraction of the total number of uridine bases are modified to a pseudouridine, a 1-methyl-pseudouridine or a 5-methoxyuridine. In some embodiments, less than 50% of the total number of uridine bases are modified to a pseudouridine, a 1-methyl-pseudouridine or a 5-methoxyuridine. In some embodiments the 5' UTR is at least 20 nucleotides in length. In some embodiments the 5' UTR is at least 30 nucleotides in length. In some embodiments the 5' UTR is at least 60 nucleotides in length. In some embodiments the 5' UTR is at least 100 nucleotides in length. In one embodiment, the nucleic acid is an mRNA comprising a poly A sequence that is enzymatically added. In one embodiment, the nucleic acid is an mRNA comprising a poly A sequence that is enzymatically added. In some embodiments, the nucleic acid is an mRNA comprising a poly A sequence that is encoded by the plasmid which comprises the template for generating the mRNA by *in vitro transcription (IVT)*. The template for IVT is a linearized plasmid. Typically, the length of the poly A is controlled when encoded by the plasmid, and is less controlled when enzymatically added. An mRNA product comprising an enzymatically

added poly A tail may be tailored at best to contain a narrowed range of the number of A- residues. The in vitro transcribed mRNA is thereafter purified prior. In some embodiments, the nucleic acid comprises a poly A sequence downstream of the 3' UTR sequence. In some embodiments, the poly A sequence is at least 50 nucleotides long (SEQ ID NO: 286). In some embodiments, the poly A sequence is at least 60, 70, 80, or 90 nucleotides long (SEQ ID NO: 287). In some embodiments, the poly A sequence is at least 100 nucleotides long (SEQ ID NO: 288). In some embodiments, the poly A sequence is at least 110 nucleotides long (SEQ ID NO: 289). In some embodiments, the poly A sequence is at least 120 nucleotides long (SEQ ID NO: 290). In some embodiments, the poly A sequence is at least 130 nucleotides long (SEQ ID NO: 291). In some embodiments, the poly A sequence is at least 140 nucleotides long (SEQ ID NO: 292). In some embodiments, the poly A sequence is at least 150, 160, 170, 180, 190 or 200 nucleotides long (SEQ ID NO: 293). In some embodiments, the within the 5' UTR, a translation start site is at least 15 nucleotides downstream of the 5' end. In some embodiments, the translation start site is at least 20 nucleotides downstream of the 5' end. In some embodiments, the translation start site is at least 25 nucleotides downstream of the 5' end. In some embodiments, the translation start site is at least 30 nucleotides downstream of the 5' end. In some embodiments, the nucleic acid comprises a single translational start site.

[00293] In some embodiments, the nucleic acid comprises a 5' methyl guanylate cap. A proper 5'-cap structure is important in the synthesis of functional messenger RNA. In some embodiments, the mRNA design as described herein comprises a proper 5'- cap structure, wherein the 5'- cap comprises a guanosine triphosphate arranged as GpppG at the 5'terminus of the nucleic acid. In some embodiments, the mRNA comprises a 5' 7-methylguanosine cap, m7-GpppG. A 5' 7-methylguanosine cap can increase mRNA translational efficiency and prevents degradation of mRNA 5'-3'exonucleases. In some embodiments, the mRNA comprises "anti-reverse" cap analog (ARCA, m7,3'-O GpppG).

[0294] In some embodiments, the nucleic acid is isolated.

[0295] In some embodiments, the nucleic acid is purified.

[0296] In some embodiments, the nucleic acid comprises at least 1 modified nucleotide.

[0297] In some embodiments, the nucleic acid comprises at least 10% modified nucleotides.

[0298] In some embodiments, the nucleic acid comprises at least 20% modified nucleotides.

[0299] In some embodiments, the nucleic acid comprises at least 30%, 40%, or 50% modified nucleotides. In some embodiments, less than 70% of the uridine residues in the nucleic acid are modified.

[0300] In some embodiments, less than 50% of the uridine residues in the nucleic acid are modified.

[0301] In some embodiments, the modified nucleotide is a pseudouridine, 1-methyl-pseudouridine or a 5-methoxyuridine that replaces a uridine.

[0302] Additionally, in some embodiments the phosphate backbone of an mRNA described herein is modified for stability. In some embodiments, the phosphate group of a chemically modified

		TTGTAATGGGGGACCTTGTACTCACGGTTCTCATAGCTCTTGCTG TCTATTTTCTCGGACGACTGGTCCCACGGGGACGAGGGGCAGCA GAAGCTGCTACACGAAAACAGAGGATTACAGAGACGGAGAGTC CCTACCAAGAACTCCAGGGGCAGAGAAGTGATGTCTATTCTGAC CTTAACACACAAAGACCATACTATAAATGA (SEQ ID NO: 251)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGCAGC (SEQ ID NO: 254)
	DAP12	CTTCGGCCTGTTCAAGCACAAGCGCAGAGTGACTGCTCTTGTA GCACGGTTTCACCTGGCGTATTGGCCGGTATTGTAATGGGGG ACCTTGTACTCACGGTTCTCATAGCTCTTGCTGTCTATTTTCTC GGACGACTGGTCCCACGGGGACGAGGGGCAGCAGAAGCTGC TACACGAAAACAGAGGATTACAGAGACGGAGAGTCCCTACC AAGAACTCCAGGGGCAGAGAAGTGATGTCTATTCTGACCTTA ACACACAAAGACCATACTATAAATGA (SEQ ID NO: 1)
TROP2-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTCAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGA AAAAGCCCGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTG

		GCTACACATTCACCAATTACGGCATGAACTGGGTCAAGCAGG CCCCTGGACAGGGCCTGAAGTGGATGGGCTGGATCAACACCT ACACCGGCGAACCTACATACACAGATGACTTCAAGGGCAGAT TCGCCTTCAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCA GATCAGCAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTG TGCCCGGGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTG TGGGGCCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGA GGATCAGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATC CAGCTGACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGC GACAGAGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCA TCGCCGTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTA AGCTGCTGATCTACAGCGCCTCCTACAGATACACCGGCGTGC CCGATAGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCC TGACAATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACT ACTGCCAGCAACACTACATCACCCCTCTGACCTTCGGCGCCG GCACCAAGGTGGAAATCAAGCGGTCAGGCGGCGGAGGAGCG GCCGCAGGAAGTGGTCTGGCCGTAAGTACCATATCCAGCTTT TTTCCGCCAGGATATCAGGTTTCCTTTTGTTTGGTCATGGTACT TCTCTTTGCGGTAGACACTGGTCTCTATTTTAGTGTCAAAACT AATATACGCTCCTCCACGAGGGATTGGAAGGACCATAAGTTC AAATGGAGGAAGGACCCGCAGGACAAATGA (SEQ ID NO: 255)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG

		CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	CD16A	GGTCTGGCCGTAAGTACCATATCCAGCTTTTTTCCGCCAGGAT ATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGCGGTA GACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGCTCCT CCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGGAAG GACCCGCAGGACAAATGA (SEQ ID NO: 2)
TROP2-CD8h-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTCAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGA AAAAGCCCGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTG GCTACACATTCACCAATTACGGCATGAACTGGGTCAAGCAGG CCCCTGGACAGGGCCTGAAGTGGATGGGCTGGATCAACACCT ACACCGGCGAACCTACATACACAGATGACTTCAAGGGCAGAT TCGCCTTCAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCA GATCAGCAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTG TGCCCGGGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTG TGGGGCCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGA GGATCAGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATC CAGCTGACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGC GACAGAGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCA TCGCCGTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTA AGCTGCTGATCTACAGCGCCTCCTACAGATACACCGGCGTGC CCGATAGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCC TGACAATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACT ACTGCCAGCAACACTACATCACCCCTCTGACCTTCGGCGCCG GCACCAAGGTGGAAATCAAGCGGTCAGGCGGCGGAGGAGCG GCCGCAACTACTACTCCAGCTCCAAGGCCTCCCACGCCAGCT CCCACTATTGCTTCTCAACCGTTGTCACTGCGACCAGAGGCCT GTAGACCTGCAGCTGGAGGCGCTGTTCACACAAGGGGTCTCG ATTTTGCGTGTGACGGATATCAGGTTTCCTTTTGTTTGGTCAT GGTACTTCTCTTTGCGGTAGACACTGGTCTCTATTTTAGTGTC

		AAAACTAATATACGCTCCTCCACGAGGGATTGGAAGGACCATAAGT TCAAATGGAGGAAGGACCCGCAGGACAAATGA (SEQ ID NO: 257)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCA (SEQ ID NO: 258)
	CD8a hinge	ACTACTACTCCAGCTCCAAGGCCTCCCACGCCAGCTCCCACTA TTGCTTCTCAACCGTTGTCACTGCGACCAGAGGCCTGTAGACC TGCAGCTGGAGGCGCTGTTCACACAAGGGGTCTCGATTTTGC GTGTGAC (SEQ ID NO: 3)
	CD16A	GGATATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGC GGTAGACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGC TCCTCCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGG AAGGACCCGCAGGACAAATGA (SEQ ID NO: 259)
TROP2-CD8hCSmut-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTCAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGA AAAAGCCCGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTG GCTACACATTCACCAATTACGGCATGAACTGGGTCAAGCAGG CCCCTGGACAGGGCCTGAAGTGGATGGGCTGGATCAACACCT

		ACACCGGCGAACCTACATACACAGATGACTTCAAGGGCAGAT TCGCCTTCAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCA GATCAGCAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTG TGCCCGGGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTG TGGGGCCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGA GGATCAGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATC CAGCTGACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGC GACAGAGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCA TCGCCGTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTA AGCTGCTGATCTACAGCGCCTCCTACAGATACACCGGCGTGC CCGATAGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCC TGACAATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACT ACTGCCAGCAACACTACATCACCCCTCTGACCTTCGGCGCCG GCACCAAGGTGGAAATCAAGCGGTCAGGCGGCGGAGGAGCG GCCGCAACTACTACTCCAGCTCCAAGGCCTCCCACGCCAGCT CCCACTATTGCTTCTCAACCGTTGTCACTGCGACCAGAGGCCA GCAGACCTGCAGCTGGAGGCGCTGTTCACACAAGGGGTCTCG ATTTTGCGAGCGACGGATATCAGGTTTCCTTTTGTTTGGTCAT GGTACTTCTCTTTGCGGTAGACACTGGTCTCTATTTTAGTGTCAA AACTAATATACGCTCCTCCACGAGGGATTGGAAGGACCATAAGT TCAAATGGAGGAAGGACCCGCAGGACAAATGA (SEQ ID NO: 260)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG

		CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCA (SEQ ID NO: 258)
	CD8aCS mut hinge	ACTACTACTCCAGCTCCAAGGCCTCCCACGCCAGCTCCCACTA TTGCTTCTCAACCGTTGTCACTGCGACCAGAGGCCAGCAGAC CTGCAGCTGGAGGCGCTGTTCACACAAGGGGTCTCGATTTTG CGAGCGAC (SEQ ID NO: 261)
	CD16A	GGATATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGC GGTAGACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGC TCCTCCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGG AAGGACCCGCAGGACAAATGA (SEQ ID NO: 259)
TROP2-CD4H-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTCAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGA AAAAGCCCGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTG GCTACACATTCACCAATTACGGCATGAACTGGGTCAAGCAGG CCCCTGGACAGGGCCTGAAGTGGATGGGCTGGATCAACACCT ACACCGGCGAACCTACATACACAGATGACTTCAAGGGCAGAT TCGCCTTCAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCA GATCAGCAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTG TGCCCGGGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTG TGGGGCCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGA GGATCAGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATC CAGCTGACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGC GACAGAGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCA TCGCCGTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTA AGCTGCTGATCTACAGCGCCTCCTACAGATACACCGGCGTGC CCGATAGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCC TGACAATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACT ACTGCCAGCAACACTACATCACCCCTCTGACCTTCGGCGCCG GCACCAAGGTGGAAATCAAGCGGTCAGGCGGCGGAGGAGCG GCCGCATCTGGTCAAGTTCTGCTGGAGTCAAACATTAAAGTG CTGCCTACTTGGAGCACTCCTGTTCAGCCTGGATATCAGGTTT CCTTTTGTTTGGTCATGGTACTTCTCTTTGCGGTAGACACTGGT

