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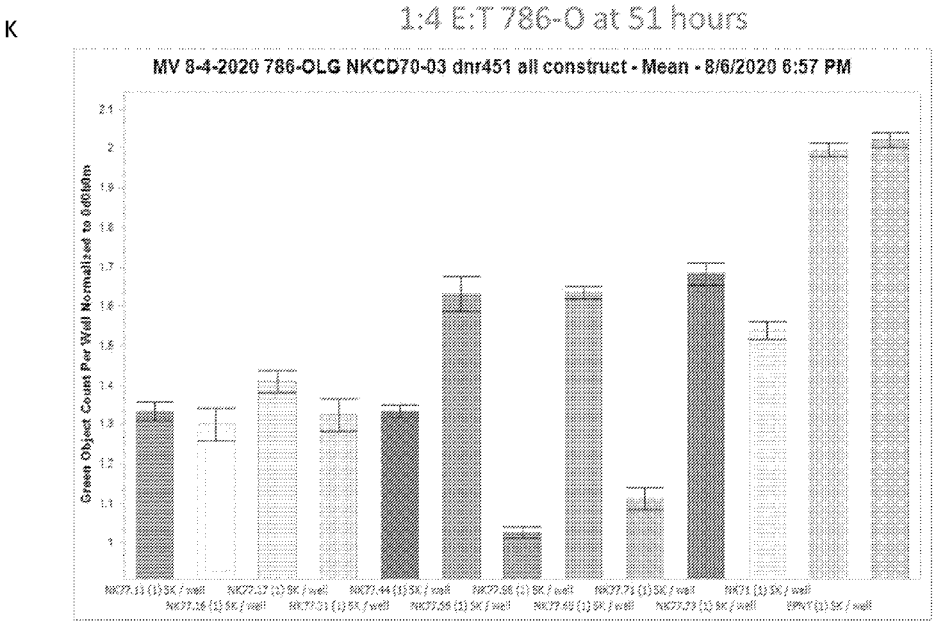
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(54) Title: GENETICALLY MODIFIED NATURAL KILLER CELLS FOR CD70-DIRECTED CANCER IMMUNOTHERAPY

Figure 60K



(57) Abstract: Several embodiments of the methods and compositions disclosed herein relate to immune cells that are engineered to express chimeric antigen receptors (CAR) and/or genetically modified to reduce potential side effects of cellular immunotherapy. Several embodiments relate to genetic modifications to the immune cells, such as Natural Killer (NK) cells, to reduce, substantially, reduce, or eliminate expression of a marker by the immune cells that would otherwise cause them to be self-targeted by the CAR. In several embodiments, the CAR targets CD70, and in some embodiments is used for renal cell carcinoma immunotherapy.

WO 2021/252804 A1

[Continued on next page]

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GENETICALLY MODIFIED NATURAL KILLER CELLS FOR CD70-DIRECTED CANCER IMMUNOTHERAPY

RELATED CASES

[0001] This application claims priority to United States Provisional Patent Application No. 63/038,645, filed June 12, 2020, United States Provisional Patent Application No. 63/090,041, filed October 9, 2020, United States Provisional Patent Application No. 63/141,411, filed January 25, 2021, and, United States Provisional Patent Application No. 63/201,490, filed April 30, 2021, the entire contents of each of which is incorporated by reference herein.

FIELD

[0002] Several embodiments disclosed herein relate to methods and compositions comprising genetically engineered cells for cancer immunotherapy, in particular cells engineered to have reduced expression of certain markers that are also present on target cells. In several embodiments, the present disclosure relates to cells engineered to express chimeric antigen receptors and have reduced expression of one or more markers that enhance the efficacy and/or reduce potential side effects when the cells are used in cancer immunotherapy

BACKGROUND

[0003] As further knowledge is gained about various cancers and what characteristics a cancerous cell has that can be used to specifically distinguish that cell from a healthy cell, therapeutics are under development that leverage the distinct features of a cancerous cell. Immunotherapies that employ engineered immune cells are one approach to treating cancers.

INCORPORATION BY REFERENCE OF MATERIAL IN ASCII TEXT FILE

[0004] This application incorporates by reference the Sequence Listing contained in the following ASCII text file being submitted concurrently herewith: File name: NKT.056WO_ST25.txt; created on June 10, 2021 and is 1,550,527 bytes in size.

SUMMARY

[0005] Immunotherapy presents a new technological advancement in the treatment of disease, wherein immune cells are engineered to express certain targeting and/or effector molecules that specifically identify and react to diseased or damaged cells. This represents a promising advance due, at least in part, to the potential for specifically targeting diseased or damaged cells, as opposed to more traditional approaches, such as chemotherapy, where all cells are impacted, and the desired outcome is that sufficient healthy cells survive to allow the patient to live. One immunotherapy approach is the recombinant

expression of chimeric receptors in immune cells to achieve the targeted recognition and destruction of aberrant cells of interest.

[0006] In some instances a population of immune cells for immunotherapy may express one or more endogenous markers that overlap in scope with those expressed by a tumor cell population. Targeting such a common marker can limit the efficacy of the therapeutic cells, insofar as the therapeutic cells target both the tumor population and other members of the therapeutic cell population. Therefore, in several embodiments, there is provided a population of genetically engineered immune cells, such as natural killer (NK) cells, T cells or combinations thereof, for cancer immunotherapy, comprising a plurality of immune cells that have been expanded in culture, wherein the plurality of immune cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex, wherein the tumor binding domain targets CD70, wherein the immune cells are genetically edited to express reduced levels of CD70 as compared to a non-edited immune cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

[0007] In several embodiments, the cells are genetically edited to express reduced levels of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene as compared to a non-edited cell. In several embodiments, the reduced (e.g., diminished, eliminated or otherwise non-detectable) CIS expression was achieved through editing of a CISH gene. Such editing imparts to the edited cells one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to cells expressing native levels of CIS. In several embodiments, additional edits are made to the cells, such as editing to yield reduced expression levels of an adenosine receptor. In several embodiments, the reduced adenosine receptor expression is achieved through editing of one or more genes encoding said adenosine receptor which results in one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to cells expressing native levels the adenosine receptor. In several embodiments, the editing and engineering of the cells works in concert in that the polynucleotide encoding the CAR is inserted into the gene that is edited. However, in several embodiments, the editing site does not include the polynucleotide encoding the CAR.

[0008] In several embodiments, the tumor binding domain of the CAR comprises a heavy chain variable region (VH), wherein the VH is encoded by a polynucleotide comprising a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1104, 1053, 1091, 1047, 1106, 1052, 1077, 1064, 1098, and 1088. In several embodiments, the tumor binding domain of the CAR comprises a light chain variable region (VL), wherein the VL is encoded by a polynucleotide comprising a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1178, 1127, 1165, 1121, 1180, 1126, 1151, 1138, 1171, and 1162. In several embodiments, the tumor binding domain comprises a single chain variable fragment (scFv), wherein the scFv is encoded by a

polynucleotide comprising a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 104, 53, 91, 47, 106, 52, 77, 64, 98, and 88.

[0009] In several embodiments, the tumor binding domain comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein the CDR-H1 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 494, 443, 481, 437, 496, 442, 467, 454, 488, and 478; the CDR-H2 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 568, 517, 555, 511, 570, 516, 541, 528, 562, and 552; the CDR-H3 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 642, 591, 629, 585, 644, 590, 615, 602, 636, and 626; the CDR-L1 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 734, 683, 721, 677, 736, 682, 707, 694, 728, and 718; the CDR-L2 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 808, 757, 795, 751, 810, 756, 781, 768, 802, and 792; and the CDR-L3 comprises a sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 882, 831, 869, 825, 884, 830, 855, 842, 876, and 855.

[0010] In several embodiments, the tumor binding domain comprises a VH, wherein the VH comprises an amino acid sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 956, 905, 943, 899, 958, 904, 929, 916, 950, and 940. In several embodiments, the tumor binding domain comprises a VL, wherein the VL comprises an amino acid sequence having at least at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 1030, 979, 1017, 973, 1032, 978, 1003, 990, 1024, and 1014.

[0011] In several embodiments, the tumor binding domain comprises an scFv, wherein the scFv comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 296, 245, 283, 239, 298, 244, 269, 256, 290, 280.

[0012] In several embodiments, the immune cells are engineered to express membrane bound IL-15 (mbIL15). In several embodiments, the mbIL15 is bicistronically encoded on a polynucleotide encoding the CAR. In several embodiments, the polynucleotide encoding the CAR and the mbIL15 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 204, 153, 191, 147, 206, 152, 177, 164, 198, and 188. In several embodiments, the CAR comprises an amino acid sequence having at least 80%, at least

85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 379, 328, 366, 322, 381, 327, 352, 339, 373, and 363. In several embodiments, the mbIL15 is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 1188.

[0013] In several embodiments, the cytotoxic signaling complex comprises an OX-40 subdomain and a CD3zeta subdomain. In several embodiments, the OX40 subdomain is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 5. In several embodiments, the CD3zeta subdomain is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 7.

[0014] In several embodiments, the expression of CIS by the edits cells is substantially reduced as compared to a cell not edited with respect to CISH. In several embodiments, the edited cells do not express a detectable level of CIS protein. In several embodiments, the expression of the adenosine receptor is substantially reduced as compared to a cell not edited with respect the adenosine receptor. In several embodiments, the edited cells do not express a detectable level of an adenosine receptor. In several embodiments, the edited adenosine receptor comprises one or more of an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, or an A1 adenosine receptor. In several embodiments, the edited adenosine receptor comprises an A2A adenosine receptor (A2AR). In several embodiments, the cells are further genetically edited to express a reduced level of one or more of a transforming growth factor beta receptor (TGFBR), beta-2 microglobulin (B2M), CIITA (class II major histocompatibility complex transactivator), Natural Killer Group 2, member A (NKG2A) receptor, Cbl proto-oncogene B protein encoded by a CBLB gene, tripartite motif-containing protein 29 protein encoded by a TRIM29 gene, and a suppressor of cytokine signaling 2 protein encoded by a SOCS2 gene as compared to a non-edited NK cell. In several embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a CRISPR-Cas system. In several embodiments, the CRISPR-Cas system comprises a Cas selected from Cas9, Csn2, Cas4, Cpf1, C2c1, C2c3, Cas13a, Cas13b, Cas13c, CasX, CasY, and combinations thereof. In one embodiment the Cas is Cas9 (optionally reduced activity Cas9).

[0015] In several embodiments, the Cas is guided to the CD70 gene by one or more guide RNA having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 121, SEQ ID NO: 122, or SEQ ID NO: 123. In several embodiments, the Cas is guided to the CISH gene by one or more guide RNA having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134. In several embodiments, the Cas is guided to the adenosine receptor gene by one or more guide RNA having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 396, SEQ ID NO: 397, or SEQ ID NO: 398. In several embodiments, the Cas is guided to the TGFBR2 gene by one or more guide RNA having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134.

[0016] In several embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a zinc finger nuclease (ZFN). In alternative embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a Transcription activator-like effector nuclease (TALEN).

[0017] In several embodiments, the immune cells that are engineered and edited comprise NK cells. In several embodiments, the immune cells that are engineered and edited consist of or consist essentially of NK cells.

[0018] In several embodiments, there are provided for herein methods of treating cancer in a subject, comprising administering to the subject the population of genetically engineered and edited immune cells, such as NK cells, as provided for herein. In several embodiments, the cancer is renal cell carcinoma, or a metastasis from renal cell carcinoma. Also provided for herein is a use of the genetically engineered and edited immune cells, such as NK cells, as provided for herein, in the treatment of cancer. Additionally provided is a use of the genetically engineered and edited immune cells, such as NK cells, as provided for herein in the manufacture of a medicament for the treatment of cancer.

[0019] Additionally provided for herein are methods for treating cancer in a subject comprising, administering to the subject a population of genetically engineered immune cells, comprising a plurality of immune cells, such as NK cells, T cells, or combinations thereof, that have been expanded in culture, wherein the plurality of NK cells is engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex, wherein the tumor binding domain targets CD70, and wherein the cells are genetically edited to express reduced levels of CD70 as compared to a non-edited cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

[0020] In several embodiments, the cells are further genetically edited to express reduced levels of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene as compared to a non-edited cell, wherein the reduced CIS expression was engineered through editing of a CISH gene and wherein the genetically edited cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to cells expressing native levels of CIS. In several embodiments, the cells are also genetically edited to express reduced expression of an adenosine receptor, wherein the reduced adenosine receptor expression was achieved through editing of a gene encoding said adenosine receptor, and wherein the genetically edited cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to cells expressing native levels the adenosine receptor.

[0021] In several embodiments, the tumor binding domain comprises a heavy chain variable region (VH), wherein the VH is encoded by a polynucleotide comprising a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1104, 1053, 1091, 1047, 1106, 1052, 1077, 1064, 1098, and 1088 and wherein the tumor binding domain comprises a light chain variable region (VL), wherein the VL is encoded by a polynucleotide

comprising a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1178, 1127, 1165, 1121, 1180, 1126, 1151, 1138, 1171, and 1162.

[0022] In several embodiments of these methods, the tumor binding domain comprises a single chain variable fragment (scFv), wherein the scFv is encoded by a polynucleotide comprising a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 104, 53, 91, 47, 106, 52, 77, 64, 98, and 88. In several embodiments of these methods, the tumor binding domain comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein the CDR-H1 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 494, 443, 481, 437, 496, 442, 467, 454, 488, and 478; the CDR-H2 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 568, 517, 555, 511, 570, 516, 541, 528, 562, and 552; the CDR-H3 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 642, 591, 629, 585, 644, 590, 615, 602, 636, and 626; the CDR-L1 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 734, 683, 721, 677, 736, 682, 707, 694, 728, and 718; the CDR-L2 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 808, 757, 795, 751, 810, 756, 781, 768, 802, and 792; and the CDR-L3 comprises a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 882, 831, 869, 825, 884, 830, 855, 842, 876, and 855.

[0023] In several embodiments of these methods, the tumor binding domain comprises a VH, wherein the VH comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 956, 905, 943, 899, 958, 904, 929, 916, 950, and 940 and wherein the tumor binding domain comprises a VL, wherein the VL comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 1030, 979, 1017, 973, 1032, 978, 1003, 990, 1024, and 1014. In several embodiments of these methods, the tumor binding domain comprises an scFv, wherein the scFv comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 296, 245, 283, 239, 298, 244, 269, 256, 290, 280.

[0024] In several embodiments of these methods, the chimeric antigen receptor comprises an OX40 subdomain and a CD3zeta subdomain and the cells are engineered to express membrane bound IL-15 (mbIL15). In several embodiments, the mbIL15 is bicistronically encoded on a polynucleotide encoding the CAR. In several embodiments, the polynucleotide encoding the CAR and the mbIL15 comprises a

sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 204, 153, 191, 147, 206, 152, 177, 164, 198, and 188. In several embodiments, the CAR comprises an amino acid sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 379, 328, 366, 322, 381, 327, 352, 339, 373, and 363. In several embodiments, the OX40 subdomain is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 5, wherein the CD3zeta subdomain is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 7, and wherein the mbIL15 is encoded by a sequence having at least 80%, at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 1188.

[0025] In several embodiments, expression of CIS is substantially reduced as compared to a cell not edited with respect to CISH and/or wherein the cells do not express a detectable level of CIS protein. In several embodiments, expression of the adenosine receptor is substantially reduced as compared to a cell not edited with respect the adenosine receptor and/or wherein the cells do not express a detectable level of an adenosine receptor. In several embodiments, the adenosine receptor comprises an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, or an A1 adenosine receptor. In several embodiments, the gene editing is made using a CRISPR-Cas system, and wherein the Cas comprises a Cas9 enzyme. In several embodiments, the immune cells that are engineered and edited comprise NK cells. In several embodiments, the immune cells that are engineered and edited consist of or consist essentially of NK cells.

[0026] Also provided for herein is a polynucleotide encoding an anti-CD70 chimeric antigen receptor, wherein the CAR comprises an anti-CD70 binding domain, wherein the anti-CD70 binding domain is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of SEQ ID NOs: 36-120, 221-229, 1038-1111, 1112-1185, and/or comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NO: 230-312, 890-963, 964-1037, or a portion thereof capable of generating cytotoxic signals upon binding to CD70 on a target cell. In several embodiments, the polynucleotide further encodes an OX40 domain, wherein the OX40 subdomain is encoded by a sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 5, and a CD3zeta domain, wherein the CD3zeta subdomain is encoded by a sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 7. In several embodiments, the polynucleotide further encodes mbIL15, wherein the mbIL15 is encoded by a sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 1188. In several embodiments, the one or more of SEQ ID NOs: 36-120, 221-229, 1038-1111, or 1112-1185, the polynucleotide encoding OX40, the polynucleotide encoding CD3zeta, and the polynucleotide encoding mbIL15 are arranged in a 5' to 3' orientation within the polynucleotide.

[0027] Additionally provided for herein is a method of enhancing the persistence of a population of immune cells to be used in cancer immunotherapy, comprising identifying a target marker on a tumor to be treated, determining if a population of immune cells to be engineered to express a CAR that binds the target marker also endogenously expresses the target marker; editing the genome of the population of immune cells to disrupt the gene encoding the endogenous target marker, and engineering the population of immune cells to express the CAR, wherein the disruption of the endogenous expression of the target marker by the immune cells reduces the ability of the CAR to bind the endogenous target marker on the immune cells, thereby enhancing the persistence of the population of immune cells. In several embodiments, the immune cells are NK cells, T cells, or a combination thereof, wherein the target marker is CD70, and wherein the gene editing is made using a CRISPR-Cas system.

[0028] In several embodiments, the method further comprises using a CRISPR-Cas system to disrupt expression of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene and/or further comprising using a CRISPR-Cas system to disrupt expression of an adenosine receptor, wherein the adenosine receptor comprises an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, and/or an A1 adenosine receptor.

[0029] Provided for herein, in several embodiments, is an anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain, wherein the anti-CD70 CAR is encoded by a polynucleotide having at least 85%, at least 90%, or at least 95% sequence identity to one or more of SEQ ID NOS: 138-220. Also provided for herein is an anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain wherein the anti-CD70 CAR comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 313-395, or a portion thereof capable of generating cytotoxic signals upon binding to CD70 on a target cell.

[0030] Additionally provided for herein is an anti-CD70 binding domain comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein: the CDR-H1 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 428-501; the CDR-H2 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 502-575; the CDR-H3 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 576-649; the CDR-L1 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 668-741; the CDR-L2 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 742-815; and the CDR-L3 comprises a sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 816-889. In several embodiments, the heavy chain variable domain is encoded by a

nucleic acid sequence having at least 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1038-1111. In several embodiments, the light chain variable domain is encoded by a nucleic acid sequence having at least80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1112-1185. Depending on the embodiment, the anti-CD70 binding domain is an antibody, Fab' fragment, $F(ab')_2$ fragment, or scFv. In several embodiments, provided for herein is a CAR comprising the anti-CD70 binding domain disclosed herein. In several embodiments, the CAR further comprises an OX40 subdomain and a CD3zeta subdomain. In several embodiments, there are provided cells, such as immune cells, comprising the anti-CD70 binding domain or the CARs provided for herein. In several embodiments, the cell comprises, consists of, or consists essentially of an NK cell. In several embodiments, the wherein the cell is genetically edited to express a reduced level of CISH, an adenosine receptor, A2A adenosine receptor, A2B adenosine receptor, A3 adenosine receptor, A1 adenosine receptor, A2AR, TGFBR, B2M, CIITA, NKG2A, CBLB, TRIM29, SOCS2, SMAD3, MAPKAPK3, CEACAM1, or DDIT4, or any combination thereof, as compared to a non-edited cell. Also provided for are methods of treating cancer in a subject comprising administering to the subject an anti-CD70 binding domain, a CAR, a cell as provided for herein. Also provided are a use of an anti-CD70 binding domain, a CAR, or a cell as provided for herein for the treatment of cancer and/or in the manufacture of a medicament for the treatment of cancer.

[0031] Provided for herein is also a population of genetically engineered immune cells for cancer immunotherapy, comprising a plurality of immune cells that have been expanded in culture, wherein the plurality of immune cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain that targets CD70, a transmembrane domain, and a cytotoxic signaling complex, wherein the immune cells are genetically edited to express reduced levels of CD70 as compared to non-edited immune cells that have been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene. In several embodiments, the population of immune cells comprises, consists of, or consists essentially of a population of NK cells.

[0032] Also provided in several embodiments, is a method of making a population of genetically engineered immune cells for cancer immunotherapy, comprising engineering a population of immune cells to express a CAR that binds a target marker, wherein at least a portion of the population of immune cells also endogenously expresses the target marker; and editing the genome of the population of immune cells to disrupt the gene encoding the endogenous target marker, wherein the disruption of the endogenous expression of the target marker by the immune cells reduces the ability of the CAR to bind the endogenous target marker on the immune cells. In several embodiments, the population of immune cells comprises, consists of, or consists essentially of a population of NK cells.

[0033] In several embodiments, there is provided herein a population of genetically engineered natural killer (NK) cells for cancer immunotherapy, comprising a plurality of NK cells that have been expanded in culture, wherein the plurality of NK cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex, wherein the tumor binding domain targets CD70. In several embodiments, the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

[0034] In several embodiments, there are provided methods for treating cancer in a subject comprising, administering to the subject a population of genetically engineered immune cells, comprising a plurality of NK cells that have been expanded in culture, wherein the plurality of NK cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex, wherein the tumor binding domain targets CD70, wherein the chimeric antigen receptor comprises an OX40 subdomain and a CD3zeta subdomain, wherein the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

[0035] In several embodiments, the chimeric antigen receptor cytotoxic signaling complex comprises an OX40 subdomain and a CD3zeta subdomain. In several embodiments, the cells are also genetically engineered to express membrane bound IL-15.

[0036] In several embodiments, the NK cells are genetically edited to express reduced levels of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene as compared to a non-engineered NK cell, wherein the reduced CIS expression was engineered through editing of a CISH gene, and wherein the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels of CIS. In several embodiments, CISH editing results in substantially reduced expression of CIS as compared to a cell not edited for CISH. In several embodiments, the edited cells do not express a detectable levels of CIS.

[0037] In several embodiments, the NK cells are genetically edited to express reduced levels of an adenosine receptor as compared to a non-engineered NK cell, wherein the reduced adenosine receptor expression was engineered through editing of a adenosine receptor encoding gene, and wherein the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels of the adenosine receptor. In several embodiments, editing of a gene encoding an adenosine receptor results in substantially reduced expression of the adenosine receptor as compared to a cell not edited for the adenosine receptor. In several embodiments, the edited cells do not express a detectable levels of an adenosine receptor. Depending on the embodiment, the edited gene may encode an A2A

adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, or an A1 adenosine receptor. In several embodiments, the gene edited encodes an A2A adenosine receptor (A2AR). In some embodiments, more than one of the adenosine receptors are edited.

[0038] In several embodiments, CISH and an adenosine receptor encoding gene are edited, resulting in substantially reduced expression of CIS and the adenosine receptor as compared to a cell not edited for CISH and the adenosine receptor. In several embodiments, the edited cells do not express a detectable levels of CIS or the adenosine receptor.

[0039] In several embodiments, the tumor binding domain is encoded by a polynucleotide comprising a sequence having at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NO: 36 to SEQ ID NOs: 120, 221-229, 1038-1111, 1112-1185, and/or comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NO: 230-312, 890-963, 964-1037. In several embodiments, the OX40 subdomain is encoded by a sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 5. In several embodiments, the OX40 subdomains comprise an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 6. In several embodiments, the CD3zeta subdomain is encoded by a sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 7. In several embodiments, the CD3zeta subdomain comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 8.

[0040] In several embodiments, there is provided for herein, an anti-CD70 binding domain comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein the CDR-H1 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 428-501, the CDR-H2 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 502-575, the CDR-H3 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 576-649, the CDR-L1 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 668-741, the CDR-L2 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 742-815, and the CDR-L3 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 816-889. In several embodiments, the heavy chain variable region comprises an amino acid sequence having at least 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 890-963. In several embodiments, the light chain variable region comprises an amino acid sequence having at least 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 964-1037. In several embodiments, the: 1) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 890 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ

ID NO: 964; 2) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 891 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 965; 3) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 892 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 966; 4) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 893 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 967; 5) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 894 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 968; 6) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 895 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 969; 7) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 896 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 970; 8) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 897 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 971; 9) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 898 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 972; 10) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 899 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 973; 11) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 900 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 974; 12) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 901 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 975; 13) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 902 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 976; 14) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 903 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 977; 15) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 904 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 978; 16) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 905 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 979; 17) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 906 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 980; 18) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 907 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 981; 19) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 908 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 982; 20) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 909 and the light chain

variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 983; 21) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 910 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 984; 22) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 911 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 985; 23) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 912 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 986; 24) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 913 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 987; 25) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 914 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 988; 26) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 915 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 989; 27) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 916 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 990; 28) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 917 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 991; 29) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 918 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 992; 30) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 919 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 993; 31) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 920 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 994; 32) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 921 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 995; 33) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 922 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 996; 34) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 923 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 997; 35) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 924 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 998; 36) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 925 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 999; 37) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 926 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1000; 38) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 927 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1001; 39) the heavy chain

variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 928 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1002; 40) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 929 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1003; 41) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 930 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1004; 42) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 931 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1005; 43) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 932 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1006; 44) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 933 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1007; 45) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 934 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1008; 46) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 935 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1009; 47) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 936 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1010; 48) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 937 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1011; 49) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 938 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1012; 50) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 939 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1013; 51) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 940 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1014; 52) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 941 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1015; 53) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 942 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1016; 54) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 943 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1017; 55) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 944 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1018; 56) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 945 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1019; 57) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 946 and the light chain

variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1020; 58) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 947 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1021; 59) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 948 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1022; 60) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 949 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1023; 61) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 950 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1024; 62) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 951 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1025; 63) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 952 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1026; 64) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 953 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1027; 65) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 954 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1028; 66) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 955 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1029; 67) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 956 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1030; 68) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 957 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1031; 69) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 958 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1032; 70) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 959 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1033; 71) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 960 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1034; 72) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 961 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1035; 73) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 962 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1036; and/or 74) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 963 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1037.

[0041] In several embodiments, 1) the heavy chain variable region comprises SEQ ID NO: 890 and the light chain variable region comprises SEQ ID NO: 964; 2) the heavy chain variable region comprises

SEQ ID NO: 891 and the light chain variable region comprises SEQ ID NO: 965; 3) the heavy chain variable region comprises SEQ ID NO: 892 and the light chain variable region comprises SEQ ID NO: 966; 4) the heavy chain variable region comprises SEQ ID NO: 893 and the light chain variable region comprises SEQ ID NO: 967; 5) the heavy chain variable region comprises SEQ ID NO: 894 and the light chain variable region comprises SEQ ID NO: 968; 6) the heavy chain variable region comprises SEQ ID NO: 895 and the light chain variable region comprises SEQ ID NO: 969; 7) the heavy chain variable region comprises SEQ ID NO: 896 and the light chain variable region comprises SEQ ID NO: 970; 8) the heavy chain variable region comprises SEQ ID NO: 897 and the light chain variable region comprises SEQ ID NO: 971; 9) the heavy chain variable region comprises SEQ ID NO: 898 and the light chain variable region comprises SEQ ID NO: 972; 10) the heavy chain variable region comprises SEQ ID NO: 899 and the light chain variable region comprises SEQ ID NO: 973; 11) the heavy chain variable region comprises SEQ ID NO: 900 and the light chain variable region comprises SEQ ID NO: 974; 12) the heavy chain variable region comprises SEQ ID NO: 901 and the light chain variable region comprises SEQ ID NO: 975; 13) the heavy chain variable region comprises SEQ ID NO: 902 and the light chain variable region comprises SEQ ID NO: 976; 14) the heavy chain variable region comprises SEQ ID NO: 903 and the light chain variable region comprises SEQ ID NO: 977; 15) the heavy chain variable region comprises SEQ ID NO: 904 and the light chain variable region comprises SEQ ID NO: 978; 16) the heavy chain variable region comprises SEQ ID NO: 905 and the light chain variable region comprises SEQ ID NO: 979; 17) the heavy chain variable region comprises SEQ ID NO: 906 and the light chain variable region comprises SEQ ID NO: 980; 18) the heavy chain variable region comprises SEQ ID NO: 907 and the light chain variable region comprises SEQ ID NO: 981; 19) the heavy chain variable region comprises SEQ ID NO: 908 and the light chain variable region comprises SEQ ID NO: 982; 20) the heavy chain variable region comprises SEQ ID NO: 909 and the light chain variable region comprises SEQ ID NO: 983; 21) the heavy chain variable region comprises SEQ ID NO: 910 and the light chain variable region comprises SEQ ID NO: 984; 22) the heavy chain variable region comprises SEQ ID NO: 911 and the light chain variable region comprises SEQ ID NO: 985; 23) the heavy chain variable region comprises SEQ ID NO: 912 and the light chain variable region comprises SEQ ID NO: 986; 24) the heavy chain variable region comprises SEQ ID NO: 913 and the light chain variable region comprises SEQ ID NO: 987; 25) the heavy chain variable region comprises SEQ ID NO: 914 and the light chain variable region comprises SEQ ID NO: 988; 26) the heavy chain variable region comprises SEQ ID NO: 915 and the light chain variable region comprises SEQ ID NO: 989; 27) the heavy chain variable region comprises SEQ ID NO: 916 and the light chain variable region comprises SEQ ID NO: 990; 28) the heavy chain variable region comprises SEQ ID NO: 917 and the light chain variable region comprises SEQ ID NO: 991; 29) the heavy chain variable region comprises SEQ ID NO: 918 and the light chain variable region comprises SEQ ID NO: 992; 30) the heavy chain variable region comprises SEQ ID NO: 919 and the light chain variable region comprises SEQ ID NO: 993; 31) the heavy chain variable region comprises SEQ ID NO: 920 and the light chain variable region comprises SEQ ID NO: 994; 32) the heavy chain variable region comprises SEQ ID NO: 921 and the light chain variable region comprises SEQ ID NO: 995; 33) the heavy

chain variable region comprises SEQ ID NO: 922 and the light chain variable region comprises SEQ ID NO: 996; 34) the heavy chain variable region comprises SEQ ID NO: 923 and the light chain variable region comprises SEQ ID NO: 997; 35) the heavy chain variable region comprises SEQ ID NO: 924 and the light chain variable region comprises SEQ ID NO: 998; 36) the heavy chain variable region comprises SEQ ID NO: 925 and the light chain variable region comprises SEQ ID NO: 999; 37) the heavy chain variable region comprises SEQ ID NO: 926 and the light chain variable region comprises SEQ ID NO: 1000; 38) the heavy chain variable region comprises SEQ ID NO: 927 and the light chain variable region comprises SEQ ID NO: 1001; 39) the heavy chain variable region comprises SEQ ID NO: 928 and the light chain variable region comprises SEQ ID NO: 1002; 40) the heavy chain variable region comprises SEQ ID NO: 929 and the light chain variable region comprises SEQ ID NO: 1003; 41) the heavy chain variable region comprises SEQ ID NO: 930 and the light chain variable region comprises SEQ ID NO: 1004; 42) the heavy chain variable region comprises SEQ ID NO: 931 and the light chain variable region comprises SEQ ID NO: 1005; 43) the heavy chain variable region comprises SEQ ID NO: 932 and the light chain variable region comprises SEQ ID NO: 1006; 44) the heavy chain variable region comprises SEQ ID NO: 933 and the light chain variable region comprises SEQ ID NO: 1007; 45) the heavy chain variable region comprises SEQ ID NO: 934 and the light chain variable region comprises SEQ ID NO: 1008; 46) the heavy chain variable region comprises SEQ ID NO: 935 and the light chain variable region comprises SEQ ID NO: 1009; 47) the heavy chain variable region comprises SEQ ID NO: 936 and the light chain variable region comprises SEQ ID NO: 1010; 48) the heavy chain variable region comprises SEQ ID NO: 937 and the light chain variable region comprises SEQ ID NO: 1011; 49) the heavy chain variable region comprises SEQ ID NO: 938 and the light chain variable region comprises SEQ ID NO: 1012; 50) the heavy chain variable region comprises SEQ ID NO: 939 and the light chain variable region comprises SEQ ID NO: 1013; 51) the heavy chain variable region comprises SEQ ID NO: 940 and the light chain variable region comprises SEQ ID NO: 1014; 52) the heavy chain variable region comprises SEQ ID NO: 941 and the light chain variable region comprises SEQ ID NO: 1015; 53) the heavy chain variable region comprises SEQ ID NO: 942 and the light chain variable region comprises SEQ ID NO: 1016; 54) the heavy chain variable region comprises SEQ ID NO: 943 and the light chain variable region comprises SEQ ID NO: 1017; 55) the heavy chain variable region comprises SEQ ID NO: 944 and the light chain variable region comprises SEQ ID NO: 1018; 56) the heavy chain variable region comprises SEQ ID NO: 945 and the light chain variable region comprises SEQ ID NO: 1019; 57) the heavy chain variable region comprises SEQ ID NO: 946 and the light chain variable region comprises SEQ ID NO: 1020; 58) the heavy chain variable region comprises SEQ ID NO: 947 and the light chain variable region comprises SEQ ID NO: 1021; 59) the heavy chain variable region comprises SEQ ID NO: 948 and the light chain variable region comprises SEQ ID NO: 1022; 60) the heavy chain variable region comprises SEQ ID NO: 949 and the light chain variable region comprises SEQ ID NO: 1023; 61) the heavy chain variable region comprises SEQ ID NO: 950 and the light chain variable region comprises SEQ ID NO: 1024; 62) the heavy chain variable region comprises SEQ ID NO: 951 and the light chain variable region comprises SEQ ID NO: 1025; 63) the heavy chain variable region comprises SEQ ID

NO: 952 and the light chain variable region comprises SEQ ID NO: 1026; 64) the heavy chain variable region comprises SEQ ID NO: 953 and the light chain variable region comprises SEQ ID NO: 1027; 65) the heavy chain variable region comprises SEQ ID NO: 954 and the light chain variable region comprises SEQ ID NO: 1028; 66) the heavy chain variable region comprises SEQ ID NO: 955 and the light chain variable region comprises SEQ ID NO: 1029; 67) the heavy chain variable region comprises SEQ ID NO: 956 and the light chain variable region comprises SEQ ID NO: 1030; 68) the heavy chain variable region comprises SEQ ID NO: 957 and the light chain variable region comprises SEQ ID NO: 1031; 69) the heavy chain variable region comprises SEQ ID NO: 958 and the light chain variable region comprises SEQ ID NO: 1032; 70) the heavy chain variable region comprises SEQ ID NO: 959 and the light chain variable region comprises SEQ ID NO: 1033; 71) the heavy chain variable region comprises SEQ ID NO: 960 and the light chain variable region comprises SEQ ID NO: 1034; 72) the heavy chain variable region comprises SEQ ID NO: 961 and the light chain variable region comprises SEQ ID NO: 1035; 73) the heavy chain variable region comprises SEQ ID NO: 962 and the light chain variable region comprises SEQ ID NO: 1036; and/or 74) the heavy chain variable region comprises SEQ ID NO: 963 and the light chain variable region comprises SEQ ID NO: 1037.

[0042] In several embodiments, the heavy chain variable region further comprises a FW-H1, FW-H2, FW-H3, and FW-H4, and the light chain variable region further comprises a FW-L1, FW-L2, FW-L3, and FW-L4, and wherein: the FW-H1 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 399-402; the FW-H2 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 403-406; the FW-H3 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 407-422; the FW-H4 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 423-427; the FW-L1 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 650-653; the FW-L2 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 654-657; the FW-L3 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 658-661; and/or the FW-L4 comprises a sequence having at least 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 662-667. In several embodiments, the heavy chain variable domain is encoded by a nucleic acid sequence having at least 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1038-1111. In several embodiments, the light chain variable domain is encoded by a nucleic acid sequence having at least 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1112-1185. In several embodiments, the anti-CD70 binding domain is an antibody, Fab' fragment, $F(ab')_2$ fragment, or scFv. In several embodiments, one or more of the anti-CD70 binding domains as disclosed above is incorporated into a CAR. In several embodiments, such a CAR further comprises an OX40 subdomain and a CD3zeta subdomain (or any signaling/co-stimulatory domain disclosed herein). In several embodiments, the CAR consists of or consists essentially

of a CD70 binding domain as disclosed herein, a transmembrane domain/hinge, an OX40 domain and a CD3zeta domain. In several embodiments, the OX40 subdomain comprises an amino sequence having at least 90%, 95%, 99%, or 100% sequence identity to SEQ ID NO: 6. In several embodiments, the OX40 subdomain is encoded by a sequence having at least 90%, 95%, 99%, or 100% sequence identity to SEQ ID NO: 5. In several embodiments, the CD3zeta subdomain comprises an amino sequence having at least 90%, 95%, 99%, or 100%, sequence identity to SEQ ID NO: 8. In several embodiments, the CD3zeta subdomain is encoded by a sequence having at least 90%, 95%, 99%, or 100% sequence identity to SEQ ID NO: 7. In several embodiments, the CAR comprises at least two anti-CD70 binding domains and the CAR is a multivalent CAR. In several embodiments, the multivalent CAR comprises at least two anti-CD70 binding domains and the CAR is a bivalent CAR. In several embodiments, the bivalent CAR comprises a first anti-CD70 binding domain and a second anti-CD70 binding domain, wherein the first anti-CD70 binding domain and second anti-CD70 binding domain each comprise: a) a heavy chain variable region comprising the sequence of SEQ ID NO: 923 and a light chain variable region comprising the sequence of SEQ ID NO: 997; b) a heavy chain variable region comprising the sequence of SEQ ID NO: 949 and a light chain variable region comprising the sequence of SEQ ID NO: 1023; c) a heavy chain variable region comprising the sequence of SEQ ID NO: 950 and a light chain variable region comprising the sequence of SEQ ID NO: 1024; d) a heavy chain variable region comprising the sequence of SEQ ID NO: 952 and a light chain variable region comprising the sequence of SEQ ID NO: 1026; and/or e) a heavy chain variable region comprising the sequence of SEQ ID NO: 953 and a light chain variable region comprising the sequence of SEQ ID NO: 1027. In several embodiments, there is provided a cell comprising an anti-CD70 binding domain and/or a CAR as disclosed above. In several embodiments, another CAR is engineered into the cell. In several embodiments, that CAR does not target NKG2D ligands. In several embodiments, that CAR does not target CD19. In several embodiments, the cell is an immune cell. In several embodiments, the cell is an NK cell. In several embodiments, the cell is used in combination with another cell type (such as, for example, an engineered T cell). In several embodiments, immune cell is not a T cell, a gamma T cell or a delta gamma T cell. In several embodiments, the cell is genetically edited to express a reduced level of CISH, an adenosine receptor, A2A adenosine receptor, A2B adenosine receptor, A3 adenosine receptor, A1 adenosine receptor, A2AR, TGFBR, B2M, CIITA, NKG2A, CBLB, TRIM29, SOCS2, SMAD3, MAPKAPK3, CEACAM1, or DDIT4, or any combination thereof, as compared to a non-engineered cell. In several embodiments, the cell is genetically edited with one or more guide RNAs having at least 90% or at least 95% sequence identity to SEQ ID NOs: 1190-1201. In several embodiments, the NK cells are genetically edited to express a reduced level of SMAD3, MAPKAPK3, CEACAM1, or DDIT4, or any combination thereof, as compared to a non-engineered NK cell. In several embodiments, the NK cells are genetically edited with one or more guide RNAs having at least 90% or at least 95% sequence identity to SEQ ID NOs: 1190-1201. In several embodiments, selected genes may not be disrupted in the engineered cells. For example, in one embodiment, the immune cells have not undergone disruption of a T Cell Receptor Alpha Constant (TRAC) gene. In one embodiment, the immune cells have not undergone

disruption of a B2M gene. In one embodiment, the immune cells have not undergone disruption of MHC Class I.

[0043] In several embodiments, there is provided a method of treating cancer in a subject comprising administering to the subject one or more anti-CD70 binding domain as described above (or elsewhere herein). In several embodiments, there is provided a use of the anti-CD70 binding domain as described above (or elsewhere herein) for the treatment of cancer and/or in the manufacture of a medicament for the treatment of cancer.

[0044] In several embodiments, the NK cells disclosed herein are engineered to express interleukin 15 (IL15, IL-15). In some embodiments, the IL15 is a membrane-bound IL15 (mbIL15). In some embodiments, the mbIL15 comprises a native IL15 sequence and at least one transmembrane domain. In some embodiments, the native IL15 sequence is a human native IL15 sequence. In some embodiments, the native IL15 sequence is encoded by a sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 11. In some embodiments, the native IL15 sequence comprises a peptide sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 12. In several embodiments, the mbIL15 is encoded by a sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 1188. In some embodiments, the mbIL15 comprises a peptide sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 1189. In some embodiments, the mbIL15 is optionally bicistronically encoded on the polynucleotide encoding the CAR. In several embodiments, the CAR is encoded by a polynucleotide having at least 85%, at least 90%, or at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NO: 138-220 or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence), and/or comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NO: 313-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[0045] In several embodiments, expression of CIS is substantially reduced as compared to a non-engineered NK cell. In several embodiments, the NK cells do not express a detectable level of CIS protein.

[0046] In several embodiments, the NK cells are further genetically engineered to express a reduced level of a transforming growth factor beta receptor (TGFBR) as compared to a non-engineered NK cell, to express a reduced level of beta-2 microglobulin (B2M) as compared to a non-engineered NK cell, to express a reduced level of CIITA (class II major histocompatibility complex transactivator) as compared to a non-engineered NK cell, to express a reduced level of a Natural Killer Group 2, member A (NKG2A) receptor as compared to a non-engineered NK cell, to express a reduced level of a Cbl proto-oncogene B protein encoded by a CBLB gene as compared to a non-engineered NK cell, to express a reduced level of a tripartite motif-containing protein 29 protein encoded by a TRIM29 gene as compared to a non-engineered NK cell, to express a reduced level of a suppressor of cytokine signaling 2 protein encoded by a SOCS2 gene as compared to a non-engineered NK cell, to express a reduced level of a mothers against decapentaplegic homolog 3 (SMAD3) protein encoded by a SMAD3 gene as compared to a non-engineered

NK cell, to express a reduced level of a MAP kinase-activated protein kinase 3 (MAPKAPK3) protein encoded by a MAPKAPK3 gene as compared to a non-engineered NK cell, to express a reduced level of a carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) protein encoded by a CEACAM1 gene as compared to a non-engineered NK cell, to express a reduced level of a DNA-damage-inducible transcript 4 (DDIT4) protein encoded by a DDIT4 gene as compared to a non-engineered NK cell, to express CD47, and/or to express HLA-E, or any combination thereof. In several embodiments, the NK cells are further genetically edited to disrupt expression of at least one immune checkpoint protein by the NK cells. In several embodiments, the at least one immune checkpoint protein is selected from CTLA4, PD-1, lymphocyte activation gene (LAG-3), NKG2A receptor, KIR2DL-1, KIR2DL-2, KIR2DL-3, KIR2DS-1 and/or KIR2DA-2, and combinations thereof.

[0047] According to several embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a CRISPR-Cas system. In several embodiments, the CRISPR-Cas system comprises a Cas selected from Cas9, Csn2, Cas4, Cpf1, C2c1, C2c3, Cas13a, Cas13b, Cas13c, CasX, CasY, and combinations thereof. In several embodiments, the Cas is Cas9.

[0048] According to several embodiments, the CRISPR-Cas system comprises a Cas selected from Cas3, Cas8a, Cas5, Cas8b, Cas8c, Cas10d, Cse1, Cse2, Csy1, Csy2, Csy3, GSU0054, Cas10, Csm2, Cmr5, Cas10, Csx11, Csx10, Csf1, and combinations thereof. In several embodiments, the one or more guide RNA having at least 95% sequence identity to SEQ ID NO: 121, SEQ ID NO: 122, or SEQ ID NO: 123 is used to edit the CD70 gene. In several embodiments, the one or more guide RNA having at least 85%, 90%, or 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134 is used to edit the CISH gene. In several embodiments, one or more guide RNA having at least 85%, 90%, or 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134 is used to edit the TGFBR2 gene.

[0049] In several embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a zinc finger nuclease (ZFN). In several embodiments, the gene editing to reduce expression or the gene editing to induce expression is made using a Transcription activator-like effector nuclease (TALEN).

[0050] Depending on the method, the cancer to be treated is renal cell carcinoma, or a metastasis from renal cell carcinoma.

[0051] In several embodiments, the methods disclosed herein further comprising optionally administering a plurality of engineered T cells, wherein the T cells are engineered to express a CAR. In several embodiments, the CAR expressed by the T cells is directed to CD70.

[0052] In several embodiments, there is provided a polynucleotide encoding an anti-CD70 chimeric antigen receptor, wherein the CAR comprises an anti-CD70 binding domain, wherein the anti-CD70 binding domain is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of SEQ ID NOs: 38-120, 221-229, 1038-1111, 1112-1185, and/or comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences

of SEQ ID NO: 230-312, 890-963, 964-1037. In several embodiments, the CAR comprises an OX40 subdomain encoded by a sequence having at least 85%, 90%, or 95% sequence identity to SEQ ID NO: 5. In several embodiments, the OX40 subdomain comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 6. In several embodiments, the CAR comprises a CD3zeta domain encoded by a sequence having at least 85%, 90%, or 95% sequence identity to SEQ ID NO: 7. In several embodiments, the CD3zeta subdomain comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 8. In several embodiments, there is further provided a polynucleotide encoding mbIL15, wherein the mbIL15 is encoded by a sequence having at least 85%, 90%, or 95% sequence identity to SEQ ID NO: 1188. In several embodiments, the mbIL15 comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 1189. In several embodiments, the one or more of SEQ ID NOs: 38-120, 221-229, 1038-1111, 1112-1185, the polynucleotide encoding OX40, the polynucleotide encoding CD3zeta, and the polynucleotide encoding mbIL15 are arranged in a 5' to 3' orientation within the polynucleotide.

[0053] Also provided for herein is a method of enhancing the persistence of a population of immune cells to be used in cancer immunotherapy, comprising identifying a target marker on a tumor to be treated, determining if a population of immune cells to be engineered to express a CAR that binds the target marker also endogenously expresses the target marker; editing the genome of the population of immune cells to disrupt the gene encoding the endogenous target marker, and engineering the population of immune cells to express the CAR, wherein the disruption of the endogenous expression of the target marker by the immune cells reduces the ability of the CAR to bind the endogenous target marker on the immune cells, thereby enhancing the persistence of the population of immune cells.

[0054] In several embodiments, the immune cells are NK cells, T cells, or a combination thereof. In several embodiments, the target marker is CD70. In several embodiments, the gene editing is made using a CRISPR-Cas system and the Cas is optionally guided to the endogenous gene by one or more of SEQ ID NOs: 121-123. In several embodiments, a CRISPR-Cas system to disrupt expression of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 130-134. In several embodiments, an adenosine receptor, such as the A2AR is edited. In several embodiments, a CRISPR-Cas system is used to edit a gene encoding an adenosine receptor. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 396-398. In several embodiments, SMAD3 is edited. In several embodiments, a CRISPR-Cas system is used to edit a gene encoding SMAD3. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 1190-1192. In several embodiments, MAPKAPK3 is edited. In several embodiments, a CRISPR-Cas system is used to edit a gene encoding MAPKAPK3. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 1193-1195. In several embodiments, CEACAM1 is edited. In several embodiments, a CRISPR-Cas system is used to edit a gene encoding CEACAM1. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 1196-1198. In several

embodiments, DDIT4 is edited. In several embodiments, a CRISPR-Cas system is used to edit a gene encoding DDIT4. In several embodiments, the Cas is guided to the endogenous gene by one or more of SEQ ID NOs: 1199-1201. In several embodiments, combinations of one or more of the above genes are edited (optionally in combination with other genes to be edited as disclosed elsewhere herein).

[0055] Provided for herein, in several embodiments, is an anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain, wherein the anti-CD70 CAR is encoded by a polynucleotide having at least 80%, 85%, 90%, or 95% sequence identity to one or more of SEQ ID NOS: 138-220, wherein SEQ ID NOS: 138-220 also bicistronically encode mbIL15.

[0056] Provided for herein, in several embodiments, is an anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain, wherein the anti-CD70 CAR comprises an amino acid sequence having at least 80%, 85%, 90%, or 95% sequence identity to one or more of the amino acid sequences of SEQ ID NO: 313-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[0057] Some embodiments relate to a method comprising administering an immune cell as described herein to a subject in need. In some embodiments, the subject has cancer. In some embodiments, the administration treats, inhibits, or prevents progression of the cancer.

[0058] Several embodiments provide for uses of the cells, anti-CD70 scFvs, anti-CD70 CARs, and/or the polynucleotides or amino acid sequences disclosed herein in the treatment or prevention of cancer. Several embodiments provide for uses of the cells, anti-CD70 scFvs, anti-CD70 CARs, and/or the polynucleotides or amino acid sequences disclosed herein in the manufacture of a medicament for treatment or prevention of cancer.

BRIEF DESCRIPTION OF THE DRAWINGS

[0059] Figure 1 depicts non-limiting schematics of tumor-directed chimeric antigen receptors.

[0060] Figure 2 depicts additional non-limiting schematics of tumor-directed chimeric antigen receptors.

[0061] Figure 3 depicts additional non-limiting schematics of tumor-directed chimeric antigen receptors.

[0062] Figure 4 depicts additional non-limiting schematics of tumor-directed chimeric antigen receptors.

[0063] Figure 5 depicts additional non-limiting schematics of tumor-directed chimeric antigen receptors.

[0064] Figure 6 depicts non-limiting schematics of tumor-directed chimeric antigen receptors directed against non-limiting examples of tumor markers.

[0065] Figure 7 depicts additional non-limiting schematics of tumor-directed chimeric antigen receptors directed against non-limiting examples of tumor markers.

[0066] Figures 8A-8C show flow cytometry data related to the degree of expression of CD70 by natural killer cells.

[0067] Figure 9 depicts a non-limiting schematic process flow for generation of engineered NK cells for use therapeutic methods for cancer therapy according to several embodiments disclosed herein.

[0068] Figures 10A-10B show schematics for non-limiting examples of protocols for CRISPR-based modification and culture of engineered NK cells according to several embodiments disclosed herein.

[0069] Figures 11A-11D show flow cytometry data related to CRISPR-mediated knockdown of CD70. Figure 11A shows data for CD70 expression on NK cells from a first donor after CRISPR-mediated knockdown using three different guide RNAs. Figure 11B shows corresponding control data for the first donor. Figure 11C shows data for CD70 expression on NK cells from a second donor after CRISPR-mediated knockdown using three different guide RNAs. Figure 11D shows corresponding control data for the first donor. These experiments were performed using the KD7 protocol.

[0070] Figures 12A-12E show flow cytometry data related to CRISPR-mediated knockdown of CD70 expression on NK cells from an additional donor. Figure 12A shows expression of CD70 using guide RNA 1. Figure 12B shows expression of CD70 using guide RNA 2. Figure 12C shows expression of CD70 using guide RNA 3. Figure 12D shows expression of CD70 by non-electroporated NK cells. Figure 12E shows unstained NK cells. These experiments were performed using the KD7 protocol.

[0071] Figures 13A-13D show flow cytometry data related to CRISPR-mediated knockdown of CD70 expression on NK cells from the same donor as in Figure 12 but using combinations of guide RNA. Figure 13A shows expression of CD70 using guide RNA 1+2. Figure 13B shows expression of CD70 using guide RNA 1+3. Figure 13C shows expression of CD70 using guide RNA 2+3. Figure 13D and 13E are the same controls as shown in Figures 12D and 12E. These experiments were performed using the KD7 protocol.

[0072] Figures 14A-14F show flow cytometry data related to CD70 expression 14 days after CRISPR-mediated CD70 knockout (21 days total). Figure 14A shows expression of CD70 using guide RNA 1. Figure 14B shows expression of CD70 using guide RNA 2. Figure 14C shows expression of CD70 using guide RNA 3. Figure 14D shows expression of CD70 by non-electroporated NK cells. Figure 14E shows unstained NK cells. These experiments were performed using the KD7 protocol, with the cells being cultured from Day 11 to Day 21 in low IL-2 media. Figure 14F shows an additional non-limiting gene editing process.

[0073] Figures 15A-15D show flow cytometry data related to CD70 expression 14 days after CRISPR-mediated CD70 knockout (21 days total), with the NK cells from the same donor as in Figures 12-14, but using combinations of guide RNA. Figure 15A shows expression of CD70 using guide RNA 1+2. Figure 15B shows expression of CD70 using guide RNA 1+3. Figure 15C shows expression of CD70 using guide RNA 2+3. Figure 15D and 15E are the same controls as shown in Figures 14D and 14E. These experiments were performed using the KD7 protocol, with the cells being cultured from Day 11 to Day 21 in low IL-2 media.

[0074] Figures 16A-16C show flow cytometry data related to knockdown of CD70 expression in two different donors. For these experiments, CRISPR-mediated CD70 knockout was performed prior to NK cell expansion, using the KD0 protocol, with the data shown from Day 5 post-electroporation. Figure 16A shows data from a first donor with each of three guide RNAs used singly. Figure 16B shows CD70 expression using the same individual guide RNAs, but with NK cells from a different donor. Figure 16C shows control data (donor 2).

[0075] Figures 17A-17C show flow cytometry data related to knockdown of CD70 expression in the same two donors as Figure 16, with expression evaluated after 8 days (day 13 of the KD0 protocol). Figure 17A shows data from a first donor with each of three guide RNAs used singly. Figure 17B shows CD70 expression using the same individual guide RNAs, but with NK cells from a different donor. Figure 17C shows control data (donor 2).

[0076] Figures 18A-18D show data related to the cytotoxicity to CD70 knockout NK cells (CD70-KO-NK) from two donors. Figure 18A shows CD70-KO-NK cell (generated using individual guide RNA 1, 2, or 3 on NK cells from a first donor) cytotoxicity against REH cells, which do not express CD27, which is the ligand for CD70, at the indicated effector:target ratios. Figure 18B shows the cytotoxicity of CD70-KO-NK cells from donor 1 against Jurkat cells, which do express CD27. Figure 18C shows CD70-KO-NK cell (NK cells from a second donor) cytotoxicity against REH cells. Figure 18D shows the cytotoxicity of CD70-KO-NK cells from donor 2 against Jurkat cells. Cytotoxicity was assessed at Day 14.

[0077] Figures 19A-19B relate to a schematic timeline for a protocol to genetically engineer and expand NK cells and data related to NK cell expansion.

[0078] Figures 20A-20C show flow cytometry data after CRISPR gene editing of NK cells. Figure 20A shows CD70 expression by NK cells using three different guide RNAs. Figure 20B shows CD70 expression by NK cells from a second donor and edited using the same guide RNAs. Figure 20C shows related control data.

[0079] Figures 21A-21B show flow cytometry data after CRISPR gene editing of Jurkat cells. Figure 21A shows CD70 expression by Jurkat cells from a first donor after editing with three different combinations of guide RNA. Figure 21B shows control data.

[0080] Figures 22A-22D show flow cytometry data after CRISPR gene editing of Jurkat cells. Figure 22A shows a sample protocol. Figure 22B shows CD70 expression by the Jurkat cells after CRISPR editing using three different guide RNA sets, with the cells being kept in culture after the gene editing. Figure 22C shows CD70 expression by the Jurkat cells after CRISPR editing using the same guide RNA sets, but with the cells being frozen after the gene editing and then thawed for flow analysis. Figure 23D shows control data.

[0081] Figure 23 shows a schematic for a non-limiting embodiment of a gene editing construct for CRISPR modification (knock-in) of the endogenous CD70 locus in NK cells to insert a CD70-directed CAR construct into the endogenous locus.

[0082] Figures 24A-24F relate to data assessing the engineered expression of CD70 on Jurkat cells and on Jurkat cells subjected to CRISPR gene editing. The left panel of each of the figures is a negative control, and the central panel a control using only the secondary antibody. Figure 24A shows data related to CD70 and GFP expression on native Jurkat cells. The right panel of Figure 24A indicates that native Jurkat cells express relatively low levels of CD70. Figure 24B shows expression of CD70 in Jurkat cells engineered to express the marker at elevated (e.g., for purposes of tonic signaling and CD70 CAR screening). As seen in the right panel of Figure 24B CD70 expression is significantly increased on these Jurkat cells (~85% of the cells are positive for human CD70 and GFP (used as a marker for transduced cells). Figure 24C shows the reduction of Jurkat native CD70 expression through the use of a first guide RNA and CRISPR gene editing. Figure 24D shows that the engineered constitutive expression of CD70 on Jurkat cells is maintained even in the face of CRISPR gene editing to reduce CD70. Figure 24E and Figure 24F show similar data regarding the maintenance of expression of CD70 on the engineered Jurkat cells.

[0083] Figure 25 shows a table summarizing CD70 expression data (MFI) for the various conditions shown in Figure 24A-24F. The data indicate that the engineered CD70-expressing Jurkat cells exhibit near constitutive expression of CD70, even higher than a known high-expressing cell line, the 786-O cells.

[0084] Figures 26A-26C relate to expression of anti-CD70 CAR constructs on Jurkat cells. As non-limiting examples of anti-CD70 CAR, Jurkat cells were transduced with NK71 or NK72 constructs (schematically depicted in Figure 6). The left panels in Figures 26A-26C is a negative control, the central panel is the control for the secondary antibody and the right panel shows data related to signal detected with an anti-Flag antibody. Figure 26A shows control data related to detecting Flag expression on Jurkat cells. The Flag tag is used in some embodiments to detect expression of a CAR construct. In several embodiments, the Flag tag is not included. Figure 26B shows expression of the NK71 anti-CD70 CAR construct and Figure 26C shows expression of the NK72 anti-CD70 CAR construct by Jurkat cells.

[0085] Figures 27A-27F show data related to the ability of anti-CD70 CAR-expressing Jurkat cells to bind human bind CD70. Figure 27A shows data from native Jurkat cells. Moving left to right are negative control, control for the antibody to human Fc, binding when 2 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and binding is detected with the human Fc-APC antibody, and binding when 10 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and binding is detected with the human Fc-APC antibody. Figure 27B shows data from native Jurkat cells. Moving left to right is a control for the antibody to murine Fc, binding when 2 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with a murine Fc-APC antibody, and binding when 10 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with the murine Fc-APC antibody, and detection of Flag tag (present in the NK71/72 CAR constructs, but not native Jurkat cells). Figure 27C shows data from NK71-expressing Jurkat cells. Moving left to right are negative control, control for the antibody to human Fc, binding when 2 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and

binding is detected with the human Fc-APC antibody, and binding when 10 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and binding is detected with the human Fc-APC antibody. Figure 27D shows data from NK71-expressing Jurkat cells. Moving left to right is a control for the antibody to murine Fc, binding when 2 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with a murine Fc-APC antibody, and binding when 10 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with the murine Fc-APC antibody, and detection of Flag tag (present in the NK71/72 CAR constructs, but not native Jurkat cells). Figure 27E shows data from NK72-expressing Jurkat cells. Moving left to right are negative control, control for the antibody to human Fc, binding when 2 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and binding is detected with the human Fc-APC antibody, and binding when 10 ug/ml of a CD70-hFc complex is incubated with the Jurkat cells and binding is detected with the human Fc-APC antibody. Figure 27F shows data from NK72-expressing Jurkat cells. Moving left to right is a control for the antibody to murine Fc, binding when 2 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with a murine Fc-APC antibody, and binding when 10 ug/ml of a CD70-murine Fc complex is incubated with the Jurkat cells and binding is detected with the murine Fc-APC antibody, and detection of Flag tag (present in the NK71/72 CAR constructs, but not native Jurkat cells).

[0086] Figures 28A-28E shows data related to CRISPR-mediated gene editing of two targets in NK cells. Figure 28A shows a non-limiting example of an electroporation protocol. In these Figures, expression of NKG2A (in conjunction with CD70) and TGFBR2 (in conjunction with CD70) were assessed. Knockout of CD70 expression is discussed in further detail below. Figure 28B shows expression of NKG2A after NK cells were exposed to CRISPR/guide RNAs targeting NKG2A. Figure 28C shows control data. Figure 28D shows expression of TGFBR2 after NK cells were exposed to CRISPR/guide RNAs targeting TGFBR2. Figure 28E shows control data.

[0087] Figures 29A-29J shows data related to CRISPR-mediated gene editing of two targets in NK cells and subsequent expression of a CAR construct at 4 days post-transduction with the CAR-encoding vector (11 days post-electroporation). Figure 29A shows expression of expression of a non-limiting embodiment of a CAR targeting CD70 after NK cells were exposed to CD70 gRNAs. Figure 29B shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs. Figure 29C shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and CISH gRNAs. Figure 29D shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and CISH gRNAs. Figure 29E shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and NKG2A gRNAs. Figure 29F shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and NKG2A gRNAs. Figure 29G shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and TGFBR2 gRNAs. Figure 29H shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and TGFBR2 gRNAs. Figure 29I shows mock control data for anti-CD70 expression on NK cells. Figure 29J shows mock control data for CD70 expression on NK cells.

[0088] Figures 30A-30J shows data related to CRISPR-mediated gene editing of two targets in NK cells and subsequent expression of a CAR construct at 11 days post-transduction with the CAR-encoding vector (18 days post-electroporation). Figure 30A shows expression of a non-limiting embodiment of a CAR targeting CD70 after NK cells were exposed to CD70 gRNAs. Figure 30B shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs. Figure 30C shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and CISH gRNAs. Figure 30D shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and CISH gRNAs. Figure 30E shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and NKG2A gRNAs. Figure 30F shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and NKG2A gRNAs. Figure 30G shows anti-CD70 CAR expression on the NK cells after NK cells were exposed to CD70 and TGFBR2 gRNAs. Figure 30H shows knockdown of expression of CD70 on NK cells through editing targeting by CD70 gRNAs and TGFBR2 gRNAs. Figure 30I shows mock control data for anti-CD70 expression on NK cells. Figure 30J shows mock control data for CD70 expression on NK cells.

[0089] Figures 31A-31C show summary expression data for a first non-limiting embodiment of an anti-CD70 CAR on NK cells subject to gene-editing knockdown of one or more targets, evaluated at 11 days post-transduction. Figure 31A shows the expression levels of a first non-limiting anti-CD70 CAR (NK71) on NK cells treated with CD70 gRNA, CD70 and CISH gRNAs, CD70 and NKG2A gRNAs, CD70 and TGFBR2 gRNAs, or with GFP. Data are the percentage of NK cells positive for the FLAG tag in the NK71 CAR construct (several embodiments do not employ a FLAG tag). Figure 31B shows the underlying raw mean fluorescence intensity (MFI) data. Figure 31C shows data related to the degree of CD70 knockout in the NK cells with the indicated gRNAs.

[0090] Figures 32A-32C show summary expression data for a second non-limiting embodiment of an anti-CD70 CAR on NK cells subject to gene-editing knockdown of one or more targets, evaluated at 11 days post-transduction. Figure 32A shows the expression levels of a first non-limiting anti-CD70 CAR (NK72) on NK cells treated with CD70 gRNA, CD70 and CISH gRNAs, CD70 and NKG2A gRNAs, CD70 and TGFBR2 gRNAs, or with GFP. Data are the percentage of NK cells positive for the FLAG tag in the NK72 CAR construct (several embodiments do not employ a FLAG tag). Figure 32B shows the underlying raw mean fluorescence intensity (MFI) data. Figure 32C shows data related to the degree of CD70 knockout in the NK cells with the indicated gRNAs.

[0091] Figures 33A-33B show data related to the changes in NK cell proliferation based on knockout of different targets in the NK cells and engineering the NK cells to express an anti-CD70 CAR. Figure 33A shows data that knockdown of CD70 expression and engineered expression of an anti-CD70 CAR (this experiment used the non-limiting NK71 construct) and knockdown of CISH expression results in enhanced NK cell proliferation (as compared to knockdown of CD70 alone. Similar data are shown when CD70 and TGFRB2 are knockout. In contrast, knockdown of NKG2A results in decreased proliferation (as compared to CD70 knockout alone). Figure 33B shows corresponding data for proliferation when the NK

cells are subjected to the same gene editing procedures, but transduced with a construct encoding the non-limiting example anti-CD70 CAR, NK72.

[0092] Figures 34A-34B show data related to NK cell survival based on knockout of different targets in the NK cells and engineering the NK cells to express an anti-CD70 CAR. Figure 34A shows survival data for NK cells engineered to express the non-limiting NK71 anti-CD70 CAR out to 35 days (post-electroporation). As shown, the double knockout of CD70 and TGFBR2 result in modestly improved survival throughout the experimental time-course (as compared to the CD70 knockout). The dual CD70 and CISH knockout resulted in significantly enhanced survival with approximately a 2-fold increase in survival (as compared to CD70 alone). The knockout of NKG2A resulted in a reduction in survival, with the NK population slowly declining from Day 21 to Day 35. The reduced survival of this group makes the survival of the CD70-CISH dual knockout nearly 3 times that of the NKG2A group. Figure 34B shows similar trends among the groups for the non-limiting NK72 anti-CD70 CAR. These data also suggest that, according to some embodiments, the NK71 construct results in enhanced survival as compared to the NK72 construct.

[0093] Figures 35A-35D show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 35A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against 786-O cells, which express high levels of CD70, at an E:T ratio of 1:1. Figure 35B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against 786-O cells at an E:T ratio of 1:2. Figure 35C shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against 786-O cells at an E:T ratio of 1:1. Figure 35B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against 786-O cells at an E:T ratio of 1:2. Data were collected at 7-days post-transduction.

[0094] Figures 36A-36D show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 36A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against ACHN cells, which express low levels of CD70, at an E:T ratio of 1:1. Figure 36B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against ACHN cells at an E:T ratio of 1:2. Figure 36C shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against ACHN cells at an E:T ratio of 1:1. Figure 36D shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against ACHN cells at an E:T ratio of 1:2. Data were collected at 7-days post-transduction.

[0095] Figures 37A-37B show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 37A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against 786-O cells, which express high levels of CD70, at an E:T ratio of 1:2. Figure 37B shows the cytotoxic effects of engineered

NK cells expressing the non-limiting NK71 anti-CD70 CAR against 786-O cells at an E:T ratio of 1:4. Data were collected at 14-days post-transduction.

[0096] Figures 38A-38B show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 38A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against ACHN cells, which express low levels of CD70, at an E:T ratio of 1:1. Figure 38B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against ACHN cells at an E:T ratio of 1:2. Data were collected at 14-days post-transduction.

[0097] Figures 39A-39B show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 39A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against 786-O cells, which express high levels of CD70, at an E:T ratio of 1:2. Figure 39B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against 786-O cells at an E:T ratio of 1:4. Data were collected at 14-days post-transduction.

[0098] Figures 40A-40B show data related to cytotoxicity of NK cells expressing an anti-CD70 CAR and subjected to knockout of various NK cell modulating targets. Figure 40A shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK72 anti-CD70 CAR against ACHN cells, which express low levels of CD70, at an E:T ratio of 1:1. Figure 40B shows the cytotoxic effects of engineered NK cells expressing the non-limiting NK71 anti-CD70 CAR against ACHN cells at an E:T ratio of 1:2. Data were collected at 14-days post-transduction.

[0099] Figures 41A-41O relate to gene editing protocol and evaluation of the expression of the various editing targets as well as expression of an anti-CD70 CAR. Figure 41A shows a non-limiting embodiment of the gene editing protocol employed. Figure 41B shows an unstained control (no anti-CD70 antibody) representing background signal. Figure 41B shows a control where CD70 expression was measured on NK cells transduced with a CAR not targeting CD70 and that does not include a CD70 subunit. This represents baseline NK cell CD70 expression. Figure 41D shows CD70 expression on NK cells subjected to gene editing to knockout CD70 expression. Figure 41E shows expression of the non-limiting NK71 anti-CD70 CAR on NK cells with knocked out CD70 expression. Figure 41F shows CD70 expression on NK cells subjected to gene editing to knockout CD70 expression. Figure 41G shows expression of the non-limiting NK72 anti-CD70 CAR on NK cells with knocked out CD70 expression. Figure 41H shows CD70 expression on NK cells subjected to gene editing to knockout CD70 and CISH expression. Figure 41F shows expression of the non-limiting NK71 anti-CD70 CAR on NK cells with knocked out CD70 and CISH expression. Figure 41J shows CD70 expression on NK cells subjected to gene editing to knockout CD70 and CISH expression. Figure 41GK shows expression of the non-limiting NK72 anti-CD70 CAR on NK cells with knocked out CD70 and CISH expression. Figure 41L shows CD70 expression on NK cells subjected to electroporation only, as a control. Figure 41M shows expression of the non-limiting NK71 anti-CD70 CAR on NK cells subjected to electroporation only, as a control. Figure 41N shows CD70 expression

on NK cells subjected to electroporation only, as a control. Figure 41O shows expression of the non-limiting NK72 anti-CD70 CAR on NK cells subjected to electroporation only, as a control.

[00100] Figures 42A-42C relate to cytotoxicity data for NK cells subjected to gene editing and engineered to express an anti-CD70 CAR. Figure 42A shows cytotoxicity of the NK cells treated in the indicated manner against 786-O cells, which express high levels of CD70, evaluated at 7 days post-transduction and at an E:T ratio of 1:2. Figure 42B shows cytotoxicity of the NK cells treated in the indicated manner against ACHN cells, which express low levels of CD70, evaluated at 7 days post-transduction and at an E:T ratio of 1:2. Figure 42C shows cytotoxicity of the NK cells treated in the indicated manner against 786-O cells, which express high levels of CD70, evaluated at 7 days post-transduction and at an E:T ratio of 1:2.

[00101] Figures 43A-43I relate to CD70 expression on NK cells (7 days post-electroporation) using various guide RNAs. Figure 43A shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNA 1. Figure 43B shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNA 2. Figure 43C shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNA 3. Figure 43D shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNAs 1 and 3. Figure 43E shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNAs 1 and 2. Figure 43F shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNAs 2 and 3. Figure 43G shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNA 1 (for CD70) and guide RNA to knockout CISH. Figure 43H shows CD70 expression levels by NK cells subjected to gene editing to knockout expression of CD70 using gRNA 1 (for CD70) and guide RNA to knockout the adenosine receptor (A2AR). Figure 43I shows control data from NK cells subject to electroporation alone (no gene editing enzymes or guide RNA).

[00102] Figures 44A-44D relate to cytotoxicity evaluation of NK cells subjected to various gene editing protocols and engineered to express an anti-CD70 CAR (used here as a non-limiting embodiment is NK71, an anti-CD70 CAR). Figure 44A shows cytotoxicity of the indicated NK cells against Reh tumor cells, at either a 1:1 or 1:2 effector:target ratio. Figure 44B shows a summary histogram of the cytotoxicity at 1:1. Figure 44C shows a summary histogram of the cytotoxicity at 1:2. Figure 44D shows cytotoxicity of the indicated constructs against Nalm-6 tumor cells.

[00103] Figures 45A-45B show cytotoxicity evaluation of NK cells subjected to various gene editing protocols and engineered to express an anti-CD70 CAR (used here as a non-limiting embodiment is NK71, an anti-CD70 CAR). Figure 45A shows cytotoxicity of the indicated NK cells against Reh tumor cells at a 1:1 E:T ratio. Figure 45B shows cytotoxicity of the indicated NK cells against Reh tumor cells at a 1:2 E:T ratio.

[00104] Figures 46A-46J show data related to the expression of an anti-CD70 CAR in NK cells subjected to gene editing to knockout native CD70 expression (and/or CISH or adenosine receptor

expression) as well as expression of native CD70 by the NK cells. Figure 46A shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNA 1 (for CD70). Figure 46B shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNA 2 (for CD70). Figure 46C shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNA 3 (for CD70). Figure 46D shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNAs 1 and 3 (both for CD70). Figure 46E shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNAs 2 and 3 (both for CD70). Figure 46F shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNAs 1 and 2 (both for CD70). Figure 46G shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNA 1 (for CD70) and additional gRNA to knockout CISH. Figure 46H shows data for antiCD70 CAR expression and native CD70 expression levels by NK cells subjected to gene editing using gRNA 1 (for CD70) and additional gRNA to knockout expression of the adenosine receptor (A2AR). Figure 46I shows control data where NK cells were subjected to electroporation only, but no gRNA or engineered CAR expression. Figure 46J shows control data with un-transduced NK cells.

[00105] Figures 47A-47F show cytotoxicity data related to anti-CD70 CAR-expressing, and gene edited, NK cells against tumor cells. Figure 47A shows cytotoxicity data of the indicated NK cells against 786-O cells at a 1:2 E:T ratio. Figure 47B shows cytotoxicity data of the indicated NK cells against 786-O cells at a 1:4 E:T ratio. Figure 47C shows cytotoxicity data of the indicated NK cells against 786-O cells at a 1:8 E:T ratio. Figure 47D shows cytotoxicity data of the indicated NK cells against ACHN cells at a 1:2 E:T ratio. Figure 47E shows cytotoxicity data of the indicated NK cells against ACHN cells at a 1:4 E:T ratio. Figure 47F shows cytotoxicity data of the indicated NK cells against ACHN cells at a 1:8 E:T ratio.

[00106] Figures 48A-48D show cytotoxicity data from various gene edited NK cells that also are engineered to express an anti-CD70 CAR against tumor cells. Figure 48A shows cytotoxicity data from the indicated gene edited NK cells expressing an anti-CD70 CAR against 786-O cells at a 1:1 ratio, with data collected at 72 hours after co-culturing with the tumor cells. Figure 48B shows summary data of GFP detection, a surrogate for live tumor cell number, measured as a percent of baseline GFP detection (as of time zero). Figure 48C shows cytotoxicity data from the indicated gene edited NK cells expressing an anti-CD70 CAR against 786-O cells at a 1:2 ratio, with data collected at 72 hours after co-culturing with the tumor cells. Figure 48D shows summary data of GFP detection, a surrogate for live tumor cell number, measured as a percent of baseline GFP detection (as of time zero).

[00107] Figures 49A-49D show schematics and knockout data from additional various gene edited NK cells that are also engineered to express an anti-CD70 CAR against tumor cells. Figure 49A shows the schematic where NK cells are first gene edited (e.g. with CRISPR) to knock out both CD70 and a target gene, expanded, and transduced with the NK71 anti-CD70 CAR construct (which is a non-limiting example of a CAR according to the present disclosure), which are then assayed for tumor killing efficacy. Figure 49B

shows consistent percent CD70 expression on day 7 following CD70 and target gene double knockout for different target gene conditions. Figure 49C shows essentially undetectable CD70 expression on day 10 following double CD70 and target gene double knockout and consistent expression of the non-limiting NK71 CAR in different target gene conditions. Figure 49D shows PCR amplification data of target gene loci for knockout NK cell populations and indel frequency of amplicons.

[00108] Figures 49E-49G show cytotoxicity data for NK cells gene edited for SMAD3. Figure 49E shows successful knockout of SMAD3 in an NK cell population. Figure 49F shows cytotoxicity data from SMAD3 or CISH gene edited NK cells expressing the NK71 CAR, against 786-O cells at a 1:4 ratio, with or without treatment with 20 ng/mL TGFb, for up to 6.5 days. Figure 49G shows the percentage of remaining 786-O cells relative to starting amount after 3 days following treatment with SMAD3 or CISH gene edited NK cells expressing a non-limiting example of a CAR, NK71, at a 1:1 ratio, with or without treatment with 20 ng/mL TGFb.

[00109] Figures 49H-49I show cytotoxicity data for NK cells gene edited for A2AR. Figure 49H shows cytotoxicity data from A2AR or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:4 ratio, with or without treatment with 10 μM NECA, for up to 6 days. Figure 49I shows the percentage of remaining 786-O cells relative to starting amount after 3 days following treatment with A2AR or CISH gene edited NK cells expressing the NK71 CAR at a 1:1 ratio, with or without treatment with 10 μM NECA.

[00110] Figures 49J-49K show cytotoxicity data for NK cells gene edited for MAPKAPK3. Figure 49J shows cytotoxicity data from MAPKAPK3 (MK3) or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:2 ratio, for up to 94 hours. Figure 49K shows the percentage of remaining 786-O cells relative to starting amount after 3 days following treatment with MK3 or CISH gene edited NK cells expressing the NK71 CAR at a 1:1 ratio.

[00111] Figures 49L-49P show cytotoxicity data for NK cells gene edited for NKG2A. Figure 49L shows cytotoxicity data from NKG2A or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:1 ratio, for up to 72 hours. Figure 49M shows cytotoxicity data from NKG2A, MK3, or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:1 ratio, for up to 94 hours. Figure 49N shows cytotoxicity data from NKG2A, MK3, or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:2 ratio, for up to 94 hours. Figure 49O shows cytotoxicity data from NKG2A or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:1 ratio, with or without treatment with 20 ng/mL TGFb, for up to 72 hours. Figure 49P shows cytotoxicity data from NKG2A or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:2 ratio, with or without treatment with 10 μM NECA, for up to 54 hours.

[00112] Figures 49Q-49R show cytotoxicity data for NK cells gene edited for DDIT4. Figure 49Q shows cytotoxicity data from DDIT4 or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:1 ratio, with or without treatment with 50 μM $CoCl_2$, for up to 94 hours. Figure 49R shows the percentage of remaining 786-O cells relative to starting amount after 3 days following treatment with DDIT4

or CISH gene edited NK cells expressing the NK71 CAR at a 1:1 ratio, with or without treatment with 50 μM $CoCl_2$.

[00113] Figures 49S-49T show cytotoxicity data for NK cells gene edited for CEACAM1. Figure 49S shows cytotoxicity data from CEACAM1 or CISH gene edited NK cells expressing the NK71 CAR against 786-O cells at a 1:2 ratio, with or without treatment with 1 μg/mL CEACAM5, for up to 72 hours. Figure 49T shows the percentage of remaining 786-O cells relative to starting amount after 3 days following treatment with CEACAM1 or CISH gene edited NK cells expressing the NK71 CAR at a 1:2 ratio, with or without treatment with 1 μg/mL CEACAM5.

[00114] Figures 49U and 49V show survival over 49 days for NK cells expressing the NK71 CAR that have been gene edited for CD70 and the various indicated gene targets.

[00115] Figure 50A depicts exemplary heavy chain variable region (VH) and light chain variable region (VL) peptide and nucleic acid sequences for the selected anti-CD70 scFvs disclosed herein. The sequences disclosed herein may be used for any of the embodiments disclosed herein.

[00116] Figure 50B depicts exemplary heavy chain variable region and light chain variable region complementarity determining regions (CDRs) for the selected anti-CD70 scFvs disclosed herein. In some embodiments, other combinations of CDRs may be used to prepare other anti-CD70 scFvs or other binding domains. The CDRS disclosed herein may be used for any of the embodiments disclosed herein.

[00117] Figure 50C depicts a schematic for selecting CARs comprising an anti-CD70 binding domain based on tonic signaling and immune cell activation.

[00118] Figure 50D shows data related detection of the degree of tonic signaling in Jurkat lines.

[00119] Figure 50E shows CAR activation relative to tonic signaling further ordered by overall CAR expression in Jurkat cells expressing the disclosed anti-CD70 CARs. The circled points depict selected non-limiting embodiments of anti-CD70 CAR constructs that result in significant on-target activation relative to tonic signaling.

[00120] Figure 50F shows a non-limiting list of 10 anti-CD70 CAR constructs that were selected for having desirable activation and limited/minimal tonic signaling effects in Jurkat cells. These constructs were tested in additional assays disclosed herein.

[00121] Figures 51A-51B shows expression levels of tested anti-CD70 CARs in a donor NK cell population gene edited to knockout CD70. Figure 51A shows flow cytometry plots detecting expression of the CAR (by anti-FLAG antibody conjugated with allophycocyanin (APC)) and loss of expression of CD70 (by anti-CD70 antibody conjugated with phycoerythrin (PE)). Figure 51B shows the quantification of anti-CD70 CAR and CD70 expression in the NK cell population of Figure 51A. NK8 refers to a control construct that expresses GFP instead of a CAR/mbIL15.

[00122] Figures 52A-52D shows expression levels of tested anti-CD70 CARs in another donor NK cell population edited to knockout CD70 and preliminary cytotoxicity assays. Figure 52A shows flow cytometry plots detecting expression of the CAR (by anti-FLAG antibody conjugated with APC) and loss of expression of CD70 (by anti-CD70 antibody conjugated with PE). Figure 52B shows the quantification of

anti-CD70 CAR and CD70 expression in the NK cell populations of Figure 52A. Figure 52C show the raw mean fluorescence intensity (MFI) used to quantify CAR expression. Figure 52D shows a cytotoxicity assay for anti-CD70 CAR NK cell populations against 786-O tumor cells at different effector:target (E:T) ratios and the calculated EC_{50} from the assay.

[00123] Figures 53A-53F shows cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells. Figure 53A shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 7 days. Figure 53B shows remaining 786-O cells at 73.5 hours following the NK cell 1:2 co-culture as measured by 786-O GFP fluorescence. Figure 53C shows cytotoxicity data of the tested NK cells of Figure 53A, but extended to 10 days. Culture was re-challenged with additional tumor cells at day 7. Figure 53D shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 7 days. Figure 53E shows remaining 786-O cells at 73.5 hours following the NK cell 1:4 co-culture as measured by 786-O GFP fluorescence. Figure 53F shows cytotoxicity data of tested NK cells against 786-O cells at a 1:8 ratio, for up to 7 days.

[00124] Figure 54A-54D show cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells against either 786-O cells or ACHN cells. Figure 54A shows cytotoxicity data for tested NK cells against 786-O cells at a 1:2 ratio, for up to 5 days. The 786-O cells express GFP. Figure 54B shows cytotoxicity data for tested NK cells against ACHN cells at a 1:2 ratio, for up to 5 days. The ACHN cells are stained with NucRed. Figure 54C shows cytotoxicity data for tested NK cells against 786-O cells at a 1:4 ratio, for up to 5 days. Figure 54D shows cytotoxicity data for tested NK cells against ACHN cells at a 1:4 ratio, for up to 5 days.

[00125] Figures 55A-55M show cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells from one donor. Figure 55A shows flow cytometry plots detecting expression of the CAR (by APC anti-FLAG) and loss of expression of CD70 (by PE anti-CD70). Figure 55B show preliminary cytotoxicity data for tested NK cells against 786-O cells at different E:T ratios at 4 hours of co-culture. Figure 55C shows quantification of the expressed anti-CD70 CAR, loss of CD70 expression, and the calculated EC_{50} from the assay of Figure 55B. Figure 55D shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 64 hours. Figure 55E shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 6 days. Figure 55F shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 7 days. Figure 55G shows cytotoxicity data of tested NK cells as seen in Figure 55F but extended to 11 days and re-challenged with additional tumor cells at day 7. Figure 55H shows remaining 786-O cells at 51 hours following the NK cell 1:2 co-culture as measured by 786-O GFP fluorescence. Figure 55I shows remaining 786-O cells at 66 hours following the NK cell 1:2 co-culture as measured by 786-O GFP fluorescence. Figure 55J shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 64 hours. Figure 55K shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 6 days. Figure 55L shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 7 days. Figure 55M shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 11 days. Cultures were re-challenged with additional tumor cells at day 7.

[00126] Figures 56A-56J show cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells from another donor. Figure 56A shows flow cytometry plots detecting expression of the CAR (by APC anti-FLAG) and loss of expression of CD70 (by PE anti-CD70). Figure 56B shows preliminary cytotoxicity data for tested NK cells against 786-O cells at different E:T ratios at 4 hours of co-culture. Figure 56C shows quantification of the expressed anti-CD70 CAR, loss of CD70 expression, and the calculated EC_{50} from the assay of Figure 56B. Figure 56D shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 5.75 days. Figure 56E shows cytotoxicity data of tested NK cells as seen in Figure 56H but extended to 10 days and re-challenge with additional tumor cells at day 6. Figure 56F shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 42 hours. Figure 56G shows cytotoxicity data of tested NK cells against 786-O cells at a 1:4 ratio, for up to 5 days. Figure 56H shows cytotoxicity data of tested NK cells against 768-O cells at a 1:4 ratio, for up to 5.75 days. Figure 56I shows cytotoxicity data of tested NK cells against 786-O cells at a 1:8 ratio, for up to 42 hours. Figure 56J shows cytotoxicity data of tested NK cells against 786-O cells at a 1:8 ratio, for up to 5 days.

[00127] Figures 57A-57H show cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells from one donor against ACHN cells. Figure 57A shows cytotoxicity data of tested NK cells against ACHN cells at a 1:2 ratio, for up to 5 days. Cultures were re-challenged with additional tumor cells at around 3.75 days. Figure 57B shows the cytotoxicity data of Figure 57A, but where cell count is normalized to day 0. Figure 57C shows cytotoxicity data of tested NK cells of Figure 57B over a longer time period following re-challenge. Figure 57D shows remaining ACHN cells at 51 hours following the NK cell 1:2 co-culture as measured by ACHN fluorescence. Figure 57E shows remaining ACHN cells at 66 hours following the NK cell 1:2 co-culture as measured by ACHN fluorescence. Figure 57F shows cytotoxicity data of tested NK cells against ACHN cells at a 1:4 ratio, for up to 5 days. Cultures were re-challenged with additional tumor cells at around 3.75 days. Figure 57G shows the cytotoxicity data of Figure 57F, but where cell count is normalized to day 0. Figure 57H shows cytotoxicity data of tested NK cells of Figure 57G over a longer time period following re-challenge.

[00128] Figures 58A-58H show cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells from another donor against ACHN cells. Figure 58A shows cytotoxicity data of tested NK cells against ACHN cells at a 1:4 ratio, for up to 5 days. Cultures were re-challenged with additional tumor cells at around 3.75 days. Figure 58B shows the cytotoxicity data of Figure 58A, but where cell count is normalized to day 0. Figure 58C shows cytotoxicity data of tested NK cells of Figure 58B over a longer time period following re-challenge. Figure 58D shows remaining ACHN cells at 51 hours following the NK cell 1:4 co-culture as measured by ACHN fluorescence. Figure 58E shows remaining ACHN cells at 66 hours following the NK cell 1:4 co-culture as measured by ACHN fluorescence. Figure 58F shows cytotoxicity data of tested NK cells against ACHN cells at a 1:8 ratio, for up to 5 days. Cultures were re-challenged with additional tumor cells at around 3.75 days. Figure 58G shows the cytotoxicity data of Figure 58D, but where cell count is normalized to day 0. Figure 58H shows cytotoxicity data of tested NK cells of Figure 58G over a longer time period following re-challenge.

[00129] Figures 59A-59D shows expression level and preliminary cytotoxicity data for additional anti-CD70 CARs in NK cells gene edited to knockout CD70 in one donor. Figure 59A shows flow cytometry plots detecting expression of the CAR (by APC anti-FLAG) and loss of expression of CD70 (by PE anti-CD70). Figure 59B shows the quantification of anti-CD70 CAR and CD70 expression in the NK cell populations of Figure 59A. Figure 59C shows the MFI used to quantify CAR expression. Figure 59D shows a cytotoxicity assay for anti-CD70 CAR NK cell populations against 786-O tumor cells at different effector:target ratios and the calculated EC_{50} from the assay.

[00130] Figures 60A-60O shows cytotoxicity data of tested anti-CD70 CARs in CD70 knockout NK cells from a donor against either 786-O or ACHN tumor cells. Figure 60A shows cytotoxicity data of tested NK cells against 786-O cells at a 1:2 ratio, for up to 51 hours. Figure 60B shows cytotoxicity data of tested NK cells of Figure 60A, extended to 90 hours and re-challenged with additional tumor cells at 70 hours. Figure 60C shows remaining 786-O cells at 51 hours following the NK cell 1:2 co-culture as measured by 786-O fluorescence. Figure 60D shows remaining 786-O cells at 66 hours following the NK cell 1:2 co-culture as measured by 786-O fluorescence. Figure 60E shows cytotoxicity data of tested NK cells against ACHN cells at a 1:2 ratio, for up to 51 hours. Figure 60F shows cytotoxicity data of tested NK cells of Figure 60E extended to 90 hours and re-challenged with additional tumor cells at 70 hours. Figure 60G shows remaining ACHN cells at 51 hours following the NK cell 1:2 co-culture as measured by ACHN fluorescence. Figure 60H shows remaining ACHN cells at 66 hours following the NK cell 1:2 co-culture as measured by ACHN fluorescence. Figure 60I shows cytotoxicity data of tested NK cells against 786-O cells at a ratio of 1:4, for up to 51 hours. Figure 60J shows cytotoxicity data of the tested NK cell cultures of Figure 60I, but extended to 90 hours and re-challenged with additional tumor cells at 70 hours. Figure 60K shows remaining 786-O cells at 51 hours following the NK cell 1:4 co-culture as measured by 786-O fluorescence. Figure 60L shows remaining 786-O cells at 66 hours following the NK cell 1:4 co-culture as measured by 786-O fluorescence. Figure 60M shows cytotoxicity data of tested NK cells against ACHN cells at a 1:4 ratio, for up to 51 hours. Figure 60N shows cytotoxicity data of the tested NK cell cultures of Figure 60M, but extended to 90 hours and re-challenged with additional tumor cells at 70 hours. Figure 60O shows remaining ACHN cells at 51 hours following the NK cell 1:4 co-culture as measured by ACHN fluorescence. Figure 60P shows remaining ACHN cells at 66 hours following the NK cell 1:4 co-culture as measured by ACHN fluorescence.

[00131] Figures 61A-61N shows expression level and cytotoxicity data for additional anti-CD70 CARs in NK cells gene edited to knockout CD70 in another donor. Figure 61A shows flow cytometry plots showing knockout of CD70 in the donor (denoted donor 512). Figure 61B shows flow cytometry plots detecting expression of the CAR (by APC anti-FLAG) and loss of expression of CD70 (by PE anti-CD70). Figure 61C shows the quantification of anti-CD70 CAR and CD70 expression in the NK cell population of Figure 61B. Figure 61D shows the raw MFI used to quantify CAR expression of Figure 61B. Figure 61E shows the % abundance of the tested anti-CD70 CARs after 1 week of culture. Figure 61F shows the raw MFI of the tested anti-CD70 CARs after 1 week of culture. Figure 61G shows the % abundance of the tested

anti-CD70 CARs after 2 weeks of culture. Figure 61H shows the raw MFI of the tested anti-CD70 CARs after 2 weeks of culture. Figure 61I shows the % abundance of the tested ant-CD70 CARs after 3 weeks of culture. Figure 61J shows the raw MFI of the tested anti-CD70 CARs after 3 weeks of culture. Figure 61K shows cytotoxicity data of the tested NK cells against 786-O cells at a 1:2 E:T ratio at 3 days of a 14 day total culture. Figure 61L shows cytotoxicity data of the tested NK cells against 786-O cells at a 1:4 E:T ratio at 3 days of a 14 day total culture. Figure 61M shows cytotoxicity data of the tested NK cells against ACHN cells at a 1:2 ratio at 3 days of a 14 day total culture. Figure 61N shows cytotoxicity data of the tested NK cells against ACHN cells at a 1:4 ratio at 3 days of a 14 day total culture.

[00132] Figures 62A-62B show NK cell survival over 5 weeks (week 0 to week 5) after transduction with tested anti-CD70 CARs. Figure 62A shows survival of NK cells from one donor (denoted donor 451). Figure 62B shows survival of NK cells from another donor (denoted donor 512).

[00133] Figures 63A-63B show cytotoxicity data of tested NK cells gene expressing anti-CD70 CARs and gene edited to knockout CD70 and optionally CISH. Figure 63A shows cytotoxicity data of tested NK cells against 786-O cells at a 1:8 ratio, for up to 64 hours. Figure 63B shows cytotoxicity data of tested NK cells against ACHN cells at a 1:8 ratio, for up to 64 hours.

[00134] Figures 64A-64J show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout. Figure 64A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a trimer of CD70 (native CD70 conformation) as measured week 1 post-transduction with the CAR (which is 1 week past the phenotypic analysis of CD70 expression post-gene editing shown in Figures 61A-61B). Figure 64B shows similar data from another donor. Figures 64C and 64D shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 64E and 64F show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 64G and 64H show flow cytometry plots depicting knockout of CD70 expression in the NK cells from two donors and Figures 64I and 64J show the summary data of the percent of NK cells expressing CD70 as a percentage and by MFI for both donors.

[00135] Figures 65A-65J show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout, measured at 2 weeks post-transduction of the NK cells with the CARs. Figure 65A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a native CD70 trimer. Figure 65B shows similar data from another donor. Figures 65C and 65D shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 65E and 65F show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 65G and 65H show flow cytometry plots depicting the maintained knockout of CD70

expression in the NK cells from each of the two donors. Figures 65I and 65J show summary data of the percent of NK cells expressing CD70 as a percentage and by MFI for both donors.

[00136] Figures 66A-66I show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout, measured at 3 weeks post-transduction of the NK cells with the CARs. Figure 66A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a native CD70 trimer. Figure 66B shows similar data from another donor. Figure 66C shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 66D and 66E show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 66F and 66G show flow cytometry plots depicting the maintained knockout of CD70 expression in the NK cells from each of the two donors. Figures 66H and 66I show summary data of the percent of NK cells expressing CD70 as a percentage and by MFI, as well a percent viability, for both donors.

[00137] Figures 67A-67J show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout, measured at 4 weeks post-transduction of the NK cells with the CARs. Figure 67A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a native CD70 trimer. Figure 67B shows similar data from another donor. Figures 67C and 67D shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 67E and 67F show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 67G and 67H show flow cytometry plots depicting the maintained knockout of CD70 expression in the NK cells from each of the two donors. Figures 67I and 67J show summary data of the percent of NK cells expressing CD70 as a percentage and by MFI for both donors.

[00138] Figures 68A-68I show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout, measured at 5 weeks post-transduction of the NK cells with the CARs. Figure 68A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a native CD70 trimer. Figure 68B shows similar data from another donor. Figures 68C and 65D shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 68E and 68F show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 68G and 68H show flow cytometry plots depicting the maintained knockout of CD70 expression in the NK cells from each of the two donors. Figures 68I shows summary data of the percent of NK cells expressing CD70 as a percentage and by MFI for both donors.

[00139] Figures 69A-69H show further data related to screening of various CD70 CAR constructs expressed by NK cells and characterization of CD70 gene knockout, measured at 7 weeks post-

transduction of the NK cells with the CARs. Figure 69A shows data for the indicated CD70 CAR constructs and their ability, when expressed by NK cells, to bind a native CD70 trimer and Figure 68B shows corresponding data from another donor. Figure 69C shows summary data from the flow cytometry binding data, expressed as a percentage of the NK cell population that is binding the CD70 trimer, or as the detected mean fluorescence intensity (MFI) for the two respective donors. Figures 69D and 69E show graphical summary data for the relative expression of each of the indicated CAR constructs by NK cells, as measured by MFI. Figures 69F and 69G show flow cytometry plots depicting the maintained knockout of CD70 expression in the NK cells from each of the two donors. Figures 69H shows summary data of the percent of NK cells expressing CD70 as a percentage and by MFI for both donors.

[00140] Figures 70A-70B show data related to the expression of selected non-limiting anti-CD70 CARs by NK cells over time. Figure 70A tracks the expression of three non-limiting CARs on NK cells from a first donor and Figure 70B tracks expression of the same CARs on NK cells from a second donor.

[00141] Figures 71A-71T show data related to cytokines released by NK cells from one of two donors that are expressing various CD70 CAR constructs (and edited to knockout CD70) when co-cultured with either ACHN or 786-O tumor cells at various effector:target ratios. Figures 71A and 71B show levels of interferon-gamma release when cells from the first donor are co-cultured at a 1:2 E:T ratio with 786-O cells (71A) or ACHN cells (71B), with data being collected at day 14 and day 28 after the inception of process for producing the gene edited and transduced cells (e.g., D0 of the non-limiting example process shown in Figure 49A). Figures 71C and 71D show corresponding data from the second donor. Figures 71E and 71F shows levels of GMCSF release when cells from the first donor are co-cultured at a 1:2 E:T ratio with 786-O cells (71E) or ACHN cells (71F), with data being collected at day 14 and day 28 after inception of the cell production process. Figures 71G and 71H show corresponding data from the second donor. Figures 71I and 71J shows levels of TNF-alpha release when cells from the first donor are co-cultured at a 1:2 E:T ratio with 786-O cells (71I) or ACHN cells (71J), with data being collected at day 14 and day 28 after inception of the cell production process. Figures 71K and 71L show corresponding data from the second donor. Figures 71M and 71N shows levels of perforin release when cells from the first donor are co-cultured at a 1:2 E:T ratio with 786-O cells (71M) or ACHN cells (71N), with data being collected at day 14 and day 28 after inception of the cell production process. Figures 71O and 71P show corresponding data from the second donor. Figures 71Q and 71R shows levels of Granzyme B release when cells from the first donor are co-cultured at a 1:2 E:T ratio with 786-O cells (71Q) or ACHN cells (71R), with data being collected at day 14 and day 28 after inception of the cell production process. Figures 71S and 71T show corresponding data from the second donor.

[00142] Figures 72A-72M show data related to the sustained persistence (both CAR expression and cell viability) and cytotoxicity of NK cells expressing CD70 CARs and edited to knockout one or both of CD70 and CISH. Figure 72A shows expression data for the indicated CARs over an 8 week period post-transduction, as measured by the percentage of the population expressing the CAR. Figure 72B shows similar data, as measured by MFI. Figure 72C shows data related to the survival of the NK cells over the

8 week in vitro period. Figure 72D shows data related to the cytotoxicity of NK cells expressing the indicated CARs against 786-O cells at 1:8 E:T. Figure 72E is a histogram that depicts the final green object count per well (indicative of remaining tumor cell population) for each of the constructs from Figure 72D. Figures 72F and 72G are histograms showing the tumor cell count at the final time point of co-culture of donor NK cells expressing the indicated CARs and the indicated edits, at an E:T of 1:4, against ACHN cells (72F) or 786-O cells (72G). Figures 72H and 72I show corresponding data at a 1:8 E:T ratio. Figures 72J and 72K show cytotoxicity curves in a re-challenge experimental setup, where the NK cells expressing the indicated CARs, edited for CD70 knockout and edited (or not) for CISH knockout, are re-challenged, at a 1:4 E:T ratio, with ACHN (72J) or 786-O (72K) cells. Figures 72L and 72M show corresponding data using a 1:8 E:T ratio.

[00143] Figures 73A-73H show data related to cytotoxicity of selected CAR-expressing NK cells against tumor cells in an in vitro assay prior to and post-rechallenge (assay initiated at 21 days after inception of the cell production process). Figure 73A shows data regarding 786-O tumor cell presence, using a 1:4 E:T ratio), 72 hours prior to rechallenge. Figure 73B shows data regarding 786-O tumor cell presence, using a 1:8 E:T ratio), 72 hours prior to rechallenge. Figure 73C shows data regarding 786-O tumor cell presence, using a 1:4 E:T ratio), 6 days after rechallenge of the NK cells with additional 786-O cells. 73D shows data regarding 786-O tumor cell presence, using a 1:8 E:T ratio), 6 days after rechallenge of the NK cells with additional 786-O cells. Figure 73E shows data regarding ACHN tumor cell presence, using a 1:4 E:T ratio), 72 hours prior to rechallenge. Figure 73F shows data regarding ACHN tumor cell presence, using a 1:8 E:T ratio), 72 hours prior to rechallenge. Figure 73G shows data regarding ACHN tumor cell presence, using a 1:4 E:T ratio), 6 days after rechallenge of the NK cells with additional ACHN cells. 73H shows data regarding ACHN tumor cell presence, using a 1:8 E:T ratio), 6 days after rechallenge of the NK cells with additional ACHN cells.

[00144] Figures 74A-74H show data related to cytotoxicity of selected CAR-expressing NK cells against tumor cells in an in vitro assay prior to and post-rechallenge (assay initiated at 28 days after inception of the cell production process). Figure 74A shows data regarding 786-O tumor cell presence, using a 1:4 E:T ratio), 72 hours prior to rechallenge. Figure 74B shows data regarding 786-O tumor cell presence, using a 1:8 E:T ratio), 72 hours prior to rechallenge. Figure 74C shows data regarding 786-O tumor cell presence, using a 1:4 E:T ratio), 6 days after rechallenge of the NK cells with additional 786-O cells. 74D shows data regarding 786-O tumor cell presence, using a 1:8 E:T ratio), 6 days after rechallenge of the NK cells with additional 786-O cells. Figure 74E shows data regarding ACHN tumor cell presence, using a 1:4 E:T ratio), 72 hours prior to rechallenge. Figure 74F shows data regarding ACHN tumor cell presence, using a 1:8 E:T ratio), 72 hours prior to rechallenge. Figure 74G shows data regarding ACHN tumor cell presence, using a 1:4 E:T ratio), 6 days after rechallenge of the NK cells with additional ACHN cells. 74H shows data regarding ACHN tumor cell presence, using a 1:8 E:T ratio), 6 days after rechallenge of the NK cells with additional ACHN cells.

[00145] Figures 75A-75F show data related to Indel frequency and assessment of CISH KO. Figure 75A shows detection of Indel frequency with respect to edits in CISH. Figure 75B shows detection of Indel frequency with respect to edits in CD70. Figure 75C shows a schematic of a CISH signaling pathway. Figure 75D shows western blot data assessing expressing of phosphorylated Stat 5, a signaling molecule downstream of CIS. Figure 75E shows quantification data normalized to the electroporation control. Figure 75F shows data normalized to the electroporation control at a value of 1.

DETAILED DESCRIPTION

[00146] Some embodiments of the methods and compositions provided herein relate to engineered immune cells and combinations of the same for use in immunotherapy. In several embodiments, the engineered cells are engineered in multiple ways, for example, to express a cytotoxicity-inducing receptor complex. As used herein, the term "cytotoxic receptor complexes" shall be given its ordinary meaning and shall also refer to (unless otherwise indicated), Chimeric Antigen Receptors (CAR), chimeric receptors (also called activating chimeric receptors in the case of NKG2D chimeric receptors). In several embodiments, the cells are further engineered to achieve a modification of the reactivity of the cells against non-tumor tissue and/or other therapeutic cells. In several embodiments, natural killer (NK) cells are also engineered to express a cytotoxicity-inducing receptor complex (e.g., a chimeric antigen receptor or chimeric receptor), such as for example targeting CD70 expressing tumor cells. In several embodiments, the NK cells are genetically edited to reduce and/or eliminate certain markers/proteins that would otherwise inhibit or limit the therapeutic efficacy of the CAR-expressing NK cells. In several embodiments, certain markers/proteins have expression that is upregulated or otherwise induced by one or more processes undertaken to engineer and/or expand the NK cells. For example, in several embodiments, the process of expanding NK cells in culture results in substantially increased CD70 expression by the NK cells. In those embodiments wherein a CD70 CAR is engineered to be expressed by expanded NK cells, the CAR would actually target, not only a CD70-expressing tumor, but other engineered and expanded NK cells as well (based on the increased expression of CD70 resulting from culture of the cells). Thus, for example, in several embodiments, therapeutic NK cells are engineered to express a CAR that targets CD70 and are likewise genetically edited to knock out CD70 expression on the NK cells themselves, which, if present, would cause the CAR-expressing NK cells to target the tumor and the therapeutic NK cells as well. This would otherwise create a self-limiting therapeutic effect, which could allow for tumor expansion and progression of the cancer.

[00147] The term "anticancer effect" refers to a biological effect which can be manifested by various means, including but not limited to, a decrease in tumor volume, a decrease in the number of cancer cells, a decrease in the number of metastases, an increase in life expectancy, decrease in cancer cell proliferation, decrease in cancer cell survival, and/or amelioration of various physiological symptoms associated with the cancerous condition.

Cell Types

[00148] Some embodiments of the methods and compositions provided herein relate to a cell such as an immune cell. For example, an immune cell, such as an NK cell or a T cell, may be engineered to include a chimeric receptor such as a CD70-directed chimeric receptor, or engineered to include a nucleic acid encoding said chimeric receptor as described herein. Additional embodiments relate to engineering a second set of cells to express another cytotoxic receptor complex, such as an NKG2D chimeric receptor complex as disclosed herein. Still additional embodiments relate to the further genetic manipulation of the cells (e.g., donor NK cells) to reduce, disrupt, minimize and/or eliminate the expression of one or more markers/proteins by the NK cells, resulting in an enhancement of the efficacy and/or persistence of the engineered NK cells.

[00149] Traditional anti-cancer therapies relied on a surgical approach, radiation therapy, chemotherapy, or combinations of these methods. As research led to a greater understanding of some of the mechanisms of certain cancers, this knowledge was leveraged to develop targeted cancer therapies. Targeted therapy is a cancer treatment that employs certain drugs that target specific genes or proteins found in cancer cells or cells supporting cancer growth, (like blood vessel cells) to reduce or arrest cancer cell growth. More recently, genetic engineering has enabled approaches to be developed that harness certain aspects of the immune system to fight cancers. In some cases, a patient's own immune cells are modified to specifically eradicate that patient's type of cancer. Various types of immune cells can be used, such as T cells, Natural Killer (NK cells), or combinations thereof, as described in more detail below.

[00150] To facilitate cancer immunotherapies, there are provided for herein polynucleotides, polypeptides, and vectors that encode chimeric antigen receptors (CAR) that comprise a target binding moiety (e.g., an extracellular binder of a ligand, or a tumor marker-directed chimeric receptor, expressed by a cancer cell) and a cytotoxic signaling complex. For example, some embodiments include a polynucleotide, polypeptide, or vector that encodes, for example a chimeric antigen receptor directed against a tumor marker, for example, CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, to facilitate targeting of an immune cell to a cancer and exerting cytotoxic effects on the cancer cell. Also provided are engineered immune cells (e.g., NK cells and/or T cells) expressing such CARs. There are also provided herein, in several embodiments, polynucleotides, polypeptides, and vectors that encode a construct comprising an extracellular domain comprising two or more subdomains, e.g., a first CD70-targeting subdomain comprising an anti-CD70 binding domain as disclosed herein and a second subdomain comprising an additional binding moiety, for example a C-type lectin-like receptor and a cytotoxic signaling complex, or alternatively another anti-CD70 binding domain. Also provided are engineered immune cells (e.g., NK cells and/or T cells) expressing such bi-specific constructs. Methods of treating cancer and other uses of such cells for cancer immunotherapy are also provided for herein.

[00151] To facilitate cancer immunotherapies, there are also provided for herein polynucleotides, polypeptides, and vectors that encode chimeric receptors that comprise a target binding moiety (e.g., an extracellular binder of a ligand expressed by a cancer cell) and a cytotoxic signaling complex. For example, some embodiments include a polynucleotide, polypeptide, or vector that encodes, for example an activating

chimeric receptor comprising an NKG2D extracellular domain that is directed against a tumor marker, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6, among others, to facilitate targeting of an immune cell to a cancer and exerting cytotoxic effects on the cancer cell. Also provided are engineered immune cells (e.g., NK cells and/or T cells) expressing such chimeric receptors. There are also provided herein, in several embodiments, polynucleotides, polypeptides, and vectors that encode a construct comprising an extracellular domain comprising two or more subdomains, e.g., first and second ligand binding receptor and a cytotoxic signaling complex. Also provided are engineered immune cells (e.g., NK cells and/or T cells) expressing such bi-specific constructs (in some embodiments the first and second ligand binding domain target the same ligand). Methods of treating cancer and other uses of such cells for cancer immunotherapy are also provided for herein.

Engineered Cells for Immunotherapy

[00152] In several embodiments, cells of the immune system are engineered to have enhanced cytotoxic effects against target cells, such as tumor cells. For example, a cell of the immune system may be engineered to include a tumor-directed chimeric receptor and/or a tumor-directed CAR as described herein. In several embodiments, white blood cells or leukocytes, are used, since their native function is to defend the body against growth of abnormal cells and infectious disease. There are a variety of types of white bloods cells that serve specific roles in the human immune system, and are therefore a preferred starting point for the engineering of cells disclosed herein. White blood cells include granulocytes and agranulocytes (presence or absence of granules in the cytoplasm, respectively). Granulocytes include basophils, eosinophils, neutrophils, and mast cells. Agranulocytes include lymphocytes and monocytes. Cells such as those that follow or are otherwise described herein may be engineered to include a chimeric antigen receptor, such as a CD70-directed CAR, or a nucleic acid encoding the CAR. In several embodiments, the cells are optionally engineered to co-express a membrane-bound interleukin 15 (mbIL15) domain. As discussed in more detail below, in several embodiments, the therapeutic cells, are further genetically modified enhance the cytotoxicity and/or persistence of the cells. In several embodiments, the genetic modification enhances the ability of the cell to resist signals emanating from the tumor microenvironment that would otherwise cause a reduced efficacy or shortened lifespan of the therapeutic cells.

Monocytes for Immunotherapy

[00153] Monocytes are a subtype of leukocyte. Monocytes can differentiate into macrophages and myeloid lineage dendritic cells. Monocytes are associated with the adaptive immune system and serve the main functions of phagocytosis, antigen presentation, and cytokine production. Phagocytosis is the process of uptake cellular material, or entire cells, followed by digestion and destruction of the engulfed cellular material. In several embodiments, monocytes are used in connection with one or more additional engineered cells as disclosed herein. Some embodiments of the methods and compositions described

herein relate to a monocyte that includes a tumor-directed CAR, or a nucleic acid encoding the tumor-directed CAR. Several embodiments of the methods and compositions disclosed herein relate to monocytes engineered to express a CAR that targets a tumor marker, for example, CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, and optionally includes a membrane-bound interleukin 15 (mbIL15) domain. Several embodiments of the methods and compositions disclosed herein relate to monocytes engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally a membrane-bound interleukin 15 (mbIL15) domain.

Lymphocytes for Immunotherapy

[00154] Lymphocytes, the other primary sub-type of leukocyte include T cells (cell-mediated, cytotoxic adaptive immunity), natural killer cells (cell-mediated, cytotoxic innate immunity), and B cells (humoral, antibody-driven adaptive immunity). While B cells are engineered according to several embodiments, disclosed herein, several embodiments also relate to engineered T cells or engineered NK cells (mixtures of T cells and NK cells are used in some embodiments, either from the same donor, or different donors). Several embodiments of the methods and compositions disclosed herein relate to lymphocytes engineered to express a CAR that targets a tumor marker, for example, CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, and optionally includes a membrane-bound interleukin 15 (mbIL15) domain. Several embodiments of the methods and compositions disclosed herein relate to lymphocytes engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally a membrane-bound interleukin 15 (mbIL15) domain.

T Cells for Immunotherapy

[00155] T cells are distinguishable from other lymphocytes sub-types (e.g., B cells or NK cells) based on the presence of a T-cell receptor on the cell surface. T cells can be divided into various different subtypes, including effector T cells, helper T cells, cytotoxic T cells, memory T cells, regulatory T cells, natural killer T cell, mucosal associated invariant T cells and gamma delta T cells. In some embodiments, a specific subtype of T cell is engineered. In some embodiments, a mixed pool of T cell subtypes is engineered. In some embodiments, there is no specific selection of a type of T cells to be engineered to express the cytotoxic receptor complexes disclosed herein. In several embodiments, specific techniques, such as use of cytokine stimulation are used to enhance expansion/collection of T cells with a specific marker profile. For example, in several embodiments, activation of certain human T cells, e.g. CD4+ T cells, CD8+ T cells is achieved through use of CD3 and/or CD28 as stimulatory molecules. In several embodiments, there is provided a method of treating or preventing cancer or an infectious disease, comprising administering a therapeutically effective amount of T cells expressing the cytotoxic receptor complex and/or a homing moiety as described herein. In several embodiments, the engineered T cells are

autologous cells, while in some embodiments, the T cells are allogeneic cells. Several embodiments of the methods and compositions disclosed herein relate to T cells engineered to express a CAR that targets a tumor marker, for example, CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, and optionally includes a membrane-bound interleukin 15 (mbIL15) domain. Several embodiments of the methods and compositions disclosed herein relate to T cells engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally a membrane-bound interleukin 15 (mbIL15) co-stimulatory domain.

NK Cells for Immunotherapy

[00156] In several embodiments, there is provided a method of treating or preventing cancer or an infectious disease, comprising administering a therapeutically effective amount of natural killer (NK) cells expressing the cytotoxic receptor complex and/or a homing moiety as described herein. In several embodiments, the engineered NK cells are autologous cells, while in some embodiments, the NK cells are allogeneic cells. In several embodiments, NK cells are preferred because the natural cytotoxic potential of NK cells is relatively high. In several embodiments, it is unexpectedly beneficial that the engineered cells disclosed herein can further upregulate the cytotoxic activity of NK cells, leading to an even more effective activity against target cells (e.g., tumor or other diseased cells). Some embodiments of the methods and compositions described herein relate to NK cells engineered to express a CAR that targets a tumor marker, for example, CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, and optionally includes a membrane-bound interleukin 15 (mbIL15) domain. Several embodiments of the methods and compositions disclosed herein relate to NK cells engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally a membrane-bound interleukin 15 (mbIL15) domain. In several embodiments, immortalized NK cells are used and are subject to gene editing and/or engineering, as disclosed herein. In some embodiments, the NK cells are derived from cell line NK-92. NK-92 cells are derived from NK cells, but lack major inhibitory receptors displayed by normal NK cells, while retaining the majority of activating receptors. Some embodiments of NK-92 cells described herein related to NK-92 cell engineered to silence certain additional inhibitory receptors, for example, SMAD3, allowing for upregulation of interferon-γ (IFNγ), granzyme B, and/or perforin production. Additional information relating to the NK-92 cell line is disclosed in WO 1998/49268 and U.S. Patent Application Publication No. 2002/0068044 and incorporated in their entireties herein by reference. NK-92 cells are used, in several embodiments, in combination with one or more of the other cell types disclosed herein. For example, in one embodiment, NK-92 cells are used in combination with NK cells as disclosed herein. In an additional embodiment, NK-92 cells are used in combination with T cells as disclosed herein.

[00157] In several embodiments, genetic manipulation of NK cells is employed to further enhance the efficacy and/or persistence of the NK cells. For example, in several embodiments, expression of various

markers/proteins is reduced, substantially reduced, or knocked out (eliminated) through gene editing techniques. Depending on the embodiment, this may include gene editing to reduce expression of one or more of a cytokine-inducible SH2-containing protein encoded by a CISH gene, a transforming growth factor beta receptor (e.g., TGFBR2), a Natural Killer Group 2, member A (NKG2A) receptor, a Cbl proto-oncogene B protein encoded by a CBLB gene, a tripartite motif-containing protein 29 protein encoded by a TRIM29 gene, a suppressor of cytokine signaling 2 protein encoded by a SOCS2 gene, a mothers against decapentaplegic homolog 3 (SMAD3) protein encoded by a SMAD3 gene, a MAP kinase-activated protein kinase 3 (MAPKAPK3) protein encoded by a MAPKAPK3 gene, a carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1) protein encoded by a CEACAM1 gene, and/or a DNA-damage-inducible transcript 4 (DDIT4) protein encoded by a DDIT4 gene. In several embodiments, reduced expression is accomplished through targeted introduction of DNA breakage, and subsequent DNA repair mechanism. In several embodiments, double strand breaks of DNA are repaired by non-homologous end joining (NHEJ), wherein enzymes are used to directly join the DNA ends to one another to repair the break. In several embodiments, however, double strand breaks are repaired by homology directed repair (HDR), which is advantageously more accurate, thereby allowing sequence specific breaks and repair. HDR uses a homologous sequence as a template for regeneration of missing DNA sequences at the break point, such as a vector with the desired genetic elements (e.g., an insertion element to disrupt the coding sequence of the target protein, such as CD70 and/or CISH) within a sequence that is homologous to the flanking sequences of a double strand break. This will result in the desired change (e.g., insertion) being inserted at the site of the DSB.

[00158] In several embodiments, gene editing is accomplished by one or more of a variety of engineered nucleases. In several embodiments, restriction enzymes are used, particularly when double strand breaks are desired at multiple regions. In several embodiments, a bioengineered nuclease is used. Depending on the embodiment, one or more of a Zinc Finger Nuclease (ZFN), transcription-activator like effector nuclease (TALEN), meganuclease and/or clustered regularly interspaced short palindromic repeats (CRISPR/Cas9) system are used to specifically edit the genes encoding one or more target proteins, such as CD70 and/or CISH.

[00159] Meganucleases are characterized by their capacity to recognize and cut large DNA sequences (from 14 to 40 base pairs). In several embodiments, a meganuclease from the LAGLIDADG family is used, and is subjected to mutagenesis and screening to generate a meganuclease variant that recognizes a unique sequence(s), such as a specific site in a gene encoding a target protein of interest. In several embodiments, two or more meganucleases, or functions fragments thereof, are fused to create a hybrid enzymes that recognize a desired target sequence within the gene encoding a target protein of interest, such as CD70 and/or CISH.

[00160] In contrast to meganucleases, ZFNs and TALEN function based on a non-specific DNA cutting catalytic domain which is linked to specific DNA sequence recognizing peptides such as zinc fingers or transcription activator-like effectors (TALEs). Advantageously, the ZFNs and TALENs thus allow

sequence-independent cleavage of DNA, with a high degree of sequence-specificity in target recognition. Zinc finger motifs naturally function in transcription factors to recognize specific DNA sequences for transcription. The C-terminal part of each finger is responsible for the specific recognition of the DNA sequence. While the sequences recognized by ZFNs are relatively short, (e.g., ~3 base pairs), in several embodiments, combinations of 2, 3, 4, 5, 6, 7, 8, 9, 10 or more zinc fingers whose recognition sites have been characterized are used, thereby allowing targeting of specific sequences, such as a portion of the gene encoding a target protein normally expressed by NK cells, such as CD70 and/or CISH. The combined ZFNs are then fused with the catalytic domain(s) of an endonuclease, such as FokI (optionally a FokI heterodimer), in order to induce a targeted DNA break. Additional information on uses of ZFNs to edit a target gene of interest, such as CD70 or CISH can be found in US Patent No. 9,597,357, which is incorporated by reference herein.

[00161] Transcription activator-like effector nucleases (TALENs) are specific DNA-binding proteins that feature an array of 33 or 34-amino acid repeats. Like ZFNs, TALENs are a fusion of a DNA cutting domain of a nuclease to TALE domains, which allow for sequence-independent introduction of double stranded DNA breaks with highly precise target site recognition. TALENs can create double strand breaks at the target site that can be repaired by error-prone non-homologous end-joining (NHEJ), resulting in gene disruptions through the introduction of small insertions or deletions. Advantageously, TALENs are used in several embodiments, at least in part due to their higher specificity in DNA binding, reduced off-target effects, and ease in construction of the DNA-binding domain.

[00162] CRISPRs (Clustered Regularly Interspaced Short Palindromic Repeats) are genetic elements that bacteria use as protection against viruses. The repeats are short sequences that originate from viral genomes and have been incorporated into the bacterial genome. Cas (CRISPR associated proteins) process these sequences and cut matching viral DNA sequences. By introducing plasmids containing Cas genes and specifically constructed CRISPRs into eukaryotic cells, the eukaryotic genome can be cut at any desired position. Additional information on CRISPR can be found in US Patent Publication No. 2014/0068797, which is incorporated by reference herein. In several embodiments, CRISPR is used to manipulate the genes encoding on or more of the TCRs of a T cell and/or the genes encoding one or more immune checkpoint inhibitors. In several embodiments, the immune checkpoint inhibitor is selected from one or more of CTLA4 and PD1. In several embodiments, native CD70 expression by NK cells is disrupted or substantially eliminated by targeting the CD70 encoding gene with a CRISPR/Cas system. In several embodiments, one or more additional target proteins, normally expressed by an NK cells is disrupted or substantially eliminated by targeting the corresponding encoding gene with a CRISPR/Cas system. Depending on the embodiment, one or more of a cytokine-inducible SH2-containing protein encoded by a CISH gene, a transforming growth factor beta receptor (e.g., TGFBR2), a Natural Killer Group 2, member A (NKG2A) receptor, a Cbl proto-oncogene B protein encoded by a CBLB gene, a tripartite motif-containing protein 29 protein encoded by a TRIM29 gene, a suppressor of cytokine signaling 2 protein encoded by a SOCS2 gene, a SMAD3 protein encoded by a SMAD3 gene, a MAPKAPK3 protein

encoded by a MAPKAPK3 gene, a CEACAM1 protein encoded by a CEACAM1 gene, and/or a DDIT4 protein encoded by a DDIT4 gene is targeted with a CRISPR/Cas system. Depending on the embodiment, a Class 1 or Class 2 Cas is used. In several embodiments, a Class 1 Cas is used, and the Cas type is selected from the following types: I, IA, IB, IC, ID, IE, IF, IU, III, IIIA, IIIB, IIIC, IIID, IV IVA, IVB, and combinations thereof. In several embodiments, the Cas is selected from the group consisting of Cas3, Cas8a, Cas5, Cas8b, Cas8c, Cas10d, Cse1, Cse2, Csy1, Csy2, Csy3, GSU0054, Cas10, Csm2, Cmr5, Cas10, Csx11, Csx10, Csf1, and combinations thereof. In several embodiments, a Class 2 Cas is used, and the Cas type is selected from the following types: II, IIA, IIB, IIC, V, VI, and combinations thereof. In several embodiments, the Cas is selected from the group consisting of Cas9, Csn2, Cas4, Cpf1, C2c1, C2c3, Cas13a (previously known as C2c2), Cas13b, Cas13c, CasX, CasY and combinations thereof. In some embodiments, class 2 CasX is used, wherein CasX is capable of forming a complex with a guide nucleic acid and wherein the complex can bind to a target DNA, and wherein the target DNA comprises a non-target strand and a target strand. In some embodiments, class 2 CasY is used, wherein CasY is capable of binding and modifying a target nucleic acid and/or a polypeptide associated with target nucleic acid.