		CTCTATTTTAGTGTCAAAACTAATATACGCTCCTCCACGAGGG ATTGGAAGGACCATAAGTTCAAATGGAGGAAGGACCCGCAG GACAAATGA (SEQ ID NO: 262)
	GM-CSF Signal Peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCA (SEQ ID NO: 258)
	CD4 hinge	TCTGGTCAAGTTCTGCTGGAGTCAAACATTAAAGTGCTGCCTA CTTGGAGCACTCCTGTTCAGCCT (SEQ ID NO: 263)
	CD16A	GGATATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGC GGTAGACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGC TCCTCCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGG AAGGACCCGCAGGACAAATGA (SEQ ID NO: 259)
TROP2-SIGLEC4H-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTCAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGA AAAAGCCCGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTG GCTACACATTCACCAATTACGGCATGAACTGGGTCAAGCAGG CCCCTGGACAGGGCCTGAAGTGGATGGGCTGGATCAACACCT

		ATACGCTCCTCCACGAGGGATTGGAAGGACCATAAGTTCAAA TGGAGGAAGGACCCGCAGGACAAATGA (SEQ ID NO: 264)
	GM-CSF Signal Peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	TROP2 scFv	CAAGTGCAGCTGCAGCAGAGCGGCAGCGAGCTGAAAAAGCC CGGAGCCAGCGTGAAAGTGTCCTGCAAGGCTTCTGGCTACAC ATTCACCAATTACGGCATGAACTGGGTCAAGCAGGCCCCTGG ACAGGGCCTGAAGTGGATGGGCTGGATCAACACCTACACCGG CGAACCTACATACACAGATGACTTCAAGGGCAGATTCGCCTT CAGCCTGGACACCAGCGTGTCCACCGCTTATCTGCAGATCAG CAGCCTGAAGGCCGACGATACCGCCGTGTACTTTTGTGCCCG GGGCGGATTTGGCTCTAGCTACTGGTACTTCGACGTGTGGGG CCAGGGCAGCCTGGTGACCGTGTCTAGCGGAGGCGGAGGATC AGGTGGCGGTGGATCTGGCGGTGGTGGCTCTGACATCCAGCT GACACAGAGCCCATCTAGCCTGAGCGCTAGCGTGGGCGACAG AGTGTCTATTACCTGTAAAGCTTCTCAGGACGTGTCCATCGCC GTCGCCTGGTATCAGCAGAAGCCCGGCAAGGCCCCTAAGCTG CTGATCTACAGCGCCTCCTACAGATACACCGGCGTGCCCGAT AGATTCAGCGGAAGCGGCAGCGGAACAGATTTTACCCTGACA ATCAGCAGCCTGCAGCCTGAGGACTTCGCCGTGTACTACTGC CAGCAACACTACATCACCCCTCTGACCTTCGGCGCCGGCACC AAGGTGGAAATCAAGCGG (SEQ ID NO: 253)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCA (SEQ ID NO: 258)
	SIGLEC4 Hinge	TATCCACCTGTCATAGTTGAAATGAATTCCAGTGTTGAGGCTA TCGAGGGCAGTCACGTATCACTCCTGTGTGGTGCAGATTCCA ATCCACCACCCCTCCTTACATGGATGCGGGATGGAACTGTTCT GAGAGAAGCGGTGGCGGAAAGTTTGCTCCTTGAATTGGAGGA GGTTACTCCCGCCGAGGACGGCGTTTATGCCTGCCTGGCCGA GAATGCGTACGGACAAGACAATCGAACGGTCGGTTTGAGCGT GATGTACGCGCCTTGGAAACCTACGGTTAACGGCACTATGGT TGCGGTAGAAGGGGAAACGGTATCCATACTCTGTAGTACACA ATCAAATCCTGATCCCATCCTCACGATCTTTAAAGAGAAACA AATCCTTTCCACAGTCATTTATGAGTCTGAGCTTCAGCTCGAA CTGCCAGCAGTCTCCCCTGAGGATGATGGAGAATATTGGTGC GTTGCCGAAAACCAGTATGGCCAGAGAGCTACAGCGTTCAAT

		CTCAGCGTAGAATTTGCTCCAGTTCTCTTGCTGGAGAGTCACT GTGCGGCGGCACGGGATACTGTCCAGTGTCTTTGTGTAGTGA AAAGCAATCCTGAGCCTTCTGTAGCTTTTGAGTTGCCTTCACG CAACGTGACGGTAAATGAGAGCGAACGCGAGTTCGTGTATAG TGAGAGAAGCGGATTGGTGCTGACTTCAATCCTCACGCTTCG GGGCCAGGCGCAGGCGCCACCTCGCGTGATTTGCACTGCTCG GAACCTTTACGGCGCAAAATCCTTGGAGCTGCCGTTTCAGGG AGCCCATCGGCTTATGTGGGCTAAGATTGGTCCTGTGGGGGC T (SEQ ID NO: 6)
	CD16A	GGATATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGC GGTAGACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGC TCCTCCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGG AAGGACCCGCAGGACAAATGA (SEQ ID NO: 259)
HER2-CD16A	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGG CCGCAGGAAGTGGTCTGGCCGTAAGTACCATATCCAGCTTTTT TCCGCCAGGATATCAGGTTTCCTTTTGTTTGGTCATGGTACTT CTCTTTGCGGTAGACACTGGTCTCTATTTTAGTGTCAAAACTA

		ATATACGCTCCTCCACGAGGGATTGGAAGGACCATAAGTTCA AATGGAGGAAGGACCCGCAGGACAAATGA (SEQ ID NO: 265)
	GM-CSF Signal Peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTG GTCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	CD16A	GGTCTGGCCGTAAGTACCATATCCAGCTTTTTTCCGCCAGGAT ATCAGGTTTCCTTTTGTTTGGTCATGGTACTTCTCTTTGCGGTA GACACTGGTCTCTATTTTAGTGTCAAAACTAATATACGCTCCT CCACGAGGGATTGGAAGGACCATAAGTTCAAATGGAGGAAG GACCCGCAGGACAAATGA (SEQ ID NO: 2)
HER2-NKG2C	Full length	ATGAATAAGCAGCGAGGGACCTTTTCAGAAGTCTCACTCGCT CAGGATCCTAAAAGACAACAAAGAAAGCCTAAGGGAAATAA GTCCAGCATATCAGGTACGGAACAGGAAATTTTTCAAGTCGA ACTGAATTTGCAGAACCCTAGCCTGAATCACCAAGGTATCGA CAAGATCTATGATTGTCAAGGGCTCCTGCCACCGCCTGAAAA GCTTACGGCGGAGGTGCTGGGCATTATTTGTATAGTCCTGATG GCAACTGTACTTAAAACTATTGTACTTATCCCGTTTCTGGAAC