[00163] .

Hematopoietic Stem Cells for Cancer Immunotherapy

[00164] In some embodiments, hematopoietic stem cells (HSCs) are used in the methods of immunotherapy disclosed herein. In several embodiments, the cells are engineered to express a homing moiety and/or a cytotoxic receptor complex. HSCs are used, in several embodiments, to leverage their ability to engraft for long-term blood cell production, which could result in a sustained source of targeted anti-cancer effector cells, for example to combat cancer remissions. In several embodiments, this ongoing production helps to offset anergy or exhaustion of other cell types, for example due to the tumor microenvironment. In several embodiments allogeneic HSCs are used, while in some embodiments, autologous HSCs are used. In several embodiments, HSCs are used in combination with one or more additional engineered cell type disclosed herein. Some embodiments of the methods and compositions described herein relate to a stem cell, such as a hematopoietic stem cell engineered to express a CAR that targets a tumor marker, for example, CD70, CD19, CD123, CD70, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others, and optionally includes a membrane-bound interleukin 15 (mbIL15) domain. Several embodiments of the methods and compositions disclosed herein relate to hematopoietic stem cells engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally includes a membrane-bound interleukin 15 (mbIL15) domain.

Induced Pluripotent Stem Cells

[00165] In some embodiments, induced pluripotent stem cells (iPSCs) are used in the method of immunotherapy disclosed herein. iPSCs are used, in several embodiments, to leverage their ability to

differentiate and derive into non-pluripotent cells, including, but not limited to, CD34 cells, hemogenic endothelium cells, HSCs (hematopoietic stem and progenitor cells), hematopoietic multipotent progenitor cells, T cell progenitors, NK cell progenitors, T cells, NKT cells, NK cells, and B cells comprising one or several genetic modifications at selected sites through differentiating iPSCs or less differentiated cells comprising the same genetic modifications at the same selected sites. In several embodiments, the iPSCs are used to generate iPSC-derived NK or T cells. In several embodiments, the cells are engineered to express a homing moiety and/or a cytotoxic receptor complex. In several embodiments, iPSCs are used in combination with one or more additional engineered cell type disclosed herein. Some embodiments of the methods and compositions described herein relate to a stem cell, such as a induced pluripotent stem cell engineered to express a CAR that targets a tumor marker, for example, CD19, CD123, CD70, Her2, mesothelin, Claudin 6, BCMA, EGFR, among any of the others disclosed herein, and optionally a membrane-bound interleukin 15 (mbIL15) co-stimulatory domain. Several embodiments of the methods and compositions disclosed herein relate to induced pluripotent stem cells engineered to express an activating chimeric receptor that targets a ligand on a tumor cell, for example, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others) and optionally a membrane-bound interleukin 15 (mbIL15) co-stimulatory domain.

Genetic Engineering of Immune Cells

[00166] As discussed above, a variety of cell types can be utilized in cellular immunotherapy. Further, as elaborated on in more detail below, and shown in the Examples, genetic modifications can be made to these cells in order to enhance one or more aspects of their efficacy (e.g., cytotoxicity) and/or persistence (e.g., active life span). As discussed herein, in several embodiments NK cells are used for immunotherapy. In several embodiments provided for herein, gene editing of an NK cells imparts to the cell various beneficial characteristics such as, for example, enhanced proliferation, enhanced cytotoxicity, and/or enhanced persistence. In several embodiments provided for herein, gene editing of the NK cell can advantageously impart to the edited NK cell the ability to resist and/or overcome various inhibitory signals that are generated in the tumor microenvironment. It is known that tumors generate a variety of signaling molecules that are intended to reduce the anti-tumor effects of immune cells. As discussed in more detail below, in several embodiments, gene editing of the NK cell limits this tumor microenvironment suppressive effect on the NK cells, T cells, combinations of NK and T cells, or any edited/engineered immune cell provided for herein.

[00167] As discussed below, in several embodiments, gene editing is employed to reduce or knockout expression of target proteins, for example by disrupting the underlying gene encoding the protein. In several embodiments, gene editing can reduce expression of a target protein by about 30%, about 40%, about 50%, about 60%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 98%, about 99%, or more (including any amount between those listed). In several embodiments, the gene is completely knocked out, such that expression of the target protein is

undetectable. In several embodiments, gene editing is used to "knock in" or otherwise enhance expression of a target protein. In several embodiments, expression of a target protein can be enhanced by about 30%, about 40%, about 50%, about 60%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, about 97%, about 98%, about 99%, or more (including any amount between those listed).

[00168] In accordance with additional embodiments, other modulators of one or more aspects of NK cell (or T cell) function are modulated through gene editing. A variety of cytokines impart either negative (as with TGF-beta above) or positive signals to immune cells. By way of non-limiting example, IL15 is a positive regulator of NK cells, which as disclosed herein, can enhance one or more of NK cell homing, NK cell migration, NK cell expansion/proliferation, NK cell cytotoxicity, and/or NK cell persistence. To keep NK cells in check under normal physiological circumstances, a cytokine-inducible SH2-containing protein (CIS, encoded by the CISH gene) acts as a critical negative regulator of IL-15 signaling in NK cells. As discussed herein, because IL15 biology impacts multiple aspects of NK cell functionality, including, but not limited to, proliferation/expansion, activation, cytotoxicity, persistence, homing, migration, among others. Thus, according to several embodiments, editing CISH enhances the functionality of NK cells across multiple functionalities, leading to a more effective and long-lasting NK cell therapeutic. In several embodiments, inhibitors of CIS are used in conjunction with engineered NK cell administration. In several embodiments, the CIS expression is knocked down or knocked out through gene editing of the CISH gene, for example, by use of CRISPR-Cas editing. Small interfering RNA, antisense RNA, TALENs or zinc fingers are used in other embodiments. In some embodiments CIS expression in T cells is knocked down through gene editing.

[00169] In several embodiments, CISH gene editing endows an NK cell with enhanced ability to home to a target site. In several embodiments, CISH gene editing endows an NK cell with enhanced ability to migrate, e.g., within a tissue in response to, for example chemoattractants or away from repellants. In several embodiments, CISH gene editing endows an NK cell with enhanced ability to be activated, and thus exert, for example, anti-tumor effects. In several embodiments, CISH gene editing endows an NK cell with enhanced proliferative ability, which in several embodiments, allows for generation of robust NK cell numbers from a donor blood sample. In addition, in such embodiments, NK cells edited for CISH and engineered to express a CAR are more readily, robustly, and consistently expanded in culture. In several embodiments, CISH gene editing endows an NK cell with enhanced cytotoxicity. In several embodiments, the editing of CISH synergistically enhances the cytotoxic effects of engineered NK cells and/or engineered T cells that express a CAR.

[00170] In several embodiments, CISH gene editing activates or inhibits a wide variety of pathways. The CIS protein is a negative regulator of IL15 signaling by way of, for example, inhibiting JAK-STAT signaling pathways. These pathways would typically lead to transcription of IL15-responsive genes (including CISH). In several embodiments, knockdown of CISH disinhibits JAK-STAT (e.g., JAK1-STAT5) signaling and there is enhanced transcription of IL15-responsive genes. In several embodiments, knockout of CISH yields enhanced signaling through mammalian target of rapamycin (mTOR), with corresponding increases in expression of genes related to cell metabolism and respiration. In several embodiments,

knockout of CISH yields IL15 induced increased expression of IL-2Rα (CD25), but not IL-15Rα or IL-2/15Rβ, enhanced NK cell membrane binding of IL15 and/or IL2, increased phosphorylation of STAT-3 and/or STAT-5, and elevated expression of the antiapoptotic proteins, such as Bcl-2. In several embodiments, CISH knockout results in IL15-induced upregulation of selected genes related to mitochondrial functions (e.g., electron transport chain and cellular respiration) and cell cycle. Thus, in several embodiments, knockout of CISH by gene editing enhances the NK cell cytotoxicity and/or persistence, at least in part via metabolic reprogramming. In several embodiments, negative regulators of cellular metabolism, such as TXNIP, are downregulated in response to CISH knockout. In several embodiments, promotors for cell survival and proliferation including BIRC5 (Survivin), TOP2A, CKS2, and RACGAP1 are upregulated after CISH knockout, whereas antiproliferative or proapoptotic proteins such as TGFB1, ATM, and PTCH1 are downregulated. In several embodiments, CISH knockout alters the state (e.g., activates or inactivates) signaling via or through one or more of CXCL-10, IL2, TNF, IFNg, IL13, IL4, Jnk, PRF1, STAT5, PRKCQ, IL2 receptor Beta, SOCS2, MYD88, STAT3, STAT1, TBX21, LCK, JAK3, IL& receptor, ABL1, IL9, STAT5A, STAT5B, Tcf7, PRDM1, and/or EOMES.

[00171] In several embodiments, gene editing of the immune cells can also provide unexpected enhancement in the expansion, persistence and/or cytotoxicity of the edited immune cell. As disclosed herein, engineered cells (e.g., those expressing a CAR) may also be edited, the combination of which provides for a robust cell for immunotherapy. In several embodiments, the edits allow for unexpectedly improved NK cell expansion, persistence and/or cytotoxicity. In several embodiments, knockout of CISH expression in NK cells removes a potent negative regulator of IL15-mediated signaling in NK cells, disinhibits the NK cells and allows for one or more of enhanced NK cell homing, NK cell migration, activation of NK cells, expansion, cytotoxicity and/or persistence. Additionally, in several embodiments, the editing can enhance NK and/or T cell function in the otherwise suppressive tumor microenvironment. In several embodiments, CISH gene editing results in enhanced NK cell expansion, persistence and/or cytotoxicity without requiring Notch ligand being provided exogenously.

[00172] By way of non-limiting example, TGF-beta is one such cytokine released by tumor cells that results in immune suppression within the tumor microenvironment. That immune suppression reduces the ability of immune cells, even engineered CAR-immune cells is some cases, to destroy the tumor cells, thus allowing for tumor progression. In several embodiments, as discussed in detail below, immune checkpoint inhibitors are disrupted through gene editing. In several embodiments, blockers of immune suppressing cytokines in the tumor microenvironment are used, including blockers of their release or competitive inhibitors that reduce the ability of the signaling molecule to bind and inhibit an immune cell. Such signaling molecules include, but are not limited to TGF-beta, IL10, arginase, inducible NOS, reactive-NOS, Arg1, Indoleamine 2,3-dioxygenase (IDO), and PGE_2. However, in additional embodiments, there are provided immune cells, such as NK cells, wherein the ability of the NK cell (or other cell) to respond to a given immunosuppressive signaling molecule is disrupted and/or eliminated. For example, in several embodiments, in several embodiments, NK cells or T cells are genetically edited to become have reduced

sensitivity to TGF-beta. TGF-beta is an inhibitor of NK cell function on at least the levels of proliferation and cytotoxicity. See, for example, Figure 8A which schematically shows some of the inhibitory pathways by which TGF-beta reduces NK cell activity and/or proliferation. Thus, according to some embodiments, the expression of the TGF-beta receptor is knocked down or knocked out through gene editing, such that the edited NK is resistant to the immunosuppressive effects of TGF-beta in the tumor microenvironment. In several embodiments, the TGFB2 receptor is knocked down or knocked out through gene editing, for example, by use of CRISPR-Cas editing. Small interfering RNA, antisense RNA, TALENs or zinc fingers are used in other embodiments. Other isoforms of the TGF-beta receptor (e.g., TGF-beta 1 and/or TGF-beta 3) are edited in some embodiments. In some embodiments TGF-beta receptors in T cells are knocked down through gene editing.

Extracellular domains (Tumor binder)

[00173] Some embodiments of the compositions and methods described herein relate to a chimeric antigen receptor that includes an extracellular domain that comprises a tumor-binding domain (also referred to as an antigen-binding protein or antigen-binding domain) as described herein. The tumor binding domain, depending on the embodiment, targets, for example CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, among others. Several embodiments of the compositions and methods described herein relate to a chimeric receptor that includes an extracellular domain that comprises a ligand binding domain that binds a ligand expressed by a tumor cell (also referred to as an activating chimeric receptor) as described herein. The ligand binding domain, depending on the embodiment, targets for example MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6 (among others).

[00174] In some embodiments, the antigen-binding domain is derived from or comprises wild-type or non-wild-type sequence of an antibody, an antibody fragment, an scFv, a Fv, a Fab, a (Fab')2, a single domain antibody (SDAB), a vH or vL domain, a camelid VHH domain, or a non-immunoglobulin scaffold such as a DARPIN, an affibody, an affilin, an adnectin, an affitin, a repebody, a fynomer, an alphabody, an avimer, an atrimer, a centyrin, a pronectin, an anticalin, a kunitz domain, an Armadillo repeat protein, an autoantigen, a receptor or a ligand. In some embodiments, the tumor-binding domain contains more than one antigen binding domain.

Antigen-Binding Proteins

[00175] There are provided, in several embodiments, antigen-binding proteins. As used herein, the term "antigen-binding protein" shall be given its ordinary meaning, and shall also refer to a protein comprising an antigen-binding fragment that binds to an antigen and, optionally, a scaffold or framework portion that allows the antigen-binding fragment to adopt a conformation that promotes binding of the antigen-binding protein to the antigen. In some embodiments, the antigen is a cancer antigen (e.g., CD70) or a fragment thereof. In some embodiments, the antigen-binding fragment comprises at least one CDR from an antibody that binds to the antigen. In some embodiments, the antigen-binding fragment comprises

all three CDRs from the heavy chain of an antibody that binds to the antigen or from the light chain of an antibody that binds to the antigen. In still some embodiments, the antigen-binding fragment comprises all six CDRs from an antibody that binds to the antigen (three from the heavy chain and three from the light chain). In several embodiments, the antigen-binding fragment comprises one, two, three, four, five, or six CDRs from an antibody that binds to the antigen, and in several embodiments, the CDRs can be any combination of heavy and/or light chain CDRs. The antigen-binding fragment in some embodiments is an antibody fragment.

[00176] Non-limiting examples of antigen-binding proteins include antibodies, antibody fragments (e.g., an antigen-binding fragment of an antibody), antibody derivatives, and antibody analogs. Further specific examples include, but are not limited to, a single-chain variable fragment (scFv), a nanobody (e.g. VH domain of camelid heavy chain antibodies; VHH fragment,), a Fab fragment, a Fab' fragment, a F(ab')2 fragment, a Fv fragment, a Fd fragment, and a complementarity determining region (CDR) fragment. These molecules can be derived from any mammalian source, such as human, mouse, rat, rabbit, or pig, dog, or camelid. Antibody fragments may compete for binding of a target antigen with an intact (e.g., native) antibody and the fragments may be produced by the modification of intact antibodies (e.g. enzymatic or chemical cleavage) or synthesized de novo using recombinant DNA technologies or peptide synthesis. The antigen-binding protein can comprise, for example, an alternative protein scaffold or artificial scaffold with grafted CDRs or CDR derivatives. Such scaffolds include, but are not limited to, antibody-derived scaffolds comprising mutations introduced to, for example, stabilize the three-dimensional structure of the antigen-binding protein as well as wholly synthetic scaffolds comprising, for example, a biocompatible polymer. In addition, peptide antibody mimetics ("PAMs") can be used, as well as scaffolds based on antibody mimetics utilizing fibronectin components as a scaffold.

[00177] In some embodiments, the antigen-binding protein comprises one or more antibody fragments incorporated into a single polypeptide chain or into multiple polypeptide chains. For instance, antigen-binding proteins can include, but are not limited to, a diabody; an intrabody; a domain antibody (single VL or VH domain or two or more VH domains joined by a peptide linker;); a maxibody (2 scFvs fused to Fc region); a triabody; a tetrabody; a minibody (scFv fused to CH3 domain); a peptibody (one or more peptides attached to an Fc region); a linear antibody (a pair of tandem Fd segments (VH-CH1-VH-CH1) which, together with complementary light chain polypeptides, form a pair of antigen binding regions); a small modular immunopharmaceutical; and immunoglobulin fusion proteins (e.g. IgG-scFv, IgG-Fab, 2scFv-IgG, 4scFv-IgG, VH-IgG, IgG-VH, and Fab-scFv-Fc).

[00178] In some embodiments, the antigen-binding protein has the structure of an immunoglobulin. As used herein, the term "immunoglobulin" shall be given its ordinary meaning, and shall also refer to a tetrameric molecule, with each tetramer comprising two identical pairs of polypeptide chains, each pair having one "light" (about 25 kDa) and one "heavy" chain (about 50-70 kDa). The amino-terminal portion of each chain includes a variable region of about 100 to 110 or more amino acids primarily responsible for

antigen recognition. The carboxy-terminal portion of each chain defines a constant region primarily responsible for effector function.

[00179] Within light and heavy chains, the variable (V) and constant regions (C) are joined by a "J" region of about 12 or more amino acids, with the heavy chain also including a "D" region of about 10 more amino acids. The variable regions of each light/heavy chain pair form the antibody binding site such that an intact immunoglobulin has two binding sites.

[00180] Immunoglobulin chains exhibit the same general structure of relatively conserved framework regions (FR) joined by three hypervariable regions, also called complementarity determining regions or CDRs. From N-terminus to C-terminus, both light and heavy chains comprise the domains FR1, CDR1, FR2, CDR2, FR3, CDR3 and FR4.

[00181] Human light chains are classified as kappa and lambda light chains. An antibody "light chain", refers to the smaller of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations. Kappa (K) and lambda (λ) light chains refer to the two major antibody light chain isotypes. A light chain may include a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin light chain variable region (VL) and a single immunoglobulin light chain constant domain (CL).

[00182] Heavy chains are classified as mu (μ), delta (Δ), gamma (γ), alpha (α), and epsilon (ε), and define the antibody's isotype as IgM, IgD, IgG, IgA, and IgE, respectively. An antibody "heavy chain" refers to the larger of the two types of polypeptide chains present in antibody molecules in their naturally occurring conformations, and which normally determines the class to which the antibody belongs. A heavy chain may include a polypeptide comprising, from amino terminus to carboxyl terminus, a single immunoglobulin heavy chain variable region (VH), an immunoglobulin heavy chain constant domain 1 (CH1), an immunoglobulin hinge region, an immunoglobulin heavy chain constant domain 2 (CH2), an immunoglobulin heavy chain constant domain 3 (CH3), and optionally an immunoglobulin heavy chain constant domain 4 (CH4).

[00183] The IgG-class is further divided into subclasses, namely, IgG1, IgG2, IgG3, and IgG4. The IgA-class is further divided into subclasses, namely IgA1 and IgA2. The IgM has subclasses including, but not limited to, IgM1 and IgM2. The heavy chains in IgG, IgA, and IgD antibodies have three domains (CH1, CH2, and CH3), whereas the heavy chains in IgM and IgE antibodies have four domains (CH1, CH2, CH3, and CH4). The immunoglobulin heavy chain constant domains can be from any immunoglobulin isotype, including subtypes. The antibody chains are linked together via inter-polypeptide disulfide bonds between the CL domain and the CH1 domain (e.g., between the light and heavy chain) and between the hinge regions of the antibody heavy chains.

[00184] In some embodiments, the antigen-binding protein is an antibody. The term "antibody", as used herein, refers to a protein, or polypeptide sequence derived from an immunoglobulin molecule which specifically binds with an antigen. Antibodies can be monoclonal, or polyclonal, multiple or single chain, or intact immunoglobulins, and may be derived from natural sources or from recombinant sources. Antibodies can be tetramers of immunoglobulin molecules. The antibody may be "humanized", "chimeric" or non-

human. An antibody may include an intact immunoglobulin of any isotype, and includes, for instance, chimeric, humanized, human, and bispecific antibodies. An intact antibody will generally comprise at least two full-length heavy chains and two full-length light chains. Antibody sequences can be derived solely from a single species, or can be "chimeric," that is, different portions of the antibody can be derived from two different species as described further below. Unless otherwise indicated, the term "antibody" also includes antibodies comprising two substantially full-length heavy chains and two substantially full-length light chains provided the antibodies retain the same or similar binding and/or function as the antibody comprised of two full length light and heavy chains. For example, antibodies having 1, 2, 3, 4, or 5 amino acid residue substitutions, insertions or deletions at the N-terminus and/or C-terminus of the heavy and/ or light chains are included in the definition provided that the antibodies retain the same or similar binding and/or function as the antibodies comprising two full length heavy chains and two full length light chains. Examples of antibodies include monoclonal antibodies, polyclonal antibodies, chimeric antibodies, humanized antibodies, human antibodies, bispecific antibodies, and synthetic antibodies. There is provided, in some embodiments, monoclonal and polyclonal antibodies. As used herein, the term "polyclonal antibody" shall be given its ordinary meaning, and shall also refer to a population of antibodies that are typically widely varied in composition and binding specificity. As used herein, the term "monoclonal antibody" ("mAb") shall be given its ordinary meaning, and shall also refer to one or more of a population of antibodies having identical sequences. Monoclonal antibodies bind to the antigen at a particular epitope on the antigen.

[00185] In some embodiments, the antigen-binding protein is a fragment or antigen-binding fragment of an antibody. The term "antibody fragment" refers to at least one portion of an antibody, that retains the ability to specifically interact with (e.g., by binding, steric hindrance, stabilizing/destabilizing, spatial distribution) an epitope of an antigen. Examples of antibody fragments include, but are not limited to, Fab, Fab', F(ab')2, Fv fragments, scFv antibody fragments, disulfide-linked Fvs (sdFv), a Fd fragment consisting of the VH and CHI domains, linear antibodies, single domain antibodies such as sdAb (either vL or vH), camelid vHH domains, multi-specific antibodies formed from antibody fragments such as a bivalent fragment comprising two Fab fragments linked by a disulfide bridge at the hinge region, and an isolated CDR or other epitope binding fragments of an antibody. An antigen binding fragment can also be incorporated into single domain antibodies, maxibodies, minibodies, nanobodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv (see, e.g., Hollinger and Hudson, Nature Biotechnology 23: 1126-1136, 2005). Antigen binding fragments can also be grafted into scaffolds based on polypeptides such as a fibronectin type III (Fn3)(see U.S. Patent No. 6,703,199, which describes fibronectin polypeptide mini bodies). An antibody fragment may include a Fab, Fab', F(ab')2, and/or Fv fragment that contains at least one CDR of an immunoglobulin that is sufficient to confer specific antigen binding to a cancer antigen (e.g., CD19). Antibody fragments may be produced by recombinant DNA techniques or by enzymatic or chemical cleavage of intact antibodies.

[00186] In some embodiments, Fab fragments are provided. A Fab fragment is a monovalent fragment having the VL, VH, CL and CH1 domains; a F(ab')2 fragment is a bivalent fragment having two

Fab fragments linked by a disulfide bridge at the hinge region; a Fd fragment has the VH and CH1 domains; an Fv fragment has the VL and VH domains of a single arm of an antibody; and a dAb fragment has a VH domain, a VL domain, or an antigen-binding fragment of a VH or VL domain. In some embodiments, these antibody fragments can be incorporated into single domain antibodies, single-chain antibodies, maxibodies, minibodies, intrabodies, diabodies, triabodies, tetrabodies, v-NAR and bis-scFv. In some embodiments, the antibodies comprise at least one CDR as described herein.

[00187] There is also provided for herein, in several embodiments, single-chain variable fragments. As used herein, the term "single-chain variable fragment" ("scFv") shall be given its ordinary meaning, and shall also refer to a fusion protein in which a VL and a VH region are joined via a linker (e.g., a synthetic sequence of amino acid residues) to form a continuous protein chain wherein the linker is long enough to allow the protein chain to fold back on itself and form a monovalent antigen binding site). For the sake of clarity, unless otherwise indicated as such, a "single-chain variable fragment" is not an antibody or an antibody fragment as defined herein. Diabodies are bivalent antibodies comprising two polypeptide chains, wherein each polypeptide chain comprises VH and VL domains joined by a linker that is configured to reduce or not allow for pairing between two domains on the same chain, thus allowing each domain to pair with a complementary domain on another polypeptide chain. According to several embodiments, if the two polypeptide chains of a diabody are identical, then a diabody resulting from their pairing will have two identical antigen binding sites. Polypeptide chains having different sequences can be used to make a diabody with two different antigen binding sites. Similarly, tribodies and tetrabodies are antibodies comprising three and four polypeptide chains, respectively, and forming three and four antigen binding sites, respectively, which can be the same or different.

[00188] In several embodiments, the antigen-binding protein comprises one or more CDRs. As used herein, the term "CDR" shall be given its ordinary meaning, and shall also refer to the complementarity determining region (also termed "minimal recognition units" or "hypervariable region") within antibody variable sequences. The CDRs permit the antigen-binding protein to specifically bind to a particular antigen of interest. There are three heavy chain variable region CDRs (CDR-H1, CDR-H2 and CDR-H3) and three light chain variable region CDRs (CDR-L1, CDR-L2 and CDR-L3). The CDRs in each of the two chains typically are aligned by the framework regions to form a structure that binds specifically to a specific epitope or domain on the target protein. From N-terminus to C-terminus, naturally-occurring light and heavy chain variable regions both typically conform to the following order of these elements: FW1, CDR1, FW2, CDR2, FW3, CDR3, FW4. For heavy chain variable regions, the order is typically: FW-H1, CDR-H1, FW-H2, CDR-H2, FW-H3, CDR-H3, and FW-H4 from N-terminus to C-terminus. For light chain variable regions, the order is typically: FW-L1, CDR-L1, FW-L2, CDR-L2, FW-L3, CDR-L3, FW-L4 from N-terminus to C-terminus. A numbering system has been devised for assigning numbers to amino acids that occupy positions in each of these domains. This numbering system is defined in Kabat Sequences of Proteins of Immunological Interest (1987 and 1991, NIH, Bethesda, MD), or Chothia & Lesk, 1987, J. Mol. Biol. 196:901-917; Chothia et al., 1989, Nature 342:878-883. Complementarity determining regions (CDRs) and framework regions

(FR) of a given antibody may be identified using this system. Other numbering systems for the amino acids in immunoglobulin chains include IMGT® (the international ImMunoGeneTics information system; Lefranc et al, Dev. Comp. Immunol. 29:185-203; 2005) and AHo (Honegger and Pluckthun, J. Mol. Biol. 309(3):657-670; 2001). The binding domains disclosed herein may utilize CDRs defined according to any of these systems. For any given embodiment containing more than one CDR, the CDRs may be defined in accordance with any of Kabat, Chothia, extended, IMGT, Paratome, AbM, and/or conformational definitions, or a combination of any of the foregoing. Any of the CDRs, either separately or within the context of variable domains, can be interpreted by one of skill in the art under any of these numbering systems as appropriate. One or more CDRs may be incorporated into a molecule either covalently or noncovalently to make it an antigen-binding protein.

[00189] In some embodiments, the antigen-binding proteins provided herein comprise one or more CDR(s) as part of a larger polypeptide chain. In some embodiments, the antigen-binding proteins covalently link the one or more CDR(s) to another polypeptide chain. In some embodiments, the antigen-binding proteins incorporate the one or more CDR(s) noncovalently. In some embodiments, the antigen-binding proteins may comprise at least one of the CDRs described herein incorporated into a biocompatible framework structure. In some embodiments, the biocompatible framework structure comprises a polypeptide or portion thereof that is sufficient to form a conformationally stable structural support, or framework, or scaffold, which is able to display one or more sequences of amino acids that bind to an antigen (e.g., CDRs, a variable region, etc.) in a localized surface region. Such structures can be a naturally occurring polypeptide or polypeptide "fold" (a structural motif), or can have one or more modifications, such as additions, deletions and/or substitutions of amino acids, relative to a naturally occurring polypeptide or fold. Depending on the embodiment, the scaffolds can be derived from a polypeptide of a variety of different species (or of more than one species), such as a human, a non-human primate or other mammal, other vertebrate, invertebrate, plant, bacteria or virus.

[00190] The term "consensus sequence" as used herein with regard to sequences refers to the generalized sequence representing all of the different combinations of permissible amino acids at each location of a group of sequences. A consensus sequence may provide insight into the conserved regions of related sequences where the unit (e.g. amino acid or nucleotide) is the same in most or all of the sequences, and regions that exhibit divergence between sequences. In the case of antibodies, the consensus sequence of a CDR may indicate amino acids that are important or dispensable for antigen binding. It is envisioned that consensus sequences may be prepared with any of the sequences provided herein, and the resultant various sequences derived from the consensus sequence can be validated to have similar effects as the template sequences.

[00191] In some embodiments, the antibody or binding fragment thereof comprises a combination of a CDR-H1, CDR-H2, CDR-H3, CDR-L1, CDR-L2, and a CDR-L3 where one or more of these CDRs is defined by a consensus sequence. The consensus sequences provided herein have been derived from the alignments of CDRs provided for herein. However, it is envisioned that alternative alignments may be done

(e.g. using global or local alignment, or with different algorithms, such as Hidden Markov Models, seeded guide trees, Needleman-Wunsch algorithm, or Smith-Waterman algorithm) and as such, alternative consensus sequences can be derived.

[00192] In some embodiments, the CDR-H1 is defined by the formula $X_1TFX_4X_5X_6X_7X_8X_9$ (SEQ ID NO: 1202), where X_1 is G or Y; X_4 is R or T; X_5 is D, E, N, or S; X_6 is N or Y; X_7 is A, D, E, G, or Y; X_8 is I, L, or M; and X_9 is H, N, or S. In some embodiments, the CDR-H1 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H1 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00193] In some embodiments, the CDR-H2 is defined by the formula $GX_2X_3X_4X_5X_6X_7GX_9X_{10}X_{11}YA$ (SEQ ID NO: 1203), where X_2 is G, I, V, or W; X_3 is I or M; X_4 is I, N, or S; X_5 is A or P; X_6 is I, N, S, or Y; X_7 is F, G, N, or S; X_9 is A, D, G, H, N, S or T; X_{10} is A or T; and X_{11} or G, I, N, or S. In some embodiments, the CDR-H2 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H2 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00194] In some embodiments, the CDR-H3 is defined by the formula $CAX_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}W$ (SEQ ID NO: 1204), where X_1 is C; X_2 is A; X_3 is G, K, or R; X_4 is D, E, G, S, or Y; X_5 is F, H, I, M, P, R, S, W, or Y; X_6 is G, S, or V; X_7 is no amino acid, A, D, G, or V; X_8 is no amino acid, A, G, N, W, or Y; X_9 is no amino acid, A, P, T, or Y; X_{10} is no amino acid, A, E, G, H, R, or Y; X_{11} is no amino acid, A, D, G, H, or S; X_{12} is no amino acid, D, F, G, or W; X_{13} is no amino acid, A, D, E, G, V, or Y; X_{14} is no amino acid, F, M, or Y; X_{15} is no amino acid or Y; X_{16} is no amino acid or Y; X_{17} is no amino acid or G; X_{18} is no amino acid or M; X_{19} is D or G; and X_{20} is I, L, V, or Y. In some embodiments, the CDR-H3 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H3 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00195] In some embodiments, the CDR-L1 is defined by the formula $X_1ASQX_5X_6X_7X_8X_9LX_{11}$ (SEQ ID NO: 1205), where X_1 is Q or R; X_5 is D, G, S, or T; X_6 is I or V; X_7 is G, R, or S; X_8 is N, R, or S; X_9 is F, W, or Y; and X_{11} is A or N. In some embodiments, the CDR-L1 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-L1 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00196] In some embodiments, the CDR-L2 is defined by the formula $X_1X_2SX_4X_5X_6X_7$ (SEQ ID NO: 1206), where X_1 is A, D, or G; X_2 is A or T; X_4 is D, N, S, or T; X_5 is L or R; X_6 is A, E, or Q; and X_7 is A, N, S or T. In some embodiments, the CDR-L2 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100%

identity to this consensus sequence. In some embodiments, the CDR-L2 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00197] In some embodiments, the CDR-L3 is defined by the formula $CQQX_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 1207), where X_4 is A, S, or Y; X_5 is D, H, I, or Y; X_6 is N, S, or T; X_7 is A, F, P, S, or T; X_8 is L or P; X_9 is L, S, T, V, W, or Y; X_{10} is no amino acid, F, or T; and X_{11} is no amino acid or F. In some embodiments, the CDR-L3 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-L3 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00198] In some embodiments, the CDR-H1 is defined by the formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}$ (SEQ ID NO: 1208), where X_1 is F, G, N or Y; X_2 is I, R, S, T, or V; X_3 is F or L; X_4 is A, D, I, N, R, S, or T; X_5 is A, D, E, G, N, R, S, or T; X_6 is no amino acid H, S, or Y; X_7 is no amino acid, A, D, G, T, or V; X_8 is no amino acid D, F, I, or M; X_9 is H, N, Q, S, or Y; X_{10} is no amino acid, A, E, F, G, H, L, S, or Y; X_{11} is no amino acid, I, L, M, T, or V; and X_{12} is no amino acid, H, or Y. In some embodiments, the CDR-H1 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H1 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00199] In some embodiments, the CDR-H2 is defined by the formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}$ (SEQ ID NO: 1209), where X_1 is A, G, or S; X_2 is A, G, I, M, R, S, T, V, or W; X_3 is no amino acid, F, I, M, or V; X_4 is D, I, N, S, or T; X_5 is A, K, P, S, or T; X_6 is D, G, H, I, M, N, R, S, T, or Y; X_7 is A, D, F, G, N, S, or T; X_8 is A, or G; X_9 is A, D, G, H, I, K, N, R, S, T, V, or Y; X_{10} is A, E, N, P, S, or T; X_{11} is A, D, G, H, I, K, L, N, Q, S, T, or Y; X_{12} is F, N, or Y; X_{13} is A or Y; and X_{14} is no amino acid, A, or V. In some embodiments, the CDR-H2 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H2 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00200] In some embodiments, the CDR-H3 is defined by the formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}X_{18}X_{19}X_{20}X_{21}X_{22}X_{23}X_{24}X_{25}X_{26}X_{27}W$ (SEQ ID NO: 1210), where X_1 is no amino acid or C; X_2 is no amino acid, A, or C; X_3 is no amino acid, A, C, K, or V; X_4 is no amino acid, A, D, G, K, M, R, S, or W; X_5 is no amino acid, A, D, E, G, H, T, or V; X_6 is no amino acid, C, D, E, F, G, H, L, M, N, P, Q, R, S, T, V, or Y; X_7 is no amino acid, A, D, E, G, I, L, M, N, Q, R, S, V, or Y; X_8 is no amino acid, A, F, I, L, P, R, T, V, W, or Y; X_9 is no amino acid, D, E, or Y; X_{10} is no amino acid, G, S, V, or Y; X_{11} is no amino acid, E, G, I, or S; X_{12} is no amino acid or G; X_{13} is no amino acid, L, or T; X_{14} is no amino acid, D, L, or T; X_{15} is no amino acid, A, C, D, G, H, or P; X_{16} is no amino acid, A, C, F, G, L, M, or Y; X_{17} is no amino acid, A, C, D, E, G, K, N, R, S, T, or V; X_{18} is no amino acid, A, C, D, E, G, I, L, N, P, R, S, T, V, W, or Y; X_{19} is no amino acid, A, D, E, F, G, H, K, L, N, Q, R, S, T, W, or Y; X_{20} is no amino acid,

A, C, D, E, G, I, M, P, Q, S, T, V, W, or Y; X_{21} is no amino acid, A, D, E, F, G, H, L, Q, S, V, W, or Y; X_{22} is no amino acid, A, D, E, F, G, H, I, L, M, N, P, Q, S, T, W, or Y; X_{23} is no amino acid, A, D, E, G, H, L, P, S, T, V, W, or Y; X_{24} is no amino acid, A, D, E, F, G, I, L, Q, S, T, V, W, or Y; X_{25} is no amino acid, A, F, I, L, M, S, V, or Y; X_{26} is no amino acid, D, G, L, or V; and X_{27} is I, L, N, P, V, or Y. In some embodiments, the CDR-H3 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-H3 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00201] In some embodiments, the CDR-L1 is defined by the formula $X_1X_2SX_4X_5X_6X_7X_8X_9X_{10}X_{11}X_{12}X_{13}X_{14}X_{15}X_{16}X_{17}$ (SEQ ID NO: 1211), where X_1 is K, Q, or R; X_2 is A, S, or T; X_4 is E, H, Q, S, or T; X_5 is no amino acid or S; X_6 is no amino acid, L, or V; X_7 is no amino acid or L; X_8 is no amino acid, H, or Y; X_9 is no amino acid or S; X_{10} is no amino acid or S; X_{11} is D, E, G, N, R, S, or T; X_{12} is G, I, N, or V; X_{13} is D, G, K, N, R, S, T, or Y; X_{14} is D, G, H, I, K, N, R, S, or T; X_{15} is D, F, G, N, S, W, or Y; X_{16} is L or V; and X_{17} is A, D, G, H, or N. In some embodiments, the CDR-L1 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-L1 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00202] In some embodiments, the CDR-L2 is defined by the formula $X_1X_2X_3X_4X_5X_6X_7$ (SEQ ID NO: 1212), where X_1 is A, D, E, G, H, L, Q, S, W, or Y; X_2 is A, G, T, or V; X_3 is S or T; X_4 is D, N, S, T, or Y; X_5 is L or R; X_6 is A, D, E, H, or Q; and X_7 is A, G, I, N, R, S, or T. In some embodiments, the CDR-L2 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-L2 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00203] In some embodiments, the CDR-L3 is defined by the formula $X_1X_2X_3X_4X_5X_6X_7X_8X_9X_{10}X_{11}$ (SEQ ID NO: 1213), where X_1 is C or L; X_2 is L, M, Q, or S; X_3 is K, Q, or T; X_4 is A, D, G, N, S, T, or Y; X_5 is A, D, F, H, I, L, N, R, T, or Y; X_6 is A, D, E, G, H, I, N, Q, R, S, or T; X_7 is A, F, G, I, P, S, T, W, or Y; X_8 is L, P, or T; X_9 is A, F, I, L, M, P, S, T, V, W, or Y; X_{10} is no amino acid, A, F, H, R, S, or T; and X_{11} is no amino acid or F. In some embodiments, the CDR-L3 comprises a sequence having at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% identity to this consensus sequence. In some embodiments, the CDR-L3 comprises a sequence having 0, 1, 2, 3, 4, 5, or 6 substitutions from this consensus sequence.

[00204] Depending on the embodiment, the biocompatible framework structures are based on protein scaffolds or skeletons other than immunoglobulin domains. In some such embodiments, those framework structures are based on fibronectin, ankyrin, lipocalin, neocarzinostain, cytochrome b, CP1 zinc finger, PST1, coiled coil, LACI-D1, Z domain and/or tendamistat domains.

[00205] There is also provided, in some embodiments, antigen-binding proteins with more than one binding site. In several embodiments, the binding sites are identical to one another while in some embodiments the binding sites are different from one another. For example, an antibody typically has two identical binding sites, while a "bispecific" or "bifunctional" antibody has two different binding sites. The two binding sites of a bispecific antigen-binding protein or antibody will bind to two different epitopes, which can reside on the same or different protein targets. In several embodiments, this is particularly advantageous, as a bispecific chimeric antigen receptor can impart to an engineered cell the ability to target multiple tumor markers. For example, CD70 and an additional tumor marker, such as CD123, CD19, Her2, mesothelin, Claudin 6, BCMA, EGFR, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6, among others, or any other marker disclosed herein or appreciated in the art as a tumor specific antigen or tumor associated antigen can be bound by a bispecific antibody.

[00206] As used herein, the term "chimeric antibody" shall be given its ordinary meaning, and shall also refer to an antibody that contains one or more regions from one antibody and one or more regions from one or more other antibodies. In some embodiments, one or more of the CDRs are derived from an anti-cancer antigen antibody (e.g., CD70, CD19, CD123, Her2, mesothelin, PD-L1, Claudin 6, BCMA, EGFR, etc.) antibody. In several embodiments, all of the CDRs are derived from an anti-cancer antigen antibody (such as an anti-CD70 antibody). In some embodiments, the CDRs from more than one anti-cancer antigen antibodies are mixed and matched in a chimeric antibody. For instance, a chimeric antibody may comprise a CDR1 from the light chain of a first anti-cancer antigen antibody, a CDR2 and a CDR3 from the light chain of a second anti-cancer antigen antibody, and the CDRs from the heavy chain from a third anti-cancer antigen antibody. Further, the framework regions of antigen-binding proteins disclosed herein may be derived from one of the same anti-cancer antigen (e.g., CD70, CD123, CD19, Her2, mesothelin, Claudin 6, BCMA, EGFR, etc.) antibodies, from one or more different antibodies, such as a human antibody, or from a humanized antibody. In one example of a chimeric antibody, a portion of the heavy and/or light chain is identical with, homologous to, or derived from an antibody from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is/are identical with, homologous to, or derived from an antibody or antibodies from another species or belonging to another antibody class or subclass. Also provided herein are fragments of such antibodies that exhibit the desired biological activity. In some embodiments, the CARs disclosed herein comprise an anti-CD70 binding domain. In some embodiments, the anti-CD70 binding domain is an scFv. In several embodiments, the CARs disclosed herein comprise an scFv as the binder for the tumor antigen. In several embodiments, the scFv is encoded by a polynucleotide comprising a sequence that has at least about 85%, about 90%, about 95%, or more, sequence identity to one or more of SEQ ID NOs: 36-120, 221-229, 1038-1111, 1112-1185. In several embodiments, the scFv comprises an amino acid sequences that has at least about 85%, about 90%, about 95%, or more, sequence identity to one or more of SEQ ID NOs: 230-312, 890-963, and/or 964-1037.

Natural Killer Group Domains that Bind Tumor Ligands

[00207] In several embodiments, engineered immune cells such as NK cells are leveraged for their ability to recognize and destroy tumor cells. For example, an engineered NK cell may include a CD70-directed chimeric antigen receptor or a nucleic acid encoding said chimeric antigen receptor (or a CAR directed against, for example, one or more of CD123, CD19, Her2, mesothelin, Claudin 6, BCMA, EGFR, etc.). NK cells express both inhibitory and activating receptors on the cell surface. Inhibitory receptors bind self-molecules expressed on the surface of healthy cells (thus preventing immune responses against "self" cells), while the activating receptors bind ligands expressed on abnormal cells, such as tumor cells. When the balance between inhibitory and activating receptor activation is in favor of activating receptors, NK cell activation occurs and target (e.g., tumor) cells are lysed.

[00208] Natural killer Group 2 member D (NKG2D) is an NK cell activating receptor that recognizes a variety of ligands expressed on cells. The surface expression of various NKG2D ligands is generally low in healthy cells but is upregulated upon, for example, malignant transformation. Non-limiting examples of ligands recognized by NKG2D include, but are not limited to, MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and ULBP6, as well as other molecules expressed on target cells that control the cytolytic or cytotoxic function of NK cells. In several embodiments, T cells are engineered to express an extracellular domain to binds to one or more tumor ligands and activate the T cell. For example, in several embodiments, T cells are engineered to express an NKG2D receptor as the binder/activation moiety. In several embodiments, engineered cells as disclosed herein are engineered to express another member of the NKG2 family, e.g., NKG2A, NKG2C, and/or NKG2E. Combinations of such receptors are engineered in some embodiments. Moreover, in several embodiments, other receptors are expressed, such as the Killer-cell immunoglobulin-like receptors (KIRs).

[00209] In several embodiments, cells are engineered to express a cytotoxic receptor complex comprising a full length NKG2D as an extracellular component to recognize ligands on the surface of tumor cells (e.g., liver cells). In one embodiment, full length NKG2D has the nucleic acid sequence of SEQ ID NO: 27. In several embodiments, the full length NKG2D, or functional fragment thereof is human NKG2D. Additional information about chimeric receptors for use in the presently disclosed methods and compositions can be found in PCT Patent Publication No. WO/2018/183385, which is incorporated in its entirety by reference herein.

[00210] In several embodiments, cells are engineered to express a cytotoxic receptor complex comprising a functional fragment of NKG2D as an extracellular component to recognize ligands on the surface of tumor cells or other diseased cells. In one embodiment, the functional fragment of NKG2D has the nucleic acid sequence of SEQ ID NO: 25. In several embodiments, the fragment of NKG2D has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% sequence identity with full-length wild-type NKG2D. In several embodiments, the fragment may have one or more additional mutations from SEQ ID NO: 25, but retains, or in some embodiments, has enhanced, ligand-binding function. In several embodiments, the functional fragment of NKG2D comprises the amino acid sequence of SEQ ID

NO: 26. In several embodiments, the NKG2D fragment is provided as a dimer, trimer, or other concatemeric format, such embodiments providing enhanced ligand-binding activity. In several embodiments, the sequence encoding the NKG2D fragment is optionally fully or partially codon optimized. In one embodiment, a sequence encoding a codon optimized NKG2D fragment comprises the sequence of SEQ ID NO: 28. Advantageously, according to several embodiments, the functional fragment lacks its native transmembrane or intracellular domains but retains its ability to bind ligands of NKG2D as well as transduce activation signals upon ligand binding. A further advantage of such fragments is that expression of DAP10 to localize NKG2D to the cell membrane is not required. Thus, in several embodiments, the cytotoxic receptor complex encoded by the polypeptides disclosed herein does not comprise DAP10. In several embodiments, immune cells, such as NK or T cells (e.g., non-alloreactive T cells engineered according to embodiments disclosed herein), are engineered to express one or more chimeric receptors that target, for example CD70, CD19, CD123, Her2, mesothelin, Claudin 6, BCMA, EGFR, and an NKG2D ligand, such as MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and/or ULBP6. Such cells, in several embodiments, also co-express mbIL15.

[00211] In several embodiments, the cytotoxic receptor complexes are configured to dimerize. Dimerization may comprise homodimers or heterodimers, depending on the embodiment. In several embodiments, dimerization results in improved ligand recognition by the cytotoxic receptor complexes (and hence the NK cells expressing the receptor), resulting in a reduction in (or lack) of adverse toxic effects. In several embodiments, the cytotoxic receptor complexes employ internal dimers, or repeats of one or more component subunits. For example, in several embodiments, the cytotoxic receptor complexes may optionally comprise a first NKG2D extracellular domain coupled to a second NKG2D extracellular domain, and a transmembrane/signaling region (or a separate transmembrane region along with a separate signaling region).

[00212] In several embodiments, the various domains/subdomains are separated by a linker such as, a GS3 linker (SEQ ID NOs: 15 and 16, nucleotide and protein, respectively) is used (or a GSn linker). Other linkers used according to various embodiments disclosed herein include, but are not limited to those encoded by SEQ ID NOs: 17, 19, 21 or 23. In several embodiments, other linkers comprise the peptide sequence of one of SEQ ID NOs: 18, 20, 22, 24. This provides the potential to separate the various component parts of the receptor complex along the polynucleotide, which can enhance expression, stability, and/or functionality of the receptor complex.

Cytotoxic Signaling Complex

[00213] Some embodiments of the compositions and methods described herein relate to a chimeric receptor, such as a chimeric antigen receptor (e.g., a CAR directed to CD70) or a chimeric receptor directed against an NKG2D ligand, such as MICA, MICB, ULBP1, ULBP2, ULBP3, ULBP4, ULBP5, and/or ULBP6) that includes a cytotoxic signaling complex. As disclosed herein, according to several embodiments, the provided cytotoxic receptor complexes comprise one or more transmembrane and/or intracellular domains

that initiate cytotoxic signaling cascades upon the extracellular domain(s) binding to ligands on the surface of target cells.

[00214] In several embodiments, the cytotoxic signaling complex comprises at least one transmembrane domain, at least one co-stimulatory domain, and/or at least one signaling domain. In some embodiments, more than one component part makes up a given domain – e.g., a co-stimulatory domain may comprise two subdomains. Moreover, in some embodiments, a domain may serve multiple functions, for example, a transmembrane domain may also serve to provide signaling function.

Transmembrane Domains

[00215] Some embodiments of the compositions and methods described herein relate to chimeric receptors (e.g., tumor antigen-directed CARs and/or ligand-directed chimeric receptors) that comprise a transmembrane domain. Some embodiments include a transmembrane domain from NKG2D or another transmembrane protein. In several embodiments in which a transmembrane domain is employed, the portion of the transmembrane protein employed retains at least a portion of its normal transmembrane domain.

[00216] In several embodiments, however, the transmembrane domain comprises at least a portion of CD8, a transmembrane glycoprotein normally expressed on both T cells and NK cells. In several embodiments, the transmembrane domain comprises CD8α. In several embodiments, the transmembrane domain is referred to as a "hinge". In several embodiments, the "hinge" of CD8α has the nucleic acid sequence of SEQ ID NO: 1. In several embodiments, the CD8α hinge is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD8α having the sequence of SEQ ID NO: 1. In several embodiments, the "hinge" of CD8α comprises the amino acid sequence of SEQ ID NO: 2. In several embodiments, the CD8α can be truncated or modified, such that it has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the sequence of SEQ ID NO: 2.

[00217] In several embodiments, the transmembrane domain comprises a CD8α transmembrane region. In several embodiments, the CD8α transmembrane domain has the nucleic acid sequence of SEQ ID NO: 3. In several embodiments, the CD8α hinge is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD8α having the sequence of SEQ ID NO: 3. In several embodiments, the CD8α transmembrane domain comprises the amino acid sequence of SEQ ID NO: 4. In several embodiments, the CD8α hinge is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD8α having the sequence of SEQ ID NO: 4.

[00218] Taken together in several embodiments, the CD8 hinge/transmembrane complex is encoded by the nucleic acid sequence of SEQ ID NO: 13. In several embodiments, the CD8 hinge/transmembrane complex is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD8 hinge/transmembrane complex

having the sequence of SEQ ID NO: 13. In several embodiments, the CD8 hinge/transmembrane complex comprises the amino acid sequence of SEQ ID NO: 14. In several embodiments, the CD8 hinge/transmembrane complex hinge is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD8 hinge/transmembrane complex having the sequence of SEQ ID NO: 14.

[00219] In some embodiments, the transmembrane domain comprises a CD28 transmembrane domain or a fragment thereof. In several embodiments, the CD28 transmembrane domain comprises the amino acid sequence of SEQ ID NO: 30. In several embodiments, the CD28 transmembrane domain complex hinge is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD28 transmembrane domain having the sequence of SEQ ID NO: 30.

Co-stimulatory Domains

[00220] Some embodiments of the compositions and methods described herein relate to chimeric receptors (e.g., tumor antigen-directed CARs and/or tumor ligand-directed chimeric receptors) that comprise a co-stimulatory domain. In addition, the various the transmembrane domains and signaling domain (and the combination transmembrane/signaling domains), additional co-activating molecules can be provided, in several embodiments. These can be certain molecules that, for example, further enhance activity of the immune cells. Cytokines may be used in some embodiments. For example, certain interleukins, such as IL-2 and/or IL-15 as non-limiting examples, are used. In some embodiments, the immune cells for therapy are engineered to express such molecules as a secreted form. In additional embodiments, such co-stimulatory domains are engineered to be membrane bound, acting as autocrine stimulatory molecules (or even as paracrine stimulators to neighboring cells).

[00221] In several embodiments, the NK cells disclosed herein are engineered to express interleukin 15 (IL15, IL-15). In some embodiments, the IL15 is expressed from a separate cassette on the construct comprising any one of the CARs disclosed herein. In some embodiments, the IL15 is expressed in the same cassette as any one of the CARs disclosed herein, optionally separated by a cleavage site, for example, a proteolytic cleavage site or a T2A, P2A, E2A, or F2A self-cleaving peptide cleavage site. In some embodiments, the IL15 is a membrane-bound IL15 (mbIL15). In some embodiments, the mbIL15 comprises a native IL15 sequence, such as a human native IL15 sequence, and at least one transmembrane domain. In some embodiments, the native IL15 sequence is encoded by a sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 11. In some embodiments, the native IL15 sequence comprise a peptide sequence having at least 85%, at least 90%, at least 95% sequence identity to SEQ ID NO: 12. In some embodiments, the at least one transmembrane domain comprises a CD8 transmembrane domain. In some embodiments, the mbIL15 may comprise additional components, such as a leader sequence and/or a hinge sequence. In some embodiments, the leader sequence is a CD8 leader sequence. In some embodiments, the hinge sequence is a CD8 hinge sequence.

[00222] In some embodiments, the tumor antigen-directed CARs and/or tumor ligand-directed chimeric receptors are encoded by a polynucleotide that encodes for one or more cytosolic protease cleavage sites. Such sites are recognized and cleaved by a cytosolic protease, which can result in separation (and separate expression) of the various component parts of the receptor encoded by the polynucleotide. In some embodiments, the tumor antigen-directed CARs and/or tumor ligand-directed chimeric receptor are encoded by a polynucleotide that encodes for one or more self-cleaving peptides, for example a T2A cleavage site, a P2A cleavage site, an E2A cleavage site, and/or an F2A cleavage site. As a result, depending on the embodiment, the various constituent parts of an engineered cytotoxic receptor complex can be delivered to an NK cell or T cell in a single vector or by multiple vectors. Thus, as shown schematically, in the Figures, a construct can be encoded by a single polynucleotide, but also include a cleavage site, such that downstream elements of the constructs are expressed by the cells as a separate protein (as is the case in some embodiments with IL-15). In several embodiments, a T2A cleavage site is used. In several embodiments, a T2A cleavage site has the nucleic acid sequence of SEQ ID NO: 9. In several embodiments, T2A cleavage site can be truncated or modified, such that it has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the sequence of SEQ ID NO: 9. In several embodiments, the T2A cleavage site comprises the amino acid sequence of SEQ ID NO: 10. In several embodiments, the T2A cleavage site is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the T2A cleavage site having the sequence of SEQ ID NO: 10.

[00223] In several embodiments, NK cells are engineered to express membrane-bound interleukin 15 (mbIL15). In such embodiments, mbIL15 expression on the NK enhances the cytotoxic effects of the engineered NK cell by enhancing the proliferation and/or longevity of the NK cells. In several embodiments, the mbIL15 is encoded by the same polynucleotide as the CAR. In some embodiments, mbIL15 is encoded by a polynucleotide comprising the sequence of SEQ ID NO: 11 and a sequence that encodes for a transmembrane domain. In some embodiments, mbIL15 comprises the amino acid sequence of SEQ ID NO: 12 functionally coupled to an amino acid sequence of a transmembrane domain. In several embodiments, mbIL15 has the nucleic acid sequence of SEQ ID NO: 1188. In several embodiments, mbIL15 can be truncated or modified, such that it has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the sequence of SEQ ID NO: 1188. In several embodiments, the mbIL15 comprises the amino acid sequence of SEQ ID NO: 1189. In several embodiments, the mbIL15 is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the mbIL15 having the sequence of SEQ ID NO: 1189. Membrane-bound IL15 sequences are explored in PCT publications WO 2018/183385 and WO 2020/056045, each of which is hereby expressly incorporated by reference in its entirety and pertaining to membrane-bound IL15 sequences.

Signaling Domains

[00224] Some embodiments of the compositions and methods described herein relate to a chimeric receptor (e.g., tumor antigen-directed CARs and/or tumor ligand-directed chimeric receptors) that includes a signaling domain. For example, immune cells engineered according to several embodiments disclosed herein may comprise at least one subunit of the CD3 T cell receptor complex (or a fragment thereof). In several embodiments, the signaling domain comprises the CD3zeta subunit. In several embodiments, the CD3zeta is encoded by the nucleic acid sequence of SEQ ID NO: 7. In several embodiments, the CD3zeta can be truncated or modified, such that it has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD3zeta having the sequence of SEQ ID NO: 7. In several embodiments, the CD3zeta domain comprises the amino acid sequence of SEQ ID NO: 8. In several embodiments, the CD3zeta domain is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD3zeta domain having the sequence of SEQ ID NO: 8.

[00225] In several embodiments, unexpectedly enhanced signaling is achieved through the use of multiple signaling domains whose activities act synergistically. For example, in several embodiments, the signaling domain further comprises an OX40 domain. In several embodiments, the OX40 domain is an intracellular signaling domain. In several embodiments, the OX40 intracellular signaling domain has the nucleic acid sequence of SEQ ID NO: 5. In several embodiments, the OX40 intracellular signaling domain can be truncated or modified, such that it has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the OX40 having the sequence of SEQ ID NO: 5. In several embodiments, the OX40 intracellular signaling domain comprises the amino acid sequence of SEQ ID NO: 6. In several embodiments, the OX40 intracellular signaling domain is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the OX40 intracellular signaling domain having the sequence of SEQ ID NO: 6. In several embodiments, OX40 is used as the sole transmembrane/signaling domain in the construct, however, in several embodiments, OX40 can be used with one or more other domains. For example, combinations of OX40 and CD3zeta are used in some embodiments. By way of further example, combinations of CD28, OX40, 4-1BB, and/or CD3zeta are used in some embodiments.

[00226] In several embodiments, the signaling domain comprises a 4-1BB domain. In several embodiments, the 4-1BB domain is an intracellular signaling domain. In several embodiments, the 4-1BB intracellular signaling domain comprises the amino acid sequence of SEQ ID NO: 29. In several embodiments, the 4-1BB intracellular signaling domain is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the 4-1BB intracellular signaling domain having the sequence of SEQ ID NO: 29. In several embodiments, 4-1BB is used as the sole transmembrane/signaling domain in the construct, however, in several embodiments, 4-1BB can be used with one or more other domains. For example, combinations of 4-1BB andCD3zeta are

used in some embodiments. By way of further example, combinations of CD28, OX40, 4-1BB, and/or CD3zeta are used in some embodiments.

[00227] In several embodiments, the signaling domain comprises a CD28 domain. In several embodiments the CD28 domain is an intracellular signaling domain. In several embodiments, the CD28 intracellular signaling domain comprises the amino acid sequence of SEQ ID NO: 31. In several embodiments, the CD28 intracellular signaling domain is truncated or modified and has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% sequence identity with the CD28 intracellular signaling domain having the sequence of SEQ ID NO: 31. In several embodiments, CD28 is used as the sole transmembrane/signaling domain in the construct, however, in several embodiments, CD28 can be used with one or more other domains. For example, combinations of CD28 andCD3zeta are used in some embodiments. By way of further example, combinations of CD28, OX40, 4-1BB, and/or CD3zeta are used in some embodiments.

Cytotoxic Receptor Complex Constructs

[00228] Some embodiments of the compositions and methods described herein relate to chimeric antigen receptors, such as a CD19-directed chimeric receptor, as well as chimeric receptors, such as an activating chimeric receptor (ACR) that targets ligands of NKG2D. The expression of these cytotoxic receptor complexes in immune cells, such as genetically modified non-alloreactive T cells and/or NK cells, allows the targeting and destruction of particular target cells, such as cancerous cells. Non-limiting examples of such cytotoxic receptor complexes are discussed in more detail below.

Chimeric Antigen Receptor Cytotoxic Receptor Complex Constructs

[00229] In several embodiments, there are provided for herein a variety of cytotoxic receptor complexes (also referred to as cytotoxic receptors) are provided for herein with the general structure of a chimeric antigen receptor. Figures 1-7 depict non-limiting schematics of constructs that include a tumor binding moiety that binds to tumor antigens or tumor-associated antigens expressed on the surface of cancer cells and activates the engineered cell expressing the chimeric antigen receptor. Figure 7 shows a schematic of a chimeric receptor complex, with an NKG2D activating chimeric receptor as a non-limiting example (see NKG2D ACRa and ACRb). Figure 6 shows a schematic of a CD70 directed CAR, as well as a bispecific CD70 CAR/chimeric receptor complex, and two non-limiting constructs, NK71 and NK72, which target CD70.

[00230] As shown in the figures, several embodiments of the CAR include an anti-tumor binder, a CD8a hinge domain, an Ig4 SH domain (or hinge), a CD8a transmembrane domain, a CD28 transmembrane domain, an OX40 domain, a 4-1BB domain, a CD28 domain, a CD3ζ ITAM domain or subdomain, a CD3zeta domain, an NKp80 domain, a CD16 IC domain, a 2A cleavage site, and/or a membrane-bound IL-15 domain (though, as above, in several embodiments soluble IL-15 is used). In several embodiments, the binding and activation functions are engineered to be performed by separate

domains. Several embodiments relate to complexes with more than one tumor binder moiety or other binder/activation moiety. In some embodiments, the binder/activation moiety targets other markers besides CD70, such as a cancer target described herein, for example, CD19, CD123, CLDN6, BCMA, HER2, Mesothelin, PD-L1, or EGFR. In several embodiments, a construct is provided that targets NKG2D ligands on tumor cells, which can be used in conjunction with the CARs disclosed herein. In several embodiments, the general structure of the chimeric antigen receptor construct includes a hinge and/or transmembrane domain. These may, in some embodiments, be fulfilled by a single domain, or a plurality of subdomains may be used, in several embodiments. The receptor complex further comprises a signaling domain, which transduces signals after binding of the homing moiety to the target cell, ultimately leading to the cytotoxic effects on the target cell. In several embodiments, the complex further comprises a co-stimulatory domain, which operates, synergistically, in several embodiments, to enhance the function of the signaling domain. Expression of these complexes in immune cells, such as NK cells and/or T cells, allows the targeting and destruction of particular target cells, such as cancerous cells that express a given tumor marker. Some such receptor complexes comprise an extracellular domain comprising an anti-CD70 moiety, or CD70-binding moiety, that binds CD70 on the surface of target cells and activates the engineered cell. The CD3zeta ITAM subdomain may act in concert as a signaling domain. The IL-15 domain, e.g., mbIL-15 domain, may act as a co-stimulatory domain. The IL-15 domain, e.g. mbIL-15 domain, may render immune cells (e.g., NK or T cells) expressing it particularly efficacious against target tumor cells. It shall be appreciated that the IL-15 domain, such as an mbIL-15 domain, can, in accordance with several embodiments, be encoded on a separate construct. Additionally, each of the components may be encoded in one or more separate constructs.

[00231] Disclosed herein in some embodiments are anti-CD70 binding domains. In some embodiments, the anti-CD70 binding domains are scFvs. These anti-CD70 binding domains are specific for and/or preferentially bind to CD70. The anti-CD70 binding domains disclosed herein may be incorporated into any one of the chimeric antigen receptor constructs disclosed herein. The anti-CD70 binding domains disclosed herein may furthermore be expressed by a cell, either separately or within an anti-CD70 CAR.

[00232] In some embodiments, the anti-CD70 binding domain comprises a polynucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of either SEQ ID NO: 36 and/or SEQ ID NO: 37.

[00233] In some embodiments, the anti-CD70 binding domain comprises a heavy chain variable region and a light chain variable region. In some embodiments, the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3 and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3. In some embodiments, the CDR-H1 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 428-501; the CDR-H2 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a

sequence selected from SEQ ID NOs: 502-575; the CDR-H3 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 576-649; the CDR-L1 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 668-741; the CDR-L2 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 742-815; and the CDR-L3 comprises a sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 816-889.

[00234] In some embodiments of the anti-CD70 binding domains, the heavy chain variable region comprises an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 890-963. In some embodiments, the light chain variable region comprises an amino acid sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 964-1037.

In some embodiments of the anti-CD70 binding domains: 1) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 890 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 964; 2) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 891 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 965; 3) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 892 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 966; 4) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 893 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 967; 5) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 894 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 968; 6) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 895 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 969; 7) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 896 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 970; 8) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 897 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 971; 9) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 898 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 972; 10) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 899 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 973; 11) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 900 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 974; 12) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 901 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 975; 13) the heavy chain variable region

comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 902 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 976; 14) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 903 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 977; 15) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 904 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 978; 16) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 905 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 979; 17) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 906 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 980; 18) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 907 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 981; 19) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 908 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 982; 20) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 909 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 983; 21) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 910 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 984; 22) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 911 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 985; 23) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 912 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 986; 24) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 913 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 987; 25) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 914 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 988; 26) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 915 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 989; 27) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 916 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 990; 28) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 917 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 991; 29) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 918 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 992; 30) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 919 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 993; 31) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 920 and the light chain variable region

comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 994; 32) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 921 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 995; 33) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 922 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 996; 34) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 923 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 997; 35) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 924 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 998; 36) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 925 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 999; 37) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 926 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1000; 38) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 927 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1001; 39) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 928 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1002; 40) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 929 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1003; 41) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 930 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1004; 42) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 931 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1005; 43) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 932 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1006; 44) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 933 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1007; 45) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 934 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1008; 46) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 935 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1009; 47) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 936 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1010; 48) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 937 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1011; 49) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 938 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1012; 50) the heavy chain variable region

comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 939 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1013; 51) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 940 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1014; 52) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 941 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1015; 53) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 942 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1016; 54) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 943 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1017; 55) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 944 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1018; 56) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 945 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1019; 57) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 946 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1020; 58) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 947 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1021; 59) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 948 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1022; 60) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 949 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1023; 61) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 950 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1024; 62) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 951 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1025; 63) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 952 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1026; 64) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 953 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1027; 65) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 954 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1028; 66) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 955 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1029; 67) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 956 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1030; 68) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 957 and the light chain variable region

comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1031; 69) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 958 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1032; 70) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 959 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1033; 71) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 960 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1034; 72) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 961 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1035; 73) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 962 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1036; or 74) the heavy chain variable region comprises the CDR-H1, CDR-H2, CDR-H3 within SEQ ID NO: 963 and the light chain variable region comprises the CDR-L1, CDR-L2, CDR-L3 within SEQ ID NO: 1037.

[00235] In some embodiments of the anti-CD70 binding domains: 1) the heavy chain variable region comprises SEQ ID NO: 890 and the light chain variable region comprises SEQ ID NO: 964; 2) the heavy chain variable region comprises SEQ ID NO: 891 and the light chain variable region comprises SEQ ID NO: 965; 3) the heavy chain variable region comprises SEQ ID NO: 892 and the light chain variable region comprises SEQ ID NO: 966; 4) the heavy chain variable region comprises SEQ ID NO: 893 and the light chain variable region comprises SEQ ID NO: 967; 5) the heavy chain variable region comprises SEQ ID NO: 894 and the light chain variable region comprises SEQ ID NO: 968; 6) the heavy chain variable region comprises SEQ ID NO: 895 and the light chain variable region comprises SEQ ID NO: 969; 7) the heavy chain variable region comprises SEQ ID NO: 896 and the light chain variable region comprises SEQ ID NO: 970; 8) the heavy chain variable region comprises SEQ ID NO: 897 and the light chain variable region comprises SEQ ID NO: 971; 9) the heavy chain variable region comprises SEQ ID NO: 898 and the light chain variable region comprises SEQ ID NO: 972; 10) the heavy chain variable region comprises SEQ ID NO: 899 and the light chain variable region comprises SEQ ID NO: 973; 11) the heavy chain variable region comprises SEQ ID NO: 900 and the light chain variable region comprises SEQ ID NO: 974; 12) the heavy chain variable region comprises SEQ ID NO: 901 and the light chain variable region comprises SEQ ID NO: 975; 13) the heavy chain variable region comprises SEQ ID NO: 902 and the light chain variable region comprises SEQ ID NO: 976; 14) the heavy chain variable region comprises SEQ ID NO: 903 and the light chain variable region comprises SEQ ID NO: 977; 15) the heavy chain variable region comprises SEQ ID NO: 904 and the light chain variable region comprises SEQ ID NO: 978; 16) the heavy chain variable region comprises SEQ ID NO: 905 and the light chain variable region comprises SEQ ID NO: 979; 17) the heavy chain variable region comprises SEQ ID NO: 906 and the light chain variable region comprises SEQ ID NO: 980; 18) the heavy chain variable region comprises SEQ ID NO: 907 and the light chain variable region comprises SEQ ID NO: 981; 19) the heavy chain variable region comprises SEQ ID NO: 908 and the light chain variable region comprises SEQ ID NO: 982; 20) the heavy chain variable region

comprises SEQ ID NO: 909 and the light chain variable region comprises SEQ ID NO: 983; 21) the heavy chain variable region comprises SEQ ID NO: 910 and the light chain variable region comprises SEQ ID NO: 984; 22) the heavy chain variable region comprises SEQ ID NO: 911 and the light chain variable region comprises SEQ ID NO: 985; 23) the heavy chain variable region comprises SEQ ID NO: 912 and the light chain variable region comprises SEQ ID NO: 986; 24) the heavy chain variable region comprises SEQ ID NO: 913 and the light chain variable region comprises SEQ ID NO: 987; 25) the heavy chain variable region comprises SEQ ID NO: 914 and the light chain variable region comprises SEQ ID NO: 988; 26) the heavy chain variable region comprises SEQ ID NO: 915 and the light chain variable region comprises SEQ ID NO: 989; 27) the heavy chain variable region comprises SEQ ID NO: 916 and the light chain variable region comprises SEQ ID NO: 990; 28) the heavy chain variable region comprises SEQ ID NO: 917 and the light chain variable region comprises SEQ ID NO: 991; 29) the heavy chain variable region comprises SEQ ID NO: 918 and the light chain variable region comprises SEQ ID NO: 992; 30) the heavy chain variable region comprises SEQ ID NO: 919 and the light chain variable region comprises SEQ ID NO: 993; 31) the heavy chain variable region comprises SEQ ID NO: 920 and the light chain variable region comprises SEQ ID NO: 994; 32) the heavy chain variable region comprises SEQ ID NO: 921 and the light chain variable region comprises SEQ ID NO: 995; 33) the heavy chain variable region comprises SEQ ID NO: 922 and the light chain variable region comprises SEQ ID NO: 996; 34) the heavy chain variable region comprises SEQ ID NO: 923 and the light chain variable region comprises SEQ ID NO: 997; 35) the heavy chain variable region comprises SEQ ID NO: 924 and the light chain variable region comprises SEQ ID NO: 998; 36) the heavy chain variable region comprises SEQ ID NO: 925 and the light chain variable region comprises SEQ ID NO: 999; 37) the heavy chain variable region comprises SEQ ID NO: 926 and the light chain variable region comprises SEQ ID NO: 1000; 38) the heavy chain variable region comprises SEQ ID NO: 927 and the light chain variable region comprises SEQ ID NO: 1001; 39) the heavy chain variable region comprises SEQ ID NO: 928 and the light chain variable region comprises SEQ ID NO: 1002; 40) the heavy chain variable region comprises SEQ ID NO: 929 and the light chain variable region comprises SEQ ID NO: 1003; 41) the heavy chain variable region comprises SEQ ID NO: 930 and the light chain variable region comprises SEQ ID NO: 1004; 42) the heavy chain variable region comprises SEQ ID NO: 931 and the light chain variable region comprises SEQ ID NO: 1005; 43) the heavy chain variable region comprises SEQ ID NO: 932 and the light chain variable region comprises SEQ ID NO: 1006; 44) the heavy chain variable region comprises SEQ ID NO: 933 and the light chain variable region comprises SEQ ID NO: 1007; 45) the heavy chain variable region comprises SEQ ID NO: 934 and the light chain variable region comprises SEQ ID NO: 1008; 46) the heavy chain variable region comprises SEQ ID NO: 935 and the light chain variable region comprises SEQ ID NO: 1009; 47) the heavy chain variable region comprises SEQ ID NO: 936 and the light chain variable region comprises SEQ ID NO: 1010; 48) the heavy chain variable region comprises SEQ ID NO: 937 and the light chain variable region comprises SEQ ID NO: 1011; 49) the heavy chain variable region comprises SEQ ID NO: 938 and the light chain variable region comprises SEQ ID NO: 1012; 50) the heavy chain variable region comprises SEQ ID NO: 939 and the light chain variable region comprises SEQ

ID NO: 1013; 51) the heavy chain variable region comprises SEQ ID NO: 940 and the light chain variable region comprises SEQ ID NO: 1014; 52) the heavy chain variable region comprises SEQ ID NO: 941 and the light chain variable region comprises SEQ ID NO: 1015; 53) the heavy chain variable region comprises SEQ ID NO: 942 and the light chain variable region comprises SEQ ID NO: 1016; 54) the heavy chain variable region comprises SEQ ID NO: 943 and the light chain variable region comprises SEQ ID NO: 1017; 55) the heavy chain variable region comprises SEQ ID NO: 944 and the light chain variable region comprises SEQ ID NO: 1018; 56) the heavy chain variable region comprises SEQ ID NO: 945 and the light chain variable region comprises SEQ ID NO: 1019; 57) the heavy chain variable region comprises SEQ ID NO: 946 and the light chain variable region comprises SEQ ID NO: 1020; 58) the heavy chain variable region comprises SEQ ID NO: 947 and the light chain variable region comprises SEQ ID NO: 1021; 59) the heavy chain variable region comprises SEQ ID NO: 948 and the light chain variable region comprises SEQ ID NO: 1022; 60) the heavy chain variable region comprises SEQ ID NO: 949 and the light chain variable region comprises SEQ ID NO: 1023; 61) the heavy chain variable region comprises SEQ ID NO: 950 and the light chain variable region comprises SEQ ID NO: 1024; 62) the heavy chain variable region comprises SEQ ID NO: 951 and the light chain variable region comprises SEQ ID NO: 1025; 63) the heavy chain variable region comprises SEQ ID NO: 952 and the light chain variable region comprises SEQ ID NO: 1026; 64) the heavy chain variable region comprises SEQ ID NO: 953 and the light chain variable region comprises SEQ ID NO: 1027; 65) the heavy chain variable region comprises SEQ ID NO: 954 and the light chain variable region comprises SEQ ID NO: 1028; 66) the heavy chain variable region comprises SEQ ID NO: 955 and the light chain variable region comprises SEQ ID NO: 1029; 67) the heavy chain variable region comprises SEQ ID NO: 956 and the light chain variable region comprises SEQ ID NO: 1030; 68) the heavy chain variable region comprises SEQ ID NO: 957 and the light chain variable region comprises SEQ ID NO: 1031; 69) the heavy chain variable region comprises SEQ ID NO: 958 and the light chain variable region comprises SEQ ID NO: 1032; 70) the heavy chain variable region comprises SEQ ID NO: 959 and the light chain variable region comprises SEQ ID NO: 1033; 71) the heavy chain variable region comprises SEQ ID NO: 960 and the light chain variable region comprises SEQ ID NO: 1034; 72) the heavy chain variable region comprises SEQ ID NO: 961 and the light chain variable region comprises SEQ ID NO: 1035; 73) the heavy chain variable region comprises SEQ ID NO: 962 and the light chain variable region comprises SEQ ID NO: 1036; or 74) the heavy chain variable region comprises SEQ ID NO: 963 and the light chain variable region comprises SEQ ID NO: 1037.

[00236] In some embodiments of the anti-CD70 binding domains, the heavy chain variable region and/or light chain variable region comprise a framework. In some embodiments, the heavy chain variable region comprises a FW-H1, FW-H2, FW-H3, and FW-H4. In some embodiments, the heavy chain variable region comprises the order of FW-H1, CDR-H1, FW-H2, CDR-H2, FW-H3, CDR-H3, and FW-H4 from N-terminus to C-terminus. In some embodiments, the light chain variable region comprises a FW-L1, FW-L2, FW-L3, and FW-L4. In some embodiments, the light chain variable region comprises the order of FW-L1, CDR-L1, FW-L2, CDR-L2, FW-L3, CDR-L3, FW-L4 from N-terminus to C-terminus. In some embodiments,

the FW-H1 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 399-402; the FW-H2 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 403-406; the FW-H3 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 407-422; the FW-H4 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 423-427; the FW-L1 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 650-653; the FW-L2 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 654-657; the FW-L3 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 658-661; the FW-L4 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 662-667.

[00237] In some embodiments of the anti-CD70 binding domains, the heavy chain variable domain is encoded by a nucleic acid sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1038-1111.

[00238] In some embodiments of the anti-CD70 binding domains, the light chain variable domain is encoded by a nucleic acid sequence having at least 75%, 80%, 85%, 90%, 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1112-1185.

[00239] In some embodiments, the anti-CD70 binding domain is an antibody, Fab' fragment, $F(ab')_2$ fragment, or scFv.

[00240] In several embodiments, the anti-CD70 binding domain is encoded by a polynucleotide sequence comprising a sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of one or more of SEQ ID NOs: 38-120, 221-229, 1038-1111, and/or 1112-1185. In several embodiments, the anti-CD70 binding domain comprises an amino acid sequences that has at least about 85%, about 90%, about 95%, or more, sequence identity to one or more of SEQ ID NOs: 230-312, 890-963, 964-1037.

[00241] Also disclosed herein are CARs. In some embodiments, the CARs are anti-CD70 CARs. In some embodiments, the CARs comprise any one or more of the anti-CD70 binding domains disclosed herein.

[00242] In some embodiments, the CARs further comprise an OX40 subdomain and a CD3zeta subdomain. In several embodiments, the OX40 subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 5. In several embodiments, the OX40 subdomain comprises an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 6. In several embodiments, the CD3zeta subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 7. In several embodiments, the CD3zeta subdomain comprises an amino acid sequence having at least 85%, at least 90%, at least 95%, at least 99%, or at least 100% sequence identity to SEQ ID NO: 8. In several embodiments, the mbIL15 is encoded by a

sequence having at least 95% sequence identity to SEQ ID NO: 1188. In several embodiments, the one or more of SEQ ID NOS: 36-120, 221-229, 1038-1111, and/or 1112-1185, the polynucleotide encoding the OX40 subdomain, the polynucleotide encoding the CD3zeta subdomain, and the polynucleotide encoding mbIL15 are arranged in a 5' to 3' orientation within the polynucleotide.

[00243] In several embodiments, an anti-CD70 CAR is provided and is encoded by a polynucleotide having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of one or more of SEQ ID NOs: 138-220 or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence). In several embodiments, the CAR comprises an amino acid sequence having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of one or more of SEQ ID NOs 313-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[00244] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8hinge/ CD8hinge-CD8TM /4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 1, CAR1a). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a 4-1BB domain, and a CD3zeta domain, as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00245] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8hinge/CD8hinge-CD8TM/4-1BB/CD3zeta/2A/mIL-15 chimeric antigen receptor complex (see Figure 1, CAR 1b). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a 4-1BB domain, a CD3zeta domain, a 2A cleavage site, and an mIL-15 domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in

accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00246] In one embodiment, there is provided a polynucleotide encoding a Tumor Binder /CD8hinge-CD8TM/OX40/CD3zeta chimeric antigen receptor complex (see Figure 1, CAR1c). The polynucleotide comprises or is composed of tumor binder, a CD8a hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00247] In several embodiments, there is provided a polynucleotide encoding a tumor binder /CD8hinge-CD8TM/OX40/CD3zeta/2A/mIL-15 chimeric antigen receptor complex (see Figure 1, CAR 1d). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, an OX40 domain, a CD3zeta domain, a 2A cleavage site, and an mIL-15 domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed

sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site). In several embodiments, the anti-CD70 binding domain comprises a polynucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of either SEQ ID NO: 36 and/or SEQ ID NO: 37. In several embodiments, the anti-CD70 binding domain comprises a polynucleotide sequence that is at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of either SEQ ID NOs: 38-120, 221-229, 1038-1111, and/or 1112-1185. In several embodiments, an anti-CD70 CAR is provided and is encoded by a polynucleotide having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of one or more of SEQ ID NOs: 138-220, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence). In several embodiments, the CAR comprises an amino acid sequences having at least 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more, or a range defined by any two of the aforementioned percentages, identical to the sequence of one or more of SEQ ID NOs 313-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[00248] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8hinge-CD28TM/CD28/CD3zeta chimeric antigen receptor complex (see Figure 1, CAR1e). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD28 transmembrane domain, a CD28 domain, and a CD3zeta domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00249] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8hinge-CD28TM/CD28/CD3zeta/2A/mIL-15 chimeric antigen receptor complex (see Figure 1, CAR1f). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD28 transmembrane domain, a CD28 domain, a CD3zeta domain, a 2A cleavage site, and an mIL-15 domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule

comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00250] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/ICOS/CD3zeta chimeric antigen receptor complex (see Figure 1, CAR1g). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, inducible costimulator (ICOS) signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 1, CAR1h). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00251] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/CD28/4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 1, CAR1i). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD28 signaling domain, a 4-1BB signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 1, CAR1j). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments,

the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00252] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/NKG2DTM/OX40/CD3zeta chimeric antigen receptor complex (see Figure 2, CAR2a). The polynucleotide comprises or is composed of a Tumor Binder (such as a light chain variable region of an scFv), a CD8a hinge, an NKG2D transmembrane domain, an OX40 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 2, CAR2b). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00253] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/OX40/CD3zeta/2A/EGFRt chimeric antigen receptor complex (see Figure 2, CAR2e). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, an OX40 signaling domain, a CD3zeta domain, a 2A cleavage side, and a truncated version of the epidermal growth factor receptor (EGFRt). In several embodiments, the chimeric antigen receptor further comprises mbIL15 (see Figure 2, CAR2f). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence

identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00254] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/NKG2DTM/OX40/CD3zeta chimeric antigen receptor complex (see Figure 2, CAR2g). The polynucleotide comprises or is composed of a Tumor Binder (such as a heavy chain variable region of an scFv), a CD8a hinge, an NKG2D transmembrane domain, an OX40 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 2, CAR2h). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00255] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ Ig4SH-CD28TM/CD28/CD3zeta chimeric antigen receptor complex (see Figure 2, CAR2i). The polynucleotide comprises or is composed of a Tumor Binder, an Ig4 SH domain, a CD28 transmembrane domain, a CD28 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 2, CAR2j). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00256] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/CD27/CD3zeta chimeric antigen receptor complex (see Figure 3, CAR3a). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD27 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 3, CAR3b). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00257] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder / CD8hinge/CD8aTM/CD70/CD3zeta chimeric antigen receptor complex (see Figure 3, CAR3c). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD70 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 3, CAR3d). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00258] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/CD161/CD3zeta chimeric antigen receptor complex (see Figure 3, CAR3e). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD161 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 3, CAR3f). In several embodiments, this receptor complex is encoded

by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00259] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/CD40L/CD3zeta chimeric antigen receptor complex (see Figure 3, CAR3g). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD40L signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 3, CAR3h). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00260] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/ CD8hinge/CD8aTM/CD44/CD3zeta chimeric antigen receptor complex (see Figure 3, CAR3i). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a CD44 signaling domain, and a CD3zeta domain. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 3, CAR3j). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the

amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00261] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/Ig4SH-CD8TM/4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 4,CAR4a). The polynucleotide comprises or is composed of a Tumor Binder, an Ig4 SH domain, a CD8a transmembrane domain, a 4-1BB domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 4, CAR4b). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00262] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/Ig4SH-CD8TM/OX40/CD3zeta chimeric antigen receptor complex (see Figure 4, CAR4c). The polynucleotide comprises or is composed of a Tumor Binder, a Ig4 SH domain, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 4, CAR4d). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain

sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00263] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder /CD8hinge-CD3αTM/CD28/CD3zeta chimeric antigen receptor complex (see Figure 4, CAR4e). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD3α transmembrane domain, a CD28 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 4, CAR4f). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00264] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8hinge-CD28TM/CD28/4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 4, CAR 4g). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD28 transmembrane domain, a CD28 domain, a 4-1BB domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 4, CAR4h). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00265] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8 alpha hinge/CD8 alpha TM/4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 5, CAR5a). The

polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD8a transmembrane domain, a 4-1BB domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 5, CAR5b). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00266] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8 alpha hinge/CD3 TM/4-1BB/CD3zeta chimeric antigen receptor complex (see Figure 5, CAR5c). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD3 transmembrane domain, a 4-1BB domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 5, CAR5d). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00267] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8 alpha hinge/CD3 TM/4-1BB/NKp80 chimeric antigen receptor complex (see Figure 5,CAR5e). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD3 transmembrane domain, a 4-1BB domain, and an NKp80 domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 5, CAR5f). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein.

In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00268] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/CD8 alpha hinge/CD3 TM/CD16 intracellular domain/4-1BB chimeric antigen receptor complex (see Figure 5, CAR5g). The polynucleotide comprises or is composed of a Tumor Binder, a CD8a hinge, a CD3 transmembrane domain, CD16 intracellular domain, and a 4-1BB domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 5, CAR5h). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00269] In several embodiments, there is provided a polynucleotide encoding a Tumor Binder/NKG2D Extracellular Domain/CD8hinge-CD8TM/OX40/CD3zeta chimeric antigen receptor complex (see Figure 5, Bi-spec CAR/ACRa). The polynucleotide comprises or is composed of a Tumor Binder, an NKG2D extracellular domain (either full length or a fragment), a CD8a hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 5, Bi-Spec CAR/ACRb). In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising a sequence obtained from a combination of sequences disclosed herein, or comprises an amino acid sequence obtained from a combination of sequences disclosed herein. In several embodiments, the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence in accordance with one or more SEQ ID NOS as described herein, such as those included herein as examples of constituent parts. In several embodiments,

the encoding nucleic acid sequence, or the amino acid sequence, comprises a sequence that shares at least about 90%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with a sequence resulting from the combination one or more SEQ ID NOS as described herein. It shall be appreciated that certain sequence variability, extensions, and/or truncations of the disclosed sequences may result when combining sequences, as a result of, for example, ease or efficiency in cloning (e.g., for creation of a restriction site).

[00270] In several embodiments, there is provided a polynucleotide encoding an anti-CD70 binding domain/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta chimeric antigen receptor complex (see Figure 6, CD70 CARa). The polynucleotide comprises or is composed of an anti-CD70 binding domain, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 6, CD70CARb). In several embodiments, this anti-CD70 binding domain comprises an scFv. In several embodiments, the anti-CD70 scFv is encoded by a nucleic acid molecule having a sequence according to any one of SEQ ID NOS: 38-111. In several embodiments, the anti-CD70 scFv is encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 38-111. In several embodiments, the scFv comprises an amino acid having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 230-303. In several embodiments, an anti-CD70 CAR is encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 138-211 or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence). In several embodiments, the anti-CD70 CAR comprises an amino acid sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 313-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[00271] In some embodiments of the CARs disclosed herein, the CAR comprises at least two anti-CD70 binding domains and the CAR is a multivalent CAR. In some embodiments, the multivalent CAR comprises two anti-CD70 binding domains and the CAR is a bivalent CAR.

[00272] In some embodiments, the bivalent CAR comprises a first anti-CD70 binding domain and a second anti-CD70 binding domain. In some embodiments, the first anti-CD70 binding domain and the second anti-CD70 binding domain are any one of the anti-CD70 binding domains disclosed herein. In some embodiments, the first anti-CD70 binding domain and the second anti-CD70 binding domain each comprise

a heavy chain variable region and a light chain variable region disclosed herein. In some embodiments, the first anti-CD70 binding domain and the second anti-CD70 binding domain each comprise: a) a heavy chain variable region comprising the sequence of SEQ ID NO: 923 and a light chain variable region comprising the sequence of SEQ ID NO: 997; b) a heavy chain variable region comprising the sequence of SEQ ID NO: 949 and a light chain variable region comprising the sequence of SEQ ID NO: 1023; c) a heavy chain variable region comprising the sequence of SEQ ID NO: 950 and a light chain variable region comprising the sequence of SEQ ID NO: 1024; d) a heavy chain variable region comprising the sequence of SEQ ID NO: 952 and a light chain variable region comprising the sequence of SEQ ID NO: 1026; or e) a heavy chain variable region comprising the sequence of SEQ ID NO: 953 and a light chain variable region comprising the sequence of SEQ ID NO: 1027.

[00273] In several embodiments, there is provided a polynucleotide encoding a bi-specific anti-CD70 binding domain/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta chimeric antigen receptor complex (see Figure 6, Bi-V CD70 CARa). The polynucleotide comprises or is composed of a first and a second anti-CD70 binding domain, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15 (see Figure 6, Bi-V CD70CARb). In several embodiments, the first and/or the second anti-CD70 binding domain comprise an scFv. In several embodiments the first and the second anti-CD70 scFv are the same, while in some embodiments the first and the second anti-CD70 scFv are different sequences. In several embodiments, the bi-specific anti-CD70 scFv is encoded by a nucleic acid molecule having a sequence according to any one of SEQ ID NOS: 112-120, and/or 221-229. In several embodiments, the anti-CD70 scFv is encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 112-120, and/or 221-229. In several embodiments, the bispecific scFv comprises an amino acid having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 304-312, 890-963, and/or 964-1037. In several embodiments, a bispecific anti-CD70 CAR is encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 212-220, or codon-optimized SEQ ID NOs: 221-229. In several embodiments, the bispecific CAR comprises an amino acid sequence having at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with any one of SEQ ID NOS: 387-395, or a portion thereof (e.g. a portion excluding the mbIL15 sequence and/or self-cleaving peptide sequence).

[00274] In several embodiments, there is provided a polynucleotide encoding an anti-CD70 scFv/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta chimeric antigen receptor complex (see Figure 6, NK71). The polynucleotide comprises or is composed of an anti CD70 scFv encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with SEQ ID NO: 36, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15. In several embodiments, there is provided a polynucleotide encoding an anti CD70 scFv/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta chimeric antigen receptor complex (see Figure 6, NK72). The polynucleotide comprises or is composed of an anti CD70 scFv encoded by a nucleic acid sequence that shares at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, sequence identity, homology and/or functional equivalence with SEQ ID NO: 37, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, the polynucleotide further encodes mbIL15. However, in several embodiments, the anti-CD70 CARs disclosed herein do not comprise the scFv of SEQ ID NO: 36 or 37.

[00275] In several embodiments, there is provided a polynucleotide encoding an CD19/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta activating chimeric receptor complex (see Figure 7, CD19 CARa). The polynucleotide comprises or is composed of an anti-CD19 scFv, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. Additionally, in several embodiments, the polynucleotide encoding this CAR construct can optionally further encode mbIL15 (Figure 7, CD19 CARb). In several embodiments, this receptor complex (including mbIL15) is encoded by a nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO: 34. In yet another embodiment, this chimeric receptor is encoded by the amino acid sequence of SEQ ID NO: 35. In some embodiments, the sequence of the chimeric receptor may vary from SEQ ID NO: 34 or 35, but remains, depending on the embodiment, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% identical with SEQ ID NO: 34 or 35. In several embodiments, while the chimeric receptor may vary from SEQ ID NO: 34 or 35, the chimeric receptor retains, or in some embodiments, has enhanced, NK cell activating and/or cytotoxic function. Additional information about chimeric receptors for use in the presently disclosed methods and compositions can be found in PCT Patent Application No. PCT/US2020/020824, filed March 3, 2020, which is incorporated in its entirety by reference herein.

[00276] In several embodiments, there is provided a polynucleotide encoding an NKG2D/CD8a hinge/CD8a transmembrane domain/OX40/CD3zeta activating chimeric receptor complex (see Figure 7, NKG2D ACRa). The polynucleotide comprises or is composed of a fragment of the NKG2D receptor capable of binding a ligand of the NKG2D receptor, a CD8alpha hinge, a CD8a transmembrane domain, an OX40 domain, and a CD3zeta domain as described herein. In several embodiments, this receptor complex is encoded by a nucleic acid molecule comprising the nucleic acid sequence of SEQ ID NO: 32.

In yet another embodiment, this chimeric receptor is encoded by the amino acid sequence of SEQ ID NO: 33. In some embodiments, the sequence of the chimeric receptor may vary from SEQ ID NO: 32 or 33, but remains, depending on the embodiment, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, or at least 95% identical to SEQ ID NO: 32 or 33. In several embodiments, while the chimeric receptor may vary from SEQ ID NO: 32 or 33, the chimeric receptor retains, or in some embodiments, has enhanced, NK cell activating and/or cytotoxic function. Additionally, in several embodiments, this construct can optionally be co-expressed with mbIL15, such as the mbIL15 encoded by SEQ ID NO: 1188 (Figure 7, NKG2D ACRb). Additional information about chimeric receptors for use in the presently disclosed methods and compositions can be found in PCT Patent Publication No. WO 2018/183385, filed March 27, 2018, which is incorporated in its entirety by reference herein.

[00277] In several embodiments, there is provided a population of genetically engineered natural killer cells for cancer immunotherapy. In some embodiments, the population comprises a plurality of NK cells that have been expanded in culture. In some embodiments, at least a portion of the plurality of NK cells is engineered to express a chimeric antigen receptor comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex. In some embodiments, the tumor binding domain targets CD70 and is encoded by a polynucleotide comprising a sequence having at least 85%, at least 90%, or at least 95% sequence identity to SEQ ID NO: 36 or 37. In some embodiments, the tumor binding domain targets CD70 and comprises an amino acid sequence having at least 85%, at least 90%, or at least 95% or greater sequence identity to SEQ ID NO: 1186 or 1187. In some embodiments, the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture. In some embodiments, the reduced CD70 expression was engineered through editing of an endogenous CD70 gene. In some embodiments, the NK cells are further genetically edited to express reduced levels of a CIS protein encoded by a CISH gene as compared to a non-engineered NK cell. In some embodiments, the reduced CIS expression was engineered through editing of a CISH gene. In some embodiments, the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels of CIS. In some embodiments, the NK cells are further genetically edited to express reduced levels of an adenosine receptor. In some embodiments, the reduced adenosine receptor expression was achieved through editing of a gene encoding said adenosine receptor. In some embodiments, the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells and enhanced persistence, as compared to NK cells expressing native levels of the adenosine receptor.

[00278] Also disclosed herein are cells comprising any one of the anti-CD70 binding domains disclosed herein and/or any one of the CARs disclosed herein. In some embodiments, the cell is an immune cell. In some embodiments, the cell is an NK cell or a T cell. In some embodiments, the cell is genetically edited to express a reduced level of CISH, an adenosine receptor, A2A adenosine receptor, A2B adenosine receptor, A3 adenosine receptor, A1 adenosine receptor, A2AR, TGFBR, B2M, CIITA, NKG2A, CBLB,

TRIM29, SOCS2, SMAD3, MAPKAPK3, CEACAM1, or DDIT4, or any combination thereof, as compared to a non-engineered cell. In some embodiments, the cell is genetically edited with one or more guide RNAs having at least 95% sequence identity to SEQ ID NOs: 1190-1201. Unless indicated otherwise to the contrary, the sequences provided for guide RNAs that are recited using deoxyribonucleotides refer to the target DNA and shall be considered as also referencing those guides used in practice (e.g., employing ribonucleotides, where the ribonucleotide uracil is used in lieu of deoxyribonucleotide thymine or vice-versa where thymine is used in lieu of uracil, wherein both are complementary base pairs to adenine when reciting either an RNA or DNA sequence). For example, a gRNA with the sequence TCACCAAGCCCGCGACCAATGGG (SEQ ID NO: 121) shall also refer to the following sequence UCACCAAGCCCGCGACCAAUGGG (SEQ ID NO: 1214) or a gRNA with sequence UCACCAAGCCCGCGACCAAUGGG (SEQ ID NO: 1214) shall also refer to the following sequence TCACCAAGCCCGCGACCAATGGG (SEQ ID NO: 121) .

Methods of Treatment

[00279] Some embodiments relate to a method of treating, ameliorating, inhibiting, or preventing cancer with a cell or immune cell comprising a chimeric antigen receptor and/or an activating chimeric receptor, as disclosed herein. In some embodiments, the method includes treating or preventing cancer. In some embodiments, the method includes administering a therapeutically effective amount of immune cells expressing a tumor-directed chimeric antigen receptor and/or tumor-directed chimeric receptor as described herein. Examples of types of cancer that may be treated as such are described herein.

[00280] Disclosed herein are methods of treating cancer in a subject. In some embodiments, the methods comprise administering to the subject any one of the anti-CD70 binding domains disclosed herein, any one of the CARs disclosed herein, or any one of the cells disclosed herein, or any combination thereof.

[00281] In certain embodiments, treatment of a subject with a genetically engineered cell(s) described herein achieves one, two, three, four, or more of the following effects, including, for example: (i) reduction or amelioration the severity of disease or symptom associated therewith; (ii) reduction in the duration of a symptom associated with a disease; (iii) protection against the progression of a disease or symptom associated therewith; (iv) regression of a disease or symptom associated therewith; (v) protection against the development or onset of a symptom associated with a disease; (vi) protection against the recurrence of a symptom associated with a disease; (vii) reduction in the hospitalization of a subject; (viii) reduction in the hospitalization length; (ix) an increase in the survival of a subject with a disease; (x) a reduction in the number of symptoms associated with a disease; (xi) an enhancement, improvement, supplementation, complementation, or augmentation of the prophylactic or therapeutic effect(s) of another therapy. Advantageously, the non-alloreactive engineered T cells disclosed herein further enhance one or more of the above. Administration can be by a variety of routes, including, without limitation, intravenous, intra-arterial, subcutaneous, intramuscular, intrahepatic, intraperitoneal and/or local delivery to an affected tissue.

[00282] Also disclosed herein are uses of any one of the anti-CD70 binding domains disclosed herein, any one of the CARs disclosed herein, any one of the cells disclosed herein, or any combination thereof for the treatment of cancer.

[00283] Also disclosed herein are uses of any one of the anti-CD70 binding domains disclosed herein, any one of the CARs disclosed herein, any one of the cells disclosed herein, or any combination thereof in the manufacture of a medicament for the treatment of cancer.

Administration and Dosing

[00284] Further provided herein are methods of treating a subject having cancer, comprising administering to the subject a composition comprising immune cells (such as NK and/or T cells) engineered to express a cytotoxic receptor complex as disclosed herein. For example, some embodiments of the compositions and methods described herein relate to use of a tumor-directed chimeric antigen receptor and/or tumor-directed chimeric receptor, or use of cells expressing a tumor-directed chimeric antigen receptor and/or tumor-directed chimeric receptor, for treating a cancer patient. Uses of such engineered immune cells for treating cancer are also provided.

[00285] In certain embodiments, treatment of a subject with a genetically engineered cell(s) described herein achieves one, two, three, four, or more of the following effects, including, for example: (i) reduction or amelioration the severity of disease or symptom associated therewith; (ii) reduction in the duration of a symptom associated with a disease; (iii) protection against the progression of a disease or symptom associated therewith; (iv) regression of a disease or symptom associated therewith; (v) protection against the development or onset of a symptom associated with a disease; (vi) protection against the recurrence of a symptom associated with a disease; (vii) reduction in the hospitalization of a subject; (viii) reduction in the hospitalization length; (ix) an increase in the survival of a subject with a disease; (x) a reduction in the number of symptoms associated with a disease; (xi) an enhancement, improvement, supplementation, complementation, or augmentation of the prophylactic or therapeutic effect(s) of another therapy. Each of these comparisons are versus, for example, a different therapy for a disease, which includes a cell-based immunotherapy for a disease using cells that do not express the constructs disclosed herein. Advantageously, the non-alloreactive engineered T cells disclosed herein further enhance one or more of the above.

[00286] Administration can be by a variety of routes, including, without limitation, intravenous, intra-arterial, subcutaneous, intramuscular, intrahepatic, intraperitoneal and/or local delivery to an affected tissue. Doses of immune cells such as NK and/or T cells can be readily determined for a given subject based on their body mass, disease type and state, and desired aggressiveness of treatment, but range, depending on the embodiments, from about 10^5 cells per kg to about 10^{12} cells per kg (e.g., 10^5-10^7, 10^7-10^{10}, 10^{10}-10^{12} and overlapping ranges therein). In one embodiment, a dose escalation regimen is used. In several embodiments, a range of immune cells such as NK and/or T cells is administered, for example between about 1 x 10^6 cells/kg to about 1 x 10^8 cells/kg. Depending on the embodiment, various types of

cancer can be treated. In several embodiments, hepatocellular carcinoma is treated. Additional embodiments provided for herein include treatment or prevention of the following non-limiting examples of cancers including, but not limited to, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, Kaposi sarcoma, lymphoma, gastrointestinal cancer, appendix cancer, central nervous system cancer, basal cell carcinoma, bile duct cancer, bladder cancer, bone cancer, brain tumors (including but not limited to astrocytomas, spinal cord tumors, brain stem glioma, glioblastoma, craniopharyngioma, ependymoblastoma, ependymoma, medulloblastoma, medulloepithelioma), breast cancer, bronchial tumors, Burkitt lymphoma, cervical cancer, colon cancer, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative disorders, ductal carcinoma, endometrial cancer, esophageal cancer, gastric cancer, Hodgkin lymphoma, non-Hodgkin lymphoma, hairy cell leukemia, renal cell cancer, leukemia, oral cancer, nasopharyngeal cancer, liver cancer, lung cancer (including but not limited to, non-small cell lung cancer, (NSCLC) and small cell lung cancer), pancreatic cancer, bowel cancer, lymphoma, melanoma, ocular cancer, ovarian cancer, pancreatic cancer, prostate cancer, pituitary cancer, uterine cancer, and vaginal cancer.

[00287] In some embodiments, also provided herein are nucleic acid and amino acid sequences that have sequence identity and/or homology of at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% (and ranges therein) as compared with the respective nucleic acid or amino acid sequences of SEQ ID NOS. 1-398 (or combinations of two or more of SEQ ID NOS: 1-398) and that also exhibit one or more of the functions as compared with the respective SEQ ID NOS. 1-398 (or combinations of two or more of SEQ ID NOS: 1-398) including but not limited to, (i) enhanced proliferation, (ii) enhanced activation, (iii) enhanced cytotoxic activity against cells presenting ligands to which NK cells harboring receptors encoded by the nucleic acid and amino acid sequences bind, (iv) enhanced homing to tumor or infected sites, (v) reduced off target cytotoxic effects, (vi) enhanced secretion of immunostimulatory cytokines and chemokines (including, but not limited to IFNg, TNFa, IL-22, CCL3, CCL4, and CCL5), (vii) enhanced ability to stimulate further innate and adaptive immune responses, and (viii) combinations thereof.

[00288] Additionally, in several embodiments, there are provided amino acid sequences that correspond to any of the nucleic acids disclosed herein, while accounting for degeneracy of the nucleic acid code. Furthermore, those sequences (whether nucleic acid or amino acid) that vary from those expressly disclosed herein, but have functional similarity or equivalency are also contemplated within the scope of the present disclosure. The foregoing includes mutants, truncations, substitutions, or other types of modifications.

[00289] In several embodiments, polynucleotides encoding the disclosed cytotoxic receptor complexes are mRNA. In some embodiments, the polynucleotide is DNA. In some embodiments, the polynucleotide is operably linked to at least one regulatory element for the expression of the cytotoxic receptor complex.

[00290] Additionally provided, according to several embodiments, is a vector comprising the polynucleotide encoding any of the polynucleotides provided for herein, wherein the polynucleotides are

optionally operatively linked to at least one regulatory element for expression of a cytotoxic receptor complex. In several embodiments, the vector is a retrovirus.

[00291] Further provided herein are engineered immune cells (such as NK and/or T cells) comprising the polynucleotide, vector, or cytotoxic receptor complexes as disclosed herein. Further provided herein are compositions comprising a mixture of engineered immune cells (such as NK cells and/or engineered T cells), each population comprising the polynucleotide, vector, or cytotoxic receptor complexes as disclosed herein. Additionally, there are provided herein compositions comprising a mixture of engineered immune cells (such as NK cells and/or engineered T cells), each population comprising the polynucleotide, vector, or cytotoxic receptor complexes as disclosed herein and the T cell population having been genetically modified to reduce/eliminate gvHD and/or HvD. In some embodiments, the NK cells and the T cells are from the same donor. In some embodiments, the NK cells and the T cells are from different donors. In several embodiments, one or more genes are edited (e.g., knockout or knock in) in order to impart one or more enhanced functions or characteristics to the edited cells. For example, in several embodiments CIS protein is substantially reduced by editing the CISH, which leads to enhanced NK cell proliferation, cytotoxicity and/or persistence.

[00292] Doses of immune cells such as NK cells or T cells can be readily determined for a given subject based on their body mass, disease type and state, and desired aggressiveness of treatment, but range, depending on the embodiments, from about 10^5 cells per kg to about 10^{12} cells per kg (e.g., 10^5 - 10^7, 10^7- 10^{10}, 10^{10}- 10^{12} and overlapping ranges therein). In one embodiment, a dose escalation regimen is used. In several embodiments, a range of NK cells is administered, for example between about 1 x 10^6 cells/kg to about 1 x 10^8 cells/kg. Depending on the embodiment, various types of cancer or infection disease can be treated.

Cancer Types

[00293] Some embodiments of the compositions and methods described herein relate to administering immune cells comprising a tumor-directed chimeric antigen receptor and/or tumor-directed chimeric receptor to a subject with cancer. Various embodiments provided for herein include treatment or prevention of the following non-limiting examples of cancers. Examples of cancer include, but are not limited to, acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, Kaposi sarcoma, lymphoma, gastrointestinal cancer, appendix cancer, central nervous system cancer, basal cell carcinoma, bile duct cancer, bladder cancer, bone cancer, brain tumors (including but not limited to astrocytomas, spinal cord tumors, brain stem glioma, craniopharyngioma, ependymoblastoma, ependymoma, medulloblastoma, medulloepithelioma), breast cancer, bronchial tumors, Burkitt lymphoma, cervical cancer, colon cancer, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative disorders, ductal carcinoma, endometrial cancer, esophageal cancer, gastric cancer, Hodgkin lymphoma, non-Hodgkin lymphoma, hairy cell leukemia, renal cell cancer, leukemia, oral cancer, nasopharyngeal cancer, liver cancer, lung cancer (including but not limited to, non-small cell lung

cancer, (NSCLC) and small cell lung cancer), pancreatic cancer, bowel cancer, lymphoma, melanoma, ocular cancer, ovarian cancer, pancreatic cancer, prostate cancer, pituitary cancer, uterine cancer, and vaginal cancer.

Cancer Targets

[00294] Some embodiments of the compositions and methods described herein relate to immune cells comprising a chimeric receptor that targets a cancer antigen. Non-limiting examples of target antigens include: CD70, CD5, CD19; CD123; CD22; CD30; CD171 ; CS1 (also referred to as CD2 subset 1, CRACC, SLAMF7, CD319, and 19A24); TNF receptor family member B cell maturation (BCMA) ; CD38; DLL3; G protein coupled receptor class C group 5, member D (GPRC5D); epidermal growth factor receptor (EGFR) CD138; prostate-specific membrane antigen (PSMA); Fms Like Tyrosine Kinase 3 (FLT3); KREMEN2 (Kringle Containing Transmembrane Protein 2), ALPPL2, Claudin 4, Claudin 6, C-type lectin-like molecule-1 (CLL-1 or CLECL1); CD33; epidermal growth factor receptor variant III (EGFRviii); ganglioside G2 (GD2); ganglioside GD3 (aNeu5Ac(2-8)aNeu5Ac(2-3)bDGalp(l-4)bDGlcp(l-l)Cer);); Tn antigen ((Tn Ag) or (GalNAca-Ser/Thr)); prostate-specific membrane antigen (PSMA); Receptor tyrosine kinase-like orphan receptor 1 (ROR1); Fms Like Tyrosine Kinase 3 (FLT3); Tumor-associated glycoprotein 72 (TAG72); CD38; CD44v6; a glycosylated CD43 epitope expressed on acute leukemia or lymphoma but not on hematopoietic progenitors, a glycosylated CD43 epitope expressed on non-hematopoietic cancers, Carcinoembryonic antigen (CEA); Epithelial cell adhesion molecule (EPCAM); B7H3 (CD276); KIT (CD117); Interleukin-13 receptor subunit alpha-2 (IL-13Ra2 or CD213A2); Mesothelin; Interleukin 11 receptor alpha (IL-llRa); prostate stem cell antigen (PSCA); Protease Serine 21 (Testisin or PRSS21); vascular endothelial growth factor receptor 2 (VEGFR2); Lewis(Y) antigen; CD24; Platelet-derived growth factor receptor beta (PDGFR-beta); Stage-specific embryonic antigen-4 (SSEA-4); CD20; Folate receptor alpha (FRa or FR1); Folate receptor beta (FRb); Receptor tyrosine-protein kinase ERBB2 (Her2/neu); Mucin 1, cell surface associated (MUC1); epidermal growth factor receptor (EGFR); neural cell adhesion molecule (NCAM); Prostase; prostatic acid phosphatase (PAP); elongation factor 2 mutated (ELF2M); Ephrin B2; fibroblast activation protein alpha (FAP); insulin-like growth factor 1 receptor (IGF-I receptor), carbonic anhydrase IX (CAIX); Proteasome (Prosome, Macropain) Subunit, Beta Type, 9 (LMP2); glycoprotein 100 (gp100); oncogene fusion protein consisting of breakpoint cluster region (BCR) and Abelson murine leukemia viral oncogene homolog 1 (Abl) (bcr-abl); tyrosinase; ephrin type-A receptor 2 (EphA2); sialyl Lewis adhesion molecule (sLe); ganglioside GM3 (aNeu5Ac(2-3)bDClalp(l-4)bDGlcp(l-l)Cer); transglutaminase 5 (TGS5); high molecular weight-melanoma associated antigen (HMWMAA); o-acetyl-GD2 ganglioside (OAcGD2); tumor endothelial marker 1 (TEM1/CD248); tumor endothelial marker 7-related (TEM7R); claudin 6 (CLDN6); thyroid stimulating hormone receptor (TSHR); G protein coupled receptor class C group 5, member D (GPRC5D); chromosome X open reading frame 61 (CXORF61); CD97; CD179a; anaplastic lymphoma kinase (ALK); Polysialic acid; placenta-specific 1 (PLAC1); hexasaccharide portion of globoH glycoceramide (GloboH); mammary gland differentiation antigen (NY-BR-1); uroplakin 2 (UPK2); Hepatitis

A virus cellular receptor 1 (HAVCR1); adrenoceptor beta 3 (ADRB3); pannexin 3 (PANX3); G protein-coupled receptor 20 (GPR20); lymphocyte antigen 6 complex, locus K 9 (LY6K); Olfactory receptor 51E2 (OR51E2); TCR Gamma Alternate Reading Frame Protein (TARP); Wilms tumor protein (WT1); Cancer/testis antigen 1 (NY-ES0-1); Cancer/testis antigen 2 (LAGE-la); Melanoma-associated antigen 1 (MAGE-A1); ETS translocation-variant gene 6, located on chromosome 12p (ETV6-AML); sperm protein 17 (SPA17); X Antigen Family, Member 1A (XAGE1); angiopoietin-binding cell surface receptor 2 (Tie 2); melanoma cancer testis antigen-1 (MAD-CT-1); melanoma cancer testis antigen-2 (MAD-CT-2); Fos-related antigen 1; tumor protein p53 (p53); p53 mutant; prostein; survivin; telomerase; prostate carcinoma tumor antigen-1 (PCT A-l or Galectin 8), melanoma antigen recognized by T cells 1 (MelanA or MARTI); Rat sarcoma (Ras) mutant; human Telomerase; reverse transcriptase (hTERT); sarcoma translocation breakpoints; melanoma inhibitor of apoptosis (ML-IAP); ERG (transmembrane protease, serine 2 (TMPRSS2) ETS fusion gene); N-Acetyl glucosaminyl-transferase V (NA17); paired box protein Pax-3 (PAX3); Androgen receptor; Cyclin Bl; v-myc avian myelocytomatosis viral oncogene neuroblastoma derived homolog (MYCN); Ras Homolog Family Member C (RhoC); Tyrosinase-related protein 2 (TRP-2); Cytochrome P450 IB 1 (CYPIB 1); CCCTC-Binding Factor (Zinc Finger Protein)-Like (BORIS or Brother of the Regulator oflmprinted Sites), Squamous Cell Carcinoma Antigen Recognized By T Cells 3 (SART3); Paired box protein Pax-5 (PAX5); proacrosin binding protein sp32 (OY-TES1); lymphocyte-specific protein tyrosine kinase (LCK); A kinase anchor protein 4 (AKAP-4); synovial sarcoma, X breakpoint 2 (SSX2); Receptor for Advanced Gly cation Endproducts (RAGE-1); renal ubiquitous 1 (RU1); renal ubiquitous 2 (RU2); legumain; human papilloma virus E6 (HPV E6); human papilloma virus E7 (HPV E7); intestinal carboxyl esterase; heat shock protein 70-2 mutated (mut hsp70-2); CD79a; CD79b; CD72; Leukocyte-associated immunoglobulin-like receptor 1 (LAIR1); Fc fragment of IgA receptor (FCAR or CD89); Leukocyte immunoglobulin-like receptor subfamily A member 2 (LILRA2); CD300 molecule-like family member f (CD300LF); C-type lectin domain family 12 member A (CLEC12A); bone marrow stromal cell antigen 2 (BST2); EGF-like module-containing mucin-like hormone receptor-like 2 (EMR2); lymphocyte antigen 75 (LY75); Glypican-3 (GPC3); Fc receptor-like 5 (FCRL5); and immunoglobulin lambda-like polypeptide 1 (IGLLl), MPL, Biotin, c-MYC epitope Tag, CD34, LAMP1 TROP2, GFRalpha4, CDH17, CDH6, NYBR1, CDH19, CD200R, Slea (CA19.9; Sialyl Lewis Antigen); Fucosyl-GMl, PTK7, gpNMB, CDH1-CD324, DLL3, CD276/B7H3, ILl lRa, IL13Ra2, CD179b-IGLll, TCRgamma-delta, NKG2D, CD32 (FCGR2A), Tn ag, Timl-/HVCR1, CSF2RA (GM-CSFR-alpha), TGFbetaR2, Lews Ag, TCR-betal chain, TCR-beta2 chain, TCR-gamma chain, TCR-delta chain, FITC, Leutenizing hormone receptor (LHR), Follicle stimulating hormone receptor (FSHR), Gonadotropin Hormone receptor (CGHR or GR), CCR4, GD3, SLAMF6, SLAMF4, HIV1 envelope glycoprotein, HTLVl-Tax, CMV pp65, EBV-EBNA3c, KSHV K8.1, KSHV-gH, influenza A hemagglutinin (HA), GAD, PDL1, Guanylyl cyclase C (GCC), auto antibody to desmoglein 3 (Dsg3), auto antibody to desmoglein 1 (Dsgl), HLA, HLA-A, HLA-A2, HLA-B, HLA-C, HLA-DP, HLA-DM, HLA-DOA, HLA-DOB, HLA-DQ, HLA-DR, HLA-G, IgE, CD99, Ras G12V, Tissue Factor 1 (TF1), AFP, GPRC5D, Claudinl 8.2 (CLD18A2 or CLDN18A.2)), P-glycoprotein, STEAP1, Livl, Nectin-4,

Cripto, gpA33, BST1/CD157, low conductance chloride channel, and the antigen recognized by TNT antibody.

EXAMPLES

[00295] The following are non-limiting descriptions of experimental methods and materials that were used in examples disclosed below.

Example 1 – CD70 Gene Editing to Reduce Expression by NK Cells

[00296] As discussed in more detail herein, certain cancer types express selected markers in an elevated manner. In several embodiments, CAR constructs are generated according to sequences disclosed herein in order to specifically target a given cancer. One such non-limiting embodiment of a cancer marker targeted by constructs disclosed herein is CD70. While various types of cancer can be treated using the cells and methods disclosed herein, in several embodiments renal cell carcinoma (RCC) is treated. RCC accounts for 90-95% of neoplasms in the kidneys, and is one of the most common kidney cancers in adults. While the 5-year survival rate is 75%, this depends heavily on the type, cell type, and stage of the cancer when it is first diagnosed. For ~ 2/3 of patients, RCC is only in the kidney (with the 5-year survival rate for these patients is 93%). However, if the kidney cancer has spread to surrounding tissues or organs and/or the regional lymph nodes, the 5-year survival rate is drops to 69%. Additionally, if the cancer has spread to a distant part of the body, the 5-year survival rate plummets to only 12%. Therapeutics to treat RCC and other CD70-expressing tumors are needed. Thus, as discussed in detail above, in several embodiments, anti-CD70 CAR constructs are provided. In several embodiments, the polynucleotides encoding those constructs are engineered to bi-cistronically express mbIL15. In several embodiments, however, in order to enhance the expansion, cytotoxicity and/or persistence of engineered immune cells (such as NK cells), the cells are subject to gene editing to enhance or disrupt expression of certain genes. In several embodiments, one such gene that is disrupted, knocked out in several embodiments, is CD70. In several embodiments, CD70 expression is disrupted (e.g., knocked out) in NK cells because NK cells naturally express relatively high levels of CD70, and if expression were maintained at native levels, an anti-CD70 CAR expressing NK cell would target not only a CD70-expressing tumor cell, but also other NK cells (whether native NK cells or those expressing the CD70 CAR). Thus, in several embodiments, gene editing is used to knockout CD70 expression by NK cells, such that engineered NK cells expressing an anti-CD70 CAR are not targeting the therapeutic NK cells as well as a CD70-expressing tumor.

[00297] To assess the expression of CD70 on native NK cell, FACS analysis was performed on donor NK cells after 9 days of expansion in culture. Figures 8A-8C show these data. Figure 8A shows that nearly 98% of NK cells from this donor were positive for CD70. Figures 8B and 8C show isotype control staining and unstained NK cells. These data demonstrate that CD70 expression on expanded NK cells would cause an anti-CD70 CAR expressing NK cells to kill the NK cell population, essentially an NK cell

suicide due to lack of differentiation between the CD70-expressing NK cells and CD70-expressing tumor cells. Figure 9 demonstrates a non-limiting schematic of various embodiments of editing and engineering NK cells to effectively target CD70-expressing tumors and exhibit enhanced NK cell persistence. In several embodiments, gene editing is used to reduce, substantially reduce, or eliminate CD70 expression by NK cells. The NK cells are then engineered to express an anti-CD70 CAR, such as those utilizing one or more of the anti-CD70 binding domain or scFv disclosed herein. This process results in a CD70-targeting, non-CD70 expressing NK cell. While this process schematically depicts editing and engineering of NK cells, in several embodiments T cells are subjected to a corresponding process.

[00298] Figures 10A and 10B depict schematic process flow diagrams for gene editing of NK cells (or T cells). These non-limiting embodiments of gene editing processes reflect the use of a CRISPR-Cas system, however in several embodiments, other editing modalities are used. Figure 10A shows a timeline for electroporation of NK cells on Day 0, followed by 5 days of culture in high IL-2 media. At Day 5, CD70 expression is assessed by FACS, followed by another 8 days of expansion of the NK cells in culture with feeder cells and low IL-2 media. CD70 expression is assessed again at Day 13. Figure 10B shows another non-limiting approach in which NK cells are first expanded by co-culture with feeder cells and using low IL-2 media, followed by electroporation to introduce guide RNA at day 7, then culture in high IL-2 media for 5 additional days. CD70 expression is assessed at Day 7 and Day 11. Non-limiting examples of CD70 guide RNAs are shown below in Table 1.

Table 1: CD70 Guide RNAs

SEQ ID NO:	Name	Sequence
121	CD70-1	TCACCAAGCCCGCGACCAATGGG
122	CD70-2	GCTTTGGTCCCATTGGTCGCGGG
123	CD70 -3	ACCCTCCTCCGGCATCGCCGCGG

[00299] Figures 11A-11B show FACS analysis of CD70 expression from a first experiment (using the KD7 approach) and Figures 11C-11D show data from a second experiment (also using KD7). Figure 11A shows CD70 expression for each of the three guide RNAs used, while Figure 11B shows CD70 expression by native NK cells, an isotype control, and an unstained control. Figure 11C and 11D show corresponding data from the second experiment (different donor). While in several embodiments, use of a single guide RNA is sufficient to achieve a desired level of reduced gene/protein expression, given that CD70 expression by edited and engineered immune cells will cause a suicide effect, greater levels of reduction of CD70 were investigated.

[00300] As is used in several embodiments disclosed herein, the effect of use of single guide RNA versus a combination of guide RNAs was investigated. Figures 12A-12E relate to use of single guide RNAs 1, 2, and 3 (12A, 12B, and 12C, respectively). The NK cells in this experiment were edited/expanded with the KD7 method (expansion followed by editing). As shown, approximately 20-50% of the NK cells retained

CD70 expression. Figures 12D and 12E are CD70 counts on non-electroporated NK cells and an unstained control. Figures 13A-13E show data for combinations of guide RNAs (again with KD7). Figure 13A shows that CD70-1 and CD70-2 guide RNAs in combination reduce CD70 expression to ~24% of NK cells. Figure 13B shows that CD70-1 and CD70-3 guide RNAs in combination reduce CD70 expression further, to ~13% of NK cells. Figure 13C shows that CD70-2 and CD70-3 guide RNAs in combination reduce CD70 expression still further, to less than 13% of NK cells. Figures 13D and 13E repeat the control data of 12D/12E. These data show that, in accordance with several embodiments, significant reductions in CD70 expression can be accomplished through the use of a plurality of guide RNAs directed against a target gene, like CD70.

[00301] As schematically illustrated in Figure 14F, provided for herein are various alternative methods for gene editing cells, such as NK cells or T cells. Figure 14F shows a modified KD7 approach with donor cells being expanded for 7 days, electroporated at Day 7, cultured for 5 days to allow gene editing to occur (done in some embodiments in high IL2 media, followed by an additional 10 days of culture (done in some embodiments with low IL2 media). CD70 expression was analyzed by FACS at Day 21. Figures 14A-14E show data related to CD70 expression by NK cells using that approach. Figure 14D shows CD70 expression on 96% of NK cells assessed, whereas Figure 14E confirms limited background signal with an unstained population. Figures 14A, 14B, and 14C show reductions in CD70 expression by NK cells ranging from about 78% to nearly 97%.

[00302] Figures 15A-15E show FACS analysis data for NK cells where double guide RNAs where used to target CD70. Figures 15D and 15E repeat the control data of 14D/14E. Figure 15A shows guide RNAs 1 and 2, which resulted in almost 80% knockdown of CD70 expression. Figure 15B shows guide RNAs 1 and 3, which resulted in almost 97% knockdown of CD70 expression. Figure 15C shows guide RNAs 2 and 3, which resulted in over 98% knockdown of CD70 expression. These data demonstrate that in some embodiments, use of a single guide RNA to edit a gene results in substantial decreases in expression of a target protein. However, in several embodiments, use of a plurality of guide RNAs to edit a gene can further reduce the expression of a target protein.

[00303] Figures 16A-16C show additional gene editing (here using the KD0 approach) on NK cells from two different donors, in order to further assess the effects of gene editing prior to expansion. Figure 16A shows the knockdown of CD70 expression on NK cells from a first donor using three different guide RNAs (CD70-1, CD70-2, CD70-3, see Table 1). Figure 16B shows results for NK cells of a second donor, while Figure 16C shows control data (native, unexpanded NK cells, which express low levels of CD70). As can be seen from these data, as in accordance with several embodiments substantially all native CD70 expression was knocked out using various guide sets. At Day 5 post expansion, guide set 1, 2, and 3, reduced expressing of native CD70 by almost 99%, 98%, and 97%, respectively for a first donor (16A). Those guide RNAs achieved almost 98%, 99% and 97% (respectively) reduction of CD70 expression on NK cells of a second donor (16B). CD70 expression was assessed at Day 13 post-editing (8 days after the first assessment of CD70 expression. Of note is that the NK cells robustly expanded, in spite of the CD70

knockout, indicating that expansion of NK cells to clinically relevant numbers is possible, even with genetic editing. Figure 17A shows the CD70 expression for a first donor, which even after an additional 8 days in culture, was still significantly reduced using guide set 1 and guide set 2 (approximately 70-80% using those gRNAs). The "recovery" of expression of CD70 is due to the expansion of NK cells in which CD70 was not knocked out or was only partially knocked down. The maintenance of CD70 expression at about 70-80% still represents a significant portion of the NK cell population that could avoid the cytotoxic effects of other NK cells expressing an anti-CD70 CAR. CD70 expression was higher (e.g., recovered) using guide set 3. Similar results are shown for a second Donor (Figure 17B), again with guide RNA set 1 and 2 maintaining over 80% CD70 knockout. Figure 17C shows control data. In several embodiments, sequential rounds of CD70 FACS can be used to obtain an NK cell population that is over about 95%, about 96%, about 97%, about 98%, about 99% or more, CD70 negative. In several embodiments, FACS can be followed by further expansion of this screened NK cell population to further increase NK cell number, and additional FACS screening could optionally be performed to further purify that expanded population.

[00304] Having shown that NK cells can be edited and expanded, experiments were performed to assess the ability of those cells to exert cytotoxic effects on target cells. Jurkat cells express CD27, which is the ligand for CD70. In contrast, Reh cells do not express CD27. Figures 18A-D show cytotoxicity data against either Jurkat or Reh cells at the indicated effector:target ratios, the experiment performed at Day 14 post-electroporation. Figures 18A and 18B are data from NK cells of a first donor, while 18C/18D are cells from a different donor. Notably, whether the target cells express the CD70 ligand, CD27, or not, NK cells can exert cytotoxic effects. The reduction of the E:T ratio (which effectively dilutes out the edited NK cells) yields an expected decrease in the overall cytotoxicity measured. Thus, as is in accordance with several embodiments disclosed herein, the relative cytotoxicity of an NK cell edited to reduce its native CD70 expression is retained against a given cell line. Figures 18A-18D also demonstrate that there are alternative mechanisms by which NK cells exert their cytotoxicity other than through a CD70-CD27 interaction. This is shown by virtue of the fact that CD70-negative NK cells can still retain cytotoxicity against Jurkat cells (which express the CD70 ligand, CD27), and can also exert cytotoxicity against Reh cells, which do not express CD27.

[00305] Experiments were also conducted to revisit the degree of impact, if any, of CD70 deletion on NK cell expansion. Figure 19A shows a schematic of a KD0 gene editing protocol (as was used to generate the cells tested in Figures 18A-18D. However, at Day 13, a fraction of the cells were seeded at a relatively low density (0.5 x 10^6 cells/well) in 24 well plates and expanded for an additional 7 days in low IL-2 media. Cell counts were performed by FACS at Day 20. Expansion data are summarized in Figure 19B. Cells from the two donors mapped out by guide RNAs used in each row show reasonably consistent viability across the experimental sample, most samples being in the mid- to high-70's in terms of percent viable cells. Fold growth of the cells is shown in a box in Figure 19B. These data demonstrate that experimental NK cells show between about 1.7 to about 2.5-fold growth over 20 days, even when CD70 expression is disrupted. FACS analysis of the expression levels of CD70 on NK cells at day 20 was performed and those

data are shown in Figures 20A-20C. Figure 20A shows CD70 expression for the first donor using the three knockout guides, and Figure 20B shows the data for the second donor. Figure 20C shows unedited NK cells and other relevant controls. The initial CD70 percentage expression, expression at Day 7 (the data discussed in Figures 16A-16B), and final CD70 expression is tabulated here. Knockout 1 and Knockout 2 maintained less than about 7% expression across those four samples, with Knockout 2 showing less than 3% of the NK cells expressing CD70 at the final Day 20 time point. Interestingly, Knockout 1 and Knockout 2, exhibited the two lowest CD70 expression levels, but also some of the highest fold-expansion values. Thus, as is in accordance with several embodiments disclosed herein, knockdown or knockout of native CD70 expression on NK cells (or T cells), does not impair the ability of the NK (or T) cells to expand in culture.

Example 2 – CD70 Knockout, CD70 Expression and Functionality of Jurkat Cells

[00306] As discussed in more detail below, several embodiments provided for herein relate to NK cells edited to reduce, substantially reduce, or eliminate native CD70 expression by the NK cells in conjunction with engineering the NK cells to express an anti-CD70 CAR. The gene editing reduces the suicide effect of the CAR-expressing engineered cells. In order to evaluate the ability of a give CAR to bind CD70, a control cell line was developed through gene editing to achieve high (e.g., at least about 100,000, at least about 150,000, at least about 200,000, at least about 250,000, or more, copies of CD70 per cell) CD70 expression. As mentioned above, Jurkat cells express relatively high levels of CD70, however, to mimic tumor-like CD70 expression, native CD70 expression was first knocked out with gene editing, then replaced achieve the desired copy numbers discussed above.

[00307] Figures 21A and 21B relate to CD70 knockout on Jurkat cells. Figure 21A shows that each of guide RNA set 1, set 2, and set 3, reduce Jurkat CD70 expression by at least 96%. Figure 21B shows control data. Figure 22A shows a schematic time frame for knockout, expansion or storage of cells and analysis of CD70 expression. Figure 22B shows data for CD70 expression after use of guide RNA set 1, 2, or 3, where the Jurkat cells were maintained in culture for the duration of the experiment, until CD70 FACS at Day 13. In these data, each of the guide RNA sets reduced expression by over 94%, with guide RNA set 2 reducing expression by over 97% and guide RNA set 1 by over 98%. Figure 22C shows data for Jurkat cells that were expanded in the same manner as the cells in 22B, until day 11, at which time they were frozen. At Day 13, those cells were thawed and CD70 expression was assessed. As shown in Figure 23C, the freeze/thaw cycle, which can often disrupt gene expression and/or viability of cells, did not appear to substantially alter the efficacy of the CD70 knockdown. This suggests that, according to several embodiments disclosed herein, Jurkat cells can be edited to reduce CD70 expression, then expanded and stored (e.g., frozen), with the storage period and the subsequent thaw cycle not adversely impacting the CD70 expression reduction. Figure 22D shows relevant control data.

[00308] Figure 23 shows a non-limiting schematic of a knock-in approach used to introduce expression of a gene or other desired construct into a particular location, ultimately for expression of that

gene by the host cell. For example, in some embodiments, the host cell is an NK cell and the target locus is the endogenous CD70 locus. By directing a targeted insertion at that point, in some embodiments, the native CD70 expression is eliminated, and a CD70-targeting CAR could be inserted. Alternatively, the target locus could be CD70 and another gene of interest could be knocked in at that point. In still additional embodiments, for example with generation of high-CD70 Jurkat cells, the endogenous locus of CD70 could be targeted/interrupted, and an enhanced CD70 could be inserted (e.g., driven by an enhanced promoter, etc. to enhance CD70 expression to a desired level) and/or perhaps including a marker, such as GFP, to enable visualization of the edited cells.

[00309] Continuing the development of a high-CD70 expressing Jurkat cells for screening of CD70 CARS, a viral construct was generated encoding human CD70 tagged with GFP (hCD70) and used to transduce either wild-type Jurkat cells or Jurkat cells previously subjected to CD70 knockdown by guide RNA set 1 or guide RNA set 2. Figure 24A shows (left to right) non-stained wild-type Jurkat cells, a secondary antibody control, and expression of the human CD70-GFP construct (which is essentially zero, as these are wild-type cells). Figure 24B shows (left to right) the same data as discussed above but with Jurkat cells that are transduced with the human CD70-GFP construct. Here, nearly 85% of the cells express the delivered construct. Figure 24C shows the corresponding data for Jurkat cells edited using guide RNA set 1. The right-most panel shows that nearly 97% of the CD70 expression has been eliminated. Figure 24D shows Jurkat cells edited with guide RNA set 1 and transduced with the human CD70-GFP construct. Nearly 85% of the edited and transduced Jurkat cells express the detectable human CD70-GFP construct. Figure 24E shows corresponding data for editing of Jurkat cells with guide RNA set 2, which resulted in over 98% reduction of CD70 expression. Figure 24F shows "replacement" expression of human CD70-GFP through the viral transduction which results in over 90% of the Jurkat cells expression hCD70-GFP. These data are summarized in Figure 25, with two different gating scenarios used to view the data in multiple ways. The MFI represents expression of human CDCD70-GFP by the indicated cells. 786-O cells are provided as a reference, as they are renal cell carcinoma cells, which is a tumor type known to highly express CD70. Notably, direct viral transduction of Jurkat cells with the human CD70-GFP construct results in robust hCD70-GFP expression, as does the reduction of endogenous CD70 expression with guide RNA set 1 or 2. However, when data is gated on the population of Jurkat cells that were transduced to a great level (rather than the entire Jurkat population), the expression of hCD70-GFP exceeds the CD70 expression of the 786-O RCC cells. This demonstrates that, according to several embodiments, an edited and engineered Jurkat cell line can be generated that is useful for the screening of anti-CD70-targeting CARs.

[00310] Jurkat cells were also subject to viral transduction with human anti-CD70 antibodies, shown as a non-limiting embodiment in Figure 26B and 26C as "NK71 scFv" and "NK72 scFv" (SEQ ID NO: 36 and SEQ ID NO: 37, respectively). Each of these antibodies has a flag tag (though according to some embodiments, none of the antibodies used in CAR constructs comprise a flag tag or any other tag). Figure 26A shows control data. Figure 26B shows expression of the NK71 antibody on the Jurkat cells and Figure 26C shows expression of the NK72 antibody, which is elevated over the expression of the NK71 antibody.

[00311] Figures 27A-27F show data related to the determination of whether the NK71 or NK72 expressing Jurkat cells can bind human CD70. Figure 27A shows (left to right) a negative control, an isotype control (hFC-APC) and Jurkat cell binding to CD70 (using a DNA sequence encoding the extracellular domain of human CD70 (NP_001243.1) (Gln 39-Pro 193) fused with the Fc region of human IgG1 at the N-terminus via a polypeptide linker) when added at two different concentrations (2ug/ml) or (10ug/ml). Figure 27B shows (left to right) control binding when Jurkat cells are exposed to a murine Fc-directed antibody, binding of murine CD70 by the Jurkat cells (again at two concentrations) and the degree of NK71/NK72 expression by an APC-tagged anti-flag antibody. These data show that Jurkat cells, which have endogenous CD27 expression (the ligand for CD70) bind to human CD70, but less so to murine CD70. Figure 27C and 27D show corresponding data for Jurkat cells transduced with the NK71 antibody. Exposure of the Jurkat cells to 2 ug/mL of CD70 resulted in almost 50% of the Jurkat cells binding the CD70, whereas use of 10ug/mL elevated that binding to over 80%. Similar patterns are seen with murine CD70 (27D), with the overall binding being less robust. The right-most panel of Figure 27D shows that the binding data was achieved with just about 16% of the Jurkat cells expressing the NK71 antibody. Figures 27E and 27F show corresponding data for Jurkat cells transduced to express NK72. Figure 27E shows (left to right, a negative control, isotype antibody control and significant binding of CD70 by the Jurkat cells at both 2 and 10ug/mL, with the latter showing that nearly 97% of the Jurkat cells binding CD70. Figure 27F shows corresponding data for murine CD70, and (right-most) that NK72 expression was quite robust, with nearly 83% of Jurkat expressing the NK72 antibody. Collectively, these data demonstrate that a target gene of interest can be knocked out efficiently through, according to several embodiments a combination of guide RNAs and that, also according to several embodiments cells can be engineered to express an antibody that binds to a target of interest. In several embodiments, such cells are beneficial for, for example, screening candidate binding moieties for one or more desired characteristics, e.g., affinity for target.

Example 3 – Editing of Multiple Genes and Engineering NK Cells With an Anti-CD70 CAR

[00312] As discussed above, in several embodiments, immune cells (e.g., NK cells) are edited, for example to knock down or knock expression of a target gene. In some embodiments, multiple genes are edited. In several embodiments, in addition to editing one or more target genes, immune cells (e.g., NK cells) are engineered to express a chimeric antigen receptor that targets one (or more) target antigens, such as a tumor marker. In several embodiments, immune cells, such as NK cells are edited to reduce, substantially reduce, and/or eliminate CD70 expression and engineered to express a CAR that targets CD70. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate CISH expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate TGFBR (e.g., TGFBR2)expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate NKG2A expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate ADORA2A (Adenosine 2a Receptor) expression. In several embodiments, the

immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate Cytokine Signaling 2 (SOCS2) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate Casitas B-lineage lymphoma-b (Cbl-b) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate Beta-2 Microglobulin (B2-microglobulin, or B2M) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate T cell immunoreceptor with Ig and ITIM domains (TIGIT) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate Programmed cell death protein-1 (PD-1) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate T-cell immunoglobulin and mucin-domain containing-3 (TIM-3) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate CD38 expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate T cell receptor alpha (TCR α) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate CEACAM1 expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate DDIT4 expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate MAPKAP Kinase 3 (MAPKAPK3) expression. In several embodiments, the immune cells are optionally also edited to reduce, substantially reduce, and/or eliminate SMAD3 expression. Non-limiting examples of guide RNAs to edit one or more of such targets (e.g., using Cas9, CasX, CasY or other endonuclease) may be found in U.S. Provisional Patent Application No. 63/201159, filed April 15, 2021, the entire contents of which is incorporated by reference herein.

[00313] The tumor microenvironment (TME), as suggested with the nomenclature, is the environment around a tumor, which includes the surrounding blood vessels and capillaries, immune cells circulating through or retained in the area, fibroblasts, various signaling molecules related by the tumor cells, the immune cells or other cells in the area, as well as the surrounding extracellular matrix. Various mechanisms are employed by tumors to evade detection and/or destruction by host immune cells, including modification of the TME. Tumors may alter the TME by releasing extracellular signals, promoting tumor angiogenesis or even inducing immune tolerance, in part by limiting immune cell entry in the TME and/or limiting reproduction/expansion of immune cells in the TME. The tumor can also modify the ECM, which can allow pathways to develop for tumor extravasation to new sites. Transforming Growth-Factor beta (TGFb) has beneficial effects when reducing inflammation and preventing autoimmunity. However, it can also function to inhibit anti-tumor immune responses, and thus, upregulated expression of TGFb has been implicated in tumor progression and metastasis. TGFb signaling can inhibit the cytotoxic function of NK cells by interacting with the TGFb receptor expressed by NK cells, for example the TGFb receptor isoform II (TGFBR2). In accordance with several embodiments disclosed herein, the reduction or elimination of expression of TGFBR2 through gene editing (e.g., by CRISPR/Cas9 guided by a TGFBR2 guide RNA) interrupts the inhibitory effect of TGFb on NK cells.

[00314] As discussed above, the CRISPR/Cas9 system was used to specifically target and reduce the expression of the TGFBR2 by NK cells. Various non-limiting examples of guide RNAs were tested, which are summarized below.

Table 2: TGFb Receptor Type 2 Isoform Guide RNAs

SEQ ID NO:	Name	Sequence
124	TGFBR2-1	CCCCTACCATGACTTTATTC
125	TGFBR2-2	ATTGCACTCATCAGAGCTAC
126	TGFBR2-3	AGTCATGGTAGGGGAGCTTG
127	TGFBR2-4	TGCTGGCGATACGCGTCCAC
128	TGFBR2-5	GTGAGCAATCCCCCGGGCGA
129	TGFBR2-6	AACGTGCGGTGGGATCGTGC

[00315] In accordance with additional embodiments, a disruption of, or elimination of, expression of a receptor, pathway or protein on an immune cell can result in the enhanced activity (e.g., cytotoxicity, persistence, etc.) of the immune cell against a target cancer cell. In several embodiments, this results from a disinhibition of the immune cell. Natural killer cells express a variety of receptors, such particularly those within the Natural Killer Group 2 family of receptors. One such receptor, according to several embodiments disclosed herein, the NKG2D receptor, is used to generate cytotoxic signaling constructs that are expressed by NK cells and lead to enhanced anti-cancer activity of such NK cells. In addition, NK cells express the NKG2A receptor, which is an inhibitory receptor. One mechanism by which tumors develop resistance to immune cells is through the expression of peptide-loaded HLA Class I molecules (HLA-E), which suppresses the activity of NK cells through the ligation of the HLA-E with the NKG2A receptor. Thus, while one approach could be to block the interaction of the HLA-E with the expressed NKG2A receptors on NK cells, according to several embodiments disclosed herein, the expression of NKG2A is disrupted, which short circuits that inhibitory pathway and allows enhanced NK cell cytotoxicity.

[00316] CRISPR/Cas9 was used to disrupt NKG2A expression using the non-limiting examples of guide RNAs shown below in Table 3.

Table 3: NKG2A Guide RNAs

SEQ ID NO:	Name	Sequence
135	NKG2A-1	GGAGCTGATGGTAAATCTGC
136	NKG2A-2	TTGAAGGTTTAATTCCGCAT
137	NKG2A -3	AACAACTATCGTTACCACAG

[00317] Other pathways that may impact immune cell signaling are edited, in several embodiments. One such example is the CIS/CISH pathway. Cytokine-inducible SH2-containing protein (CIS) is a negative

regulator of IL-15 signaling in NK cells, and is encoded by CISH gene in humans. IL-15 signaling can have positive impacts on the NK cell expansion, survival, cytotoxicity and cytokine production. Thus, a disruption of CISH could render NK cells more sensitive to IL-15, thereby increasing their anti-tumor effects.

[00318] As discussed above, CRISPR/CAS9 was used to disrupt expression of CISH, though in additional embodiments, other gene editing approaches can be used. Non-limiting examples of CISH-targeting guide RNAs are shown below in Table 4.

Table 4: CISH Guide RNAs

SEQ ID NO:	Name	Sequence
130	CISH-1	CTCACCAGATTCCCGAAGGT
131	CISH-2	CCGCCTTGTCATCAACCGTC
132	CISH-3	TCTGCGTTCAGGGGTAAGCG
133	CISH-4	GCGCTTACCCCTGAACGCAG
134	CISH-5	CGCAGAGGACCATGTCCCCG

[00319] Figure 28A shows a schematic of a non-limiting embodiment of a gene editing approach used according to embodiment disclosed herein. Cells (e.g., NK cells) are electroporated at Day 0 in order to initiate gene editing though use of gene editing machinery. In several embodiments, CRISPR-Cas-based editing is used. Cells are cultured in high IL-2 media for one day, then expanded on feeder cells in low IL-2 media for an additional 6 days. At Day 7, cells are transduced with a viral construct encoding a CAR directed against a tumor and then expanded again for at least another 5 days prior to FACS analysis. In this experiment, double gene editing was performed to knock down expression of CD70 and the inhibitory receptor, NKG2A, or the combination of CD70 and TGFBR2 (CD70 knockout is shown above). Figure 28B shows FACS analysis for expression of NKG2A after editing, while Figure 28C shows the related control. Gene editing reduced NKG2A expression by over 50%, with less than 20% of the edited NK cells expressing the inhibitory receptor. Figure 28D shows data for TGFBR2 expression post-editing, with Figure 28E showing the related control. TGFBR2 express was reduced such that only about 3% of cells expressed the receptor. These data, in conjunction with the data above related to CD70 editing, demonstrate that immune cells, such as NK cells, can successfully be edited to alter expression of two or more target genes.

[00320] Having established that double knock out can be performed, the ability to express CARs as disclosed herein on the NK cells was also assessed. Figure 29A shows expression of the NK71 CD70-targeting CAR on NK cells that were edited to reduce expression of CD70 (using CD70-1 guide RNA). Nearly 90% of the NK cells expressed the NK71 CAR. Figure 29B shows the substantially eliminated expression of CD70 in those NK cells (only about 5% of the cells expressed CD70). Figure 29B shows expression of the NK71 CAR by cells doubly edited to reduce CD70 and CISH expression. Again, nearly 90% of the doubly-edited NK cells expressed the NK71 CAR. Figure 29D again confirms substantial reduction in CD70 expression on the NK cells. Figure 29E shows expression of the NK71 CAR by cells

doubly edited for CD70 and NKG2A. Over 90% of the doubly-edited NK cells expressed the CAR. As shown in Figure 29F, CD70 expression was substantially reduced in these doubly-edited NK cells as well. Figure 29G shows NK71 expression on NK cells doubly-edited to reduce expression of CD70 and TGFBR2, with over 87% of the cells expressing the CAR. As shown in Figure 29H, CD70 expression was reduced by nearly 90% in these cells. Figure 29I and 29J show control data (mock gene editing, e.g., electroporation only). All data presented in Figure 29 was obtained at Day 11 (4 days after transduction).

[00321] Data was collected on these say groups at Day 18 (11 days after transduction) to assess the persistence of the gene editing and the stability of CAR expression. Data for NK71 expression in CD70 knockouts is shown in Figure 30A with corresponding CD70 expression data in Figure 30B. Data for NK71 expression in CD70-CISH knockouts is shown in Figure 30C with corresponding CD70 expression data in Figure 30D. Data for NK71 expression in CD70-NKG2A knockouts is shown in Figure 30E with corresponding CD70 expression data in Figure 30F. Data for NK71 expression in CD70-TGFRB2 knockouts is shown in Figure 30G with corresponding CD70 expression data in Figure 30H. Corresponding control data is shown in Figure 30I and 30J. Of note in this data is that NK71 expression was maintained across each of the knockout groups and also that CD70 expression was further diminished in each group, with all groups showing 97% or more reduction in CD70 expression.

[00322] Viewing the expression data in another way, Figure 31A shows a plot of the mean fluorescence intensity (MFI) detected, representing NK71 expression, after each of the gene editing approaches undertaken. As can be seen, each of the gene edited cells, regardless of single or double gene editing, expressed the NK71 CAR at elevated levels over control, with relatively consistent MFI across each gene editing approach. The percentage of NK71 positive cells (out of the entire population tested) is shown in Figure 31B. Regardless of the gene editing approach undertaken, at least 60% of the NK cells expressed NK71. The single CD70 knockout and the combination CD70/CISH knockout expressed the greatest percentage of NK71, at almost 80% and about 85%, respectively. Figure 31C shows the percentage of CD70 expression (in terms of percent reduction). As can be seen, each of the gene editing techniques, whether targeting CD70 alone, or in combination with other targets, yielded nearly 100% reduction in CD70 expression. Figures 32A-32B show corresponding data for the NK72-expressing NK cells. Together these data show that gene edited cells, whether with respect to editing a single target, or two targets, are still capable of expressing a CAR at significant levels of expression.

[00323] As various gene edits can impact signaling pathways (and thus increase or enhance, proliferation, cytotoxicity, and/or persistence), an experiment was performed to assess the impact of gene editing of proliferation of edited/engineered NK cells. 3 $X10^5$ NK cells were transduced (on Day 7 after gene editing) with a viral construct encoding either the NK71 or NK72 CAR. Gene edits, single or double, were made as discussed above. Figure 33A shows that, at Day 12 (5 days post-transduction), proliferation of CD70 knockout and CD70/TGFBR2 knockouts proliferated at about the same rate over the 5 days in culture. Interestingly, CD70/CISH showed substantially more (about 30%) more proliferation than either the CD70 knockout or the CD70/TGFBR2 knockout. In contrast, the CD70/NKG2A knockout showed

reduced proliferation compared to all other groups. Figure 33B shows a similar pattern in cell proliferation for cells transduced with the NK72 CAR.

[00324] Additional data was collected to evaluate the longer-term viability/proliferation of engineered/edited NK cells. Culturing of the engineered and edited NK cells was carried out to 35 days, with cell population viability measured at Day 14, 21, 28 and 35. The results are shown in Figured 34A and 34B for NK71-expressing and NK72-expressing NK cells, respectively. The pattern of viability in this experiment parallels the proliferation data discussed above. Regardless of the editing approach used, all the groups showed an upswing in overall viability between days 14 and 21. The CD70/NKG2DA group had the smallest increase, CD70 alone and CD70/TGFBR2 performed similarly and CD70/CISH outpaced each of the other groups. Moving from Day 21 to 28 and on to 35, each of the groups showed a decline in the viability of the populations, however, CD70/CISH edited cells showed the least decline over time, with the overall viability being substantially higher than the other groups as Day 35. In accordance with several embodiments, gene editing can enhance not only the ability of the edited cells to proliferate, but also enhance their viability as compared to unedited cells. In several embodiments, a dual modification (or more) can synergistically interact to yield robustly proliferating cells expressing a CAR, with enhanced viability of those cells. Advantageously, in several embodiments, these modifications lead to an easier generation of clinically relevant cell numbers.

[00325] Having confirmed that edited and engineered cells express a CAR, proliferate successfully in culture, and have enhanced viability compared to un-edited cells, their anti-tumor effects were investigated. Figure 35A shows cytotoxicity data of the indicated edited and engineered NK cells against 786-O cells, a renal cell carcinoma line expressing high levels of CD70. These edited NK cells were transduced with the NK71 CAR and cytotoxicity was measured starting at Day 14 post editing. TGFb, a cytokine that acts as an NK cell inhibitor in the tumor microenvironment, was not added here. A CD19-targeting CAR construct expressed by NK cells (unedited) was used as a control, as were 786-O cells cultured alone. At the E:T ratio of 1:1 each of the gene edited groups substantially reduced 786-O growth over the course of the experiment, with the end results being largely indistinguishable across the groups. Figure 35B shows the same setup, but with an E:T ratio of 1:2. With the reduction in the number of effector NK cells, the various gene editing approaches begin to show distinct results. Each of the CD70, CD70/TGFBR2 and CD70/NKG2A groups successfully controlled 786-O tumor cell growth, but not to the same extent as the CD70/CISH edited NK71-expressing NK cells. This group showed not only a more rapid anti-tumor effect, but also an overall greater reduction in the tumor cell number. Figure 35C shows corresponding data for NK cells edited and engineered to express the NK72 CAR, and using an E:T of 1:1. The data are similar to that of the NK71 construct, with all editing groups successfully controlling tumor growth. Figure 35D shows NK72 cytotoxicity data at an E:T of 1:2. Similar to the NK71 cells, the editing approach undertaken causes some separation in the cytotoxicity of the NK cells, though less pronounced than with the NK71 CAR. Here, CD70 and CD70/NKG2A edited cells showed less robust tumor growth control. CD70/CISH edited NK cells successfully controlled growth (slightly improved over the prior two

groups) and CD70/TGFBRR2 modestly outperformed the CD70/CISH cells. In accordance with several embodiments, the editing approach undertaken works in concert with a given CAR, and in some embodiments, a specific CAR may be more effective with a specific knockout or knockouts of target genes in the engineered cell.

[00326] Figures 36A-36D show corresponding data to that of 35A-35D, but using the ACHN tumor cell line as the target, as it expresses low levels of CD70. These data are indicative of not only the cytotoxicity of the engineered/edited NK cells through CD70-mediated means, but also through the normal cytotoxicity that NK cells would provide. Figure 36A shows each of the edited NK-71 expressing cell groups effectively halting ACHN tumor cell growth at 1:1: E:T. Figure 36B shows a large separation in the groups, with CD70/CISH edited cells showing robust anti-tumor effects. Figures 36C and 36D show similar patterns with CD70/CISH edited NK72-expressing cells showing the most effective tumor growth control. Thus, in several embodiments, gene editing enhances the cytotoxicity of engineered immune cells in a target-independent fashion. For example, according to several embodiments CD70/CISH editing imparts to NK cells expressing an anti-CD70 CAR a heightened ability to exert cytotoxic effects against the tumor, whether the target tumor is rich or sparse in marker identified by the CAR.

[00327] Figure 37A shows additional cytotoxicity data against the 786-O RCC tumor cells, now at 14 days post-transduction (21 days post gene editing). A 1:2 E:T ratio is used here and an NKG2D-directed CAR-expressing NK cell (NKX101) is added for comparison. Those cells, from another donor, were previously engineered to express the NKG2D-OX40-CD3Z construct, expanded, frozen and were thawed for this comparative assay. NK71-expressing edited NK cells each showed robust tumor control, though the CD70/NKG2A group allowed greater amounts of tumor growth before leveling off and suppressing further increases. Further dilution of the effector cells (a 1:4 E:T ratio) again caused differences in the cytotoxicity of the various groups. CD70/NKG2A edited NK71-expressing NK cells showed the least amount of tumor growth control, with singly-edited CD70 edited NK71-expressing NK cells showing modest improvement. CD70/TGFBR2 edited cells exhibited a relatively consistent reduction in 786-O cell numbers after an initial peak about 2 days into the experiment. Notably the CD70/CISH edited NK cells reduced the growth of the tumor cells to the lowest level of any group, including those NK cells operating through a non-CD70 route. Figure 38A shows corresponding data at a 1:2 ratio against ACHN cells. Given the lower CD70 expression on these cells, the CD70/NKG2A edited NK cells failed to control tumor growth, given that groups previously discussed reduced proliferation and viability. Each of the CD70 and CD70/TGFBR2 edited groups exhibited reasonable control of tumor growth. Most notable, however was that the CD70/CISH edited group nearly paralleled the significant suppression of tumor growth exhibited by NKG2D-targeting NK cells, despite the CD70/CISH cells being directed to a target that has reduced presence on this tumor cell line. This is in accordance with embodiments as discussed above, where the CD70/CISH gene editing positively impacts the edited NK cell in a non-target dependent manner, for example through enhanced generation of cytotoxic signals, improved metabolic profiles of the NK cell such that the edited NK cell population can expand to change the starting E:T ratio from the 1:2 starting point. This point is

made more clear when seeing the results presented in Figure 38B, wherein a 1:4 E:T ratio was used and all groups other than CD70/CISH-edited NK71-expressing NK cells allowed substantial tumor growth. In accordance with several embodiments disclosed herein, gene editing of CD70 and CISH in combination results in edited immune cells, e.g., NK cells, that are unexpectedly effective against tumor cells, even those expressing limited quantities of the targeted marker. Figures 39A-39B show corresponding data for NK cells expressing the NK72 CAR, with generally similar trends in the data, in that, of the edited cells, the CD70/CISH edited cells outperform the other editing approaches undertaken in terms of controlling 786-O cell growth. Likewise, Figures 40A and 40B show corresponding data for NK72-expressing edited NK cells against low-CD70 ACHN cells. As above, CD70/CISH edited cells showed the most robust tumor cell growth control. In accordance with several embodiments, CD70 and CISH editing drive the edited NK cells (or T cells) to exhibit unexpectedly superior anti-tumor effects, even at lower initial E:T ratios. As discussed above, in several embodiments, the CD70 and CISH editing allow the NK cells to avoid the suicide effect of the anti-CD70 CAR and also upregulate various aspects of the edited NK cell metabolism and/or cytotoxic actions.

[00328] Further experiments were conducted to evaluate the CD70/CISH knockouts and their enhanced anti-tumor effects. Figure 41A shows the embodiment of gene editing and engineering used for this example and Figures 41B-41O show the expression results. Guide RNAs used were CD70-1 and CISH-1, in this experiment. Edited NK cells were transduced at Day 7 with viral constructs encoding either NK71 or NK72. Figure 41B is an unstained control and Figure 41C is a CD70 positive control cell. Figure 41D shows CD70 expression on NK cells after editing and Figure 41D shows NK71 expression. Figures 41F-41G show corresponding data for CD70 and NK72 expression, respectively. Figures 41H-41I show corresponding data for CD70 and NK71 expression, respectively, when both CD70 and CISH were edited. Figures 41J-41K show corresponding data for CD70 and NK72 expression, respectively, when both CD70 and CISH were edited. Figures 41L-41M show corresponding data for CD70 and NK71 expression, respectively, when cells were exposed only to electroporation (no guide RNA/CRISPR) and transduction with NK71. Figures 41N-41O show corresponding data for CD70 and NK72 expression, respectively, when cells were exposed only to electroporation (no guide RNA/CRISPR) and transduction with NK72. As discussed above, these approaches yield substantial, if not total reduction in the amount of CD70 and/or CISH expressed by the NK cells. If expression is not reduced to below detectable levels, according to several embodiments, the function of the related pathways of CD70 and/or CISH is substantial or significantly disrupted. Having disrupted both CD70 and CISH expression, the cytotoxicity of NK71 and NK72 expressing NK cells was evaluated. Figure 42A shows cytotoxicity data against 786-O cells by NK71-expressing NK cells having been edited in the indicated manner. An E:T of 1:2 was used and as indicated the NK cells were pre-treated overnight with (or without) TGFbeta in culture prior to the experiment and during the experiments. As mentioned above, TGFbeta is a cytokine that is released by tumor cells into the tumor microenvironment and is one way by which certain tumors evade immune cells. As with the data discussed above, CD70/CISH-edited NK cells were able to control tumor growth. Notably, however, is the

ability of CD70/CISH-edited NK cells to substantially control tumor growth after pre-treatment with and in the presence of TGFb. Given that TGFb inhibits immune cell activity, the presence of TGFb would be expected to limit the ability of the NK71-expressing NK cells to effectively control the growth of the tumor cells, an effect seen in the CD70-edited NK71-expressing NK cells treated with TGFb, which controlled tumor growth in a manner indistinguishable from control. Unexpectedly, the CD70/CISH edited cells exposed to TGFb controlled tumor growth nearly as well as those cells not inhibited by the presence of TGFb. These effects are seen on the low-CD70-expressing ACHN cells, in Figure 42B. In this experiment, one would have expected the experimental groups with TGFb present to show limited ability to control ACHN cell growth, as the ACHN cells lack the robust CD70 expression of certain cells, like 786-O, and the TGFb would be expected to inhibit the NK cells. What the data in Figure 42B show, unexpectedly, is that the CD70/CISH editing, even in the presence of the inhibitory TGFb, enables NK cells to achieve tumor growth control on par with those experimental groups not exposed to the inhibitory signals of TGFb. In some embodiments, the CISH knockout enables the edited cells to overcome the inhibitory effect of TGFb, in a substantial, if not complete manner. In several embodiments, this endows the CD70-CISH edited NK cells expressing a CAR, such as an anti-CD70 CAR with enhanced ability to effectively control tumor progression, with the cytotoxic effects limiting, if not reducing and/or eliminating tumor cells. Figure 42C shows corresponding cytotoxicity data for edited NK cells engineered to express the NK72 CAR. As discussed above, the CD70/CISH edited NK cells show substantial anti-tumor effects, even in the presence of the inhibitory TGFb cytokine, which corresponds to several embodiments of the edited and engineered NK cells disclosed herein.

Example 4 – Further Editing of Multiple Genes, Including Tumor Microenvironment-Related Genes

[00329] According to several embodiments disclosed herein, gene editing of NK and/or T cells results in the edited cells having increased resistance to inhibitory factors that may be present in the tumor microenvironment. In addition to the experiments discussed above, additional experiments were conducted to further evaluate the effects of gene editing on NK (or T cell) cytotoxicity.

[00330] As discussed above, NK cells express endogenous CD70 and expression of an anti-CD70 CAR (designed to target a CD70-expressing tumor) would result in destruction of the engineered NK cell population due to lack of differentiation between the CD70-expressing NK cells and CD70-expressing tumor cells. Thus, several embodiments in which NK cells are engineered to express CD70 also include gene editing to reduce, or knockout, CD70 expression by the NK cells. Figures 43A-43I show data related to the gene editing of NK cells to knockout CD70 expression using different guide RNAs, or combinations of guide RNAs (expression evaluated at 7 days post-electroporation). Figure 43A shows that use of CRISPR-Cas9 gene editing with CD70-1 guide RNA reduced CD70 expression by over 75%. Editing using CD70-2 guide RNA reduced CD70 expression by over 60% (43B). Editing using CD70-3 guide RNA reduced CD70 expression by over 55% (43C). The combination of guide RNA 1 and 3 reduced CD70 expression on NK cells by over 75% (43D). The combination of guide RNA 1 and 2 also reduced CD70 expression on NK

cells by over 75% (43E). The combination of guide RNA 2 and 3 reduced CD70 expression on NK cells by nearly 85% (43F). As discussed herein, in several embodiments, multiple genes are edited in combination. Figure 43G shows reduced expression of CD70 (by almost 80%) when NK cells were edited using CD70-1 guide RNA in combination with guide RNA (CISH-1) targeting CISH. Similarly, CD70 expression was reduced by over 80% when CD70-1 guide RNA was used in combination with three guide RNAs targeting the adenosine receptor (A2AR). The three, non-limiting examples of guide RNAs targeting A2AR are shown in Table 5.

Table 5: Adenosine Receptor (A2AR) Guide RNAs

SEQ ID NO:	Name	Sequence
396	A2AR -1	CGAGGAGCCCATGATGGGCA
397	A2AR -2	GGGCAATGTGCTGGTGTGCT
398	A2AR -3	CAGTGACACCACAAAGTAGT

[00331] These data demonstrate that targeting multiple genes in combination does not reduce the effectiveness of CD70 gene editing. Figure 43I show control (electroporation only) CD70 expression on NK cells.

[00332] Data regarding the cytotoxicity of these various constructs. Figure 44A shows the percent cytotoxicity of the gene edited NK (note, for this data, the NK cells were not engineered to express a CAR) cells against REH tumor cells at either a 1:1: or 1:2 E:T ratio. These gene edited cells exhibited between about 35-50% cytotoxicity against the REH tumor cells at a 1:1 E:T ratio, while the electroporation only (EP) and un-edited (UN) NK cells yielded about 20-25% cytotoxicity at 1:1 E:T ratio. Shifting to a 1:2 E:T ratio decreased the cytotoxicity of all groups, with the controls dropping to about 10% and the majority of the edited cells yielding between about 20-30% cytotoxicity. These data are also shown in a different manner in Figures 44B (1:1) and 44C (1:2), which allow for additional insight into how various edits may impact the efficacy of NK cells. Editing of NK cells with any of CD70-1, or -2 guide RNAs alone resulted in similar cytotoxicity. Use of guide RNA CD70-3 or CD70-1+3 appeared to slightly improve cytotoxicity. In contrast, the combination of guide RNA CD70-2+3 or 1+2 appeared to lower cytotoxicity. CISH and A2AR edited NK cells each exhibited cytotoxicity in the same (CISH) or slightly higher (A2AR) as the CD70 edited cells at a 1:1 E:T ratio. A similar pattern is shown in Figure 44C, with a 1:2 E:T ratio. These data demonstrate that, in some embodiments, a particular guide RNA can work particularly well. However, these data also show that, even with some slight variance in the change in cytotoxicity between the editing machinery used, editing causes an increase in cytotoxicity (e.g., through resistance to TME signaling) as compared to non-edited cells.

[00333] Figure 44D shows additional data evidencing further increases in cytotoxicity when gene edited cells are engineered to express anti-tumor CARs. In this experiment Nalm6 cells were used as the target tumor cell and were incubated with various NK cells at a 1:1 E:T ratio (20,000 target cells). As

expected, Nalm6 cells alone increased throughout the course of the experiment. Nalm6 cells incubated with control NK cells (either electroporated only (EP) or un-electroporated (UN) showed reduced growth over time, as compared to Nalm6 alone. Editing NK cells (but not engineering) further reduced Nalm6 grown as shown by the two traces for CD70-1 and CD70-2. Those NK cells edited using CD70-1 or CD70-2 guide RNA and engineered to express a non-limiting embodiment of a CD19-targeting CAR, as well as non-edited NK cells engineered to express the same CAR resulted in complete eradication of the target Nalm6 tumor cells. Thus, according to several embodiments, expression of an anti-tumor CAR and gene editing of an immune cell, such as an NK cell, yields a highly cytotoxic edited/engineered cell. In several embodiments, other aspects of the edited/engineered cell are enhanced, such as the life span of the cell (e.g., persistence), particularly persistence in vivo, the ability of the cells to be expanded and/or stored, and the like. In several embodiments, the editing allows the edited and engineered cells to be used at lower E:T ratios, but still effectively control tumor growth.

[00334] Figure 45A further explores the effects of gene editing, with CD70-knockout NK cells also being edited for either CISH knockout or adenosine receptor (A2AR) knockout. The indicated edited cells (non-engineered) or control cells (electroporation only (EP) or un-electroporated (UN)) were incubated with Reh tumor cells at a 1:1 E:T ratio (20,000 NK cells). Control Reh cells expanded significantly in the first several days of the experiment with growth plateauing and maintaining elevated population levels for the duration of the experiment. Control EP and UN NK cells delayed Reh cell expansion in the initial phases, but eventually the Reh cells began rapid expansion near the close of the co-culturing. In contrast, CD70-edited cells (CD70-1 gRNA) allowed only modest growth in the last day of the experiment. Likewise, editing with CD70-1 gRNA in combination with editing CISH resulted in even further control to Reh tumor cell growth. Following in this trend, editing with CD70-1 gRNA in combination with editing the adenosine receptor resulted in the greatest control of Reh cell growth. Figure 45B shows similar experimental results, but with an E:T ratio of 1:2. These data shows that the relative performance of the dually-edited NK cells is more condensed, making it more difficult to determine which set of cells is exhibiting the greater cytotoxicity. However, this data also confirms either single, or multiple, gene edits to reduce, or eliminate in several embodiments, expression of certain genes, such as CISH, A2AR, or other genes related to the immune suppressive nature of the tumor microenvironment, yield immune cells (e.g., NK cells or T cells, depending on the embodiment) with enhanced tumor-directed cytotoxicity. As discussed above, in several embodiments, other characteristics of the edited immune cells may also be enhanced, e.g., persistence, expansion capacity, etc.

[00335] Further investigation into the enhanced anti-tumor effects of gene edited immune cells was undertaken by gene editing certain tumor microenvironment related genes in conjunction with engineering the immune cells, here NK cells, to express an anti-CD70 CAR (to target CD70-expressing tumor cells). Figures 46A-46J show FACS analysis of various gene edits in conjunction with engineering to induce expression of a non-limiting embodiment of an anti-CD70 CAR, here NK71. Figure 46A shows the distribution of NK cells that are (i) positive for NK71 expression and (ii) negative for CD70 express (based

on editing the NK cells used with guide RNA CD70-1). Approximately 84% of the NK cells sampled met this expression profile. Similarly, about 85% of the NK cells sampled exhibited NK71 expression and reduced CD70 expression with the editing of the cells using CD70-2 guide RNA (Figure 46B). Slightly higher degrees of NK71-expressing/CD70-edited cells were detected when CD70 was edited using guide RNA CD70-3 or the combination of guide RNA CD70-1 and -3 (nearly 87% for both; Figures 46C-46D). Use of guide RNAs CD70-2 and -3 yielded almost 90% of the NK cells sampled with this phenotype (Figure 46E). Similarly, use of guide RNA CD70-1 and -2 yielded over 85% of the NK cells sampled with this phenotype (Figure 46F). Similar numbers resulted when editing the cells using both CD70-1 to knockdown CD70 expression and CISH-1 guide RNA to knock down CISH expression (~84%, Figure 46G) and CD70-1 to knockdown CD70 expression and A2AR-1, -2, and -3 guide RNA to knock down A2AR expression (Figure 46H). Figures 46I and 46J show control data. Together, these data confirm that significant numbers of immune cells, such as NK cells, can successfully be both edited (with multiple targets, in several embodiments) and engineered to express a tumor-targeting CAR.

[00336] Having shown that immune cells, such as NK cells, could be both edited (multiple targets in several embodiments) and engineered to express a CAR, experiments were performed to determine the cytotoxicity of such cells. 786-O cells, a renal cell carcinoma cell line known to express high levels of CD70, was used as the target tumor cell for a portion of this experiment. Figure 47A shows the experimental results when the various NK cell constructs are present in a 1:2 E:T ratio (10,000 NK cells). As would be expected the negative control 786-O cells alone expanded quickly and maintained a relatively high cell count throughout the experiment. Electroporated only cells (EP) allowed for a fairly robust early stage increase followed by a long, tapered decline, starting around 2 days after co-culture with the 786-O cells. CD70-1 guide RNA edited cells showed a similar pattern but with improved overall control in tumor cell numbers. With an overall cytotoxicity profile resembling those of CD70-1 guide RNA edited cells in shape only, those cells that were additionally engineered to express NK71 (a non-limiting CD70-targeting CAR) exhibited profoundly more favorable control of tumor expansion. Notably, in this experiment, the profound control of tumor growth is at a 1:2 E:T ratio, indicative of the highly effective nature of cells according to embodiments disclosed herein against tumor cells generally, but in particular against cells expressing elevated levels of the target of a CAR expressed by edited/engineered cells.

[00337] Further demonstrating the enhanced cytotoxicity against cells expressing elevated levels of a tumor marker targeted by a CAR expressed by edited and/or engineered immune cells is the data shown in Figure 47B. The experimental setup here reduced the E:T ratio to 1:4 (5,000 NK cells) and used high-CD70 expressing Reh cells and the indicated edited and/or edited and engineered NK cells. As can be seen in this data, the editing of NK cells to reduce expression of NK cells continued to allow the edited CD70 knockout cells (CD70-1) to control tumor growth more effectively than control NK cells. The additional engineering of the edited NK cells to express an anti-CD70 CAR (CD70+NK71) further improved the cytotoxic effects. Advantageously, editing multiple genes in the NK cells, either CD70 + CISH or CD70 + A2AR, coupled with engineering the cells to express an anit-CD70 CAR yielded still further improvements

in cytotoxicity against the target 786-O cells, most notably with A2AR editing. Similar trends are shown in Figure 47C, where the E:T ratio was further reduced (1:8, 2,500 NK cells). These data further demonstrate the enhanced cytotoxicity against target cells that is induced as a result not only of editing an immune cell, like an NK cell, but the unexpectedly enhanced cytotoxicity that results from editing multiple targets (such as TME-related genes) in conjunction with engineering of the cells to express a CAR.

[00338] Further demonstrating the advantage of targeting a tumor marker that is prevalent on a target cell with a CAR specific to that marker is the data presented in Figures 47D-47F, which employed co-culture of various edited and/or edited and engineered NK cells against ACHN tumor cells, which express relatively low levels of CD70. As can be seen in Figure 47D (1:2 E:T, 10,000 NK cells), editing of CD70 alone resulted in NK cells with cytotoxicity on par with that of NK cells subjected to electroporation alone (EP). Tumor growth in this experimental setup was similar, whether NK cells were present or not, suggesting the ACHN cells grow and expand through a series of signals that does not involve expression of CD27, the binder for CD70 (normally expressed by NK cells), or involves some other TME-signaling moiety that blocks/reduces immune cell function, otherwise, the CD70-1 guide RNA NK cells would have been expected to perform more poorly than EP cells alone. Even with the relatively low expression of CD70 in ACHN cells, the engineering of the NK cells to express NK71, a non-limiting example of an anti-tumor CAR, yielded substantial improvements in reducing tumor growth as compared to control, though overall, there was still increased tumor cell count over time. These trends are exemplified in Figures 47E and 47F, which employed 1:4 and 1:8 E:T ratios, respectively (target cell number is held constant at 20,000 cells in these cytotoxicity assays). This effectively dilutes the effector cells as compared to the targets, and without the ability to bind an overexpressed CD70 via the CAR, ACHN tumor growth progressed to levels indistinguishable from control. These data support the approach that, for a given cancer, gene editing in conjunction with engineering an immune cell with a CAR targeting a marker expressed by the target tumor cell can yield enhanced resistance to immune suppressive signals from the tumor microenvironment and ultimately yield enhanced cytotoxicity, persistence and/or overall efficacy against a tumor.

[00339] To further elucidate the ability of gene editing of immune cells, such as NK cells, additional experiments were conducted comparing the cytotoxicity of gene edited cells engineered to express a non-limiting embodiment of a CAR directed against CD70, here NK71 in the presence and absence of an inhibitor of the gene that was edited. In this experiment, NECA, a high affinity adenosine receptor agonist was used. NECA has Ki (inhibitory concentration) of 6.2, 14, and 20 nM for human adenosine receptor subtypes A3, A1 and A2A receptors respectively and an EC50 of 2.4 μM for human A2B receptor. Adenosine (e.g., extracellular adenosine in the blood stream) acts on immune cells, including NK cells, by binding to one of these four adenosine receptors, most notably the A2A receptor (A2AR), with a resultant suppression of NK cell immune function. Thus, the presence of NECA in the co-culture of tumor cells and NK cells would be expected to negatively impact the cytotoxic function of the NK cells. As can be seen in Figure 48A (in the cytotoxicity plot) and 48B (histogram), as compared to NK cells expressing NK71 alone with NECA in the co-culture with 786-O cells, NK cells expressing NK71 and edited for A2AR disruption,

the latter NK cells exhibited a greater degree of cytotoxicity. Comparisons of these two groups are indicated by dashed lines. Note that Figure 48A does not include a trace for 786-O cells alone, which allows for greater visual separation of the cytotoxicity curves for the various treatment groups. Additional data is shown on Figures 48C and 48D. Here, an E:T of 1:2 was used (1:1 used in 48A) and the tested constructs show relatively similar cytotoxicity profiles (again with a control not shown to reduce compaction of the line graphs in Figure 48C. The histogram of 48D summarizes this data. As can be seen CISH editing of NK cells increases the cytotoxic effects of NK cells expressing NK71 (compare 1st vs. 2nd histogram bar). Interestingly, editing of CISH (5th bar) as well as editing of A2AR (6th bar) resulted in increased cytotoxicity (less signal detection from tumor cells), even when NECA was present (4th bar). It is contemplated that there may be some common downstream signaling between CISH and A2AR that account for this resistance to NECA, which mimics an agonist-based suppression of NK cell function as may be seen in the tumor micro-environment. Thus, according to several embodiments, editing CISH and/or A2AR (or another target involved in tumor micro-environment-related immune cell suppression) in an immune cell, such as an NK cells, can not only provide a degree of resistance to immune suppressive effects of the tumor microenvironment, but can act synergistically with an anti-tumor CAR expressed by the immune cell, such as an anti-CD70 CAR to result in enhanced cytotoxicity against a tumor. This approach can also, according to several embodiments, result in other improved characteristics of the cells, such as enhanced persistence (especially in the tumor microenvironment), increased expansion capacity; increased target specificity, and reduced dosage requirements (either lower numbers of administered cells or increased time between doses, among others.

[00340] Additional genes known to affect NK cell activity were also investigated. More specifically, the genes mothers against decapentaplegic homolog 3 (SMAD3), MAP kinase-activated protein kinase 3 (MAPKAPK3), carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1), and DNA-damage-inducible transcript 4 (DDIT4) were investigated. SMAD3 is an intracellular downstream signaling protein for the TGFb ligand superfamily. SMAD3-mediated TGFb receptor or ALK4 signaling may lead to inhibition in NK cells. MAPKAPK3 activity suppresses IFN-gamma gene expression and attenuates NK cell cytotoxicity. CEACAM1 is a checkpoint molecule on the NK cell surface, and is highly upregulated during NK cell feeder expansion. DDIT4 is a negative regulator of mTORC1; mTORC1 enables IL-15 mediated NK cell survival, proliferation, cytotoxicity, and glucose metabolism. Therefore, it was examined whether knocking out these genes would improve efficacy of anti-CD70 CAR NK cells. Non-limiting embodiments of guide RNAs for disrupting SMAD3, MAPKAPK3, CEACAM1, and DDIT4 are provided in Table 6.

Table 6: Additional guide RNAs

SEQ ID NO:	Target	Name	Sequence
1190	SMAD3	SMAD3 guide RNA 1	CCGATCGTGAAGCGCCTGCT
1191	SMAD3	SMAD3 guide RNA 2	CGAGAAGGCGGTCAAGAGCC
1192	SMAD3	SMAD3 guide RNA 3	CTTGGTGTTGACGTTCTGCG

1193	MAPKAPK3	MAPKAPK guide RNA 1	CTCTGCTGTTTCACCATCCA
1194	MAPKAPK3	MAPKAPK guide RNA 2	CCCGGCTTGGGCGGTGCTCC
1195	MAPKAPK3	MAPKAPK guide RNA 3	CGACTACCAGTTGTCCAAGC
1196	CEACAM1	CEACAM1 guide RNA 1	GACTGAGTTATTGGCGTGGC
1197	CEACAM1	CEACAM1 guide RNA 2	GAATGTTCCATTGATAAGCC
1198	CEACAM1	CEACAM1 guide RNA 3	GAGAGGCTGAGGTTTGCCCC
1199	DDIT4	DDIT4 guide RNA 1	CCTCACCATGCCTAGCCTTT
1200	DDIT4	DDIT4 guide RNA 2	CGATCTGGGGTGGGAGTTCG
1201	DDIT4	DDIT4 guide RNA 3	GTTTGACCGCTCCACGAGCC

[00341] An non-limiting schematic of an anti-CD70 CAR and a gene editing/expansion protocol is provided in Figure 49A. NK cells were first gene edited (e.g. using CRISPR/Cas electroporation) to doubly knockout CD70 and one of these target genes. Electroporated cells were cultured in high IL-2 conditions and subsequently with IL-12 and IL-18 to expand NK cells. At day 7 after gene editing, NK cells were transduced with a virus harboring a CAR genetic sequence, for example NK71 (as seen in Figure 6). Following transduction, NK cells were assessed for CAR expression and used for cytotoxicity assays. At day 7 following double knockout of CD70 and a target genes (SMAD3, MAPKAPK3 [MK3], CEACAM1, DDIT4, A2AR, NKG2A, CISH), CD70 expression was reduced consistently among different conditions (Figure 49B). At day 10 following double knockout (and NK71 CAR transduction at day 7), CD70 expression was essentially undetectable and NK71 expression was consistent among different conditions (Figure 49C). NK cell populations gene edited for the targets were amplified at the targeted loci at their respective exons as shown in Figure 49D. Gene loci amplicons were sequenced to determine indel frequency within the NK cell population (Figure 49D).

[00342] SMAD3 was knocked out in an NK cell population expressing the NK71 CAR. Loss of SMAD3 protein was confirmed by Western blot as well as loss of phosphorylated SMAD3 signal after TGFb treatment (Figure 49E). Cytotoxicity assays were performed with NK cell populations knocked out for SMAD3 or CISH and expressing the NK71 CAR, with or without treatment of 20 ng/mL TGFb (Figures 49F-49G). Unlike the CISH knockout population, the SMAD3 knockout could not overcome TGFb inhibition of NK71 cell cytotoxicity, as seen by the greater number of remaining tumor cells in the SMAD3 KO+TGFb treated condition compared to TGFb treated only condition.

[00343] A2AR was knocked out in an NK cell population expressing the NK71 CAR. Cytotoxicity assays were performed with NK cell populations knocked out for A2AR or CISH and expressing the NK71 CAR, with or without treatment of the adenosine receptor agonist NECA at 10 uM (Figure 49H-49I). The results observed here were similar to those discussed above (e.g. Figure 48). The cytotoxicity assay results suggest that A2AR knockout or CISH knockout may overcome NECA inhibition of NK71 cell cytotoxicity.

[00344] MAPKAPK3 (MK3) was knocked out in an NK cell population expressing the NK71 CAR. Cytotoxicity assays were performed with NK cell populations knocked out for MK3 or CISH and expressing the NK71 CAR (Figures 49J-49K). MK3 knockout moderately enhances NK cell cytotoxicity.

[00345] NKG2A was knocked out in an NK cell population expressing the NK71 CAR. Cytotoxicity assays were performed with NK cell populations knocked out for NKG2A or CISH (or MK3 for comparison) and expressing the NK71 CAR. NKG2A knockout increases NK cell cytotoxicity against 786-O tumor cells (Figures 49L-49N) under normal conditions. However, NKG2A knockout fails to overcome inhibition of NK cells when tested in either 20 ng/mL TGFb (1:1 E:T; Figure 49O) or 10 μM NECA (1:2 E:T; Figure 49P).

[00346] DDIT4 was knocked out in an NK cell population expressing the NK71 CAR. Cytotoxicity assays were performed with NK cell populations knocked out for DDIT4 or CISH and expressing the NK71 CAR (Figure 49Q-49R). Cells were treated with 50 μM $CoCl_2$ to induce a hypoxic state, which induces DIT4 to inhibit mTor. DDIT4 knockout was not found to enhance NK cell cytotoxicity.

[00347] CEACAM1 was knocked out in an NK cell population expressing the NK71 CAR. Cytotoxicity assays were performed with NK cell populations knocked out for CEACAM1 or CISH and expressing the NK71 CAR (Figures 49S-49T). CEACAM5, which can be found on tumor cell surfaces and interacts with CEACAM1, was added at 1 μg/mL. CEACAM1 knockout was not found to enhance NK cell cytotoxicity.

[00348] NK cell populations edited to knock out CISH, A2AR, SMAD3, MK3, DDIT4, or CEACAM1 (over 42 days, Figure 49U); or CISH or NKG2A (over 49 days, Figure 49V) were assessed to observe NK cell proliferation and survival as measured by cell counts. CISH knockout was found to have the greatest benefit for NK cell survival at the final time point tested. Thus, in several embodiments, CISH is edited to impart beneficial effects to NK or T cells expressing one or more of the anti-CD70 CAR constructs disclosed herein. In additional embodiments, genes in addition to CISH are edited to provide further benefits, which in some embodiments synergistically work with those of CISH-edited cells to result in highly efficacious and persistent edited cells for use in CD70-expressing tumor therapy.

Example 5 – Anti-CD70 Binding Domain Screening and Characterization

[00349] As discussed above, various anti-CD70 binding domains were produced and evaluated for expression, cytotoxicity against target cells and otherwise were characterized according to the non-limiting methodologies and experiments described herein.

[00350] A pool of 1600 candidate anti-CD70 binding domains were screened to identify nearly 1000 unique scFvs. These were further screened based on their ability to bind either or both a monomer or trimer of CD70 epitopes and their ability to compete with (or block) binding of a known anti-CD70 binder to such CD70 epitopes. Testing against CD70 trimers allows for identification of binders selective for the naturally occurring trimeric conformation of CD70, whereas testing against CD70 monomers allows for selection of high affinity binders.

[00351] Based on the CD70 binding assays, 74 individual scFvs were identified and selected for further characterization. Non-limiting examples of nucleotide sequences for the selected scFvs are provided in SEQ ID NOs: 38-111. Non-limiting examples of nucleotide sequences for separate heavy chain variable regions (VH) of the selected scFvs are provided in SEQ ID NOs: 1038-1111. Non-limiting examples of nucleotide sequences for separate light chain variable regions (VL) of the selected scFvs are provided in SEQ ID NOs: 1112-1185. Peptide sequences for the selected scFvs are provided in SEQ ID NOs: 230-303. Peptide sequences for separate VH of the selected scFvs are provided in SEQ ID NOs: 890-963. Peptide sequences for separate VL of the selected scFvs are provided in SEQ ID NOs: 964-1037. It is envisioned that other nucleotide sequences that the ones provided (e.g. sequences having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% homology) can be translated to the same peptide scFv sequences as conventionally understood. Non-limiting examples of nucleic acid and peptide sequences for each of the 74 selected anti-CD70 scFvs are depicted in Figure 50A.

[00352] Bivalent scFvs were prepared from some of the selected anti-CD70 scFvs. The bivalent scFvs that were prepared include: 1) NK77.38/NK77.38, 2) NK77.64/NK77.64, 3) NK77.65/NK77.65, 4) NK77.38/NK77.67, 5) NK77.38/NK77.68, 6) NK77.64/NK77.67, 7) NK77.64/NK77.68, 8) NK77.65/NK77.67, 9) NK77.65/NK77.68. The names of the bivalent combinations correspond to the nomenclature used for the monovalent scFvs as disclosed herein (e.g. in Figure 50A). Non-limiting examples of nucleotide sequences for these bivalent scFvs are provided in SEQ ID NOs: 112-120. Corresponding peptide sequences for these bivalent scFvs are provided in SEQ ID NOs: 304-312.

[00353] Also provided are individual heavy chain variable region and light chain variable region complementarity determining regions (CDRs). Non-limiting examples of CDR-H1 are provided in SEQ ID NOs: 428-501. Non-limiting examples of CDR-H2 are provided in SEQ ID NOs: 502-575. Non-limiting examples of CDR-H3 are provided in SEQ ID NOs: 576-649. Non-limiting examples of CDR-L1 are provided in SEQ ID NOs: 668-741. Non-limiting examples of CDR-L1 are provided in SEQ ID NOs: 742-815. Non-limiting examples of CDR-L1 are provided in SEQ ID NOs: 816-889. Combinations for each of the selected anti-CD70 scFvs are provided in Figure 50B. It is envisioned that other anti-CD70 scFvs (or sdAbs) can be produced by other combinations of the heavy chain and light chain CDRs provided herein.

[00354] The anti-CD70 scFvs disclosed herein are produced within immunoglobulin frameworks conventionally known in the art. For example, each heavy chain variable region and light chain variable region framework used has 4 framework sequences (FW-1, FW-2, FW-3, FW-4) in which the three CDRs are provided. Non-limiting examples of FW-H1 are provided in SEQ ID NOs: 399-402. Non-limiting examples of FW-H2 are provided in SEQ ID NOs: 403-406. Non-limiting examples of FW-H3 are provided in SEQ ID NOs: 407-422. Non-limiting examples of FW-H4 are provided in SEQ ID NOs: 423-427. Non-limiting examples of FW-L1 are provided in SEQ ID NOs: 650-653. Non-limiting examples of FW-L2 are provided in SEQ ID NOs: 654-657. Non-limiting examples of FW-L3 are provided in SEQ ID NOs: 658-661. Exemplary FW-L4 are provided in SEQ ID NOs: 662-667. It is envisioned that alternative frameworks may be substituted for any of the frameworks disclosed herein as understood by one skilled in the art.

[00355] CARs were prepared from these selected 74 anti-CD70 scFvs. The CARs were constructed with the anti-CD70 scFv, a CD8a hinge, a CD8a transmembrane domain, an OX40 subdomain, and a CD3zeta subdomain, as depicted in Figure 6, however, according to additional embodiments, other domains disclosed herein may also be used (e.g., 4-1BB, CD28, etc.). Non-limiting examples of nucleotide sequences for the monovalent CARs are provided in SEQ ID NOs: 138-211. Non-limiting examples of nucleotide sequences for the bivalent CARs are provided in SEQ ID NOs: 212-220. Additional non-limiting examples of codon-optimized sequences for the bivalent CARs are provided in SEQ ID NOs: 221-229. Corresponding peptide sequences for the monovalent CARs are provided in SEQ ID NOs: 313-386. Corresponding peptide sequences for the bivalent CARs are provided in SEQ ID NOs: 387-395.

[00356] These initial 74 CARs were assayed for tonic signaling and activation capability in Jurkat cells. A schematic for this is depicted in Figure 50C. Briefly, Jurkat cells that previously have been gene edited to knock out CD70 are transduced with a standard titer of virus harboring anti-CD70 CAR genetic sequences, expanded, and the cultured either alone (to test tonic signaling) or co-cultured with tumor cells to test CAR-mediated activation. Activation was measured by CD69 expression. Most of the prepared anti-CD70 CARs do not exhibit substantial tonic signaling, with the exception of clones NK77.48 and two bivalent CARs NK77.78 (NK77.65 duplicate bivalent) and NK77.83 (NK77.65/NK77.67 bivalent) (Figure 50D). The ratio of activation after tumor cell co-culture to tonic signaling indicates which constructs function efficiently to transduce immune cell activation (Figure 50E). From this screening, a set of 10 CAR constructs (NK77.11, NK77.16, NK77.17, NK77.31, NK77.44, NK77.55, NK77.58, NK77.65, NK77.71, NK77.73) (Figure 50F). The majority of anti-CD70 CARs tested in subsequent assays are part of this set of 10 selected CARs, although any of the anti-CD70 CARs disclosed herein, in any combination, may be similarly assayed and/or used in a cell therapy composition or method disclosed herein.

[00357] In some embodiments, also provided herein are nucleic acid or amino acid sequences that have sequence identity and/or homology of at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% (and ranges therein) as compared with the respective nucleic acid or amino acid sequences of SEQ ID NOS. 138-395 (or combinations of two or more of SEQ ID NOS: 138-395) and that also exhibit one or more of the functions as compared with the respective SEQ ID NOS. 138-395 (or combinations of two or more of SEQ ID NOS: 138-395) including but not limited to, (i) enhanced proliferation, (ii) enhanced activation, (iii) enhanced cytotoxic activity against cells presenting ligands to which NK cells harboring receptors encoded by the nucleic acid and amino acid sequences bind, (iv) enhanced homing to tumor or infected sites, (v) reduced off target cytotoxic effects, (vi) enhanced secretion of immunostimulatory cytokines and chemokines (including, but not limited to IFNg, TNFa, IL-22, Perforin, CCL3, CCL4, and CCL5), (vii) enhanced ability to stimulate further innate and adaptive immune responses, and (viii) combinations thereof.

Example 6 - Anti-CD70 CAR Screening and Characterization

[00358] Several *in vitro* experimental examples are provided herein to characterize and validate cytotoxic ability of the anti-CD70 CAR constructs expressed by CD70-deficient NK cells.

[00359] As shown in Figures 51A-51B, NK cells from one donor (denoted donor 451) were transduced to express anti-CD70 CARs and gene edited to reduce expression of CD70. Constructs NK77.55, NK77.58, NK77.65, NK77.71, and NK77.73 were tested, though (as throughout the disclosure, unless otherwise indicated) any of the CD70 CARs disclosed herein may be used, depending on the embodiment. Flow cytometry plots detecting the anti-CD70 CAR (by allophycocyanin (APC)-conjugated anti-FLAG antibody) and loss of CD70 expression (by phycoerythrin (PE)-conjugated anti-CD70 antibody) shows variability among tested CAR constructs expressed by NK cell populations (Figure 51A). Clones with higher transduction efficiencies (e.g. NK77.58 and NK77.71) exhibited greater killing of CD70+ NK cells (i.e. where the CD70 knockout was unsuccessful or incomplete), resulting in the low abundance of CD70+ cells in the plots (Figure 51B). NK8 refers to a control construct expressing GFP instead of a CAR/mbIL15.

[00360] As shown in Figures 52A-52D, NK from another donor (denoted donor 454) were transduced to express anti-CD70 CARs and gene edited to lose expression of CD70. Constructs NK77.55, NK77.58, NK77.65, NK77.71, and NK77.73 were tested, with no transduction and NK71 construct as controls. Flow cytometry plots detecting the anti-CD70 CAR (APC-anti-FLAG) and loss of CD70 expression (PE-anti-CD70) shows robust expression of the anti-CD70 CARs and virtually no CD70+ cells (Figure 52A). High frequency of CAR transduction and low CD70+ abundance suggests that the transduced NK cells killed off any remaining CD70+ cells where the CD70 knockout was either unsuccessful or incomplete (Figure 52B). Measurement of the raw mean fluorescence intensity (MFI) suggests that while transduction efficiency was high, relative expression levels per cell for each CAR may vary (Figure 52C). CAR NK cells of this set were subjected to a cytotoxicity assay against 786-O cancer cells at varying effector:target (E:T) ratios and the EC_{50} was calculated. The NK71 CAR was used as a control. Each tested CAR resulted in EC_{50} ranging from about 0.25 E:T or lower, indicating that these CAR NK cells were effective in clearing co-cultured tumor cells.

[00361] As shown in Figures 53A-53F, the CAR NK cells from donor 454 (seen in Figure 52) were subjected to cytotoxicity assays. As provided above, anti-CD70 CARs NK77.55, NK77.58, NK77.65, NK77.71, and NK77.73 were tested, with NK71 as a control. Cytotoxicity was tested at E:T ratios of 1:2 (Figures 53A-53C), 1:4 (Figures 53D-53E), and 1:8 (Figure 53F). For the 1:2 ratio condition, the NK cells were re-challenged with additional tumor cells at day 7, and cytotoxicity was continued to be measured until day 10 (Figure 53C). Each of the tested anti-CD70 CAR constructs resulted in increased cytotoxicity of the 786-O cells relative to the negative control. Constructs NK77.58 and NK77.71 consistently had the greatest relative cytotoxicity over the other CARs and the positive control CAR NK71.

[00362] As shown in Figures 54A-54D, the CAR NK cells from donor 454 (seen in Figures 52, 53) or similarly transduced to NK92 (an immortalized NK cell-like cell line) were subjected to additional cytotoxicity assays. NK cell populations with NK77.58 and NK77.71 were tested, as a non-limiting example, as they had the greatest activity as seen in Figure 53. Cytotoxicity was tested at E:T ratios of 1:2 (Figures 54A-54B) or 1:4 (Figures 54C-54D) against either 786-O expressing GFP or ACHN cells stained with NucRed. Cytotoxicity of these two CAR constructs is consistent among the different conditions, resulting in

substantial reduction of tumor cells relative to negative controls. Only the NK71 transduced to NK92 cells was found to have greater cytotoxicity compared to these two constructs.

[00363] As shown in Figures 55A-55M, additional anti-CD70 CARs were tested with NK cells from donor 451. CD70 knockout NK cells from donor 451 were transduced to express constructs NK77.11, NK77.16, NK77.17, NK77.31, and NK77.44, with NK71 as a positive control. Flow cytometry plots detecting the anti-CD70 CAR (APC-anti-FLAG) and loss of CD70 expression (PE-anti-CD70) shows robust expression of the CARs and negligible presence of CD70+ cells (Figure 55A). These CAR NK cells were subjected to a cytotoxicity assay against 786-O cells at varying E:T ratios and the EC_{50} was calculated (Figures 55B-55C). Constructs NK77.11, NK77.16, NK77.17, NK77.31, and NK77.44 had EC_{50} ranging from about 0.5-0.63, which was lower than the EC_{50} measured for the NK71 construct. NK77.44 resulted in an EC_{50} of about 1.5, which may suggest lower cytotoxic efficacy. These CAR NK cells were further subjected to a time course cytotoxicity assay at either E:T ratios of 1:2 (Figures 55D-55I) or 1:4 (Figures 55J-55M). For longer time periods, the NK cell cultures were re-challenged with additional tumor cells (Figures 55G and 55M). In this case, re-challenge was at day 7, and cytotoxicity was measured until day 11. Each of the tested anti-CD70 CARs resulted in cytotoxicity relative to negative control. Construct NK77.11 performed the best overall. As suggested by the EC_{50} data of Figures 55B-55C, NK77.44 did not perform as well as the other tested CARs. Interestingly, control CAR NK71 performed the best for earlier time points, but after re-challenge and longer culture, NK71 did not perform as well as the experimental CAR constructs, potentially suggesting improved persistence of these constructs.

[00364] As shown in Figures 56A-56J, the same additional anti-CD70 CARs tested in Figures 55A-55M were tested with NK cells from donor 454. CD70 knockout NK cells from donor 454 were transduced to express constructs NK77.11, NK77.16, NK77.17, NK77.31, and NK77.44, with NK71 as a positive control. Flow cytometry plots detecting the anti-CD70 CAR (APC-anti-FLAG) and loss of CD70 expression (PE-anti-CD70) shows robust expression of the CARs and negligible presence of CD70+ cells (Figure 56A). These CAR NK cells were subjected to a cytotoxicity assay against 786-O cells at varying E:T ratios and the EC_{50} was calculated (Figures 56B-56C). Consistent with what was seen with donor 451 (Figures 55B-55C), the EC_{50} for NK77.11, NK77.16, NK77.17, and NK77.31 were generally lower than that of NK71, while NK77.44 was higher. These CAR NK cells were further subjected to a time course cytotoxicity assay at E:T ratios of 1:2 (Figures 56D-56E), 1:4 (Figures 56F-56H), or 1:8 (Figures 56I-56J). For the 1:2 ratio, the NK cell cultures were re-challenged with additional tumor cells at day 6 with cytotoxicity measurements until day 10 (Figure 56E). As seen in Figure 55, the CAR constructs resulted in cytotoxicity relative to negative control. Construct NK77.11 still generally performed well, but in some cases, construct NK77.17 resulted in even greater cytotoxicity. In the longer time period test with re-challenge, the control NK71 did not perform as well as in Figure 55G and 55M, with most tested CARs having greater cytotoxicity both before and after the re-challenge. This variability may be due to the NK cell donor source tested or variable CAR transduction

[00365] As shown in Figures 57A-57H, the CAR NK cells from donor 451 (seen in Figure 55) were subjected to additional cytotoxicity assays. All CARs tested in Figure 55 (NK77.11, NK77.16, NK77.17, NK77.31, NK77.44) were tested. Cytotoxicity was tested at E:T ratios of 1:2 (Figures 57A-57E) or 1:4 (Figures 57F-57H) against ACHN cells. Cytotoxicity of the tested CARs is consistent with what is seen in Figure 55.

[00366] As shown in Figures 58A-58H, the CAR NK cells from donor 454 (seen in Figure 56) were subjected to additional cytotoxicity assays. All CARs tested in Figure 56 (NK77.1, NK77.16, NK77.17, NK77.31, NK77.44) were tested. Cytotoxicity was tested at E:T ratios of 1:4 (Figures 58A-58E) or 1:8 (Figures 58F-58H) against ACHN cells. Cytotoxicity of the tested CARs is consistent with what is seen in Figure 56.

[00367] As shown in Figures 59A-59D, NK cells from donor 451 were transduced to express the 10 anti-CD70 CARs shown in Figure 50G and gene edited to lose expression of CD70. Constructs NK77.11, NK77.16, NK77.17, NK77.31, NK77.44, NK77.55, NK77.58, NK77.65, NK77.71, NK77.73 were tested, with NK71 as a positive control. These CAR constructs were also tested in the previous experiments provided in this example. Flow cytometry plots detecting the anti-CD70 CAR (APC-anti-FLAG) and loss of CD70 expression (PE-anti-CD70) shows expression of each of the 10 tested CARs and negligible presence of CD70+ cells (Figure 59A). High frequency of CAR transduction and low CD70+ abundance suggests that the transduced NK cells killed off any remaining CD70+ cells where the CD70 knockout was either unsuccessful or incomplete (Figure 59B). Measurement of the raw MFI suggests that while transduction efficiency was high, relative expression levels per cell for each CAR may vary (Figure 59C). CAR NK cells were subjected to a cytotoxicity assay against 786-O cancer cells at varying E:T ratios and the EC_{50} was calculated. While there is some variability in the calculated EC_{50} compared to the previous experiments (such as the EC_{50} for NK77.44, which appears to be competitive here but higher in Figure 55C and 56C), this indicates that these selected anti-CD70 CARs confer cytotoxic activity relative to negative control.

[00368] As shown in Figures 60A-60O, the NK cells from donor 451 as seen in Figure 59 with the 10 anti-CD70 CARs were subjected to additional cytotoxicity assays. Cytotoxicity was tested at E:T ratios of 1:2 against 786-O (Figures 60A-60D), 1:2 against ACHN (Figures 60E-60H), 1:4 against 786-O (Figures 60I-60L) or 1:4 against ACHN (Figures 60M-60P). All of the tested CARs confer cytotoxicity compared to negative control. Based on these cytotoxicity assays, it generally appears that anti-CD70 CAR constructs NK77.11, NK77.16, NK77.17, NK77.31, NK77.58, NK77.71 have greater cytotoxicity compared to the NK71 CAR control. Conversely, NK77.55, NK77.65, and NK77.73 do not perform better than the NK71 control, and NK77.44 experiences some variability in this aspect.

[00369] As shown in Figures 61A-61O, NK cells from another donor (denoted donor 512) were transduced to express anti-CD70 CARs and gene edited to lose expression of CD70. Flow cytometry plots show a lower percentage of NK cells expressing CD70 after transfection of CD70-directed CRISPR/Cas9 knockout constructs (Figure 61A). All 10 CAR constructs seen in Figure 50G (NK77.11, NK77.16, NK77.17, NK77.31, NK77.44, NK77.55, NK77.58, NK77.65, NK77.71, NK77.73) were tested, with NK71 as positive

control. Flow cytometry pots show robust expression of the CAR and negligible presence of CD70+ cells (Figure 61B). High frequency of CAR transduction and low CD70+ abundance suggests that the transduced NK cells killed off any remaining CD70+ cells where the CD70 knockout was either unsuccessful or incomplete (Figure 61C). Measurement of the raw MFI suggests that while transduction efficiency was high, relative expression levels per cell for each CAR may vary (Figure 61D). CAR NK cell populations with NK77.11, NK77.16, NK77.17, NK77.58, and NK77.71 were tested for persistence of the CAR over time. Over a three week period, these tested CARs were robustly maintained, while the NK71 control experienced some reduction in expression over the same length of time (Figures 61E-61J). In a cytotoxicity assay, the tested NK constructs NK77.11, NK77.16, NK77.17, NK77.58, and NK77.71 in donor 512 NK cells all exhibited greater cytotoxicity at E:T ratios of either 1:2 or 1:4 against 786-O cells (Figures 61K-61L) or ACHN cells (Figures 61M-61N) relative to NK71 control and negative control. These anti-CD70 CAR constructs were the ones that performed the best in the previous experiments disclosed herein.

[00370] As shown in Figures 62A-62B, NK cell survival is not affected by expression of anti-CD70 CAR constructs. NK cells from either donor 451 or 512 that were transduced with the anti-CD70 constructs NK77.11, NK77.16, NK77.17, NK77.58, or NK77.71 were cultured over a 5 week span and total viable cells were quantified every week. NK cells expressing the anti-CD70 CAR persisted comparably to control cells (Figures 62A-62B).

[00371] As shown in Figures 63A-63B, NK cells from donor 512 (seen in Figures 61 and 62) were gene edited to knockout CD70 and optionally CISH, transduced with anti-CD70 CAR constructs, and subjected to cytotoxicity assays. Constructs NK77.17, NK77.58, and NK77.71 were tested. Cytotoxicity was tested at an E:T ratio of 1:8 against either 786-O cells (Figure 63A) or ACHN cells (Figure 63B). Each anti-CD70 CAR construct was effective in conferring tumor cytotoxic effects to the NK cells. These data show that anti-CD70 CAR expressing cells according to several embodiments disclosed herein are effective at controlling and/or reducing tumor cell growth. According to several embodiments, gene editing of the cells expressing the anti-CD70 CAR (e.g., CISH editing) further enhances one or more aspects of the engineered cells, including but not limited to cytotoxicity and/or persistence.

Example 7 – Further Screening of Anti-CD70 CARs and Related Characterization

[00372] Additional experiments were performed to further evaluate the characteristics of cells that are engineered to express anti-CD70 CARs and edited to knockout CD70 expression, and optionally are further edited in respect of one or more of the additional editing targets disclosed herein, such as CISH. Cells, as a non-limiting example, donor-derived NK cells are used, were engineered and edited as discussed herein.

[00373] Initially, NK cells engineered and edited according to embodiments disclosed herein were tracked over time in two respects – first for target binding ability of the expressed CD70 CAR over time and for the durability CD70 knockout over time – in other words, the persistence of the engineering and editing. Figure 64A shows the data for a first donor's NK cells with respect to the ability of the CD70 CAR to bind

the naturally occurring CD70 trimer. As shown, the electroporation-only control NK cells (EPNT) show essentially zero binding of the trimer (see Trimer+2nd panel in lower right of 64A). In contrast, each of non-limiting CD70 CAR construct-expressing NK cell populations showed robust binding to the trimer. This assessment was performed 1 week after transducing the cells with the CAR construct. Figure 64B shows corresponding data from a second donor. Figure 64C and Figure 64D provide a table that depicts summary data for each of the CAR constructs, with the data presented as both the percentage of cells expressing a CAR that can bind the CD70 trimer (out of the entire population of CD70 cells evaluated) and also as the MFI value. Reflecting the flow cytometry scatter plots, the numerical data confirms expression of CARs capable of binding their target at one week post-transduction. Figures 64E and 64F show this data graphically, with CAR constructs NK77.71, 77.11 and 77.16 showing the highest ability to bind their target.

[00374] Turning to the knockout of CD70, Figure 64G shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 64H confirms the same effect for donor two. Figures 64I and 64J show the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00375] Figure 65A shows data related to the first donor's cells at two weeks post-transduction in terms of the ability of the cells to bind the native CD70 trimer. As was seen at 1-week post-transduction, the ability of the CAR-expressing cells to bind the target was significant in comparison to EPNT cells, and even in comparison to NK71-expressing cells. Similar maintenance of ability to bind is shown in Figure 65B, for the second donor. These data are tabulated in Figures 65C and 65D for each donor, expressed both as the percentage of the NK cell population expresses the CAR that binds the native CD70 trimer and based on the MFI detected. Figures 65E and 65F graphically depict this summary data for each donor, with CAR constructs NK77.71, 77.11 and 77.16 again showing the highest ability to bind their target.

[00376] Turning to the knockout of CD70, Figure 65G shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 65H confirms the same effect for donor two. Figures 65I and 65J show the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00377] Figure 66A shows data related to the first donor's cells at three weeks post-transduction in terms of the ability of the cells to bind the native CD70 trimer. As was seen at 1-week and 2-week post-transduction, the ability of the CAR-expressing cells to bind the target was significant in comparison to EPNT cells, and even in comparison to NK71-expressing cells. Similar maintenance of ability to bind is shown in Figure 66B, for the second donor. These data are tabulated in Figure 66C for each donor, expressed both as the percentage of the NK cell population expresses the CAR that binds the native CD70

trimer and based on the MFI detected. Figures 66D and 66E graphically depict this summary data for each donor, with CAR constructs NK77.71, 77.11 and 77.16 again showing the highest ability to bind their target.

[00378] Turning to the knockout of CD70, Figure 66F shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 66G confirms the same effect for donor two. Figures 66H and 66I show the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00379] Figure 67A shows data related to the first donor's cells at four weeks post-transduction in terms of the ability of the cells to bind the native CD70 trimer. As was seen at 1-week, 2-week, and three-week post-transduction, the ability of the CAR-expressing cells to bind the target was significant in comparison to EPNT cells, and even in comparison to NK71-expressing cells. Similar maintenance of ability to bind is shown in Figure 67B, for the second donor. These data are tabulated in Figures 67C and 67D for each donor, expressed both as the percentage of the NK cell population expresses the CAR that binds the native CD70 trimer and based on the MFI detected. Figures 67E and 67F graphically depict this summary data for each donor, with CAR constructs NK77.71, 77.11 and 77.16 again (and also 77.58) showing the highest ability to bind their target.

[00380] Turning to the knockout of CD70, Figure 67G shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 67H confirms the same effect for donor two. Figures 67I and 67J show the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00381] Figure 68A shows data related to the first donor's cells at five weeks post-transduction in terms of the ability of the cells to bind the native CD70 trimer. As was seen for weeks 1 through 4 post-transduction, the ability of the CAR-expressing cells to bind the target was significant in comparison to EPNT cells, and even in comparison to NK71-expressing cells. Similar maintenance of ability to bind is shown in Figure 68B, for the second donor. These data are tabulated in Figures 68C and 68D for each donor, expressed both as the percentage of the NK cell population expresses the CAR that binds the native CD70 trimer and based on the MFI detected. Figures 678 and 68F graphically depict this summary data for each donor, with CAR constructs NK77.71, 77.11 and 77.16 again showing the highest ability to bind their target.

[00382] Turning to the knockout of CD70, Figure 68G shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 68H confirms the same effect for donor two. Figures 68I shows the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited

cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00383] Figure 69A shows data related to the first donor's cells at seven weeks post-transduction in terms of the ability of the cells to bind the native CD70 trimer. As was seen for weeks 1 through 5 post-transduction, the ability of the CAR-expressing cells to bind the target was significant in comparison to EPNT cells, and even in comparison to NK71-expressing cells. Similar maintenance of ability to bind is shown in Figure 69B, for the second donor. These data are tabulated in Figure 69C for both donors, expressed both as the percentage of the NK cell population expresses the CAR that binds the native CD70 trimer and based on the MFI detected. Figures 69D and 69E graphically depict this summary data for each donor, with CAR constructs NK77.71, 77.11 and 77.16 again showing the highest ability to bind their target.

[00384] Turning to the knockout of CD70, Figure 69F shows that, for donor one, endogenous CD70 expression is near zero for all experimental groups, as compared to the EPNT control. Figure 69G confirms the same effect for donor two. Figures 69H shows the numerical data for CD70 expression, both by the percentage of the total NK cell population that express CD70, as well as MFI. As shown, the CD70-edited cells expressing any of the non-limiting examples of CD70 CARs express vastly lower amounts of CD70, as compared to the unedited EPNT CD70 controls, for both donors.

[00385] Figures 70A-70B show data related to CAR expression (by MFI) over the course of the 7 weeks post-transduction for the indicated non-limiting CAR constructs. These data confirm that, as compared to controls, the selected non-limiting CAR constructs exhibited elevated CAR expression. Importantly, as in the prior figures, this is also expression of functional CARs (as shown with CD70 trimer binding). Thus, according to several embodiments, CAR constructs as disclosed herein exhibit durable expression and function over extended periods in culture. Advantageously, in several embodiments, this stable expression imparts to the cells expressing the CAR (such as an NK cell) an elongated functional life span in vivo, which, in turn, lends to the longer effective treatment of a tumor against which the CAR is directed.

[00386] Additional data characterizing cells expressing the CARs was collected. At Day 14 after inception of the cell production process (e.g,. electroporation for gene editing, followed by transduction with a vector encoding a particular CAR construct), and again at day 28 after inception of the cell production process, NK cells expressing the indicated anti-CD70 CAR constructs (and also edited to knockout endogenous CD70 expression) were cocultured at the indicated E:T ratio with either 786-O tumor cells or ACHN tumor cells (experimental setup as discussed elsewhere herein). After 3 days of coculture, the culture media was assessed for concentrations of selected cytokines. Figure 71A shows levels of interferon gamma in the media of co-cultures with 786-O (71A) or ACHN (71B) cells. As shown, the cytokine release level was elevated in the 14-day cell batches, with interferon production decreasing over time to day 28. Even at 28 days after inception of the cell production process, certain CAR constructs, such as NK77.71, still induced release of relatively elevated interferon gamma levels, particular as compared to ACHN cells also or electroporation negative controls. Figures 71C-71D show corresponding data for the second donor

tested, with a similar overall profile of interferon gamma release, in that there was a trend to decreasing amounts of interferon production as the cells remained in culture longer, although in most groups, the degree of release was still elevated over control.

[00387] Figures 71E-71F show data related to detection of GM-CSF at the same time points as described above. Interestingly, the edited and engineered NK cells shows a trend towards increase GMCSF production over time, with most of the constructs tested resulting in elevated levels of GMCSF at day 28, as compared to corresponding points at day 14. There was some amount of de novo production of GMCSF from the 786-O and ACHN cells on their own, but those levels were constant over time, indicating that the GMCSF release is likely induced through the coculture with the tumor cells and reflective of the cytotoxic activation of the NK cells. Figures 71G-71H show corresponding data for the second donor tested, with a similar overall profile of GMCSF release.

[00388] Figures 71I-71J show data related to the levels of TNF alpha in the culture media from donor one after coculture as described above. In this experiment, the levels of TNF alpha generally trended up between 14 and 28 days, though certain CAR-expressing cells remained more steady between the two time points. Similar data were for donor two, at least with respect TNF alpha release during coculture with ACHN cells. The general trend for TNF alpha release in donor two was downward between the 14 and 28 day time points. In several embodiments, this may be an artifact of the overall cytokine milieu in the co-culture, in that increases, or decreases, in just one cytokine in isolation may be accounted for based on corresponding increases or decreases of other cytokines.

[00389] Similar changes in the trend of cytokine production are also shown in Figures 71M-71N (donor one, perforin release) and Figures 71O-71P (donor two, perforin release). While donor one showed a clear trend to increasing perforin release with time in culture (against both tumor cell types), donor two showed a general trend to decreased perforin release between the 14 and 28 day time points. As discussed above with respect to TNF alpha, the overall cytokine release profile is one aspect of the overall cytotoxic effects a given cell delivers, and there may be donor to donor variability in terms of what an individual batch of cells exhibits in terms of the profiles of any given cytokine in isolation.

[00390] Figures 71Q-71R (donor one) and 71S-71T (donor two) related to Granzyme B production at the two coculture time points. Generally, Granzyme B levels remained steady or were increased between the 14 and 28 day timepoints for both donors and with respect to both types of tumor cells. Taken together, these data demonstrate that edited and engineered immune cells, such as NK cells, retain the capacity to release cytotoxic cytokines, even after nearly 1 month in culture, indicating that the gene edits (e.g., gene knockout) are stable, the CAR expression is stable, and the CAR function is stable. Altogether, these impart to the edited and engineered cells an enhanced degree of persistence and cytotoxicity, leading to a more effective cellular immunotherapy product.

[00391] In several embodiments, more than one gene edited is made. For example, in some embodiments, an endogenous gene is knocked out that improves the survival of the edited cells, such as removing expression of a marker or protein that has overlap with a tumor marker being targets (e.g.,. CD70).

In several embodiments, other genes are also edited. In several embodiments, CISH is edited (as discussed in more detail above). In several embodiments, multiple edits act through enhanced signaling or disrupted signaling along one or more non-redundant pathways to enhance the viability, persistence and/or cytotoxicity of the resultant immune cells. Figures 72A-72B show data related to the in vitro persistence of cells edited for both CD70 and CISH knockout, and expressing anti-CD70 CARs as measured by the percentage of the cell population expressing the CAR (72A) and by overall MFI detected (72B). As compared to control cells (electroporated, but not transduced with a CAR), these edited and engineered cells display enhanced persistence in culture, with notably elevated levels of CAR expression over time (week 1 timepoint is two weeks post-transduction, 20 days post-electroporation). Regardless of the method by which the expression is measured, the indicated CAR constructs were relatively stably expressed over 8 weeks in culture, demonstrating the persistence of expression. Not only is the expression stable over time, but the additional edit of CISH imparts an enhanced survival to the edited cells. Figure 72C shows longitudinal survival data over 8 weeks of culture (assessed at 0 weeks (inception of culture), 4 weeks, and 8 weeks). As shown based on total cell count, the cells that are further edited to knock out CISH (CIS protein expression substantially or completely eliminated) show improved survival (right panels) as compared to cells edited for CD70. This is in line with several embodiments disclosed herein, in that the multiple edits add synergistic improvements to one or more characteristics of the edited cells.

[00392] Turning to the cytotoxicity of the various anti-CD70 CAR expressing cells, Figure 72D shows cytotoxicity profiles (experimental setup discussed elsewhere herein) for the cells of one donor against 786-O tumor cells. As can be seen from the data, the addition of any CAR construct results in a dramatic reduction in the tumor cell population. The tested cells (edited CD70 and in paired groups, doubly edited for CD70 and CISH) showed a CISH-editing-dependent increase in the overall cytotoxicity at the final timepoint measured. Thus, in several embodiments, immune cells, such as NK cells, are doubly edited (or edited at a greater number of targets) for knocking out CISH and another endogenous target (here CD70 as a non-limiting example), with the CISH edit imparting an enhanced functionality (e.g., persistence and/or cytotoxicity) to the resulting cell. Figure 72E summarizes the cytotoxicity curve data in a histogram that depicts the detection of tumor cell fluorescent signal at the final time point. CD70 edited cells are shown on the left panel while doubly edited cells (CD70 and CISH) are shown on the right. Each of the matched pairs show a reduction in the presence of tumor cells with the additional edit of CISH, indicating that CISH knockout by gene editing enhances the cytotoxicity of such edited NK cells expressing a cytotoxic CAR.

[00393] Figures 72F and 72G show data related to the edited cells as tested at E:T of 1:4 against ACHN or 786-O cells at day 14 after inception of the cell production process. Data are shown for the final time-point but not for the interim points (e.g., cytotoxicity curves are not shown). Corresponding data for 1:8 E:T ratios are shown in Figures 72H-72I. Regardless of whether the E:T is higher or lower, the data repeatedly show the editing to knock out CISH results in modest to notable further increases in the cytotoxicity of a given NK cell population edited for CD70 knockout and expression of an anti-CD70 CAR.

[00394] As was performed in several prior examples, gene edited and engineered immune cells (e.g., NK cells) were assayed in a rechallenge format, wherein the experimental cells are introduced to a new dose of tumor cells at an interim timepoint during co-culture. Figure 72J shows rechallenge data for ACHN cells at a 1:4 E:T while 72K shows the corresponding data for 786-O cells (at day 14 after inception of the cell production process). Consistent with the data just described above, the additional edit of CISH resulted in modest to notable increases in the cytotoxicity (as measured by remaining tumor cell signal at the final timepoint). Figures 72L and 72M show corresponding data for 1:8 E:T ratios for each target tumor cell type. At the lower effector cell ratio, the reduction in tumor cell numbers over the first portion of the experiment was consistent, but tumor cells trended to increases in numbers after re-challenge. However, despite this trend, within an experimental pair, again, the CISH knockout editing resulted in relatively consistent enhancements in cytotoxicity.

[00395] Additional cytotoxicity analyses were performed at longer time points, in particular day 21 and day 28 after inception of the cell production process to edit CD70 and either edited for CISH, or not, followed by transduction with the indicated non-limiting CAR constructs. A rechallenge format was used here as well. Summarized data are presented both for time-points just prior to rechallenge as well as for the final time point (cytotoxicity curves are not shown). Figures 72A and 73B show data for the indicated CD70- CAR constructs expressed by NK cells (initial co-culture at 21 days after inception of the cell production process) and the cytotoxic effects against 786-O cells as measured after 72 hours of co-culture at either 1:4 (73A) or 1:8 (73B) E:T ratio. While discerning notable differences across all constructs is difficult in those that yielded the most significant cytotoxicity, positive impact of CISH editing can be seen in those with less robust cytotoxicity (noting that all CD70 CAR expressing cells were significantly more effective than control cells. For example the NK77.17 construct exhibited a decrease in the signal detected between the non-edited population (1st histogram bar in 73A) and the CISH edited population (5th histogram bar in 73A. At a reduced effector cell concentration (73B) a general stable to downward trend in signal detection (indicative of increased cytotoxicity) was observed.

[00396] Figures 73C and 73D show the corresponding data collected 6 days after the rechallenge. As shown at both the 1:4 and 1:8 E:T ratios the gene editing to knockout CISH resulted in notable decreases in tumor cells at either ratio tested. This increase in cytotoxicity with CISH editing is particularly notable in the rechallenge context, as fresh tumor cells were introduced, yet the edited cells were able to substantially inhibit tumor cell growth.

[00397] Figures 73E and 73F show data at 72 hours after inception of co-culture of the NK cells (edited or not) with ACHN cells (21 days after inception of the cell production process) at 1:4 (73E) or 1:8 (73F) E:T ratios. As with the 786-O cells discussed above, CISH editing did not show major changes in those construct where cytotoxicity was already quite robust. Again, NK77.17, which allowed more tumor growth than the other CAR constructs, at least in this experiment, showed a noticeable reduction in signal (enhanced cytotoxicity) with the editing to knockout CISH. At the lower, 1:8 E:T, increased cytotoxicity was seen with each of the test constructs (other than internal control NK71). Figures 73G and 73H show the

data collected at the final time point, 6 days post-rechallenge. Seen in both the 1:4 and 1:8 E:T ratios, in each instance, CISH knockout resulted in a notable reduction in tumor burden at the final timepoint. These data, in combination with the other data discussed herein, are indicative of the positive effects of CISH editing on the persistence and cytotoxicity of the cells that are so-edited.

[00398] Moving to testing of cells at 28 days after inception of the cell production process, Figures 74A-74B show data for the indicated CD70 CAR-expressing NK cells against 786-O cells at 1:4 or 1:8 E:T ratios. As with day 21 cells, the highly effective nature of the NK cells at 1:4 tend to mask some of the positive CISH-editing effects, though construct 77.71 and internal control NK71 showed some further enhanced cytotoxicity with CISH editing. The impact of CISH editing was more evident at the 1:8 ratio, which saw more notable reductions in tumor cell growth with the 77.71 and NK71 constructs. At 6 days post-rechallenge, more noticeable positive effects of CISH were detected. Using a 1:4 E:T, all of the constructs tested showed either a stable pattern (77.17) or a further increase in cytotoxicity with CISH editing (77.58, 77.71, and NK71). Likewise a similar pattern was seen at the lower 1:8 E:T ratio, indicative of the enhanced effects imparted by CISH editing.

[00399] Figures 74E and 74F show corresponding data prior to rechallenge with ACHN cells. Each of the non-limiting constructs tested showed robust cytotoxicity at 1:4 E:T, though CISH editing did further enhance cytotoxicity in the NK771.71 and NK71 constructs. At 1:8 E:T, the editing of CISH recapitulated the enhanced cytotoxicity in those two constructs, with the other two holding relatively steady. After rechallenge similar patterns were noted. In this non-limiting experiment, CISH editing enhanced the cytotoxicity of two constructs both before and after rechallenge, which is in line with several embodiments disclosed herein. In some embodiments, the combination of CD70 editing and CISH edited, with expression of an anti-CD70 CAR results in significantly enhanced persistence and/or cytotoxicity of the cells so edited and engineered.

[00400] Figures 75A and 75B show data related to the Indel (insertions or deletions) frequency as measured in the bulk population that was edited with respect to CISH (75A) or CD70 (75B). These data show that random Indel frequency is low and that editing of CISH results in a much higher detection of Indels in the region of DNA anticipated to be edited based on the complementary guide RNA. With respect to CD70, edits are detected in both the CISH edited and non-CISH edited cell populations, as both are edited with respect to CD70. An uptick in Indel frequency is seen with the additional CISH editing, which, in some embodiments, is related to CISH editing inducing an increased number of CD70 editing events. However, in several embodiments, the impact of CISH editing is not directly impacting CD70 editing events, but rather a result of the double-edited cells being enriched over time after the editing and transduction with the CD70 CAR. In other words, a cell edited for CISH would have increased cytotoxicity (as seen with the data above) and a cell edited for CD70 would be more robustly protected from fratricide due to the CD70 CAR expression. Thus, the double knockout cells are enriched in the population over time as compared to those not edited for CD70, which would be reduced as a result of CD70 CAR-based fratricide. Regardless,

in several embodiments, the double editing provide multiple benefits (enhanced viability, persistence and/or cytotoxicity) to the edited and engineered cells.

[00401] Assessing CD70 editing is a relatively straightforward undertaking, as endogenous CD70 is expressed on the surface of NK cells. Thus, flow cytometry or other such can be used to detect degree of successful editing of CD70 in a population of cells. As a mechanism to analyze the impacts of editing for CISH, which is an intracellular protein, a surrogate approach was assessed. Figure 75C depicts a schematic representation of CISH signaling. Since CISH encoded CIS protein, which acts as a negative regulator of STAT5/JAK signaling, the knockout of CISH would disinhibit this pathway, resulting in an increase in Stat5 phosphorylation, which could then be detected, for example, by Western blotting or intracellular staining followed by flow cytometry. By way of example, Figure 75D shows a Western blot for phosphorylated Stats5, using protein isolated from cells expressing the NK77.71 CAR construct, edited for CD70, expressing a CD70 CAR and either not edited for CISH, or edited for CISH (denoted by the "CISH" indicator). Figures 75E and 75F show two sets of normalized data. 75E shows data normalized to the intensity of the band on the Western that corresponds to the electroporated control signal (EP). 75F shows data normalized to the EP control, but set as a value of 1. With either analysis, these data show that editing CISH results in an increase in the phosphorylated Stat5. Thus, in several embodiments, edited cells for CISH are further analyzed for the degree of pStat5 present, as a surrogate for direct assessment of CISH on a genomic level.

[00402] It is contemplated that various combinations or subcombinations of the specific features and aspects of the embodiments disclosed above may be made and still fall within one or more of the inventions. Further, the disclosure herein of any particular feature, aspect, method, property, characteristic, quality, attribute, element, or the like in connection with an embodiment can be used in all other embodiments set forth herein. Accordingly, it should be understood that various features and aspects of the disclosed embodiments can be combined with or substituted for one another in order to form varying modes of the disclosed inventions. Thus, it is intended that the scope of the present inventions herein disclosed should not be limited by the particular disclosed embodiments described above. Moreover, while the invention is susceptible to various modifications, and alternative forms, specific examples thereof have been shown in the drawings and are herein described in detail. It should be understood, however, that the invention is not to be limited to the particular forms or methods disclosed, but to the contrary, the invention is to cover all modifications, equivalents, and alternatives falling within the spirit and scope of the various embodiments described and the appended claims. Any methods disclosed herein need not be performed in the order recited. The methods disclosed herein include certain actions taken by a practitioner; however, they can also include any third-party instruction of those actions, either expressly or by implication. In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[00403] The ranges disclosed herein also encompass any and all overlap, sub-ranges, and combinations thereof. Language such as "up to," "at least," "greater than," "less than," "between," and the like includes the number recited. Numbers preceded by a term such as "about" or "approximately" include the recited numbers. For example, "about 90%" includes "90%." In some embodiments, at least 95% sequence identity or homology includes 96%, 97%, 98%, 99%, and 100% sequence identity or homology to the reference sequence. In addition, when a sequence is disclosed as "comprising" a nucleotide or amino acid sequence, such a reference shall also include, unless otherwise indicated, that the sequence "comprises", "consists of" or "consists essentially of" the recited sequence. Any titles or subheadings used herein are for organization purposes and should not be used to limit the scope of embodiments disclosed herein.

[00404] All references cited herein, including but not limited to published and unpublished applications, patents, and literature references, are incorporated herein by reference in their entirety and are hereby made a part of this specification. To the extent publications and patents or patent applications incorporated by reference contradict the disclosure contained in the specification, the specification is intended to supersede and/or take precedence over any such contradictory material.

Sequences

[00405] In several embodiments, there are provided amino acid sequences that correspond to any of the nucleic acids disclosed herein (and/or included in the accompanying sequence listing), while accounting for degeneracy of the nucleic acid code. Furthermore, those sequences (whether nucleic acid or amino acid) that vary from those expressly disclosed herein (and/or included in the accompanying sequence listing), but have functional similarity or equivalency are also contemplated within the scope of the present disclosure. The foregoing includes mutants, truncations, substitutions, codon optimization, or other types of modifications.

[00406] In accordance with some embodiments described herein, any of the sequences may be used, or a truncated or mutated form of any of the sequences disclosed herein (and/or included in the accompanying sequence listing) may be used and in any combination.

WHAT IS CLAIMED IS:

1. A population of genetically engineered natural killer (NK) cells for cancer immunotherapy, comprising:

a plurality of NK cells that have been expanded in culture,

wherein the plurality of NK cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex,

wherein the tumor binding domain targets CD70,

wherein the cytotoxic signaling complex comprises an OX-40 subdomain and a CD3zeta subdomain,

wherein the NK cells are engineered to express membrane bound IL-15 (mbIL15),

wherein the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

2. The population of genetically engineered NK cells of Claim 1, wherein the NK cells are genetically edited to express reduced levels of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene as compared to a non-edited NK cell,

wherein the reduced CIS expression was engineered through editing of a CISH gene, and

wherein the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels of CIS.

3. The population of genetically engineered NK cells of Claim 2 wherein the NK cells are genetically edited to express reduced levels of an adenosine receptor,

wherein the reduced adenosine receptor expression was achieved through editing of a gene encoding said adenosine receptor, and

wherein the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels the adenosine receptor.

4. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a heavy chain variable region (VH), wherein the VH is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1104, 1053, 1091, 1047, 1106, 1052, 1077, 1064, 1098, and 1088.

5. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a light chain variable region (VL), wherein the VL is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1178, 1127, 1165, 1121, 1180, 1126, 1151, 1138, 1171, and 1162.

6. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a single chain variable fragment (scFv), wherein the scFv is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 104, 53, 91, 47, 106, 52, 77, 64, 98, and 88.

7. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein

the CDR-H1 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 494, 443, 481, 437, 496, 442, 467, 454, 488, and 478;

the CDR-H2 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 568, 517, 555, 511, 570, 516, 541, 528, 562, and 552;

the CDR-H3 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 642, 591, 629, 585, 644, 590, 615, 602, 636, and 626;

the CDR-L1 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 734, 683, 721, 677, 736, 682, 707, 694, 728, and 718;

the CDR-L2 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 808, 757, 795, 751, 810, 756, 781, 768, 802, and 792; and

the CDR-L3 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 882, 831, 869, 825, 884, 830, 855, 842, 876, and 855.

8. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a VH, wherein the VH comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 956, 905, 943, 899, 958, 904, 929, 916, 950, and 940.

9. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises a VL, wherein the VL comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 1030, 979, 1017, 973, 1032, 978, 1003, 990, 1024, and 1014.

10. The population of genetically engineered NK cells of Claim 1, wherein the tumor binding domain comprises an scFv, wherein the scFv comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 296, 245, 283, 239, 298, 244, 269, 256, 290, 280.

11. The population of genetically engineered NK cells according to Claim 1, wherein the mbIL15 is bicistronically encoded on a polynucleotide encoding the CAR.

12. The population of genetically engineered NK cells according to Claim 11, wherein polynucleotide encoding the CAR and the mbIL15 comprises a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 204, 153, 191, 147, 206, 152, 177, 164, 198, and 188.

13. The population of genetically engineered NK cells of Claim 1, wherein the CAR comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 379, 328, 366, 322, 381, 327, 352, 339, 373, and 363.

14. The population of genetically engineered NK cells according to any one of Claims 1 to 13, wherein the OX40 subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 5.

15. The population of genetically engineered NK cells according to any one of Claims 1 to 14, wherein the CD3zeta subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 7.

16. The population of genetically engineered NK cells according to any one of Claims 1 to 15, wherein the mbIL15 is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 1188.

17. The population of genetically engineered NK cells of any one of Claims 2-16, wherein expression of CIS is substantially reduced as compared to an NK cell not edited with respect to CISH.

18. The population of genetically engineered NK cells of any one of Claims 2-17, wherein the NK cells do not express a detectable level of CIS protein.

19. The population of genetically engineered NK cells of any one of Claims 3-18, wherein expression of the adenosine receptor is substantially reduced as compared to an NK cell not edited with respect the adenosine receptor.

20. The population of genetically engineered NK cells of any one of Claims 3-18, wherein the NK cells do not express a detectable level of an adenosine receptor.

21. The population of genetically engineered NK cell of Claim 19 or 20, wherein the adenosine receptor comprises an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, or an A1 adenosine receptor.

22. The population of genetically engineered NK cell of Claim 19, 20, or 21, wherein the adenosine receptor comprises an A2A adenosine receptor (A2AR).

23. The population of genetically engineered NK cells of any one of Claims 1 to 22, wherein the NK cells are further genetically edited to express a reduced level of a transforming growth factor beta receptor (TGFBR) as compared to a non-edited NK cell.

24. The population of genetically engineered NK cells of any one of Claims 1-23, wherein the NK cells are further genetically edited to express a reduced level of beta-2 microglobulin (B2M) as compared to a non-edited NK cell.

25. The population of genetically engineered NK cells of any one of Claims 1-24, wherein the NK cells are further genetically edited to express a reduced level of CIITA (class II major histocompatibility complex transactivator) as compared to a non-edited NK cell.

26. The population of genetically engineered NK cells of any one of Claims 1-25, wherein the NK cells are further genetically edited to express a reduced level of a Natural Killer Group 2, member A (NKG2A) receptor as compared to a non-edited NK cell.

27. The population of genetically engineered NK cells of any one of Claims 1-26, wherein the NK cells are further genetically edited to express a reduced level of a Cbl proto-oncogene B protein encoded by a CBLB gene as compared to a non-edited NK cell.

28. The population of genetically engineered NK cells of any one of Claims 1-27, wherein the NK cells are further genetically edited to express a reduced level of a tripartite motif-containing protein 29 protein encoded by a TRIM29 gene as compared to a non-edited NK cell.

29. The population of genetically engineered NK cells of any one of Claims 1-28, wherein the NK cells are further genetically edited to express a reduced level of a suppressor of cytokine signaling 2 protein encoded by a SOCS2 gene as compared to a non-edited NK cell.

30. The population of genetically engineered NK cells according to any one of Claims 1 to 29, wherein the gene editing to reduce expression or the gene editing to induce expression is made using a CRISPR-Cas system.

31. The population of genetically engineered NK cells of Claim 30 wherein the CRISPR-Cas system comprises a Cas selected from Cas9, Csn2, Cas4, Cpf1, C2c1, C2c3, Cas13a, Cas13b, Cas13c, CasX, CasY, and combinations thereof.

32. The population of genetically engineered NK cells of Claim 31, wherein the Cas is Cas9.

33. The population of genetically engineered NK cells according to any one of Claims 1 to 28, wherein one or more guide RNA having at least 95% sequence identity to SEQ ID NO: 121, SEQ ID NO: 122, or SEQ ID NO: 123 is used to edit the CD70 gene.

34. The population of genetically engineered NK cells according to any one of Claims 2 to 29, wherein one or more guide RNA having at least 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134 is used to edit the CISH gene.

35. The population of genetically engineered NK cells according to any one of Claims 2 to 30, wherein one or more guide RNA having at least 95% sequence identity to SEQ ID NO: 396, SEQ ID NO: 397, or SEQ ID NO: 398 is used to edit the adenosine receptor gene.

36. The population of genetically engineered NK cells according to any one of Claims 23 to 35, wherein one or more guide RNA having at least 95% sequence identity to SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 132, SEQ ID NO: 133, or SEQ ID NO: 134 is used to edit the TGFBR2 gene.

37. The population of genetically engineered NK cells according to any one of Claims 1 to 29, wherein the gene editing to reduce expression or the gene editing to induce expression is made using a zinc finger nuclease (ZFN).

38. The population of genetically engineered NK cells according to any one of Claims 1 to 29, wherein the gene editing to reduce expression or the gene editing to induce expression is made using a Transcription activator-like effector nuclease (TALEN).

39. A method of treating cancer in a subject, comprising administering to the subject the population of genetically engineered NK cells according to any one of the preceding Claims.

40. The method of Claim 39, wherein the cancer is renal cell carcinoma, or a metastasis from renal cell carcinoma.

41. Use of the population of genetically engineered NK cells according to any one of the preceding Claims in the treatment of cancer.

42. Use of the mixed population of immune cells according to any one of the preceding Claims in the manufacture of a medicament for the treatment of cancer.

43. A method for treating cancer in a subject comprising,

administering to the subject a population of genetically engineered immune cells, comprising:

a plurality of NK cells that have been expanded in culture,

wherein the plurality of NK cells is engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain, a transmembrane domain, and a cytotoxic signaling complex,

wherein the tumor binding domain targets CD70,

wherein the chimeric antigen receptor comprises an OX40 subdomain and a CD3zeta subdomain,

wherein the NK cells are engineered to express membrane bound IL-15 (mbIL15),

wherein the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene.

44. The method of Claim 43, wherein the NK cells are further genetically edited to express reduced levels of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene as compared to a non-engineered NK cell, wherein the reduced CIS expression was engineered through editing of a CISH gene and wherein the genetically engineered NK cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels of CIS.

45. The method of Claim 44, wherein the NK cells are genetically edited to express reduced expression of an adenosine receptor, wherein the reduced adenosine receptor expression was achieved through editing of a gene encoding said adenosine receptor, and wherein the genetically engineered NK

cells exhibit one or more of enhanced expansion capability, enhanced cytotoxicity against target cells, and enhanced persistence, as compared to NK cells expressing native levels the adenosine receptor.

46. The method of any one of Claims 43 to 45, wherein the tumor binding domain comprises a heavy chain variable region (VH), wherein the VH is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1104, 1053, 1091, 1047, 1106, 1052, 1077, 1064, 1098, and 1088, and wherein the tumor binding domain comprises a light chain variable region (VL), wherein the VL is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 1178, 1127, 1165, 1121, 1180, 1126, 1151, 1138, 1171, and 1162.

47. The method of any one of Claims 43 to 46, wherein the tumor binding domain comprises a single chain variable fragment (scFv), wherein the scFv is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 104, 53, 91, 47, 106, 52, 77, 64, 98, and 88.

48. The method of any one of Claims 43 to 47, wherein the tumor binding domain comprises a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein

the CDR-H1 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 494, 443, 481, 437, 496, 442, 467, 454, 488, and 478;

the CDR-H2 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 568, 517, 555, 511, 570, 516, 541, 528, 562, and 552;

the CDR-H3 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 642, 591, 629, 585, 644, 590, 615, 602, 636, and 626;

the CDR-L1 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 734, 683, 721, 677, 736, 682, 707, 694, 728, and 718;

the CDR-L2 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 808, 757, 795, 751, 810, 756, 781, 768, 802, and 792; and

the CDR-L3 comprises a sequence having at least 95% sequence identity to one or more sequences selected from SEQ ID NOs: 882, 831, 869, 825, 884, 830, 855, 842, 876, and 855.

49. The method of any one of Claims 43 to 48, wherein the tumor binding domain comprises a VH, wherein the VH comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 956, 905, 943, 899, 958, 904, 929, 916, 950, and 940 , and wherein the tumor binding domain comprises a VL, wherein the VL comprises an amino acid sequence

having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 1030, 979, 1017, 973, 1032, 978, 1003, 990, 1024, and 1014.

50. The method of any one of Claims 43 to 49, wherein the tumor binding domain comprises an scFv, wherein the scFv comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 296, 245, 283, 239, 298, 244, 269, 256, 290, 280.

51. The method of any one of Claims 43 to 50, wherein the mbIL15 is bicistronically encoded on a polynucleotide encoding the CAR.

52. The population of genetically engineered NK cells according to Claim 51, wherein polynucleotide encoding the CAR and the mbIL15 comprises a sequence having at least 95% sequence identity to one or more of the polynucleotides of SEQ ID NOs: 204, 153, 191, 147, 206, 152, 177, 164, 198, and 188.

53. The method of any one of Claims 43 to 52, wherein the CAR comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 379, 328, 366, 322, 381, 327, 352, 339, 373, and 363.

54. The method of any one of Claims 43 to 53, wherein the OX40 subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 5, wherein the CD3zeta subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 7, and wherein the mbIL15 is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 1188.

55. The method of any one of Claims 44 to 54, wherein expression of CIS is substantially reduced as compared to an NK cell not edited with respect to CISH and/or wherein the NK cells do not express a detectable level of CIS protein.

56. The method of any one of Claims 48 to 55, wherein expression of the adenosine receptor is substantially reduced as compared to an NK cell not edited with respect the adenosine receptor and/or wherein the NK cells do not express a detectable level of an adenosine receptor.

57. The method of Claim 56, wherein the adenosine receptor comprises an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, or an A1 adenosine receptor.

58. The method according to any one of Claims 43 to 57, wherein the gene editing is made using a CRISPR-Cas system, and wherein the Cas comprises a Cas9 enzyme.

59. A polynucleotide encoding an anti-CD70 chimeric antigen receptor, wherein the CAR comprises an anti-CD70 binding domain,

wherein the anti-CD70 binding domain is encoded by a polynucleotide comprising a sequence having at least 95% sequence identity to one or more of SEQ ID NOs: 36-120, 221-229, 1038-1111, 1112-1185, and/or comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NO: 230-312, 890-963, 964-1037, or a portion thereof capable of generating cytotoxic signals upon binding to CD70 on a target cell;

an OX40 domain,

wherein the OX40 subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 5, and

a CD3zeta domain,

wherein the CD3zeta subdomain is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 7.

60. The polynucleotide of Claim 59, further comprising a polynucleotide encoding mbIL15, wherein the mbIL15 is encoded by a sequence having at least 95% sequence identity to SEQ ID NO: 1188.

61. The polynucleotide of Claim 59 or 60, wherein the one or more of SEQ ID NOs: 38-120, 221-229, 1038-1111, or 1112-1185, the polynucleotide encoding OX40, the polynucleotide encoding CD3zeta, and the polynucleotide encoding mbIL15 are arranged in a 5' to 3' orientation within the polynucleotide.

62. A method of enhancing the persistence of a population of immune cells to be used in cancer immunotherapy, comprising:

identifying a target marker on a tumor to be treated,

determining if a population of immune cells to be engineered to express a CAR that binds the target marker also endogenously expresses the target marker;

editing the genome of the population of immune cells to disrupt the gene encoding the endogenous target marker, and

engineering the population of immune cells to express the CAR,

wherein the disruption of the endogenous expression of the target marker by the immune cells reduces the ability of the CAR to bind the endogenous target marker on the immune cells, thereby enhancing the persistence of the population of immune cells.

63. The method of Claim 62, wherein the immune cells are NK cells, T cells, or a combination thereof, wherein the target marker is CD70, and wherein the gene editing is made using a CRISPR-Cas system.

64. A method according to any one of Claims 62 to 63, further comprising using a CRISPR-Cas system to disrupt expression of a cytokine-inducible SH2-containing (CIS) protein encoded by a CISH gene and/or further comprising using a CRISPR-Cas system to disrupt expression of an adenosine receptor, wherein the adenosine receptor comprises an A2A adenosine receptor, an A2B adenosine receptor, an A3 adenosine receptor, and/or an A1 adenosine receptor.

65. An anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain,

wherein the anti-CD70 CAR is encoded by a polynucleotide having at least 95% sequence identity to one or more of SEQ ID NOS: 138-220.

66. An anti-CD70 chimeric antigen receptor (CAR), wherein the CAR comprises an anti-CD70 binding domain, an OX40 domain, and a CD3zeta domain

wherein the anti-CD70 CAR comprises an amino acid sequence having at least 95% sequence identity to one or more of the amino acid sequences of SEQ ID NOs: 313-395, or a portion thereof capable of generating cytotoxic signals upon binding to CD70 on a target cell.

67. An anti-CD70 binding domain comprising a heavy chain variable region and a light chain variable region, wherein the heavy chain variable region comprises a CDR-H1, CDR-H2, and CDR-H3, and the light chain variable region comprises a CDR-L1, CDR-L2, and CDR-L3, and wherein:

the CDR-H1 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 428-501;

the CDR-H2 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 502-575;

the CDR-H3 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 576-649;

the CDR-L1 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 668-741;

the CDR-L2 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 742-815; and

the CDR-L3 comprises a sequence having at least 95%, 99%, or 100% sequence identity to a sequence selected from SEQ ID NOs: 816-889.

68. The anti-CD70 binding domain of Claim 67, wherein the heavy chain variable domain is encoded by a nucleic acid sequence having at least 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1038-1111.