		AAAACAATTTTTCTCCGAACACTCGGACACAAAAGGCCCGAC ATTGTGGTCACTGTCCAGAAGAGTGGATAACTTACTCTAATA GCTGTTACTATATCGGAAAAGAGAGGAGAACGTGGGAAGAA AGCTTGCTCGCATGCACTTCCAAAAACTCTTCACTCTTGTCCA TTGATAACGAGGAGGAGATGAAATTTCTGGCCTCAATCCTGC CATCATCTTGGATAGGCGTATTCCGCAACTCAAGTCATCACCC TTGGGTAACTATAAATGGTTTGGCGTTCAAGCACAAGATTAA AGACTCTGATAATGCCGAGTTGAACTGCGCTGTTCTTCAGGTG AACCGCCTCAAATCTGCCCAGTGCGGAAGTTCTATGATATATC ACTGCAAACATAAACTGTCAGGCGGCGGAGGAGCGGCCGCA GGAAGTGACATCCAGATGACACAGAGCCCTAGCAGCCTGTCT GCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGC CAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCT GGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTG TACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGC ACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACT TCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTGA (SEQ ID NO: 267)
	NKG2C (cytoplasmic, TM and extracellular)	ATGAATAAGCAGCGAGGGACCTTTTCAGAAGTCTCACTCGCT CAGGATCCTAAAAGACAACAAAGAAAGCCTAAGGGAAATAA GTCCAGCATATCAGGTACGGAACAGGAAATTTTTCAAGTCGA ACTGAATTTGCAGAACCCTAGCCTGAATCACCAAGGTATCGA CAAGATCTATGATTGTCAAGGGCTCCTGCCACCGCCTGAAAA GCTTACGGCGGAGGTGCTGGGCATTATTTGTATAGTCCTGATG GCAACTGTACTTAAAACTATTGTACTTATCCCGTTTCTGGAAC AAAACAATTTTTCTCCGAACACTCGGACACAAAAGGCCCGAC

		ATTGTGGTCACTGTCCAGAAGAGTGGATAACTTACTCTAATA GCTGTTACTATATCGGAAAAGAGAGGAGAACGTGGGAAGAA AGCTTGCTCGCATGCACTTCCAAAAACTCTTCACTCTTGTCCA TTGATAACGAGGAGGAGATGAAATTTCTGGCCTCAATCCTGC CATCATCTTGGATAGGCGTATTCCGCAACTCAAGTCATCACCC TTGGGTAACTATAAATGGTTTGGCGTTCAAGCACAAGATTAA AGACTCTGATAATGCCGAGTTGAACTGCGCTGTTCTTCAGGTG AACCGCCTCAAATCTGCCCAGTGCGGAAGTTCTATGATATATC ACTGCAAACATAAACTG (SEQ ID NO: 8)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTG GTCACAGTTTCTTCTTGA (SEQ ID NO: 268)
HER2-NKG2C TMCyto	Full length	ATGAATAAGCAGCGAGGGACCTTTTCAGAAGTCTCACTCGCT CAGGATCCTAAAAGACAACAAAGAAAGCCTAAGGGAAATAA GTCCAGCATATCAGGTACGGAACAGGAAATTTTTCAAGTCGA ACTGAATTTGCAGAACCCTAGCCTGAATCACCAAGGTATCGA CAAGATCTATGATTGTCAAGGGCTCCTGCCACCGCCTGAAAA GCTTACGGCGGAGGTGCTGGGCATTATTTGTATAGTCCTGATG GCAACTGTACTTAAAACTATTGTACTTTCAGGCGGCGGAGGA GCGGCCGCAGGAAGTGACATCCAGATGACACAGAGCCCTAGC

		AGCCTGTCTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTA GAGCCAGCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGC AGAAGCCTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCA GCTTTCTGTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCA GATCTGGCACCGACTTCACCCTGACCATCTCTAGCCTGCAGCC TGAGGACTTCGCCACCTACTACTGCCAGCAGCACTACACCAC ACCTCCAACCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAG AACAGGCAGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGA AGGATCTGAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGT TCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGC TTCAACATCAAGGACACCTACATCCACTGGGTCCGACAGGCC CCTGGAAAGGGACTTGAATGGGTCGCCAGAATCTACCCCACC AACGGCTACACCAGATACGCCGATAGCGTGAAGGGCAGATTC ACCATCAGCGCCGACACCAGCAAGAACACCGCCTACCTGCAG ATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGT TCTAGATGGGGAGGCGACGGCTTCTACGCCATGGATTACTGG GGACAGGGCACCCTGGTCACAGTTTCTTCTTGA (SEQ ID NO: 269)
	NKG2C (cytoplasmic and TM)	ATGAATAAGCAGCGAGGGACCTTTTCAGAAGTCTCACTCGCT CAGGATCCTAAAAGACAACAAAGAAAGCCTAAGGGAAATAA GTCCAGCATATCAGGTACGGAACAGGAAATTTTTCAAGTCGA ACTGAATTTGCAGAACCCTAGCCTGAATCACCAAGGTATCGA CAAGATCTATGATTGTCAAGGGCTCCTGCCACCGCCTGAAAA GCTTACGGCGGAGGTGCTGGGCATTATTTGTATAGTCCTGATG GCAACTGTACTTAAAACTATTGTACTT (SEQ ID NO: 270)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC

		ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCTTGA (SEQ ID NO: 268)
HER2-NKG2D	Full length	ATGGGGTGGATACGAGGCAGGAGGTCTCGGCACAGCTGGGA GATGTCAGAGTTTCACAACTACAACCTCGACCTGAAAAAATC CGACTTCTCTACCCGATGGCAAAAGCAGCGATGTCCGGTAGT GAAGTCAAAATGTCGGGAAAACGCATCTCCGTTTTTTTTTTGC TGCTTCATAGCCGTCGCGATGGGCATAAGATTCATCATTATGG TGACTATTTGGTCTGCCGTGTTTCTTAATAGCTTGTTCAACCA AGAAGTGCAAATACCCCTTACCGAGAGTTACTGTGGTCCGTG TCCTAAGAACTGGATATGTTACAAGAACAACTGCTACCAATT CTTCGATGAAAGTAAAAACTGGTATGAGTCACAGGCAAGCTG CATGAGCCAAAACGCTAGTCTCCTCAAAGTCTACAGTAAAGA GGATCAGGACCTGCTGAAACTTGTGAAAAGTTATCACTGGAT GGGTTTGGTACACATTCCAACTAACGGTTCCTGGCAATGGGA AGATGGATCAATCCTTAGCCCCAATCTCCTCACTATTATAGAA ATGCAAAAGGGTGACTGTGCTCTGTACGCGTCCAGCTTTAAG GGGTATATCGAGAATTGTAGCACACCCAATACTTACATCTGT ATGCAACGAACCGTGTCAGGCGGCGGAGGAGCGGCCGCAGG AAGTGACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGC CTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCA GGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGG AAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTAC AGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACC GACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCG CCACCTACTACTGCCAGCAGCACTACACCACACCTCCAACCTT TGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCA CCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGG TGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCG GCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAA GGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGG ACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCTACAC

		CAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGC CGACACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCT GAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGG AGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACC CTGGTCACAGTTTCTTCTTGA (SEQ ID NO: 271)
	NKG2D (cytoplasmic, TM and extracellular)	ATGGGGTGGATACGAGGCAGGAGGTCTCGGCACAGCTGGGA GATGTCAGAGTTTCACAACTACAACCTCGACCTGAAAAAATC CGACTTCTCTACCCGATGGCAAAAGCAGCGATGTCCGGTAGT GAAGTCAAAATGTCGGGAAAACGCATCTCCGTTTTTTTTTTGC TGCTTCATAGCCGTCGCGATGGGCATAAGATTCATCATTATGG TGACTATTTGGTCTGCCGTGTTTCTTAATAGCTTGTTCAACCA AGAAGTGCAAATACCCCTTACCGAGAGTTACTGTGGTCCGTG TCCTAAGAACTGGATATGTTACAAGAACAACTGCTACCAATT CTTCGATGAAAGTAAAAACTGGTATGAGTCACAGGCAAGCTG CATGAGCCAAAACGCTAGTCTCCTCAAAGTCTACAGTAAAGA GGATCAGGACCTGCTGAAACTTGTGAAAAGTTATCACTGGAT GGGTTTGGTACACATTCCAACTAACGGTTCCTGGCAATGGGA AGATGGATCAATCCTTAGCCCCAATCTCCTCACTATTATAGAA ATGCAAAAGGGTGACTGTGCTCTGTACGCGTCCAGCTTTAAG GGGTATATCGAGAATTGTAGCACACCCAATACTTACATCTGT ATGCAACGAACCGTG (SEQ ID NO: 272)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC

		ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCTTGA (SEQ ID NO: 268)
HER2-NKp30	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGG CACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGC CGCAGGAAGTCTGTGGGTTAGCCAGCCACCCGAGATTCGAAC CCTCGAAGGCAGTAGTGCTTTCTTGCCGTGTAGCTTCAATGCG TCCCAAGGGCGACTGGCAATCGGTTCAGTCACATGGTTTCGC GACGAAGTTGTACCTGGCAAGGAGGTCAGGAATGGGACACC GGAATTTCGCGGCCGACTGGCCCCGTTGGCATCTTCCCGATTT CTTCATGATCACCAGGCAGAGCTTCACATTCGCGACGTACGA GGACACGACGCAAGCATCTATGTATGTAGAGTTGAAGTTTTG GGACTTGGAGTAGGCACAGGGAATGGGACTAGGTTGGTAGTG GAAAAGGAGCATCCCCAGTTGGGCGCAGGTACCGTACTTCTT CTGCGGGCAGGGTTCTATGCTGTCAGCTTTCTGTCTGTGGCAG TTGGGTCCACAGTCTATTACCAGGGTAAGTGTCTCACGTGGA AGGGACCACGGCGGCAATTGCCTGCGGTTGTTCCCGCACCCC

		TCCCTCCTCCATGCGGTTCAAGTGCACATCTCCTTCCGCCAGT TCCAGGCGGCTGA (SEQ ID NO: 273)
	GM-CSF Signal Peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTG GTCACAGTTTCTTCT (SEQ ID NO: 266)
	LINKER	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKP30 (extracellular, TM, cytoplasmic)	CTGTGGGTTAGCCAGCCACCCGAGATTCGAACCCTCGAAGGC AGTAGTGCTTTCTTGCCGTGTAGCTTCAATGCGTCCCAAGGGC GACTGGCAATCGGTTCAGTCACATGGTTTCGCGACGAAGTTG TACCTGGCAAGGAGGTCAGGAATGGGACACCGGAATTTCGCG GCCGACTGGCCCCGTTGGCATCTTCCCGATTTCTTCATGATCA CCAGGCAGAGCTTCACATTCGCGACGTACGAGGACACGACGC AAGCATCTATGTATGTAGAGTTGAAGTTTTGGGACTTGGAGT AGGCACAGGGAATGGGACTAGGTTGGTAGTGGAAAAGGAGC ATCCCCAGTTGGGCGCAGGTACCGTACTTCTTCTGCGGGCAG GGTTCTATGCTGTCAGCTTTCTGTCTGTGGCAGTTGGGTCCAC AGTCTATTACCAGGGTAAGTGTCTCACGTGGAAGGGACCACG GCGGCAATTGCCTGCGGTTGTTCCCGCACCCCTCCCTCCTCCA

		TGCGGTTCAAGTGCACATCTCCTTCCGCCAGTTCCAGGCGGCT GA (SEQ ID NO: 10)
HER2-NKp30 TM Cyto	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGCC GCAGGAAGTGCAGGTACCGTACTTCTTCTGCGGGCAGGGTTCTA TGCTGTCAGCTTTCTGTCTGTGGCAGTTGGGTCCACAGTCTATTA CCAGGGTAAGTGTCTCACGTGGAAGGGACCACGGCGGCAATTGC CTGCGGTTGTTCCCGCACCCCTCCCTCCTCCATGCGGTTCAAGTG CACATCTCCTTCCGCCAGTTCCAGGCGGCTGA (SEQ ID NO: 274)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG

		CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKp30 (TM, cytoplasmic)	GCAGGTACCGTACTTCTTCTGCGGGCAGGGTTCTATGCTGTCA GCTTTCTGTCTGTGGCAGTTGGGTCCACAGTCTATTACCAGGG TAAGTGTCTCACGTGGAAGGGACCACGGCGGCAATTGCCTGC GGTTGTTCCCGCACCCCTCCCTCCTCCATGCGGTTCAAGTGCA CATCTCCTTCCGCCAGTTCCAGGCGGCTGA (SEQ ID NO: 11)
HER2-NKp44	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGG CACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGC CGCAGGAAGTCAGTCAAAAGCACAAGTTCTGCAGAGTGTAGC