69. The anti-CD70 binding domain of any one of Claims 67 to 68, wherein the light chain variable domain is encoded by a nucleic acid sequence having at least 95%, 99%, or 100% sequence identity to any sequence selected from SEQ ID NOs: 1112-1185.

70. The anti-CD70 binding domain of any one of claims 67 to 69, wherein the anti-CD70 binding domain is an antibody, Fab' fragment, $F(ab')_2$ fragment, or scFv.

71. A CAR comprising the anti-CD70 binding domain of any one of Claims 67 to 69.

72. The CAR of Claim 71, further comprising an OX40 subdomain and a CD3zeta subdomain.

73. A cell comprising the anti-CD70 binding domain of any one of Claims 67 to 70 or the CAR of any one of claims 71 or 72.

74. The cell of Claim 73, wherein the cell is an immune cell.

75. The cell of Claim 73 or 74, wherein the cell is an NK cell.

76. The cell of any one of Claims 73 to 75, wherein the cell is genetically edited to express a reduced level of CISH, an adenosine receptor, A2A adenosine receptor, A2B adenosine receptor, A3 adenosine receptor, A1 adenosine receptor, A2AR, TGFBR, B2M, CIITA, NKG2A, CBLB, TRIM29, SOCS2, SMAD3, MAPKAPK3, CEACAM1, or DDIT4, or any combination thereof, as compared to a non-edited cell.

77. A method of treating cancer in a subject comprising administering to the subject the anti-CD70 binding domain of any one of Claims 67 to 70, the CAR of any one of Claims 71 or 72, or the cell of any one of Claims 73 to 76.

78. Use of the anti-CD70 binding domain of any one of Claims 67 to 70, the CAR of any one of Claims 71 or 72, or the cell of any one of Claims 73 to 76 for the treatment of cancer.

79. Use of the anti-CD70 binding domain of any one of Claims 67 to 70, the CAR of any one of Claims 71 or 72, or the cell of any one of Claims 73 to 76 in the manufacture of a medicament for the treatment of cancer.

80. A population of genetically engineered natural killer (NK) cells for cancer immunotherapy, comprising:

a plurality of NK cells that have been expanded in culture,

wherein the plurality of NK cells are engineered to express a chimeric antigen receptor (CAR) comprising a tumor binding domain that targets CD70, a transmembrane domain, and a cytotoxic signaling complex,

wherein the NK cells are genetically edited to express reduced levels of CD70 as compared to a non-edited NK cell that has been expanded in culture, and wherein the reduced CD70 expression was engineered through editing of an endogenous CD70 gene

81. A method of making a population of genetically engineered immune cells for cancer immunotherapy, comprising:

engineering a population of immune cells to express a CAR that binds a target marker, wherein at least a portion of the population of immune cells also endogenously expresses the target marker; and

editing the genome of the population of immune cells to disrupt the gene encoding the endogenous target marker,

wherein the disruption of the endogenous expression of the target marker by the immune cells reduces the ability of the CAR to bind the endogenous target marker on the immune cells.

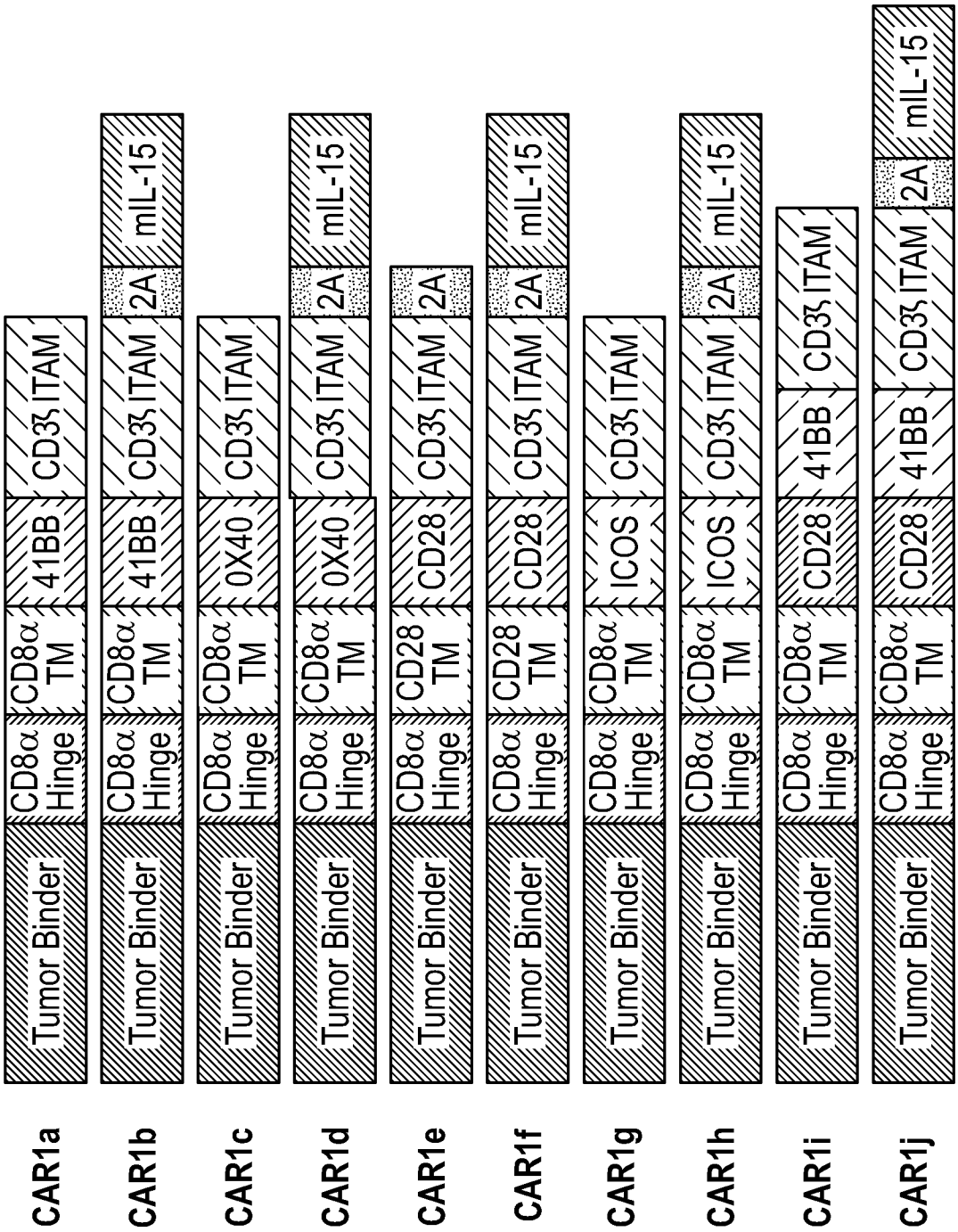

CAR1a
Tumor Binder
CD8α Hinge
CD8α TM
41BB
CD3ζ ITAM
CAR1b
Tumor Binder
CD8α Hinge
CD8α TM
41BB
CD3ζ ITAM
2A
mIL-15
CAR1c
Tumor Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
CAR1d
Tumor Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mIL-15
CAR1e
Tumor Binder
CD8α Hinge
CD28 TM
CD28
CD3ζ ITAM
2A
CAR1f
Tumor Binder
CD8α Hinge
CD28 TM
CD28
CD3ζ ITAM
2A
mIL-15
CAR1g
Tumor Binder
CD8α Hinge
CD8α TM
ICOS
CD3ζ ITAM
CAR1h
Tumor Binder
CD8α Hinge
CD8α TM
ICOS
CD3ζ ITAM
2A
mIL-15
CAR1i
Tumor Binder
CD8α Hinge
CD8α TM
CD28
41BB
CD3ζ ITAM
CAR1j
Tumor Binder
CD8α Hinge
CD8α TM
CD28
41BB
CD3ζ ITAM
2A
mIL-15

FIG. 1


CAR2a
Tumor Binder
CD8α Hinge
NKG2D TM
0X40
CD3ζ ITAM
CAR2b
Tumor Binder
CD8α Hinge
NKG2D TM
0X40
CD3ζ ITAM
2A
mIL-15
CAR2c
Tumor Binder
CD8α Hinge
CD8α TM
CD40
CD3ζ ITAM
CAR2d
Tumor Binder
CD8α Hinge
CD8α TM
Cd40
CD3ζ ITAM
2A
mIL-15
CAR2e
Tumor Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
EGFRt
CAR2f
Tumor Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mIL-15
2A
EGFRt
CAR2g
Tumor Binder
CD8α Hinge
CD8α TM
CD40
CD3ζ ITAM
CAR2h
Tumor Binder
CD8α Hinge
CD8α TM
CD40
CD3ζ ITAM
2A
mIL-15
CAR2i
Tumor Binder
Ig4 SH
CD28 TM
CD28
CD3ζ ITAM
CAR2j
Tumor Binder
Ig4 SH
CD28 TM
CD28
CD3ζ ITAM
2A
mbIL-15

FIG. 2

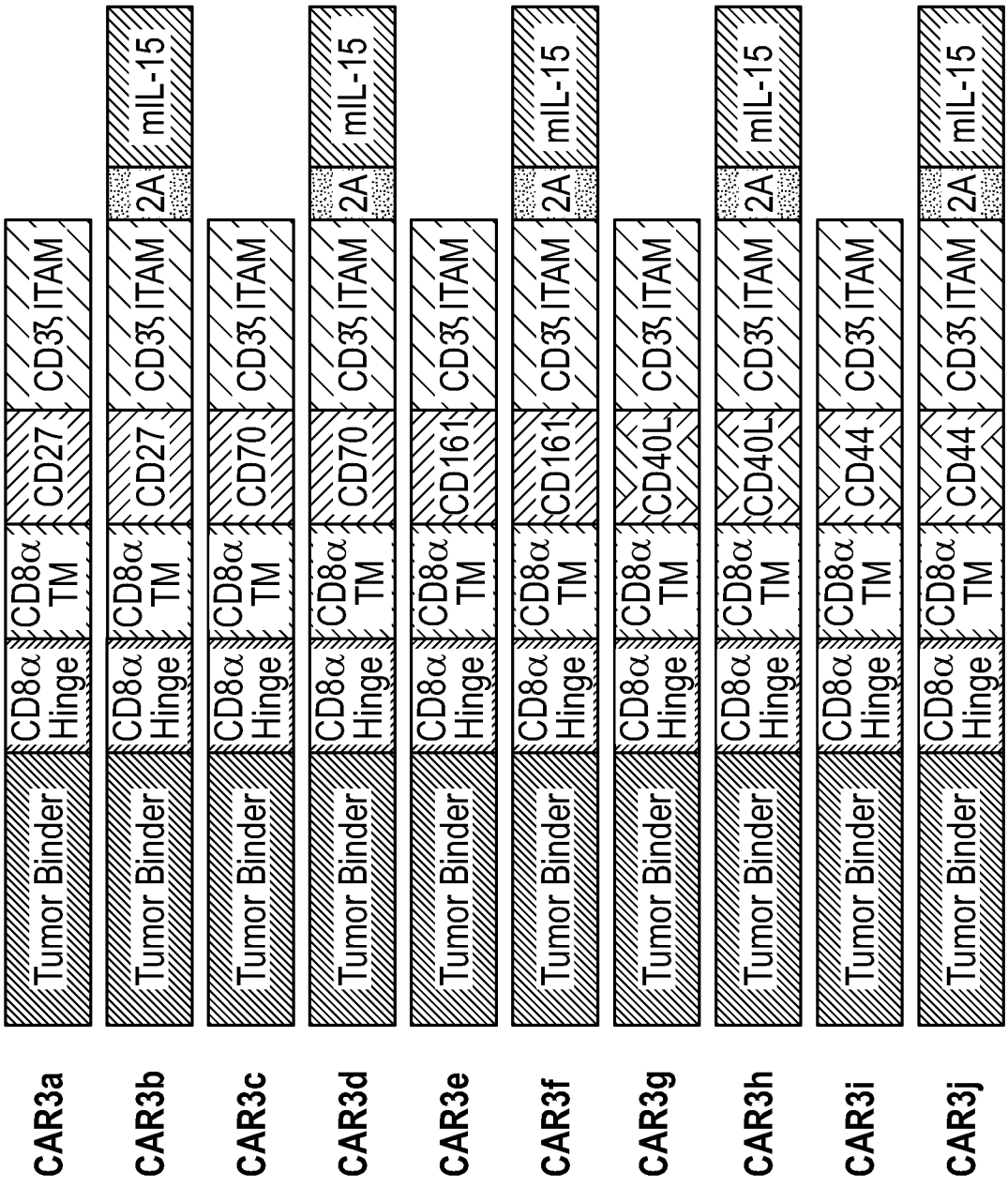

CAR3a
Tumor Binder
CD8α Hinge
CD8α TM
CD27
CD3ζ ITAM
CAR3b
Tumor Binder
CD8α Hinge
CD8α TM
CD27
CD3ζ ITAM
2A
mIL-15
CAR3c
Tumor Binder
CD8α Hinge
CD8α TM
CD70
CD3ζ ITAM
CAR3d
Tumor Binder
CD8α Hinge
CD8α TM
CD70
CD3ζ ITAM
2A
mIL-15
CAR3e
Tumor Binder
CD8α Hinge
CD8α TM
CD161
CD3ζ ITAM
CAR3f
Tumor Binder
CD8α Hinge
CD8α TM
CD161
CD3ζ ITAM
2A
mIL-15
CAR3g
Tumor Binder
CD8α Hinge
CD8α TM
CD40L
CD3ζ ITAM
CAR3h
Tumor Binder
CD8α Hinge
CD8α TM
CD40L
CD3ζ ITAM
2A
mIL-15
CAR3i
Tumor Binder
CD8α Hinge
CD8α TM
CD44
CD3ζ ITAM
CAR3j
Tumor Binder
CD8α Hinge
CD8α TM
CD44
CD3ζ ITAM
2A
mIL-15

FIG. 3

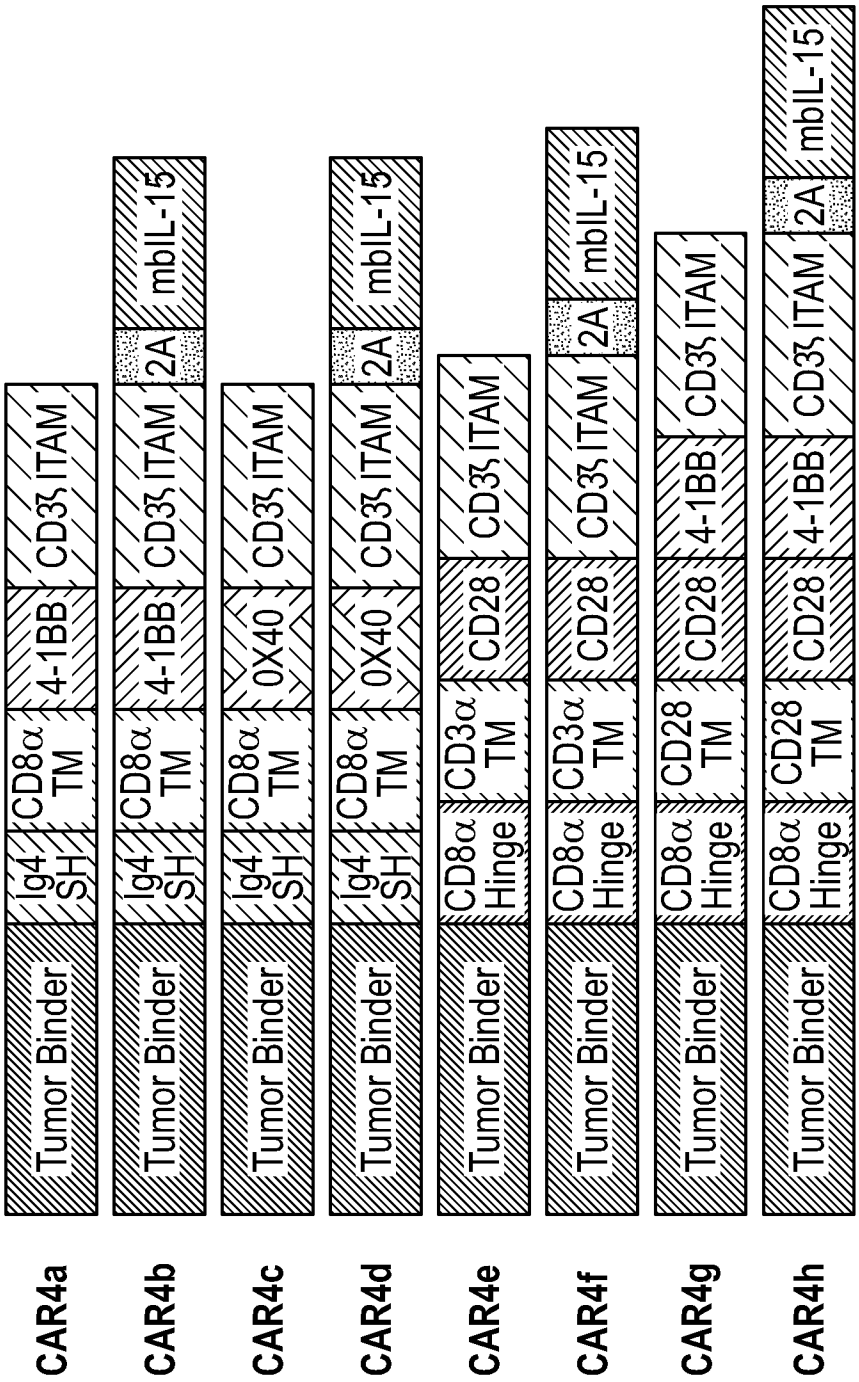

CAR4a
Tumor Binder
lg4 SH
CD8α TM
4-1BB
CD3ζ ITAM
CAR4b
Tumor Binder
lg4 SH
CD8α TM
4-1BB
CD3ζ ITAM
2A
mbIL-15
CAR4c
Tumor Binder
lg4 SH
CD8α TM
0X40
CD3ζ ITAM
CAR4d
Tumor Binder
lg4 SH
CD8α TM
0X40
CD3ζ ITAM
2A
mbIL-15
CAR4e
Tumor Binder
CD8α Hinge
CD3α TM
CD28
CD3ζ ITAM
CAR4f
Tumor Binder
CD8α Hinge
CD3α TM
CD28
CD3ζ ITAM
2A
mbIL-15
CAR4g
Tumor Binder
CD8α Hinge
CD28 TM
CD28
4-1BB
CD3ζ ITAM
CAR4h
Tumor Binder
CD8α Hinge
CD28 TM
CD28
4-1BB
CD3ζ ITAM
2A
mbIL-15

FIG. 4

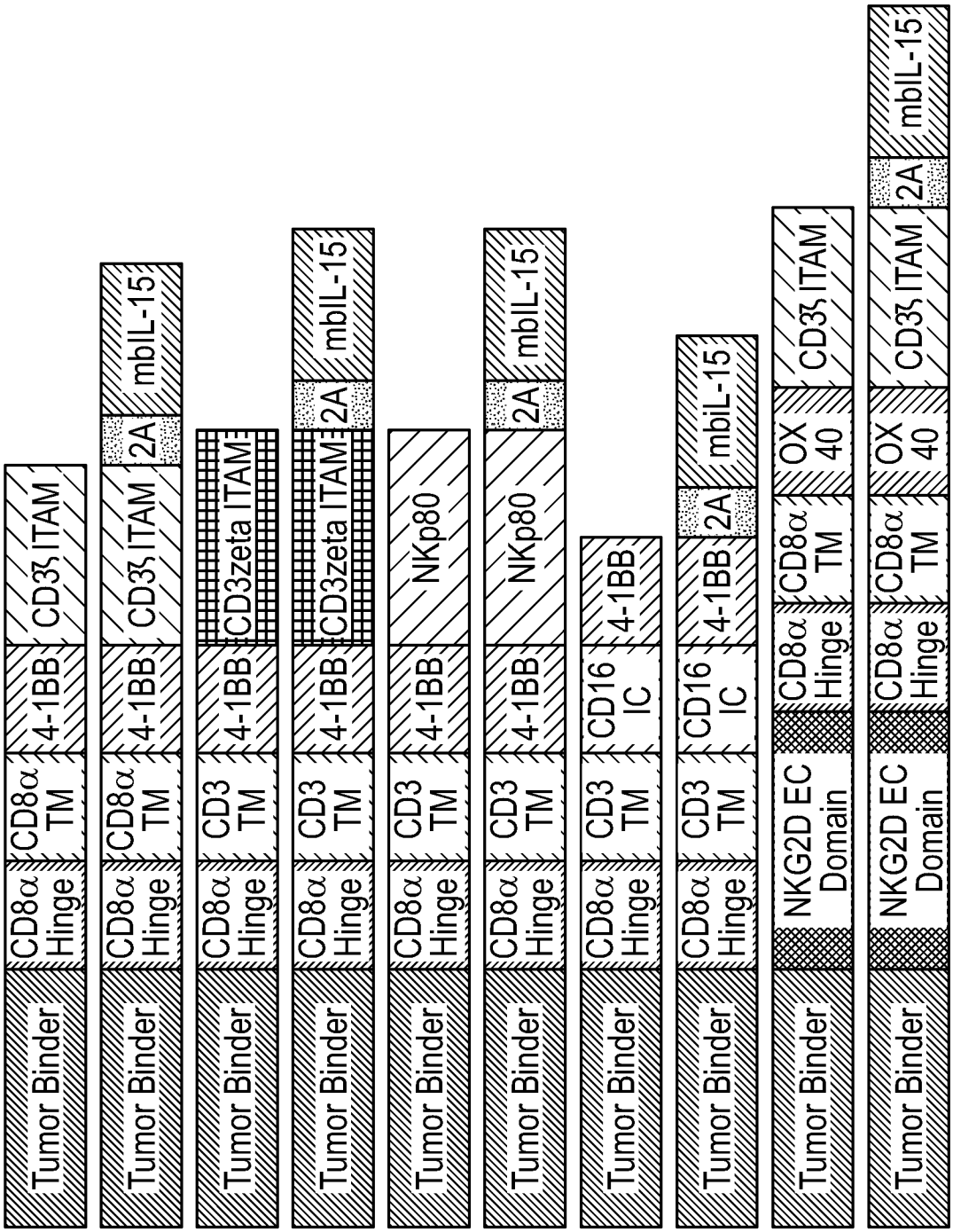

CAR5a
Tumor Binder
CD8α Hinge
CD8α TM
4-1BB
CD3ζ ITAM
CAR5b
Tumor Binder
CD8α Hinge
CD8α TM
4-1BB
CD3ζ ITAM
2A
mbIL-15
CAR5c
Tumor Binder
CD8α Hinge
CD3 TM
4-1BB
CD3zeta ITAM
CAR5d
Tumor Binder
CD8α Hinge
CD3 TM
4-1BB
CD3zeta ITAM
2A
mbIL-15
CAR5e
Tumor Binder
CD8α Hinge
CD3 TM
4-1BB
NKp80
CAR5f
Tumor Binder
CD8α Hinge
CD3 TM
4-1BB
NKp80
2A
mbIL-15
CAR5g
Tumor Binder
CD8α Hinge
CD3 TM
CD16 IC
4-1BB
CAR5h
Tumor Binder
CD8α Hinge
CD3 TM
CD16 IC
4-1BB
2A
mbIL-15
Bi-spec CAR/ACRa
Tumor Binder
NKG2D EC Domain
CD8α Hinge
CD8α TM
OX 40
CD3ζ ITAM
Bi-spec CAR/ARCb
Tumor Binder
NKG2D EC Domain
CD8α Hinge
CD8α TM
OX 40
CD3ζ ITAM
2A
mbIL-15

FIG. 5

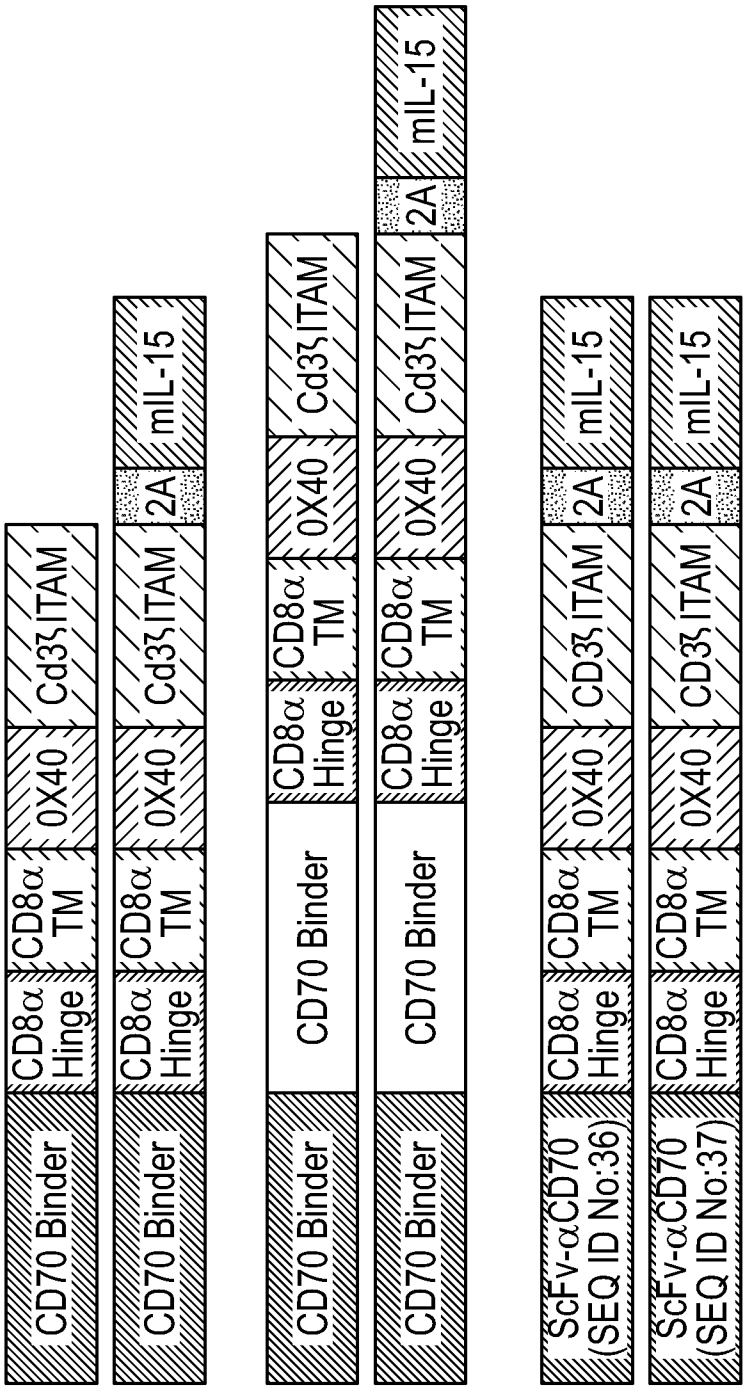

CD70 CARa
CD70 Binder
CD8α Hinge
CD8α TM
0X40
Cd3ζ ITAM
CD70 CARb
CD70 Binder
CD8α Hinge
CD8α TM
0X40
Cd3ζ ITAM
2A
mIL-15
Bi-v CD70 CARa
CD70 Binder
CD8α Hinge
CD8α TM
0X40
Cd3ζ ITAM
Bi-v CD70 CARb
CD70 Binder
CD8α Hinge
CD8α TM
0X40
Cd3ζ ITAM
2A
mIL-15
NK71
ScFv-αCD70 (SEQ ID No:36)
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mIL-15
NK72
ScFv-αCD70 (SEQ ID No:37)
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mIL-15

FIG. 6

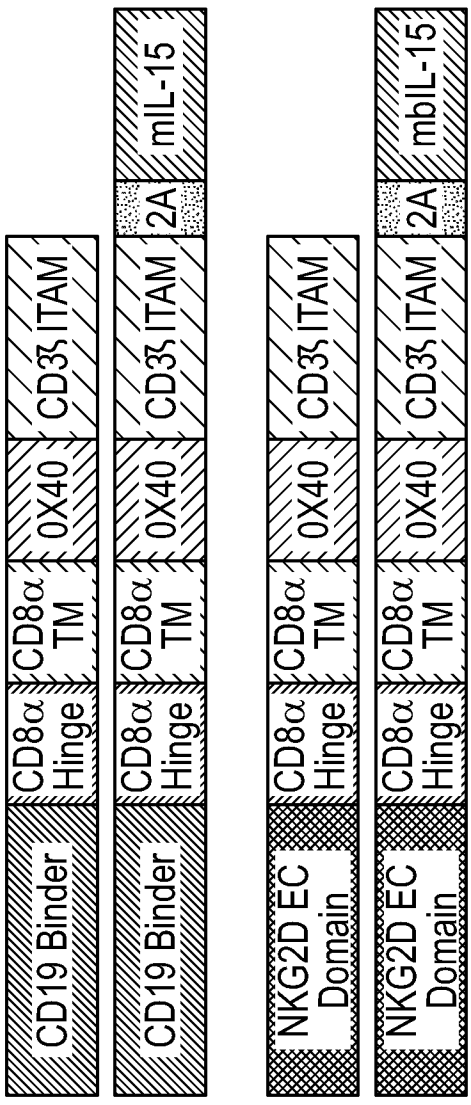

CD19 CARa
CD19 Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
CD19 CARb
CD19 Binder
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mIL-15
NKG2D ACRa
NKG2D EC Domain
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
NKG2D ACRb
NKG2D EC Domain
CD8α Hinge
CD8α TM
0X40
CD3ζ ITAM
2A
mbIL-15

FIG. 7

Figures 8A-8C

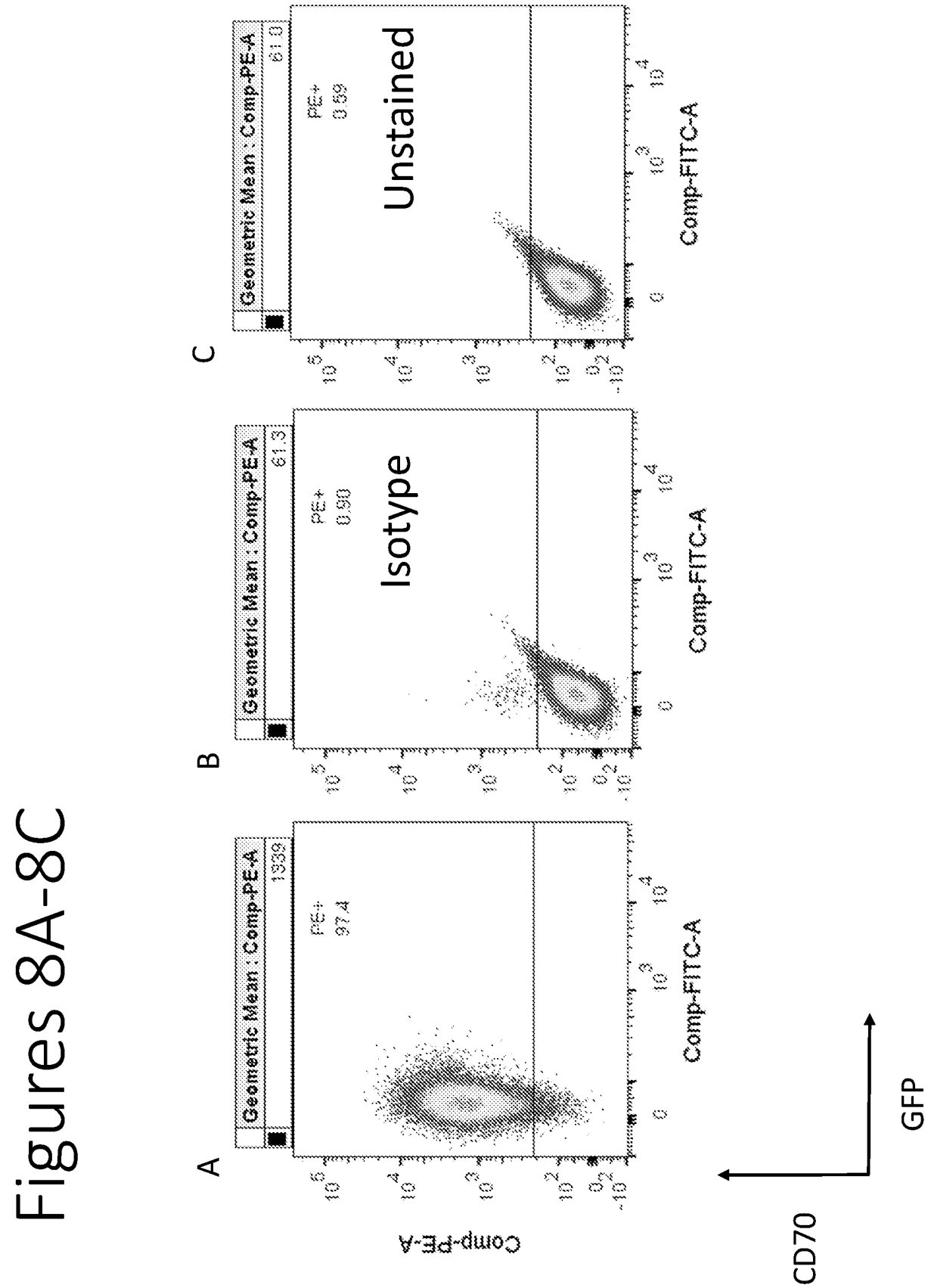
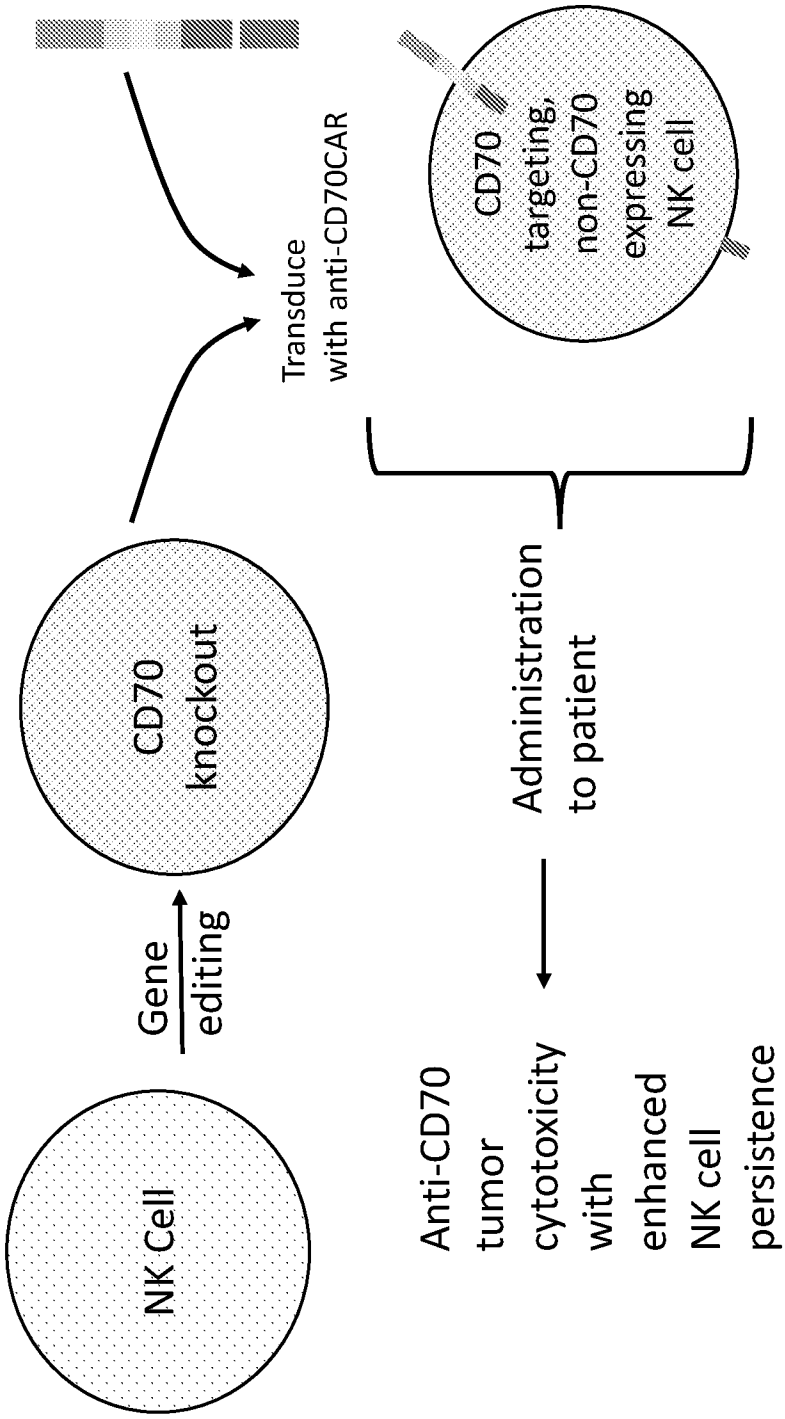
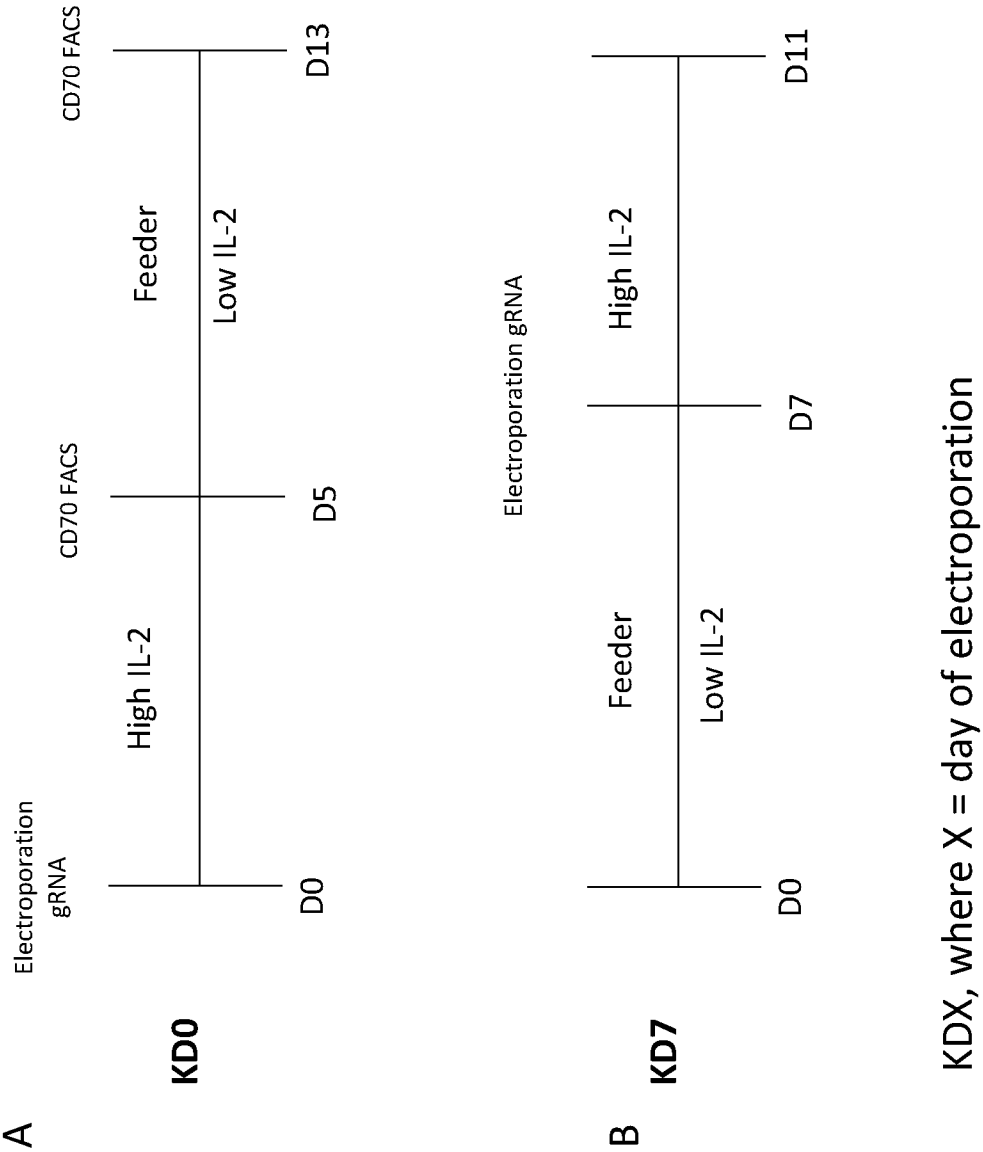


Figure 9

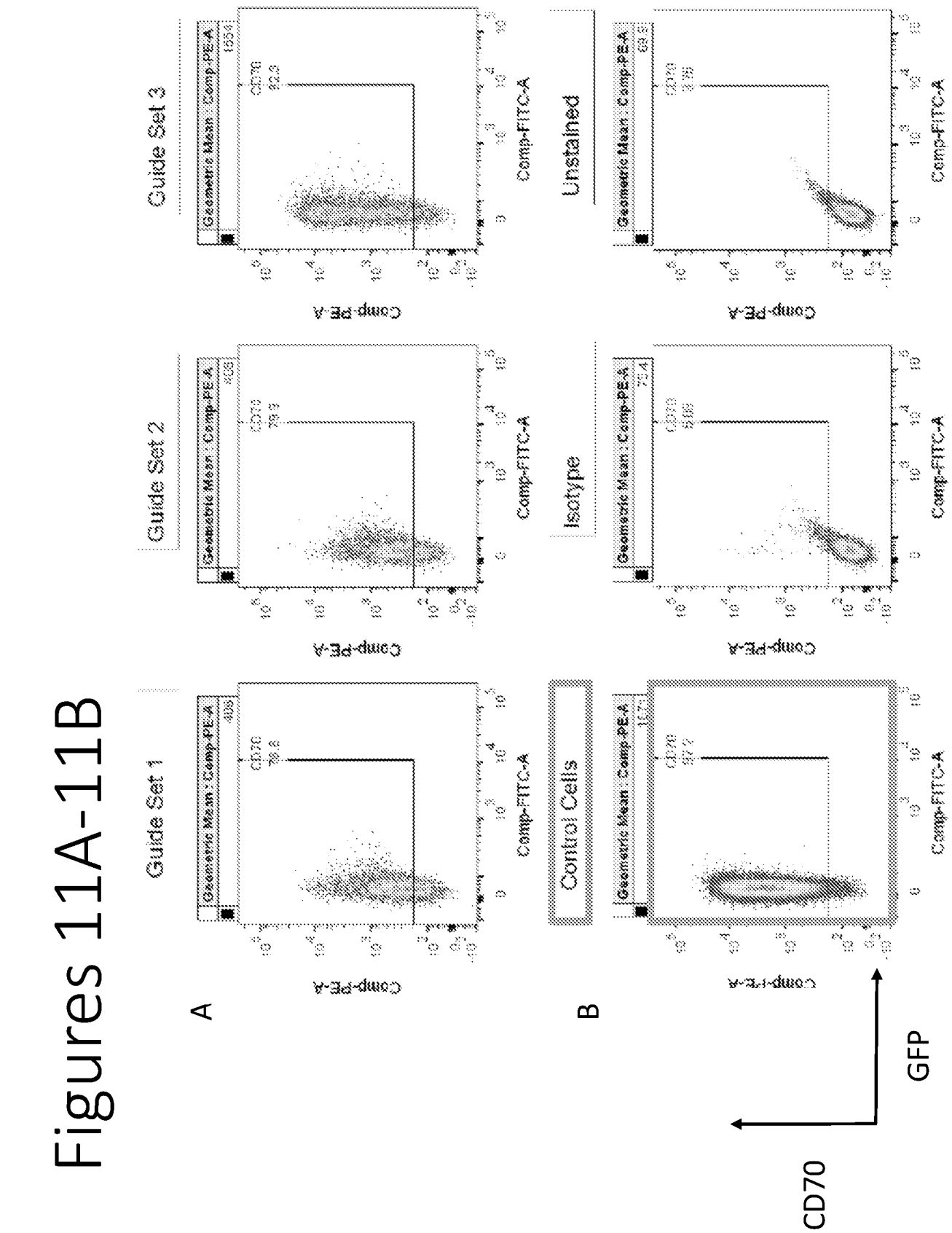

NK Cell
Gene editing
CD70 knockout
Transduce with anti-CD70CAR
CD70 targeting, non-CD70 expressing NK cell
Administration to patient
Anti-CD70 tumor cytotoxicity with enhanced NK cell persistence

Figures 10A-10B

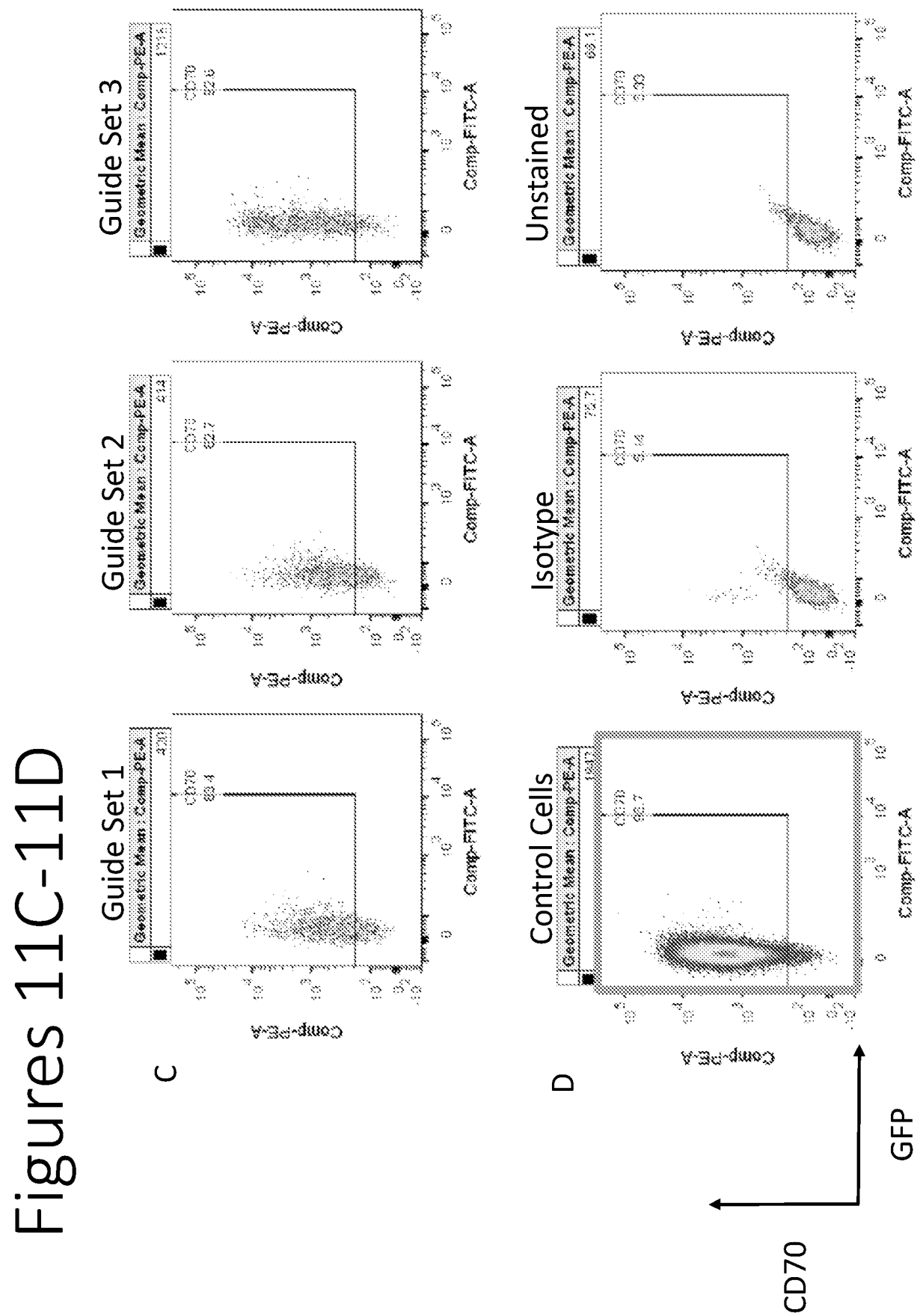


KDX, where X = day of electroporation

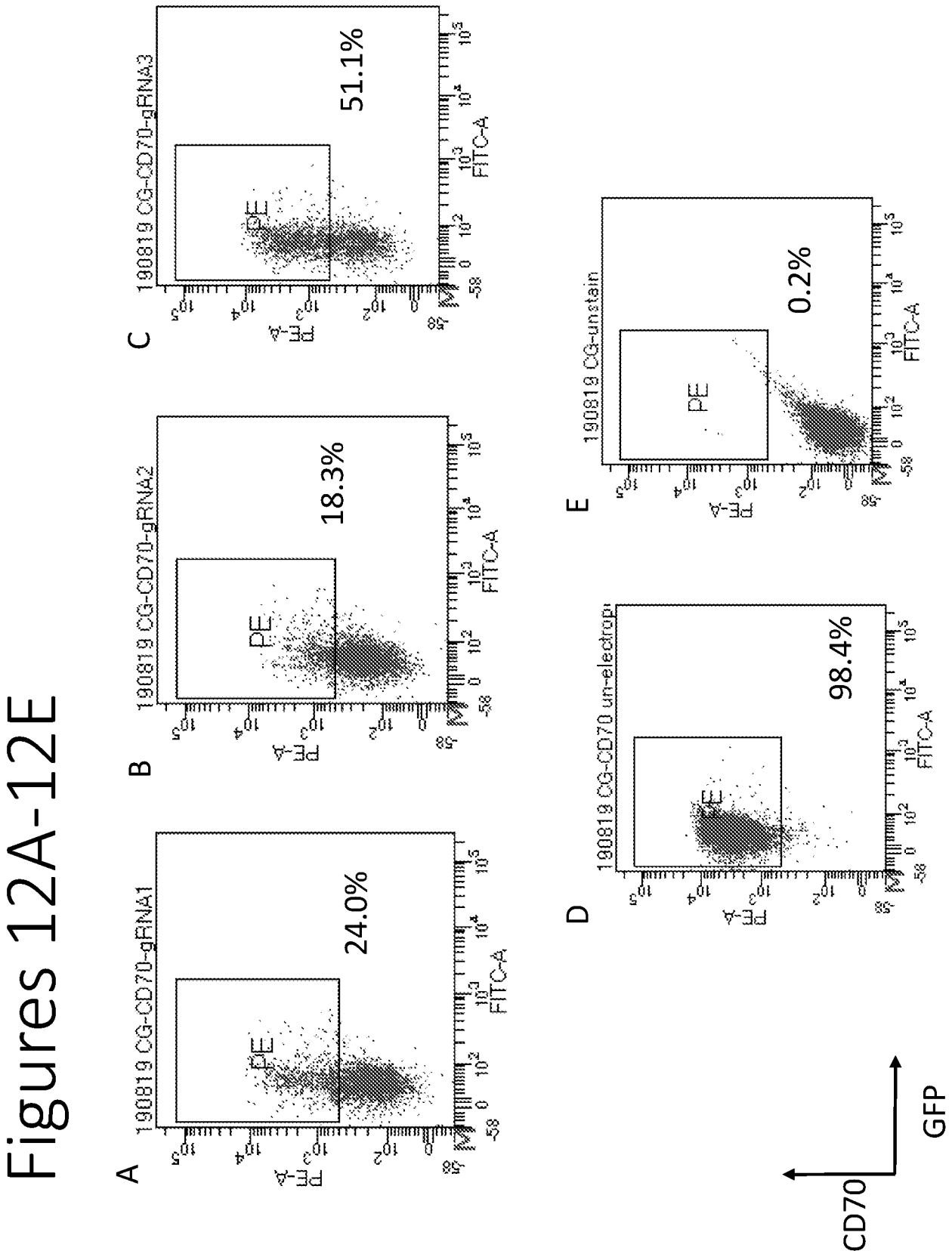
Figures 11A-11B



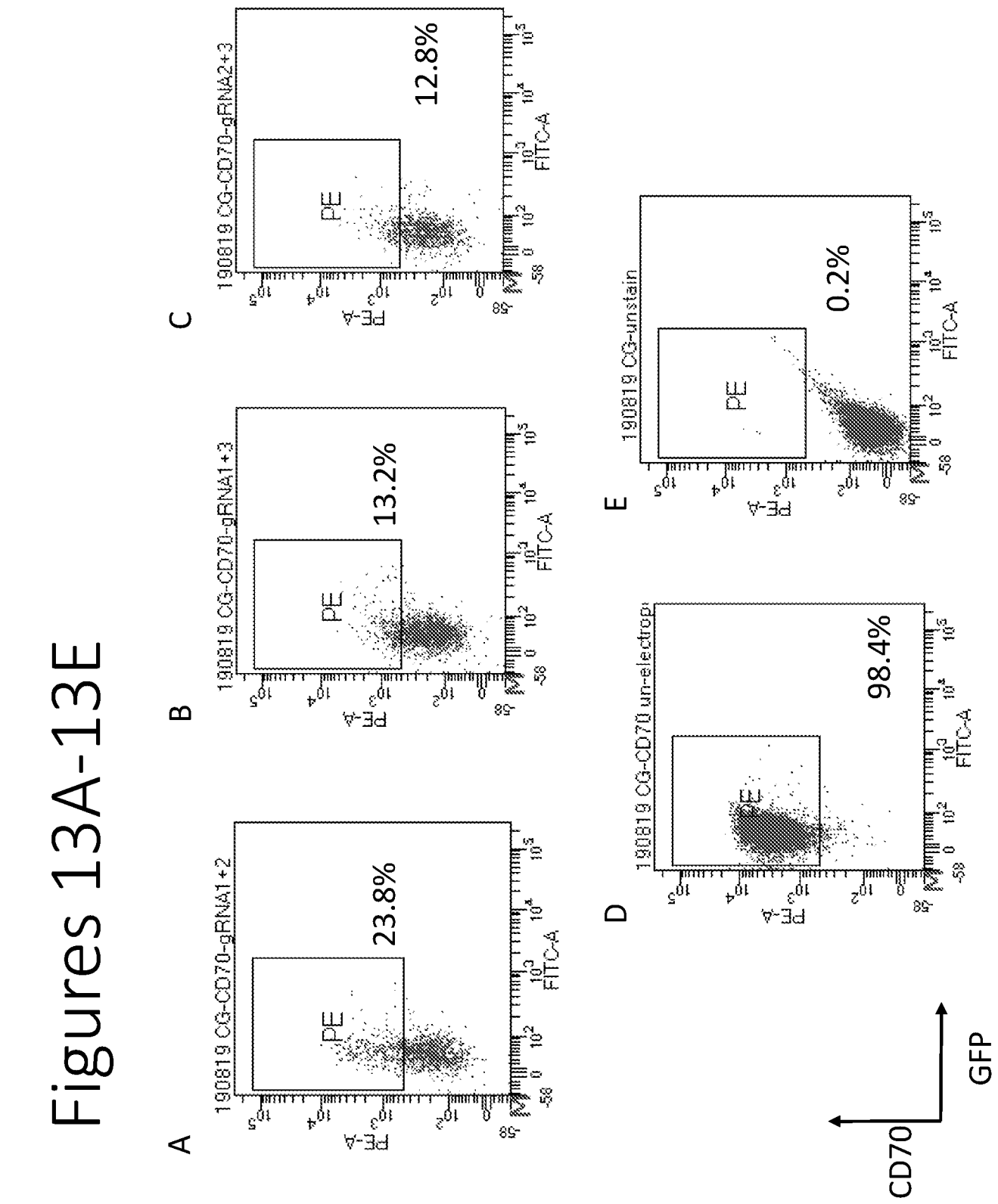
Figures 11C-11D



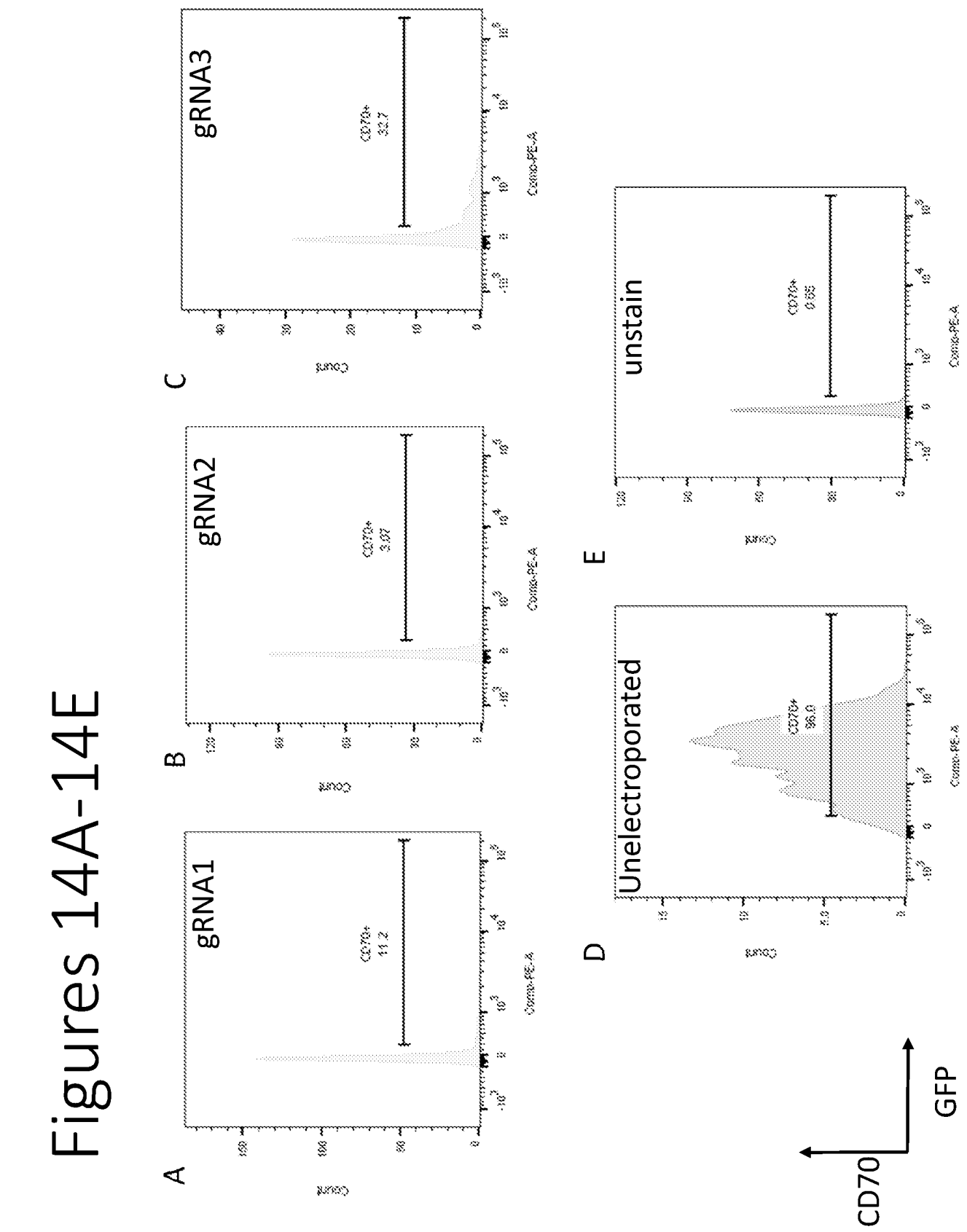
Figures 12A-12E



Figures 13A-13E

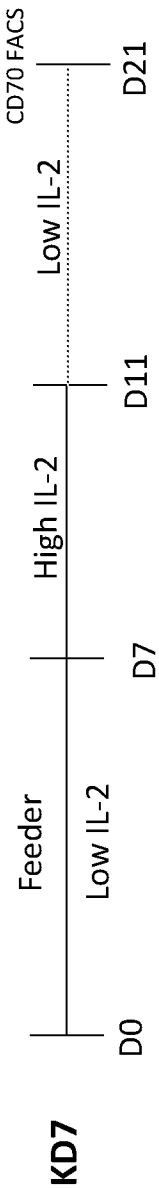


Figures 14A-14E

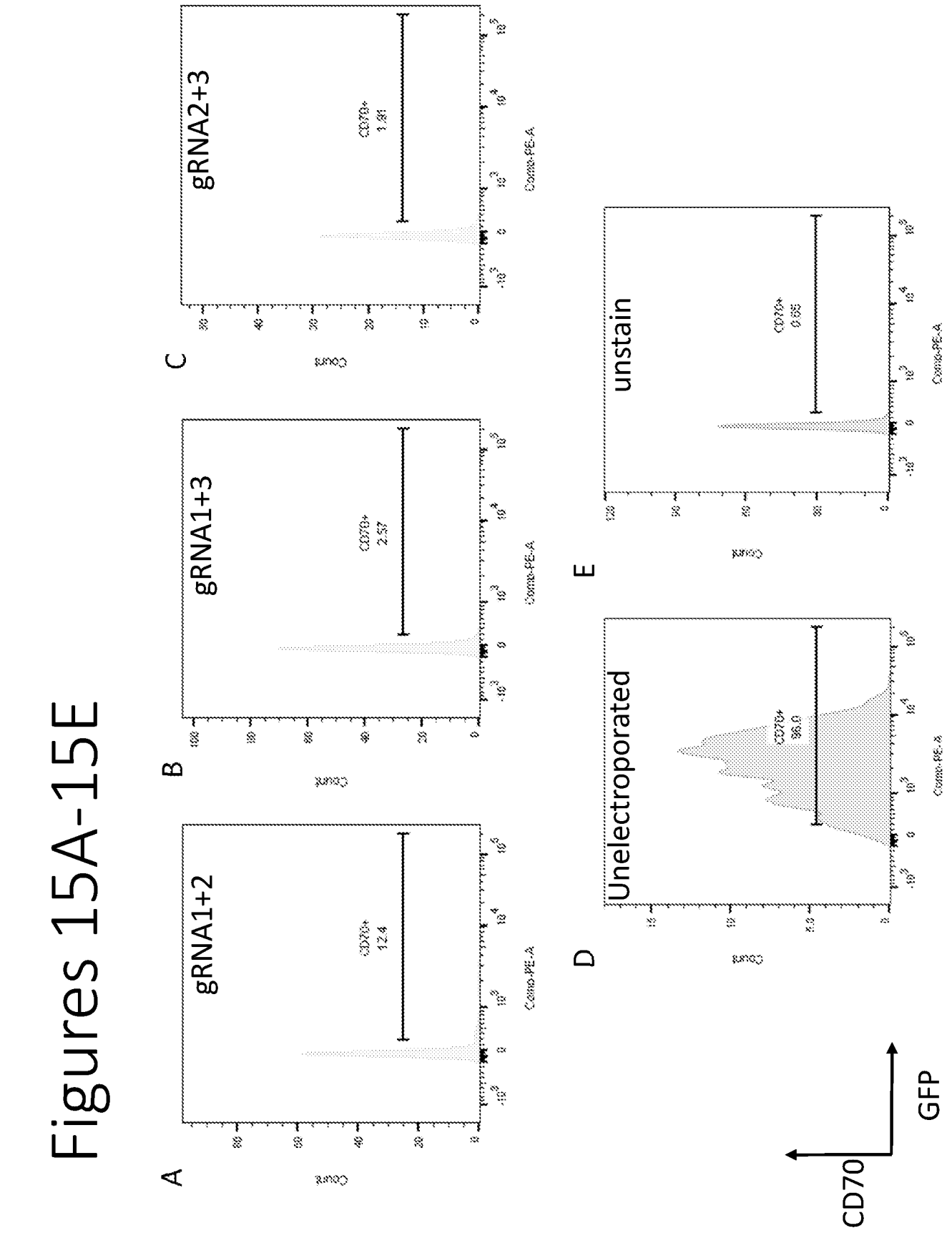


Figures 14F

F



Figures 15A-15E



Figures 16A-16B

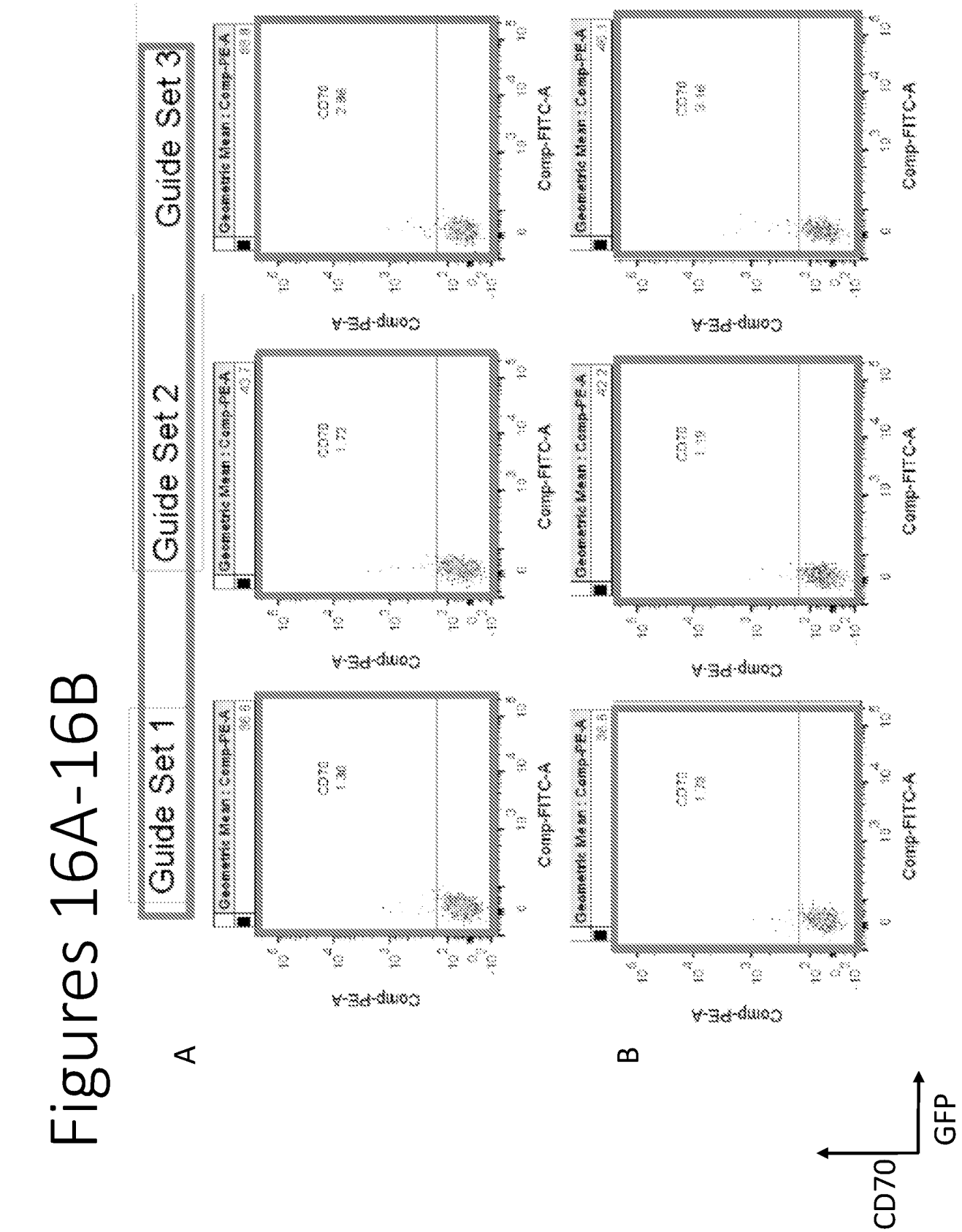
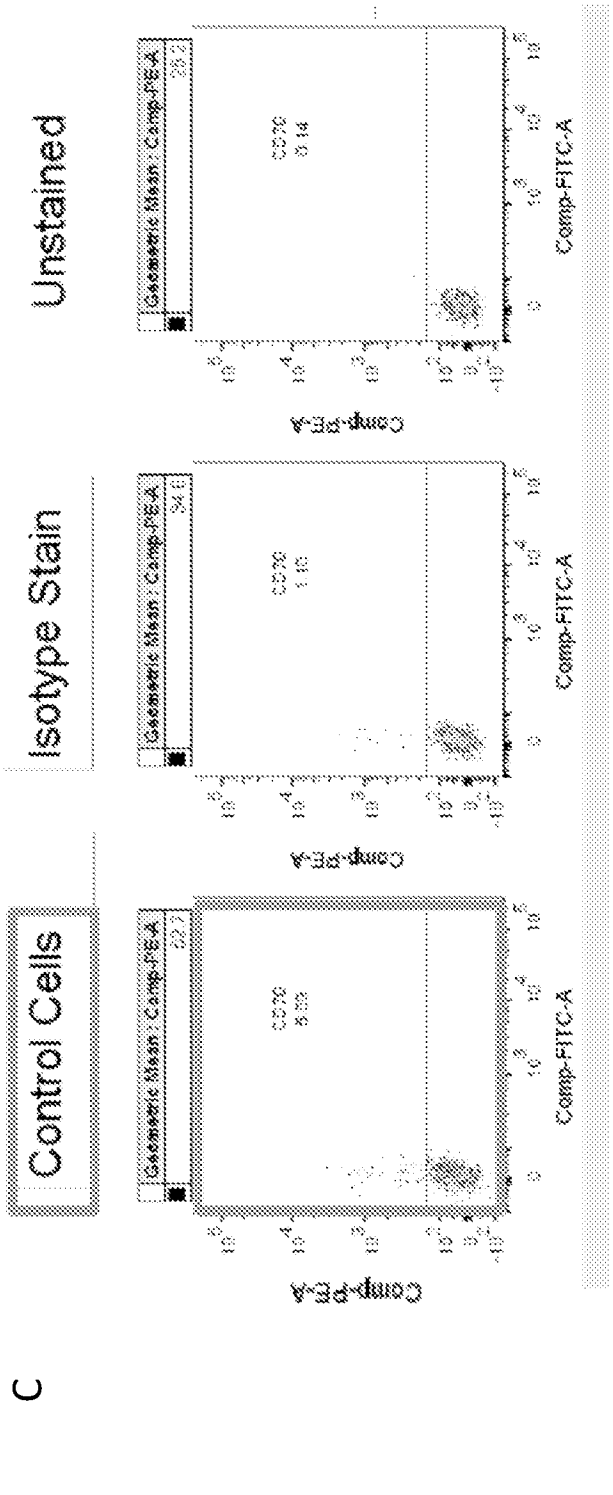


Figure 16C


C
Control Cells
Isotype Stain
Unstained
Comp-PE-A
Comp-FITC-A
CD70
GFP

Figures 17A-17B

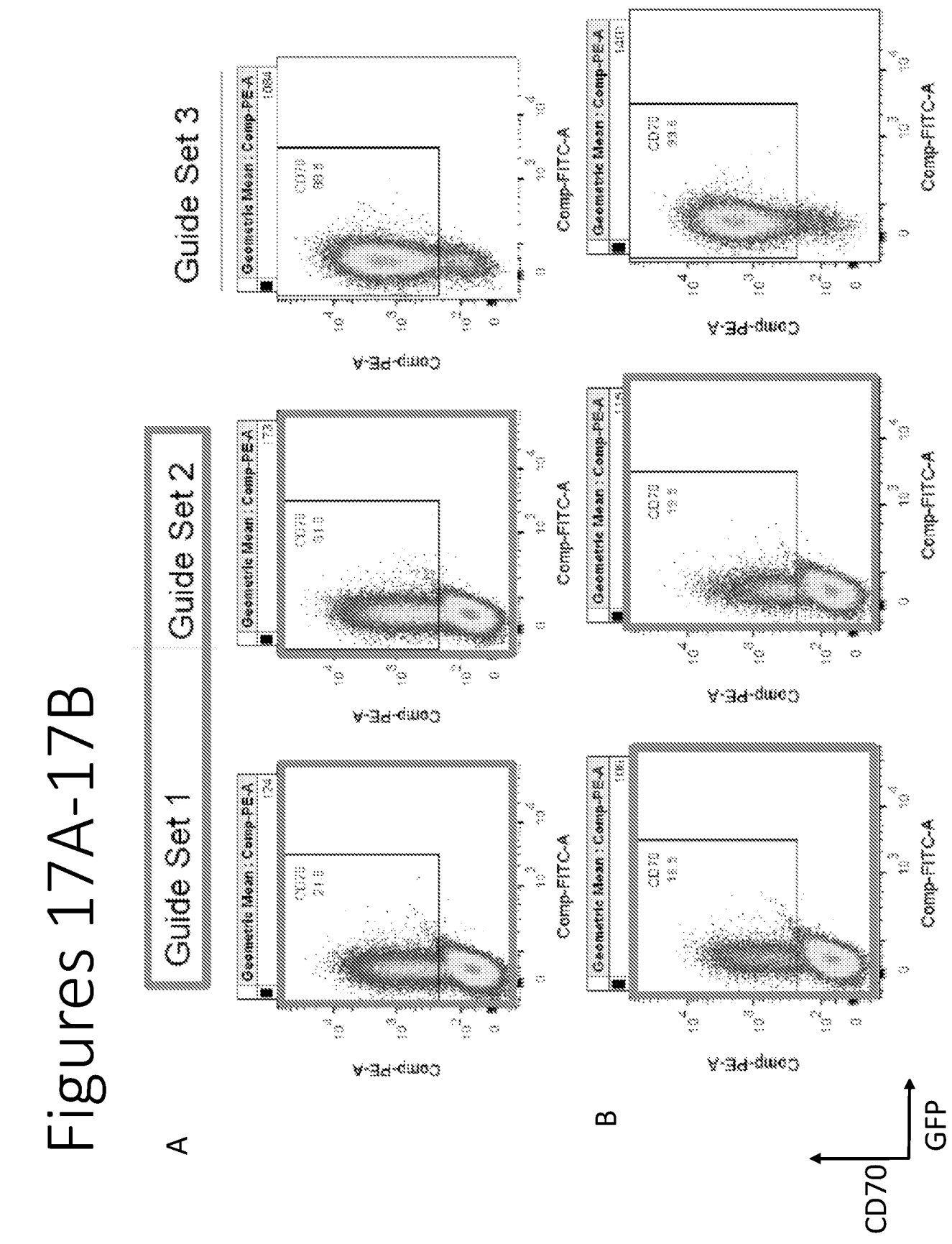
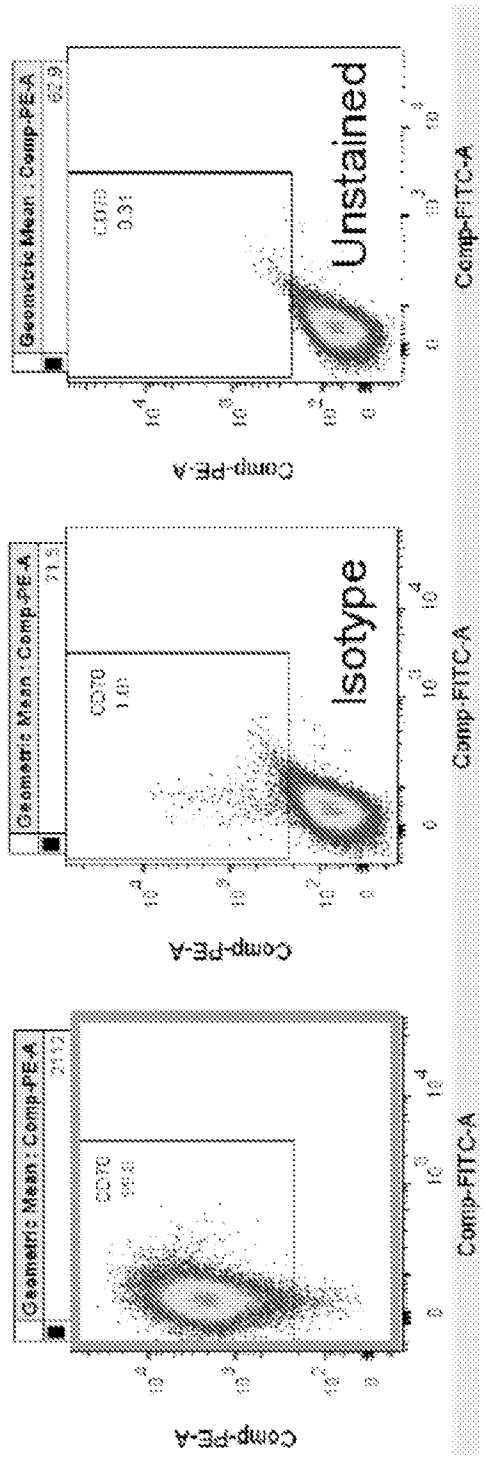
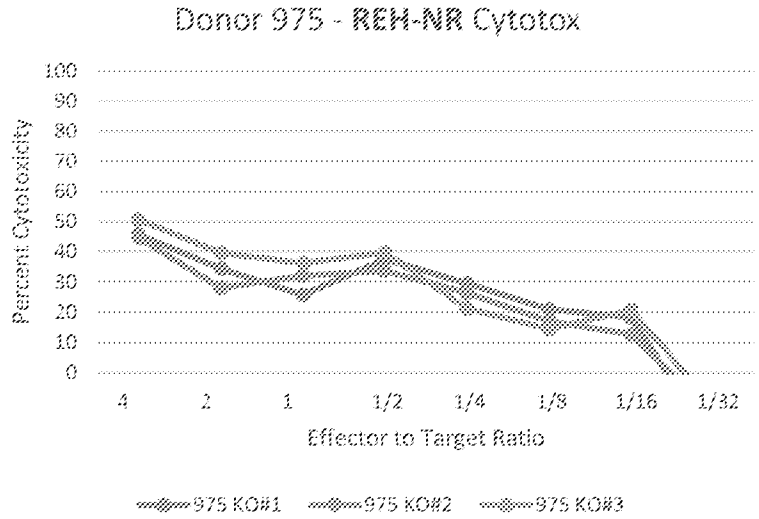


Figure 17C

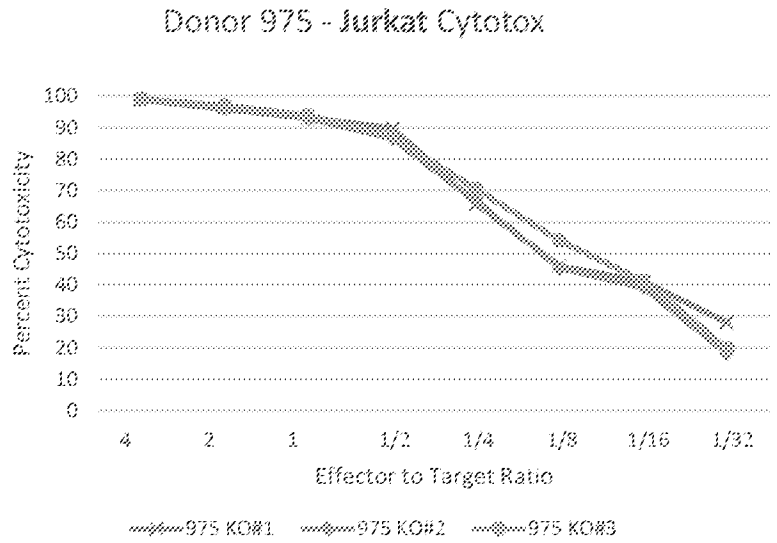

C
Comp-PE-A
Comp-FITC-A
Geometric Mean : Comp-PE-A
CD70
95.8
Isotype
CD70
1.48
Unstained
CD70
0.31
CD70
GFP

Figures 18A-18B

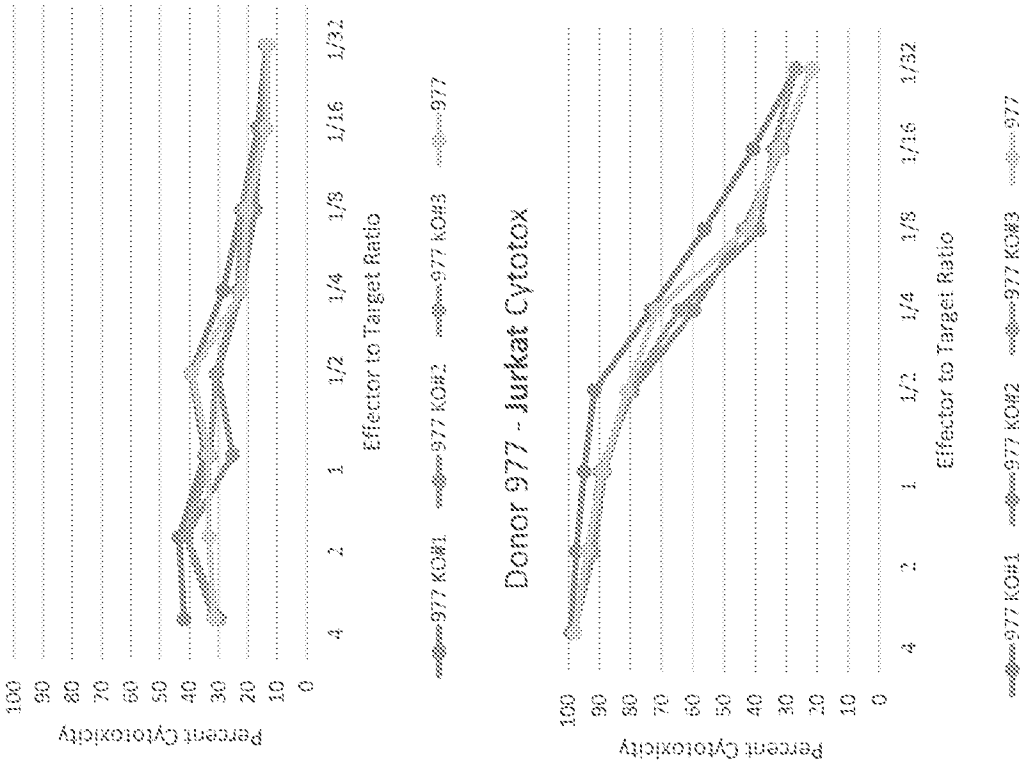
A



B

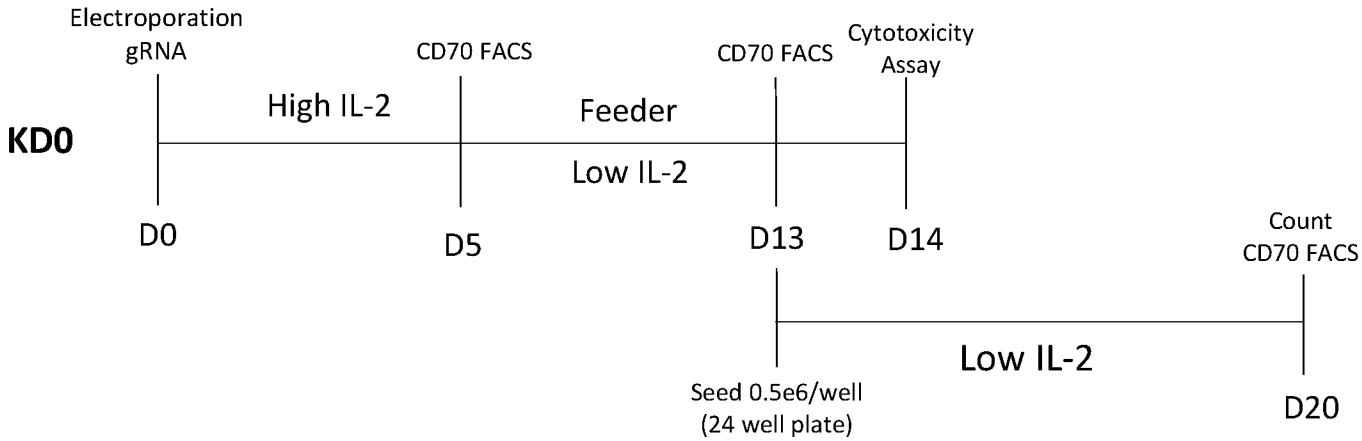


Figures 18C-18D



Figures 19A-19B

A



B

Donor	Knockout	Viability %	E6 Viable/mL	uL for 1e5	E6 Total Viable	Fold Growth	CD70% Initial	CD70% D7 Post Expansion	CD70% Final
975	1	74.8	0.417	239.8	0.834	1.668	1.3	21.8	6.09
975	2	77.1	0.491	203.7	0.982	1.964	1.72	31	15.4
975	3	79.6	0.446	224.2	0.892	1.784	2.86	88.5	57.2
977	1	78.5	0.626	159.7	1.252	2.504	1.73	16.5	5.04
977	2	73.3	0.502	199.2	1.004	2.008	1.19	19.5	2.91
977	3	79.8	0.625	160.0	1.25	2.5	3.16	93.6	49
977	c	67.2	0.383	261.1	0.766	1.532	5.09	99.3	80.9

Figures 20A-20B

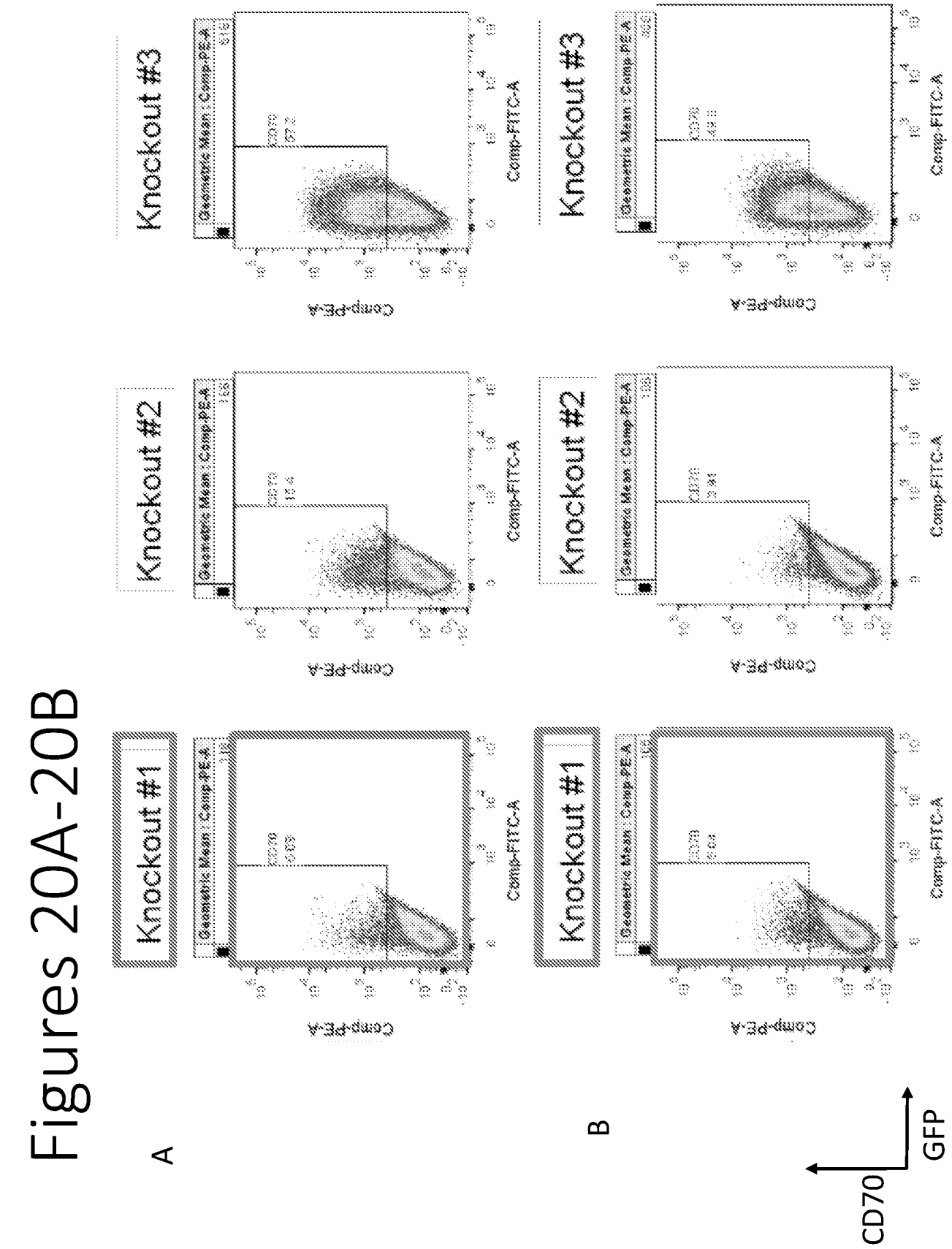
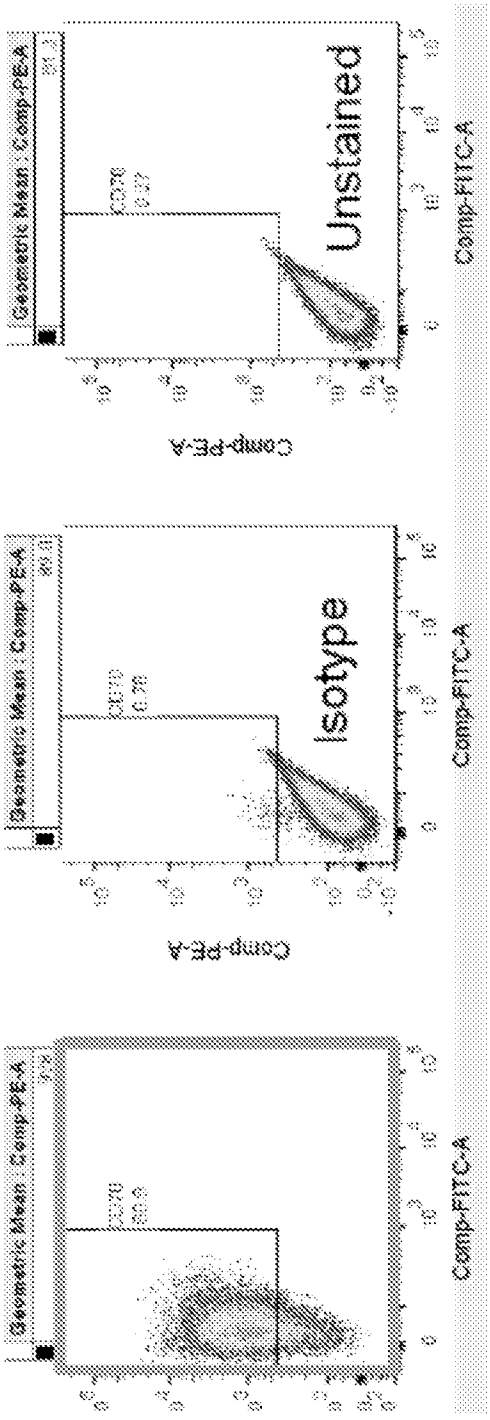
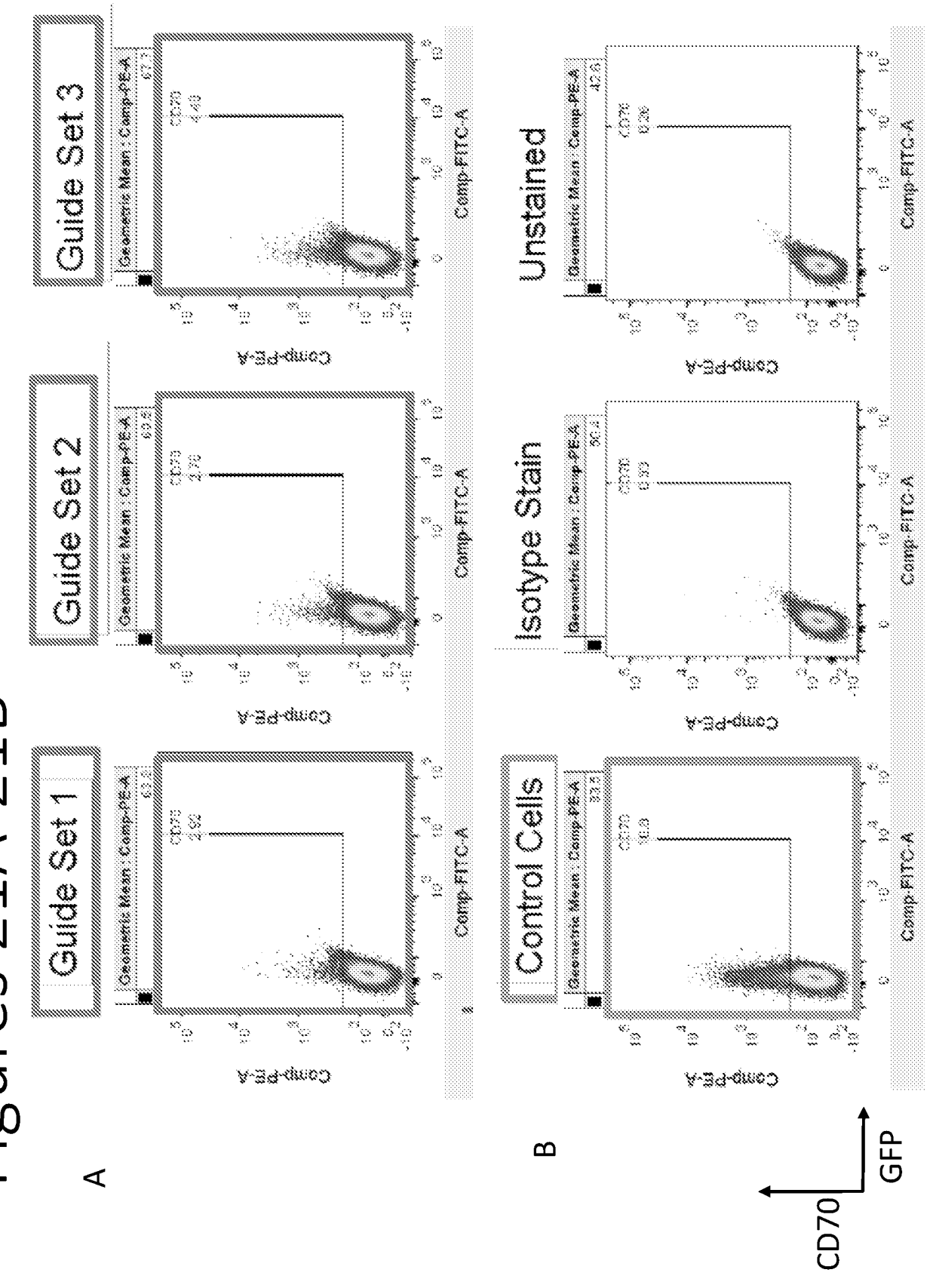


Figure 20C

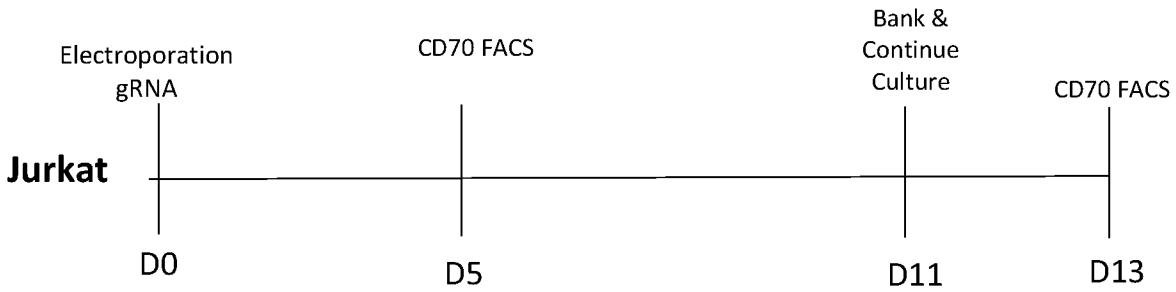


Figures 21A-21B

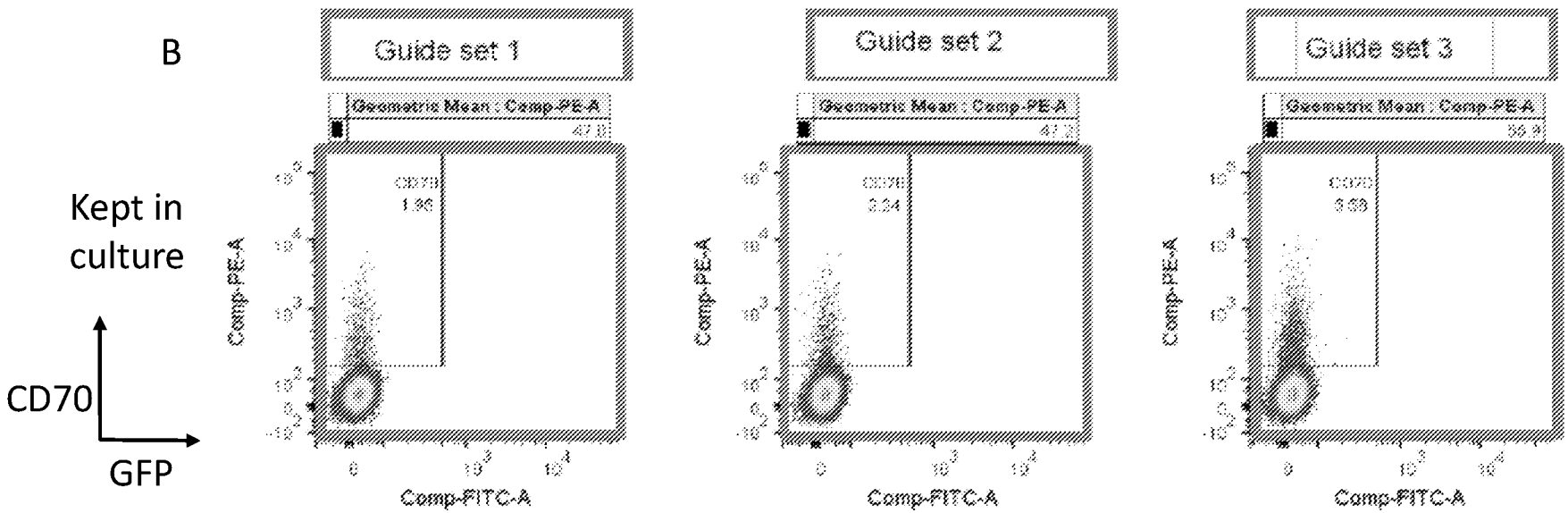


Figures 22A-22B

A



B



Figures 22C-22D

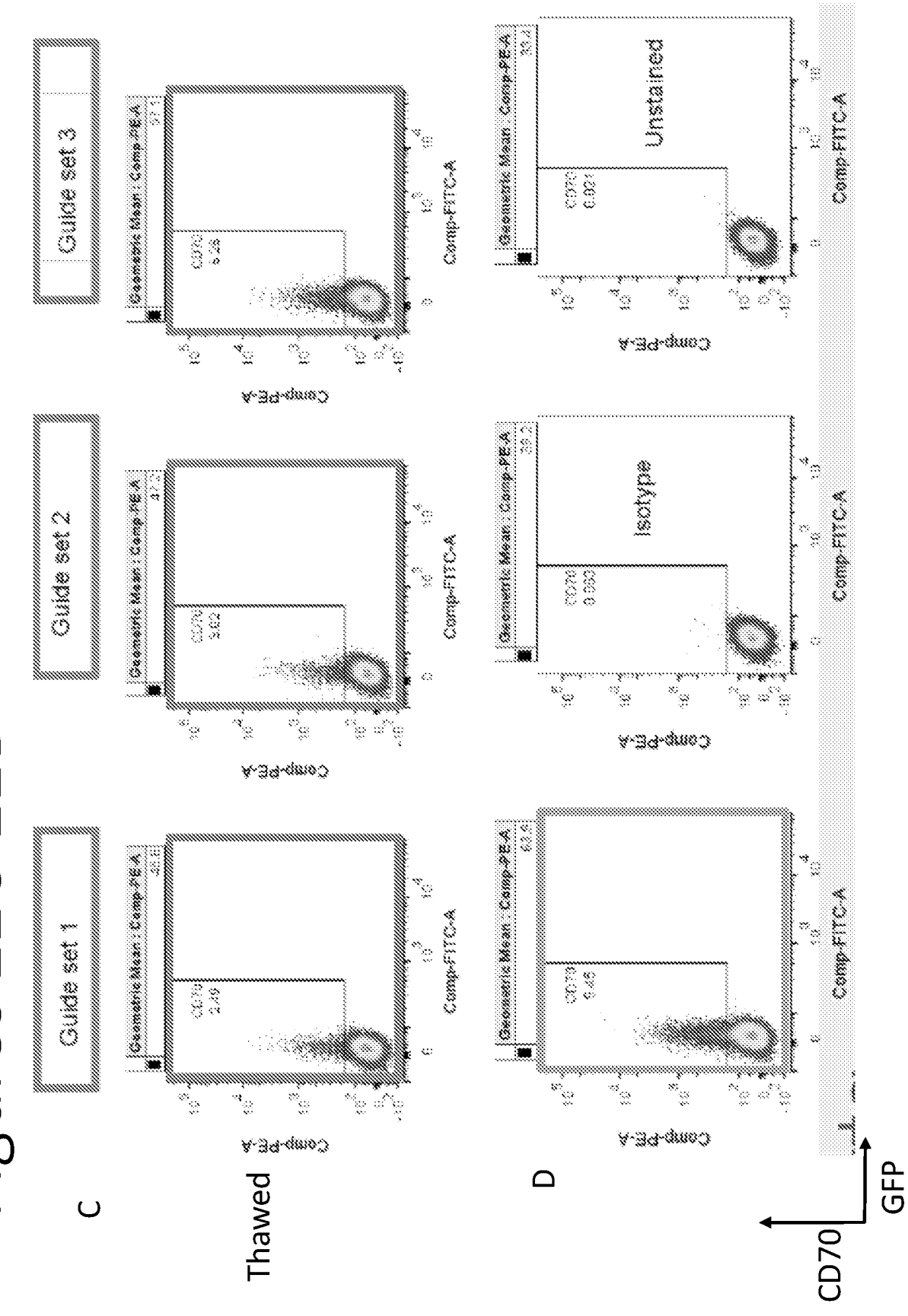
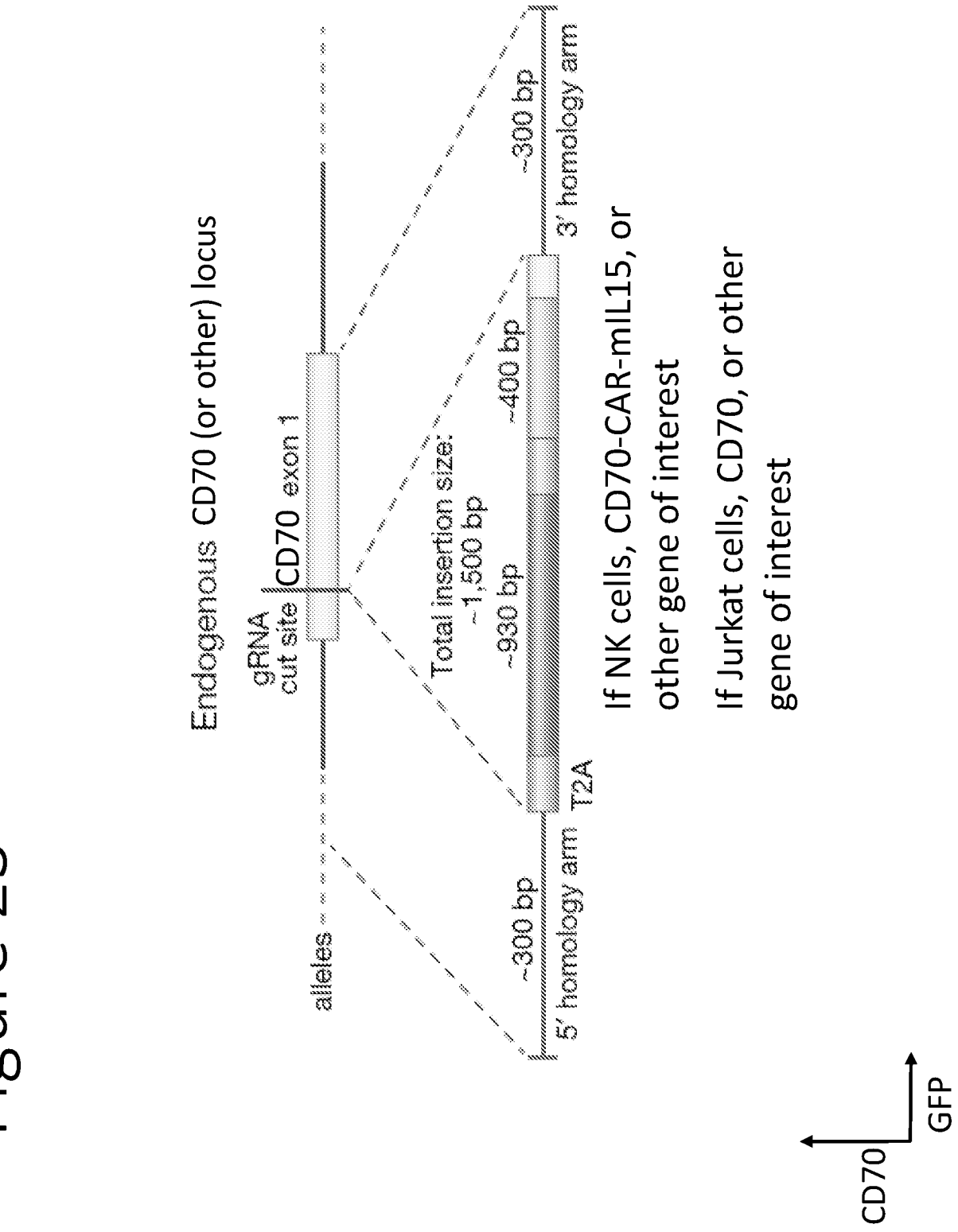
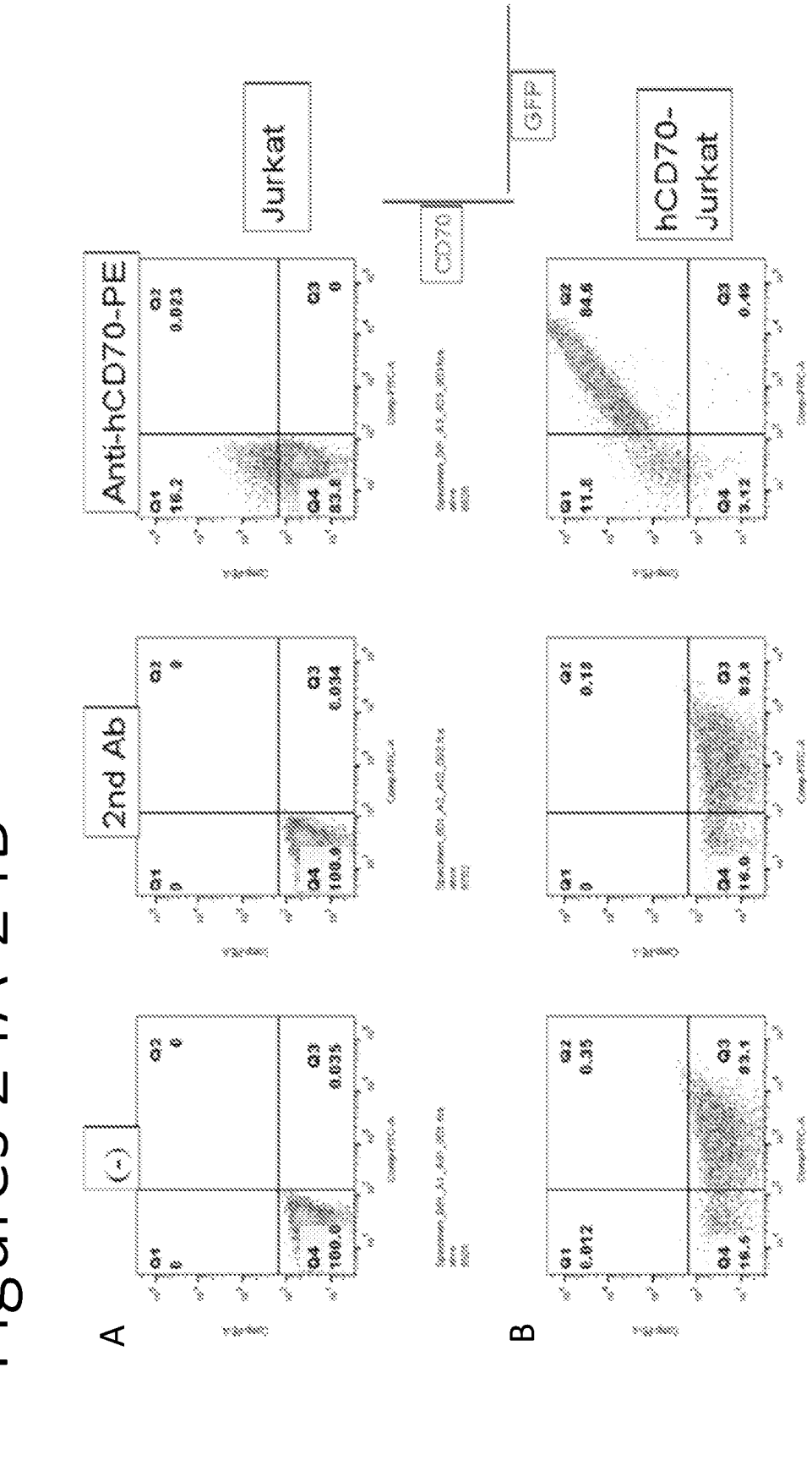


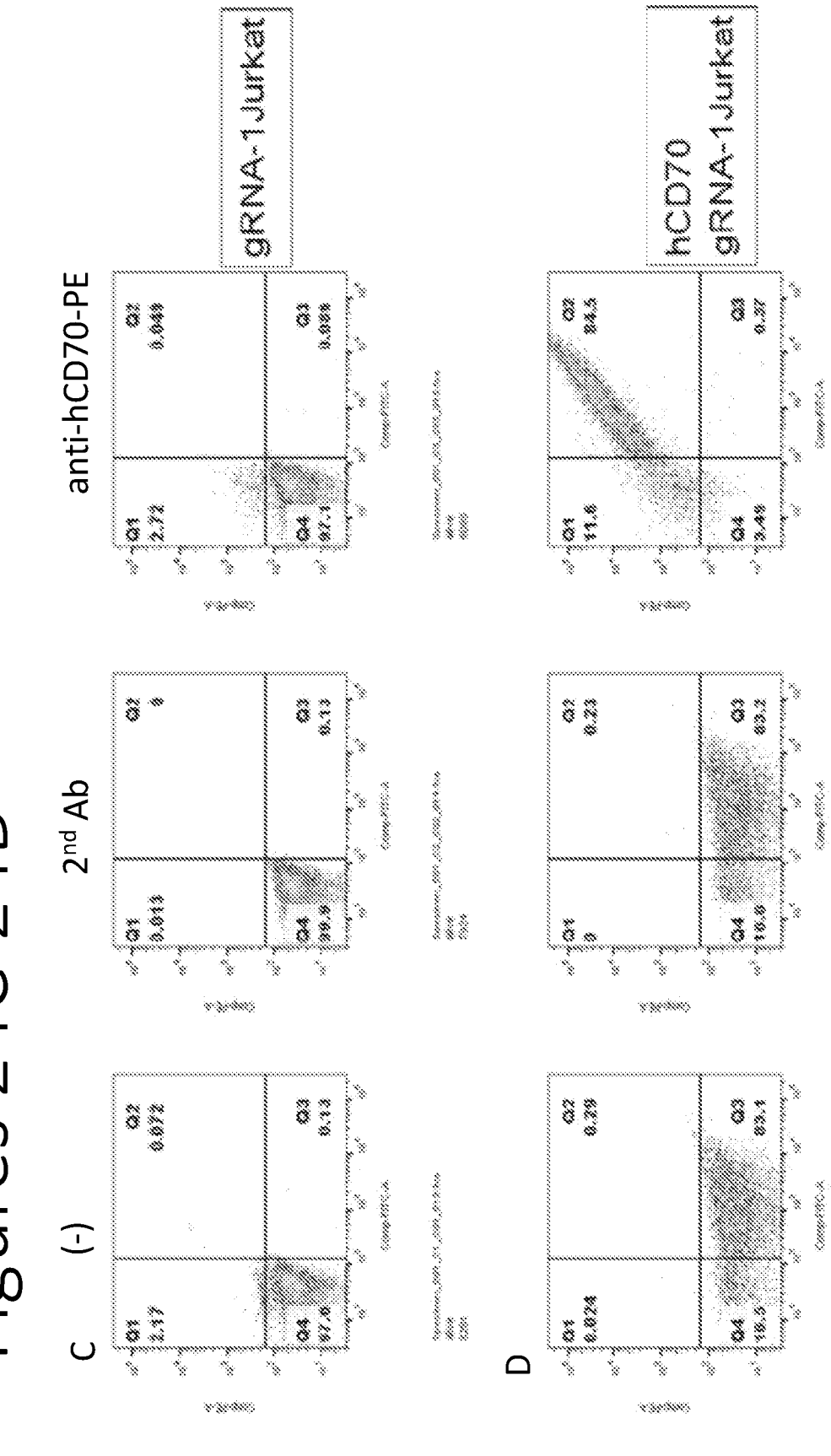
Figure 23


Endogenous CD70 (or other) locus
gRNA cut site
CD70 exon 1
alleles
Total insertion size:
~1,500 bp
~930 bp
~400 bp
~300 bp
~300 bp
5' homology arm
T2A
3' homology arm
If NK cells, CD70-CAR-mIL15, or other gene of interest
If Jurkat cells, CD70, or other gene of interest
CD70
GFP

Figures 24A-24B



Figures 24C-24D



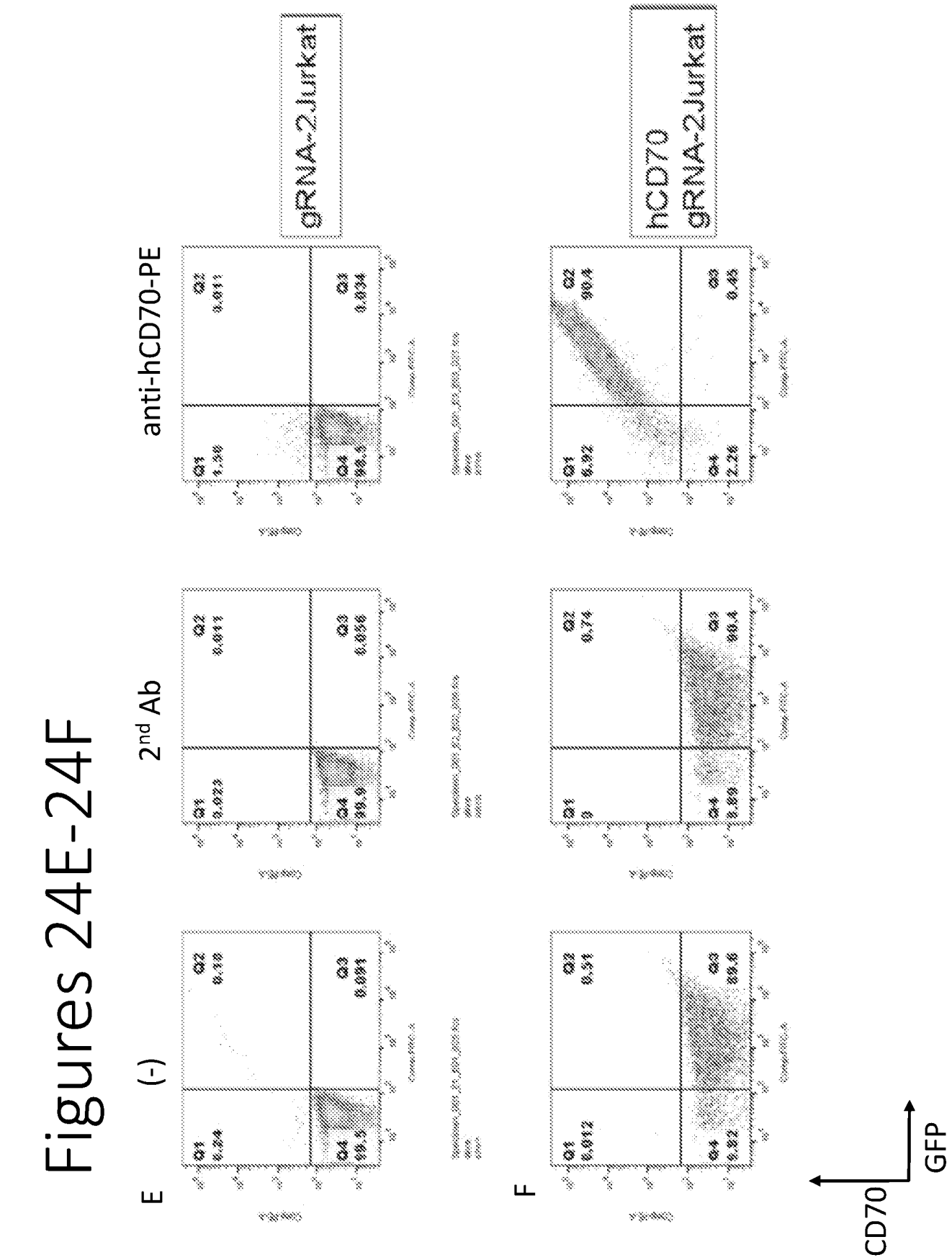

Figures 24E-24F
E
F
(-)
2nd Ab
anti-hCD70-PE
gRNA-2Jurkat
hCD70
gRNA-2Jurkat
CD70
GFP

Figure 25

	MFI				MFI on higher PE	
			CD70 Ab		CD70 Ab	
Cells	(-)	2nd Ab	1 ul	5 ul	1 ul	5 ul
Jurkat cells	30	35	87	117		
gRNA-2 Jurkat	29	32	41	56		
CD70 Jurkat	35	38	20511	21788	47196	49167
CD70 on gRNA-1 Jurkat	75	37	16799	17640	45339	46083
CD70 on gRNA-2 Jurkat	236	36.8	21736	23500	47454	46558
786-O cells	411	146	42251	46484	35508	37612

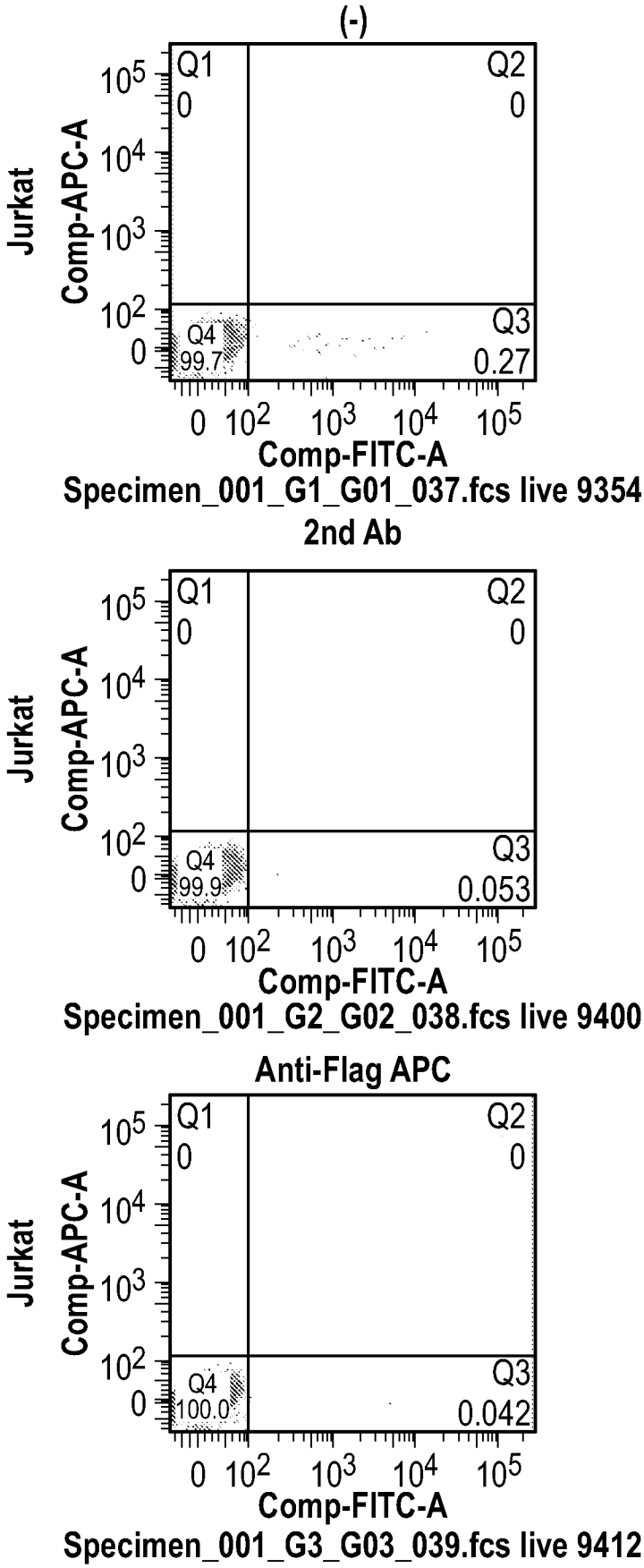

(-)
Q1
0
Q2
0
Q4
99.7
Q3
0.27
Jurkat
Comp-APC-A
Comp-FITC-A
Specimen_001_G1_G01_037.fcs live 9354
2nd Ab
Q1
0
Q2
0
Q4
99.9
Q3
0.053
Jurkat
Comp-APC-A
Comp-FITC-A
Specimen_001_G2_G02_038.fcs live 9400
Anti-Flag APC
Q1
0
Q2
0
Q4
100.0
Q3
0.042
Jurkat
Comp-APC-A
Comp-FITC-A
Specimen_001_G3_G03_039.fcs live 9412

FIG. 26A

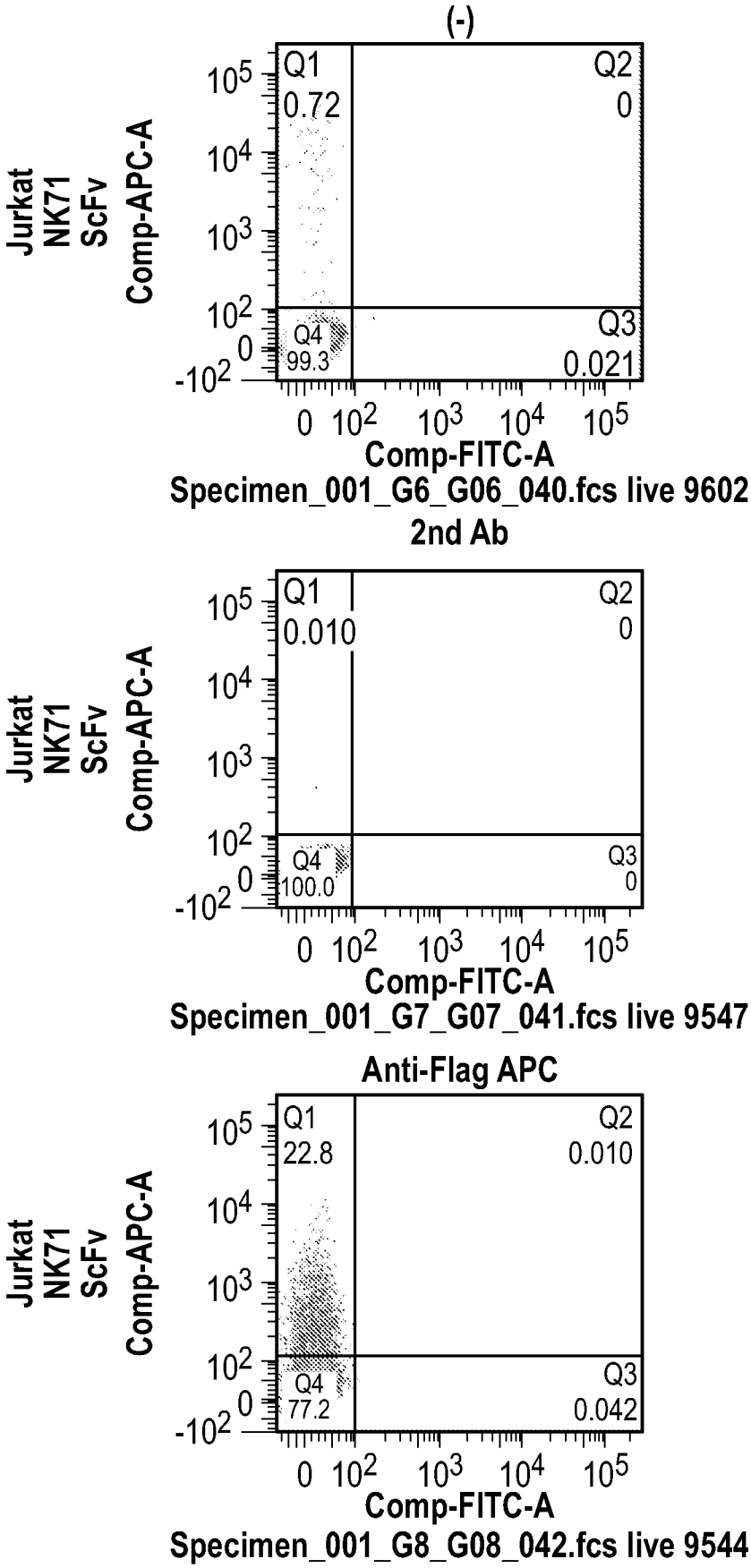

(-)
Jurkat
NK71
ScFv
Comp-APC-A
Q1
0.72
Q2
0
Q4
99.3
Q3
0.021
Comp-FITC-A
Specimen_001_G6_G06_040.fcs live 9602
2nd Ab
Q1
0.010
Q2
0
Q4
100.0
Q3
0
Specimen_001_G7_G07_041.fcs live 9547
Anti-Flag APC
Q1
22.8
Q2
0.010
Q4
77.2
Q3
0.042
Specimen_001_G8_G08_042.fcs live 9544

FIG. 26B

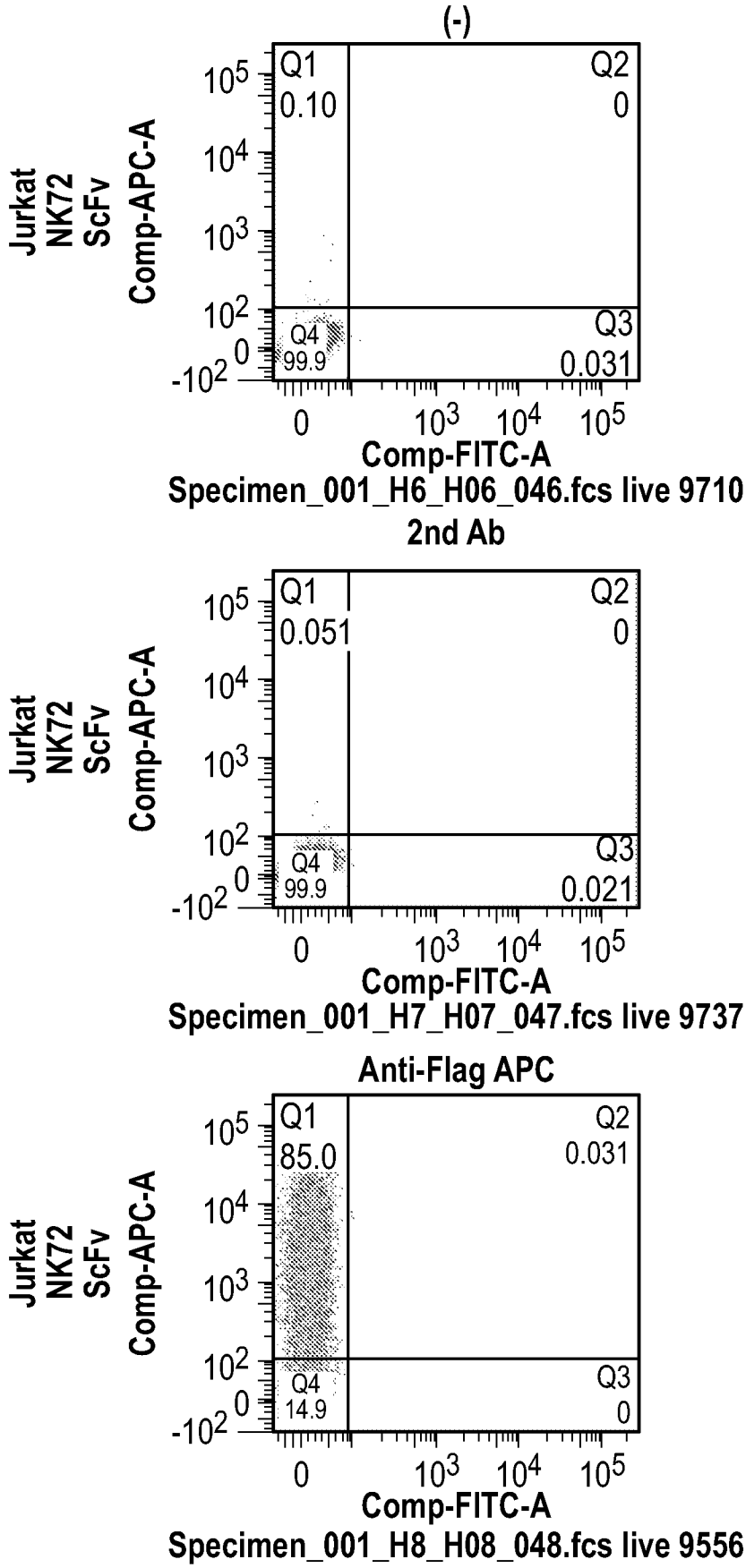

(-)
Jurkat NK72 ScFv
Comp-APC-A
Q1 0.10
Q2 0
Q4 99.9
Q3 0.031
Comp-FITC-A
Specimen_001_H6_H06_046.fcs live 9710
2nd Ab
Q1 0.051
Q2 0
Q4 99.9
Q3 0.021
Specimen_001_H7_H07_047.fcs live 9737
Anti-Flag APC
Q1 85.0
Q2 0.031
Q4 14.9
Q3 0
Specimen_001_H8_H08_048.fcs live 9556

FIG. 26C

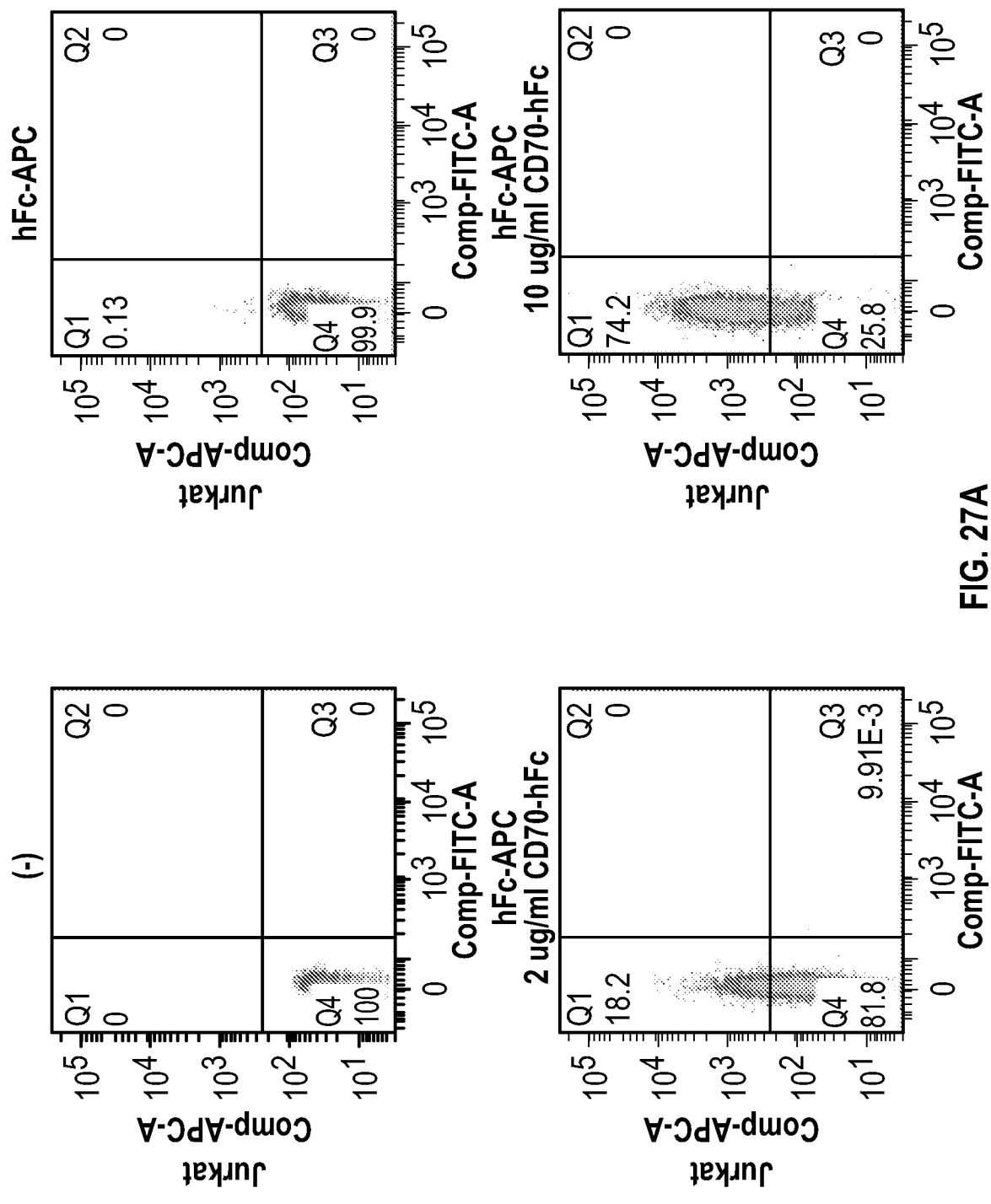

hFc-APC
Jurkat
Comp-APC-A
Comp-FITC-A
Q1 0.13
Q2 0
Q4 99.9
Q3 0
(-)
Q1 0
Q2 0
Q4 100
Q3 0
hFc-APC
10 ug/ml CD70-hFc
Q1 74.2
Q2 0
Q4 25.8
Q3 0
hFc-APC
2 ug/ml CD70-hFc
Q1 18.2
Q2 0
Q4 81.8
Q3 9.91E-3

FIG. 27A

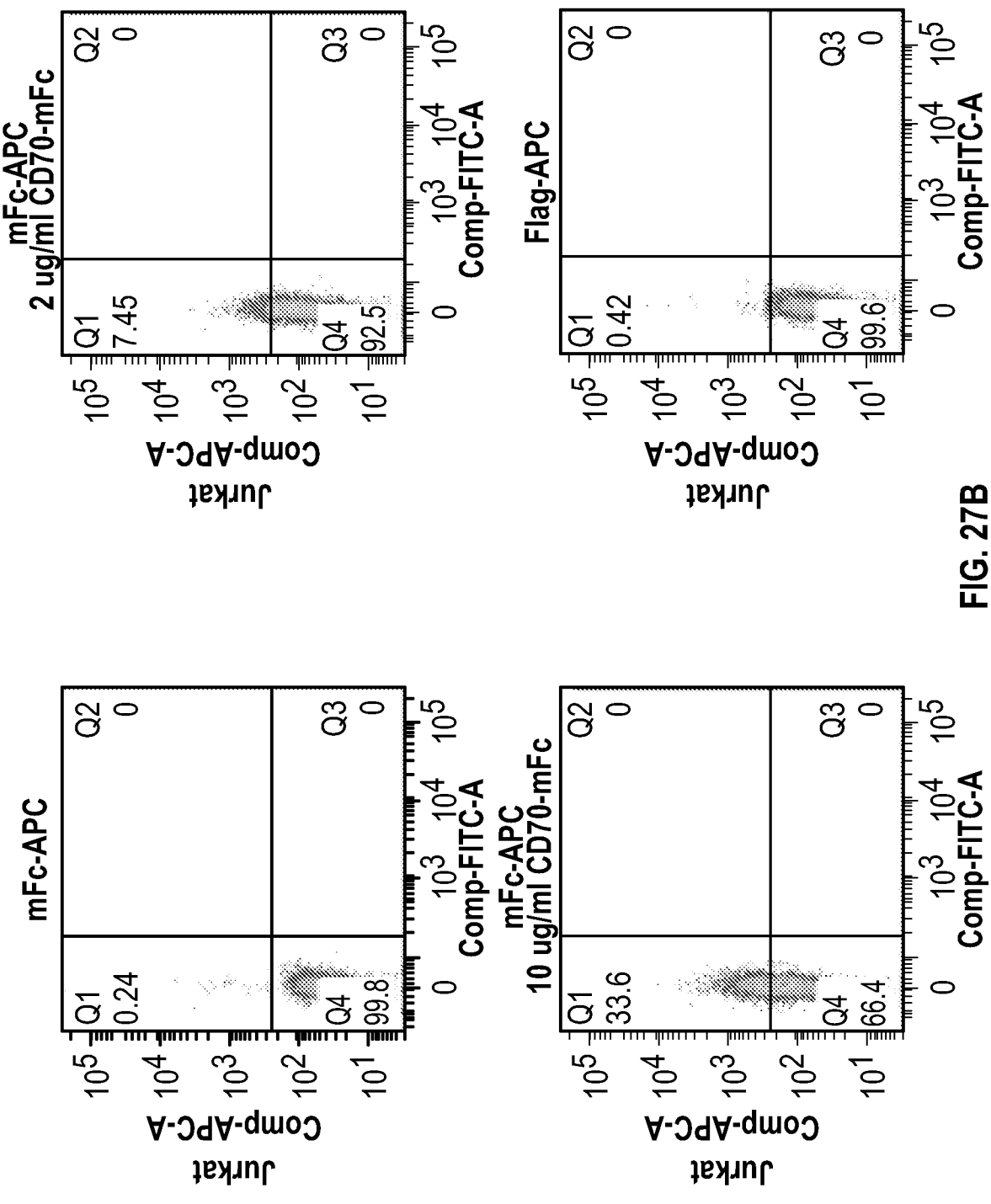

mFc-APC
2 ug/ml CD70-mFc
Flag-APC
10 ug/ml CD70-mFc
Jurkat
Comp-APC-A
Comp-FITC-A
Q1
7.45
Q2
0
Q3
0
Q4
92.5
Q1
0.42
Q2
0
Q3
0
Q4
99.6
Q1
0.24
Q2
0
Q3
0
Q4
99.8
Q1
33.6
Q2
0
Q3
0
Q4
66.4

FIG. 27B

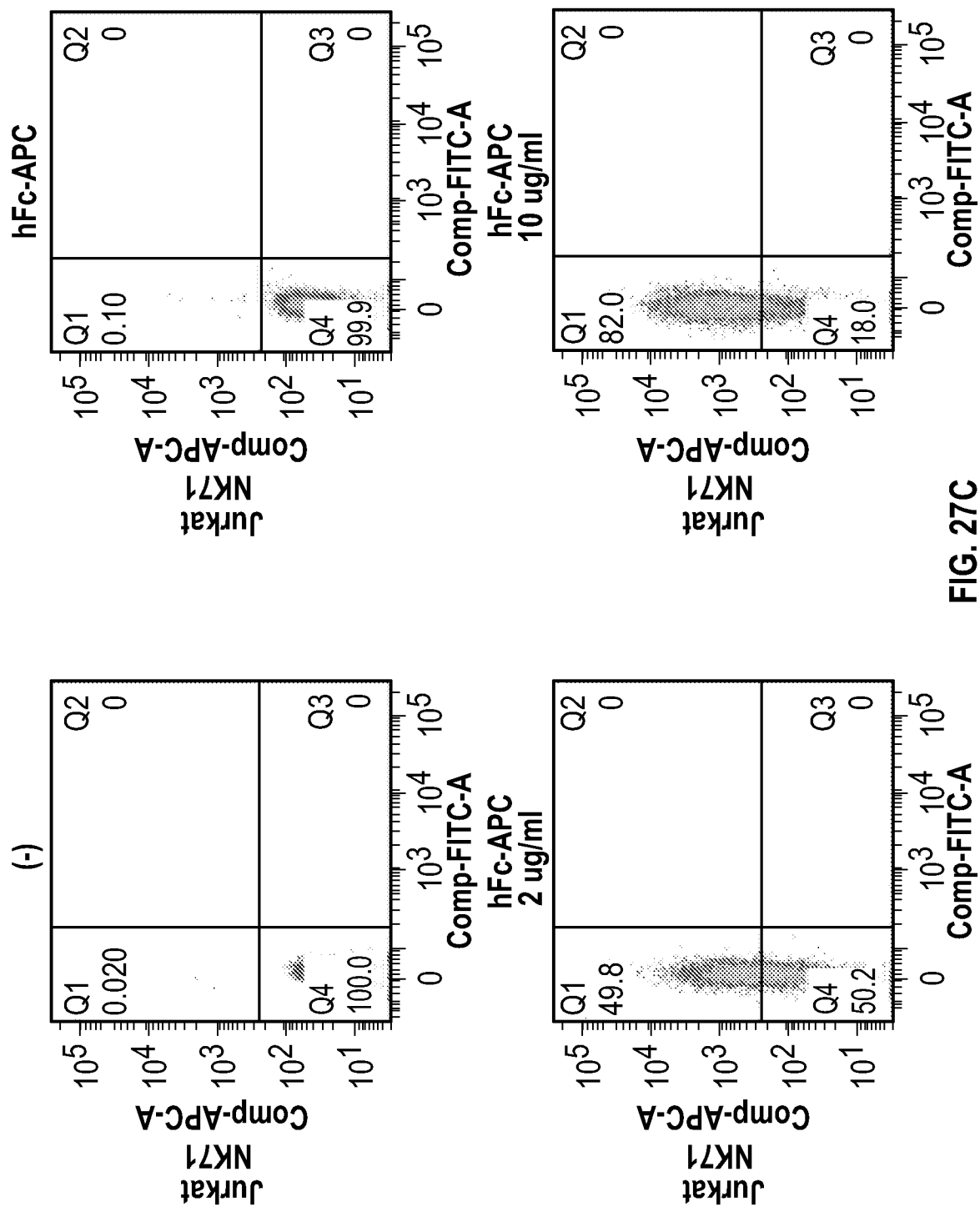

(-)
hFc-APC 2 ug/ml
hFc-APC 10 ug/ml
hFc-APC
Jurkat
NK71
Comp-APC-A
Comp-FITC-A
Q1 0.020
Q2 0
Q3 0
Q4 100.0
Q1 49.8
Q2 0
Q3 0
Q4 50.2
Q1 82.0
Q2 0
Q3 0
Q4 18.0
Q1 0.10
Q2 0
Q3 0
Q4 99.9
0
10^3
10^4
10^5
10^1
10^2

FIG. 27C

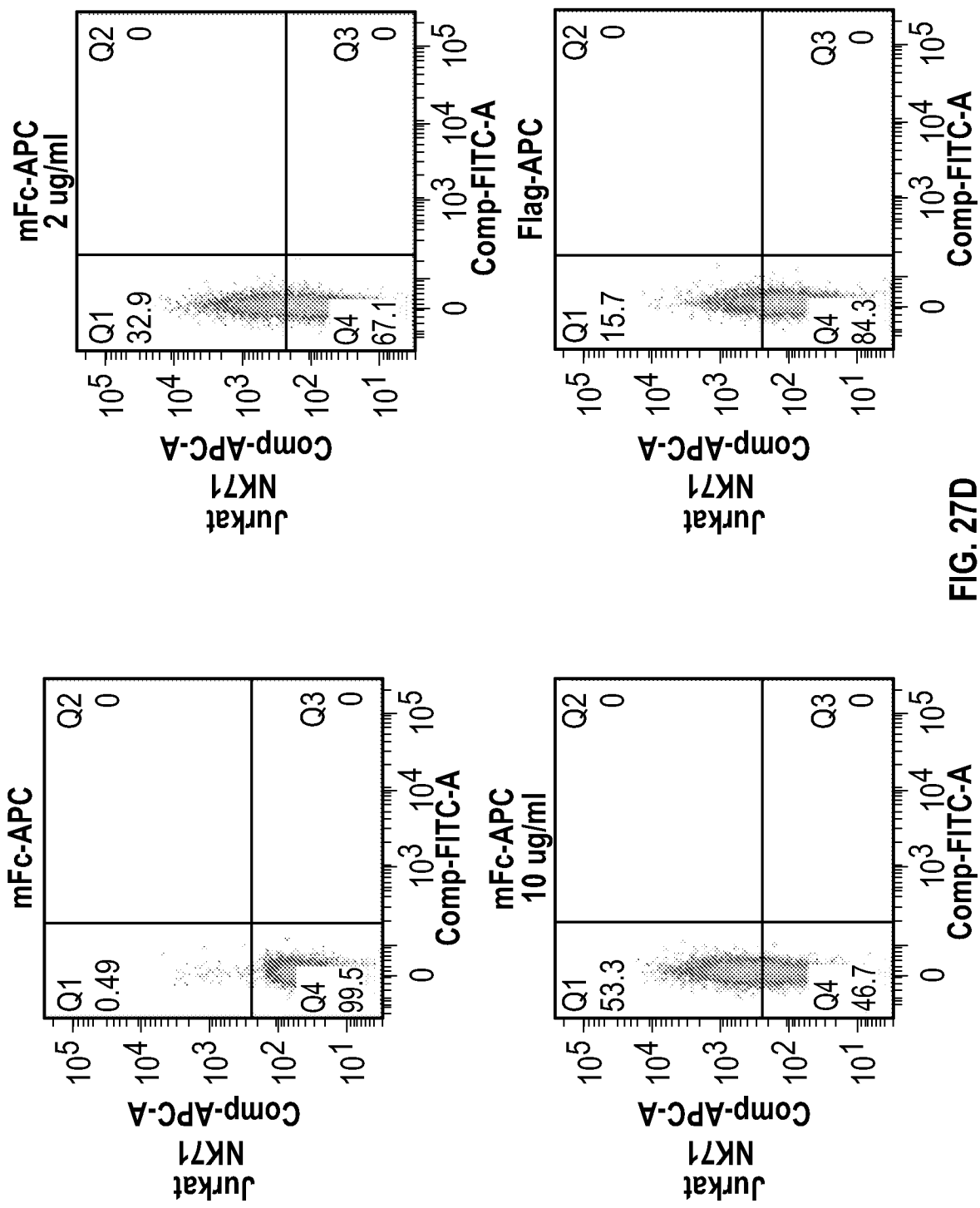

mFc-APC
2 ug/ml
Flag-APC
mFc-APC
10 ug/ml
Jurkat
NK71
Comp-APC-A
Comp-FITC-A
Q1
32.9
Q2
0
Q4
67.1
Q3
0
Q1
15.7
Q2
0
Q4
84.3
Q3
0
Q1
0.49
Q2
0
Q4
99.5
Q3
0
Q1
53.3
Q2
0
Q4
46.7
Q3
0

FIG. 27D

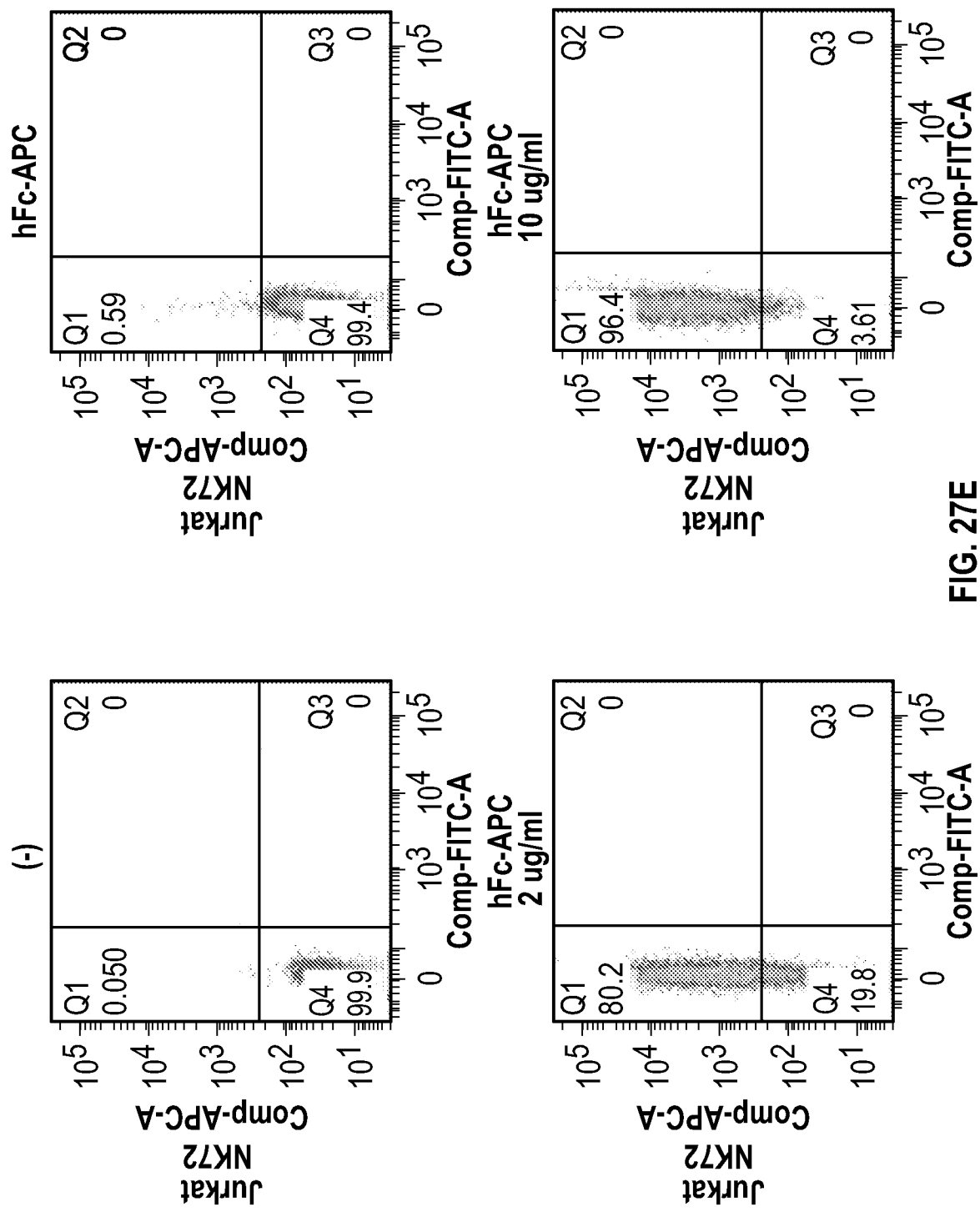

(-)
hFc-APC 2 ug/ml
hFc-APC 10 ug/ml
hFc-APC
Jurkat NK72
Comp-APC-A
Comp-FITC-A
Q1 0.050
Q2 0
Q3 0
Q4 99.9
Q1 80.2
Q2 0
Q3 0
Q4 19.8
Q1 96.4
Q2 0
Q3 0
Q4 3.61
Q1 0.59
Q2 0
Q3 0
Q4 99.4
0
10^3
10^4
10^5
10^1
10^2
10^3
10^4
10^5

FIG. 27E

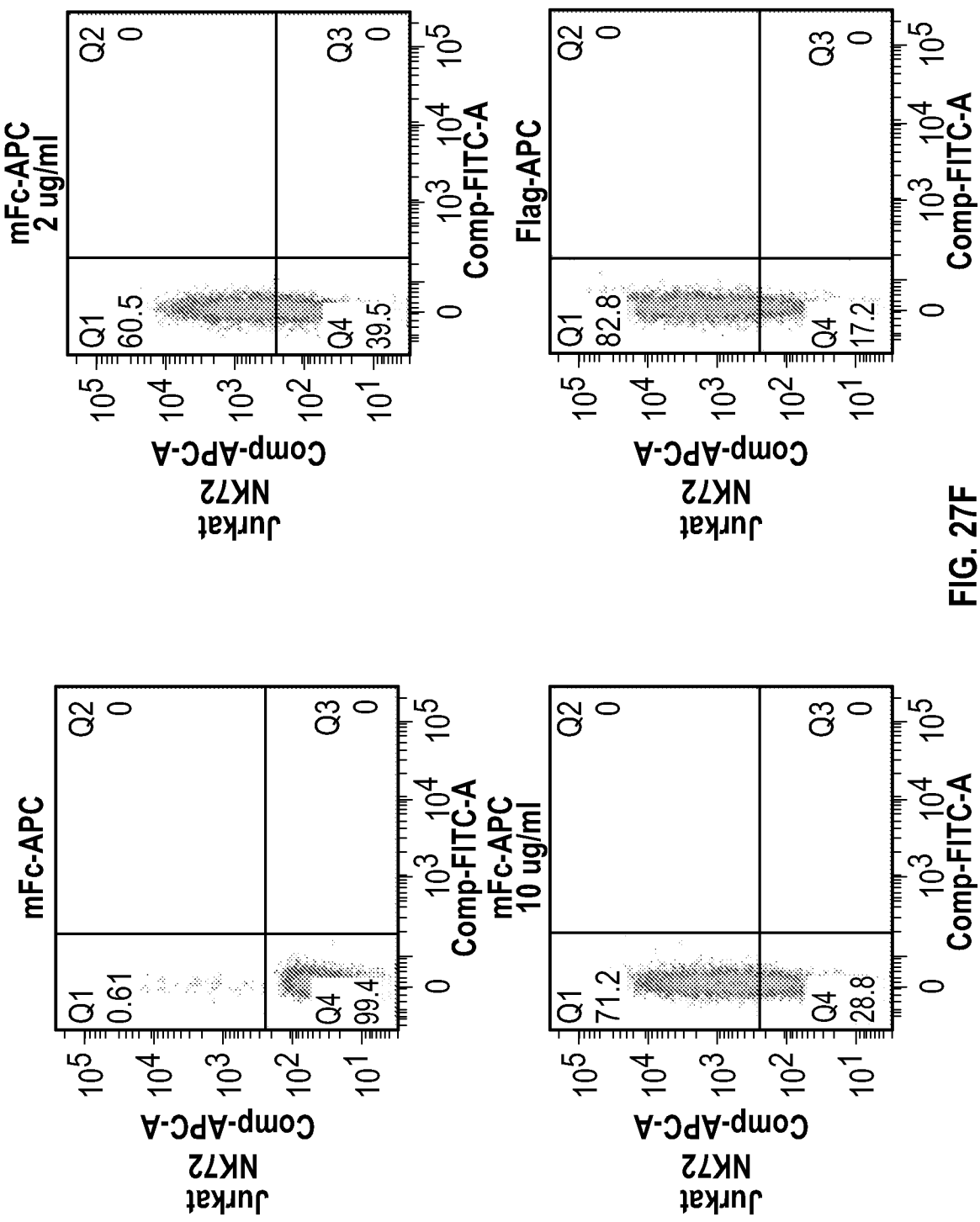
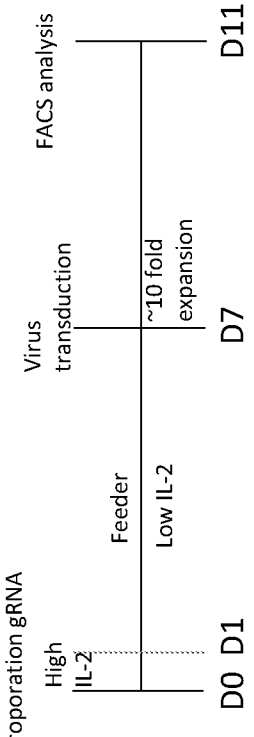
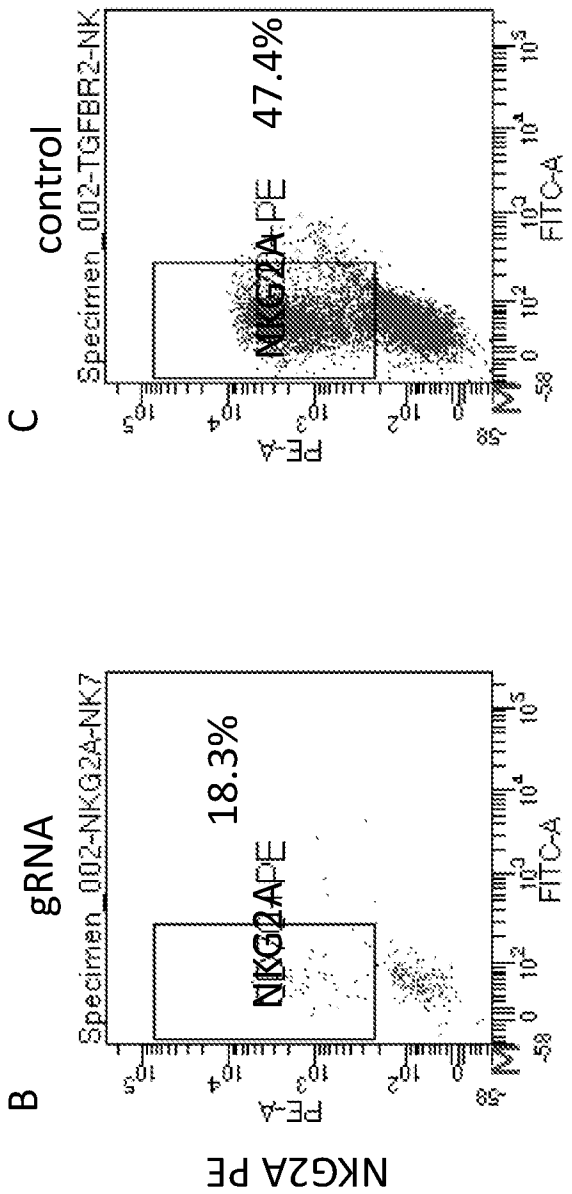

mFc-APC
Q1
0.61
Q2
0
Q4
99.4
Q3
0
Jurkat
NK72
Comp-APC-A
Comp-FITC-A
mFc-APC
2 ug/ml
Q1
60.5
Q2
0
Q4
39.5
Q3
0
Jurkat
NK72
Comp-APC-A
Comp-FITC-A
mFc-APC
10 ug/ml
Q1
71.2
Q2
0
Q4
28.8
Q3
0
Jurkat
NK72
Comp-APC-A
Comp-FITC-A
Flag-APC
Q1
82.8
Q2
0
Q4
17.2
Q3
0
Jurkat
NK72
Comp-APC-A
Comp-FITC-A

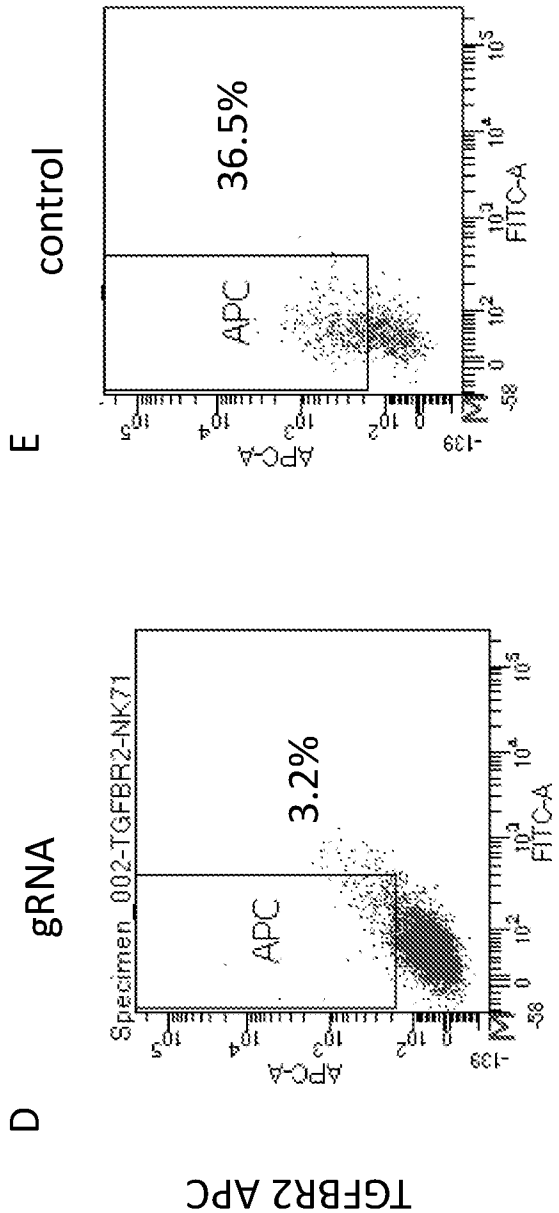
FIG. 27F

Figures 28A-28C

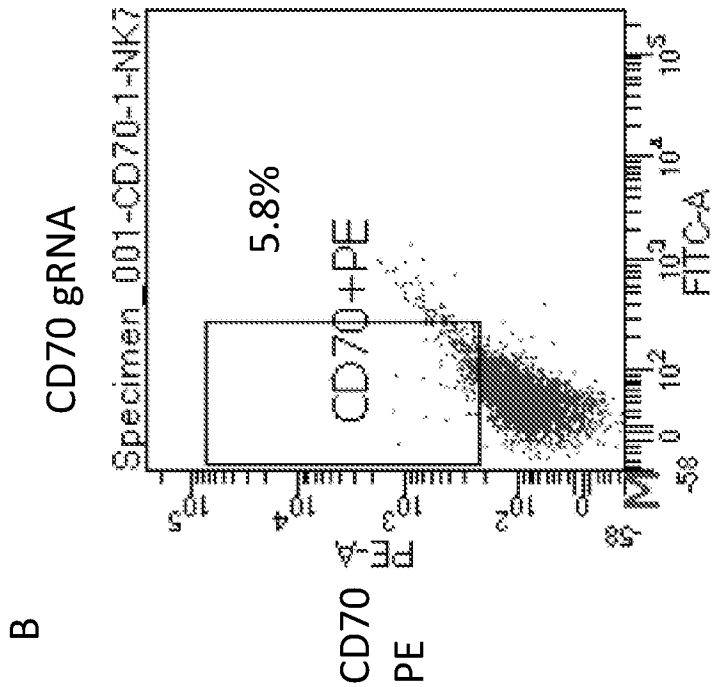




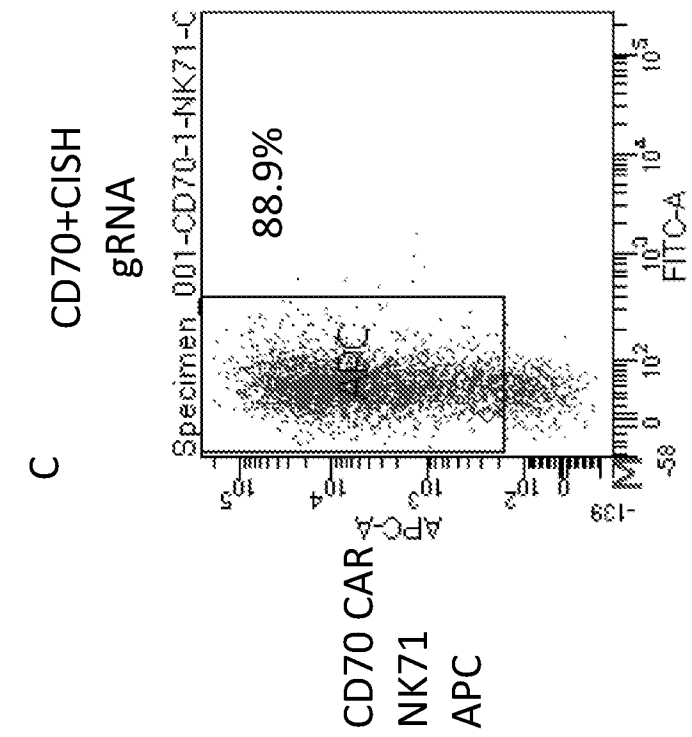
Figures 28D-28E



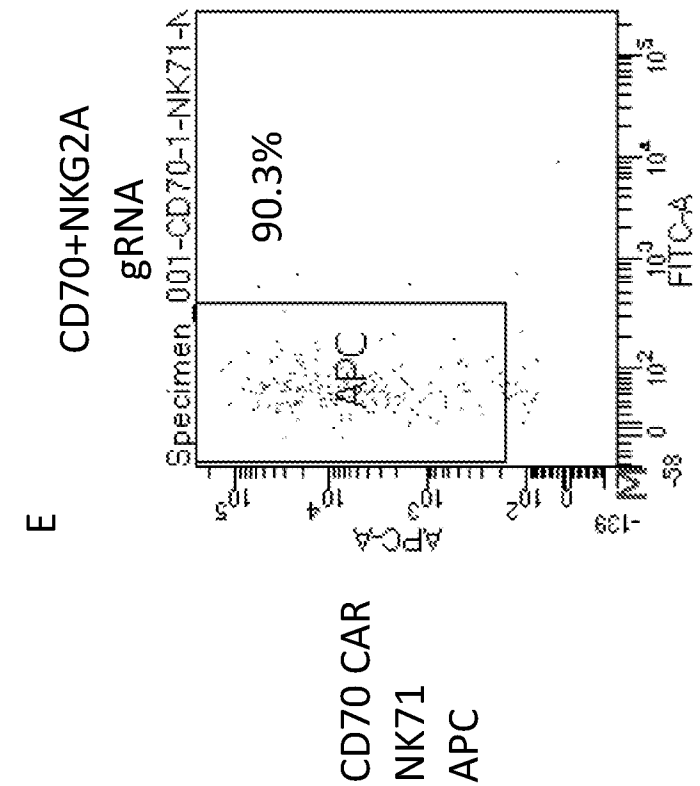
Figures 29A-29B

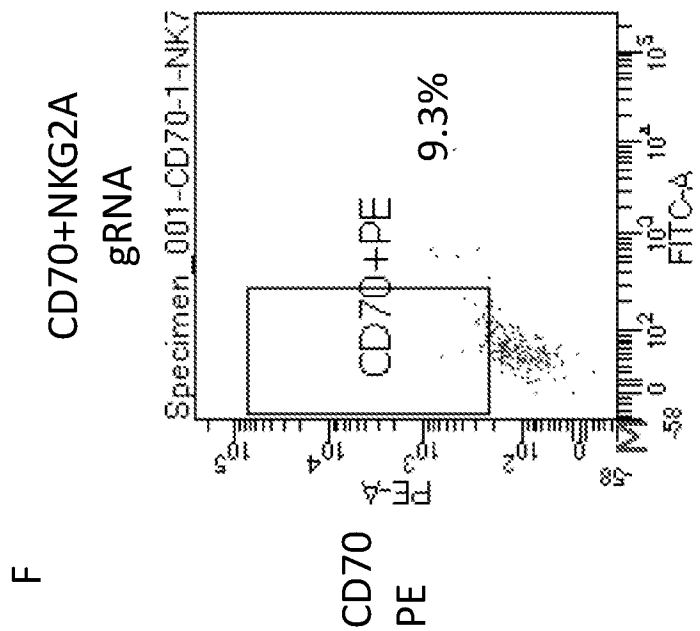


Figures 29C-29D

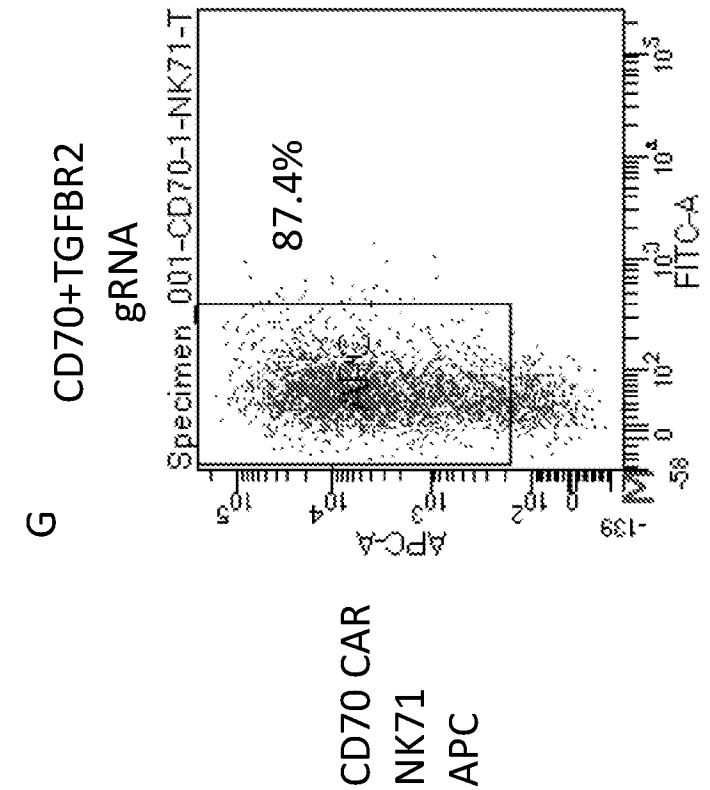


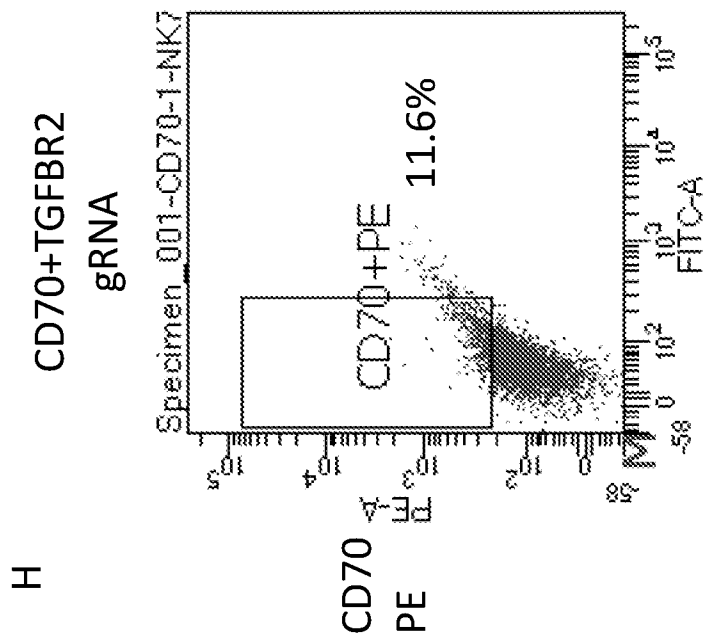
Figures 29E-29F





Figures 29G-29H

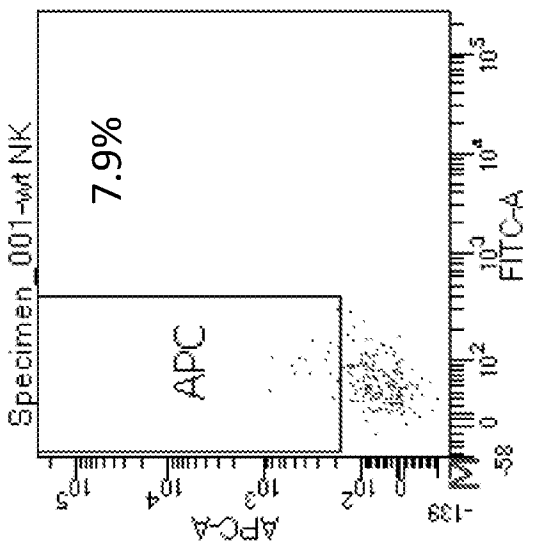




Figures 29I-29J

I

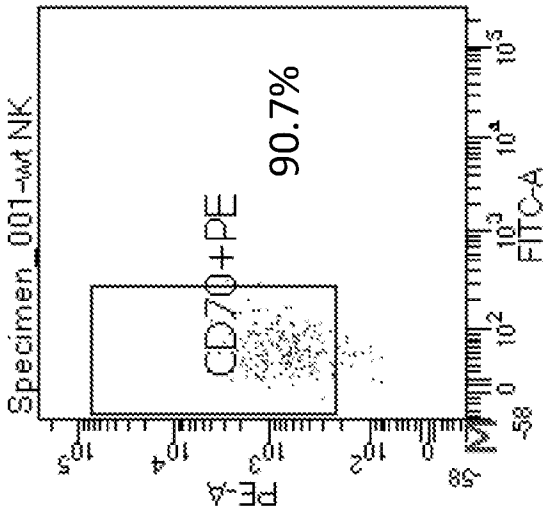
MOCK



CD70 CAR
NK71
APC

J

MOCK

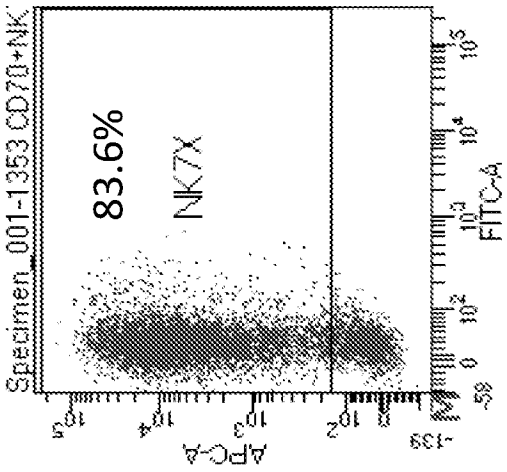


CD70
PE

Figures 30A-30B

A

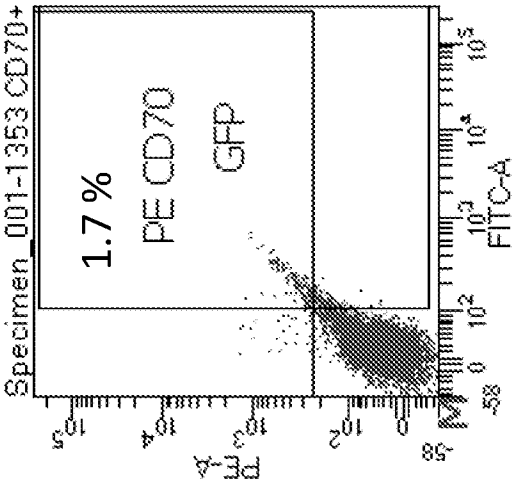
CD70 gRNA



CD70 CAR
NK71
APC

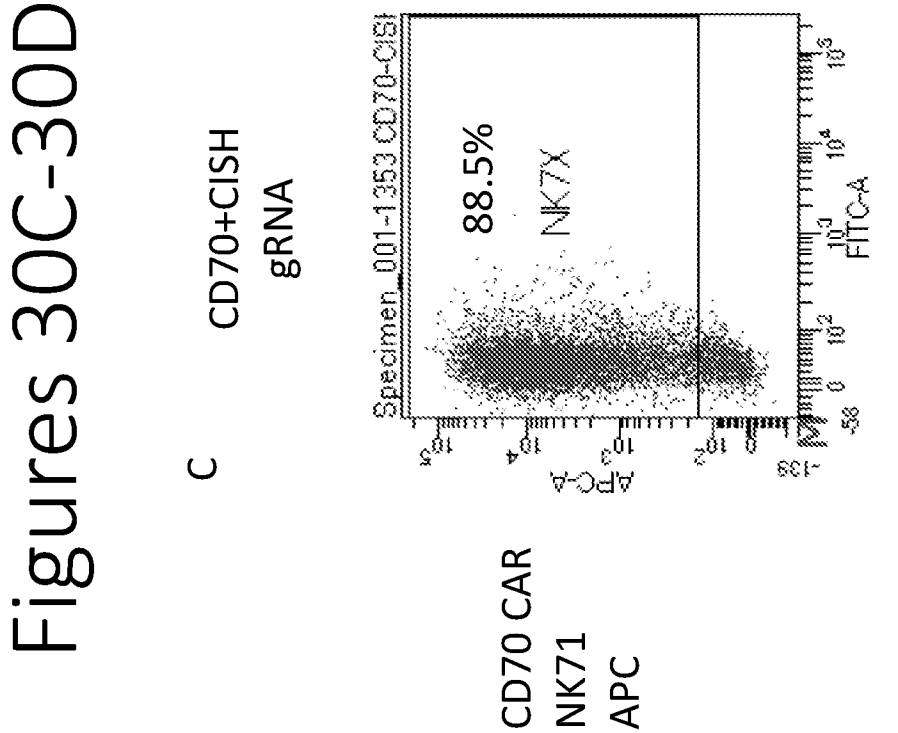
B

CD70 gRNA

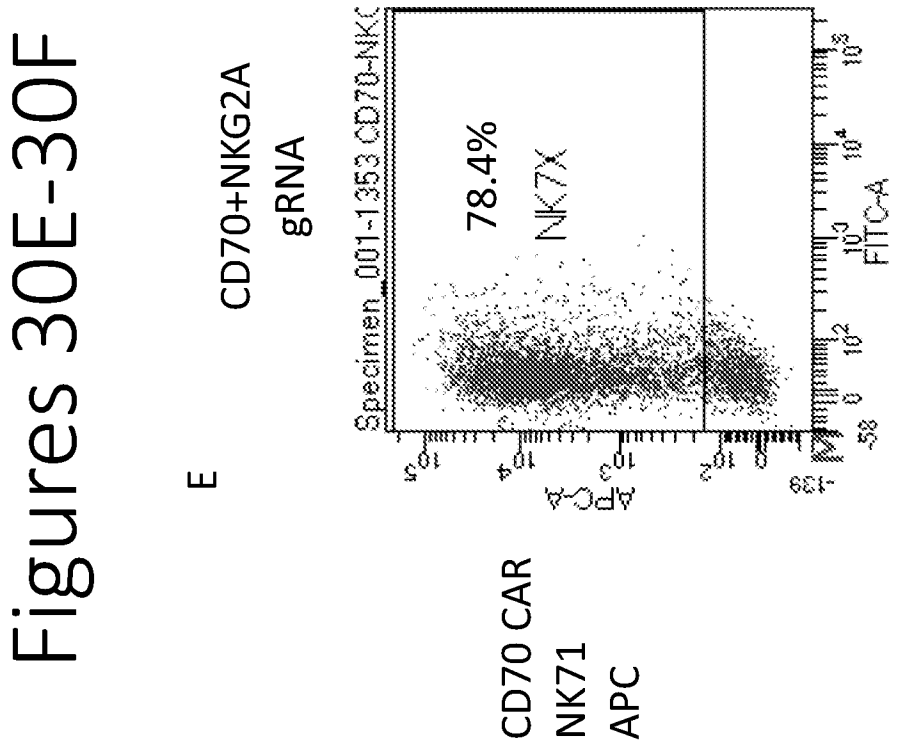


CD70
PE

Figures 30C-30D



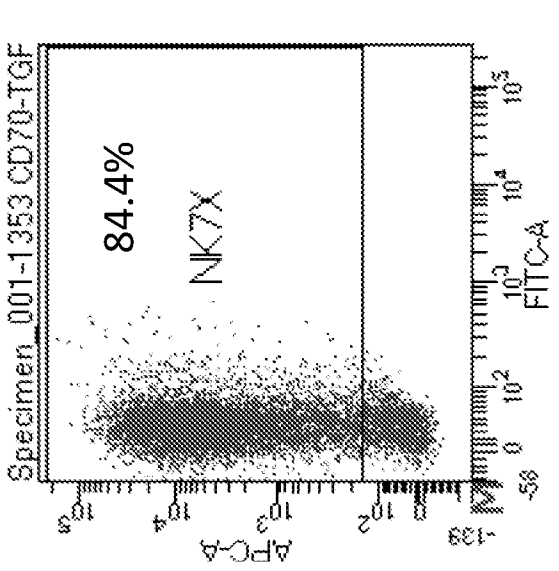
Figures 30E-30F



Figures 30G-30H

G

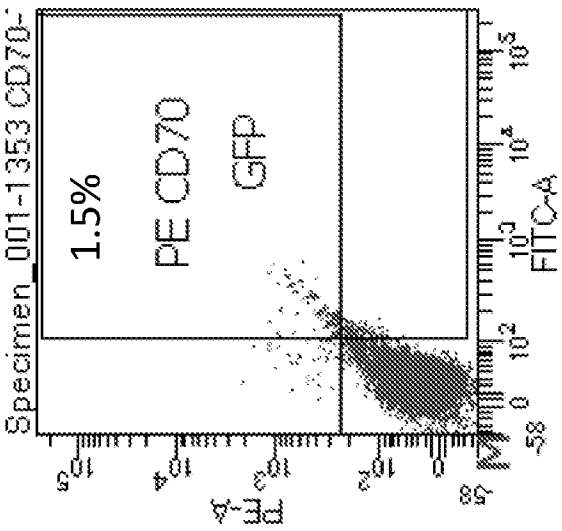
CD70+TGFBR2
gRNA



CD70 CAR
NK71
APC

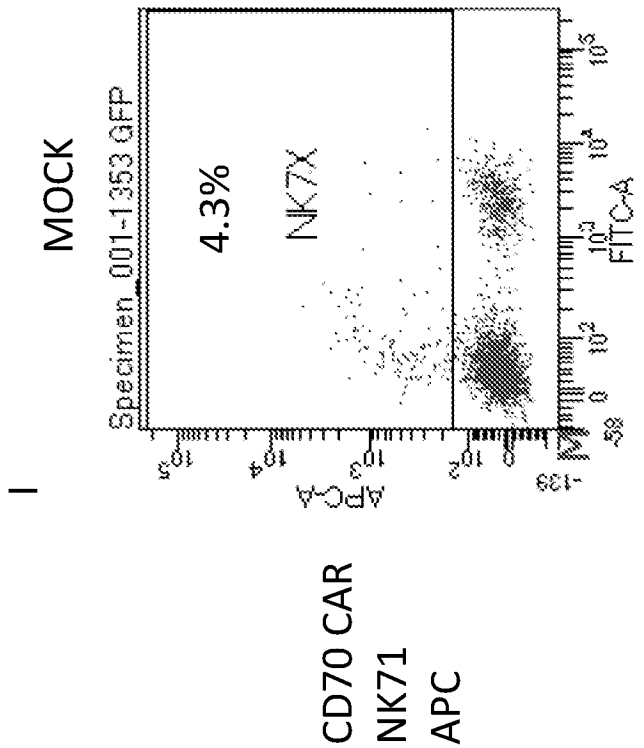
H

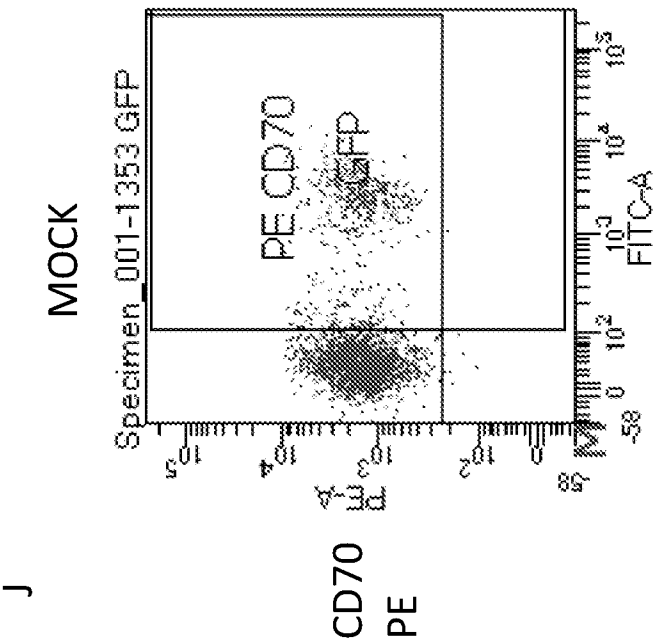
CD70+TGFBR2
gRNA



CD70
PE

Figures 30I-30J





Figures 31A-31B

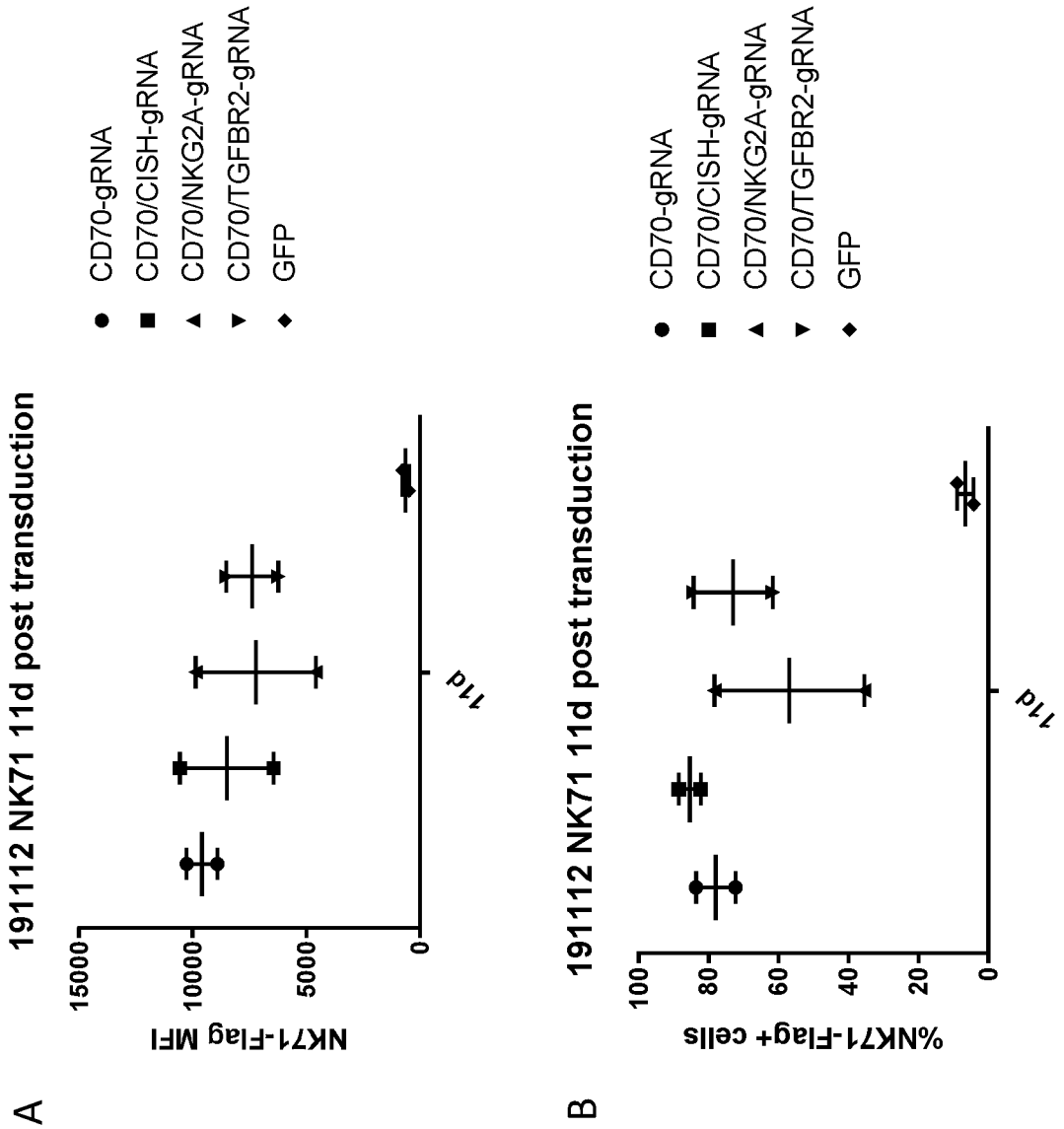
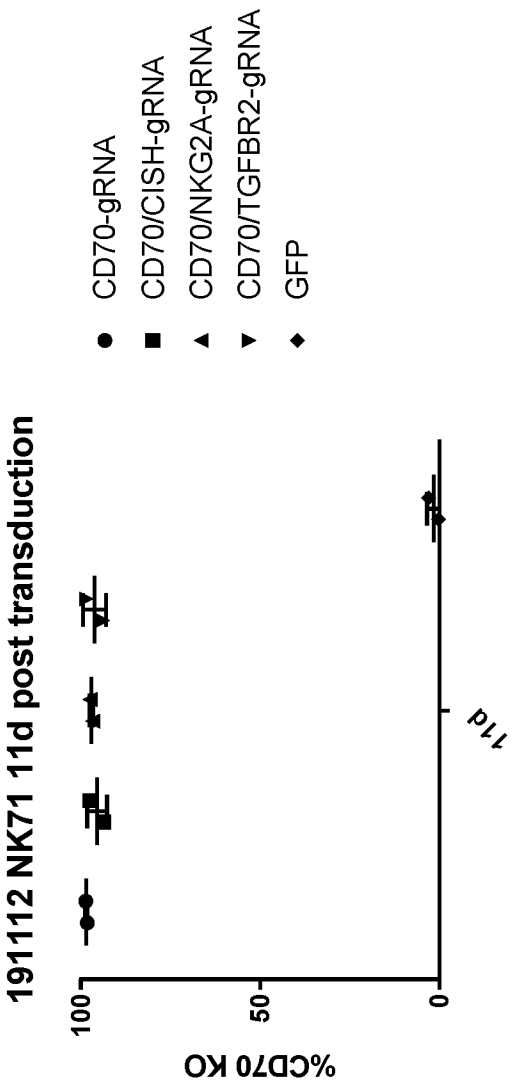


Figure 31C


CD70 KO %
C
191112 NK71 11d post transduction
CD70-gRNA
CD70/CISH-gRNA
CD70/NKG2A-gRNA
CD70/TGFBR2-gRNA
GFP
%CD70 KO
100
50
0
11d

Figures 32A-32B

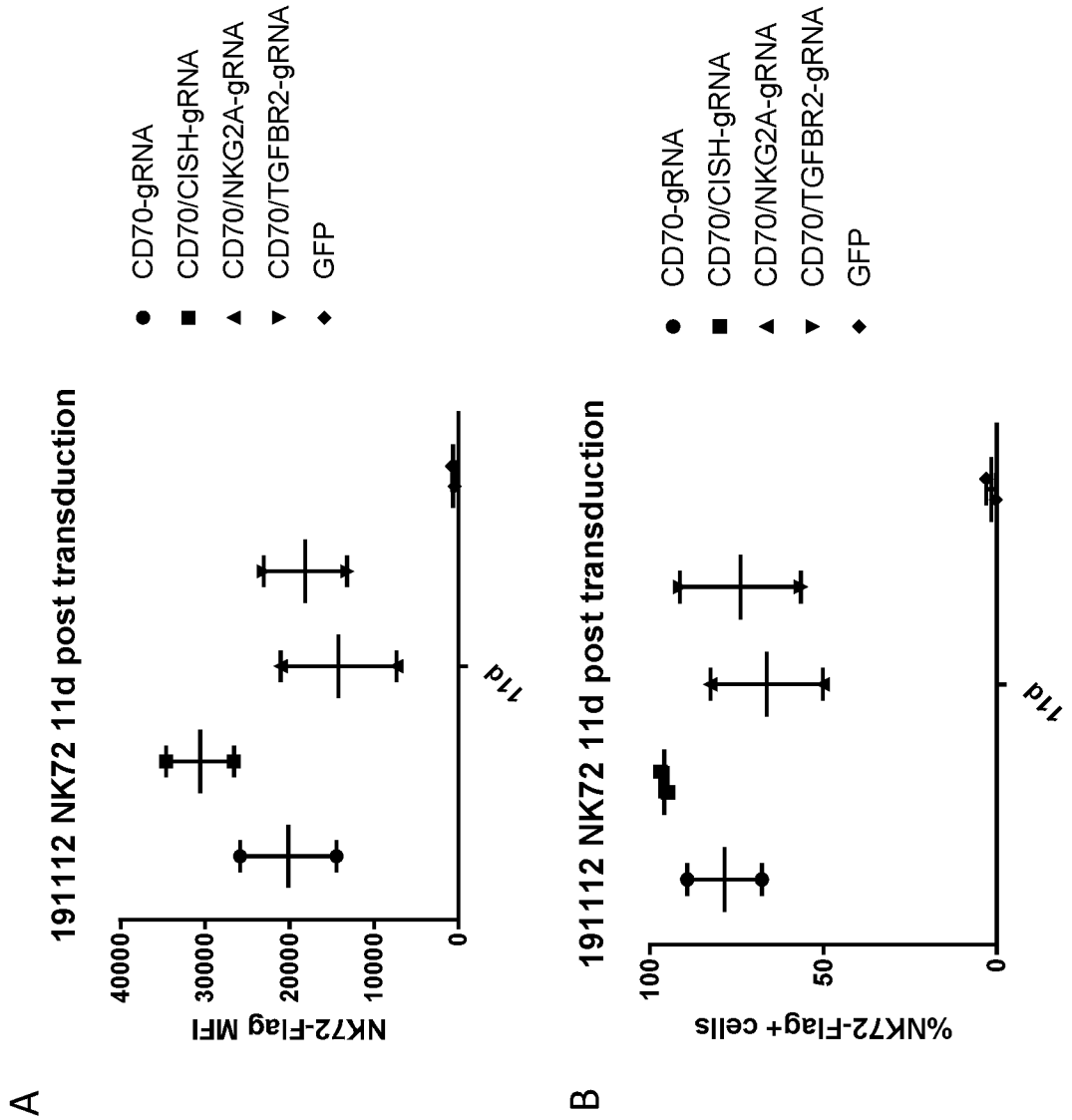
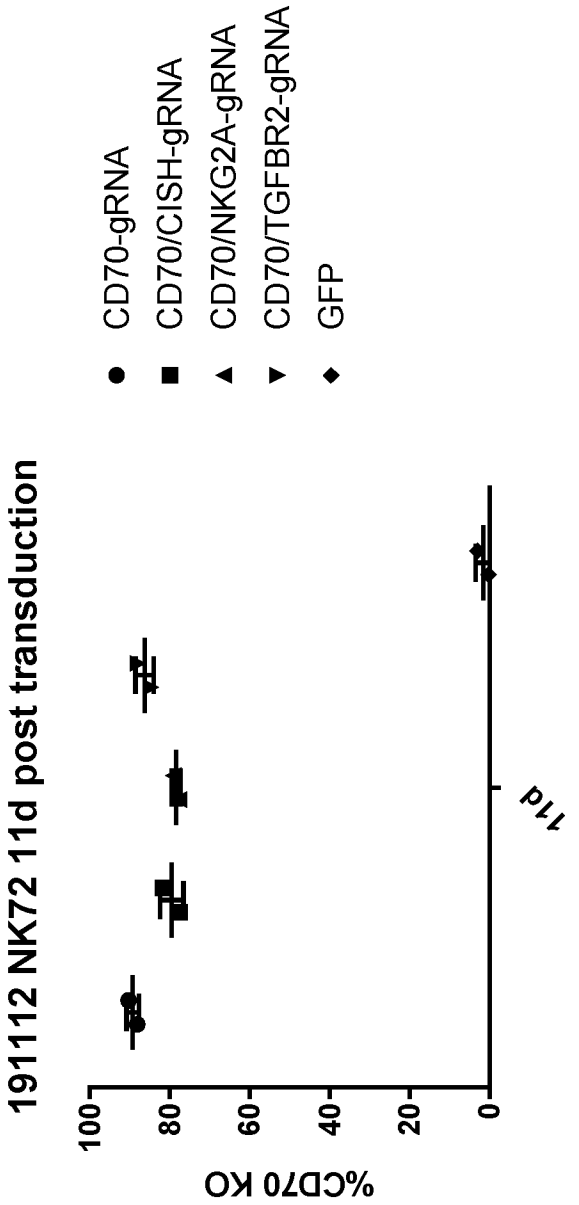
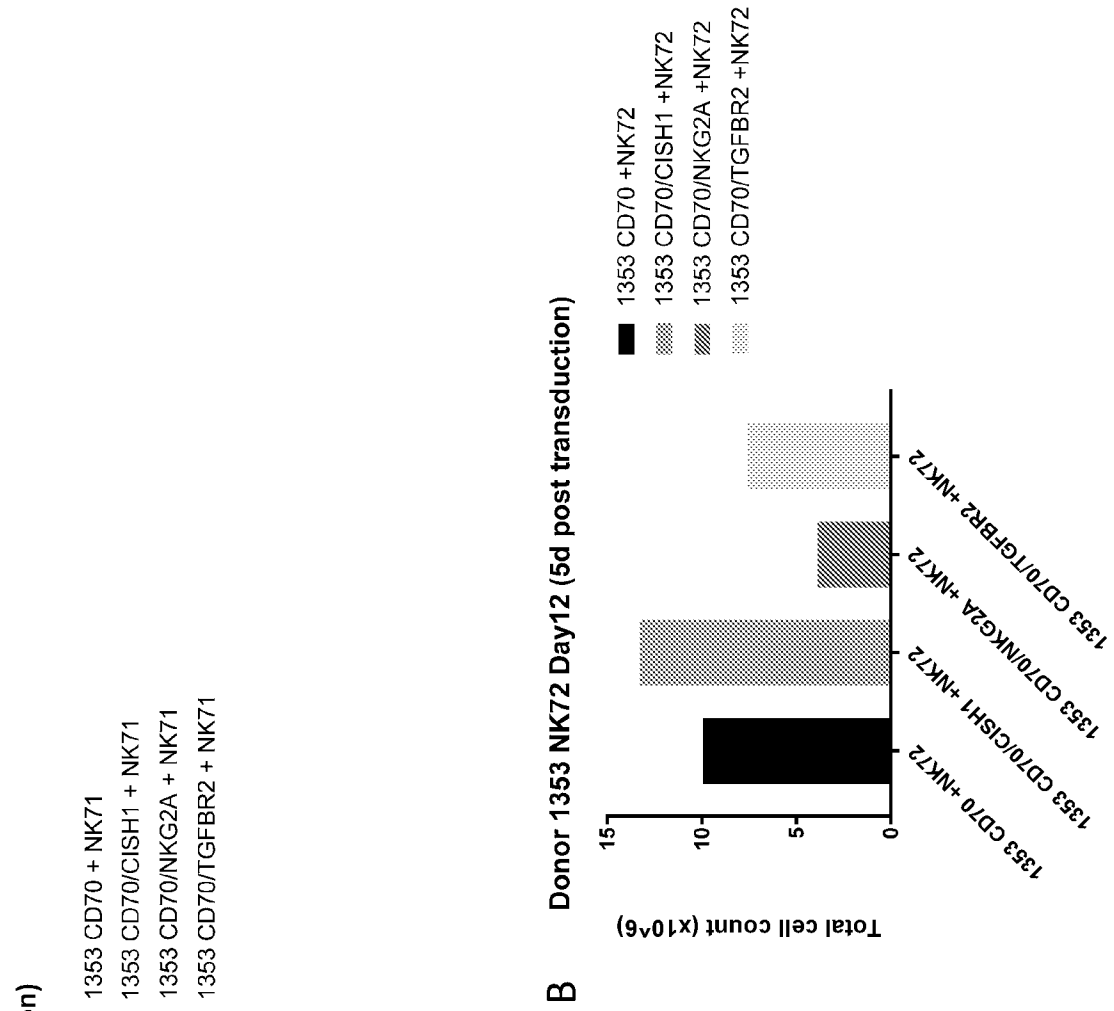


Figure 32C


c
CD70 KO %
191112 NK72 11d post transduction
CD70-gRNA
CD70/CISH-gRNA
CD70/NKG2A-gRNA
CD70/TGFBR2-gRNA
GFP
%CD70 KO
100
80
60
40
20
0
11d

Figures 33A-33B



$3x10^5$ NK cells/condition transduced on day7

Figures 34A-34B

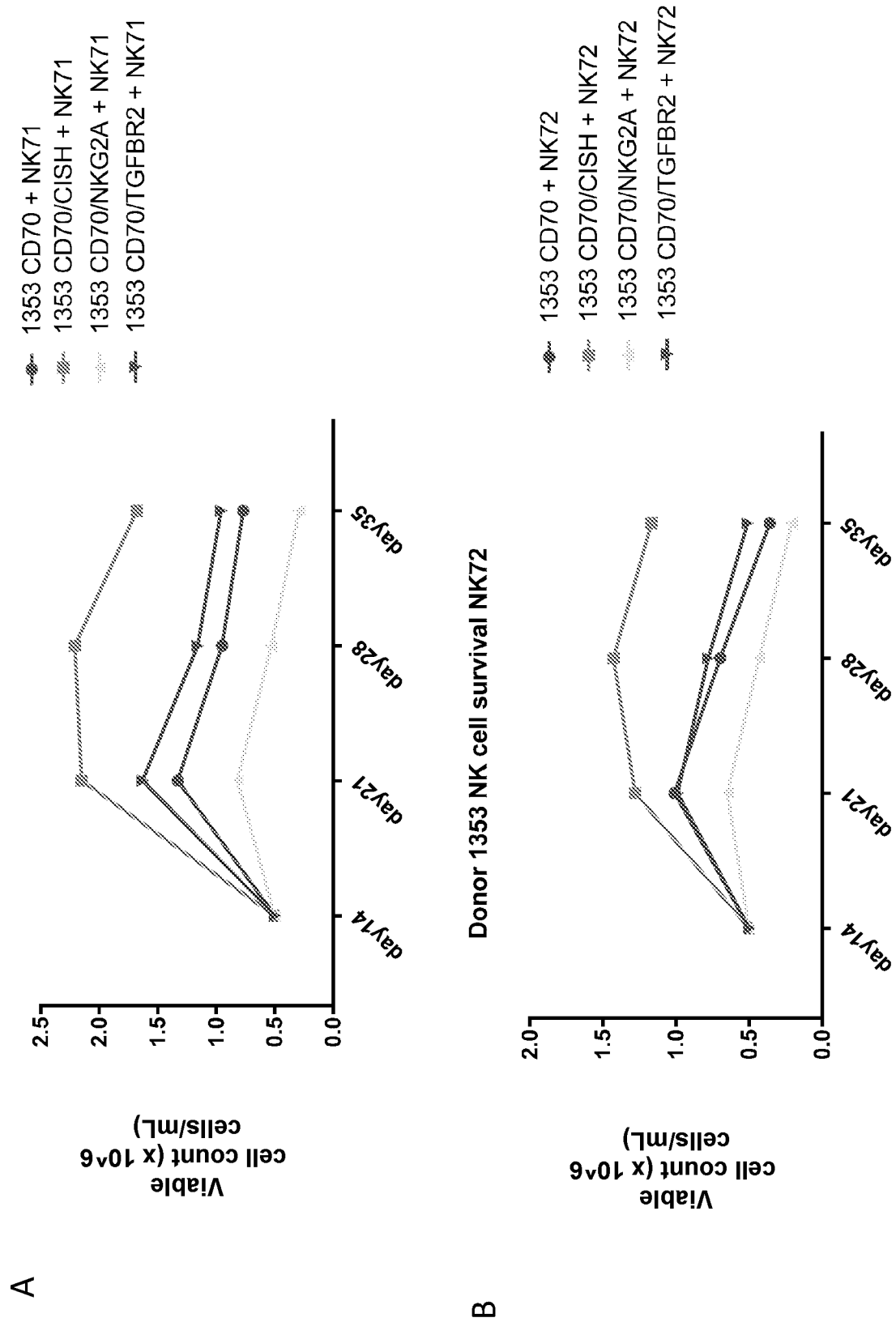


Figure 35A

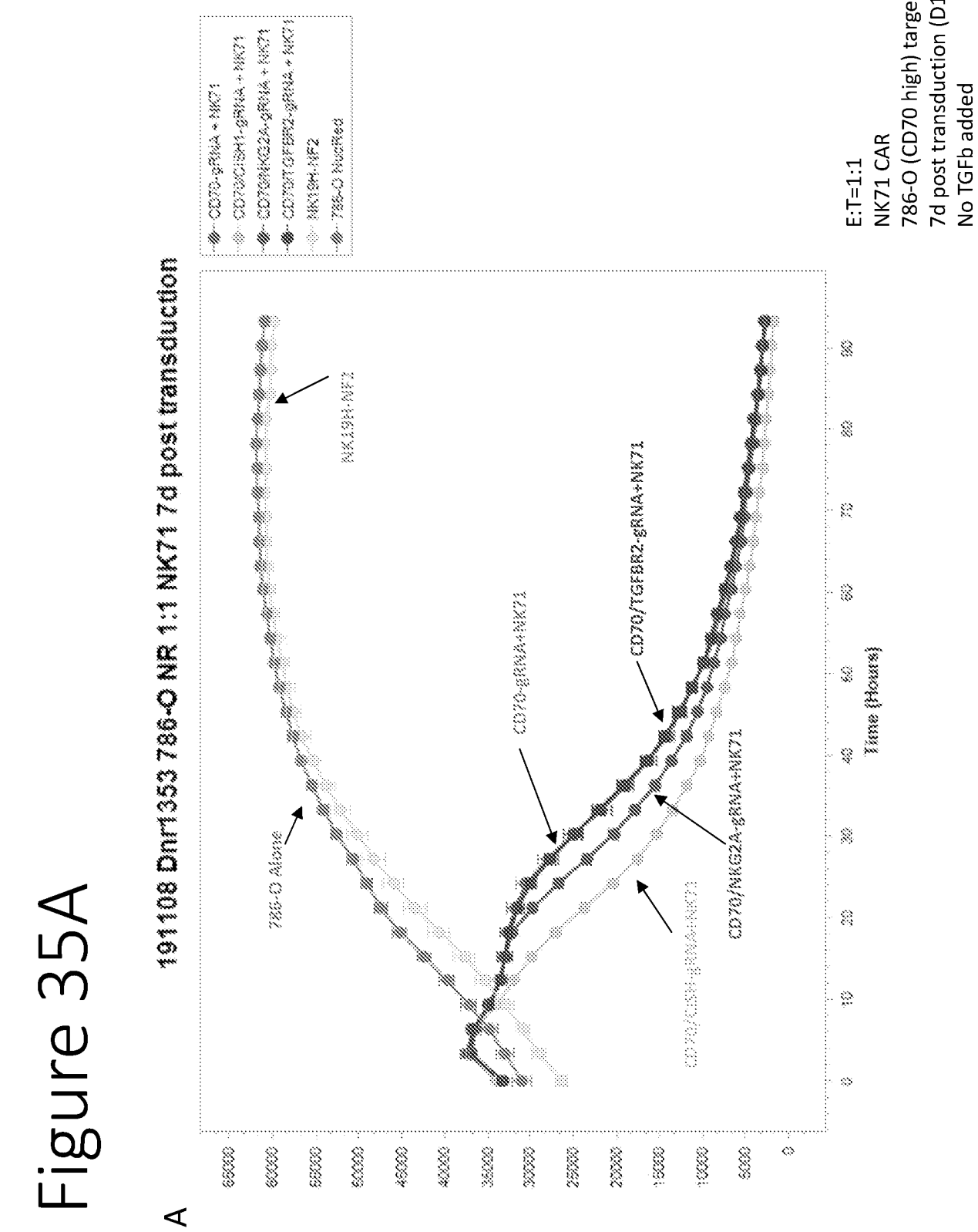

A
191108 Dnr1353 786-O NR 1:1 NK71 7d post transduction
786-O Alone
NK19H-NF2
CD70-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
CD70/NKG2A-gRNA+NK71
CD70-gRNA + NK71
CD70/CISH-gRNA + NK71
CD70/NKG2A-gRNA + NK71
CD70/TGFBR2-gRNA + NK71
NK19H-NF2
786-O Nucleus
Time (Hours)
E:T=1:1
NK71 CAR
786-O (CD70 high) target
7d post transduction (D14)
No TGFb added

Figure 35B

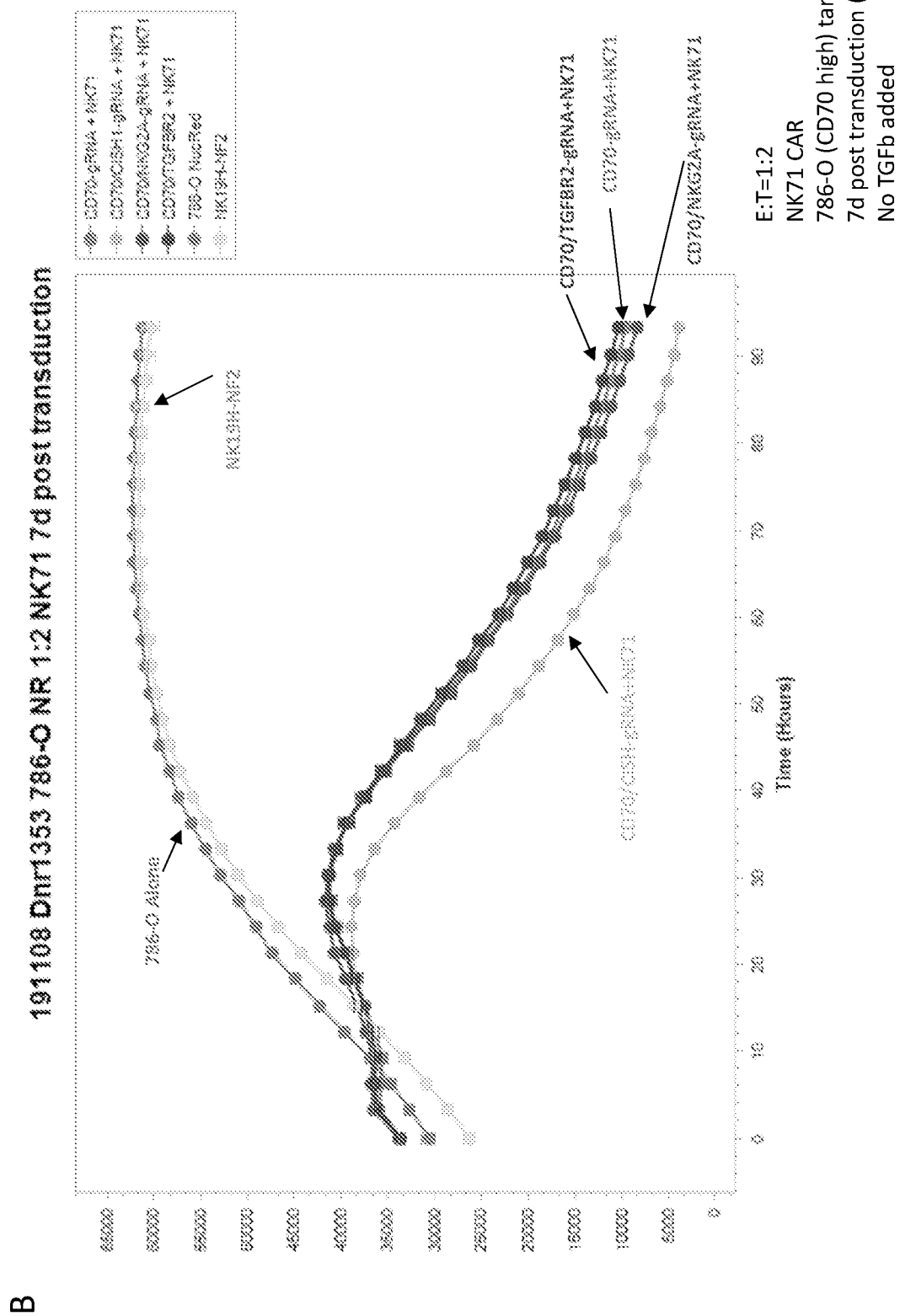

B
191108 Dnr1353 786-O NR 1:2 NK71 7d post transduction
786-O Alone
NK19H-NF2
CD70/TGFBR2-gRNA+NK71
CD70-gRNA+NK71
CD70/NKG2A-gRNA+NK71
CD70/CD5H-gRNA+NK71
Time (Hours)
E:T=1:2
NK71 CAR
786-O (CD70 high) target
7d post transduction (D14)
No TGFb added

Figure 35C

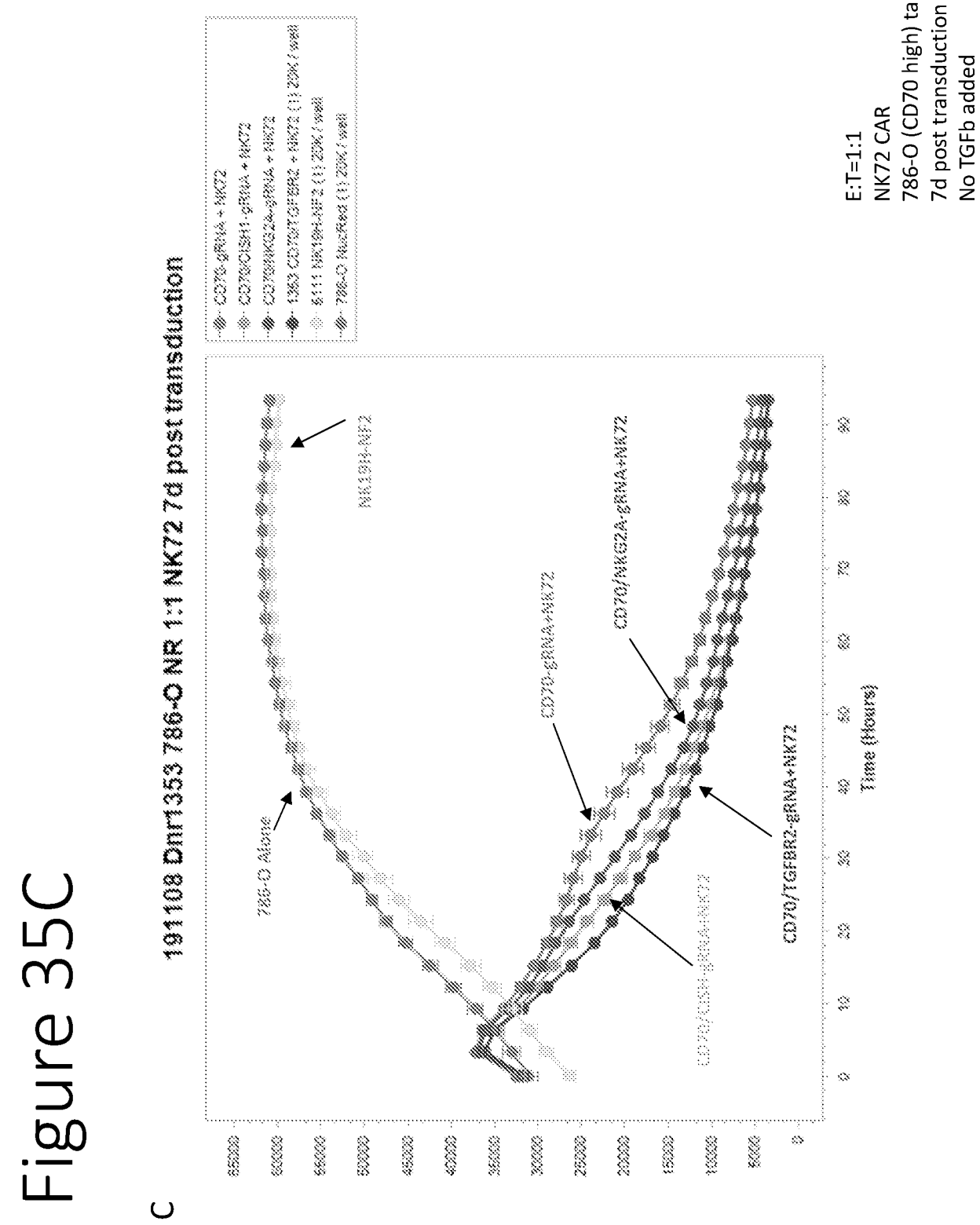

C
191108 Dnr1353 786-O NR 1:1 NK72 7d post transduction
CD70-gRNA + NK72
CD70/CISH1-gRNA + NK72
CD70/NKG2A-gRNA + NK72
1353 CD70/TGFBR2 + NK72 (1) 20K / well
6111 NK1914-NF2 (1) 20K / well
786-O NucRed (1) 20K / well
786-O Alone
NK1914-NF2
CD70-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/CISH1-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
Time (Hours)
E:T=1:1
NK72 CAR
786-O (CD70 high) target
7d post transduction (D14)
No TGFb added

Figure 35D

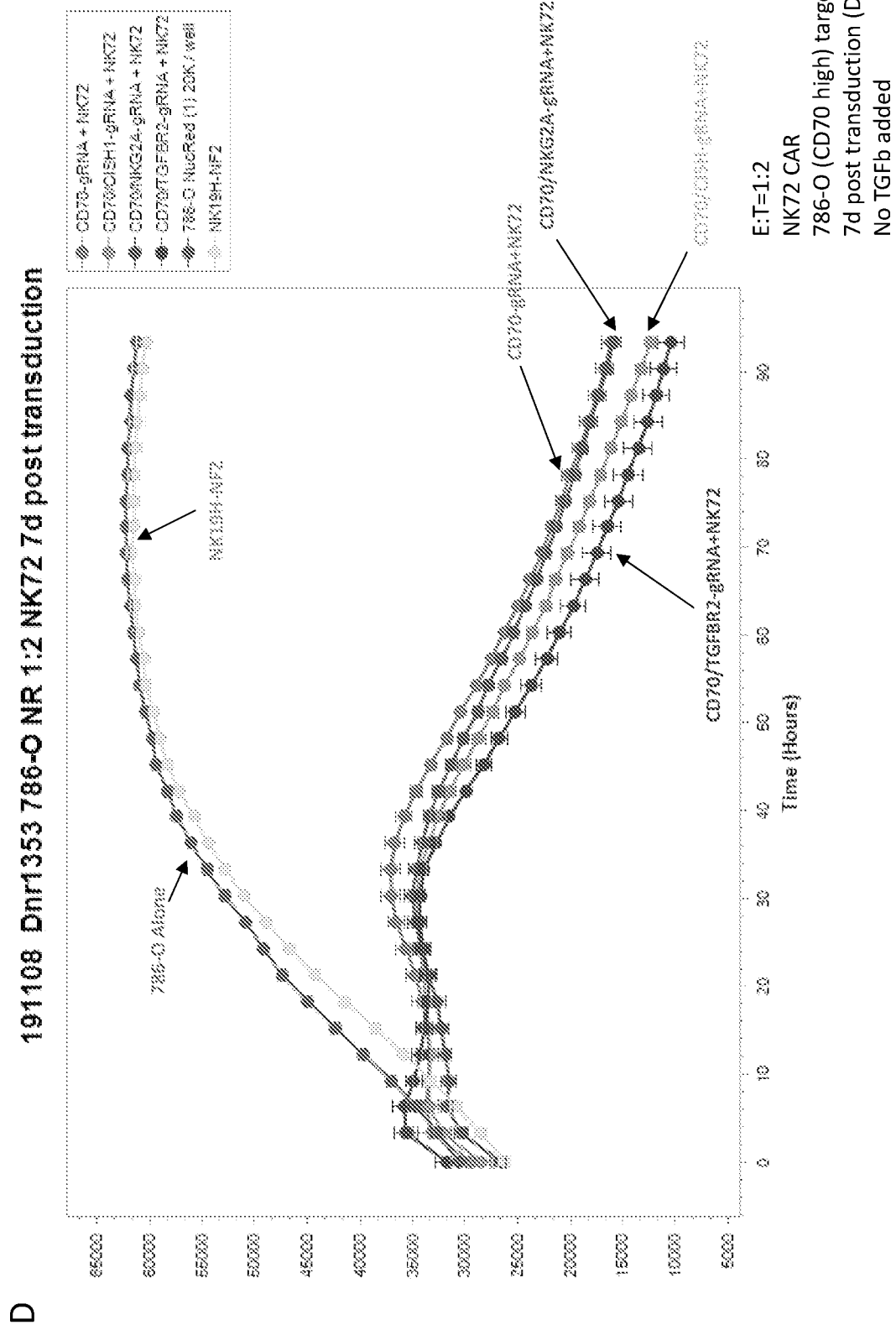

D
191108 Dnr1353 786-O NR 1:2 NK72 7d post transduction
CD70-gRNA + NK72
CD70/CISH1-gRNA + NK72
CD70/NKG2A-gRNA + NK72
CD70/TGFBR2-gRNA + NK72
786-O NucRed (1) 20K / well
NK19H-NF2
786-O Alone
NK19H-NF2
CD70-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/CISH1-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
Time (Hours)
E:T=1:2
NK72 CAR
786-O (CD70 high) target
7d post transduction (D14)
No TGFb added

Figure 36A

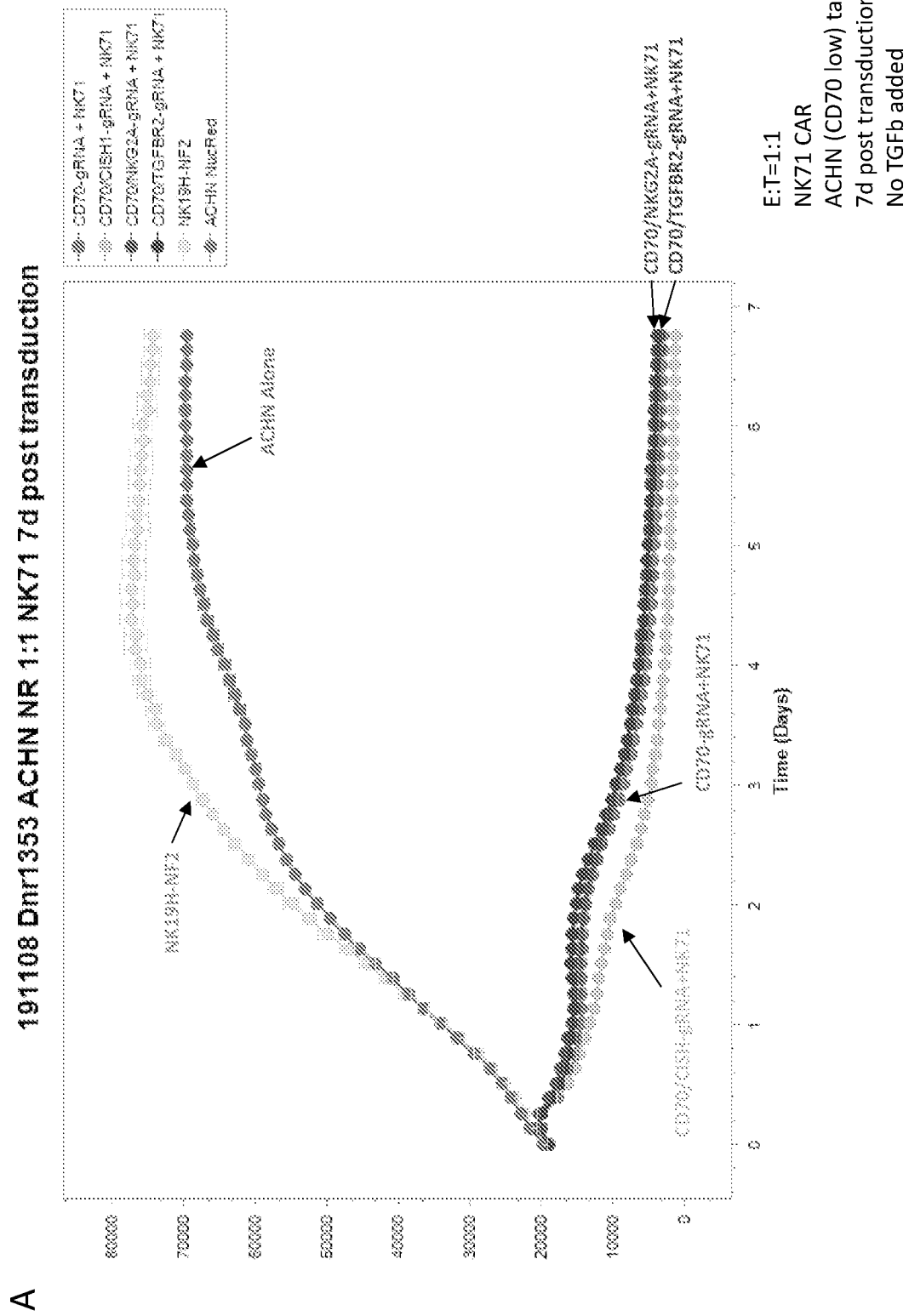

A
191108 Dnr1353 ACHN NR 1:1 NK71 7d post transduction
CD70-gRNA + NK71
CD70/CIS1-gRNA + NK71
CD70/NKG2A-gRNA + NK71
CD70/TGFBR2-gRNA + NK71
NK139-NF2
ACHN NucRed
NK139-NF2
ACHN Alone
CD70/NKG2A-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
CD70-gRNA+NK71
CD70/CIS1-gRNA+NK71
Time (Days)
E:T=1:1
NK71 CAR
ACHN (CD70 low) target
7d post transduction (D14)
No TGFb added

Figure 36B

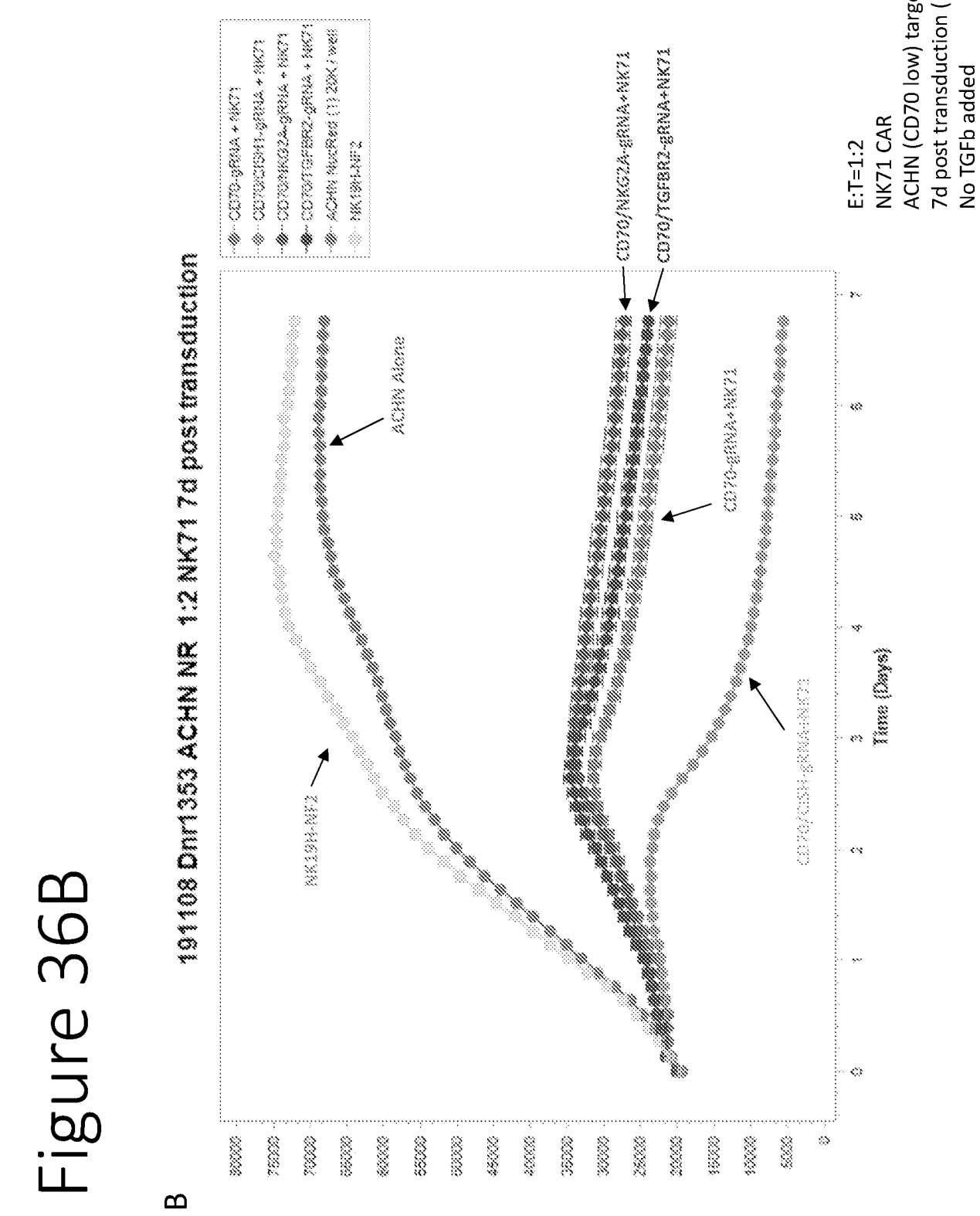

B
191108 Dnr1353 ACHN NR 1:2 NK71 7d post transduction
CD70-gRNA + NK71
CD70/CISH-gRNA + NK71
CD70/NKG2A-gRNA + NK71
CD70/TGFBR2-gRNA + NK71
ACHN Alone (1) 22K / well
NK71H-NF2
ACHN Alone
NK71H-NF2
CD70/NKG2A-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
CD70-gRNA+NK71
CD70/CISH-gRNA+NK71
Time (Days)
E:T=1:2
NK71 CAR
ACHN (CD70 low) target
7d post transduction (D14)
No TGFb added

Figure 36C

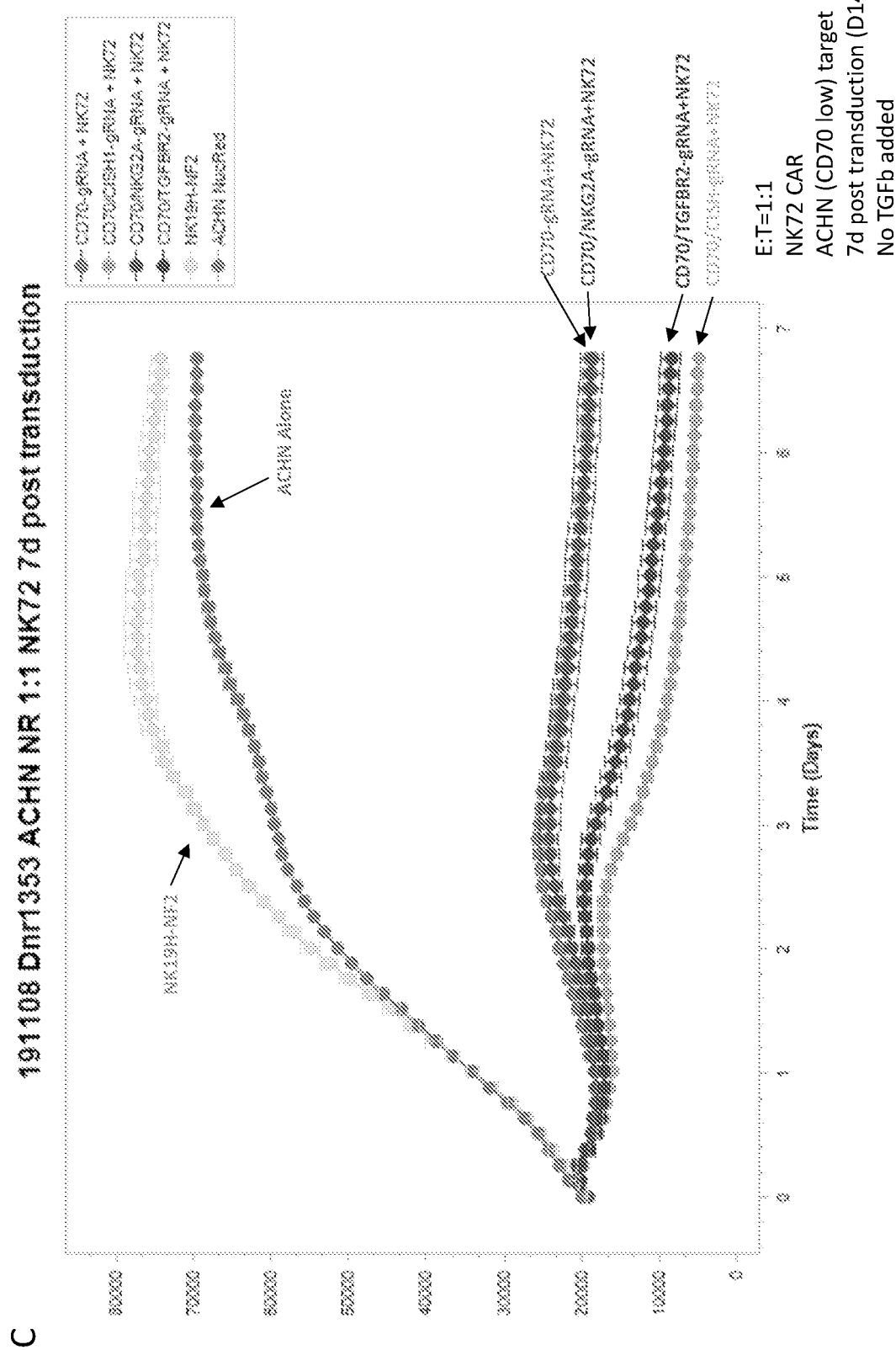

C
191108 Dnr1353 ACHN NR 1:1 NK72 7d post transduction
CD70-gRNA + NK72
CD70CBH1-gRNA + NK72
CD70NKG2A-gRNA + NK72
CD70TGFBR2-gRNA + NK72
NK19H-NF2
ACHN Nuc/Red
NK19H-NF2
ACHN Alone
CD70-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
CD70/CBH-gRNA+NK72
800000
700000
600000
500000
400000
300000
200000
100000
0
0
1
2
3
4
5
6
7
8
Time (Days)
E:T=1:1
NK72 CAR
ACHN (CD70 low) target
7d post transduction (D14)
No TGFb added

Figure 36D

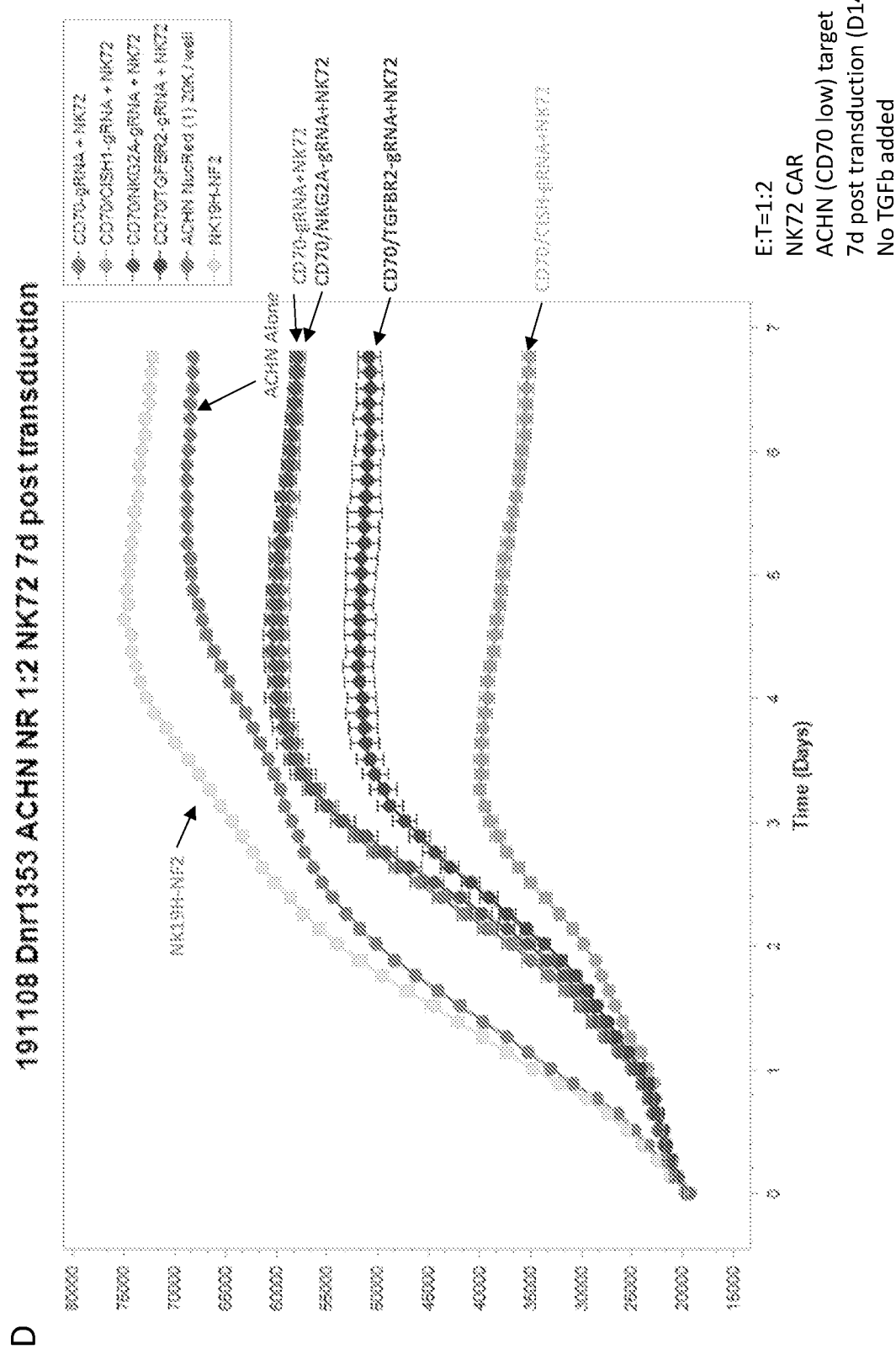

D
191108 Dnr1353 ACHN NR 1:2 NK72 7d post transduction
CD70-gRNA + NK72
CD70/SH1-gRNA + NK72
CD70/NKG2A-gRNA + NK72
CD70/TGFBR2-gRNA + NK72
ACHN NucRed (1) 30K / well
NK72H-NF2
ACHN Alone
CD70-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
CD70/SH1-gRNA+NK72
NK72H-NF2
Time (Days)
E:T=1:2
NK72 CAR
ACHN (CD70 low) target
7d post transduction (D14)
No TGFb added

Figure 37A

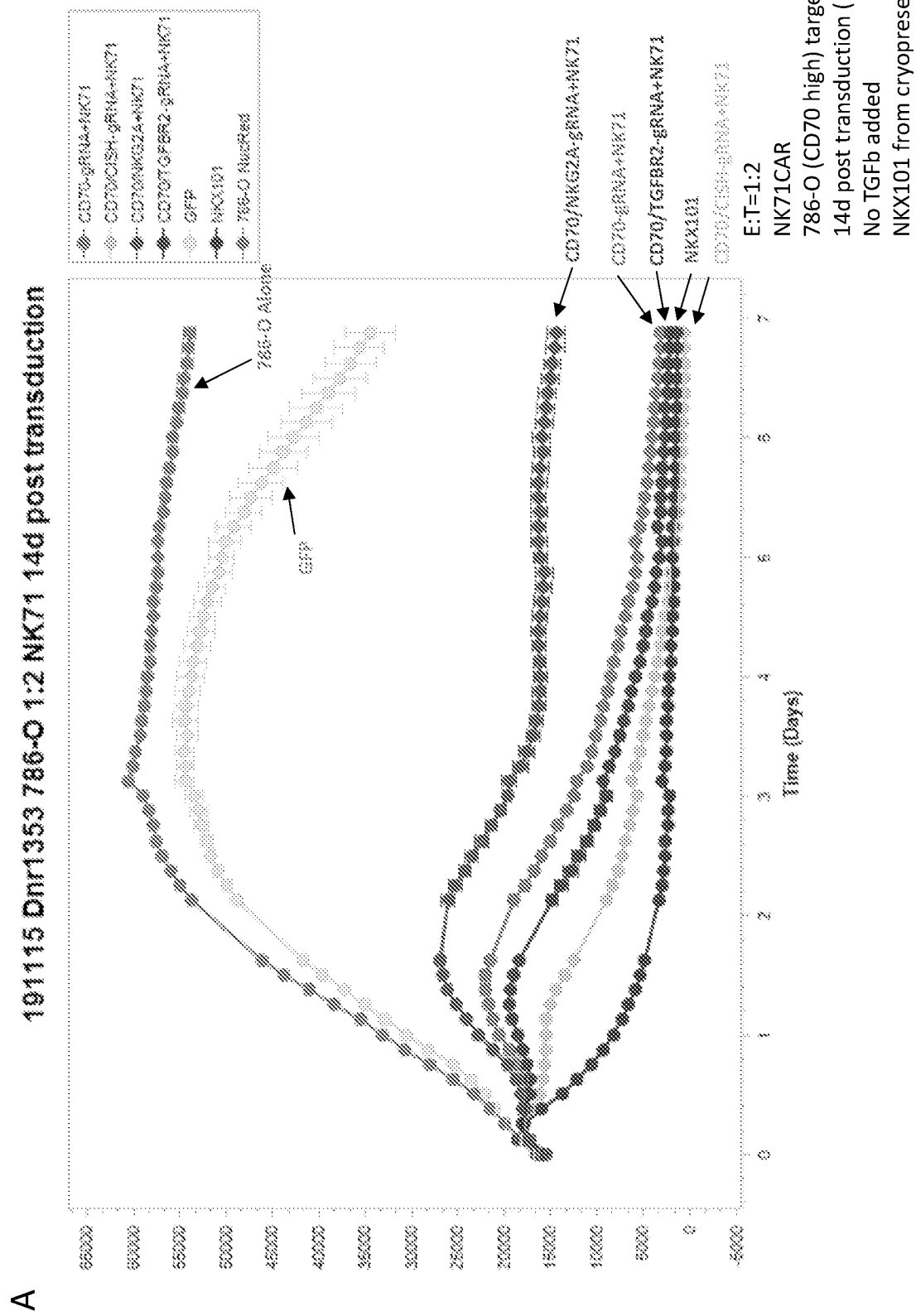

A
191115 Dmr1353 786-O 1:2 NK71 14d post transduction
786-O Alone
GFP
CD70/NKG2A-gRNA+NK71
CD70-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
NKX101
Time (Days)
E:T=1:2
NK71CAR
786-O (CD70 high) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 37B