		AGGCCAGACACTTACGGTTAGGTGTCAATATCCGCCTACCGG CAGTCTGTATGAGAAAAAGGGCTGGTGTAAAGAAGCGTCCGC GTTGGTTTGCATTCGGCTCGTAACGAGCTCCAAGCCTCGGACT ATGGCATGGACATCACGGTTCACTATATGGGACGACCCTGAT GCAGGATTTTTTACTGTCACCATGACGGACCTTCGGGAGGAG GATTCCGGCCACTATTGGTGTAGAATCTATAGACCGTCAGAC AATTCTGTCAGCAAGAGCGTGCGCTTCTACCTTGTGGTCTCTC CGGCTTCCGCCTCCACCCAAACATCTTGGACTCCGAGGGATCT CGTGTCATCACAAACCCAGACACAGAGTTGTGTGCCGCCCAC GGCGGGAGCAAGACAGGCTCCGGAGAGCCCATCTACAATTCC GGTCCCTAGCCAACCACAGAACTCTACCTTGAGGCCCGGACC CGCTGCACCCATCGCTTTGGTTCCAGTGTTTTGCGGACTCCTT GTTGCCAAGTCACTTGTCCTTTCTGCTCTCCTGGTATGGTGGG GCGACATTTGGTGGAAAACGATGATGGAGCTTCGATCCTTGG ACACACAGAAGGCGACATGTCATCTCCAACAGGTGACAGACC TGCCATGGACTAGTGTGTCAAGTCCCGTCGAGCGCGAAATCC TTTATCATACCGTGGCCCGAACCAAAATAAGCGACGATGACG ATGAGCACACTCTGTGA (SEQ ID NO: 275)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC

		GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKp44 (extracellular, TM, cytoplasmic)	CAGTCAAAAGCACAAGTTCTGCAGAGTGTAGCAGGCCAGACA CTTACGGTTAGGTGTCAATATCCGCCTACCGGCAGTCTGTATG AGAAAAAGGGCTGGTGTAAAGAAGCGTCCGCGTTGGTTTGCA TTCGGCTCGTAACGAGCTCCAAGCCTCGGACTATGGCATGGA CATCACGGTTCACTATATGGGACGACCCTGATGCAGGATTTTT TACTGTCACCATGACGGACCTTCGGGAGGAGGATTCCGGCCA CTATTGGTGTAGAATCTATAGACCGTCAGACAATTCTGTCAGC AAGAGCGTGCGCTTCTACCTTGTGGTCTCTCCGGCTTCCGCCT CCACCCAAACATCTTGGACTCCGAGGGATCTCGTGTCATCAC AAACCCAGACACAGAGTTGTGTGCCGCCCACGGCGGGAGCAA GACAGGCTCCGGAGAGCCCATCTACAATTCCGGTCCCTAGCC AACCACAGAACTCTACCTTGAGGCCCGGACCCGCTGCACCCA TCGCTTTGGTTCCAGTGTTTTGCGGACTCCTTGTTGCCAAGTC ACTTGTCCTTTCTGCTCTCCTGGTATGGTGGGGCGACATTTGG TGGAAAACGATGATGGAGCTTCGATCCTTGGACACACAGAAG GCGACATGTCATCTCCAACAGGTGACAGACCTGCCATGGACT AGTGTGTCAAGTCCCGTCGAGCGCGAAATCCTTTATCATACCG TGGCCCGAACCAAAATAAGCGACGATGACGATGAGCACACTC TGTGA (SEQ ID NO: 13)
HER2-NKp44 TM Cyto	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT

		ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGG CACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGC CGCAGGAAGTTTGGTTCCAGTGTTTTGCGGACTCCTTGTTGCC AAGTCACTTGTCCTTTCTGCTCTCCTGGTATGGTGGGGCGACA TTTGGTGGAAAACGATGATGGAGCTTCGATCCTTGGACACAC AGAAGGCGACATGTCATCTCCAACAGGTGACAGACCTGCCAT GGACTAGTGTGTCAAGTCCCGTCGAGCGCGAAATCCTTTATC ATACCGTGGCCCGAACCAAAATAAGCGACGATGACGATGAGC ACACTCTGTGA (SEQ ID NO: 276)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKp44 (TM, cytoplasmic)	TTGGTTCCAGTGTTTTGCGGACTCCTTGTTGCCAAGTCACTTG TCCTTTCTGCTCTCCTGGTATGGTGGGGCGACATTTGGTGGAA

		AACGATGATGGAGCTTCGATCCTTGGACACACAGAAGGCGAC ATGTCATCTCCAACAGGTGACAGACCTGCCATGGACTAGTGT GTCAAGTCCCGTCGAGCGCGAAATCCTTTATCATACCGTGGCC CGAACCAAAATAAGCGACGATGACGATGAGCACACTCTGTGA (SEQ ID NO: 277)
HER2-NKp46	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGG CCGCAGGAAGTCAGCAACAGACGCTGCCCAAACCATTTATTT GGGCTGAACCTCACTTTATGGTCCCCAAGGAAAAACAAGTTA CAATCTGTTGCCAGGGGAATTACGGAGCTGTGGAGTACCAGC TGCATTTCGAGGGATCTCTTTTTGCGGTTGATAGGCCCAAGCC GCCCGAGCGGATCAACAAGGTGAAGTTTTACATACCAGATAT GAACTCCAGGATGGCGGGACAGTACTCCTGTATCTATCGCGT GGGCGAGCTGTGGAGTGAGCCTTCCAATCTGCTTGATCTTGTC GTCACCGAGATGTACGATACACCTACGCTGAGCGTTCATCCC GGGCCGGAAGTTATTAGTGGCGAAAAGGTCACTTTCTATTGC CGCCTTGACACGGCTACGTCAATGTTCCTCTTGCTGAAAGAAG GAAGATCTTCCCATGTCCAACGAGGATACGGAAAAGTCCAAG CGGAATTTCCCCTGGGACCAGTAACTACCGCTCATAGGGGAA