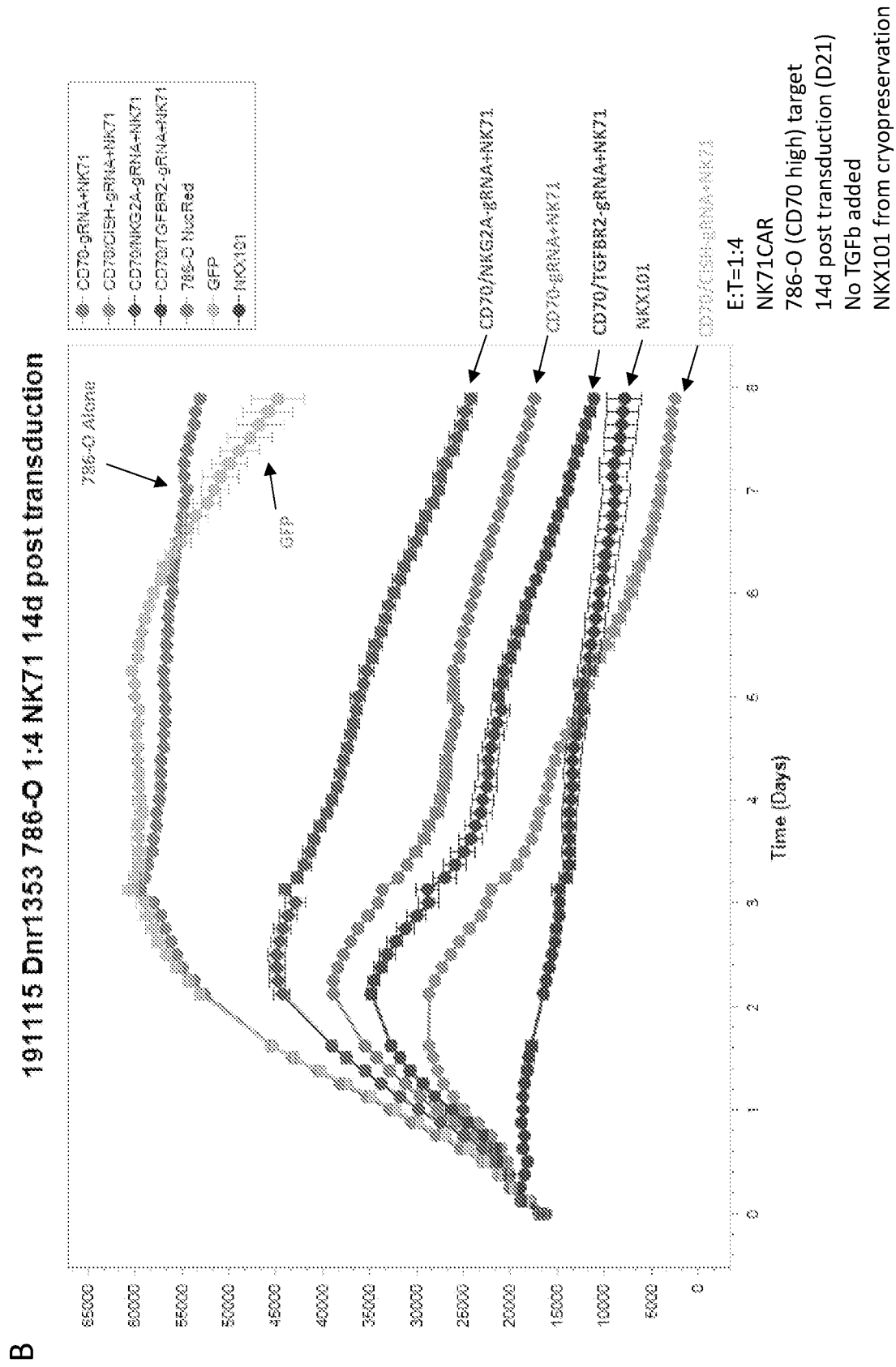

B
191115 Dnr1353 786-O 1:4 NK71 14d post transduction
786-O Alone
GFP
CD70-gRNA+NK71
CD70/CISH-gRNA+NK71
CD70/NKG2A-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
786-O NucRed
GFP
NKX101
CD70/NKG2A-gRNA+NK71
CD70-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
NKX101
CD70/CISH-gRNA+NK71
Time (Days)
E:T=1:4
NK71CAR
786-O (CD70 high) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 38A

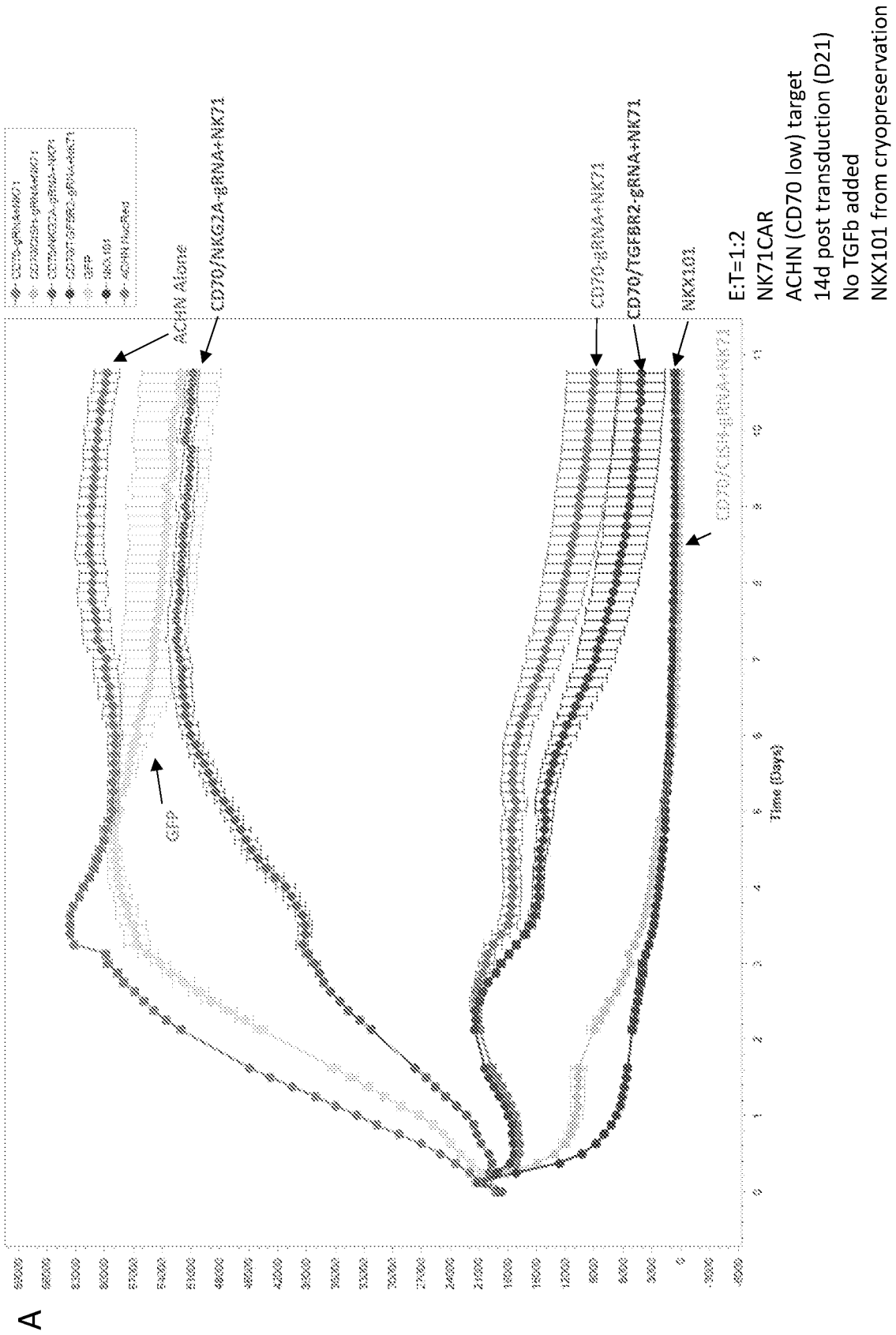

A
191115 Dnr1353 ACHN NK71 1:1 14d post transduction
ACHN Alone
CD70/NKG2A-gRNA+NK71
CD70-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
NKX101
GFP
E:T=1:2
NK71CAR
ACHN (CD70 low) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 38B

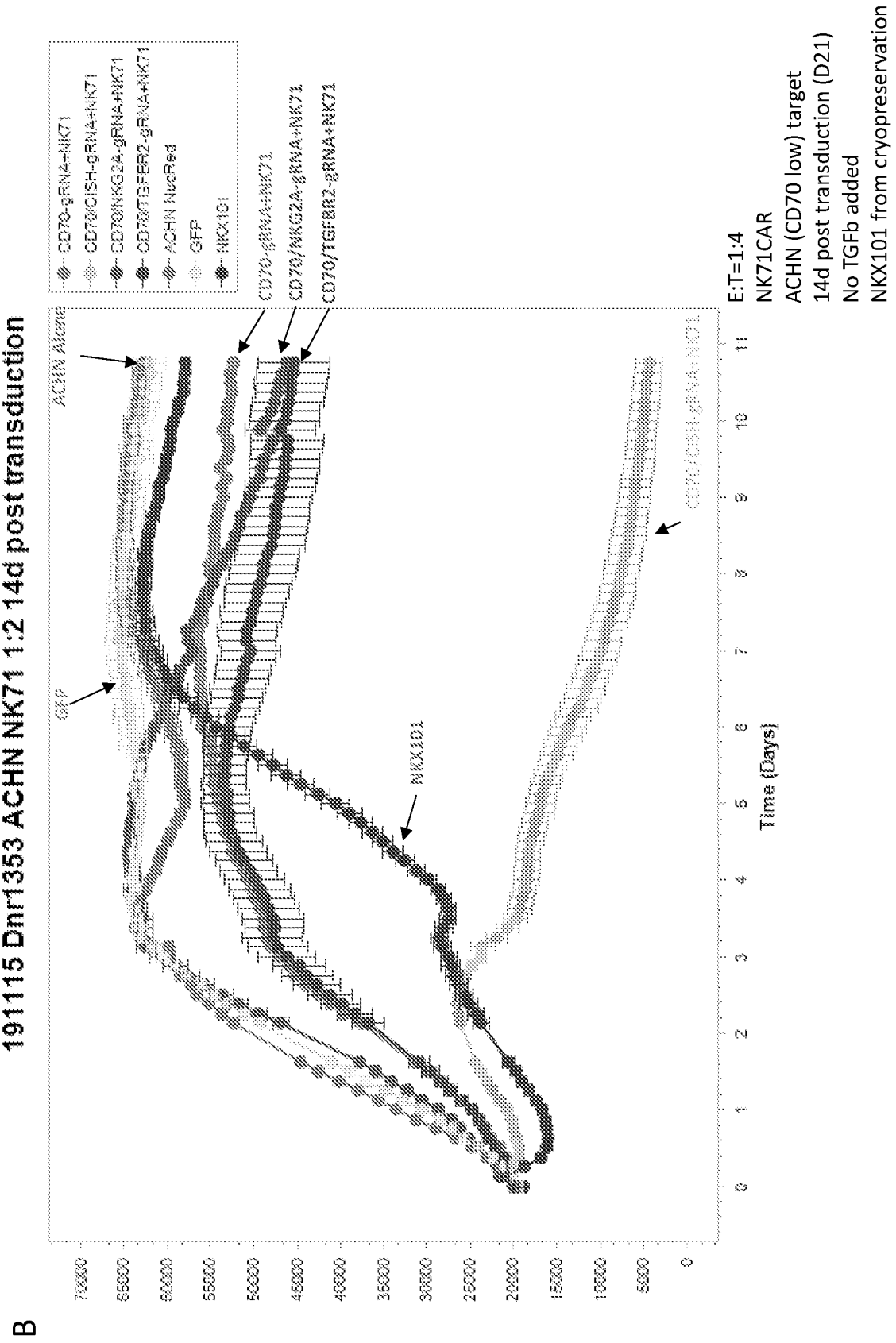

B
191115 Dnr1353 ACHN NK71 1:2 14d post transduction
CD70-gRNA+NK71
CD70/CISH-gRNA+NK71
CD70/NKG2A-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
ACHN NucRed
GFP
NKX101
ACHN Alone
GFP
NKX101
CD70-gRNA+NK71
CD70/NKG2A-gRNA+NK71
CD70/TGFBR2-gRNA+NK71
Confluence (Green Area)
Time (Days)
E:T=1:4
NK71CAR
ACHN (CD70 low) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 39A

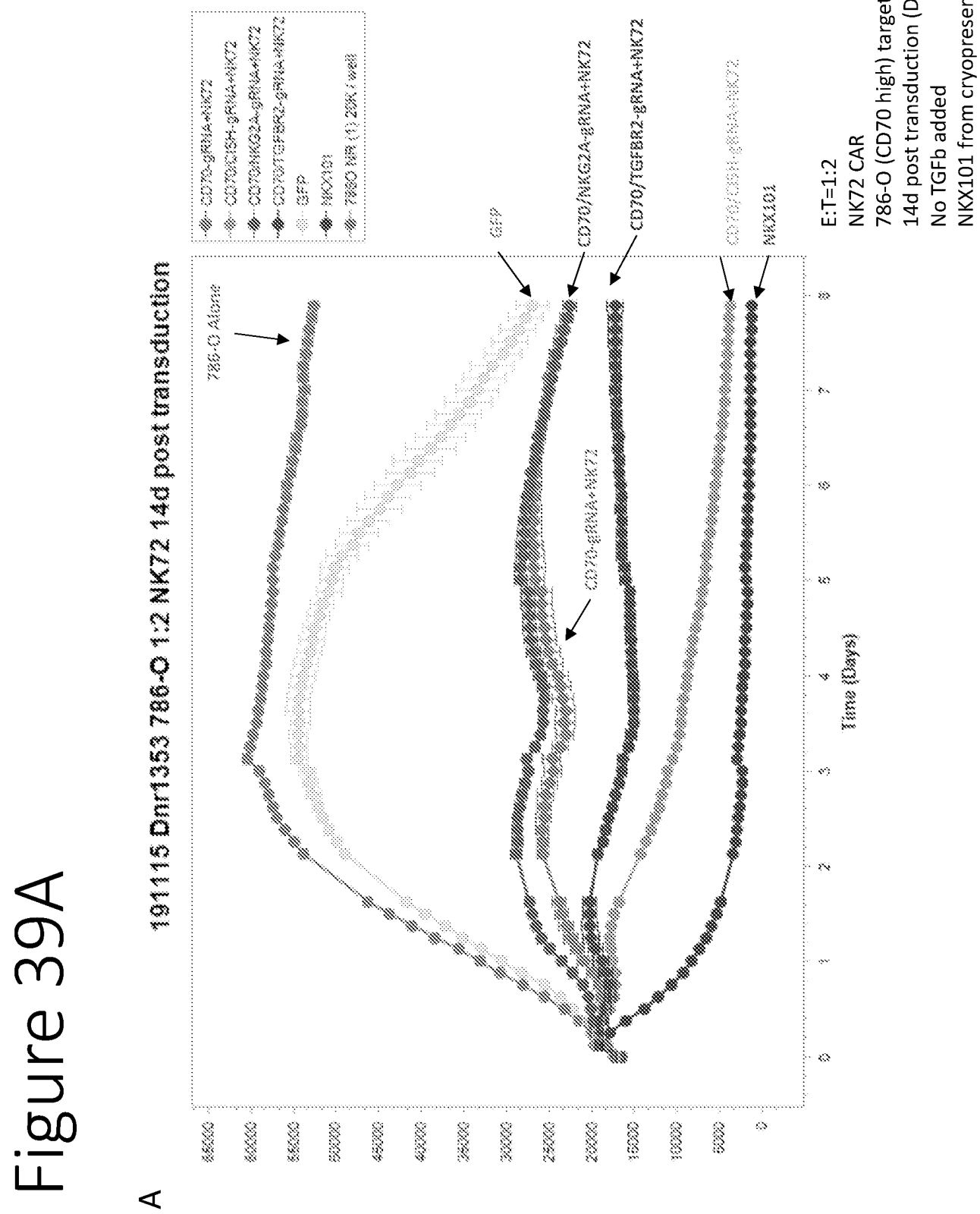

A
191115 Dnr1353 786-O 1:2 NK72 14d post transduction
786-O Alone
GFP
CD70-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
NKX101
Time (Days)
E:T=1:2
NK72 CAR
786-O (CD70 high) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 39B

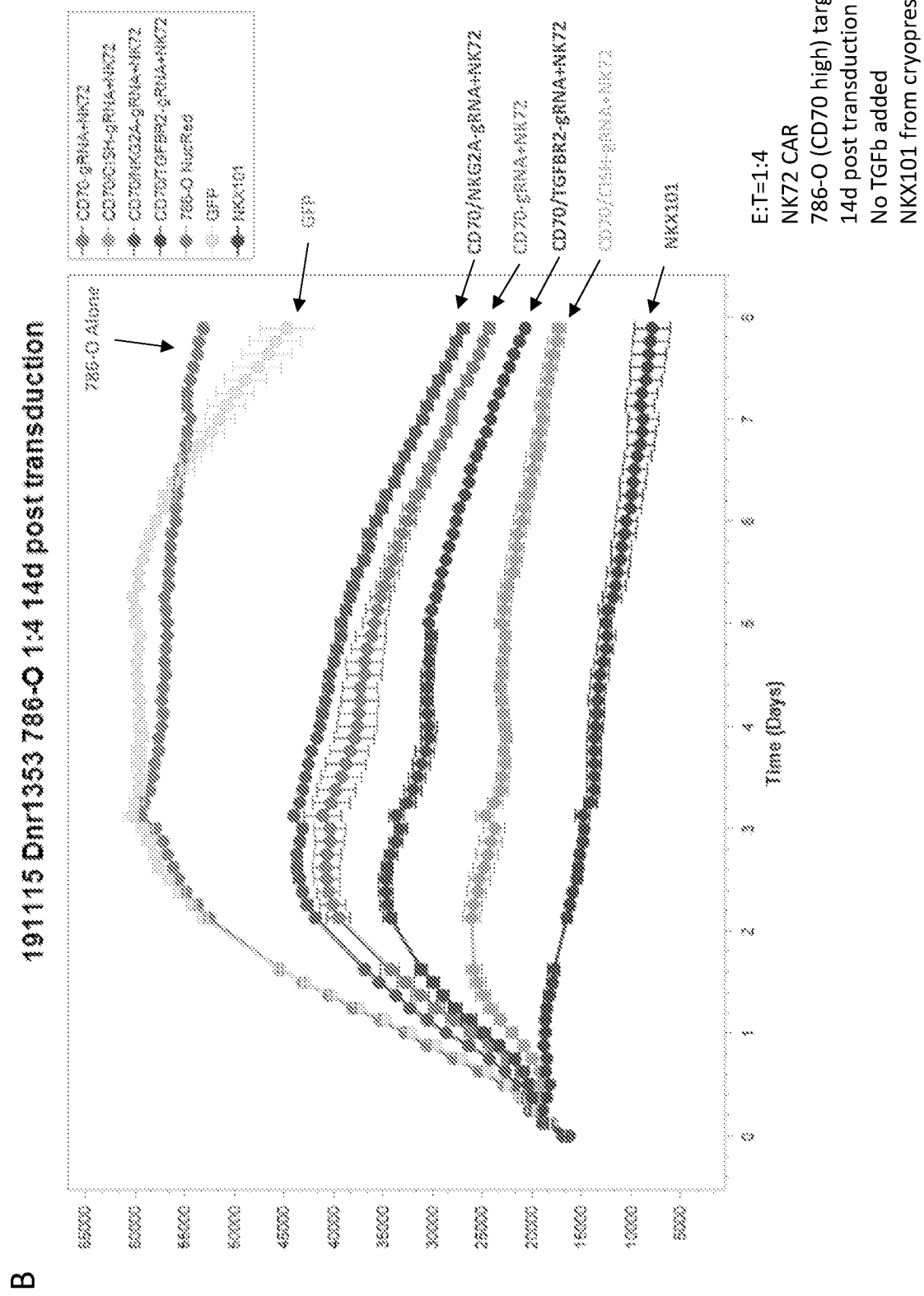

B
191115 Dnr1353 786-O 1:4 14d post transduction
786-O Alone
GFP
CD70/NKG2A-gRNA+NK72
CD70-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
NKX101
CD70-gRNA+NK72
CD70/CISH-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
786-O NucRed
GFP
NKX101
Time (Days)
E:T=1:4
NK72 CAR
786-O (CD70 high) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figure 40A

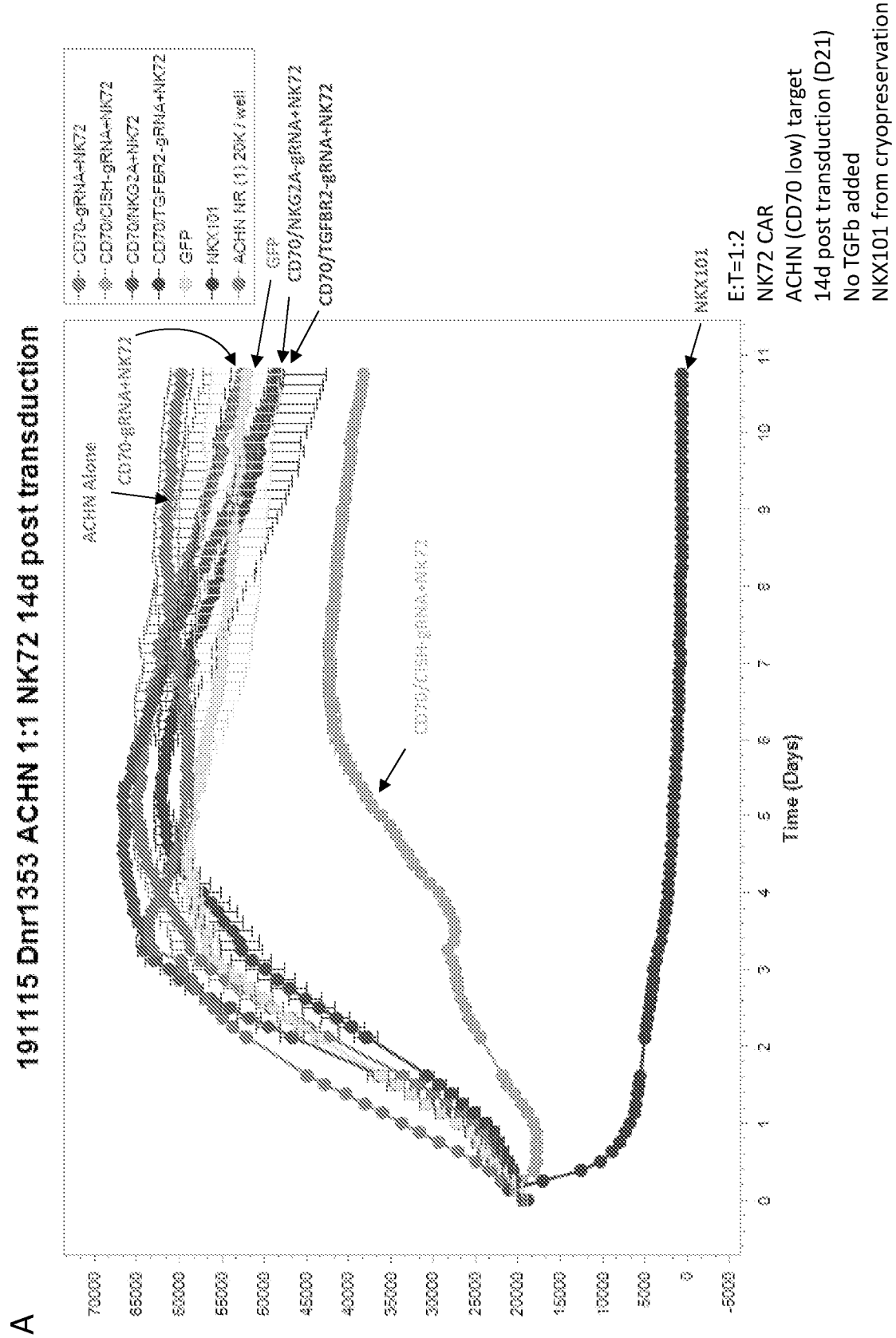
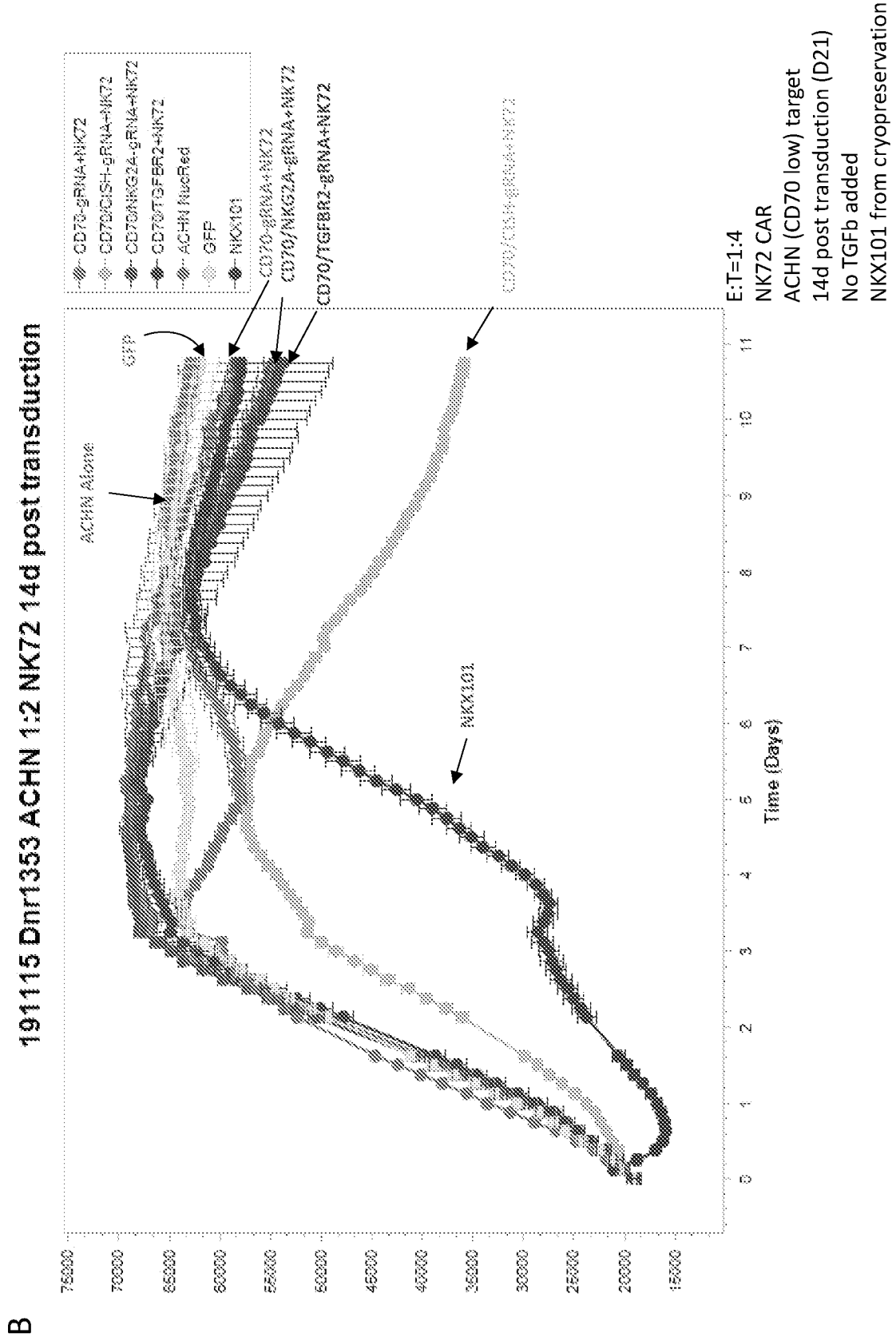
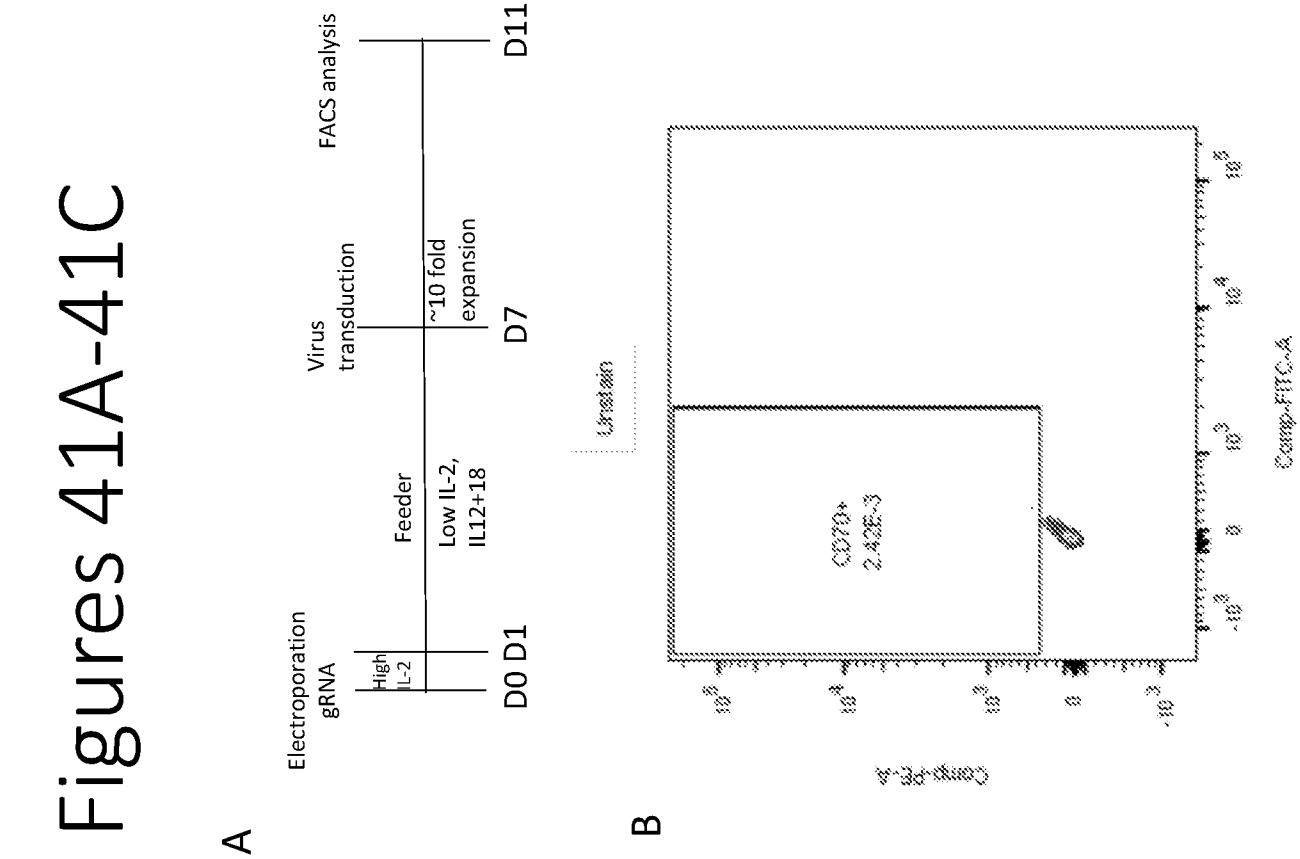

A
191115 Dnr1353 ACHN 1:1 NK72 14d post transduction
CD70-gRNA+NK72
CD70/CIS-gRNA+NK72
CD70/NKG2A+NK72
CD70/TGFBR2-gRNA+NK72
GFP
NKX101
ACHN NR (1) 20K / well
ACHN Alone
CD70-gRNA+NK72
GFP
CD70/NKG2A-gRNA+NK72
CD70/TGFBR2-gRNA+NK72
NKX101
Time (Days)
E:T=1:2
NK72 CAR
ACHN (CD70 low) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

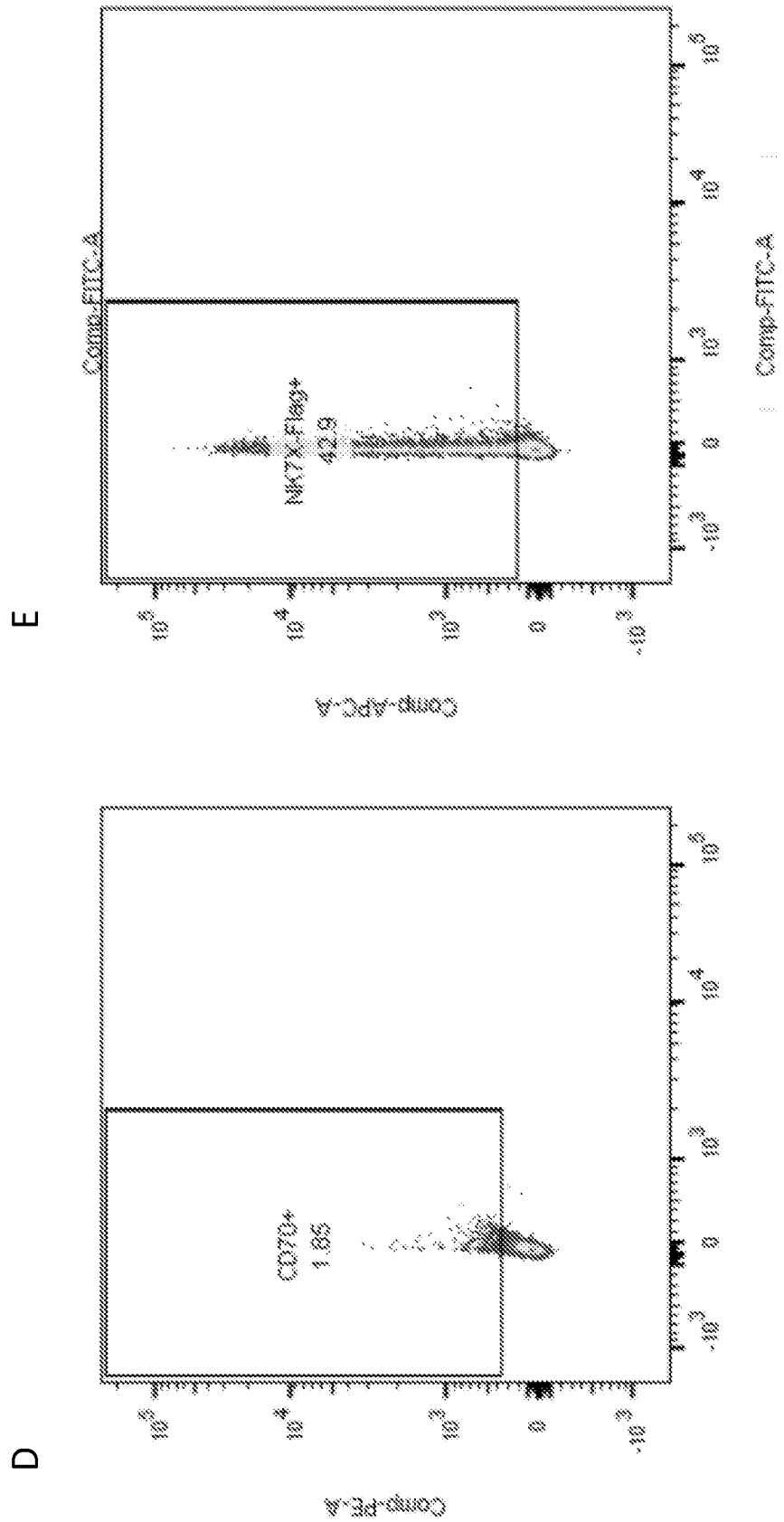
Figure 40B


B
191115 Dmr1353 ACHN 1:2 NK72 14d post transduction
CD70-gRNA+NK72
CD70DGK-gRNA+NK72
CD70NKG2A-gRNA+NK72
CD70TGFBR2-gRNA+NK72
ACHN NucRed
GFP
NKX101
ACHN Alone
GFP
CD70/TGFBR2-gRNA+NK72
CD70/NKG2A-gRNA+NK72
CD70-gRNA+NK72
NKX101
Time (Days)
E:T=1:4
NK72 CAR
ACHN (CD70 low) target
14d post transduction (D21)
No TGFb added
NKX101 from cryopreservation

Figures 41A-41C

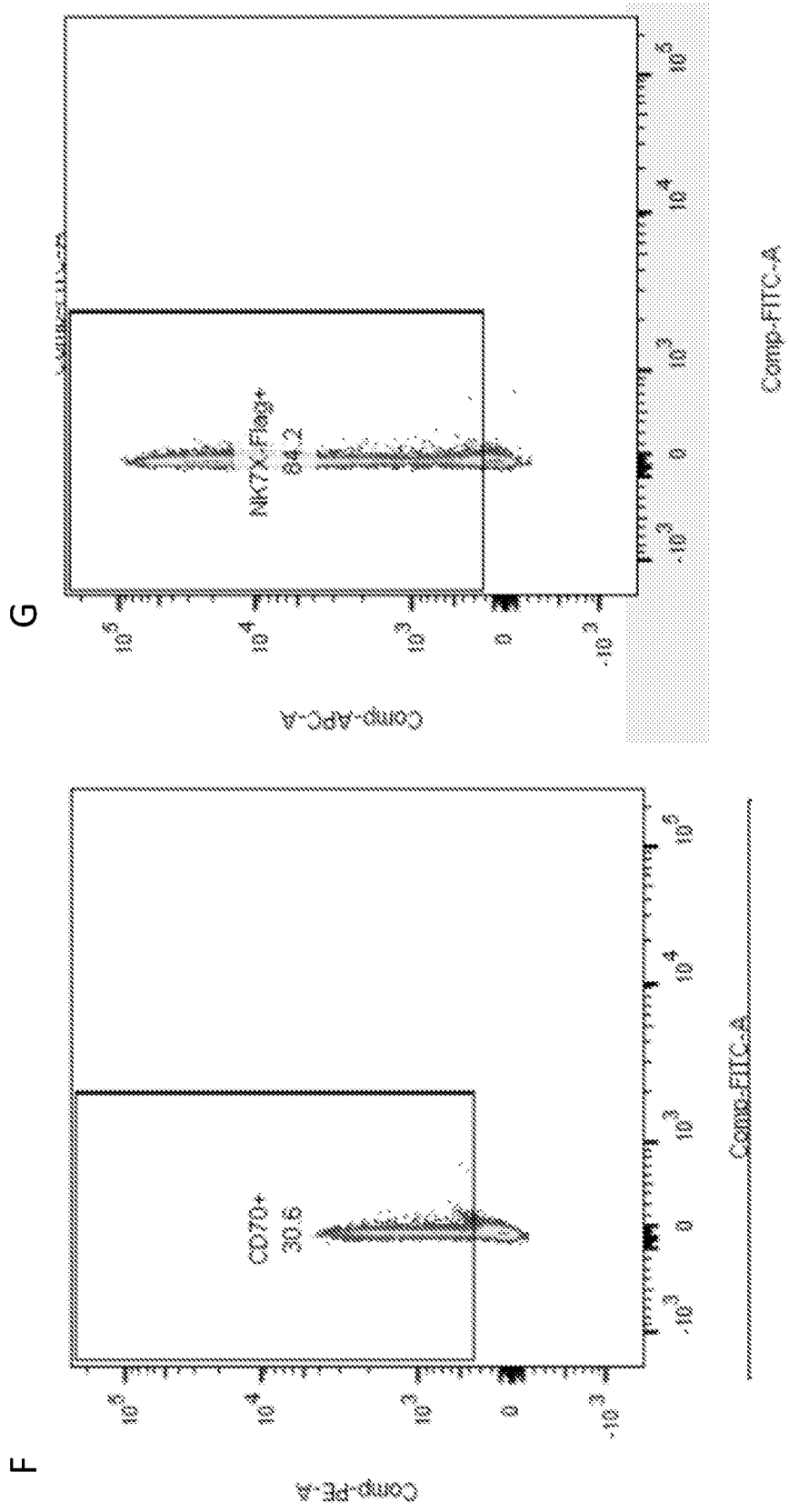


Figures 41D-41E



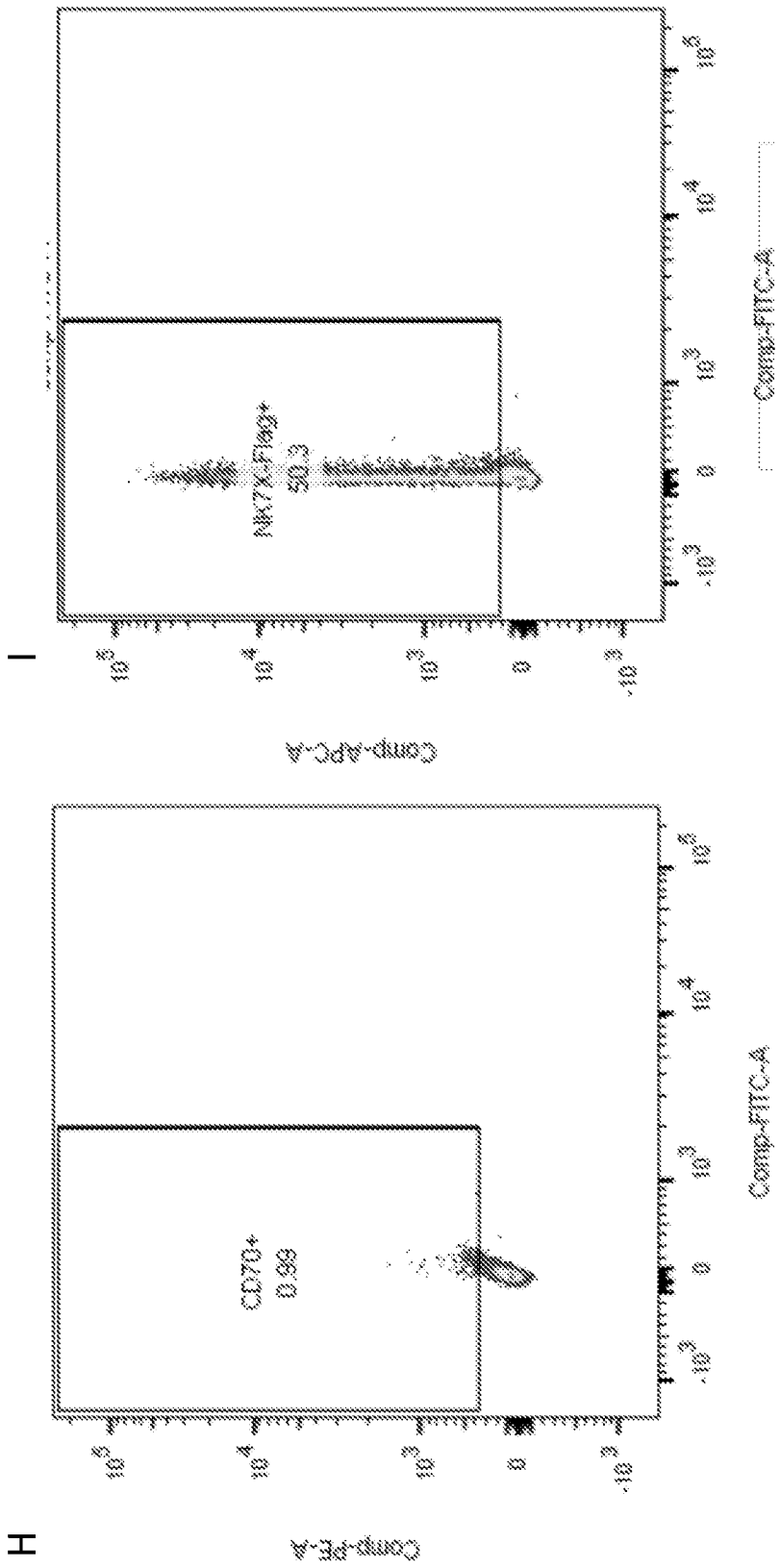
CD70 gRNA+NK71

Figures 41F-41G



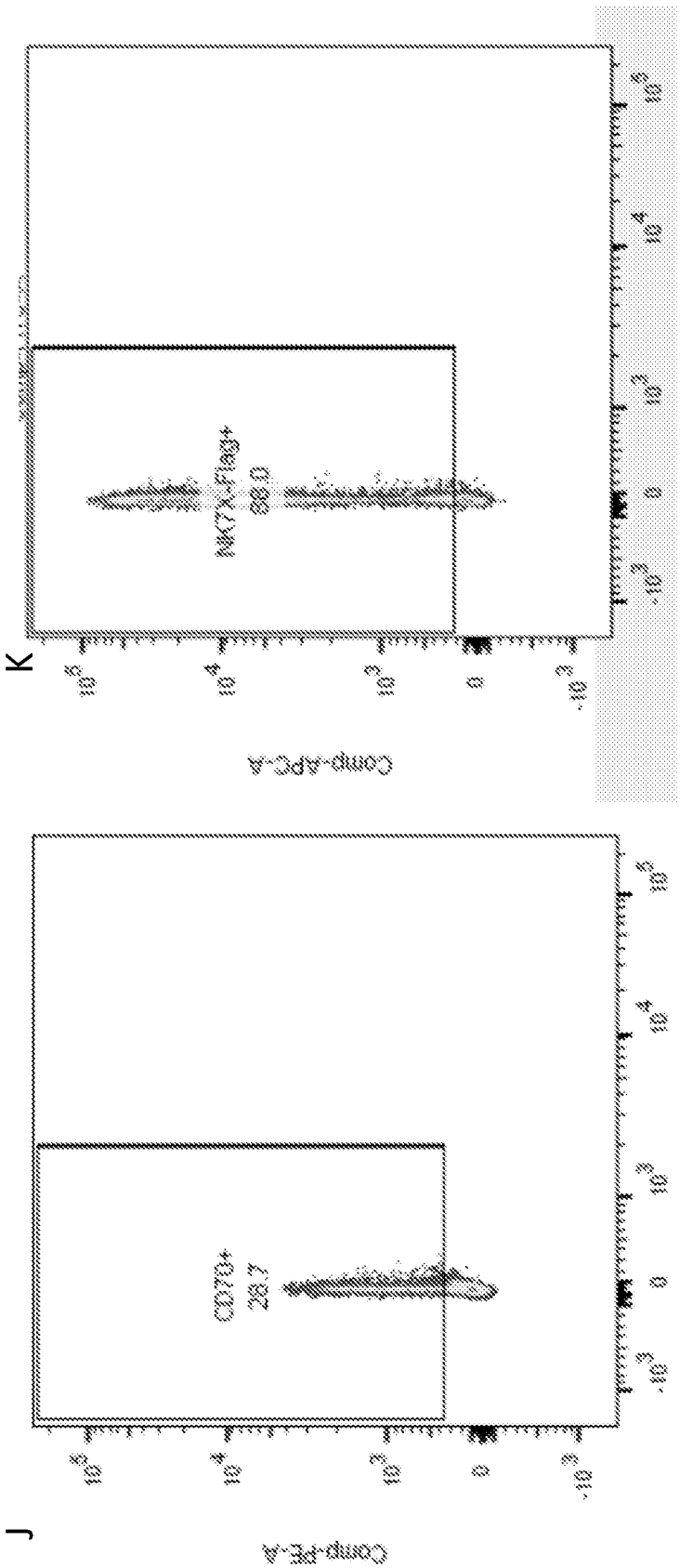
CD70 gRNA+NK72

Figures 41H-41I



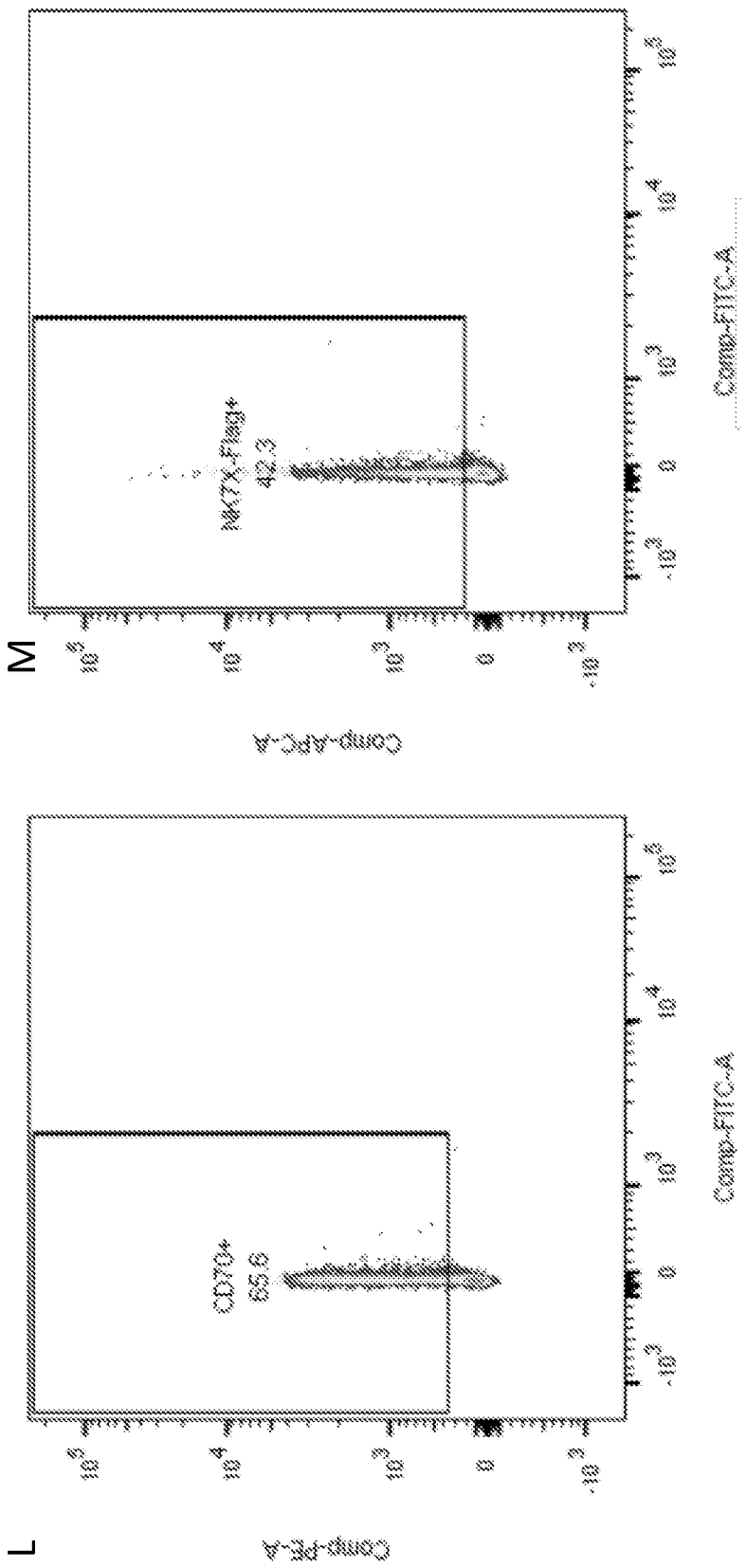
CD70 gRNA CISH gRNA + NK71

Figures 41J-41K



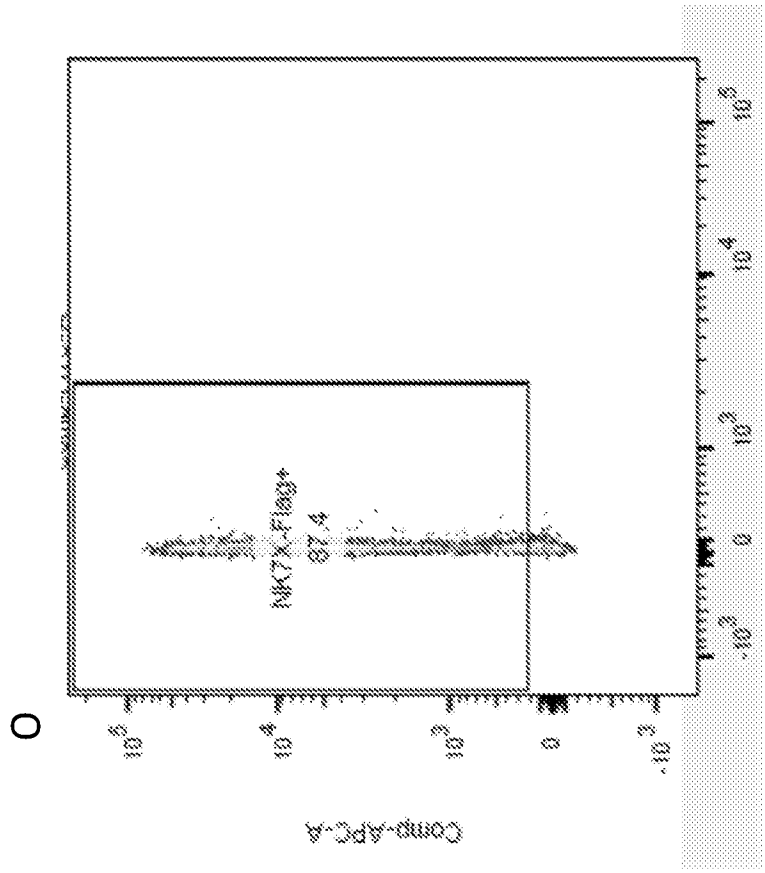
CD70 gRNA CISH gRNA + NK72

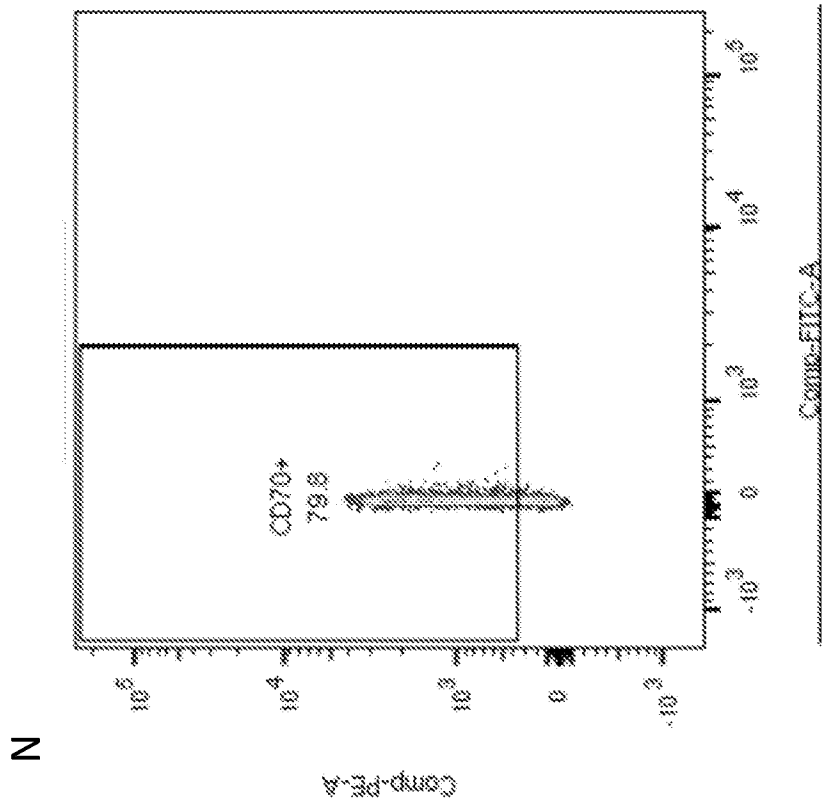
Figures 41L-41M



Electroporation + NK71

Figures 41N-41O





Electroporation + NK72

Figure 42A

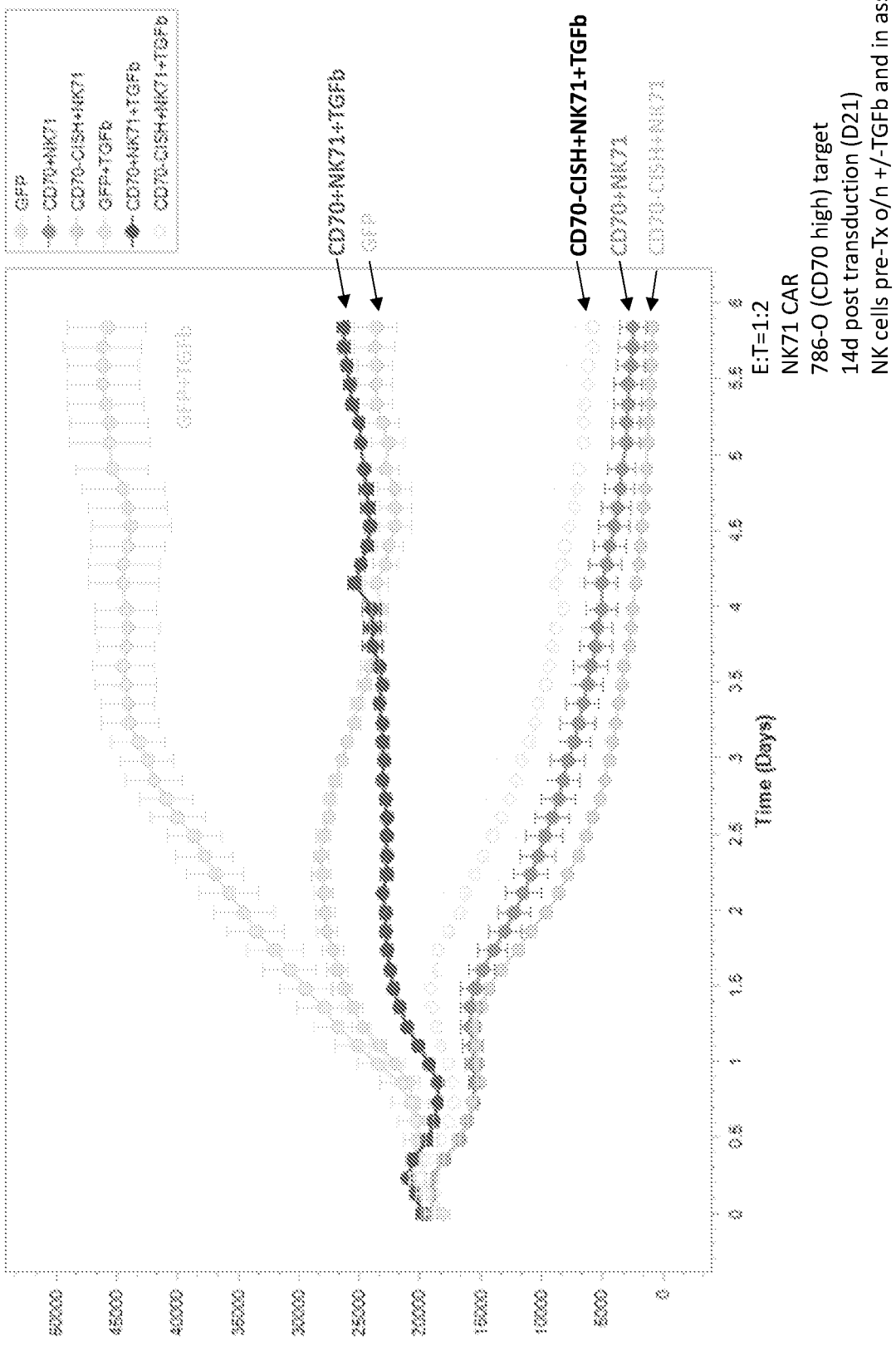

A
200122 Dnr 962 CD70 CISH NK71 7d post transduction
GFP
CD70+NK71
CD70-CISH+NK71
GFP+TGFb
CD70+NK71+TGFb
CD70-CISH+NK71+TGFb
CD70+NK71+TGFb
GFP
CD70-CISH+NK71+TGFb
CD70+NK71
CD70-CISH+NK71
Time (Days)
E:T=1:2
NK71 CAR
786-O (CD70 high) target
14d post transduction (D21)
NK cells pre-Tx o/n +/-TGFb and in assay

Figure 42B

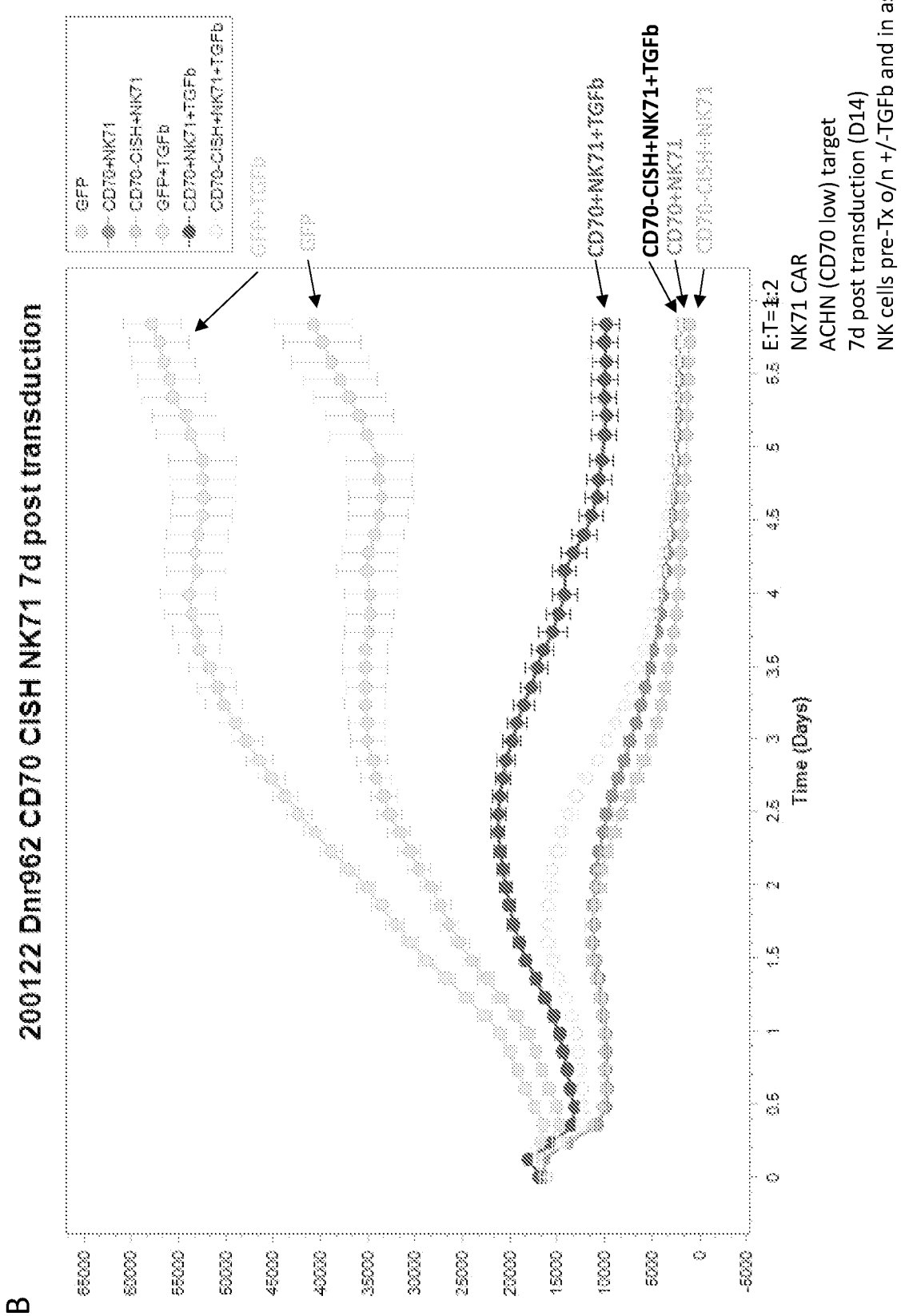

B
200122 Dnr962 CD70 CISH NK71 7d post transduction
GFP
CD70+NK71
CD70-CISH+NK71
GFP+TGFb
CD70+NK71+TGFb
CD70-CISH+NK71+TGFb
GFP+TGFb
GFP
CD70+NK71+TGFb
CD70-CISH+NK71+TGFb
CD70+NK71
CD70-CISH+NK71
65000
60000
55000
50000
45000
40000
35000
30000
25000
20000
15000
10000
5000
0
-5000
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
5.5
Time (Days)
E:T=1:2
NK71 CAR
ACHN (CD70 low) target
7d post transduction (D14)
NK cells pre-Tx o/n +/-TGFb and in assay

Figure 42C

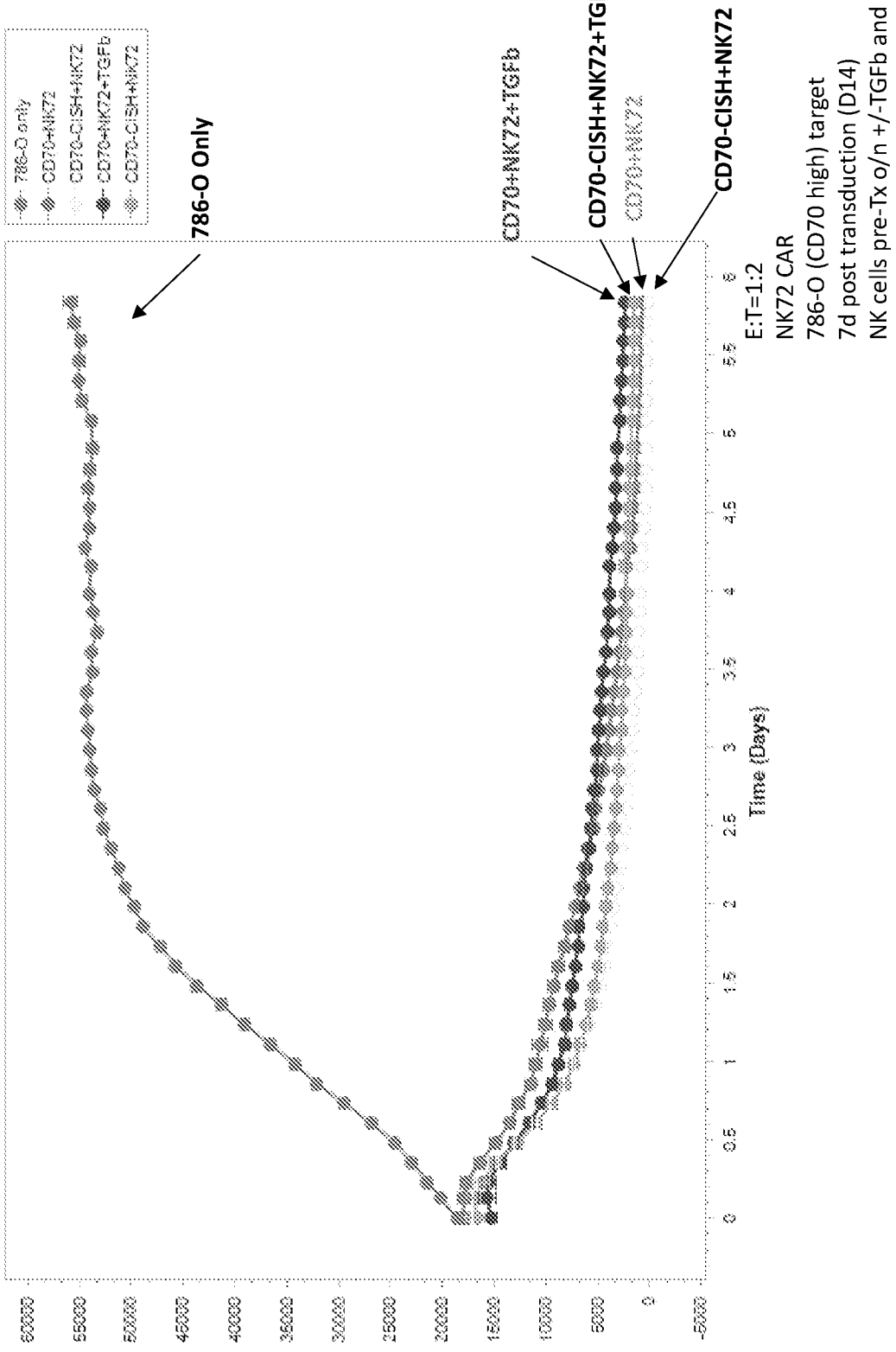

C
200122 Dnr 962 CD70 CISH NK7245-4 7d post transduction
786-O only
CD70+NK72
CD70-CISH+NK72
CD70+NK72+TGFb
CD70-CISH+NK72
786-O Only
CD70+NK72+TGFb
CD70-CISH+NK72+TGFb
CD70+NK72
CD70-CISH+NK72
Time (Days)
E:T=1:2
NK72 CAR
786-O (CD70 high) target
7d post transduction (D14)
NK cells pre-Tx o/n +/-TGFb and in assay

Figure 43A-43B

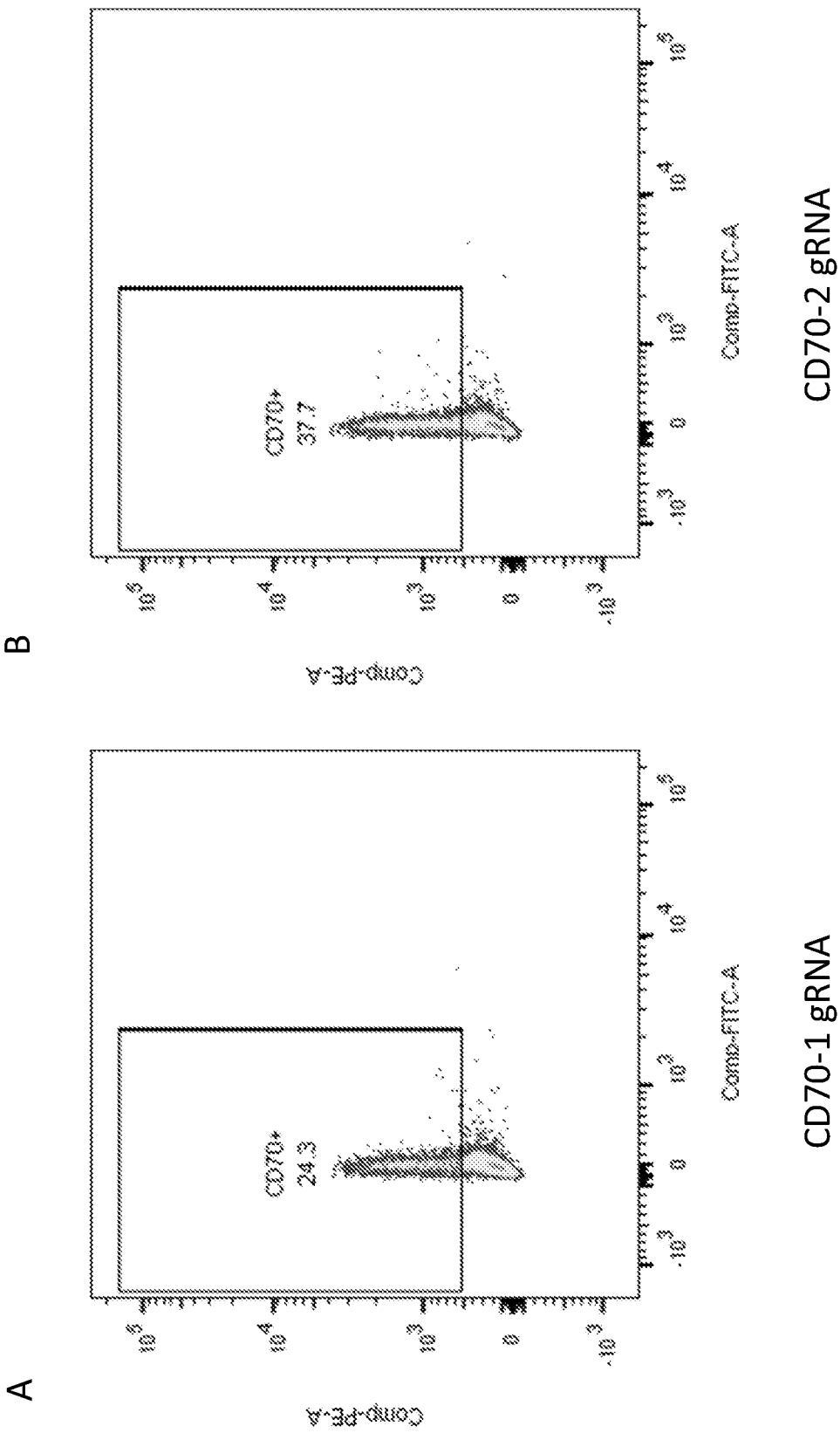
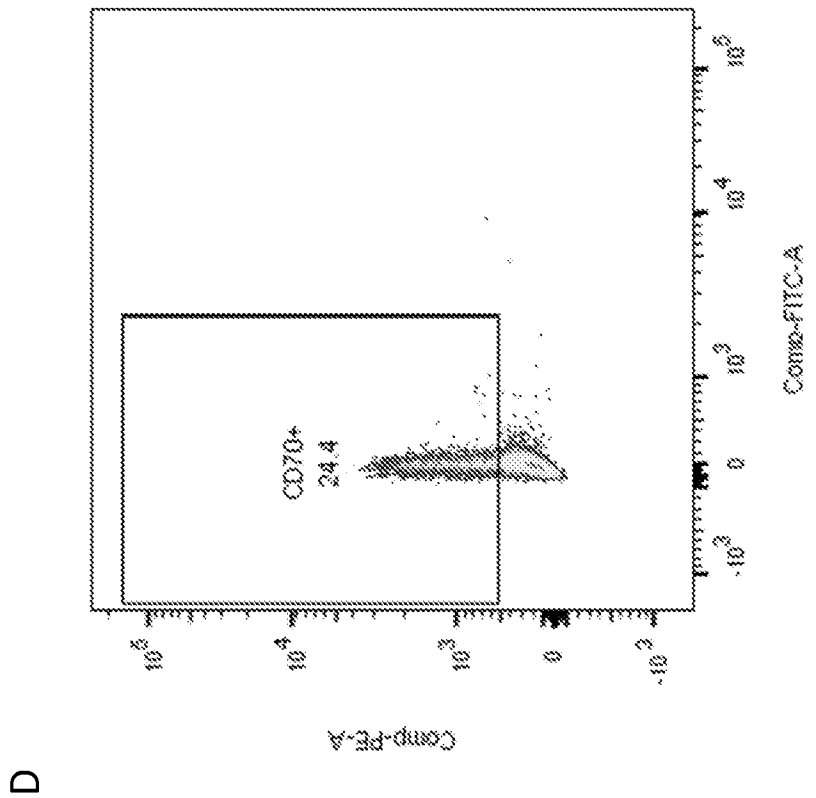


Figure 43C-43D



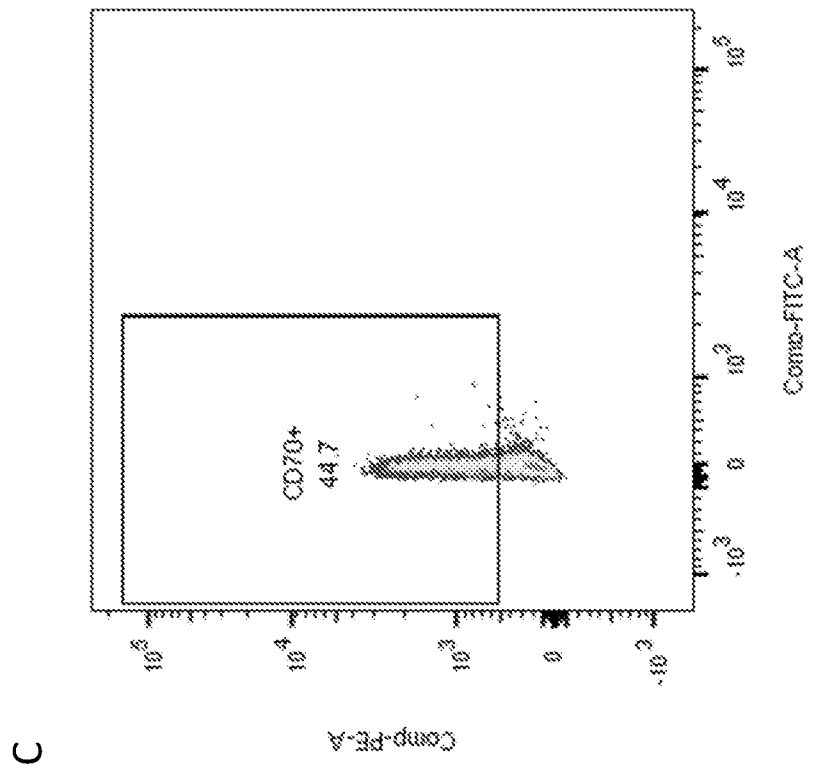


Figure 43E-43F

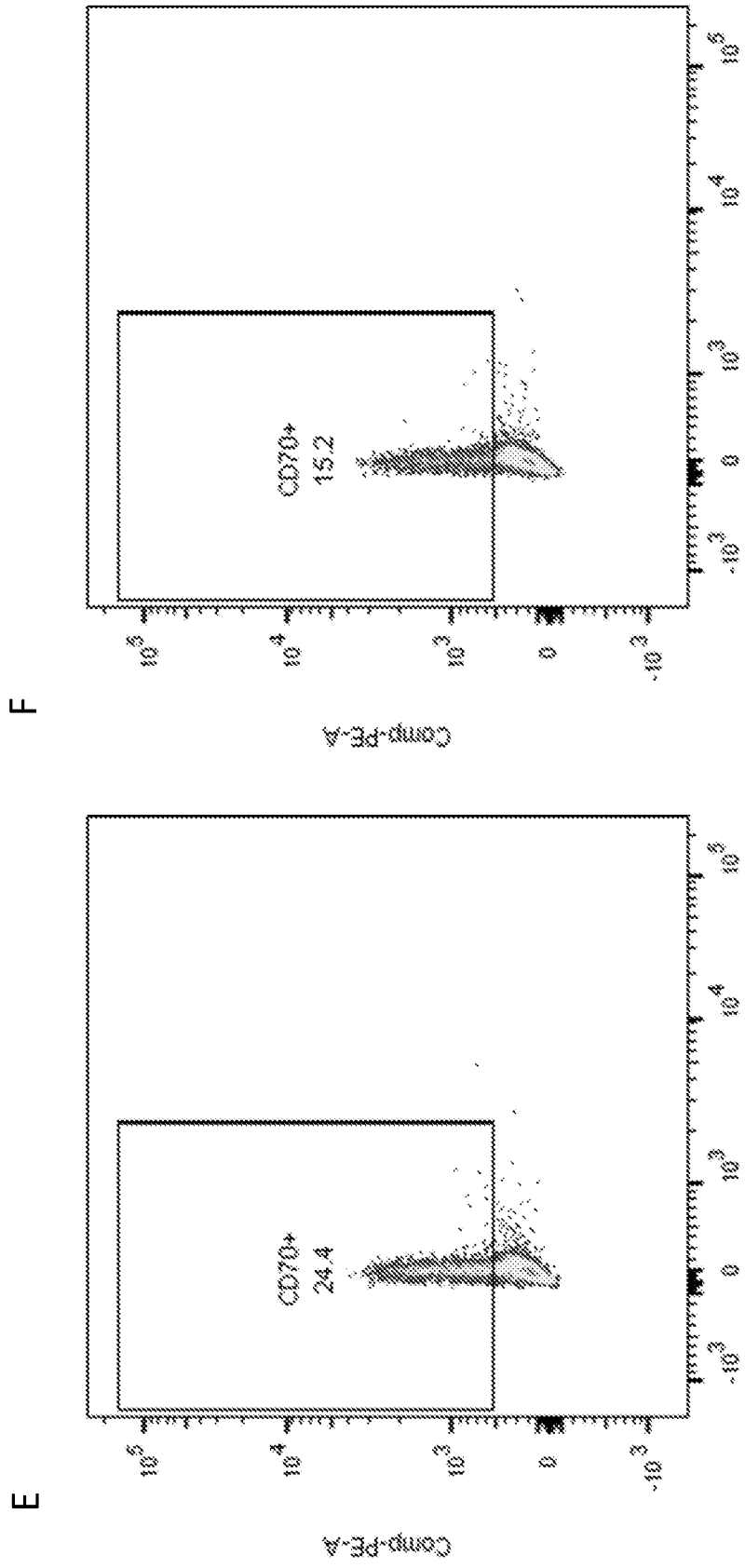
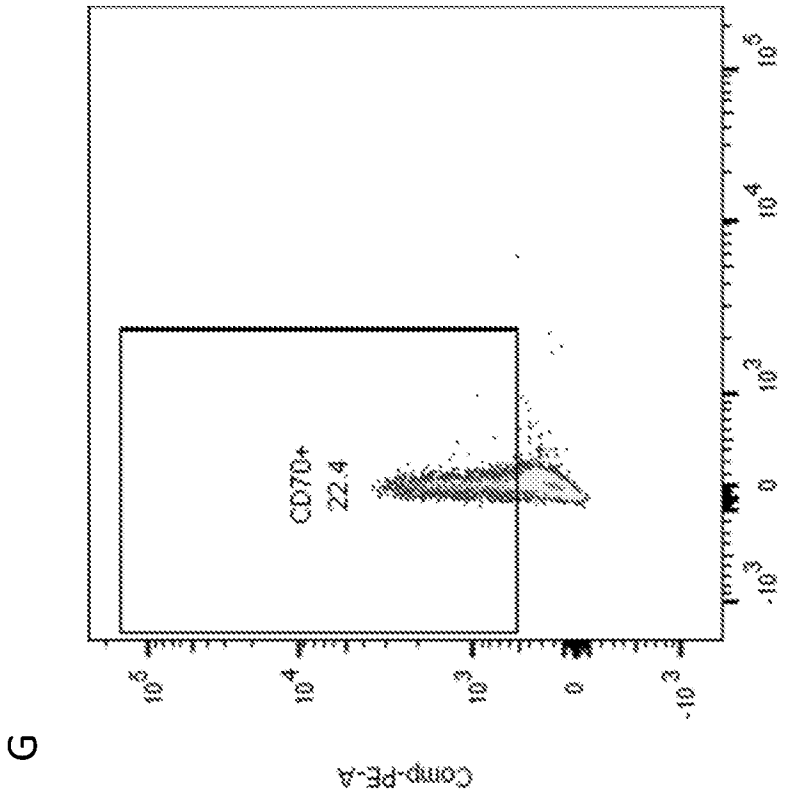


Figure 43G-43H



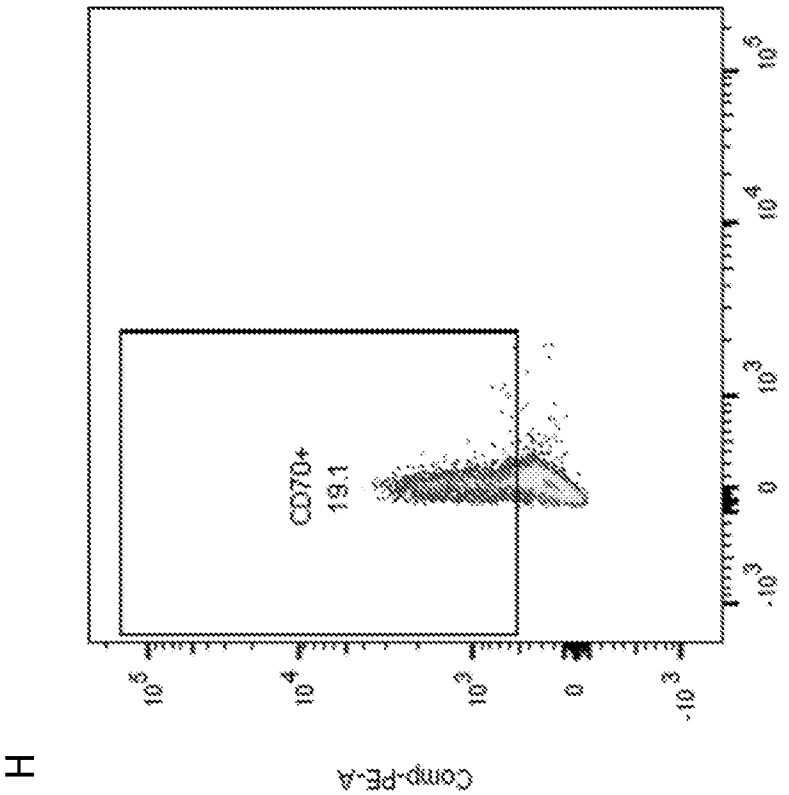


Figure 43I

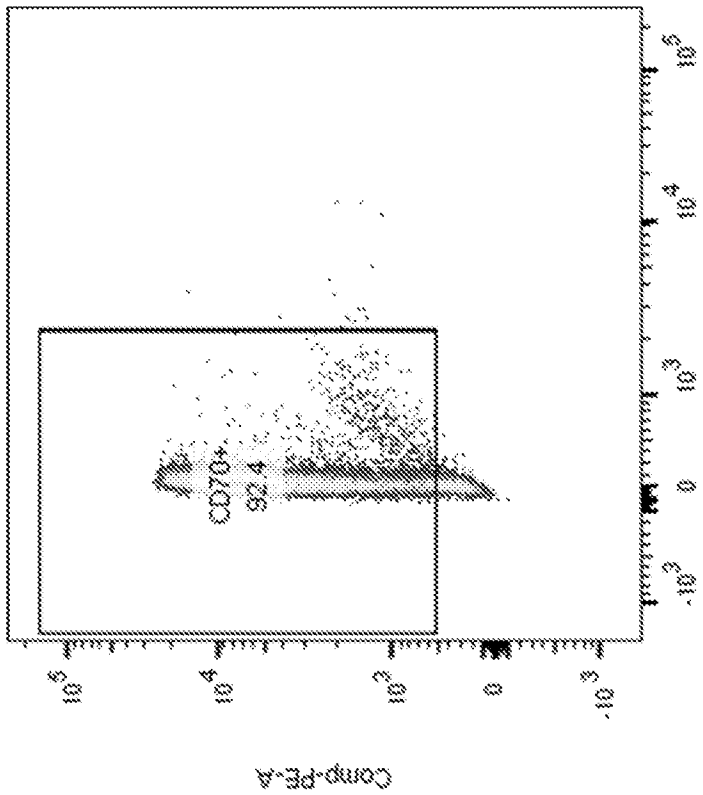


Figure 44A

A

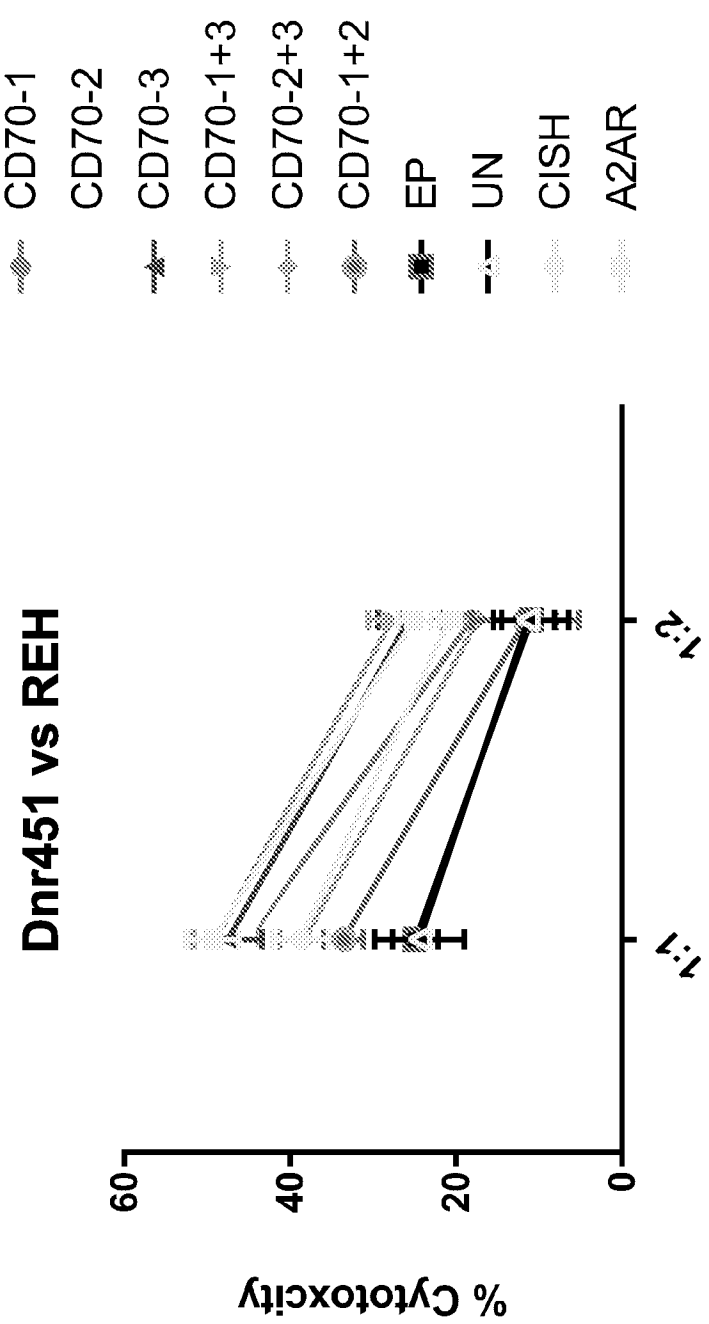

Dnr451 vs REH
% Cytotoxicity
60
40
20
0
1:1
1:2
CD70-1
CD70-2
CD70-3
CD70-1+3
CD70-2+3
CD70-1+2
EP
UN
CISH
A2AR

Figure 44B-C

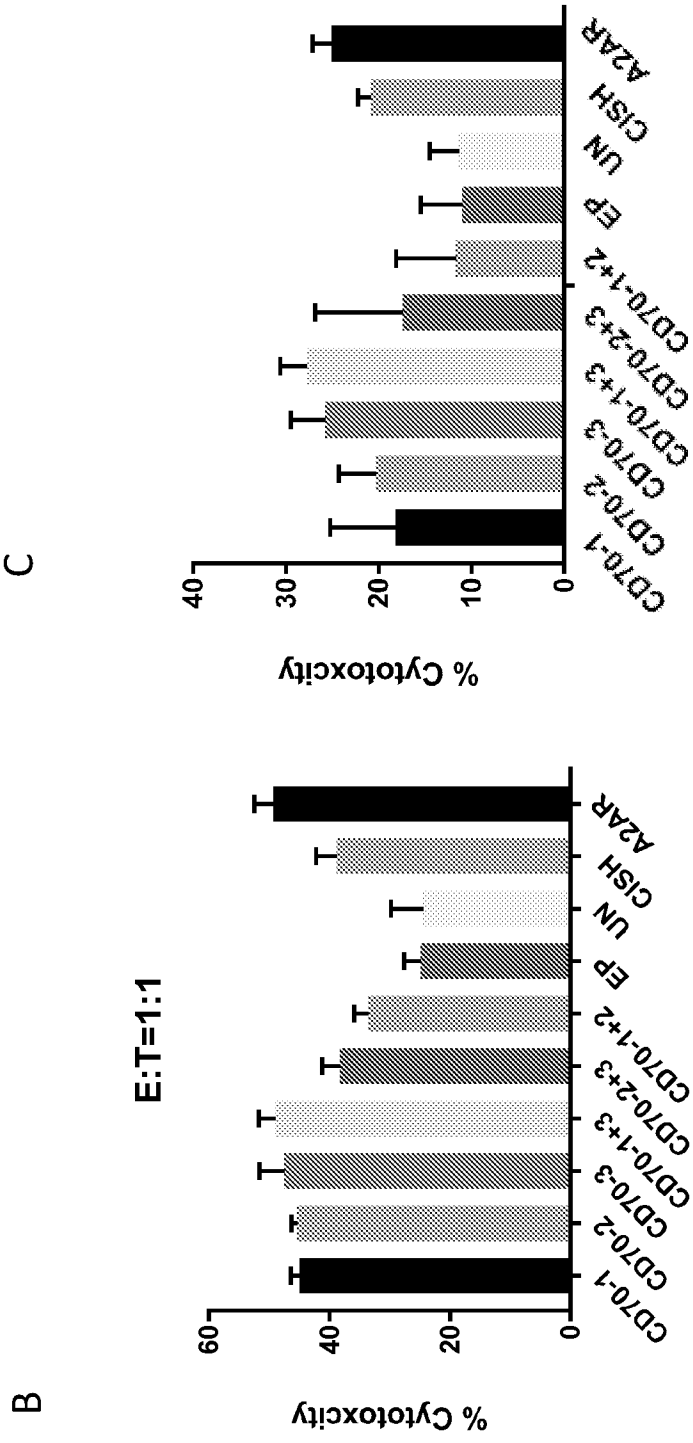
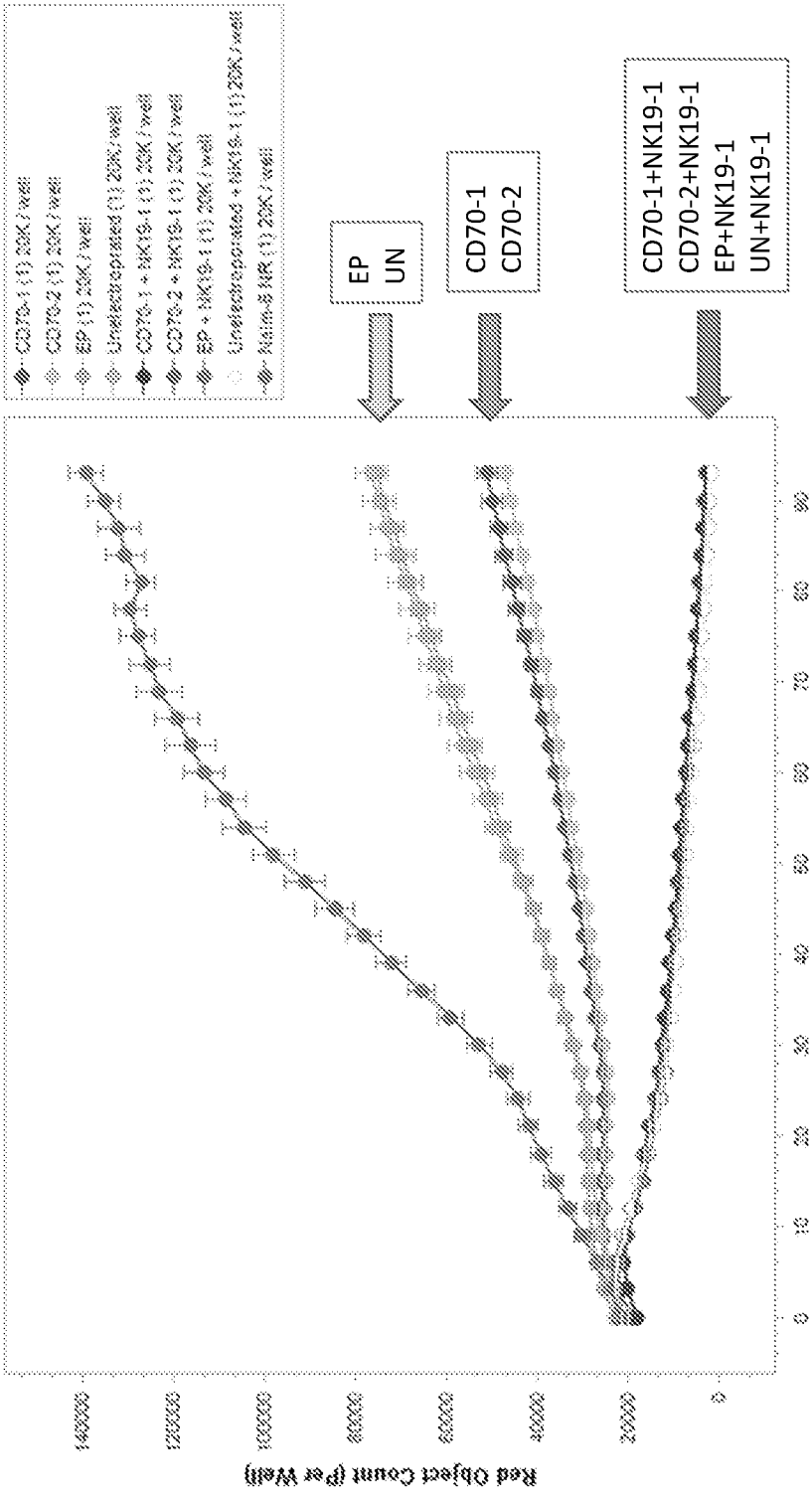

B
% Cytotoxicity
E:T=1:1
0
20
40
60
CD70-1
CD70-2
CD70-3
CD70-1+3
CD70-2+3
CD70-1+2
EP
UN
CISH
A2AR
C
% Cytotoxicity
0
10
20
30
40
CD70-1
CD70-2
CD70-3
CD70-1+3
CD70-2+3
CD70-1+2
EP
UN
CISH
A2AR

Figure 44D



E:T=1:1

Figure 45A

A

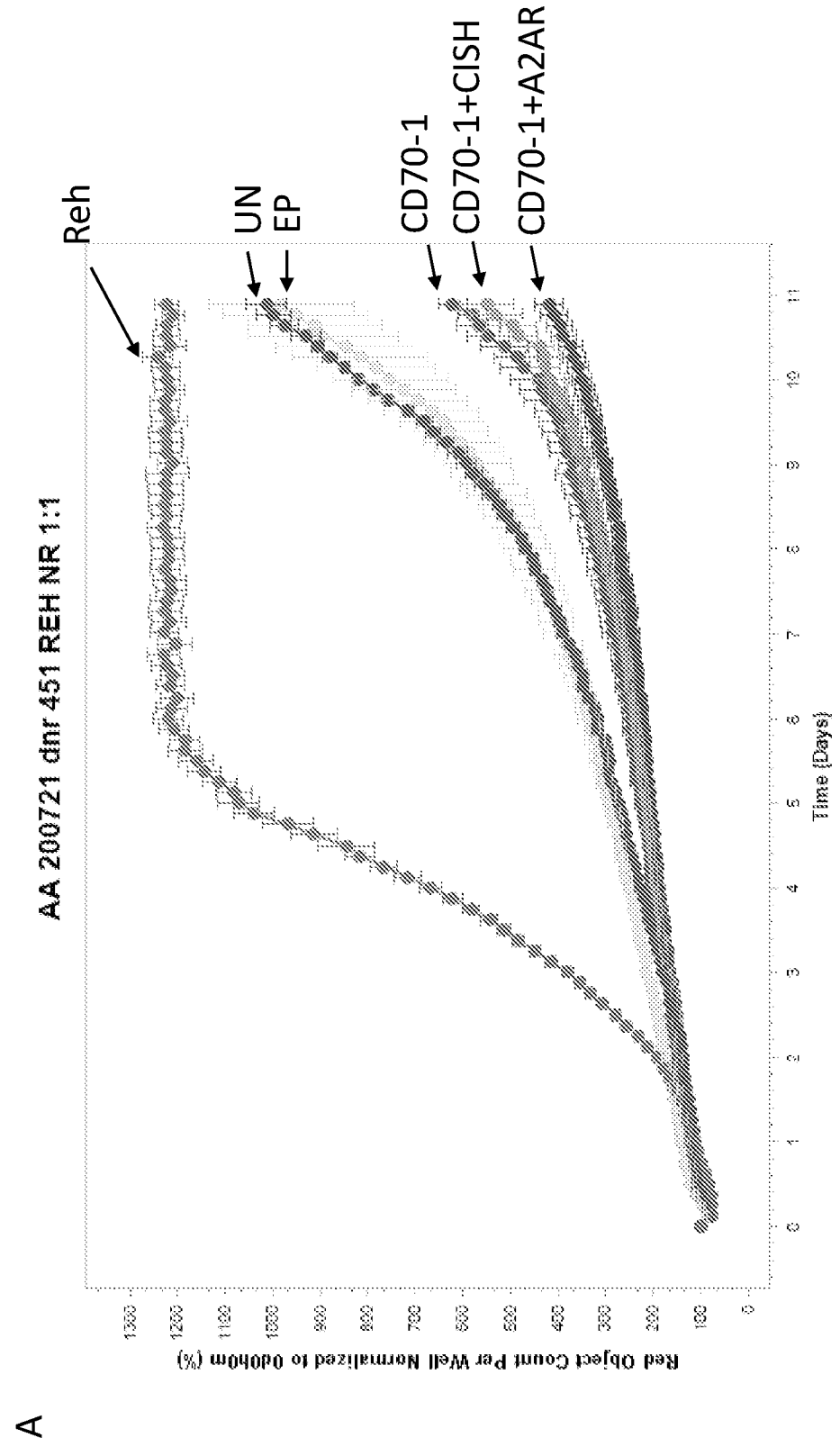

AA 200721 dnr 451 REH NR 1:1
Reh
UN
EP
CD70-1
CD70-1+CISH
CD70-1+A2AR
Red Object Count Per Well Normalized to 0dohom (%)
Time (Days)

Figure 45B

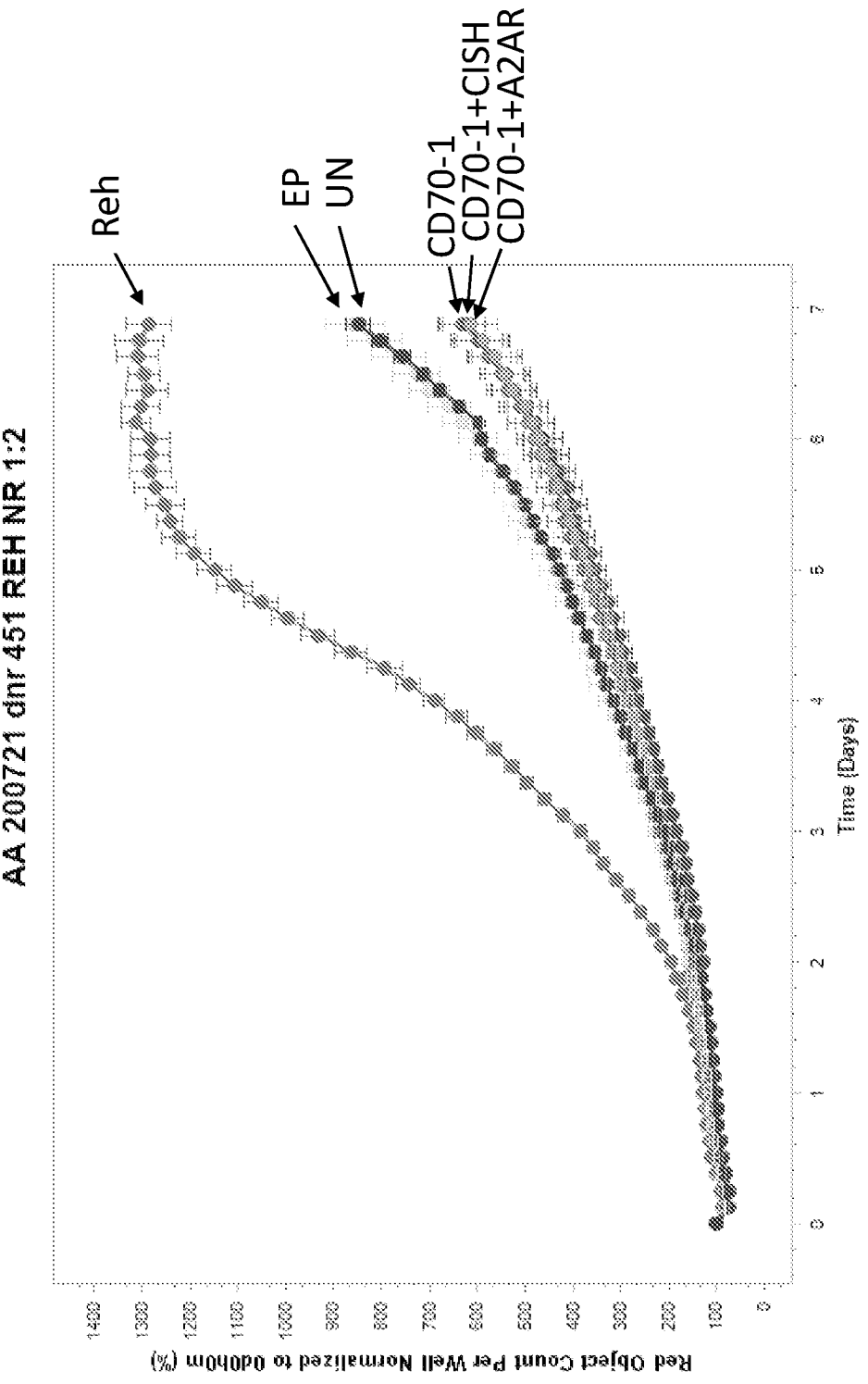

B
AA 200721 dnr 451 REH NR 1:2
Red Object Count Per Well Normalized to 0d0h0m (%)
Time (Days)
Reh
EP
UN
CD70-1
CD70-1+CISH
CD70-1+A2AR

Figure 46A-46B

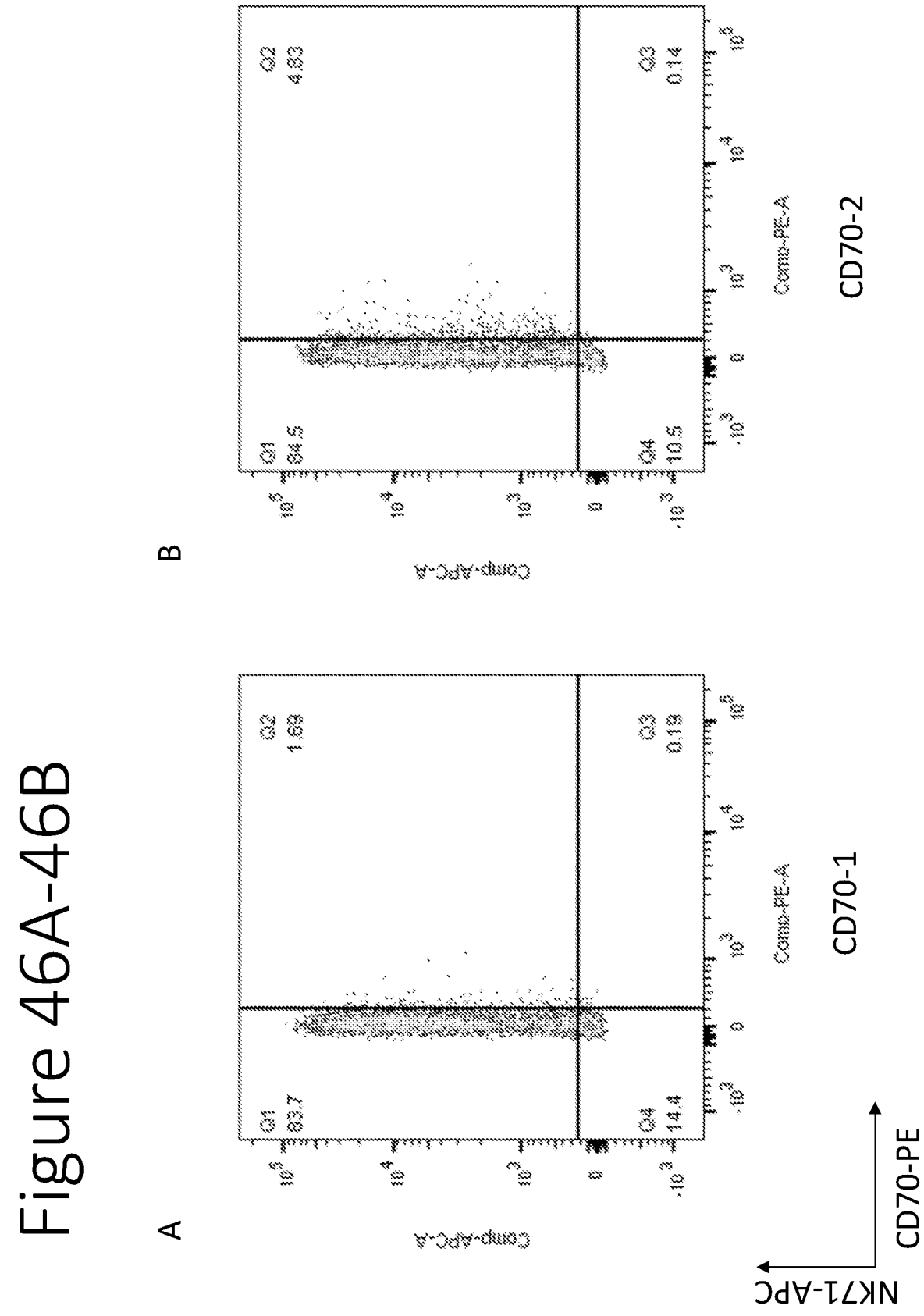


Figure 46C-46D

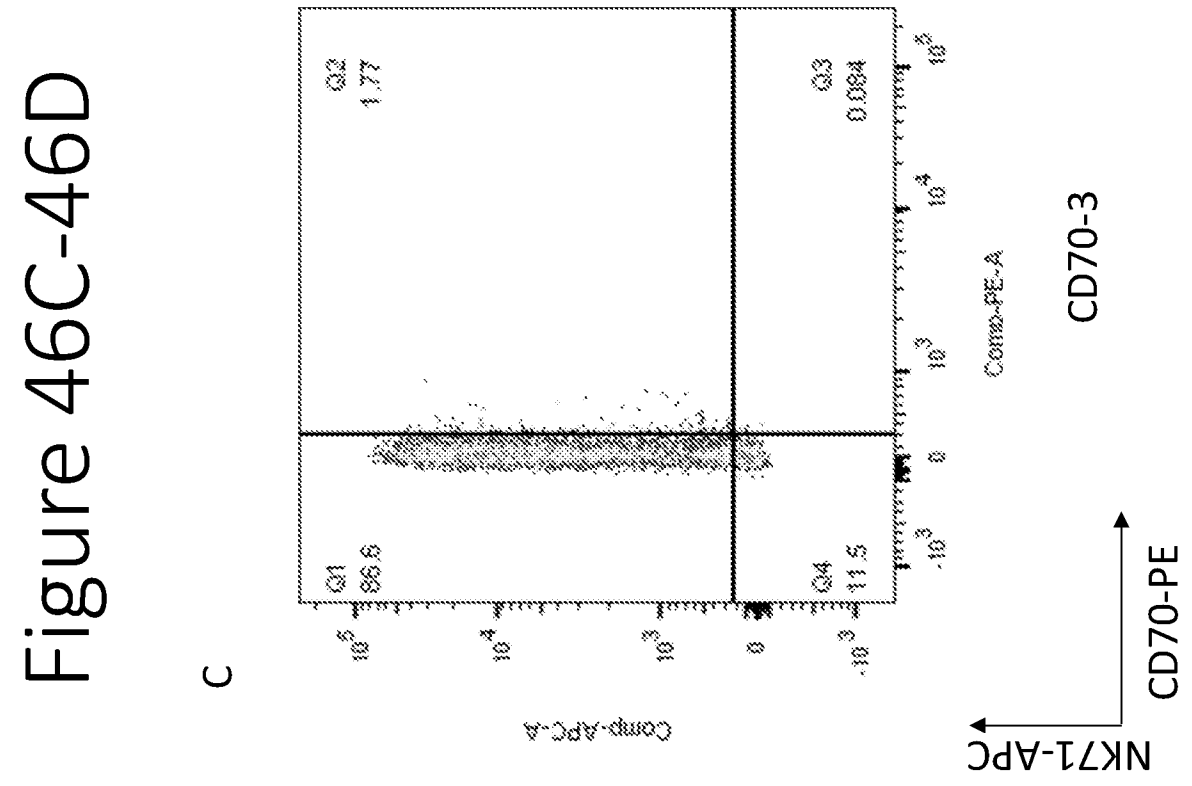


Figure 46E-46F

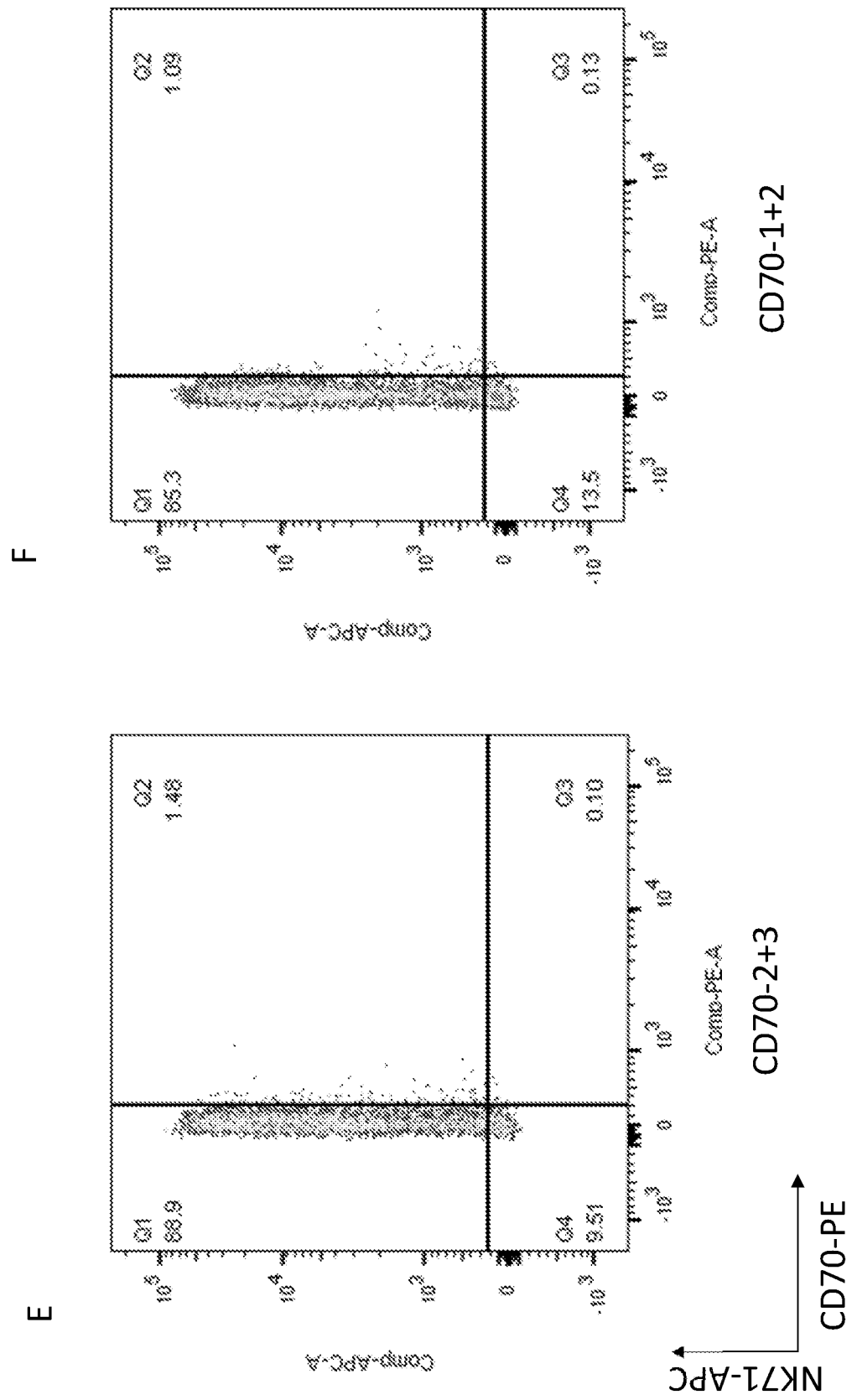


Figure 46G-46H

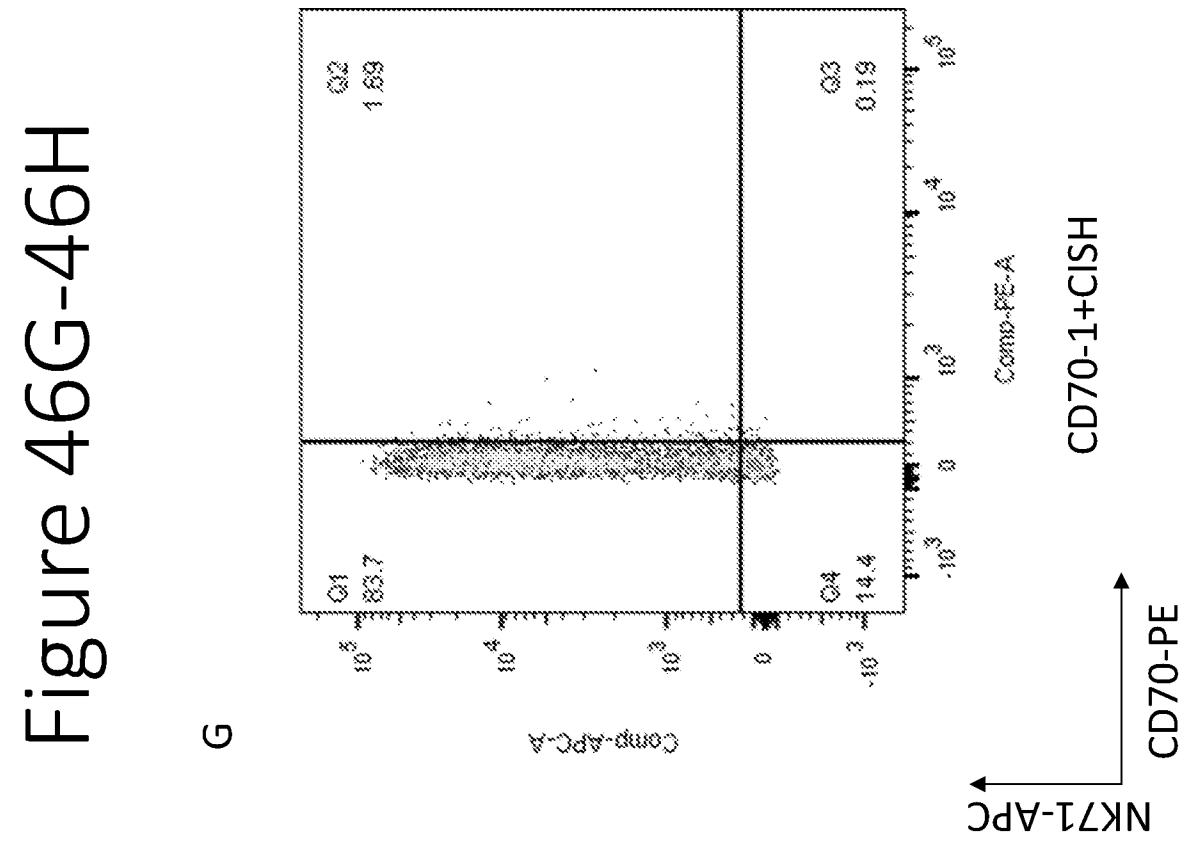


Figure 46I-46J

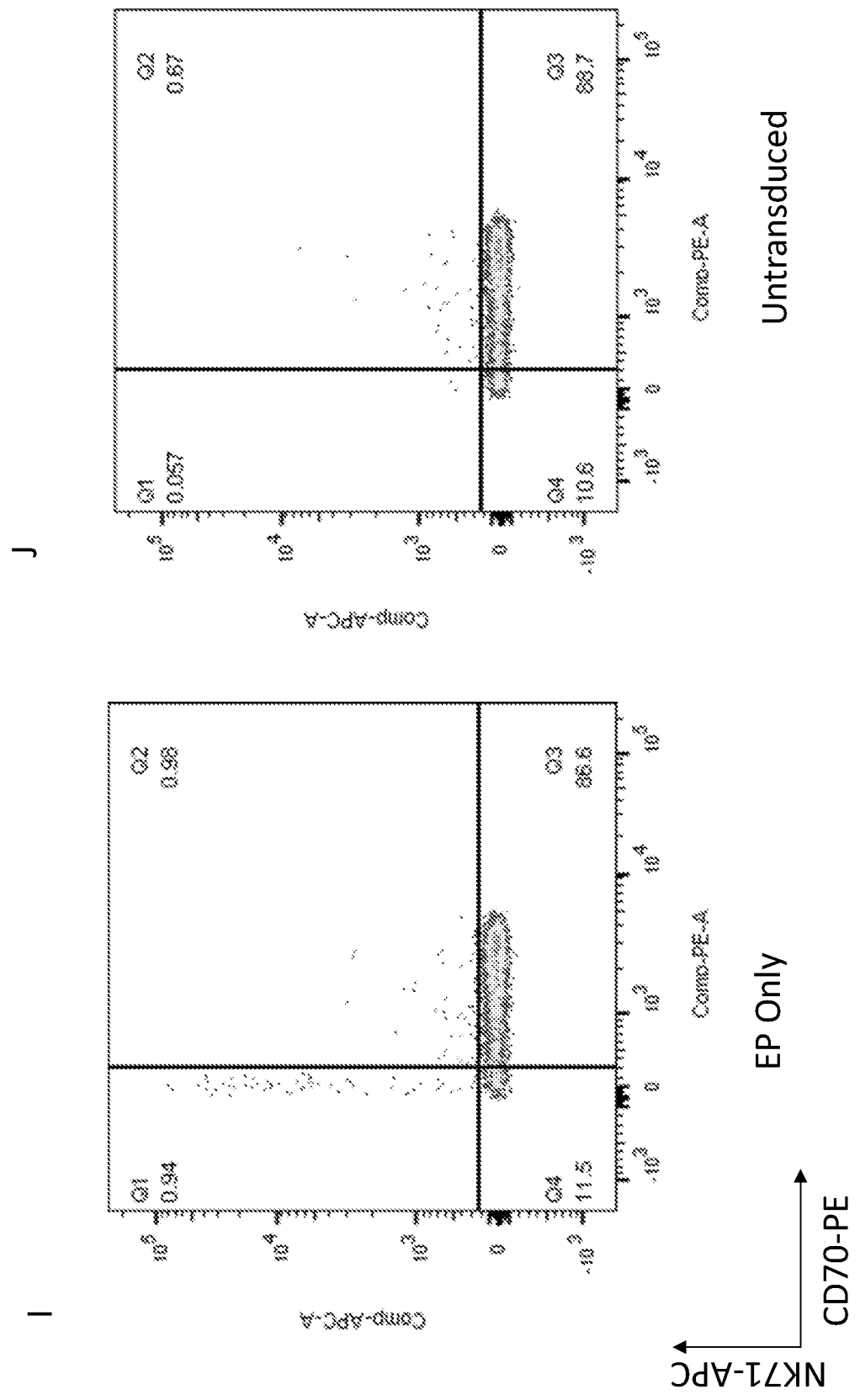


Figure 47A

A

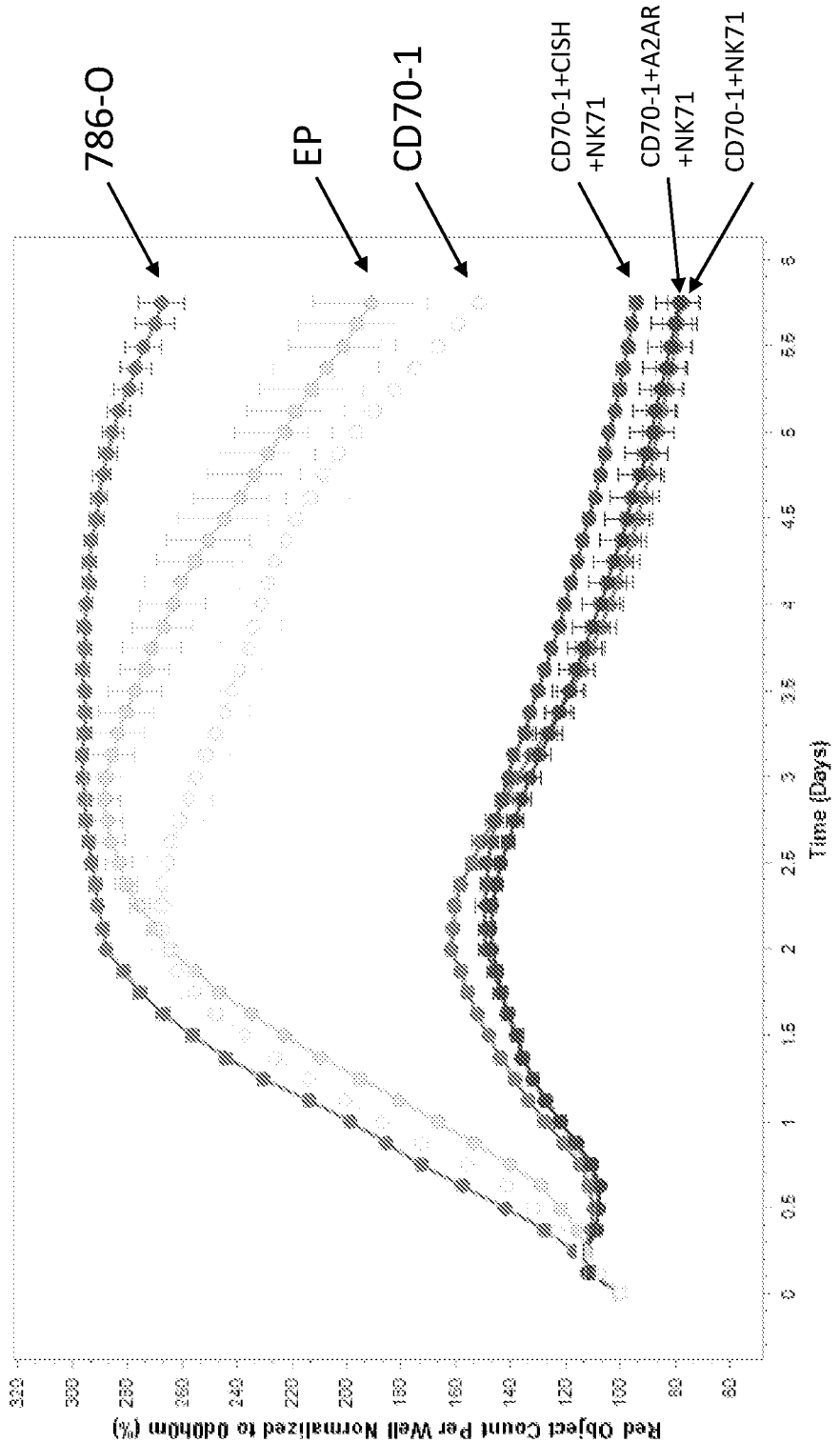

AA 200728 dnr 451 786-O NR 1:2
786-O
EP
CD70-1
CD70-1+CISH +NK71
CD70-1+A2AR +NK71
CD70-1+NK71
Red Object Count Per Well Normalized to 0dohm (%)
Time (Days)

Figure 47B

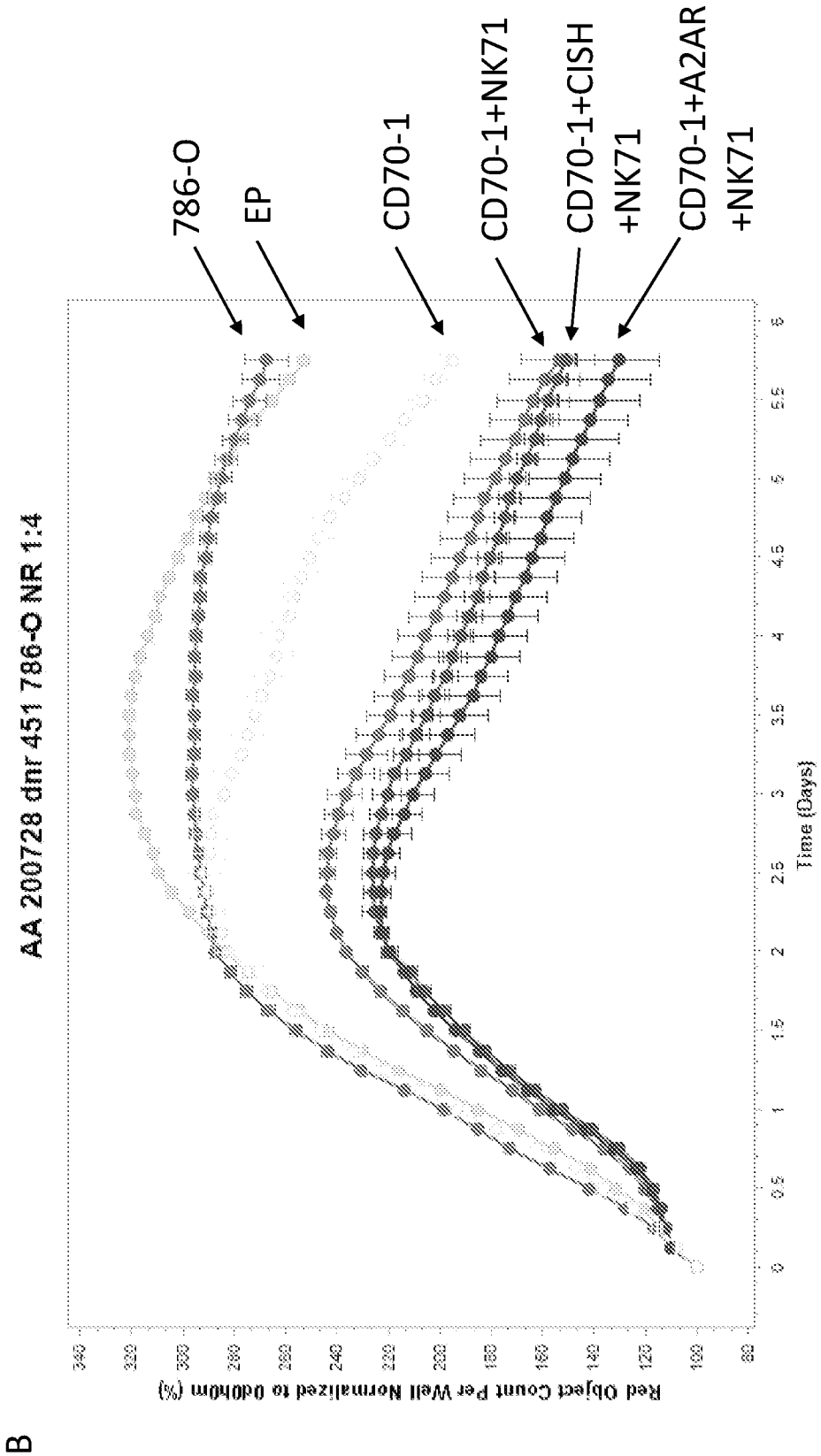

B
AA 200728 dnr 451 786-O NR 1:4
786-O
EP
CD70-1
CD70-1+NK71
CD70-1+CISH +NK71
CD70-1+A2AR +NK71
Red Object Count Per Well Normalized to 0d0h0m (%)
Time (Days)

Figure 47C

c

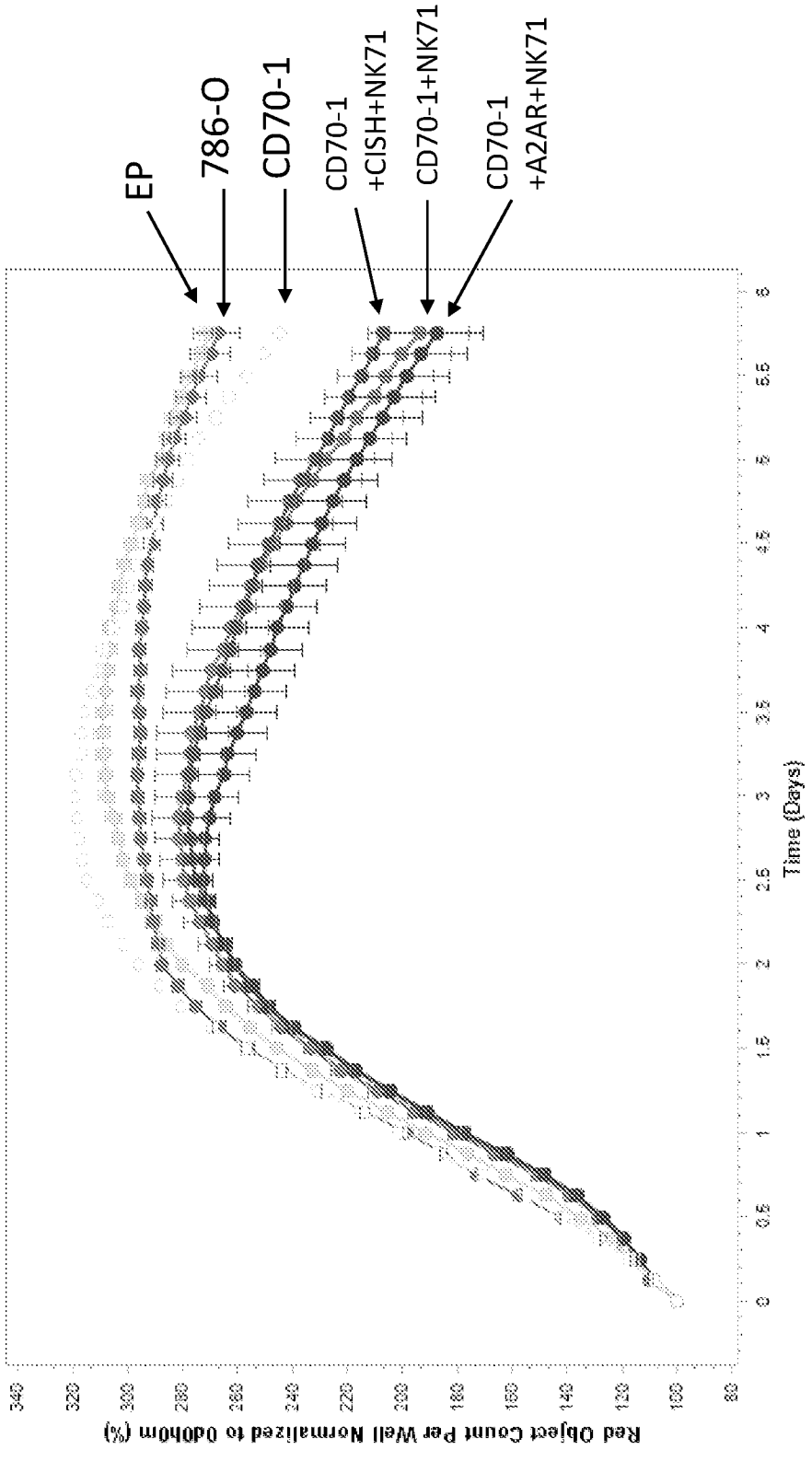

AA 200728 dnr 451 786-O NR 1:8
Red Object Count Per Well Normalized to 0d0h0m (%)
Time (Days)
EP
786-O
CD70-1
CD70-1 +CISH+NK71
CD70-1+NK71
CD70-1 +A2AR+NK71

Figure 47D

D

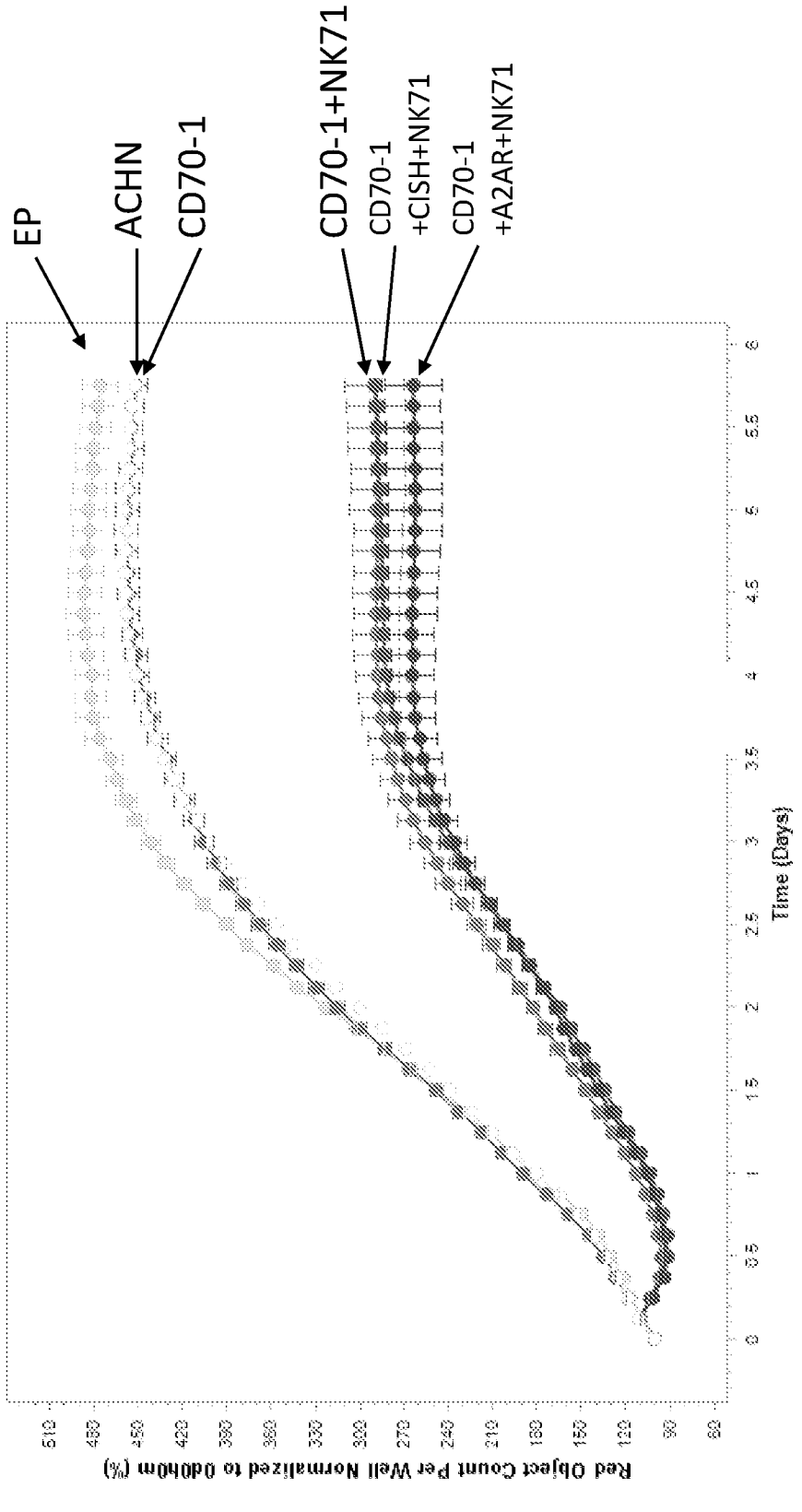

AA 200728 dnr 451 ACHN NR 1:2
EP
ACHN
CD70-1
CD70-1+NK71
CD70-1 +CISH+NK71
CD70-1 +A2AR+NK71
Red Object Count Per Well Normalized to 0d0h0m (%)
Time (Days)

Figure 47E

E

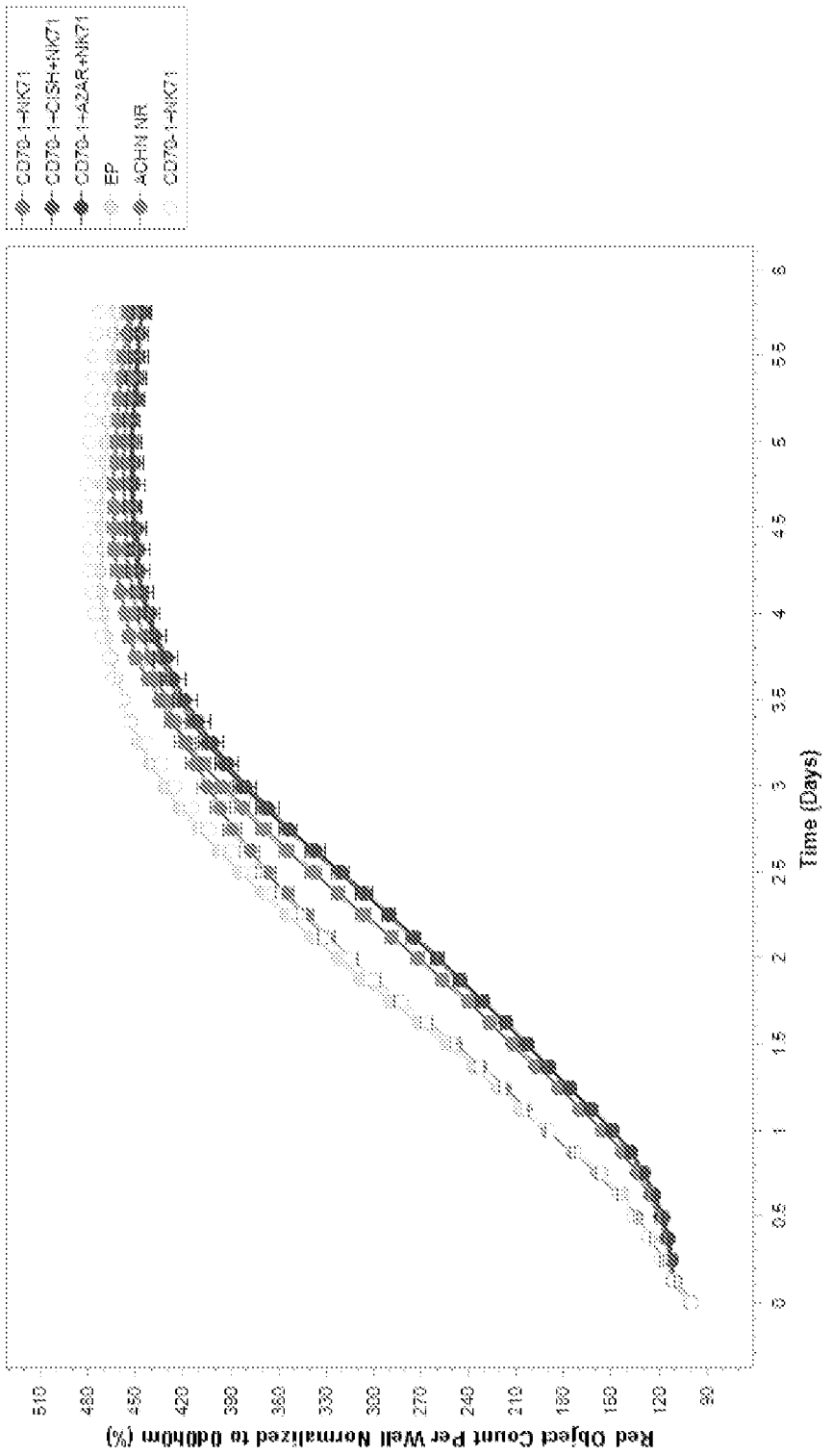

AA 200728 dnr 451 ACHN NR 1:4
Red Object Count Per Well Normalized to 0dhOm (%)
Time (Days)
CD70-1-NK71
CD70-1-CISH+NK71
CD70-1-A2AR+NK71
EP
ACHN NR
CD70-1-NK71

Figure 47F

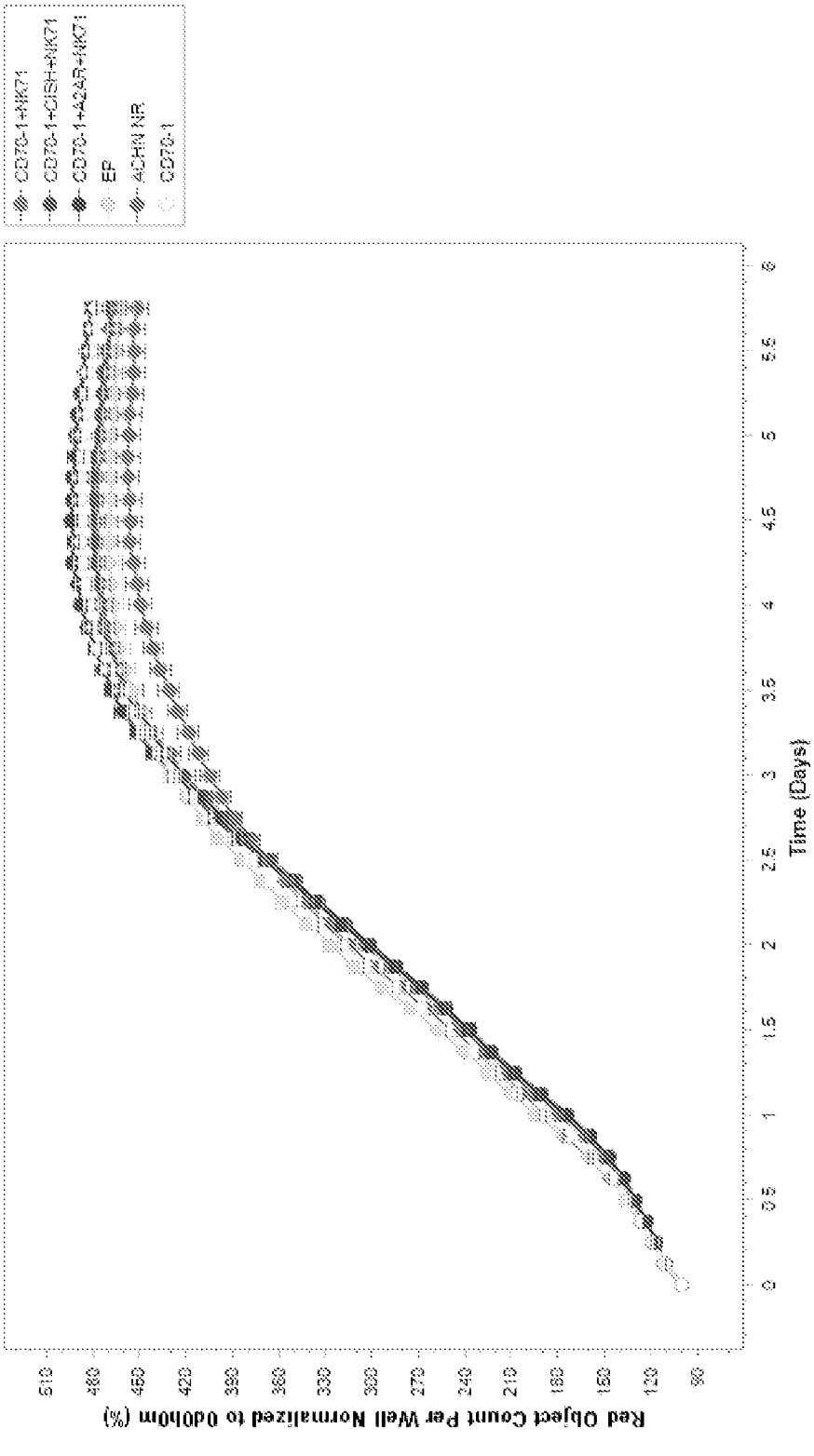
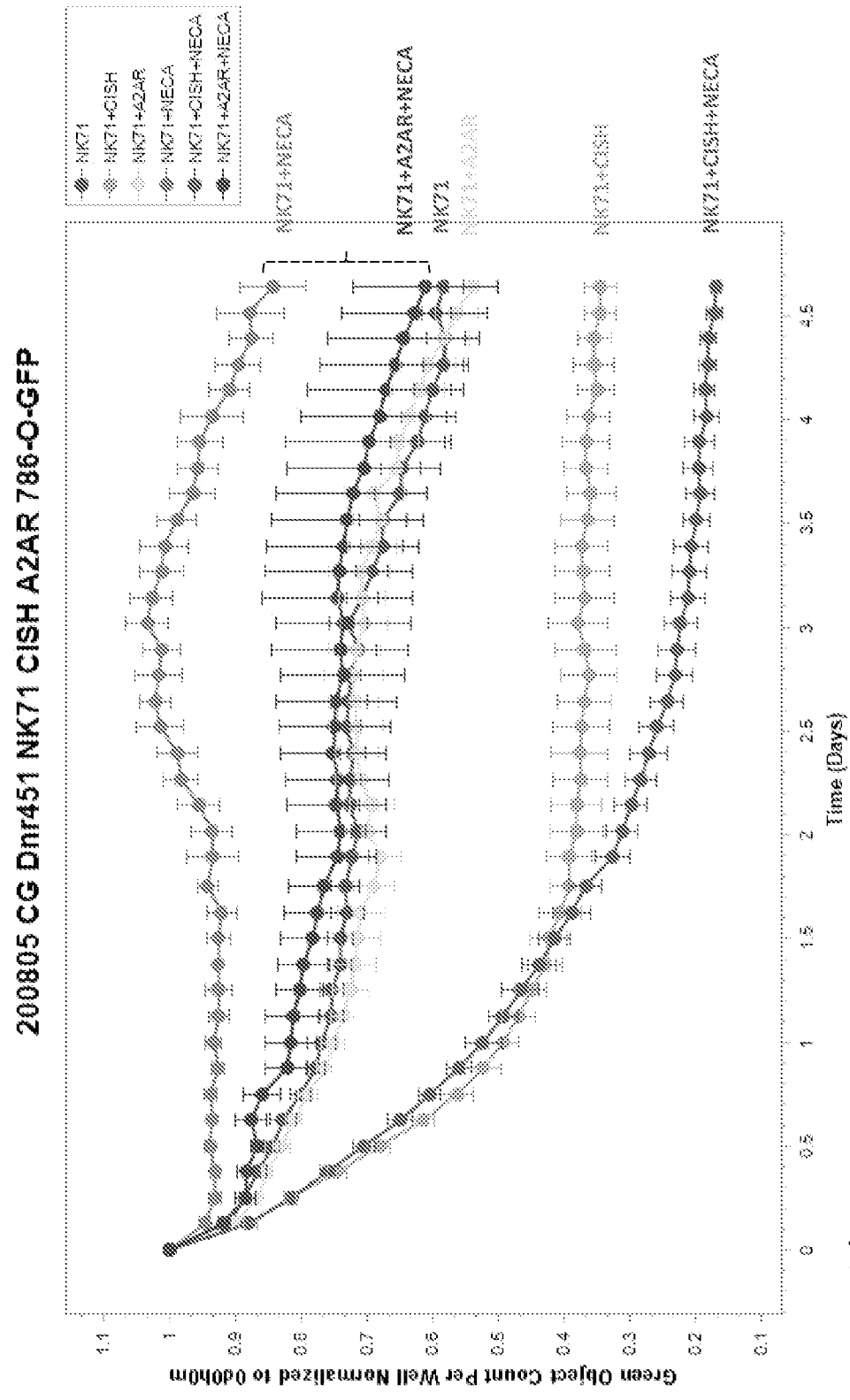

AA 200728 dnr 451 ACHN NR 1:8
CD70-1+NK71
CD70-1+CISH+NK71
CD70-1+A2AR+NK71
EP
ACHN NR
CD70-1
Red Object Count Per Well Normalized to 0dohom (%)
Time (Days)
510
480
450
420
390
360
330
300
270
240
210
180
150
120
90
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
5
5.5
6

Figure 48A



E:T=1:1 at 72 hrs
NECA at 1 μM

Figure 48B

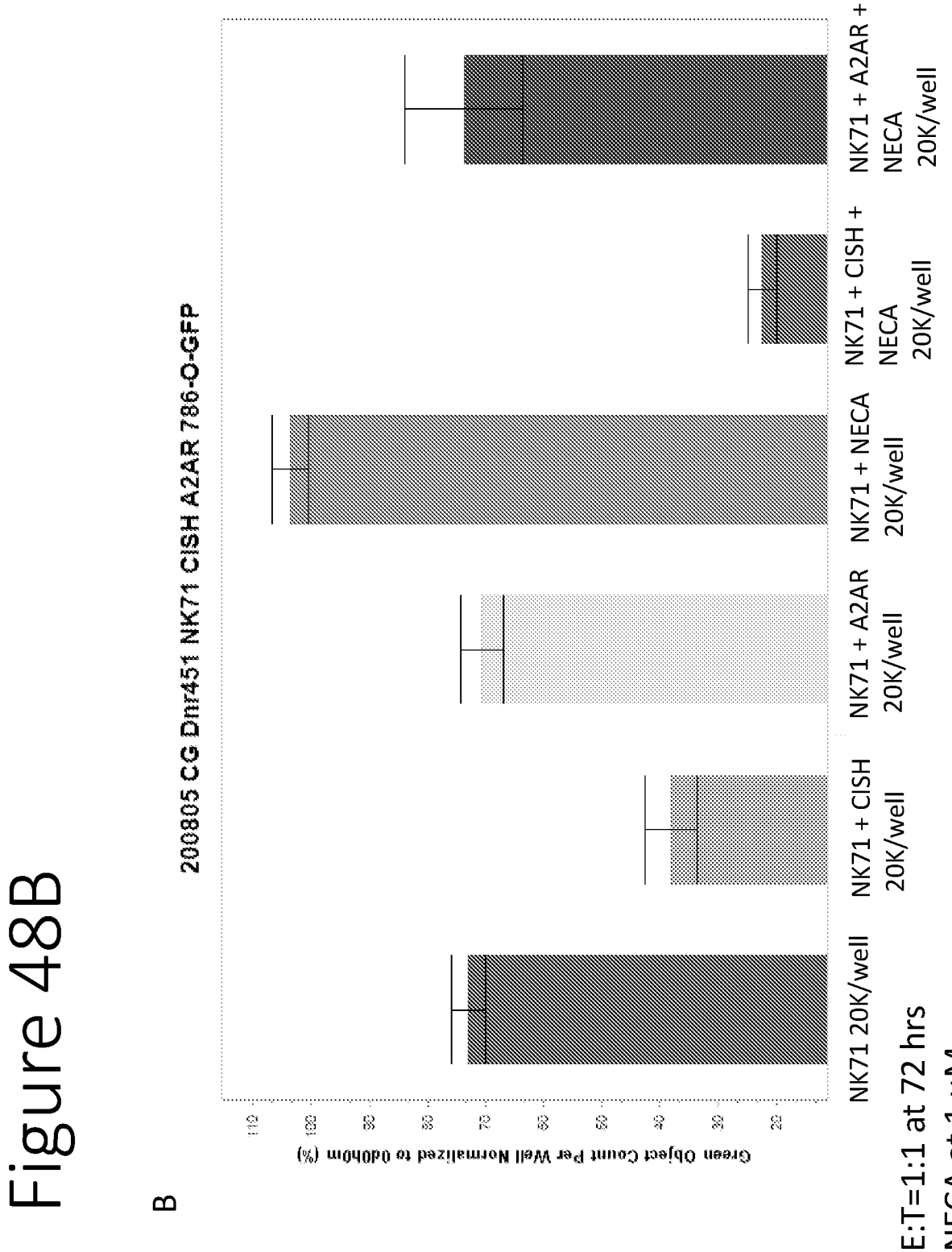
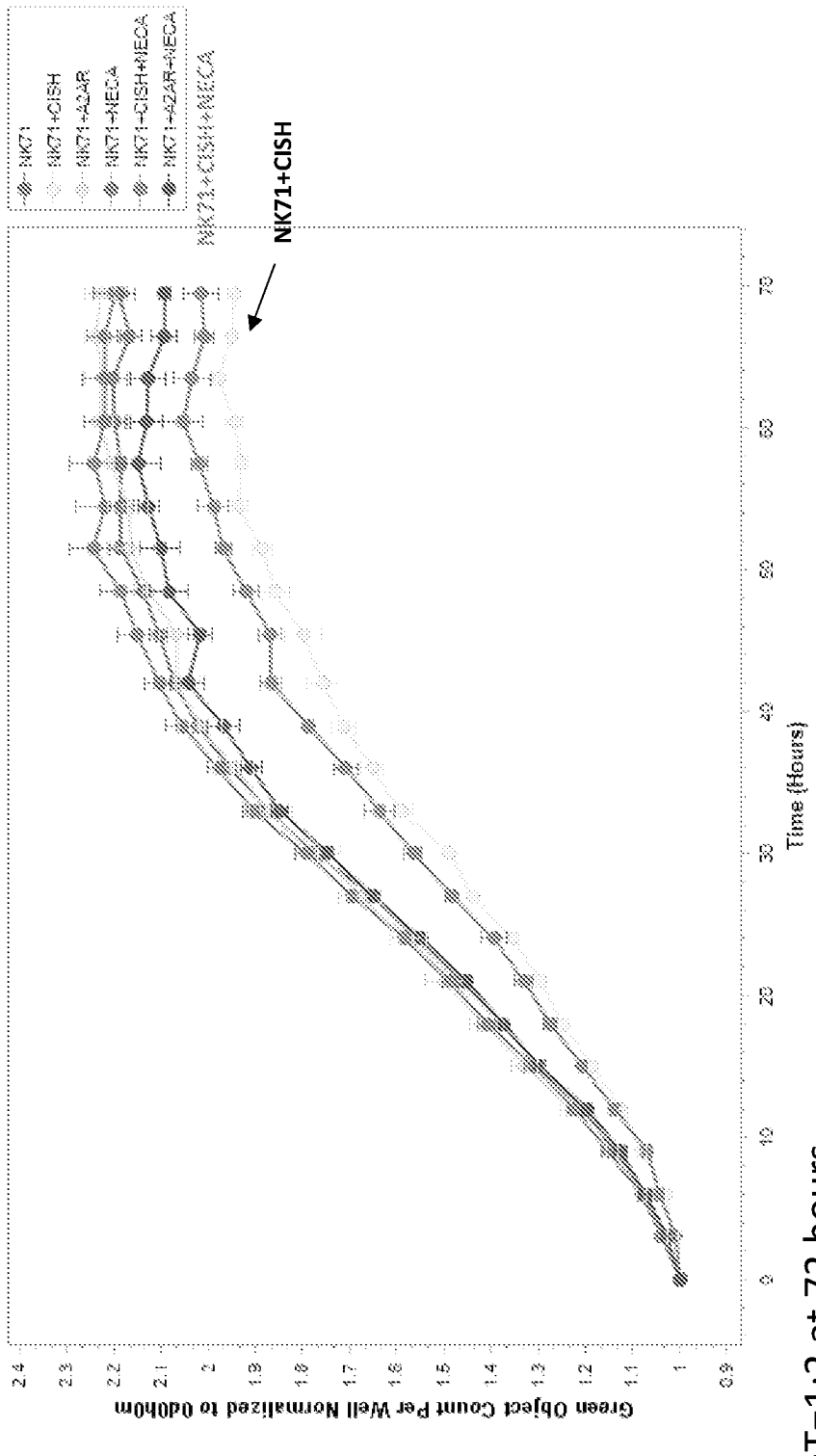

B
200805 CG Dnr451 NK71 CISH A2AR 786-O-GFP
Green Object Count Per Well Normalized to 0d0h0m (%)
110
100
90
80
70
60
50
40
30
20
NK71 20K/well
NK71 + CISH 20K/well
NK71 + A2AR 20K/well
NK71 + NECA 20K/well
NK71 + CISH + NECA 20K/well
NK71 + A2AR + NECA 20K/well
E:T=1:1 at 72 hrs
NECA at 1 µM

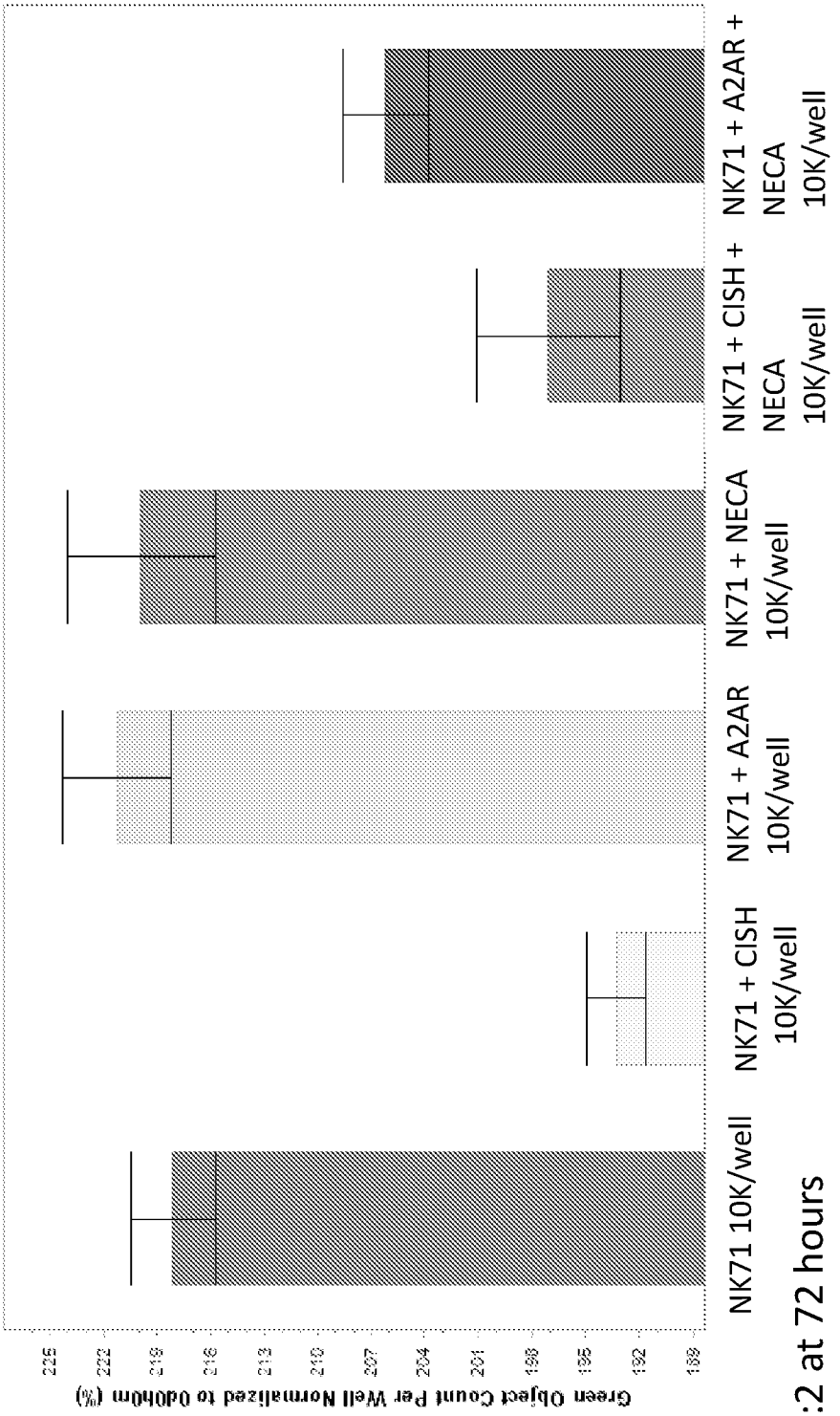
Figure 48C



C

E:T=1:2 at 72 hours
NECA at 0.75 µM

Figure 48D



E:T=1:2 at 72 hours
NECA at 0.75 µM

Figure 49A

A


NK71
Anti CD70 4F11 scFv
2A
mIL-15

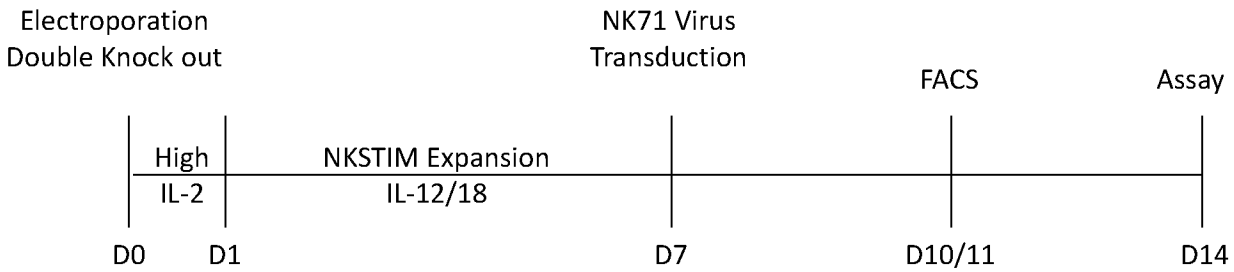

Electroporation
Double Knock out
NK71 Virus
Transduction
FACS
Assay
High
IL-2
NKSTIM Expansion
IL-12/18
D0
D1
D7
D10/11
D14

Figure 49B

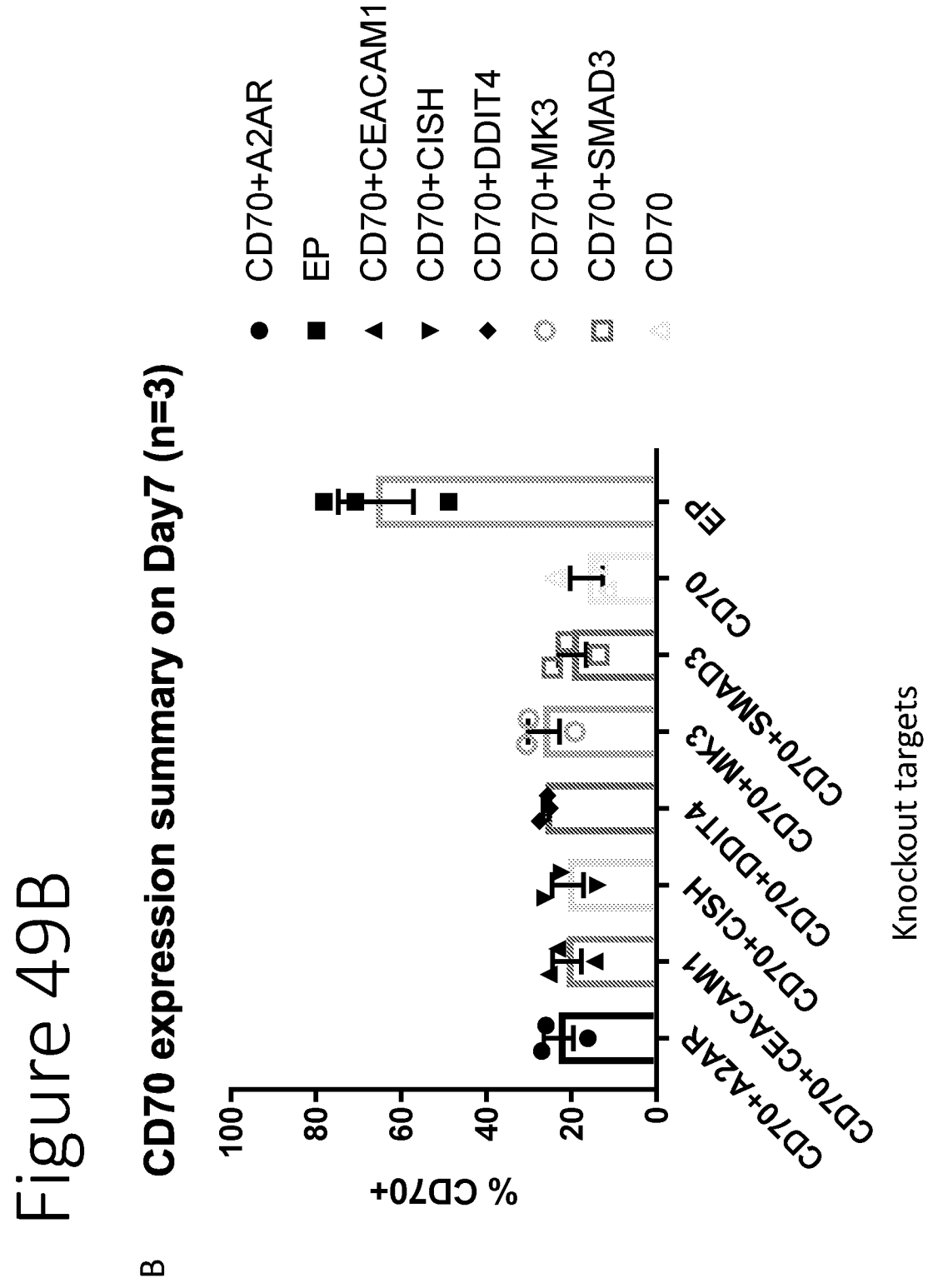
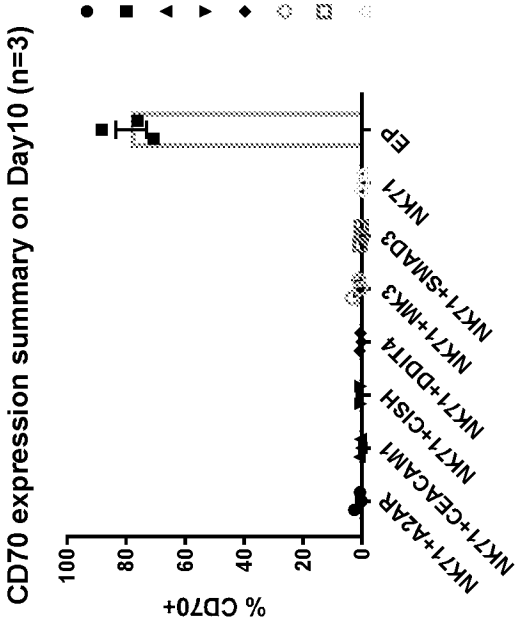
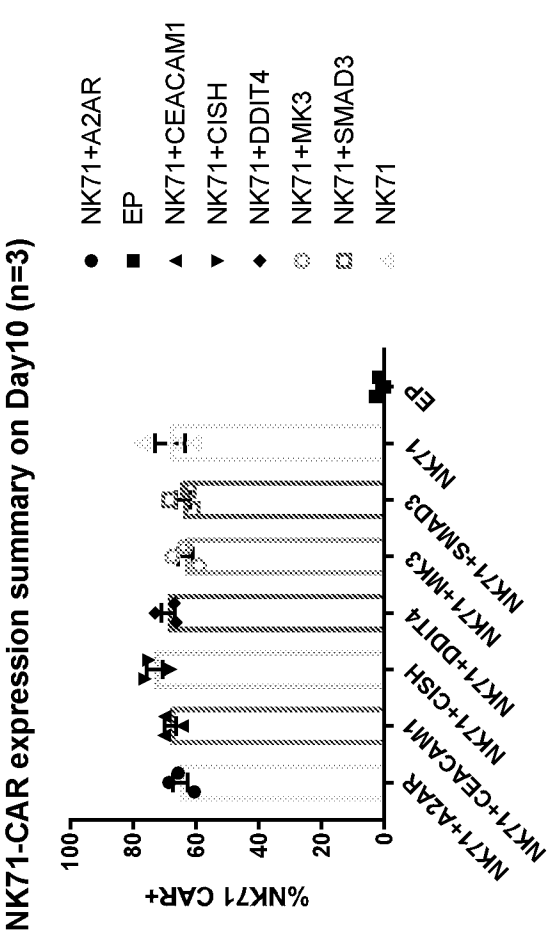

B
CD70 expression summary on Day7 (n=3)
% CD70+
100
80
60
40
20
0
CD70+A2AR
CD70+CEACAM1
CD70+CISH
CD70+DDIT4
CD70+MK3
CD70+SMAD3
CD70
EP
Knockout targets
CD70+A2AR
EP
CD70+CEACAM1
CD70+CISH
CD70+DDIT4
CD70+MK3
CD70+SMAD3
CD70

Figure 49C

C


CD70 expression summary on Day10 (n=3)
% CD70+
100
80
60
40
20
0
NK71+A2AR
EP
NK71+CEACAM1
NK71+CISH
NK71+DDIT4
NK71+MK3
NK71+SMAD3
NK71
NK71+A2AR
NK71+CEACAM1
NK71+CISH
NK71+DDIT4
NK71+MK3
NK71+SMAD3
NK71
EP


NK71-CAR expression summary on Day10 (n=3)
%NK71 CAR+
100
80
60
40
20
0
NK71+A2AR
EP
NK71+CEACAM1
NK71+CISH
NK71+DDIT4
NK71+MK3
NK71+SMAD3
NK71
NK71+A2AR
NK71+CEACAM1
NK71+CISH
NK71+DDIT4
NK71+MK3
NK71+SMAD3
NK71
EP

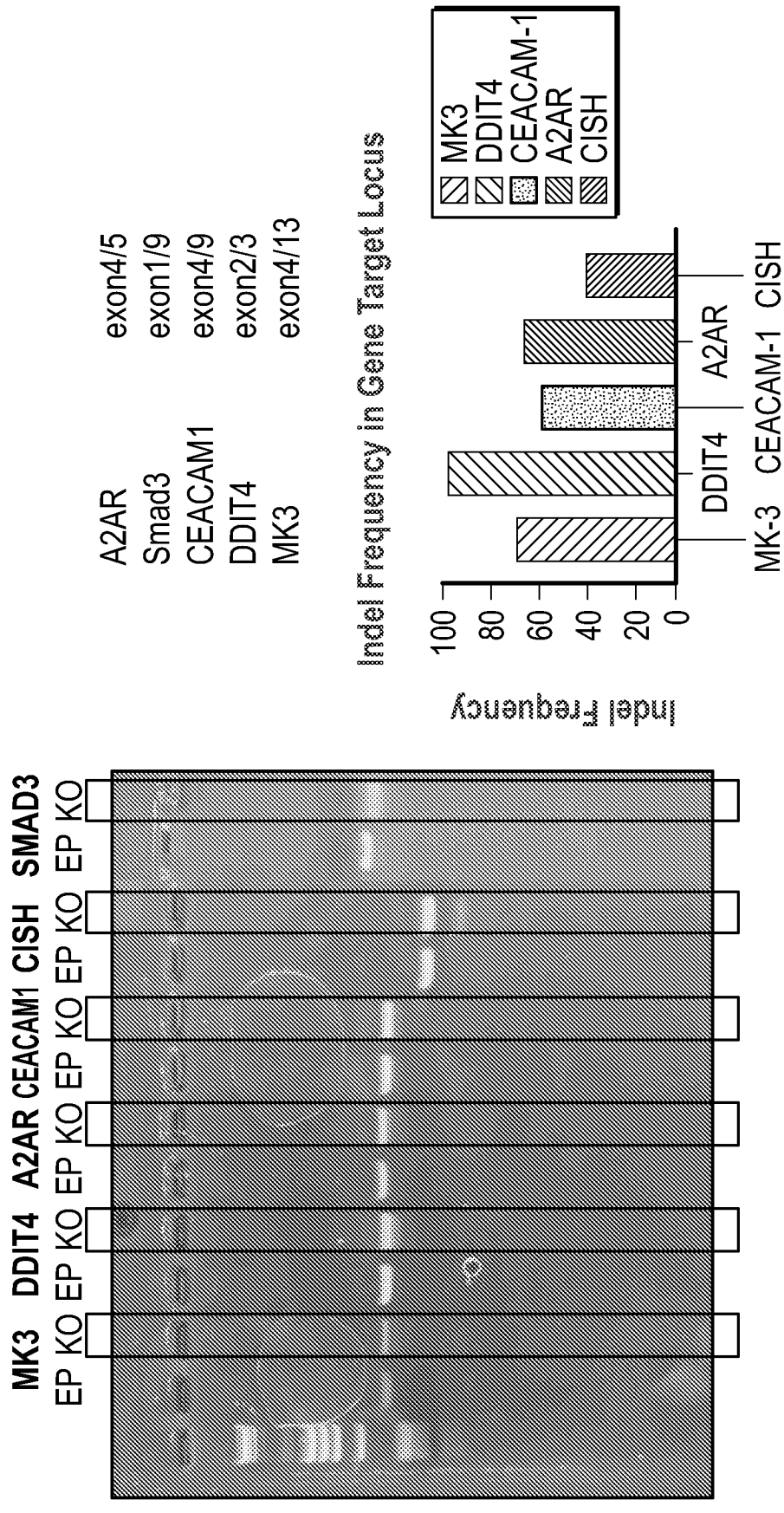

A2AR exon4/5
Smad3 exon1/9
CEACAM1 exon4/9
DDIT4 exon2/3
MK3 exon4/13
Indel Frequency in Gene Target Locus
MK3
DDIT4
CEACAM-1
A2AR
CISH
100
80
60
40
20
0
Indel Frequency
DDIT4
A2AR
MK-3 CEACAM-1 CISH
MK3 DDIT4 A2AR CEACAM1 CISH SMAD3
EP KO EP KO EP KO EP KO EP KO EP KO

FIG. 49D

Figure 49E

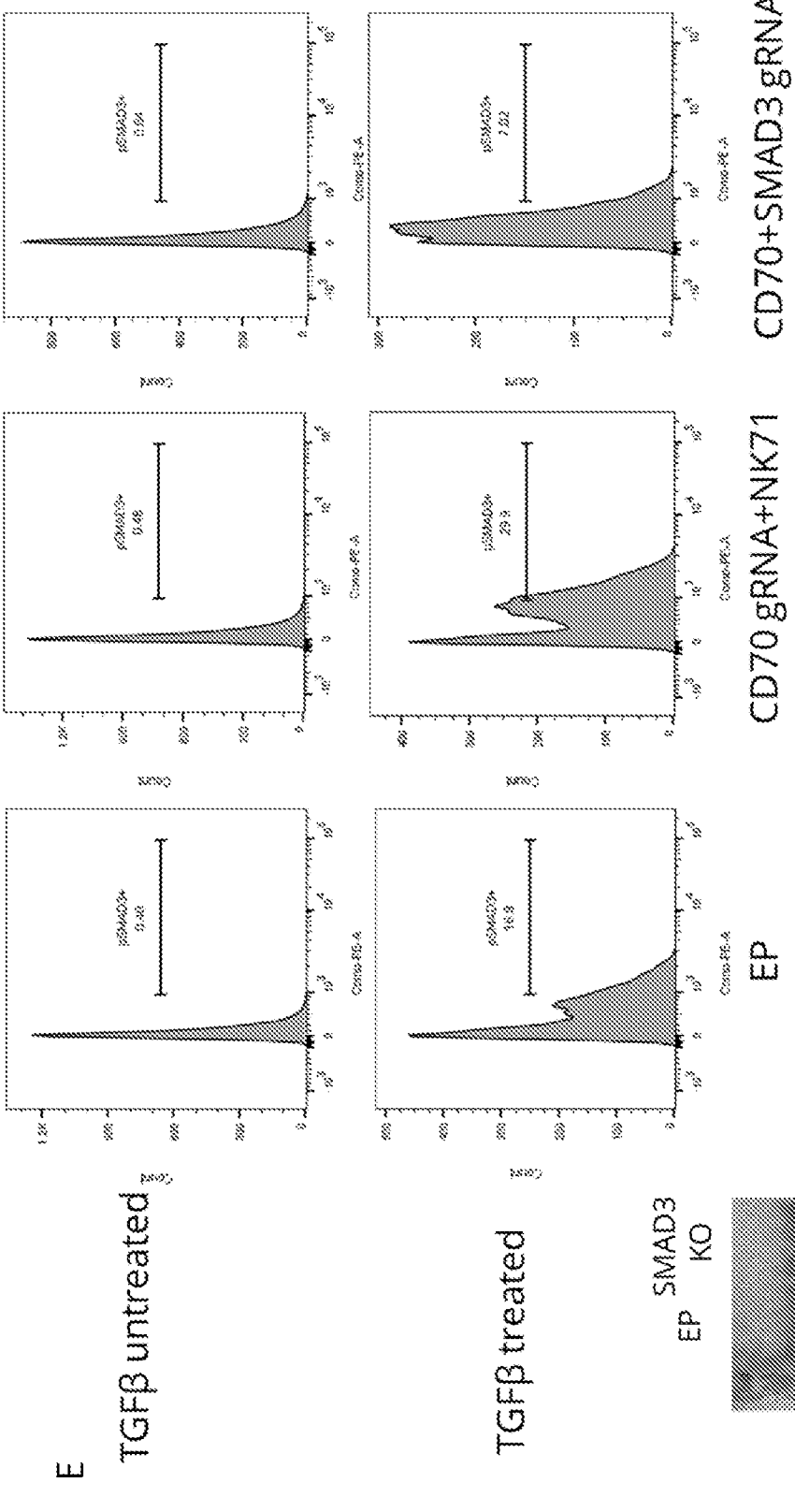
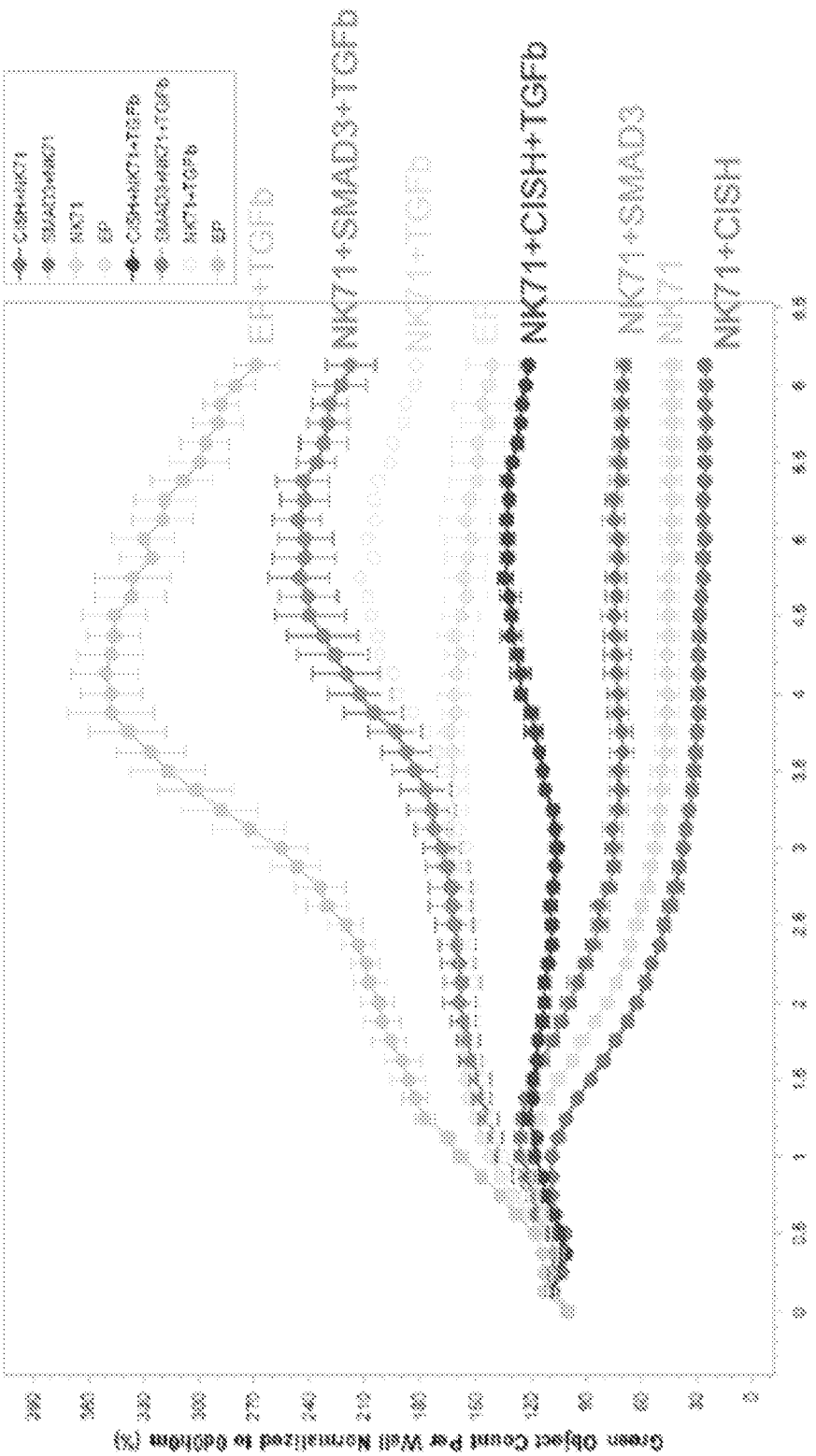
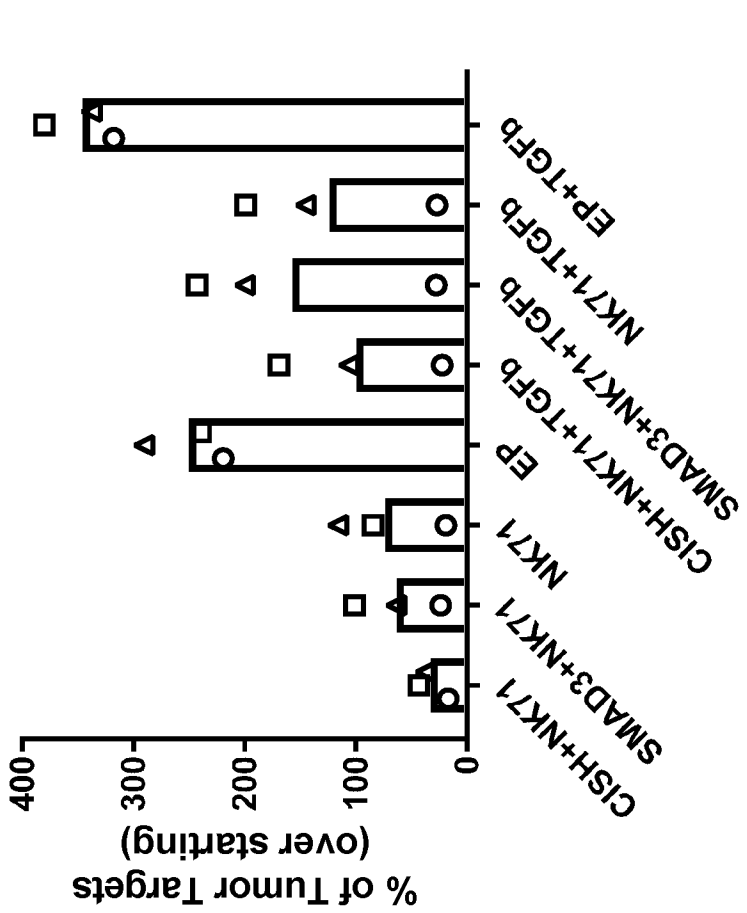

E
TGFβ untreated
TGFβ treated
EP
CD70 gRNA+NK71
CD70+SMAD3 gRNA+NK71
SMAD3 KO
EP
SSKD

Figure 49F



1:4 E:T; TGFb at 20 ng/mL

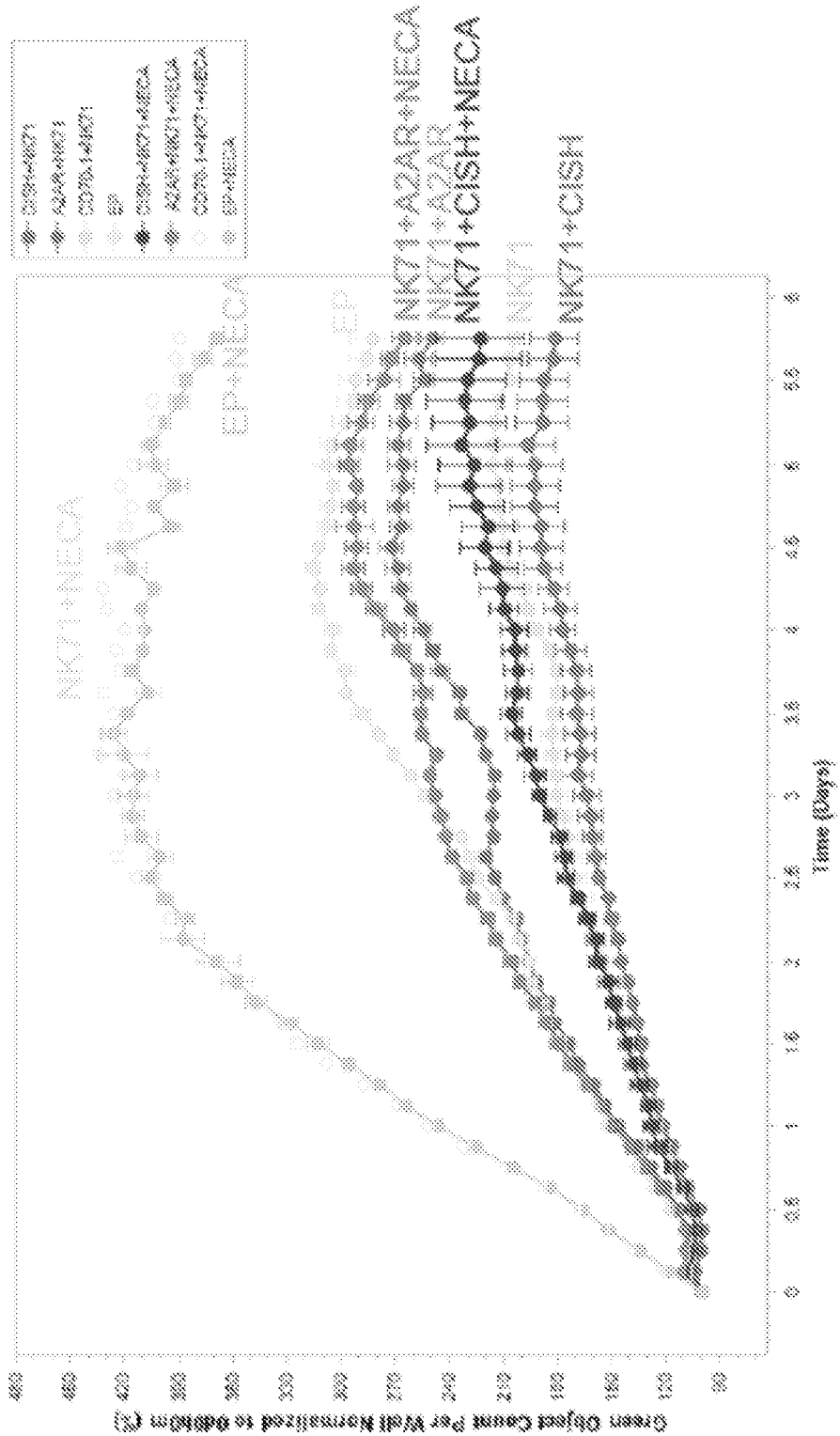
Figure 49G


CISH SMAD3 NK71 TGFb E:T=1:1 Day3
% of Tumor Targets (over starting)
400
300
200
100
0
CISH+NK71
SMAD3+NK71
NK71
EP
CISH+NK71+TGFb
SMAD3+NK71+TGFb
NK71+TGFb
EP+TGFb

G

Figure 49H

H



1:4 E:T; NECA at 10 uM

Figure 49I

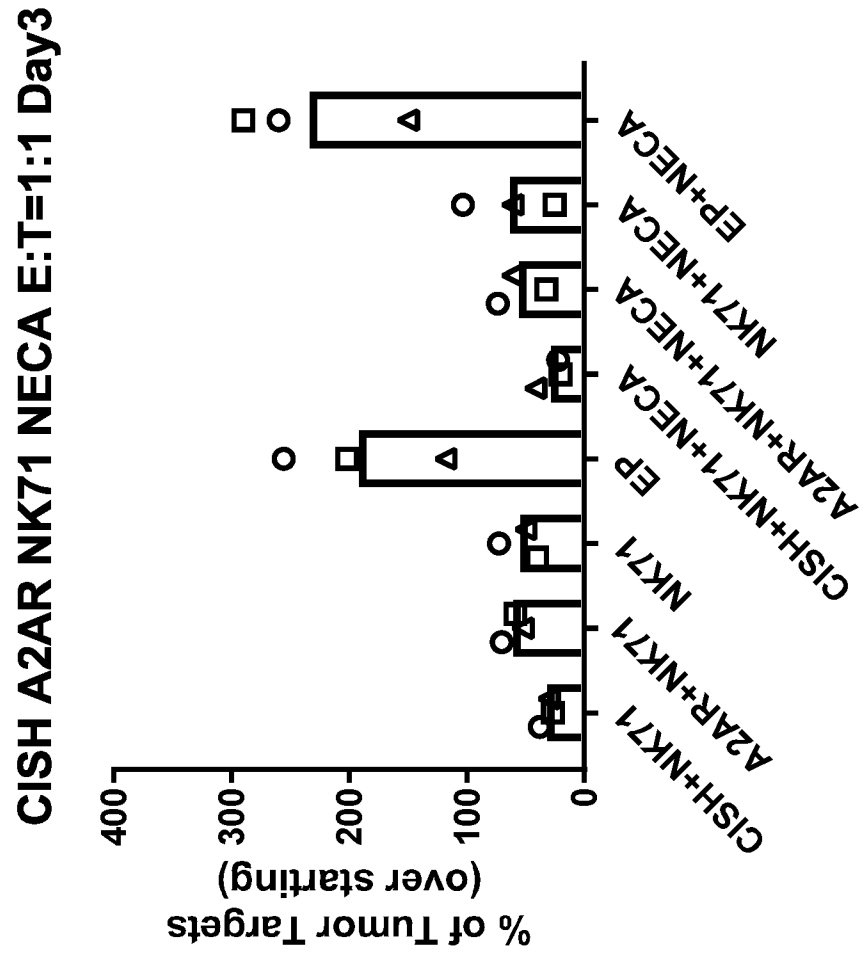

CISH A2AR NK71 NECA E:T=1:1 Day3
% of Tumor Targets (over starting)
400
300
200
100
0
CISH+NK71
A2AR+NK71
NK71
EP
CISH+NK71+NECA
A2AR+NK71+NECA
NK71+NECA
EP+NECA

Figure 49J

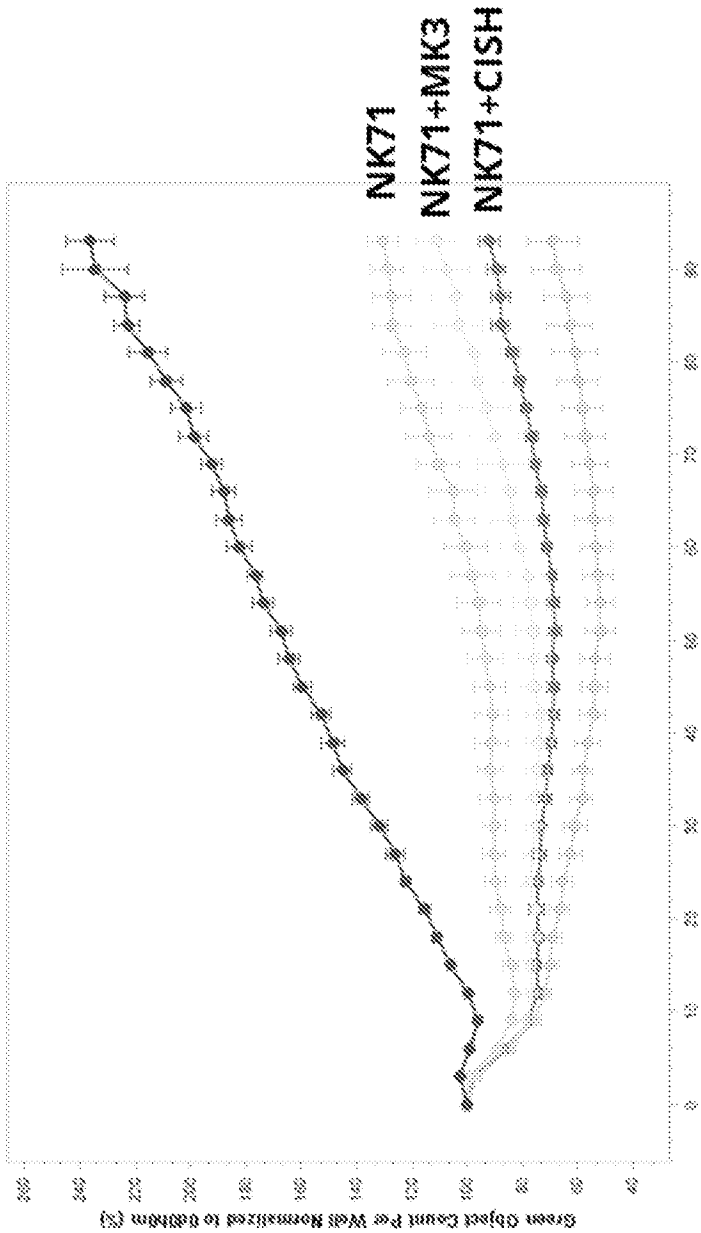
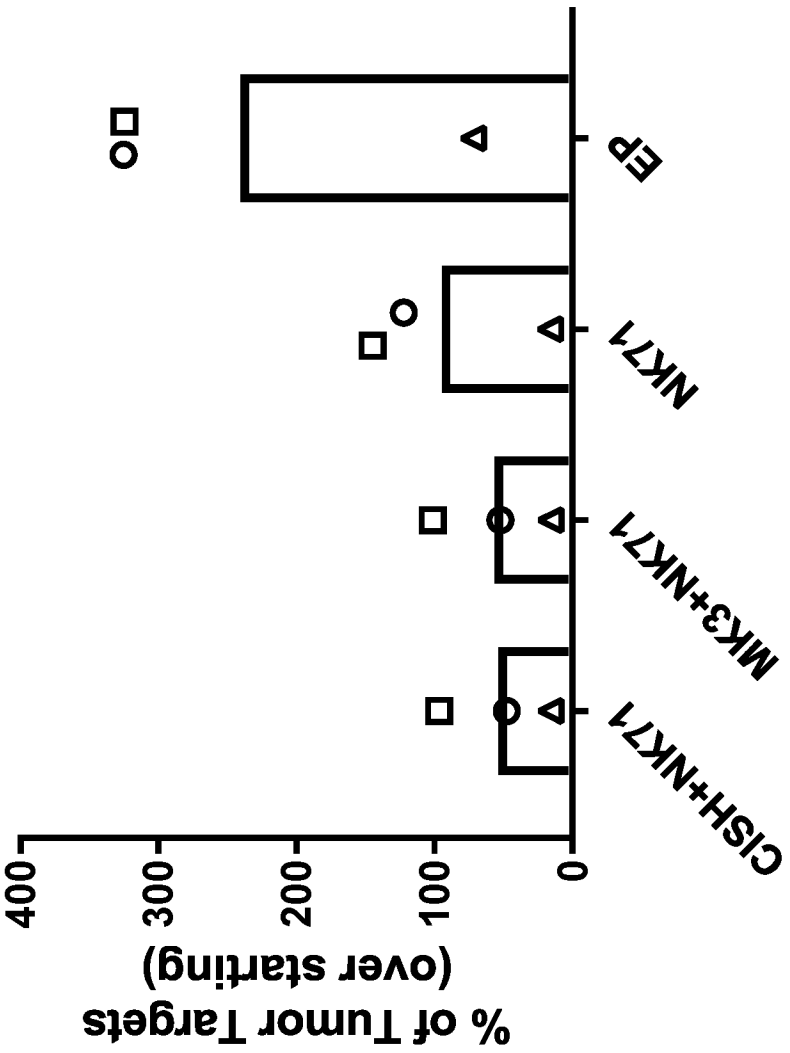


Figure 49K


CISH MK3 NK71 E:T=1:1 Day3
% of Tumor Targets (over starting)
400
300
200
100
0
CISH+NK71
MK3+NK71
NK71
EP

K

Figure 49L

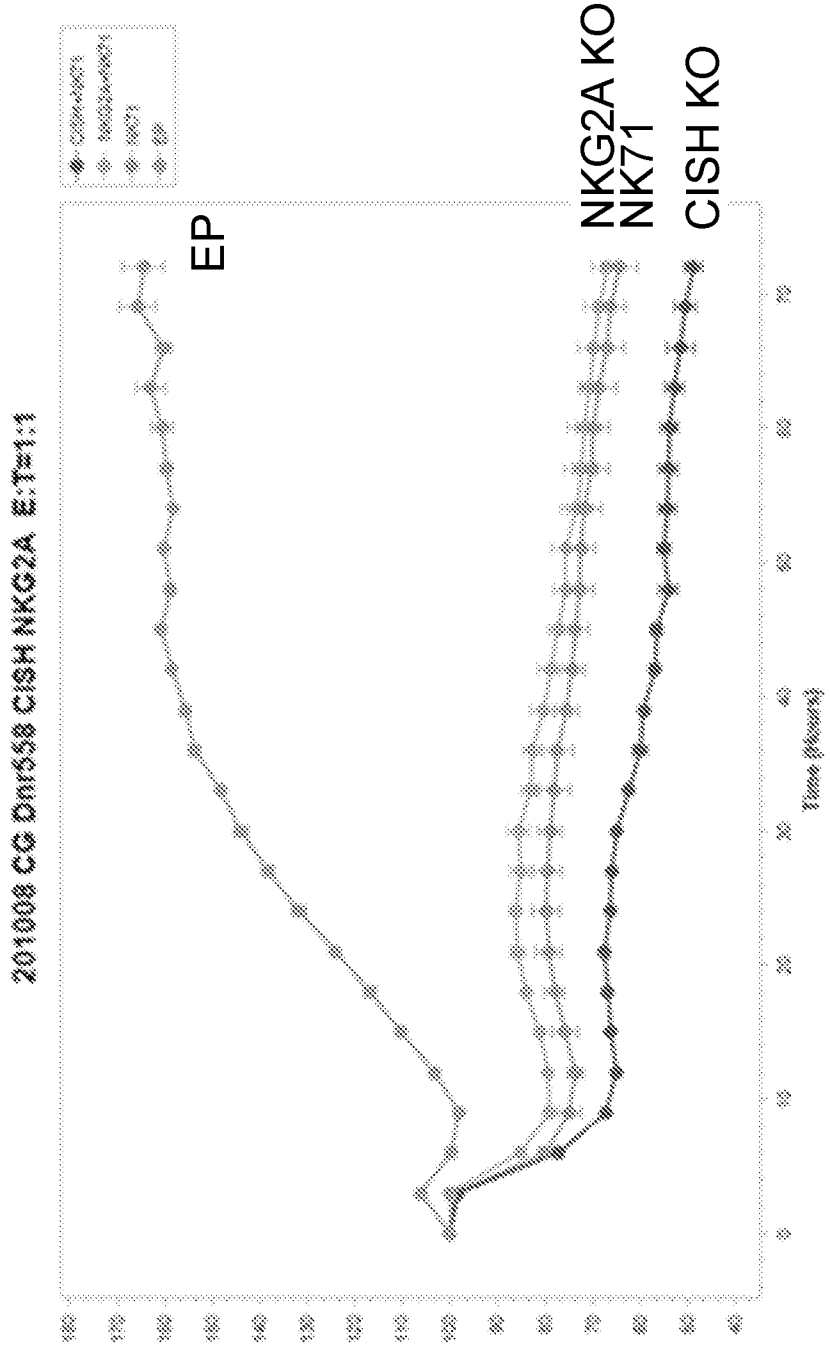

20100B CG Dn558 CISH NKG2A E:T=1:1
EP
NKG2A KO
NK71
CISH KO
Time (hours)

Figure 49M

M

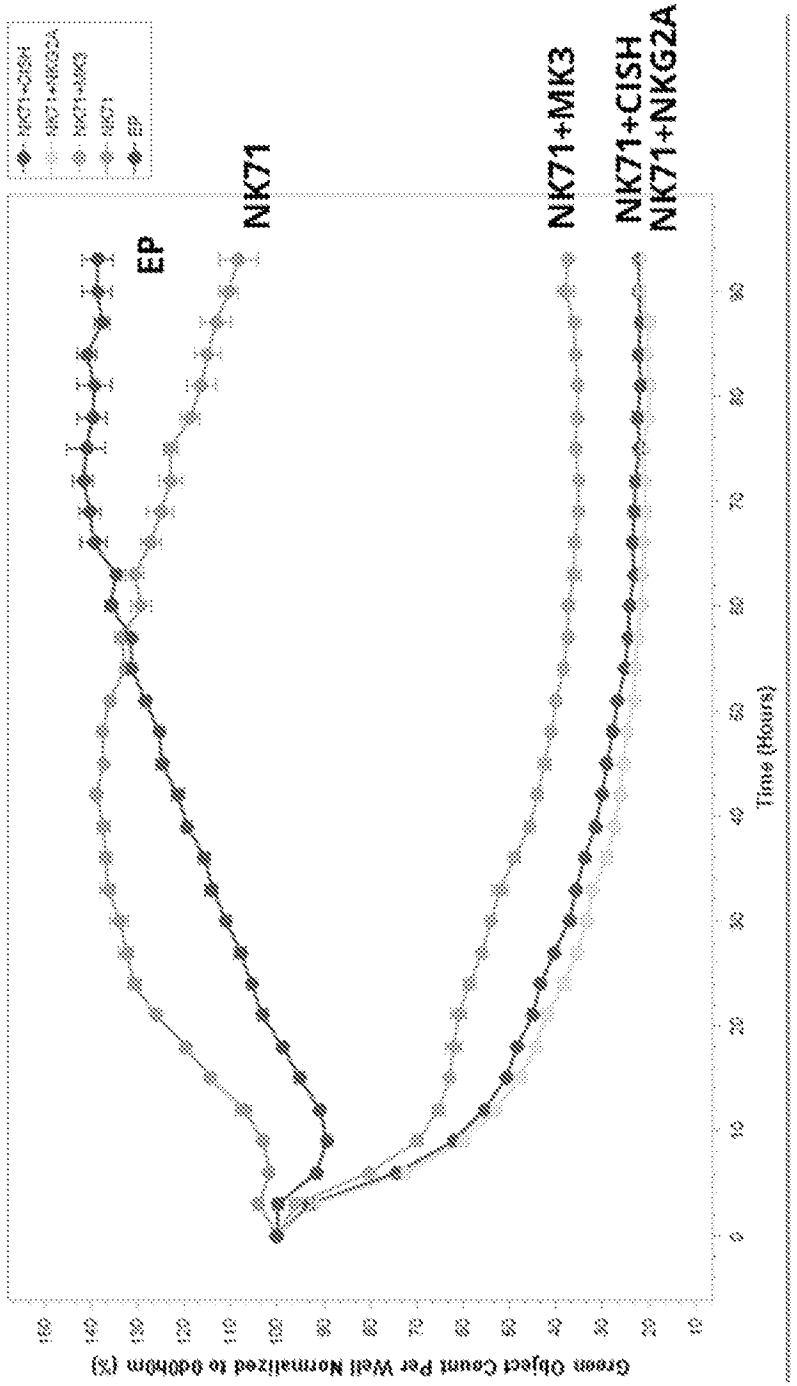

200924 CG Dnr558 CISH NKG2A MK3
Green Object Count Per Well Normalized to bottom (%)
Time (Hours)
EP
NK71
NK71+MK3
NK71+CISH
NK71+NKG2A
E:T=1:1

Figure 49N

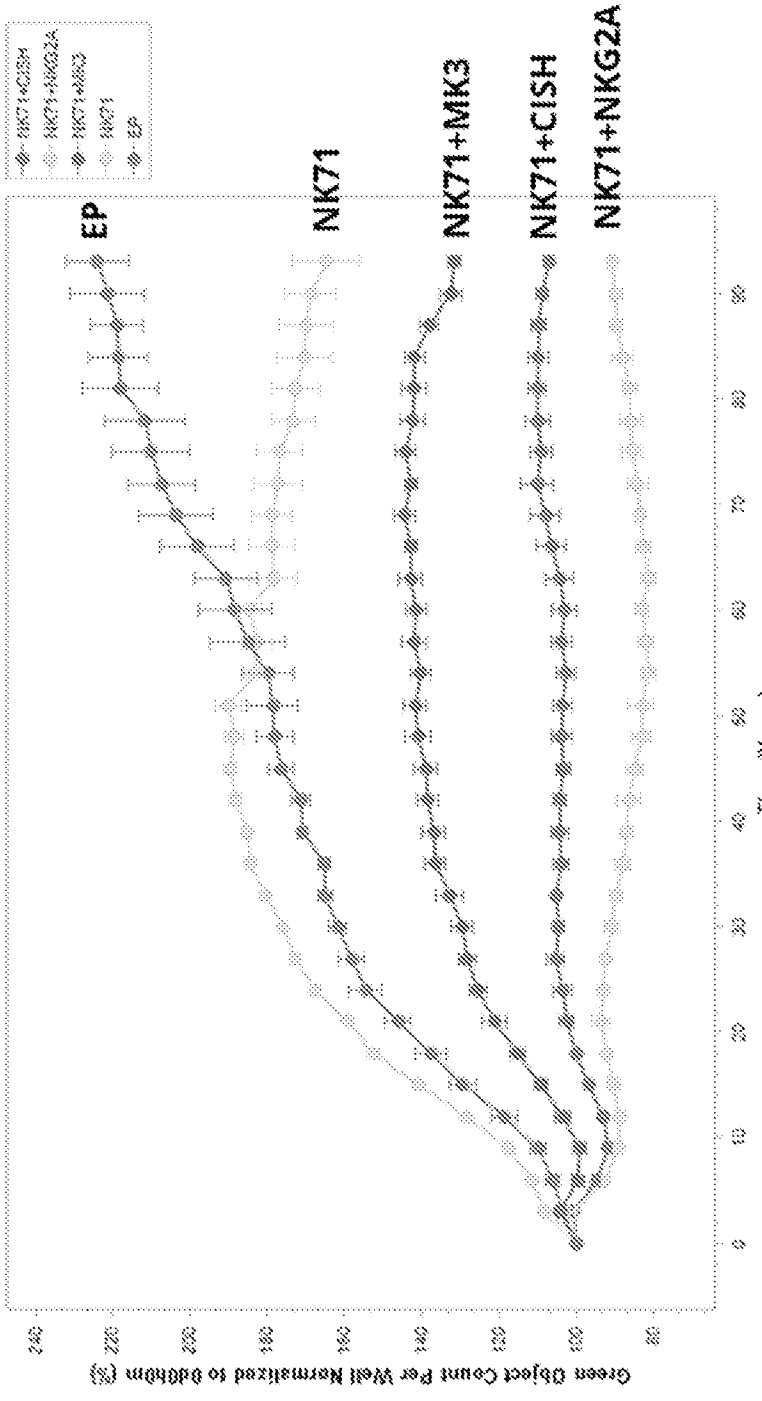
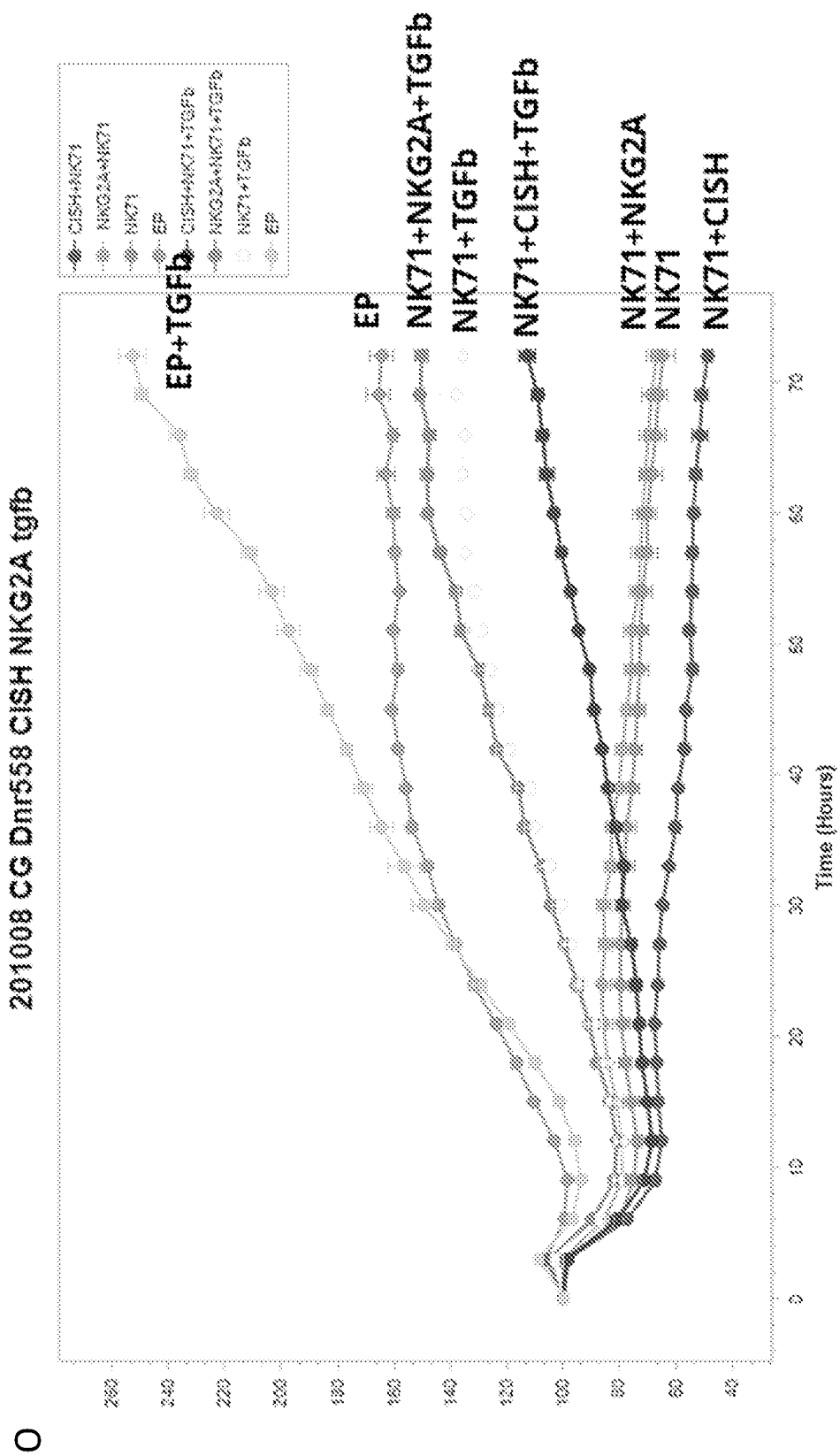
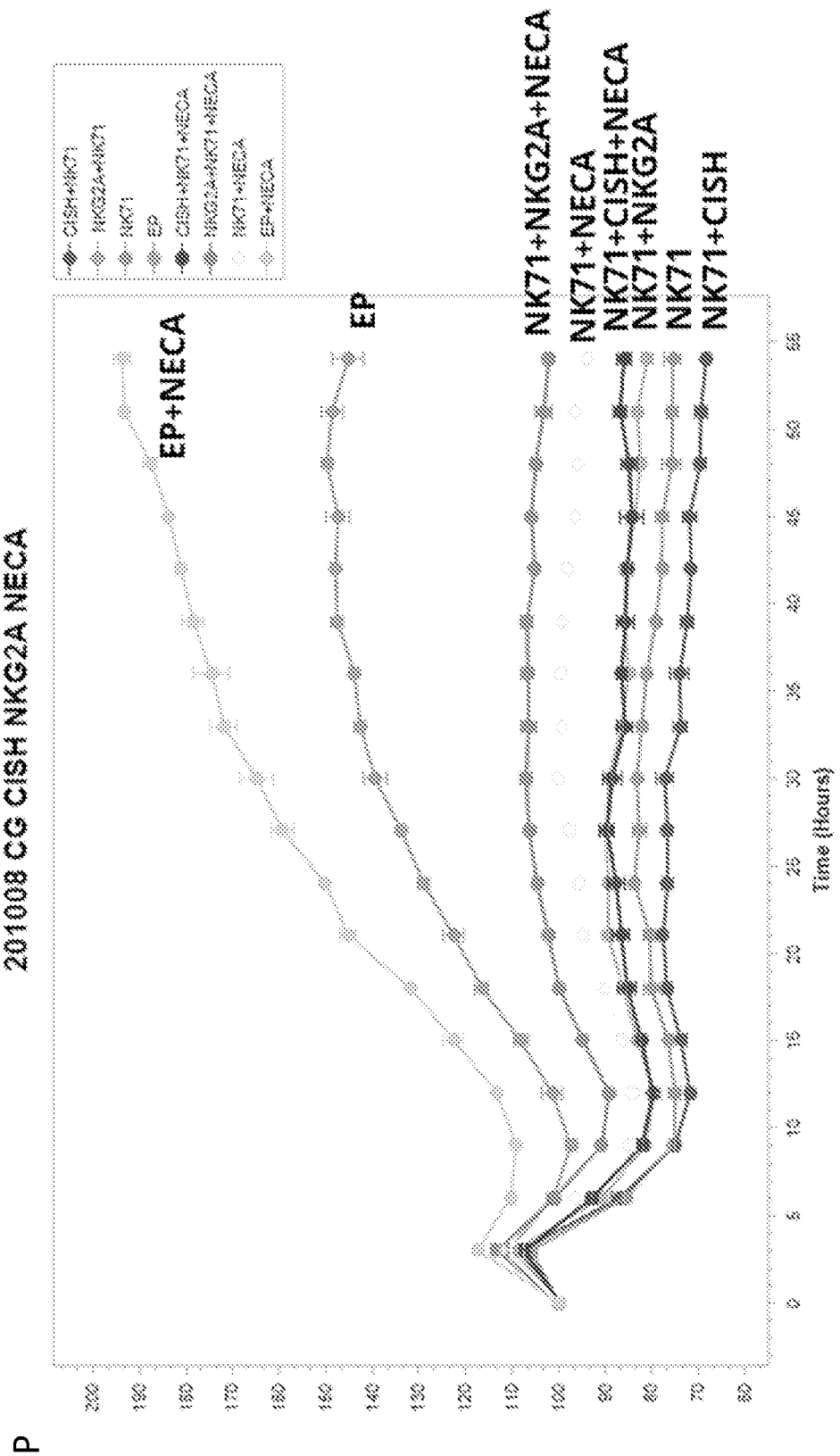

200924 CG Dm558 CISH NKG2A MK3
NK71+CISH
NK71+NKG2A
NK71+MK3
NK71
EP
EP
NK71
NK71+MK3
NK71+CISH
NK71+NKG2A
Green Object Count Per Well Normalized to baseline (%)
Time (Hours)
E:T=1:2

Figure 49O



E:T = 1:1 TGFb at 20 ng/mL

Figure 49P



E:T = 1:2 NECA at 10 uM

Figure 49Q

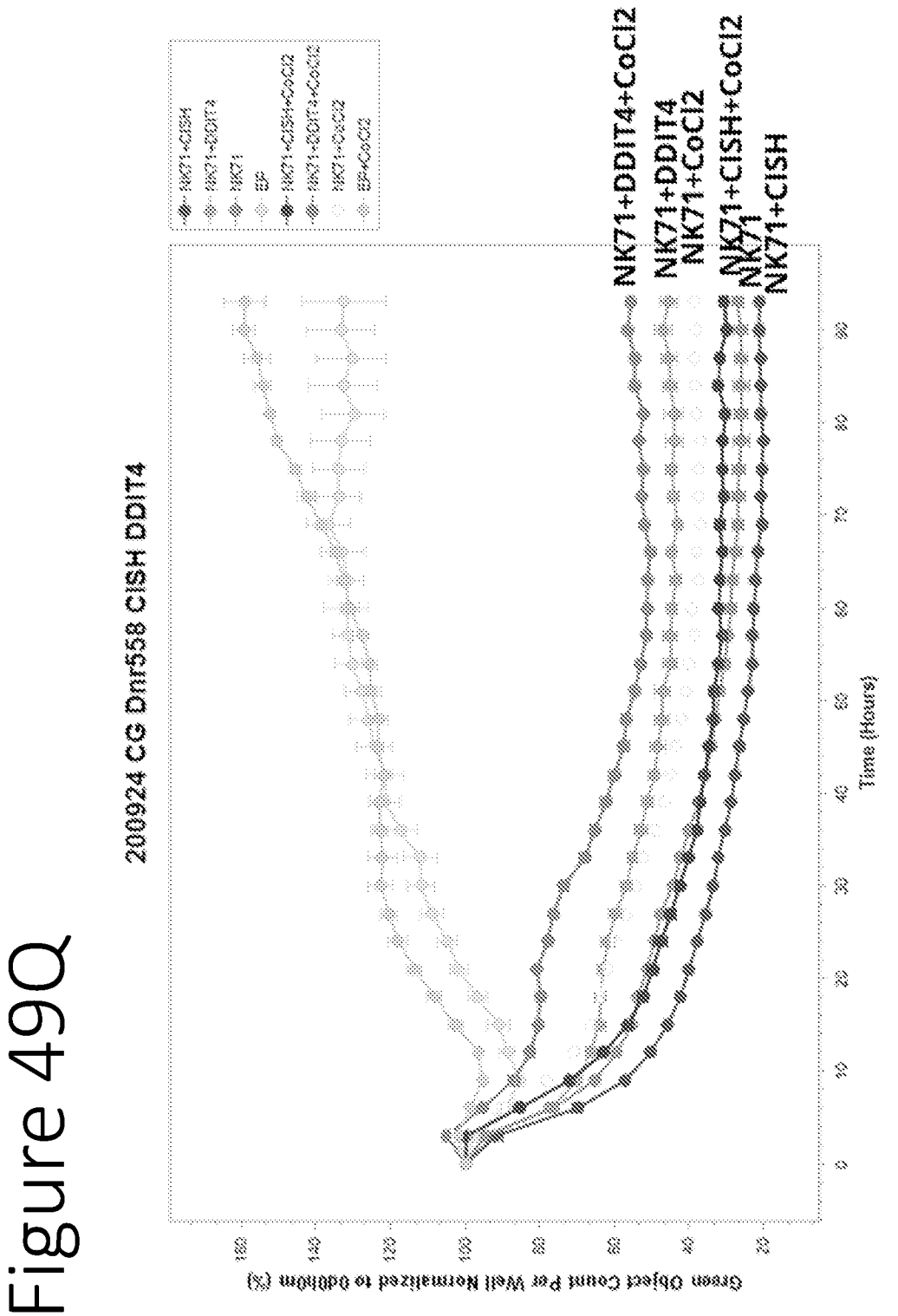
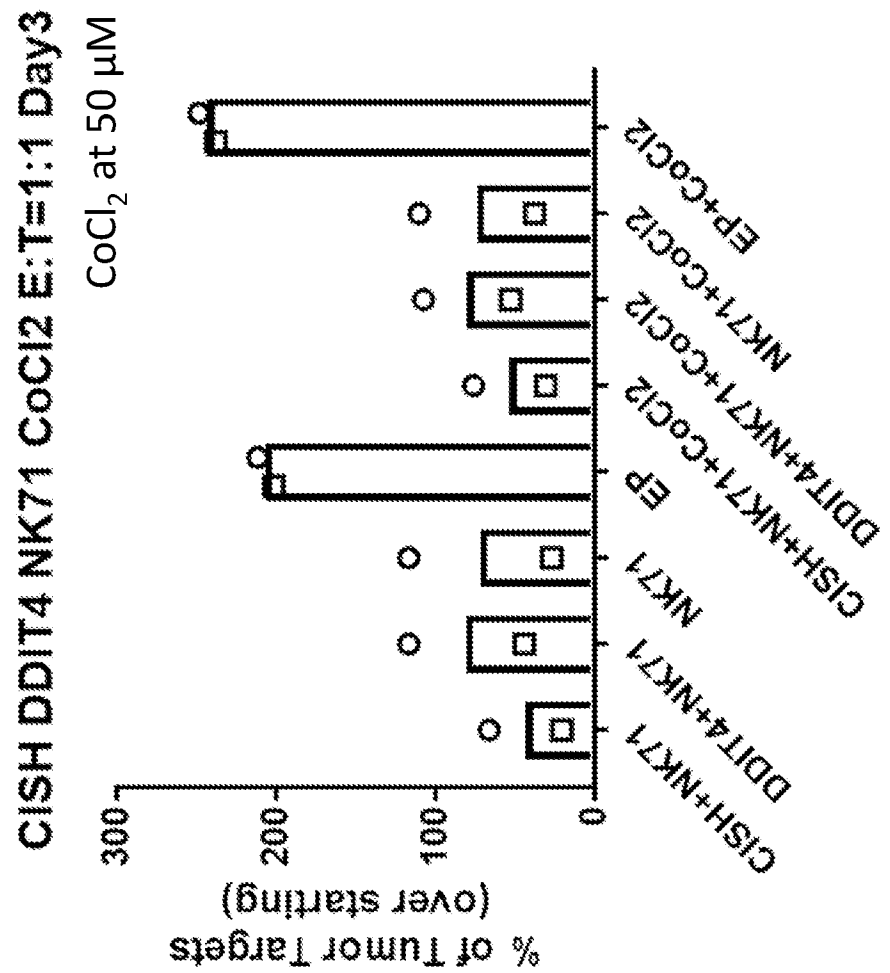

Q
200924 CG Dmr558 CISH DDIT4
Green Object Count Per Well Normalized to 0dMom (%)
Time (Hours)
NK71+DDIT4+CoCl2
NK71+DDIT4
NK71+CoCl2
NK71+CISH+CoCl2
NK71
NK71+CISH
E:T=1:1
CoCl2 at 50 µM

Figure 49R


CISH DDIT4 NK71 CoCl2 E:T=1:1 Day3
CoCl2 at 50 µM
% of Tumor Targets (over starting)
300
200
100
0
CISH+NK71
DDIT4+NK71
NK71
EP
CISH+NK71+CoCl2
DDIT4+NK71+CoCl2
NK71+CoCl2
EP+CoCl2

R

Figure 49S

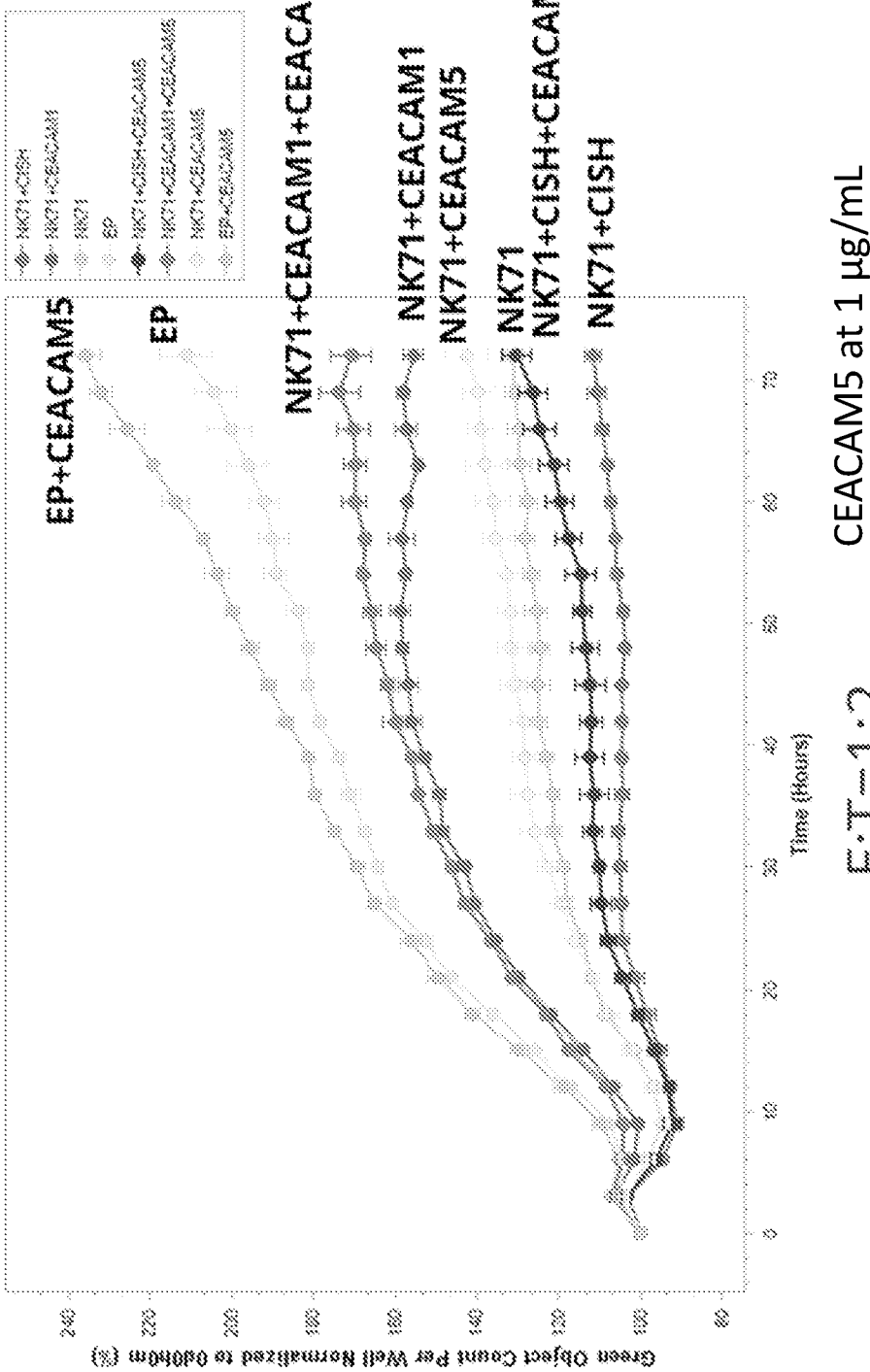

200924 CG Dmr558 CISH CEACAM1
Green Object Count Per Well Normalized to Outside (%)
Time (Hours)
EP+CEACAM5
EP
NK71+CEACAM1+CEACAM5
NK71+CEACAM1
NK71+CEACAM5
NK71
NK71+CISH+CEACAM5
NK71+CISH
E:T=1:2
CEACAM5 at 1 µg/mL

Figure 49T

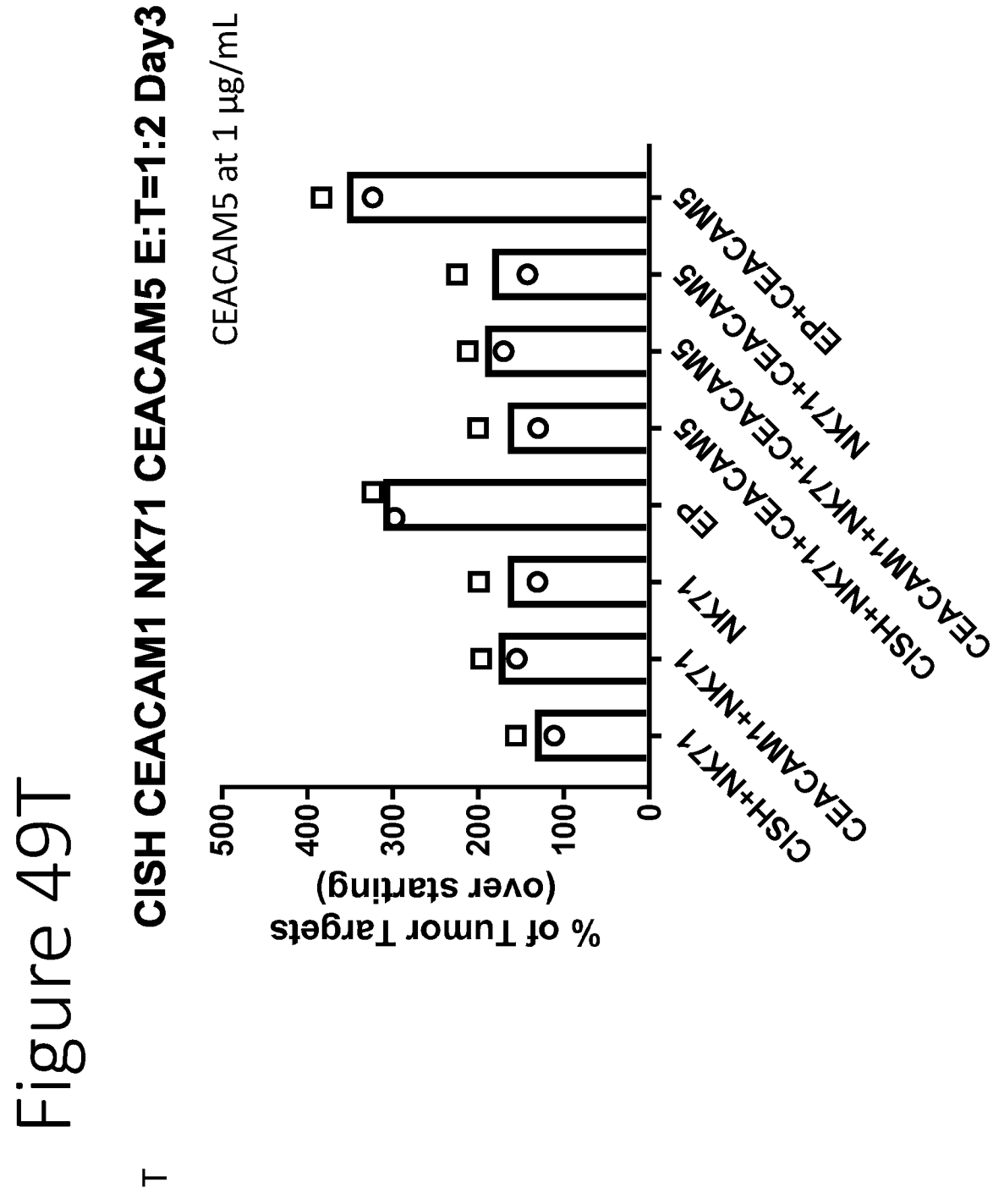

T
CISH CEACAM1 NK71 CEACAM5 E:T=1:2 Day3
CEACAM5 at 1 µg/mL
% of Tumor Targets (over starting)
500
400
300
200
100
0
CISH+NK71
CEACAM1+NK71
NK71
EP
CISH+NK71+CEACAM5
CEACAM1+NK71+CEACAM5
NK71+CEACAM5
EP+CEACAM5

Figure 49U

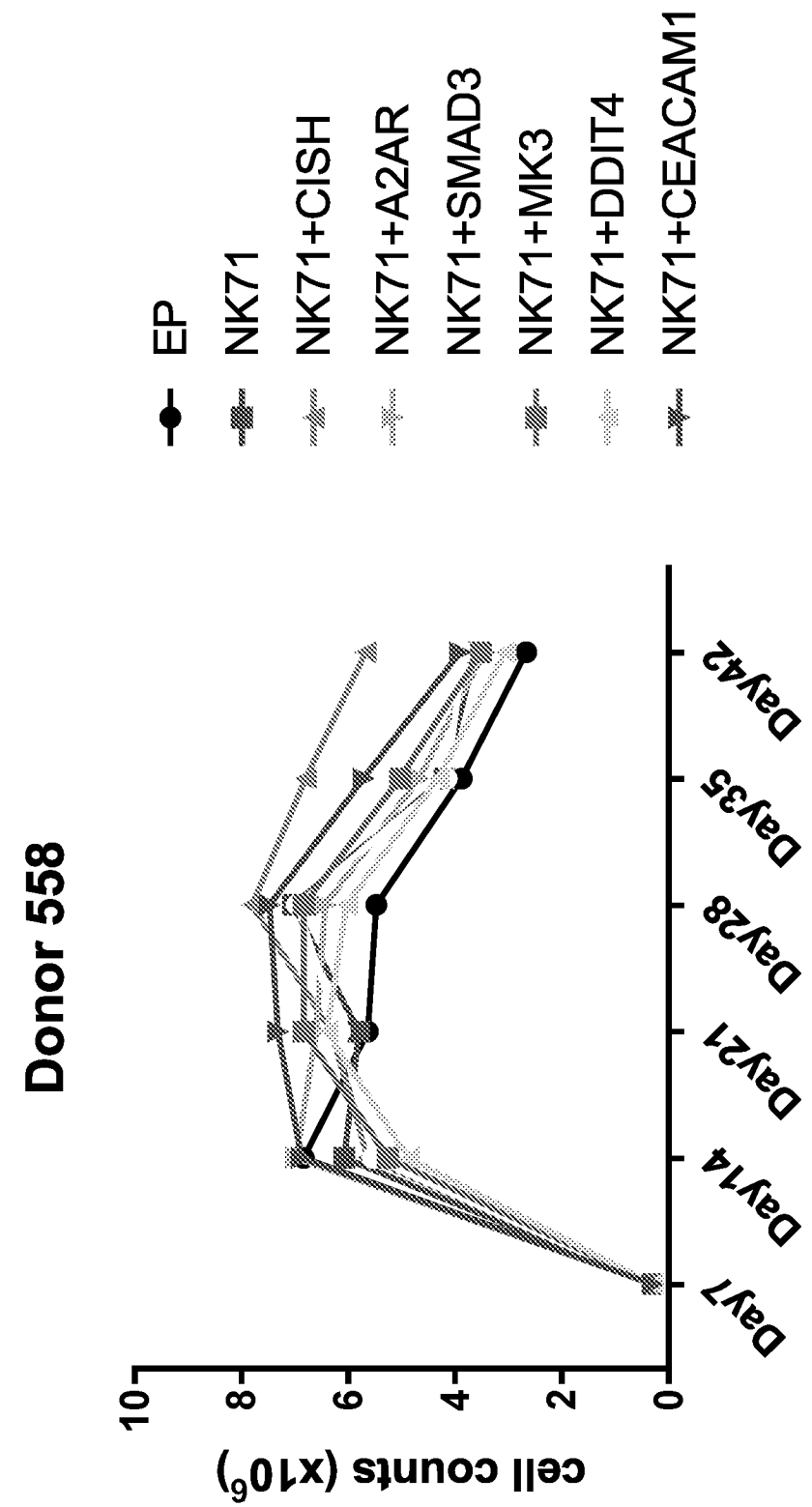

U
Donor 558
cell counts (x10^6)
10
8
6
4
2
0
Day7
Day14
Day21
Day28
Day35
Day42
EP
NK71
NK71+CISH
NK71+A2AR
NK71+SMAD3
NK71+MK3
NK71+DDIT4
NK71+CEACAM1

Figure 49V

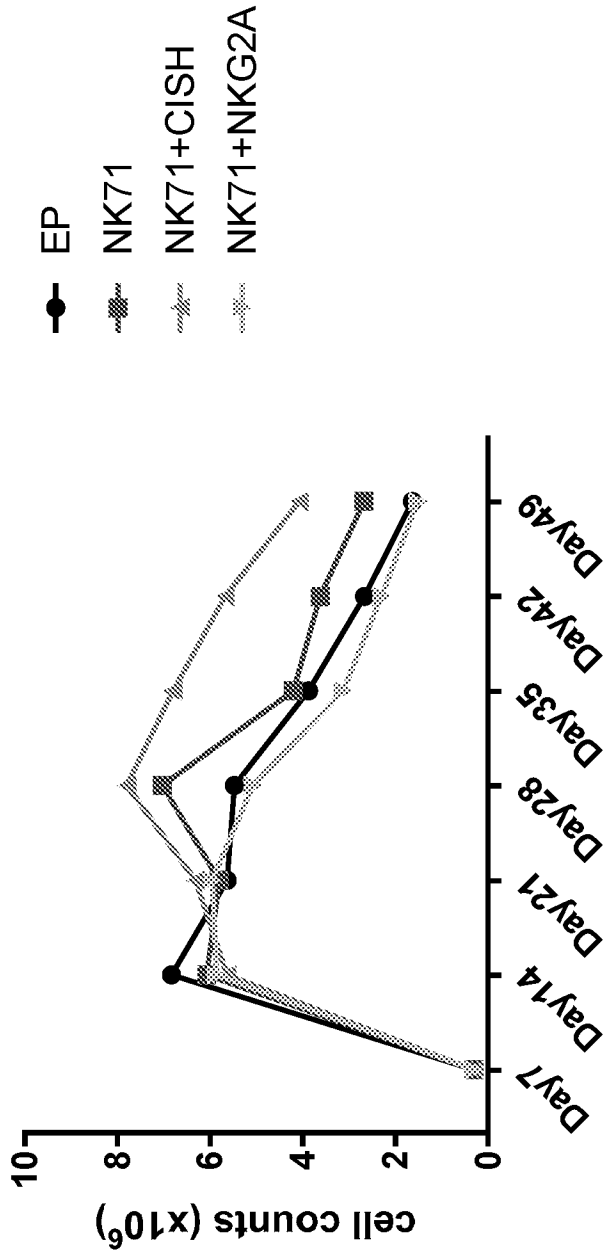

Donor 558
EP
NK71
NK71+CISH
NK71+NKG2A
cell counts (x10^6)
0
2
4
6
8
10
Day7
Day14
Day21
Day28
Day35
Day42
Day49

Figure 50A

A

scFv	VH peptide sequence SEQ ID NO:	VL peptide sequence SEQ ID NO:	VH nucleic acid sequence SEQ ID NO:	VL nucleic acid sequence SEQ ID NO:
NK77.1_CD70_DB01_C03	890	964	1038	1112
NK77.2_CD70_DB01_D02	891	965	1039	1113
NK77.3_CD70_DB01_E06	892	966	1040	1114
NK77.4_CD70_DB01_G04	893	967	1041	1115
NK77.5_CD70_DB01_G05	894	968	1042	1116
NK77.6_CD70_DB01_G07	895	969	1043	1117
NK77.7_CD70_DB01_G11	896	970	1044	1118
NK77.9_CD70_DB02_A03	897	971	1045	1119
NK77.10_CD70_DB02_A04	898	972	1046	1120
NK77.11_CD70_DB02_A05	899	973	1047	1121
NK77.12_CD70_DB02_A06	900	974	1048	1122
NK77.13_CD70_DB02_A07	901	975	1049	1123
NK77.14_CD70_DB02_A08	902	976	1050	1124
NK77.15_CD70_DB02_A09	903	977	1051	1125
NK77.16_CD70_DB02_A11	904	978	1052	1126
NK77.17_CD70_DB02_B06	905	979	1053	1127
NK77.18_CD70_DB02_B09	906	980	1054	1128
NK77.19_CD70_DB02_C03	907	981	1055	1129
NK77.20_CD70_DB02_C04	908	982	1056	1130
NK77.22_CD70_DB02_C07	909	983	1057	1131
NK77.24_CD70_DB02_D02	910	984	1058	1132
NK77.25_CD70_DB02_D04	911	985	1059	1133
NK77.26_CD70_DB02_D10	912	986	1060	1134
NK77.27_CD70_DB02_D11	913	987	1061	1135
NK77.28_CD70_DB02_E04	914	988	1062	1136
NK77.29_CD70_DB02_F06	915	989	1063	1137
NK77.31_CD70_DB02_F08	916	990	1064	1138
NK77.32_CD70_DB02_G07	917	991	1065	1139
NK77.33_CD70_DB02_H04	918	992	1066	1140
NK77.34_CD70_DB02_H05	919	993	1067	1141
NK77.35_CD70_DB02_H08	920	994	1068	1142
NK77.36_CD70_DB03_A06	921	995	1069	1143
NK77.37_CD70_DB03_A07	922	996	1070	1144
NK77.38_CD70_DB03_A08	923	997	1071	1145
NK77.39_CD70_DB03_A09	924	998	1072	1146
NK77.40_CD70_DB03_A11	925	999	1073	1147
NK77.41_CD70_DB03_A12	926	1000	1074	1148

Figure 50A cont.