		CATACCGATGCTTCGGCAGCTACAACAACCACGCTTGGAGTT TTCCGTCTGAGCCTGTAAAATTGCTCGTTACCGGAGACATTGA GAACACGAGCCTTGCCCCTGAAGATCCGACGTTCCCAGCAGA TACATGGGGGACTTATCTGTTGACTACGGAGACAGGACTTCA AAAGGACCATGCGTTGTGGGATCATACAGCTCAGAACTTGCT CCGCATGGGCCTGGCCTTTCTTGTACTCGTTGCACTCGTTTGG TTCCTTGTTGAGGATTGGCTCTCTAGAAAGAGAACTAGAGAA CGGGCCTCCAGGGCATCCACGTGGGAAGGCCGCAGACGACTC AATACCCAGACCCTGTGA (SEQ ID NO: 278)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTG GTCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKp46 (extracellular, TM, cytoplasmic)	CAGCAACAGACGCTGCCCAAACCATTTATTTGGGCTGAACCT CACTTTATGGTCCCCAAGGAAAAACAAGTTACAATCTGTTGC CAGGGGAATTACGGAGCTGTGGAGTACCAGCTGCATTTCGAG GGATCTCTTTTTGCGGTTGATAGGCCCAAGCCGCCCGAGCGG ATCAACAAGGTGAAGTTTTACATACCAGATATGAACTCCAGG ATGGCGGGACAGTACTCCTGTATCTATCGCGTGGGCGAGCTG

		TGGAGTGAGCCTTCCAATCTGCTTGATCTTGTCGTCACCGAGA TGTACGATACACCTACGCTGAGCGTTCATCCCGGGCCGGAAG TTATTAGTGGCGAAAAGGTCACTTTCTATTGCCGCCTTGACAC GGCTACGTCAATGTTCCTCTTGCTGAAAGAAGGAAGATCTTCC CATGTCCAACGAGGATACGGAAAAGTCCAAGCGGAATTTCCC CTGGGACCAGTAACTACCGCTCATAGGGGAACATACCGATGC TTCGGCAGCTACAACAACCACGCTTGGAGTTTTCCGTCTGAGC CTGTAAAATTGCTCGTTACCGGAGACATTGAGAACACGAGCC TTGCCCCTGAAGATCCGACGTTCCCAGCAGATACATGGGGGA CTTATCTGTTGACTACGGAGACAGGACTTCAAAAGGACCATG CGTTGTGGGATCATACAGCTCAGAACTTGCTCCGCATGGGCCT GGCCTTTCTTGTACTCGTTGCACTCGTTTGGTTCCTTGTTGAGG ATTGGCTCTCTAGAAAGAGAACTAGAGAACGGGCCTCCAGGG CATCCACGTGGGAAGGCCGCAGACGACTCAATACCCAGACCC TGTGA (SEQ ID NO: 16)
HER2-NKp46TMCyto		ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGG CCGCAGGAAGTATGGGCCTGGCCTTTCTTGTACTCGTTGCACT CGTTTGGTTCCTTGTTGAGGATTGGCTCTCTAGAAAGAGAACT

		AGAGAACGGGCCTCCAGGGCATCCACGTGGGAAGGCCGCAG ACGACTCAATACCCAGACCCTGTGA (SEQ ID NO: 279)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC GACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTG GTCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGAAGT (SEQ ID NO: 256)
	NKp46 (TM, cytoplasmic)	ATGGGCCTGGCCTTTCTTGTACTCGTTGCACTCGTTTGGTTCCT TGTTGAGGATTGGCTCTCTAGAAAGAGAACTAGAGAACGGGC CTCCAGGGCATCCACGTGGGAAGGCCGCAGACGACTCAATAC CCAGACCCTGTGA (SEQ ID NO: 17)
HER2-revNKG2D	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC

		AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGG CCGCAGGATGCTACAGCGAGACCCTGCCCATCCAGGTGGAGC AGAACTTCCTGAGCAACCTGTTCGTGGCCAGCTGGATCACCG TGATGATCATCTTCAGGATCGGCATGGCCGTGGCCATCTTCTG CTGCTTCTTCTTCCCCAGCGCCAACGAGAGGTGCAAGAGCAA GGTGGTGCCCTGCAGGCAGAAGCAGTGGAGGACCAGCTTCGA CAGCAAGAAGCTGGACCTGAACTACAACCACTTCGAGAGCAT GGAGTGGAGCCACAGGAGCAGGAGGGGCAGGATCTGGGGCA TGTGA (SEQ ID NO: 280)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC

		GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGA (SEQ ID NO: 281)
	NKG2D (reverse orientation-extracellular, TM, cytoplasmic)	TGCTACAGCGAGACCCTGCCCATCCAGGTGGAGCAGAACTTC CTGAGCAACCTGTTCGTGGCCAGCTGGATCACCGTGATGATC ATCTTCAGGATCGGCATGGCCGTGGCCATCTTCTGCTGCTTCT TCTTCCCCAGCGCCAACGAGAGGTGCAAGAGCAAGGTGGTGCCC TGCAGGCAGAAGCAGTGGAGGACCAGCTTCGACAGCAAGAAGC TGGACCTGAACTACAACCACTTCGAGAGCATGGAGTGGAGCCAC AGGAGCAGGAGGGGCAGGATCTGGGGCATGTGA (SEQ ID NO: 19)
HER2-NKp30 ecto TMCyto	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGG GCACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGG CCGCAGGAAATGGGACTAGGTTGGTAGTGGAAAAGGAGCAT CCCCAGTTGGGCGCAGGTACCGTACTTCTTCTGCGGGCAGGG TTCTATGCTGTCAGCTTTCTGTCTGTGGCAGTTGGGTCCACAG TCTATTACCAGGGTAAGTGTCTCACGTGGAAGGGACCACGGC GGCAATTGCCTGCGGTTGTTCCCGCACCCCTCCCTCCTCCATG CGGTTCAAGTGCACATCTCCTTCCGCCAGTTCCAGGCGGCTGA (SEQ ID NO: 282)

	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTAGCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGCGACGGCTTCTACGCCATGGATTACTGGGGACAGGGCACCCTGGTCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGA (SEQ ID NO: 281)
	NKp30 (short extracellular (15aa), TM, cytoplasmic)	AATGGGACTAGGTTGGTAGTGGAAAAGGAGCATCCCCAGTTGGGCGCAGGTACCGTACTTCTTCTGCGGGCAGGGTTCTATGCTGTCAGCTTTCTGTCTGTGGCAGTTGGGTCCACAGTCTATTACCAGGGTAAGTGTCTCACGTGGAAGGGACCACGGCGGCAATTGCCTGCGGTTGTTCCCGCACCCCTCCCTCCTCCATGCGGTTCAAGTGCACATCTCCTTCCGCCAGTTCCAGGCGGCTGA (SEQ ID NO: 12)
HER2-NKp44 ecto TMCyto	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTAGCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC

		AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGG CACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGC CGCAGGAGTCCCTAGCCAACCACAGAACTCTACCTTGAGGCC CGGACCCGCTGCACCCATCGCTTTGGTTCCAGTGTTTTGCGGA CTCCTTGTTGCCAAGTCACTTGTCCTTTCTGCTCTCCTGGTATG GTGGGGCGACATTTGGTGGAAAACGATGATGGAGCTTCGATC CTTGGACACACAGAAGGCGACATGTCATCTCCAACAGGTGAC AGACCTGCCATGGACTAGTGTGTCAAGTCCCGTCGAGCGCGA AATCCTTTATCATACCGTGGCCCGAACCAAAATAAGCGACGA TGACGATGAGCACACTCTGTGA (SEQ ID NO: 283)
	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCT GTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGAT GTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAA GCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCG GCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACT TCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCAC CTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGC CAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAG CGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCA GCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCT CTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGAC ACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTT GAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGA TACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGAC ACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGA GCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGC

		GACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGG TCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGA (SEQ ID NO: 281)
	NKp44 (short extracellular (19aa), TM, cytoplasmic)	GTCCCTAGCCAACCACAGAACTCTACCTTGAGGCCCGGACCC GCTGCACCCATCGCTTTGGTTCCAGTGTTTTGCGGACTCCTTG TTGCCAAGTCACTTGTCCTTTCTGCTCTCCTGGTATGGTGGGG CGACATTTGGTGGAAAACGATGATGGAGCTTCGATCCTTGGA CACACAGAAGGCGACATGTCATCTCCAACAGGTGACAGACCT GCCATGGACTAGTGTGTCAAGTCCCGTCGAGCGCGAAATCCT TTATCATACCGTGGCCCGAACCAAAATAAGCGACGATGACGA TGAGCACACTCTGTGA (SEQ ID NO: 15)
HER2-NKp46 ecto TMCyto	Full length	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTA GCATCTCTGACATCCAGATGACACAGAGCCCTAGCAGCCTGT CTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCA GCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGC CTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCT GTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGG CACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGAC TTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAA CCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGC AGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCT GAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCT GGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACA TCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAA AGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCT ACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCA GCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACA GCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGAT GGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGG CACCCTGGTCACAGTTTCTTCTTCAGGCGGCGGAGGAGCGGC CGCAGGAGGACTTCAAAAGGACCATGCGTTGTGGGATCATAC AGCTCAGAACTTGCTCCGCATGGGCCTGGCCTTTCTTGTACTC GTTGCACTCGTTTGGTTCCTTGTTGAGGATTGGCTCTCTAGAA AGAGAACTAGAGAACGGGCCTCCAGGGCATCCACGTGGGAA GGCCGCAGACGACTCAATACCCAGACCCTGTGA (SEQ ID NO: 284)

	GM-CSF signal peptide	ATGTGGCTGCAGTCTCTGCTGCTGCTGGGAACAGTGGCCTGTAGCATCTCT (SEQ ID NO: 252)
	HER2 scFv	GACATCCAGATGACACAGAGCCCTAGCAGCCTGTCTGCCTCTGTGGGCGATAGAGTGACCATCACCTGTAGAGCCAGCCAGGATGTGAATACCGCCGTGGCCTGGTATCAGCAGAAGCCTGGAAAAGCCCCTAAGCTGCTGATCTACAGCGCCAGCTTTCTGTACAGCGGCGTGCCAAGCAGATTCAGCGGCAGCAGATCTGGCACCGACTTCACCCTGACCATCTCTAGCCTGCAGCCTGAGGACTTCGCCACCTACTACTGCCAGCAGCACTACACCACACCTCCAACCTTTGGCCAGGGCACCAAGGTGGAAATCAAGAGAACAGGCAGCACCAGCGGCTCTGGAAAGCCTGGATCTGGCGAAGGATCTGAGGTGCAGCTGGTTGAATCTGGCGGAGGACTTGTTCAGCCTGGCGGCTCTCTGAGACTGTCTTGTGCCGCCAGCGGCTTCAACATCAAGGACACCTACATCCACTGGGTCCGACAGGCCCCTGGAAAGGGACTTGAATGGGTCGCCAGAATCTACCCCACCAACGGCTACACCAGATACGCCGATAGCGTGAAGGGCAGATTCACCATCAGCGCCGACACCAGCAAGAACACCGCCTACCTGCAGATGAACAGCCTGAGAGCCGAGGACACCGCCGTGTACTACTGTTCTAGATGGGGAGGCGACGGCTTCTACGCCATGGATtacTGGGGACAGGGCACCCTGGTCACAGTTTCTTCT (SEQ ID NO: 266)
	Linker	TCAGGCGGCGGAGGAGCGGCCGCAGGA (SEQ ID NO: 281)
	NKp46 (short extracellular (18aa), TM, cytoplasmic)	GGACTTCAAAAGGACCATGCGTTGTGGGATCATACAGCTCAGAACTTGCTCCGCATGGGCCTGGCCTTTCTTGTACTCGTTGCACTCGTTTGGTTCCTTGTTGAGGATTGGCTCTCTAGAAAGAGAACTAGAGAACGGGCCTCCAGGGCATCCACGTGGGAAGGCCGCAGACGACTCAATACCCAGACCCTGTGA (SEQ ID NO: 18)

[0362] A general protocol for testing expression and functional characterization of the constructs is provided in a schematic form in **FIG. 3** indicating the timeline in days for treatments, expansion and assay. NK cells are isolated from primary human donors, usually leukopak samples. Cells were expand and activated in vitro for 7 days using IMMUNOCULT NK cell expansion kit. 2x10^6 cells were then electroporated (EP) with 20 microgram/ml mRNA encoding a CFP, e.g., a TROP2 expressing CFP in a MaxCyte system using the NK-2 program. Cell surface expression of receptor detected by TROP2-AF647 labeling 24 hours post-EP. The schematic diagrams of each CFP polypeptides are graphically shown in **FIGs 2A** (Top: for myeloid cell-specific expression, Bottom: myeloid/NK cell-specific expression), **FIGs 2B** (for NK cell-specific expression). **FIG. 13**, diagram on the left of the graph shows exemplary CFP structures for T cell-specific expression. For instance, a CFP designed for