scFv	VH peptide sequence SEQ ID NO:	VL peptide sequence SEQ ID NO:	VH nucleic acid sequence SEQ ID NO:	VL nucleic acid sequence SEQ ID NO:
NK77.42_CD70_DB03_B01	927	1001	1075	1149
NK77.43_CD70_DB03_B04	928	1002	1076	1150
NK77.44_CD70_DB03_B06	929	1003	1077	1151
NK77.45_CD70_DB03_B09	930	1004	1078	1152
NK77.46_CD70_DB03_C05	931	1005	1079	1153
NK77.47_CD70_DB03_D11	932	1006	1080	1154
NK77.48_CD70_DB03_E01	933	1007	1081	1155
NK77.49_CD70_DB03_E03	934	1008	1082	1156
NK77.50_CD70_DB03_E09	935	1009	1083	1157
NK77.51_CD70_DB03_F02	936	1010	1084	1158
NK77.52_CD70_DB03_F05	937	1011	1085	1159
NK77.53_CD70_DB03_F06	938	1012	1086	1160
NK77.54_CD70_DB03_F09	939	1013	1087	1161
NK77.55_CD70_DB03_F12	940	1014	1088	1162
NK77.56_CD70_DB03_G06	941	1015	1089	1163
NK77.57_CD70_DB03_G11	942	1016	1090	1164
NK77.58_CD70_DB03_H08	943	1017	1091	1165
NK77.59_CD70_DB03_H10	944	1018	1092	1166
NK77.60_CD70_DB04_A05	945	1019	1093	1167
NK77.61_CD70_DB04_A07	946	1020	1094	1168
NK77.62_CD70_DB04_A10	947	1021	1095	1169
NK77.63_CD70_DB04_A11	948	1022	1096	1170
NK77.64_CD70_DB04_B03	949	1023	1097	1171
NK77.65_CD70_DB04_B05	950	1024	1098	1172
NK77.66_CD70_DB04_B07	951	1025	1099	1173
NK77.67_CD70_DB04_C01	952	1026	1100	1174
NK77.68_CD70_DB04_C04	953	1027	1101	1175
NK77.69_CD70_DB04_C06	954	1028	1102	1176
NK77.70_CD70_DB04_C07	955	1029	1103	1177
NK77.71_CD70_DB04_D02	956	1030	1104	1178
NK77.72_CD70_DB04_D05	957	1031	1105	1179
NK77.73_CD70_DB04_D07	958	1032	1106	1180
NK77.74_CD70_DB04_D08	959	1033	1107	1181
NK77.75_CD70_DB04_D10	960	1034	1108	1182
NK77.85_CD70_DB03_B02	961	1035	1109	1183
NK77.86_CD70_DB04_A06	962	1036	1110	1184
NK77.87_CD70_DB04_A09	963	1037	1111	1185

Figure 50B

B

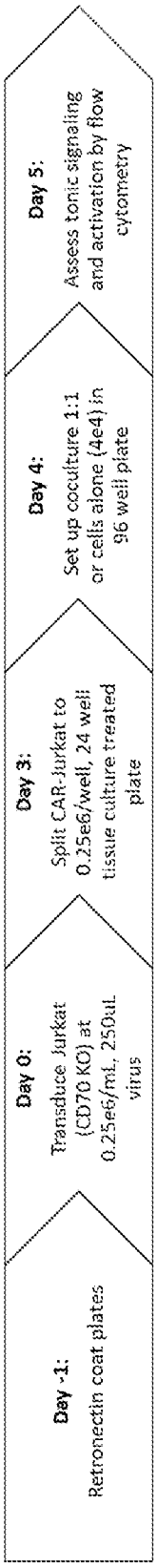
scFv	CDR-H1 SEQ ID NO:	CDR-H2 SEQ ID NO:	CDR-H3 SEQ ID NO:	CDR-L1 SEQ ID NO:	CDR-L2 SEQ ID NO:	CDR-L3 SEQ ID NO:
NK77.1_CD70_DB01_C03	428	502	576	668	742	816
NK77.2_CD70_DB01_D02	429	503	577	669	743	817
NK77.3_CD70_DB01_E06	430	504	578	670	744	818
NK77.4_CD70_DB01_G04	431	505	579	671	745	819
NK77.5_CD70_DB01_G05	432	506	580	672	746	820
NK77.6_CD70_DB01_G07	433	507	581	673	747	821
NK77.7_CD70_DB01_G11	434	508	582	674	748	822
NK77.9_CD70_DB02_A03	435	509	583	675	749	823
NK77.10_CD70_DB02_A04	436	510	584	676	750	824
NK77.11_CD70_DB02_A05	437	511	585	677	751	825
NK77.12_CD70_DB02_A06	438	512	586	678	752	826
NK77.13_CD70_DB02_A07	439	513	587	679	753	827
NK77.14_CD70_DB02_A08	440	514	588	680	754	828
NK77.15_CD70_DB02_A09	441	515	589	681	755	829
NK77.16_CD70_DB02_A11	442	516	590	682	756	830
NK77.17_CD70_DB02_B06	443	517	591	683	757	831
NK77.18_CD70_DB02_B09	444	518	592	684	758	832
NK77.19_CD70_DB02_C03	445	519	593	685	759	833
NK77.20_CD70_DB02_C04	446	520	594	686	760	834
NK77.22_CD70_DB02_C07	447	521	595	687	761	835
NK77.24_CD70_DB02_D02	448	522	596	688	762	836
NK77.25_CD70_DB02_D04	449	523	597	689	763	837
NK77.26_CD70_DB02_D10	450	524	598	690	764	838
NK77.27_CD70_DB02_D11	451	525	599	691	765	839
NK77.28_CD70_DB02_E04	452	526	600	692	766	840
NK77.29_CD70_DB02_F06	453	527	601	693	767	841
NK77.31_CD70_DB02_F08	454	528	602	694	768	842
NK77.32_CD70_DB02_G07	455	529	603	695	769	843
NK77.33_CD70_DB02_H04	456	530	604	696	770	844
NK77.34_CD70_DB02_H05	457	531	605	697	771	845
NK77.35_CD70_DB02_H08	458	532	606	698	772	846
NK77.36_CD70_DB03_A06	459	533	607	699	773	847
NK77.37_CD70_DB03_A07	460	534	608	700	774	848
NK77.38_CD70_DB03_A08	461	535	609	701	775	849
NK77.39_CD70_DB03_A09	462	536	610	702	776	850
NK77.40_CD70_DB03_A11	463	537	611	703	777	851
NK77.41_CD70_DB03_A12	464	538	612	704	778	852

Figure 50B cont.

scFv	CDR-H1 SEQ ID NO:	CDR-H2 SEQ ID NO:	CDR-H3 SEQ ID NO:	CDR-L1 SEQ ID NO:	CDR-L2 SEQ ID NO:	CDR-L3 SEQ ID NO:
NK77.42_CD70_DB03_B01	465	539	613	705	779	853
NK77.43_CD70_DB03_B04	466	540	614	706	780	854
NK77.44_CD70_DB03_B06	467	541	615	707	781	855
NK77.45_CD70_DB03_B09	468	542	616	708	782	856
NK77.46_CD70_DB03_C05	469	543	617	709	783	857
NK77.47_CD70_DB03_D11	470	544	618	710	784	858
NK77.48_CD70_DB03_E01	471	545	619	711	785	859
NK77.49_CD70_DB03_E03	472	546	620	712	786	860
NK77.50_CD70_DB03_E09	473	547	621	713	787	861
NK77.51_CD70_DB03_F02	474	548	622	714	788	862
NK77.52_CD70_DB03_F05	475	549	623	715	789	863
NK77.53_CD70_DB03_F06	476	550	624	716	790	864
NK77.54_CD70_DB03_F09	477	551	625	717	791	865
NK77.55_CD70_DB03_F12	478	552	626	718	792	866
NK77.56_CD70_DB03_G06	479	553	627	719	793	867
NK77.57_CD70_DB03_G11	480	554	628	720	794	868
NK77.58_CD70_DB03_H08	481	555	629	721	795	869
NK77.59_CD70_DB03_H10	482	556	630	722	796	870
NK77.60_CD70_DB04_A05	483	557	631	723	797	871
NK77.61_CD70_DB04_A07	484	558	632	724	798	872
NK77.62_CD70_DB04_A10	485	559	633	725	799	873
NK77.63_CD70_DB04_A11	486	560	634	726	800	874
NK77.64_CD70_DB04_B03	487	561	635	727	801	875
NK77.65_CD70_DB04_B05	488	562	636	728	802	876
NK77.66_CD70_DB04_B07	489	563	637	729	803	877
NK77.67_CD70_DB04_C01	490	564	638	730	804	878
NK77.68_CD70_DB04_C04	491	565	639	731	805	879
NK77.69_CD70_DB04_C06	492	566	640	732	806	880
NK77.70_CD70_DB04_C07	493	567	641	733	807	881
NK77.71_CD70_DB04_D02	494	568	642	734	808	882
NK77.72_CD70_DB04_D05	495	569	643	735	809	883
NK77.73_CD70_DB04_D07	496	570	644	736	810	884
NK77.74_CD70_DB04_D08	497	571	645	737	811	885
NK77.75_CD70_DB04_D10	498	572	646	738	812	886
NK77.85_CD70_DB03_B02	499	573	647	739	813	887
NK77.86_CD70_DB04_A06	500	574	648	740	814	888
NK77.87_CD70_DB04_A09	501	575	649	741	815	889

Figure 50C-50D

C



D

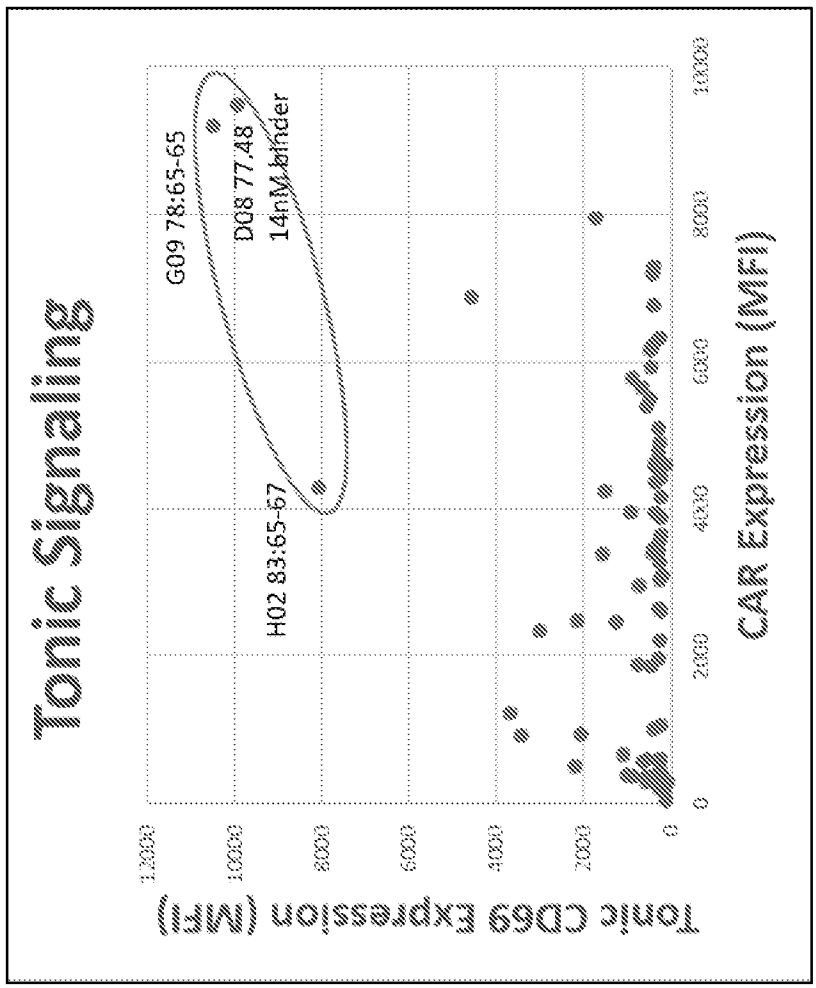


Figure 50E

E

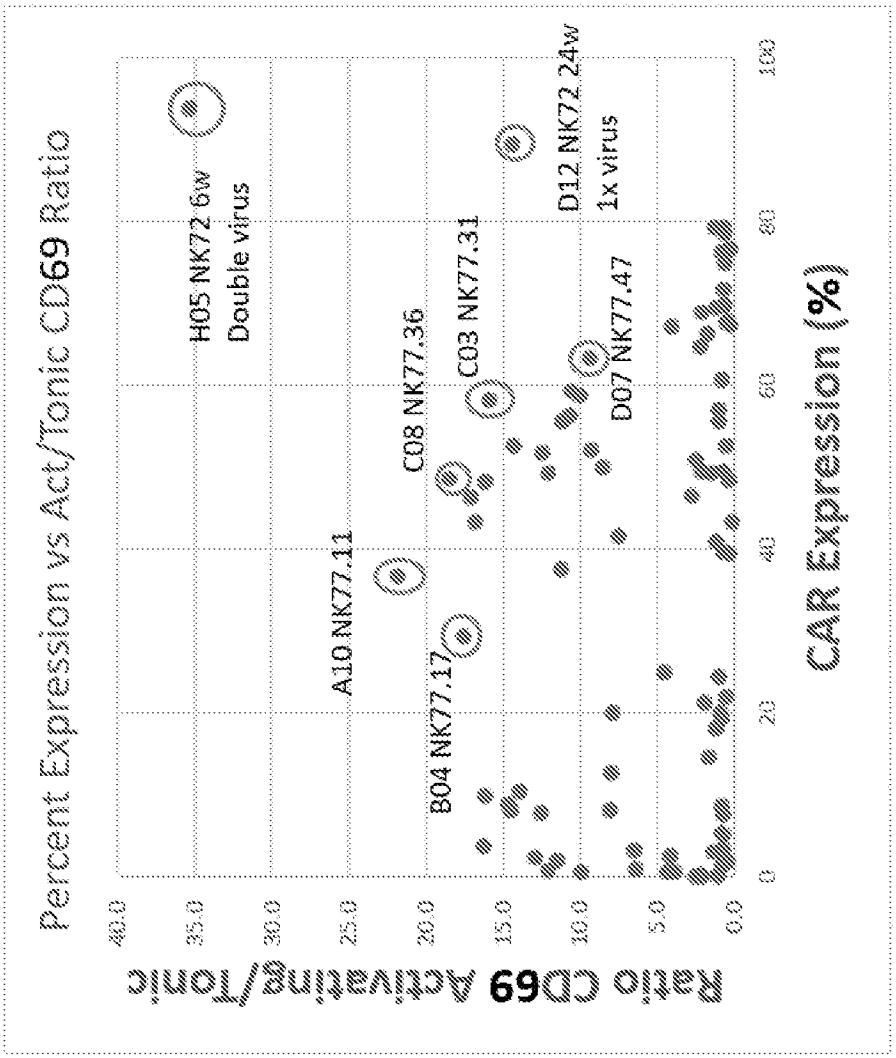

Percent Expression vs Act/Tonic CD69 Ratio
Ratio CD69 Activating/Tonic
CAR Expression (%)
H05 NK72 6w
Double virus
A10 NK77.11
C08 NK77.36
C03 NK77.31
B04 NK77.17
D07 NK77.47
D12 NK72 24w
1x virus

Figure 50F

F

NK Plasmid Number	KD (nM)	NKM34 Blocking	Tonic CD69 (MFI)	Tonic CD25 (MFI)	Expression (%)	Activation CD69 (MFI)	Activation CD25 (MFI)	High Flag Act/Tonic 69 Ratio	High Flag Act/Tonic 25 Ratio	Low Flag Trimer MFI
NK77.11_CD70_DB02_A05	24.34	Blocker Strong	288	81.5	63.2	6301	1921	21.9	24	143
NK77.71_CD70_DB04_D02	11.84	Blocker Strong	285	155	8.66	5427	2309	19.0	14.9	249
NK77.58_CD70_DB03_H08	9.65	Blocker Strong	289	135	8.4	5488	2191	19.0	16.2	191
NK77.73_CD70_DB04_D07	2.62	Blocker Strong	215	131	9.42	4054	1757	18.9	13.4	149
NK77.17_CD70_DB02_B06	3.87	Blocker Strong	415	86.9	60.7	7288	2519	17.6	29	125
NK77.16_CD70_DB02_A11	8.57	Blocker Strong	297	76.1	58.1	5090	1423	17.1	19	161
NK77.44_CD70_DB03_B06	31.69	Blocker Strong	290	71.7	58.8	4883	1124	16.8	16	142
NK77.31_CD70_DB02_F08	5.56	Blocker	299	61.5	73.3	4760	1439	15.9	23	116
NK77.65_CD70_DB04_B05	0.62	Blocker Strong	362	161	2.89	2844	844	7.9	5.2	253
NK77.55_CD70_DB03_F12	8.57	Neg	669	178	2.26	4806	1262	7.2	7.1	256

Figure 51A

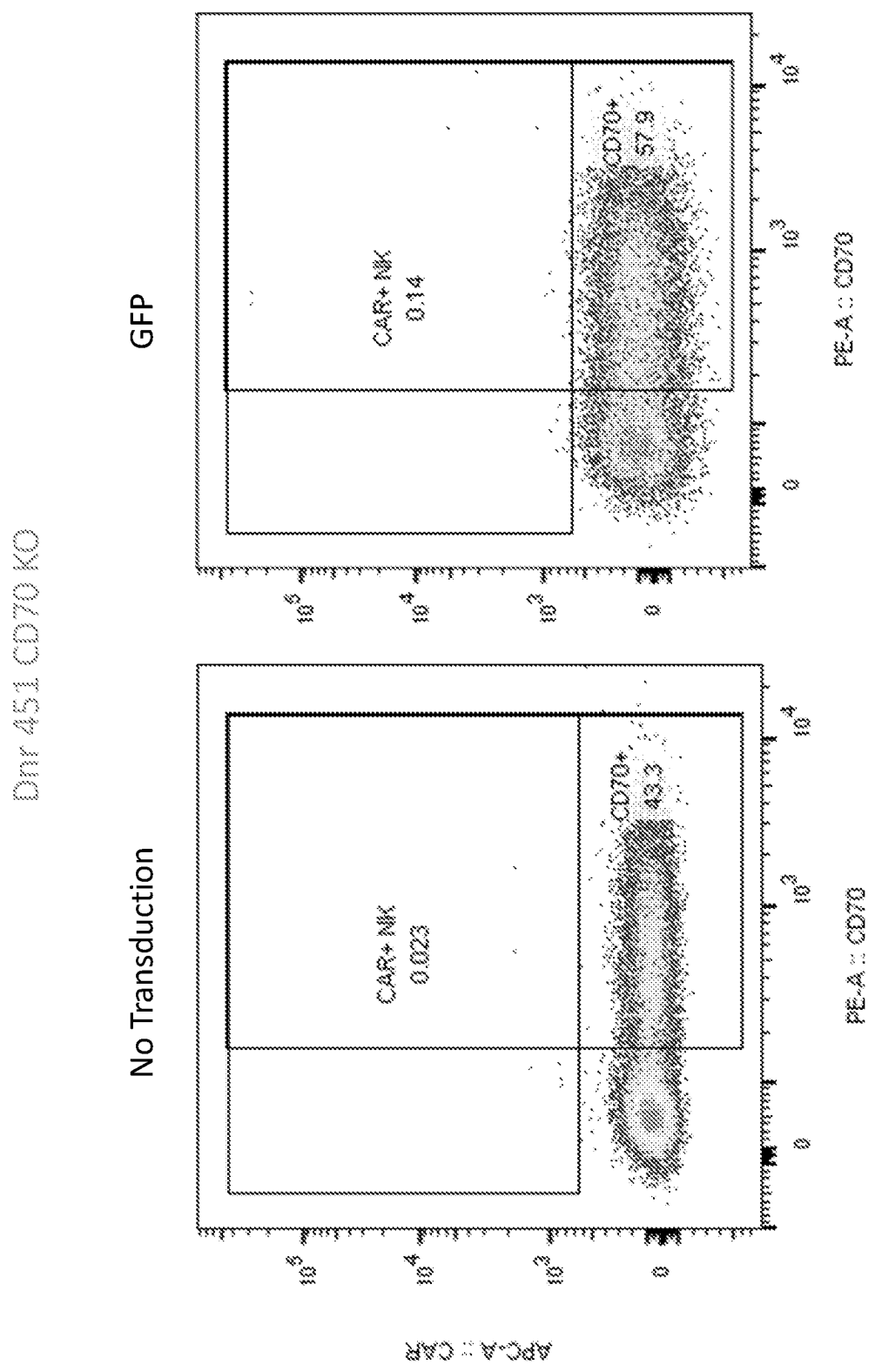

Dnr 451 CD70 KO
No Transduction
GFP
CAR+ NK
0.023
CD70+
43.3
CAR+ NK
0.14
CD70+
57.9
APC-A :: CAR
PE-A :: CD70
PE-A :: CD70
0
10^3
10^4
10^5

Figure 51A Cont.

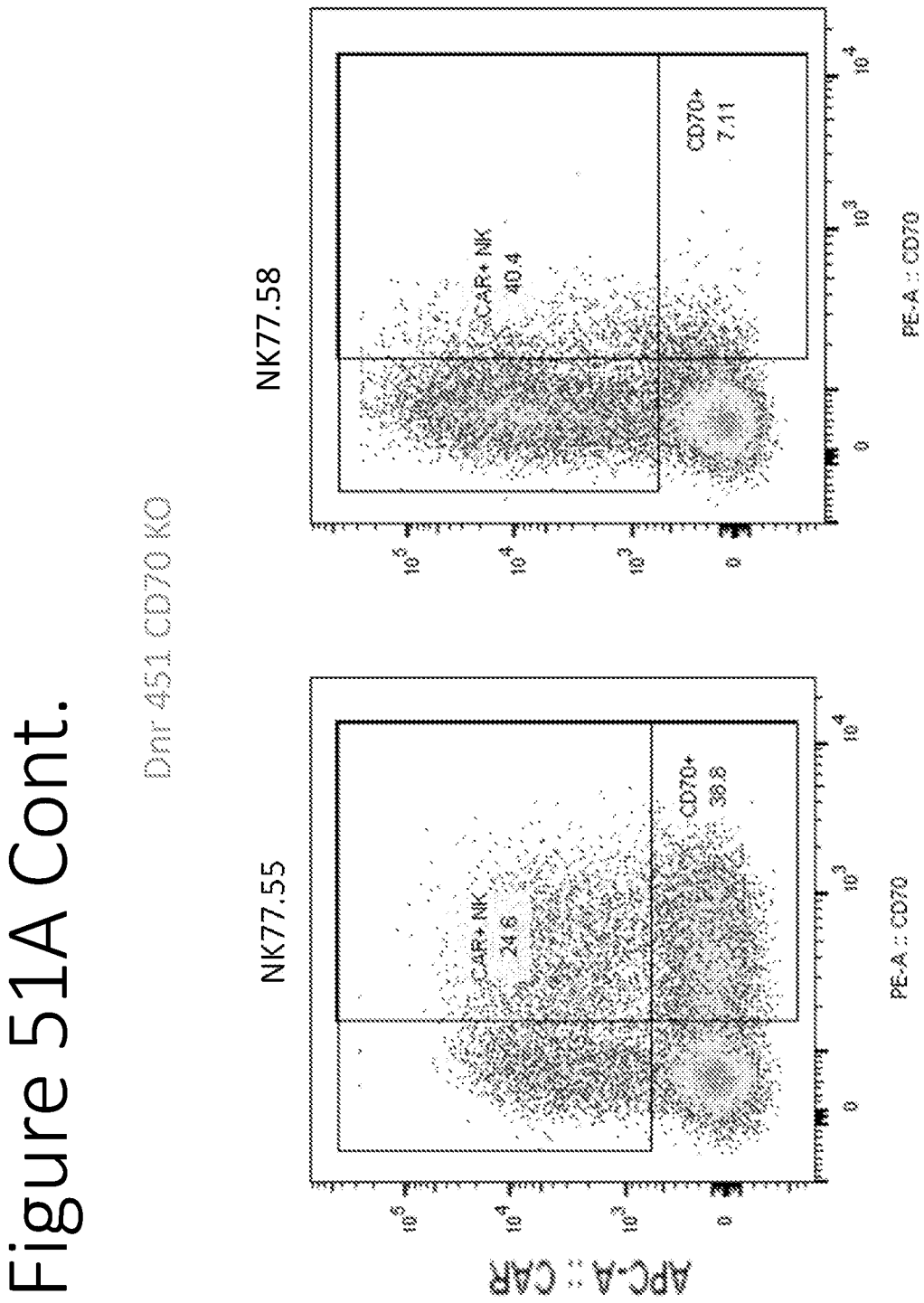


Figure 51A Cont.

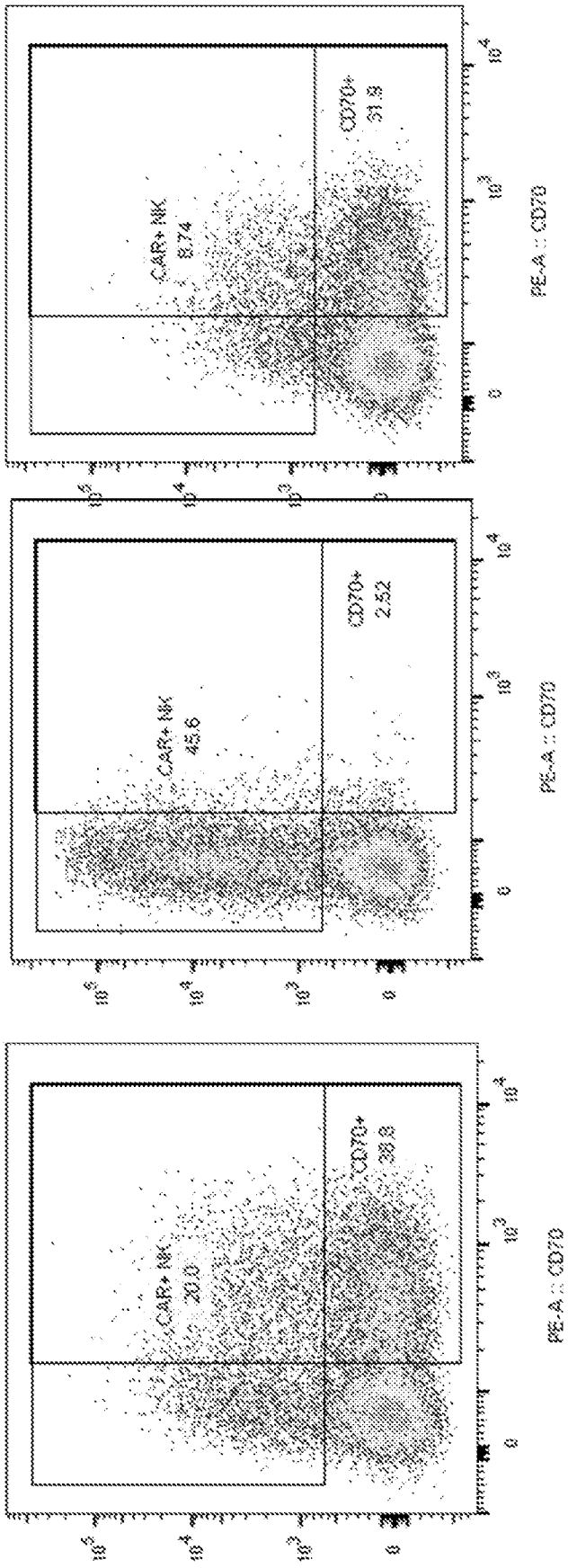


Figure 51B

B

Construct (Dnr 451 CD70 KO)	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)
NK77.55	1.03E+06	38.8%	24.6%
NK77.58	1.40E+06	7.11%	40.4%
NK77.65	5.95E+05	38.8%	20.0%
NK77.71	1.50E+06	2.52%	45.6%
NK77.73	9.17E+05	31.9%	8.74%
NK8	1.84E+06	57.9%	0.14%

Figure 52A

Dnr 454 CD70 KO

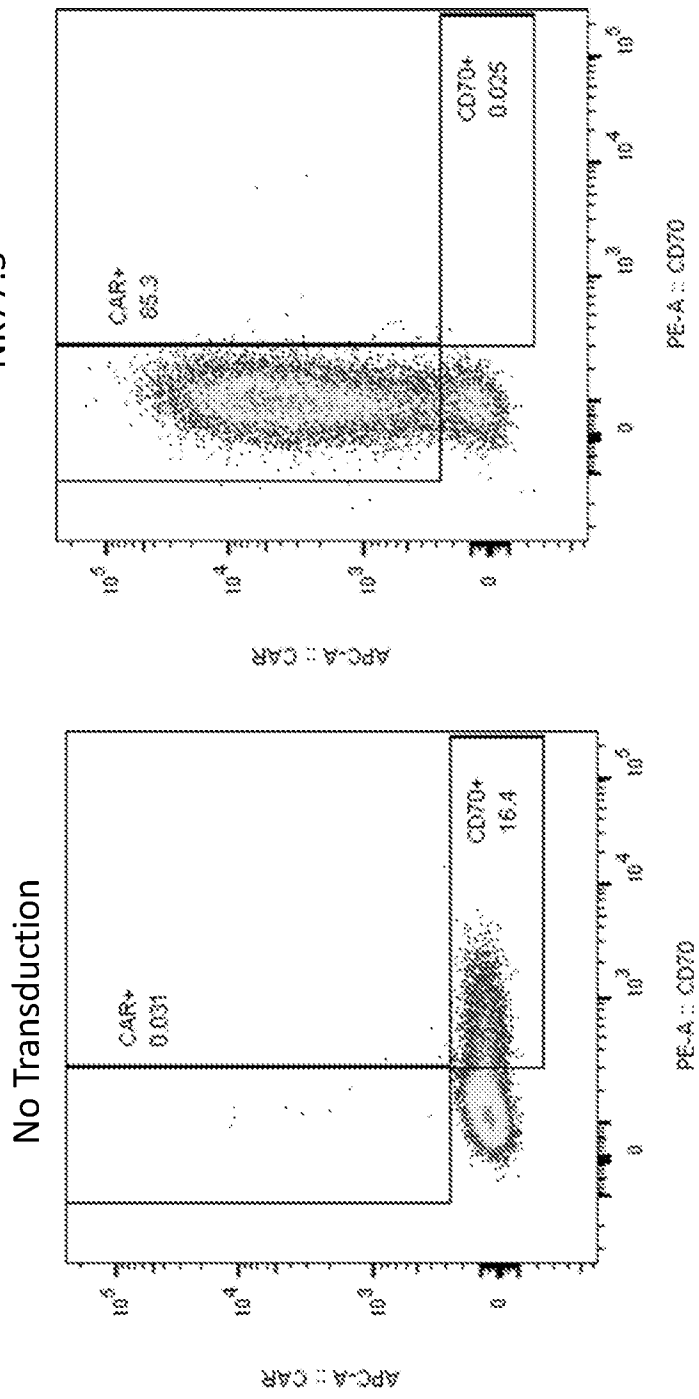


Figure 52A Cont.

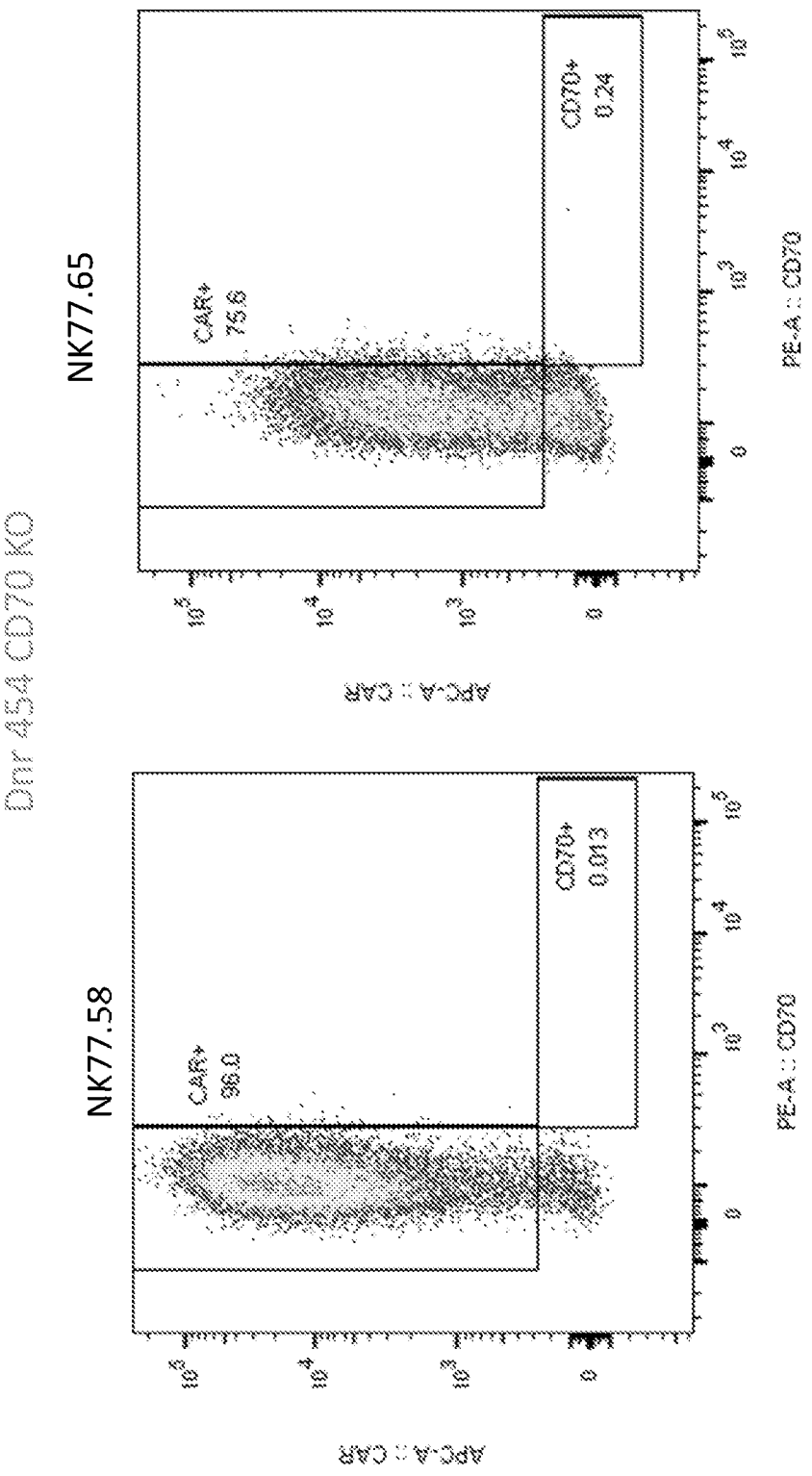


Figure 52A Cont.

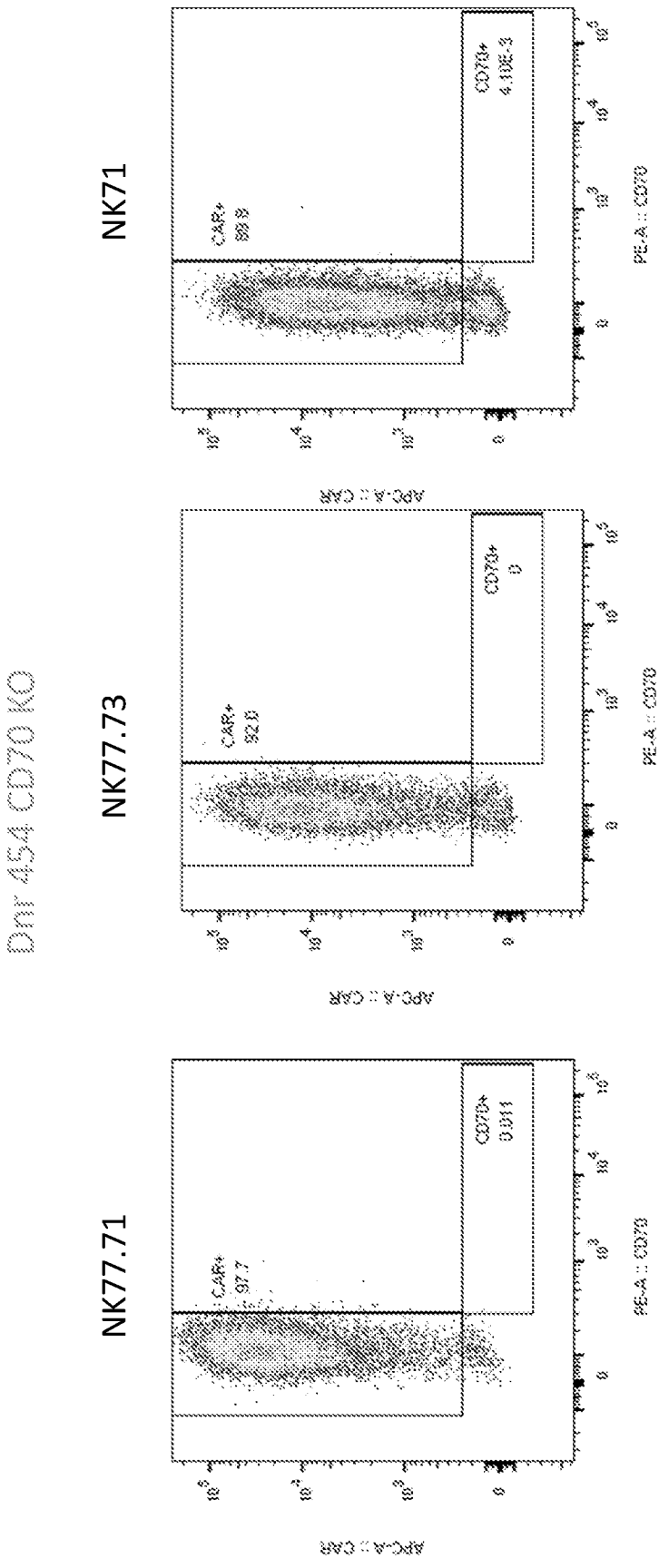


Figure 52B-52C

B

Construct	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)
NK77.55	1.03E+06	0.025%	85.3%
NK77.58	1.40E+06	0.013%	96.0%
NK77.65	5.95E+05	0.24%	75.6%
NK77.71	1.50E+06	0.011%	97.7%
NK77.73	9.17E+05	0.00%	92.0%
EPNT	-	16.4%	-
NK71	1.20E+06	0.004%	89.8%

C

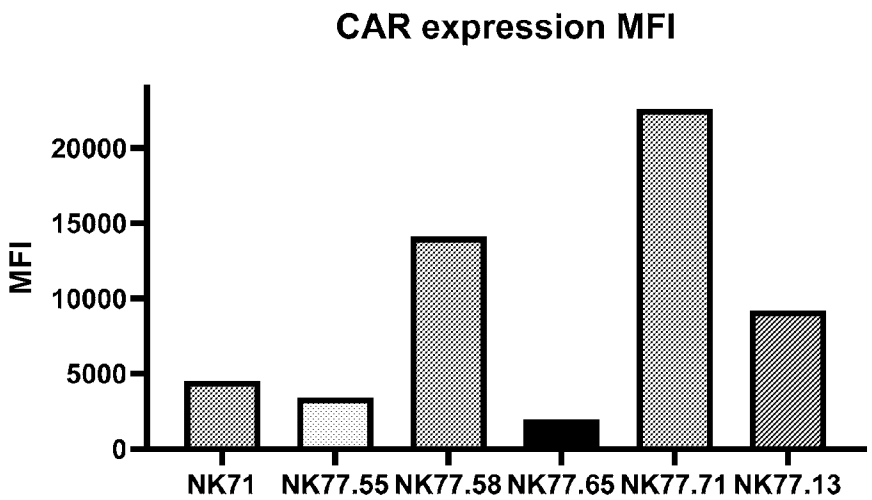
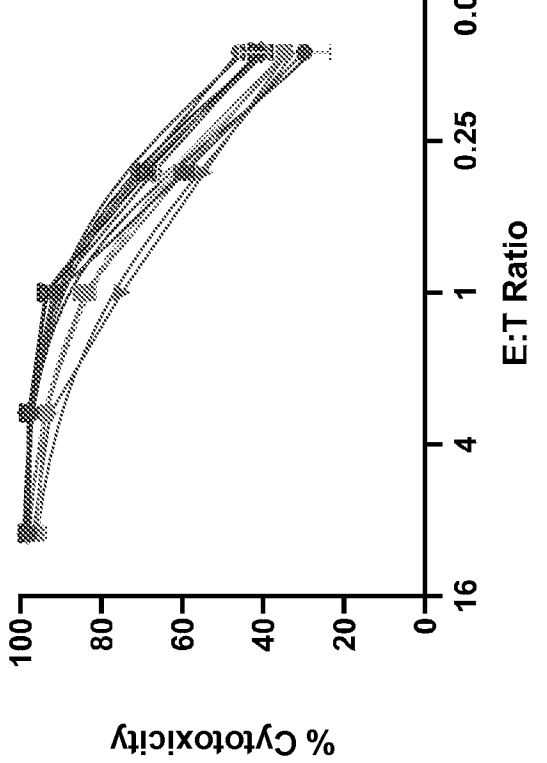


Figure 52D

D



Construct	EC_{50}
NK77.55	0.1544
NK77.58	0.1618
NK77.65	0.1340
NK77.71	0.2255
NK77.73	0.2126
NT	0.2016
NK71	0.2560

Figure 53A

A

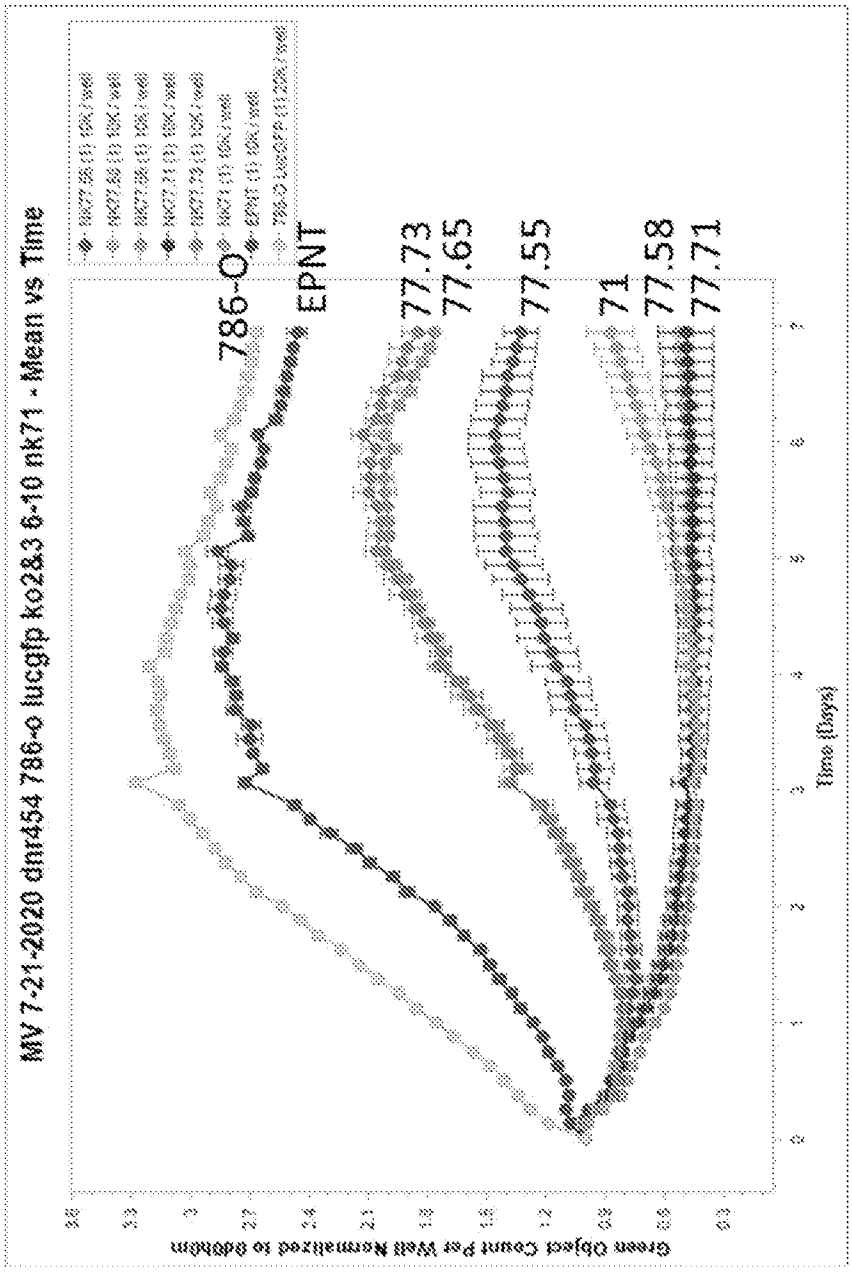

1:2 E:T
MV 7-21-2020 dnr454 786-o lucgfp ko2&3 6-10 nk71 - Mean vs Time
Green Object Count Per Well Normalized to 0dhhm
Time (Days)
786-O
EPNT
77.73
77.65
77.55
71
77.58
77.71

Figure 53B

B

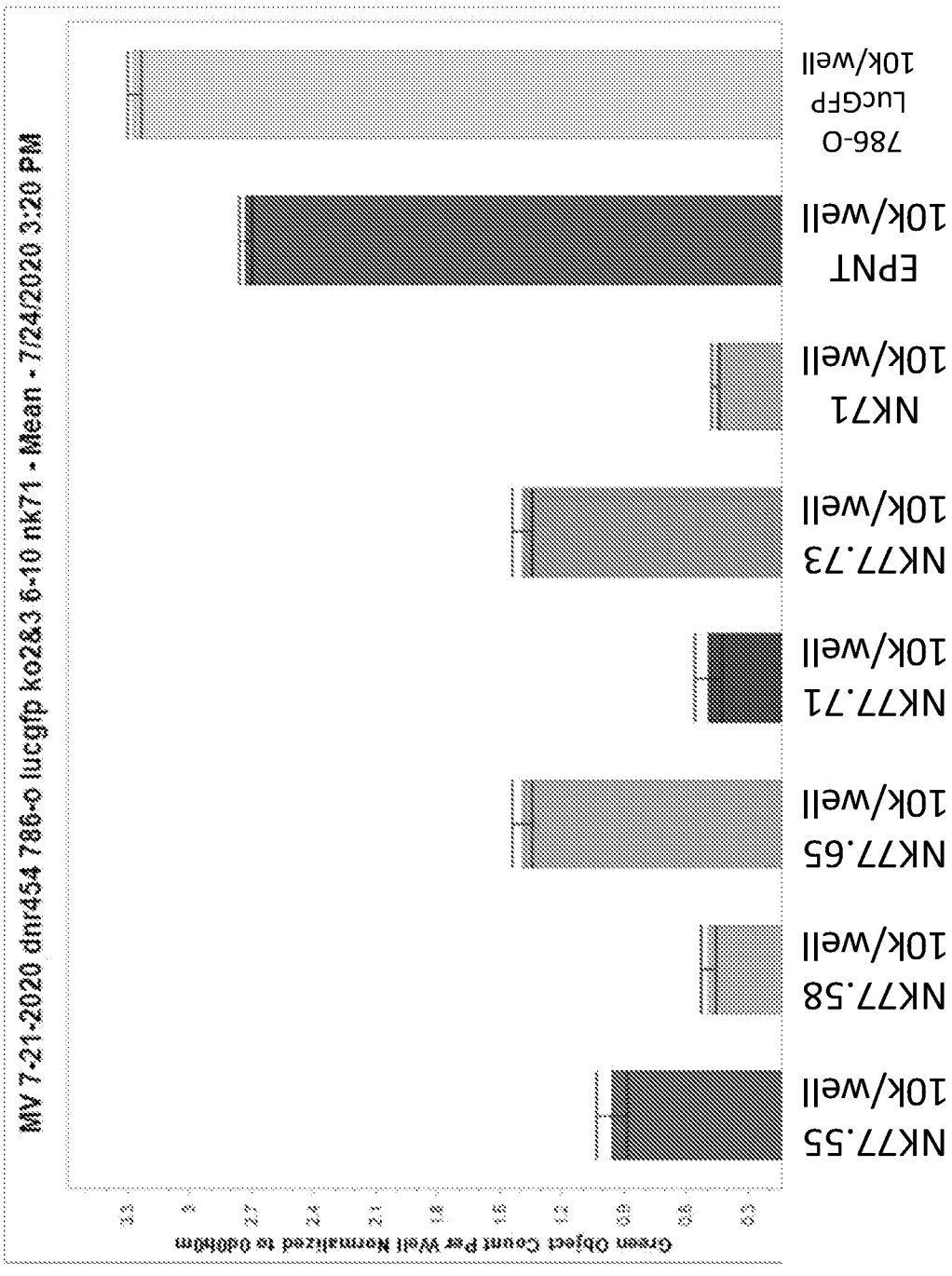

1:2 E:T at 73.5 hours (3 days)
MV 7-21-2020 dnr454 786-o lucgfp ko2&3 6-10 nk71 - Mean - 7/24/2020 3:20 PM
Green Object Count Per Well Normalized to 0dohlm
NK77.55 10k/well
NK77.58 10k/well
NK77.65 10k/well
NK77.71 10k/well
NK77.73 10k/well
NK71 10k/well
EPNT 10k/well
786-O LucGFP 10k/well

Figure 53C

c

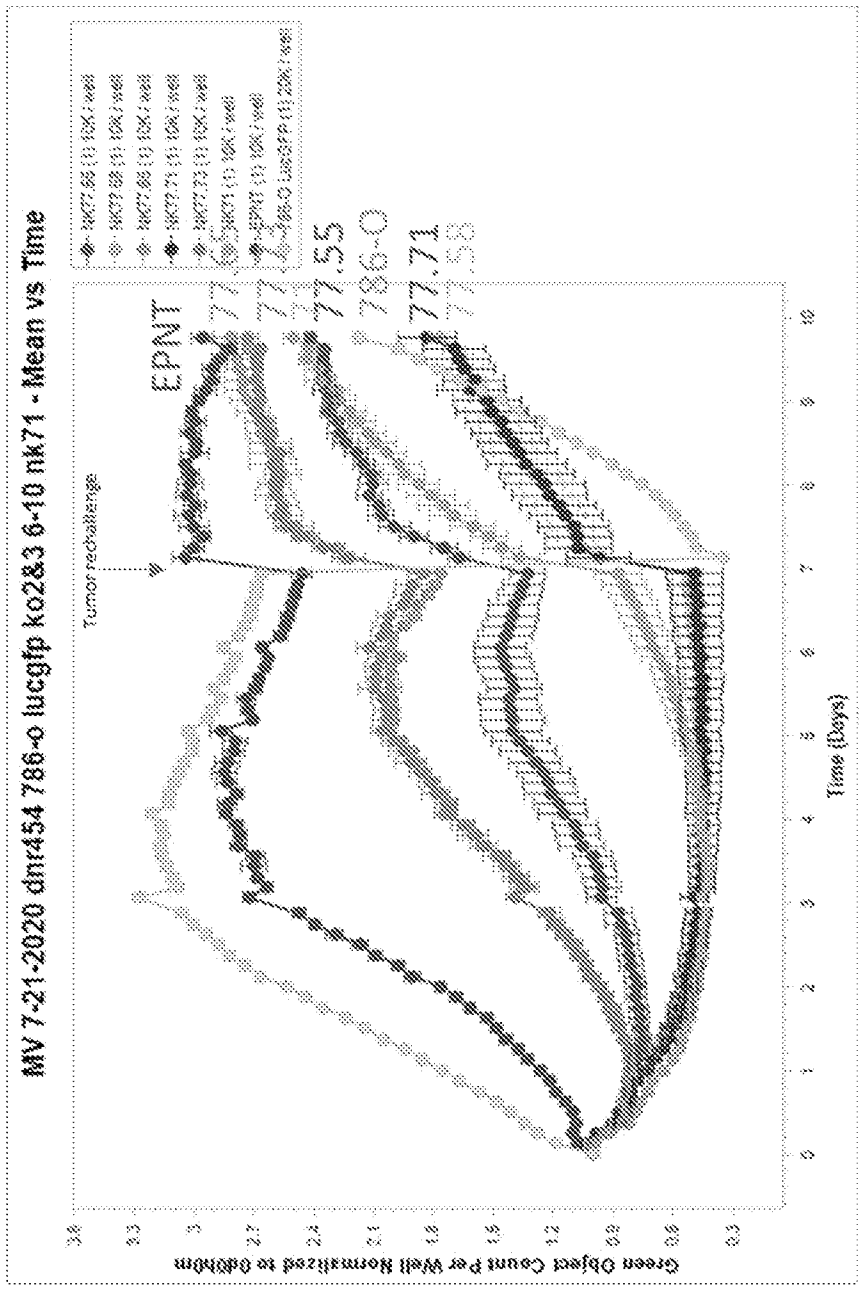

1:2 E:T
MV 7-21-2020 dnr454 786-o lucgfp ko2&3 6-10 nk71 - Mean vs Time
Tumor rechallenge
EPNT
77,55
786-O
77,71
Green Object Count Per Well Normalized to Cobblm
Time (Days)

Figure 53D

D

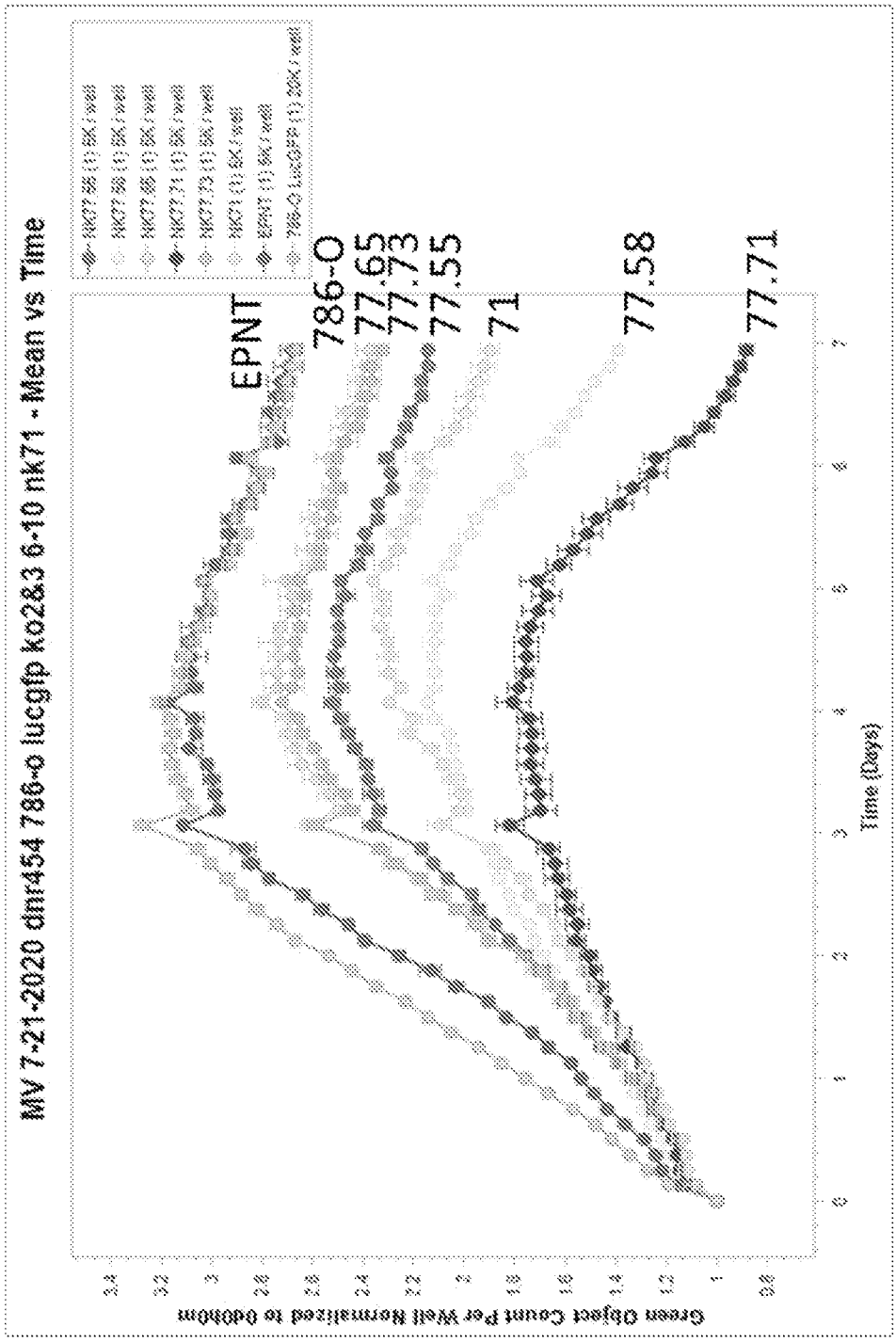

1:4 E:T
MV 7-21-2020 dnr454 786-o lucgfp ko2&3 6-10 nk71 - Mean vs Time
Green Object Count Per Well Normalized to 0dothom
Time (Days)
EPNT
786-O
77.65
77.73
77.55
71
77.58
77.71

Figure 53E

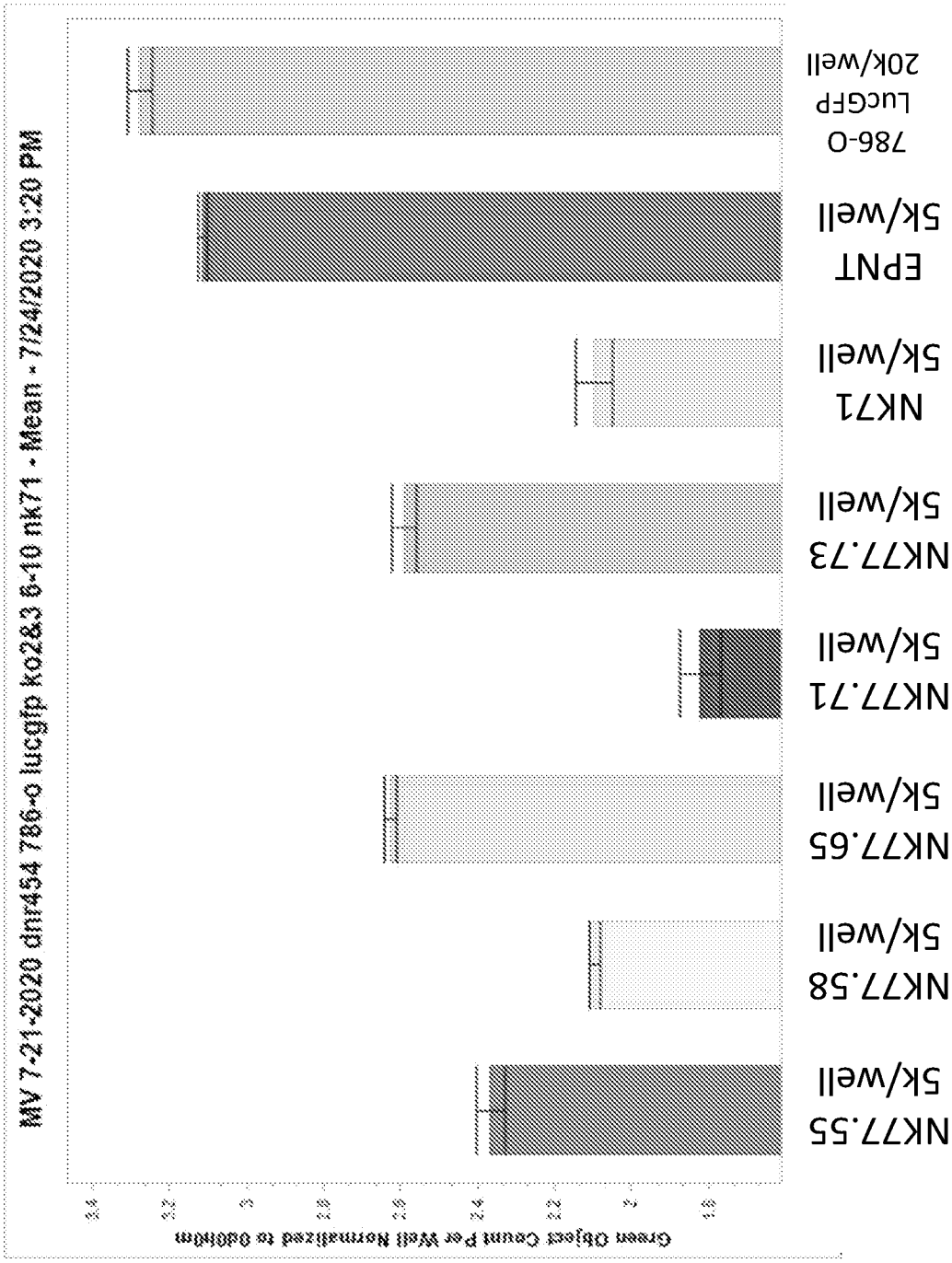

E
1:4 E:T at 73.5 hours (3 days)
MV 7-21-2020 dnr454 786-o lucgfp ko2&3 6-10 nk71 - Mean - 7/24/2020 3:20 PM
Green Object Count Per Well Normalized to 0dohm
3.4
3.2
3
2.8
2.6
2.4
2.2
2
1.8
NK77.55 5k/well
NK77.58 5k/well
NK77.65 5k/well
NK77.71 5k/well
NK77.73 5k/well
NK71 5k/well
EPNT 5k/well
786-O LucGFP 20k/well

Figure 53F

F

1:8 E:T

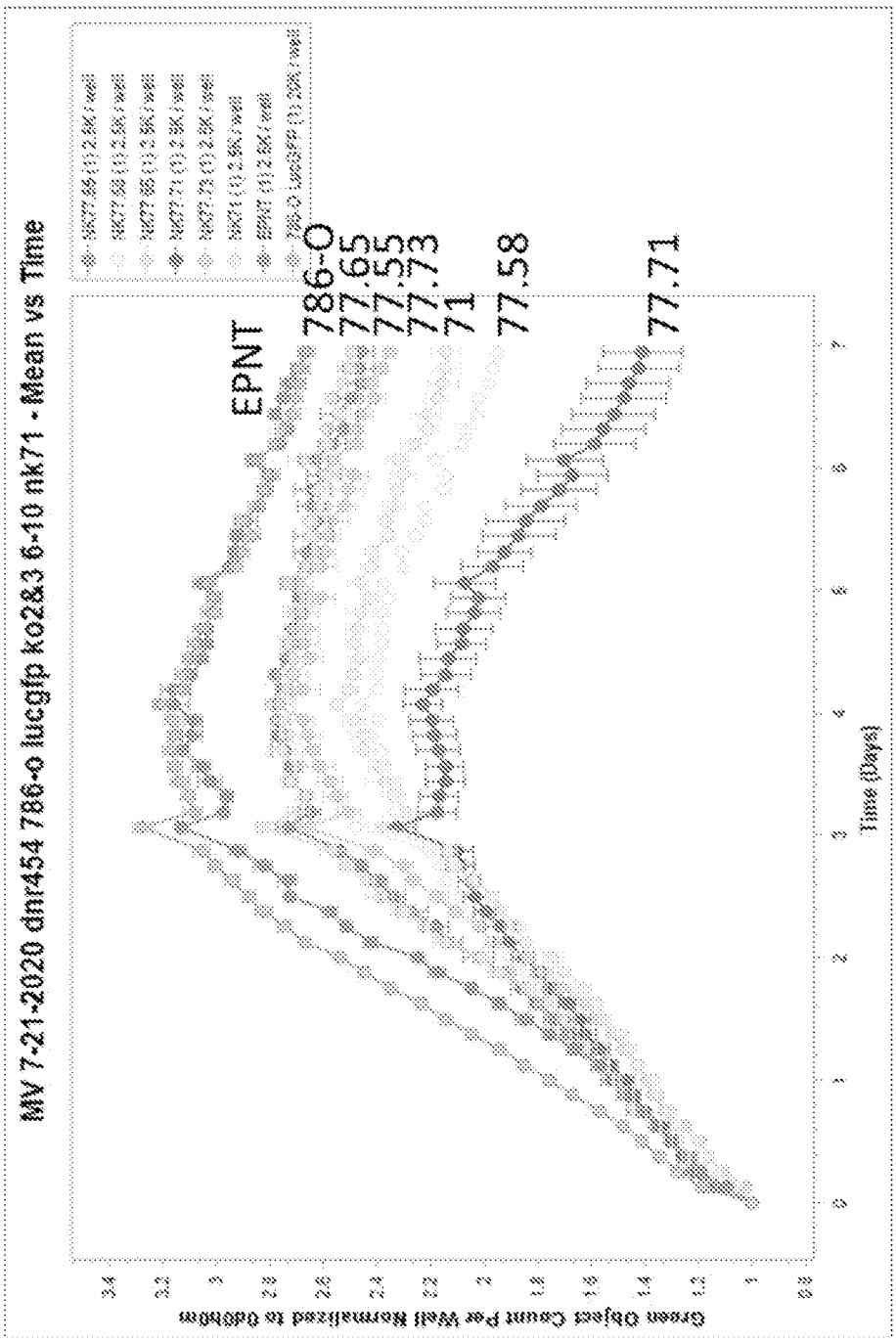


Figure 54A

A

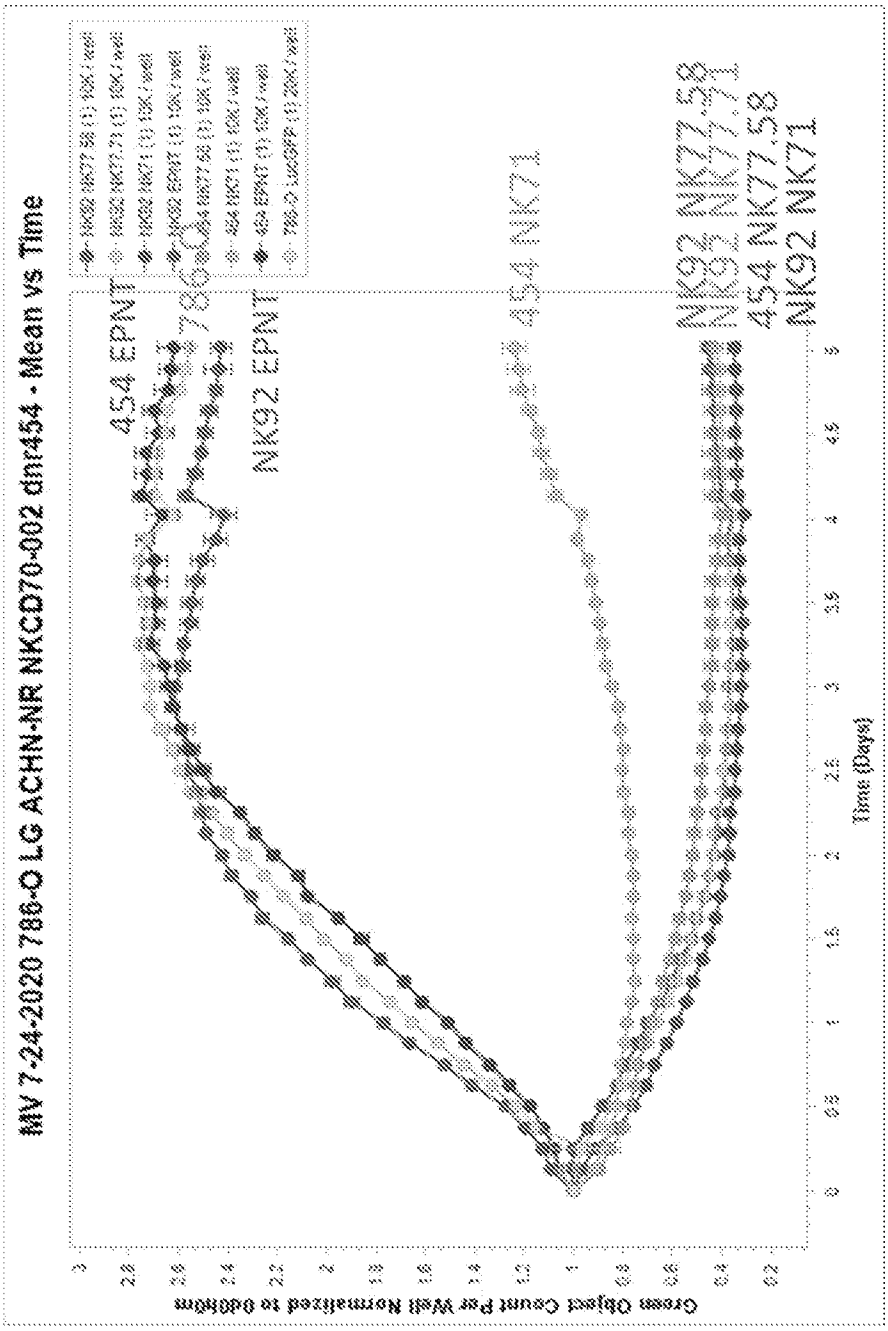

1:2 E:T 786-O (GFP)
MV 7-24-2020 786-O LG ACHN-NR NKCD70-002 dnr454 - Mean vs Time
Green Object Count Per Well Normalized to 0dMin
Time (Days)
454 EPNT
786-O
NK92 EPNT
454 NK71
NK92 NK77.58
NK92 NK77.71
454 NK77.58
NK92 NK71

Figure 54B

B

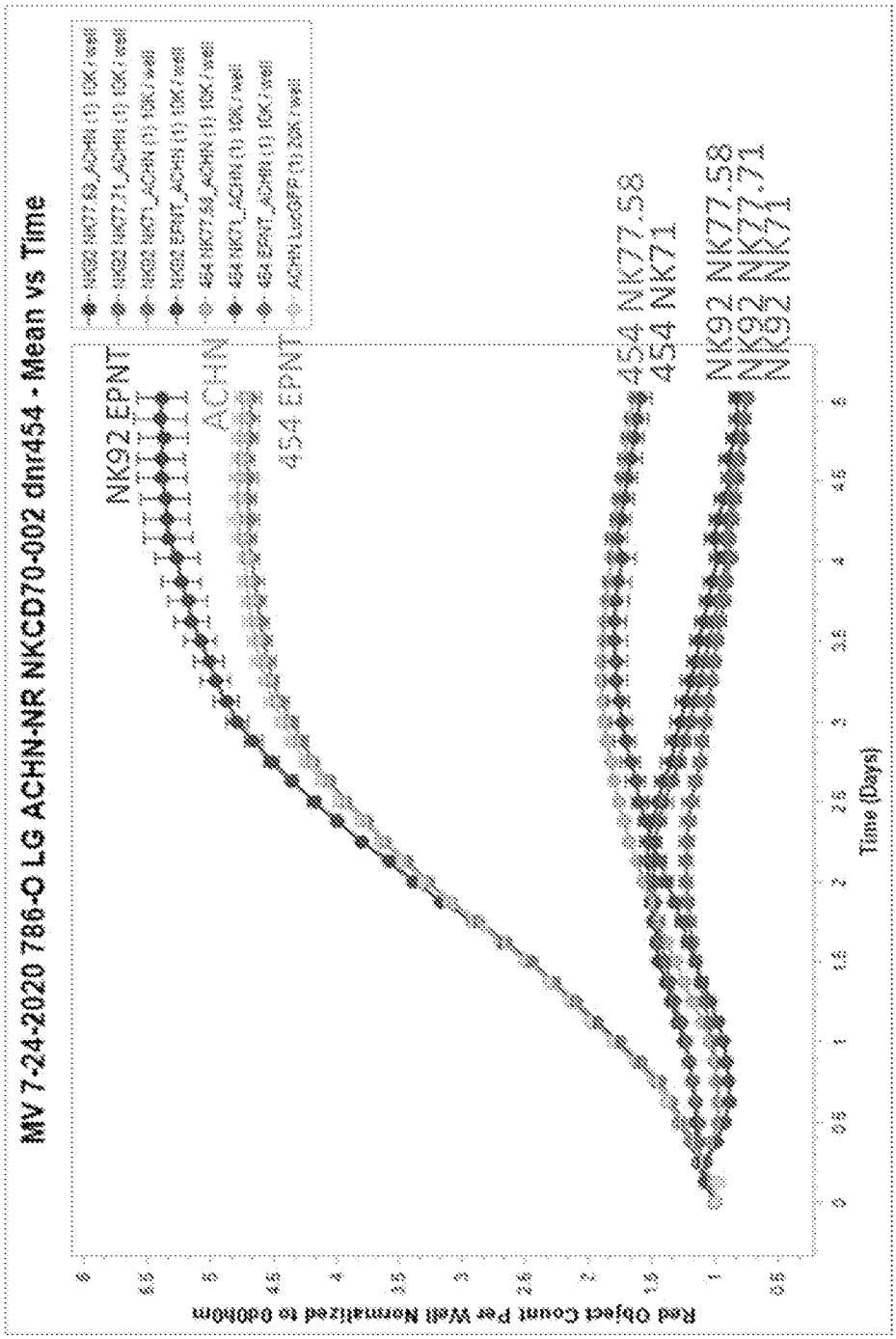

1:2 E:T ACHN (NucRed)
MV 7-24-2020 786-O LG ACHN-NR NKCD70-002 dnr454 - Mean vs Time
Red Object Count Per Well Normalized to 0dhour
Time (Days)
NK92 EPNT
ACHN
454 EPNT
454 NK77.58
454 NK71
NK92 NK77.58
NK92 NK71.71

Figure 54C

c

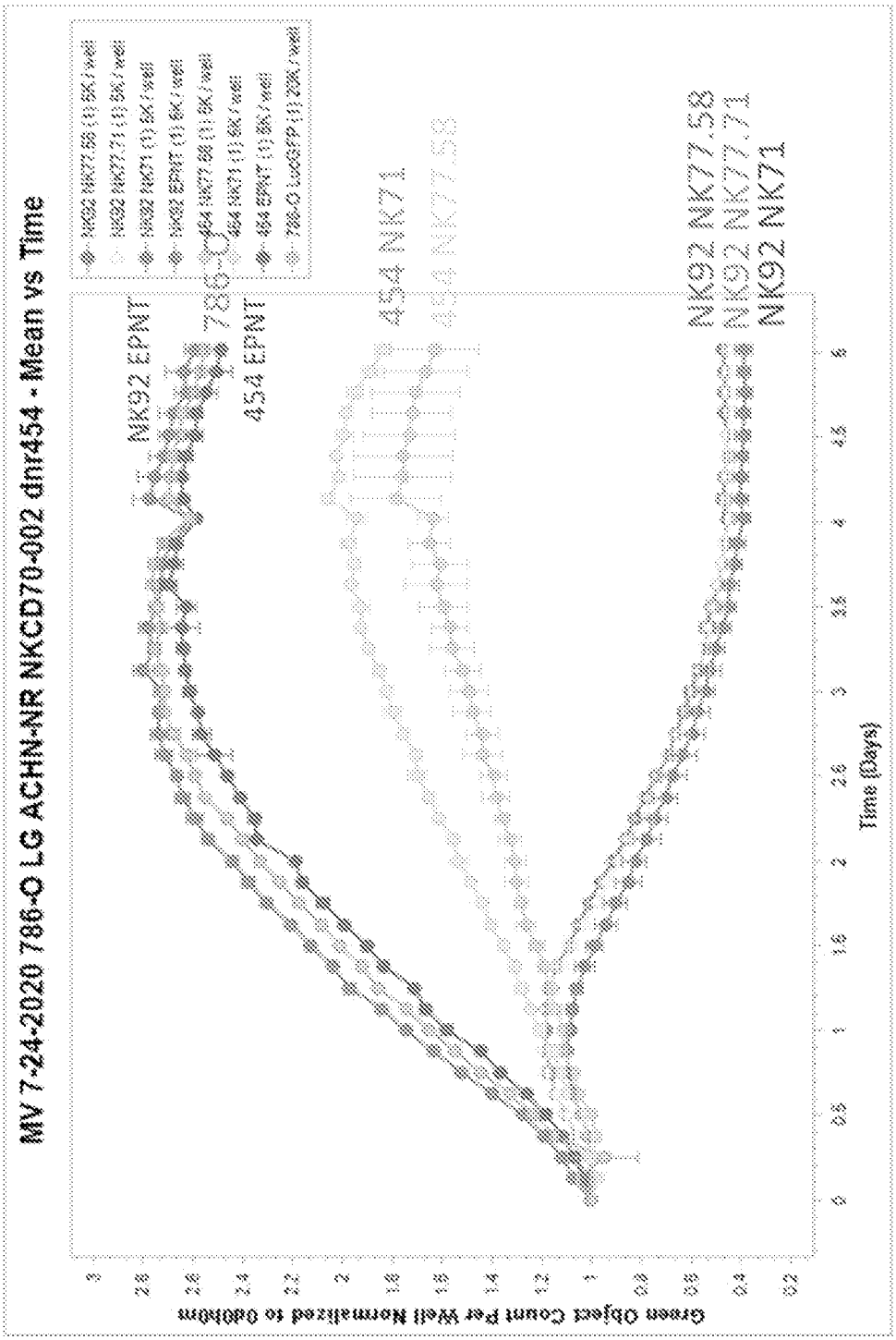
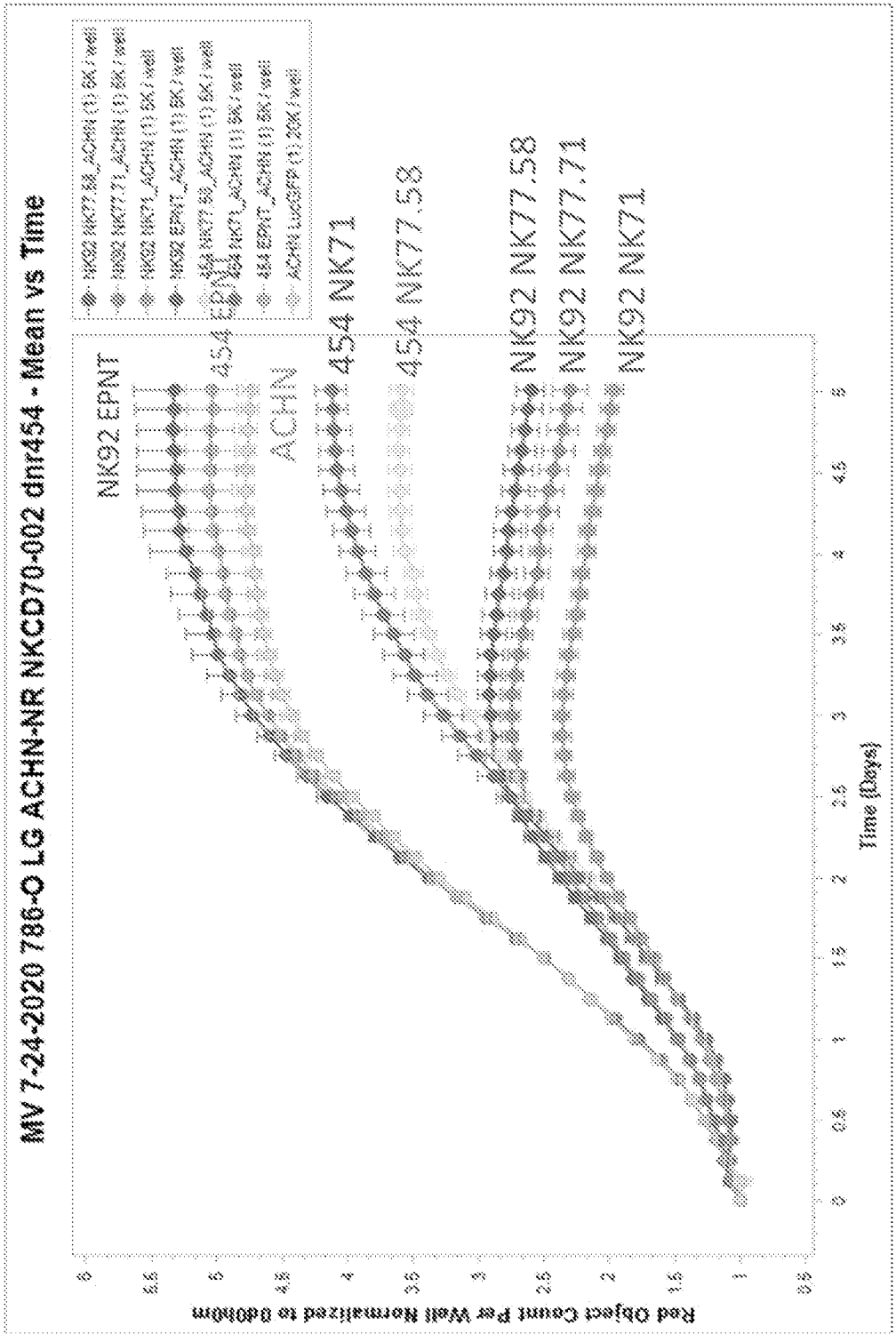
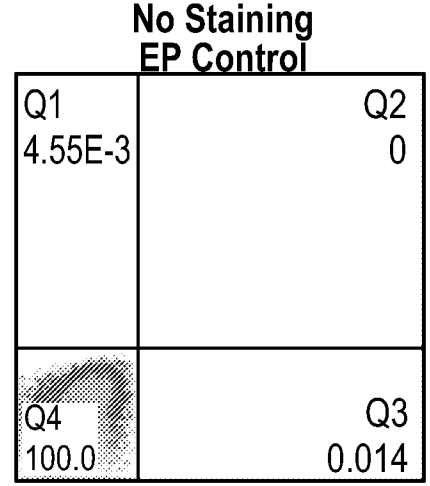

1:4 E:T 786-O (GFP)
MV 7-24-2020 786-O LG ACHN-NR NKCD70-002 dnr454 - Mean vs Time
Green Object Count Per Well Normalized to 0dohm
Time (Days)
NK92 EPNT
454 EPNT
454 NK71
NK92 NK77.58
NK92 NK77.71
NK92 NK71

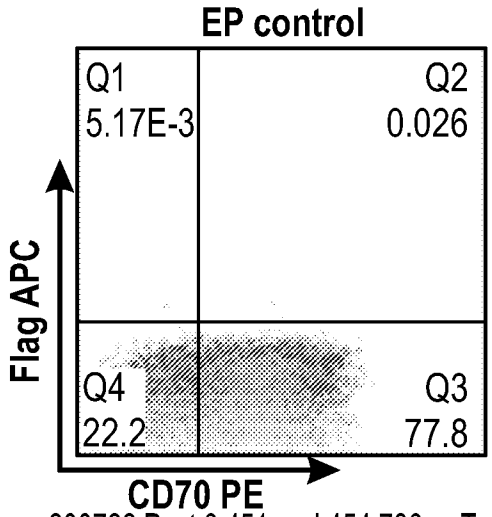
Figure 54D

D

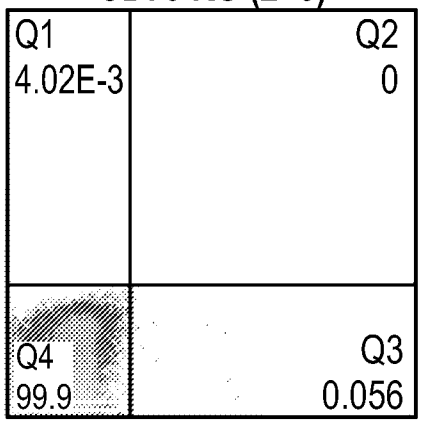

1:4 E:T ACHN (NucRed)
MV 7-24-2020 786-O LG ACHN-NR NKCD70-002 dnr454 - Mean vs Time
NK92 EPNT
454 EPNT
ACHN
454 NK71
454 NK77.58
NK92 NK77.58
NK92 NK77.71
NK92 NK71
Red Object Count Per Well Normalized to Bottom
Time (Days)



200722 Post 6 451 and 454 786-o_Tube_001_001.fcs
FSC-A, Comp-BV421-A Subset 21962

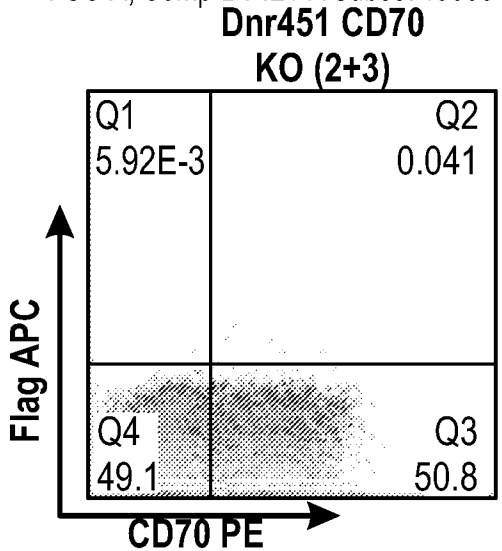


200722 Post 6 451 and 454 786-o_Tube_002_002.fcs
FSC-A, Comp-BV421-A Subset 19358



200722 Post 6 451 and 454 786-o_Tube_003_003.fcs
FSC-A, Comp-BV421-A Subset 24858

FIG. 55A



200722 Post 6 451 and 454 786-o_Tube_004_004.fcs FSC-A, Comp-BV421-A Subset 16905

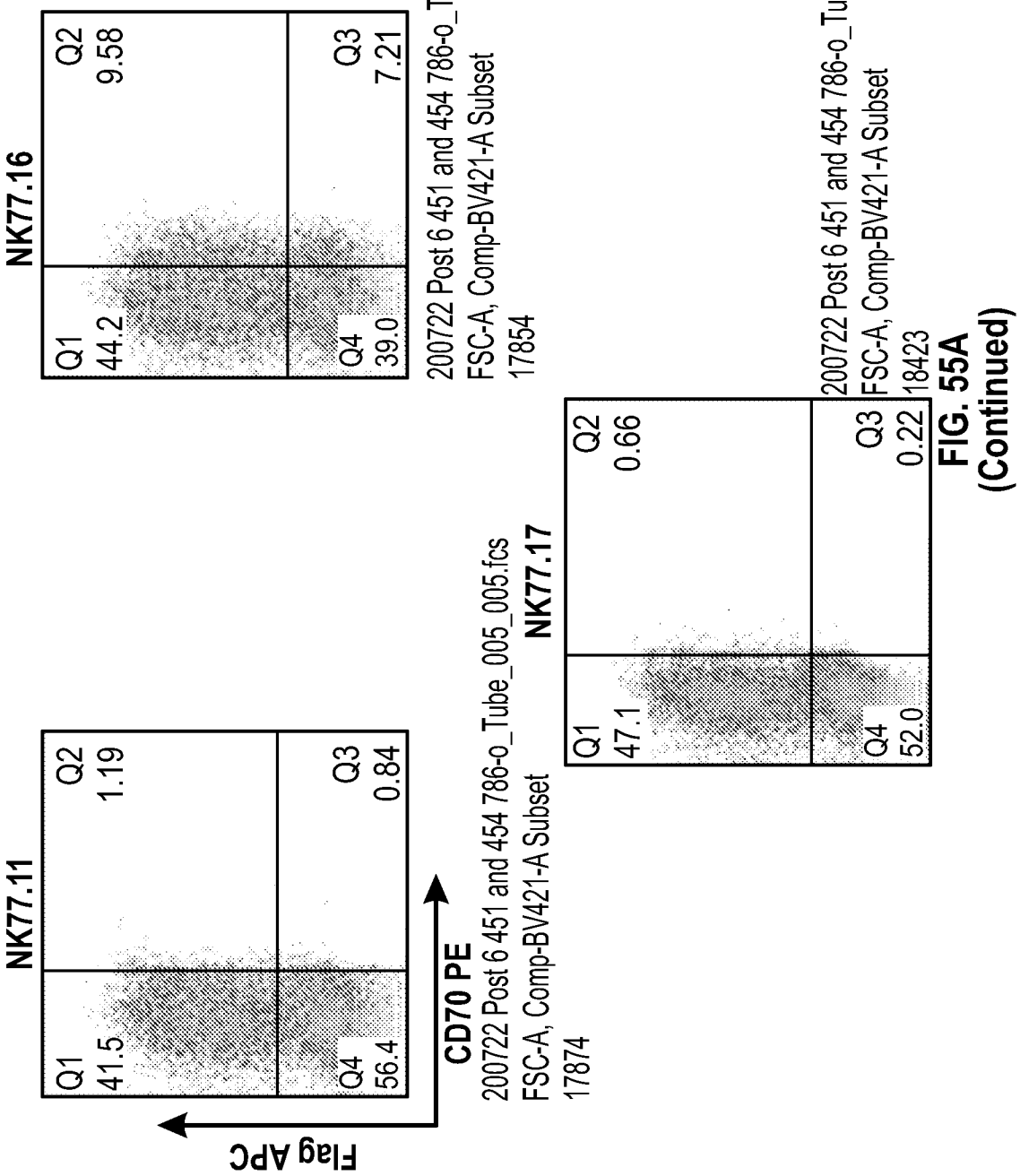
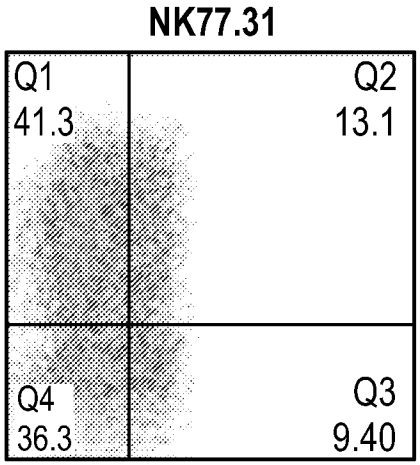
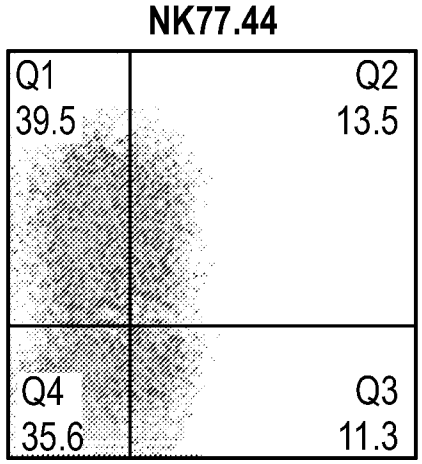


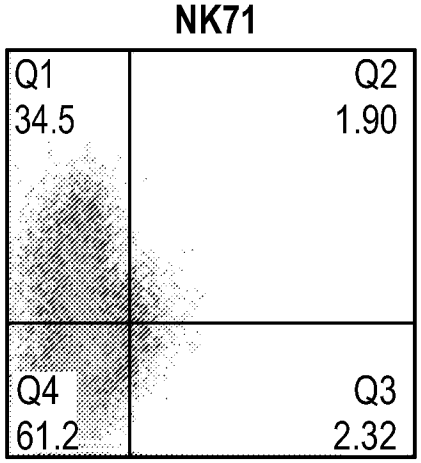
FIG. 55A (Continued)



200722 Post 6 451 and 454 786-o_Tube_008_008.fcs
FSC-A, Comp-BV421-A Subset
18996



200722 Post 6 451 and 454 786-o_Tube_009_009.fcs
FSC-A, Comp-BV421-A Subset
20711

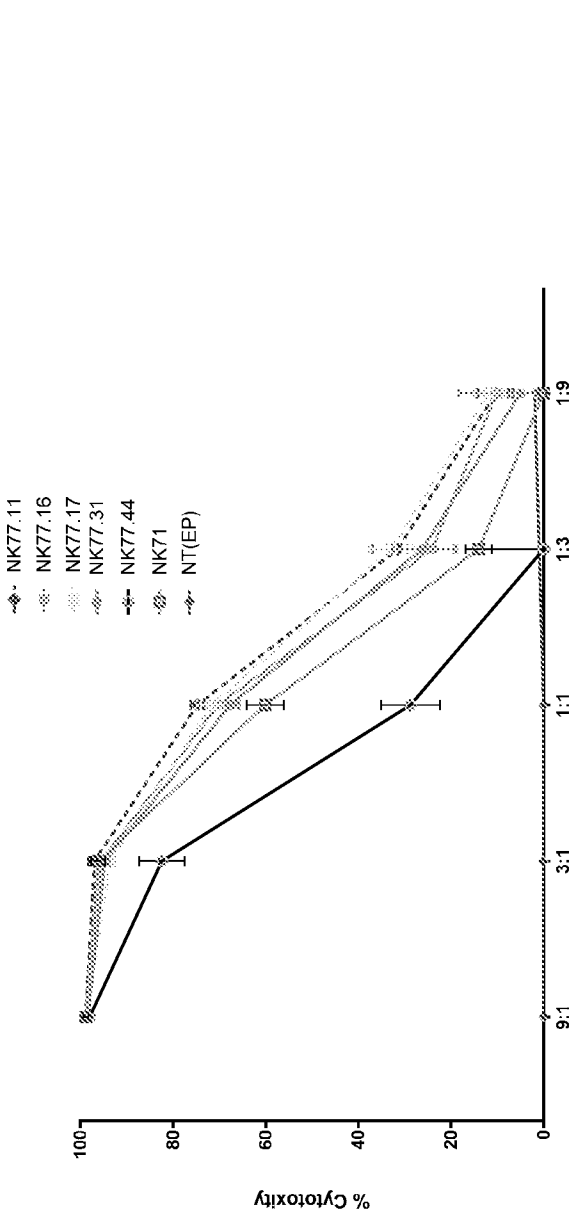


200722 Post 6 451 and 454 786-o_Tube_010_010.fcs
FSC-A, Comp-BV421-A Subset
18778

FIG. 55A
(Continued)

Figure 55B-55C

B

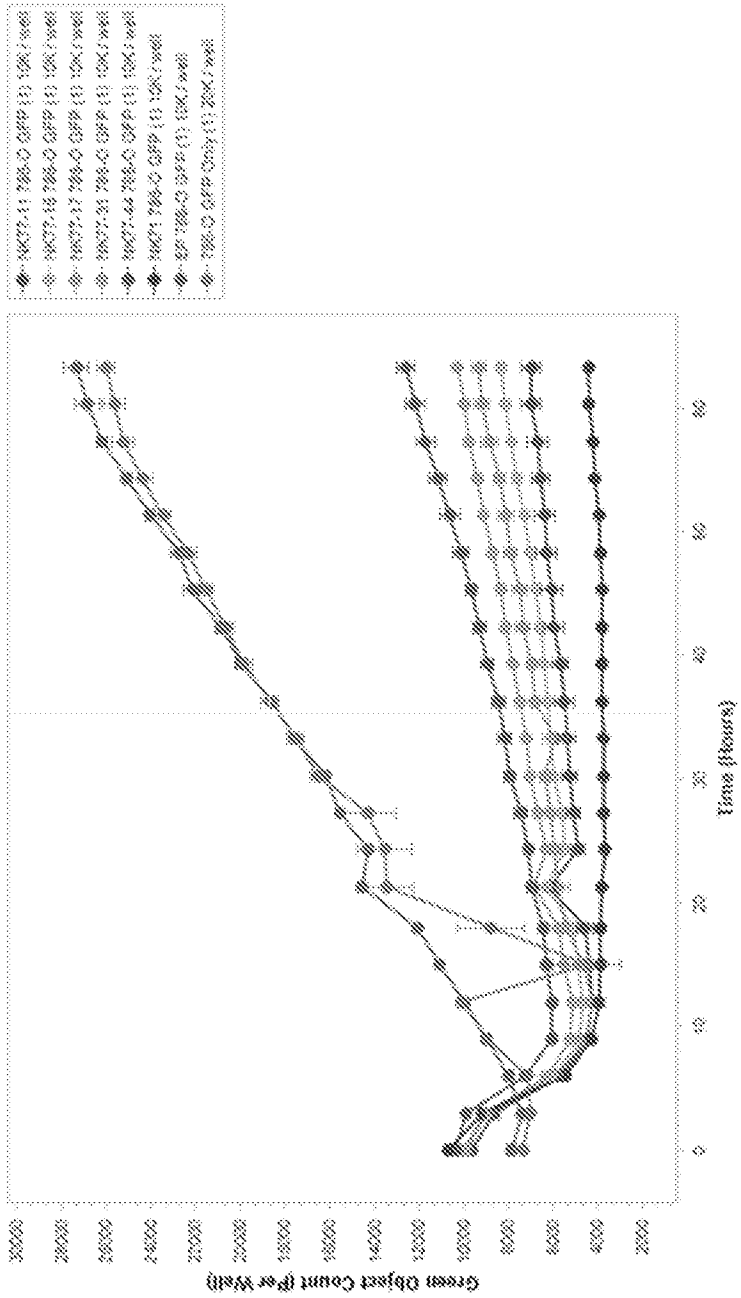


C

Construct	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)	EC50
NK77.11	2.85E+06	0.84%	45%	0.5154
NK77.16	3.15E+06	7.21%	54.7%	0.6104
NK77.17	2.88E+06	0.22%	53.7%	0.5257
NK77.31	3.51E+06	9.4%	49%	0.6293
NK77.44	3.57E+06	11.3	54%	1.513
EPNT	-	77.8%	-	-
NK71	1.20E+06	2.32%	37.5%	0.8364

Figure 55D

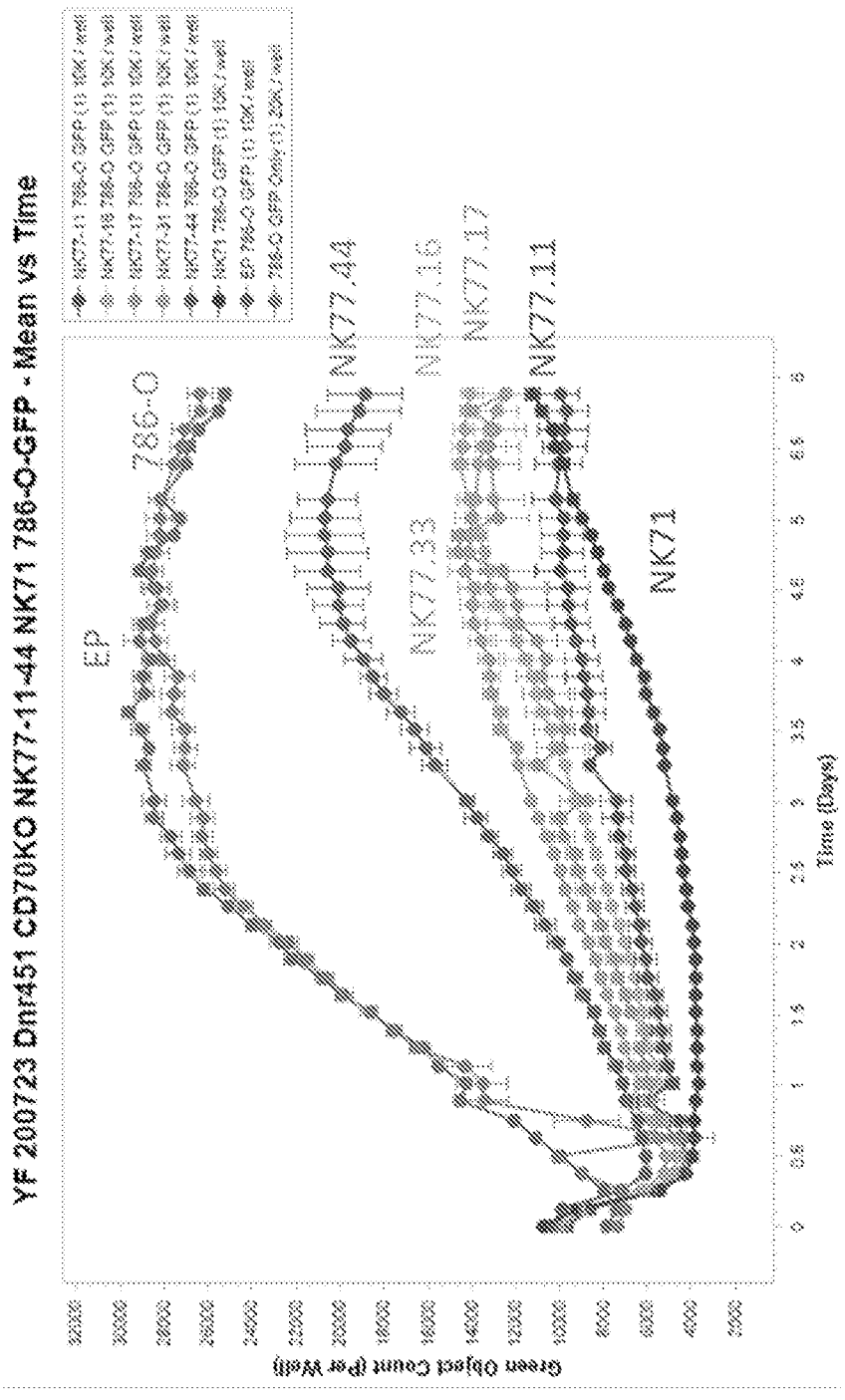
D



E:T=1:2

Figure 55E

E



E:T=1:2

Figure 55F

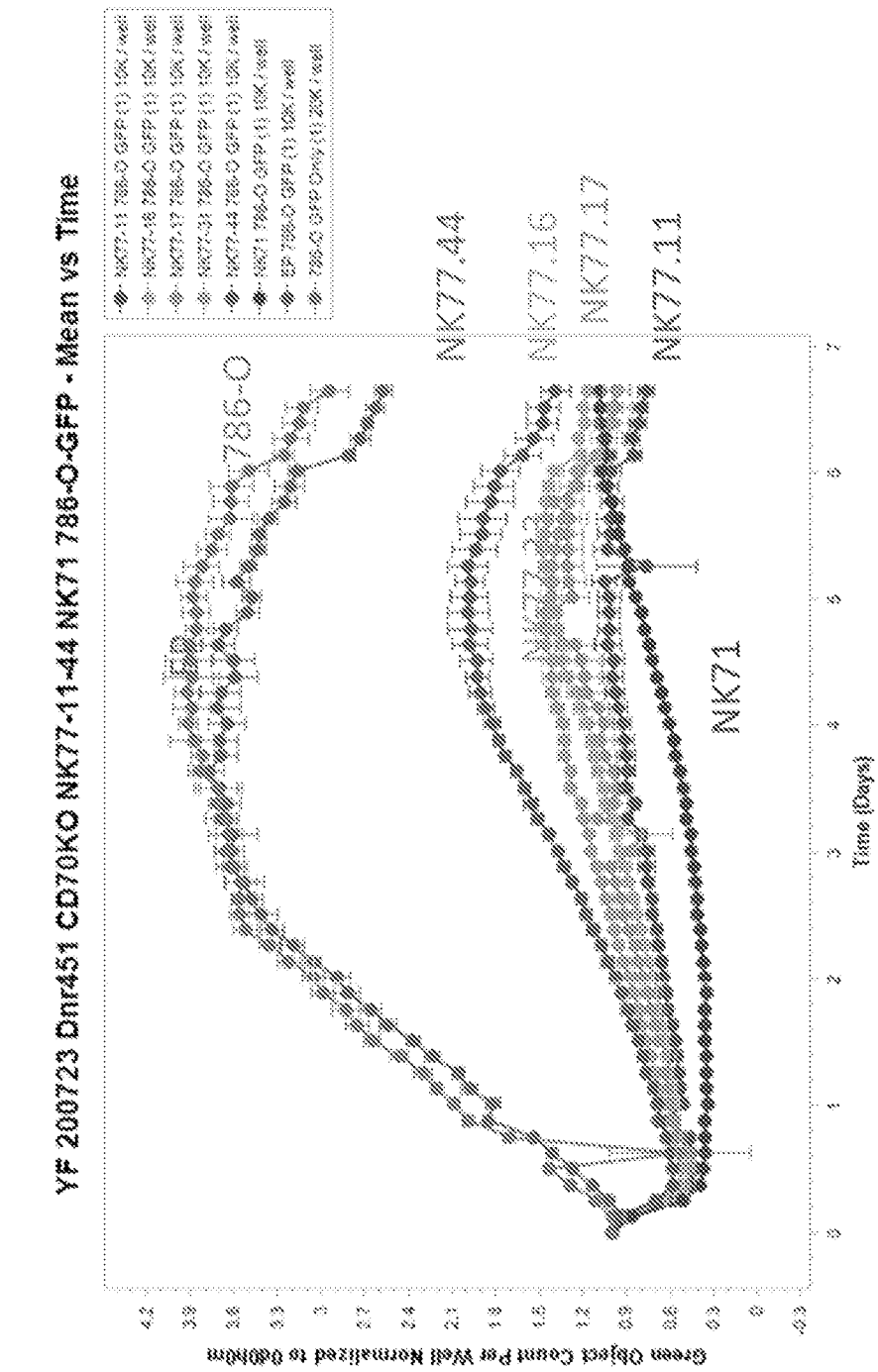

YF 200723 Dnr451 CD70KO NK77-11-44 NK71 786-O-GFP - Mean vs Time
Green Object Count Per Well Normalized to 0dhhr
Time (Days)
NK77.44
NK77.16
NK77.17
NK77.11
NK71
786-O
E:T=1:2

Figure 55G

G

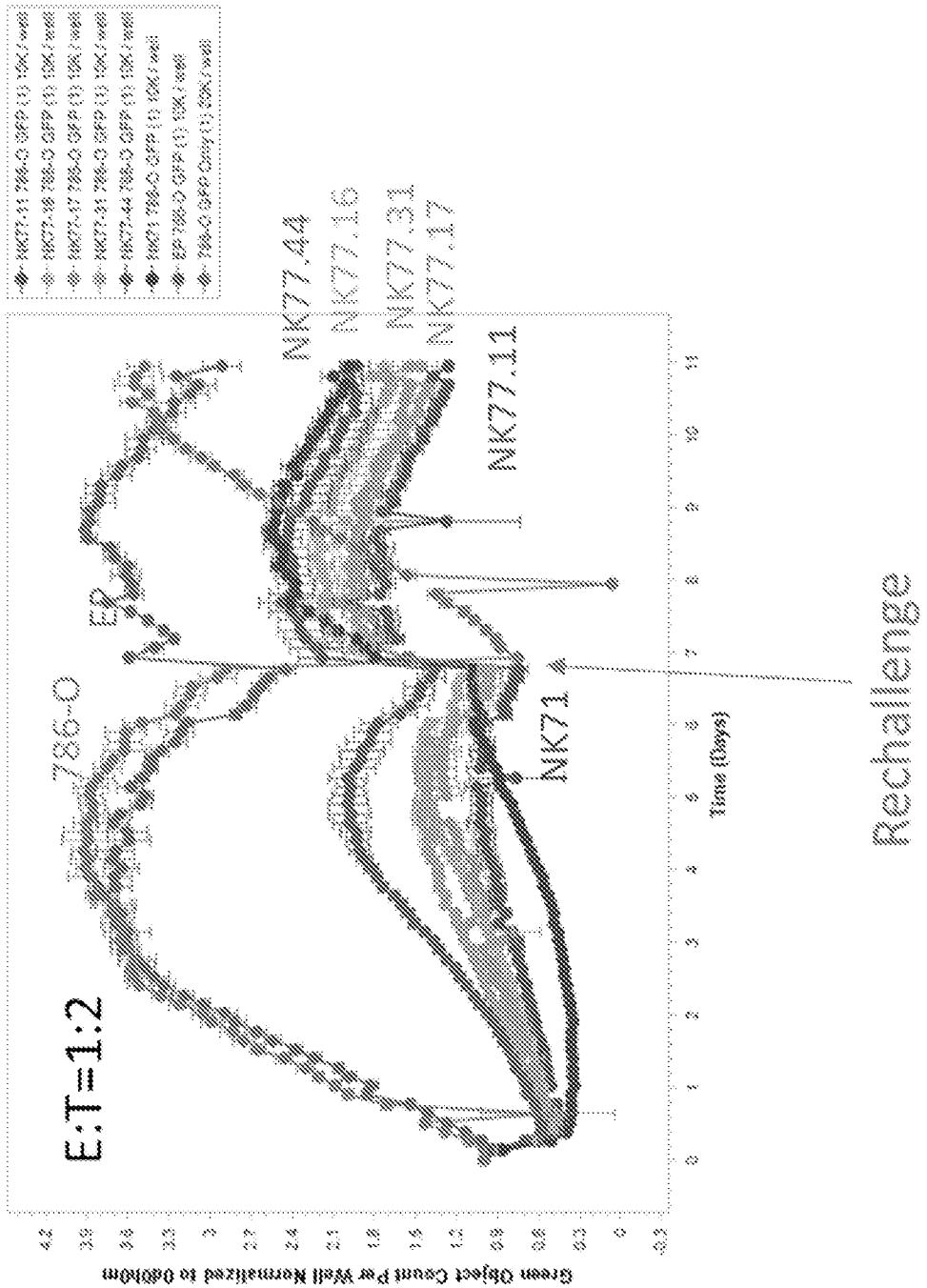

YF 200723 Dnr451 CD70KO NK77-11-44 NK71 786-O-GFP - Mean vs Time
E:T=1:2
786-O
ER
NK77.44
NK77.16
NK77.31
NK77.17
NK77.11
NK71
Rechallenge
Time (Days)
Green Object Count Per Well Normalized to 0dhhm

Figure 55H

H

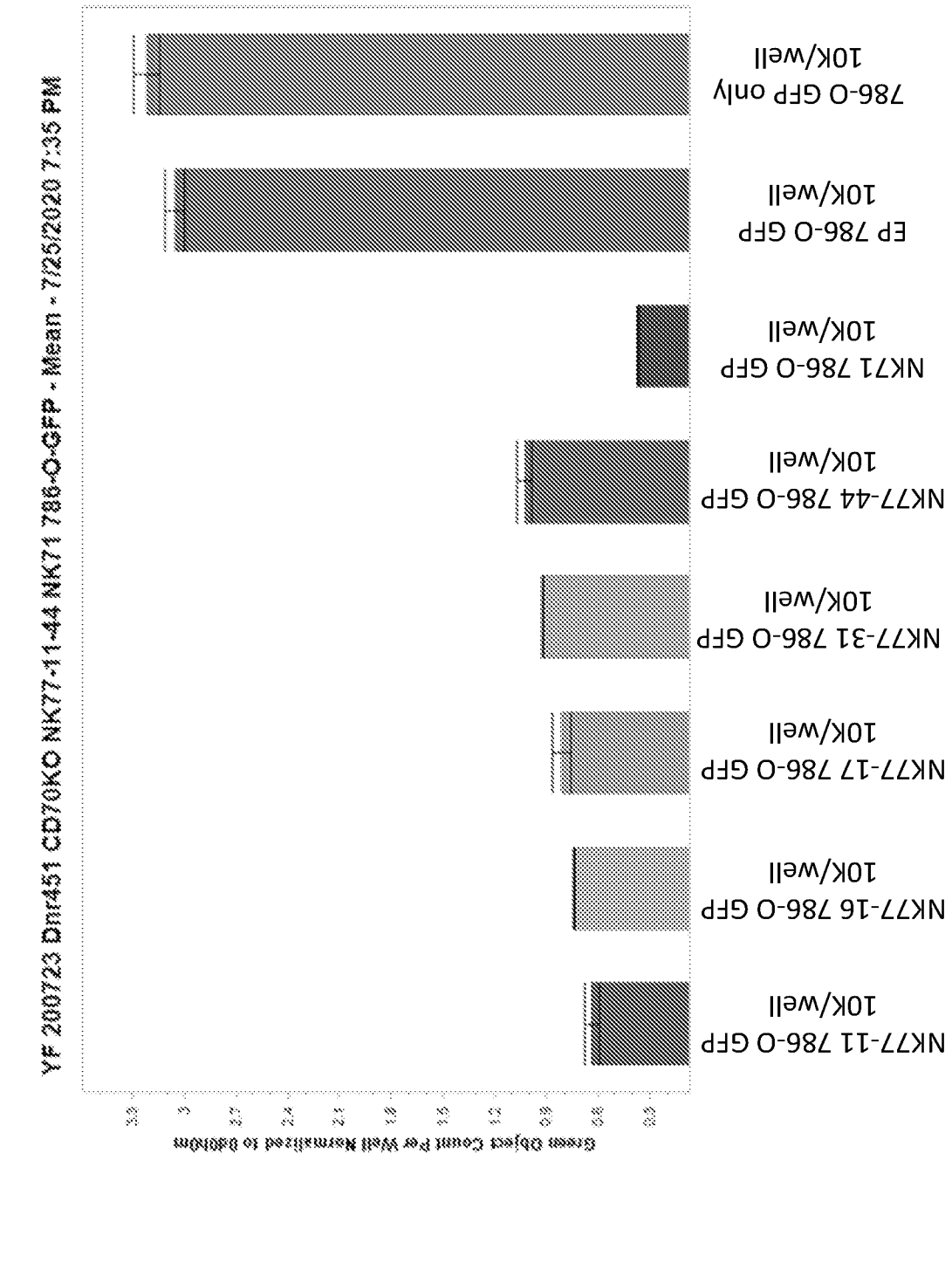

1:2 E:T 786-O at 51 hours
YF 200723 Dnr451 CD70KO NK77-11-44 NK71 786-O-GFP - Mean - 7/25/2020 7:35 PM
Green Object Count Per Well Normalized to Baseline
NK77-11 786-O GFP 10K/well
NK77-16 786-O GFP 10K/well
NK77-17 786-O GFP 10K/well
NK77-31 786-O GFP 10K/well
NK77-44 786-O GFP 10K/well
NK71 786-O GFP 10K/well
EP 786-O GFP 10K/well
786-O GFP only 10K/well

Figure 55I

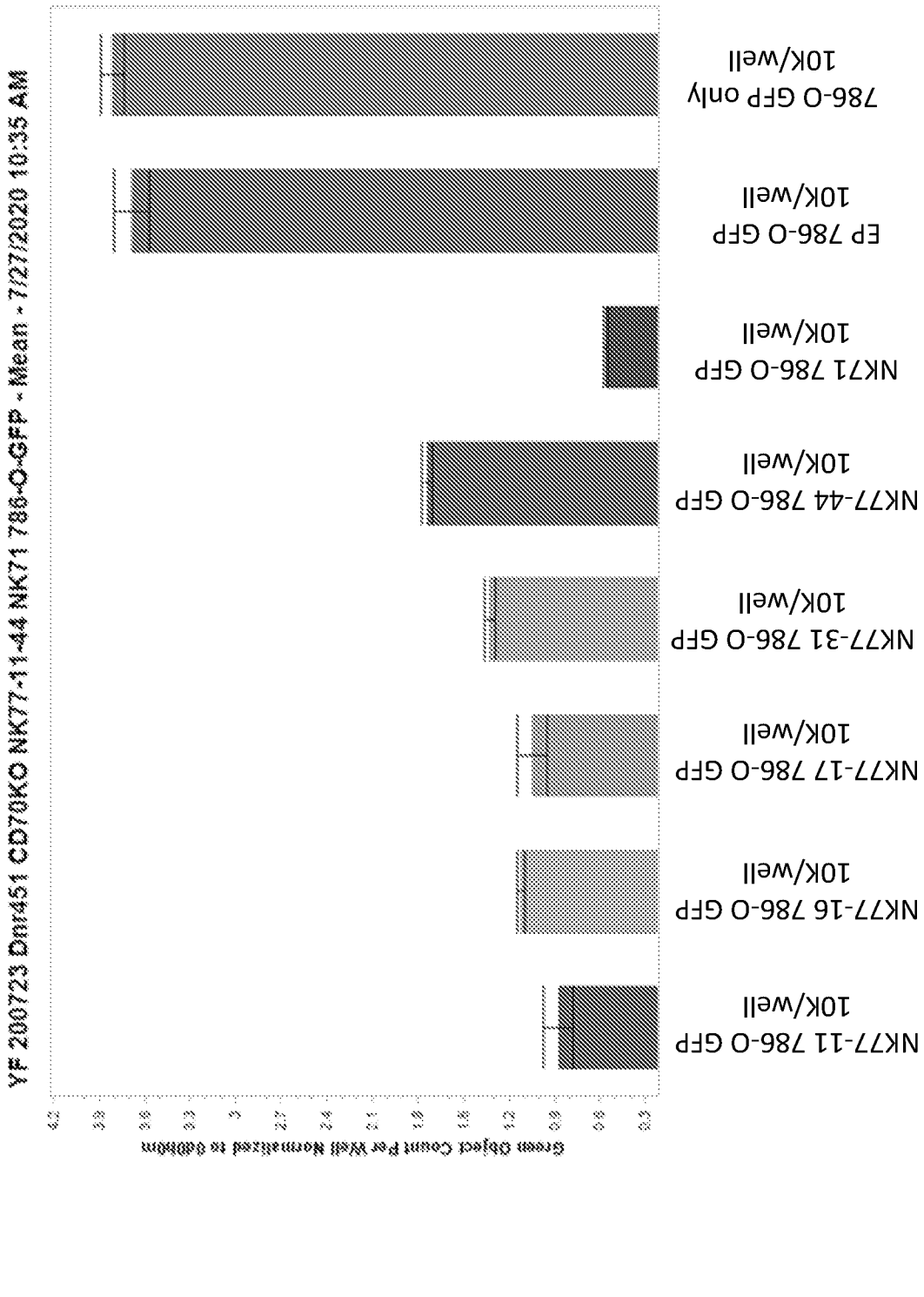
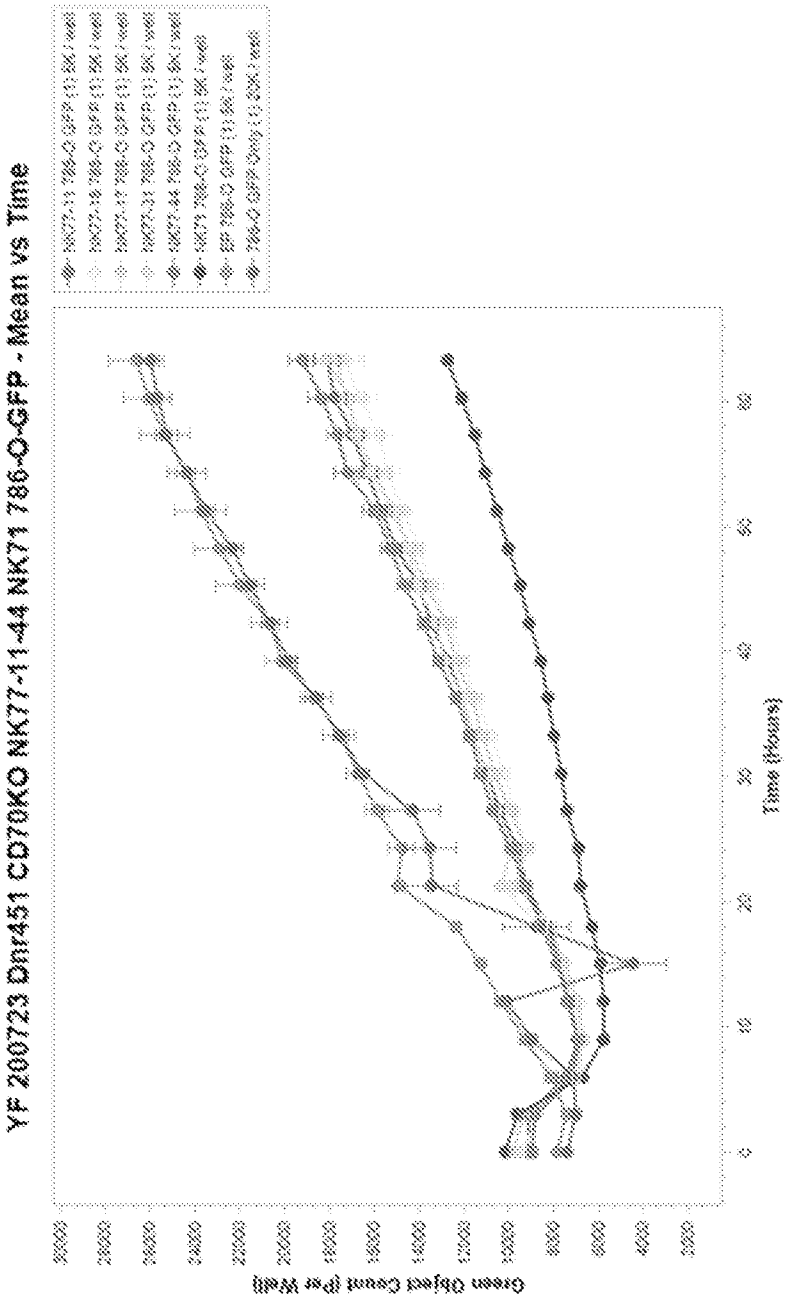

1:2 E:T 786-O at 66 hours
YF 200723 Dnr451 CD70KO NK77-11-44 NK71 786-O-GFP - Mean - 7/27/2020 10:35 AM
Green Object Count Per Well Normalized to Baseline
4.2
3.9
3.6
3.3
3
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0.3
NK77-11 786-O GFP 10K/well
NK77-16 786-O GFP 10K/well
NK77-17 786-O GFP 10K/well
NK77-31 786-O GFP 10K/well
NK77-44 786-O GFP 10K/well
NK71 786-O GFP 10K/well
EP 786-O GFP 10K/well
786-O GFP only 10K/well

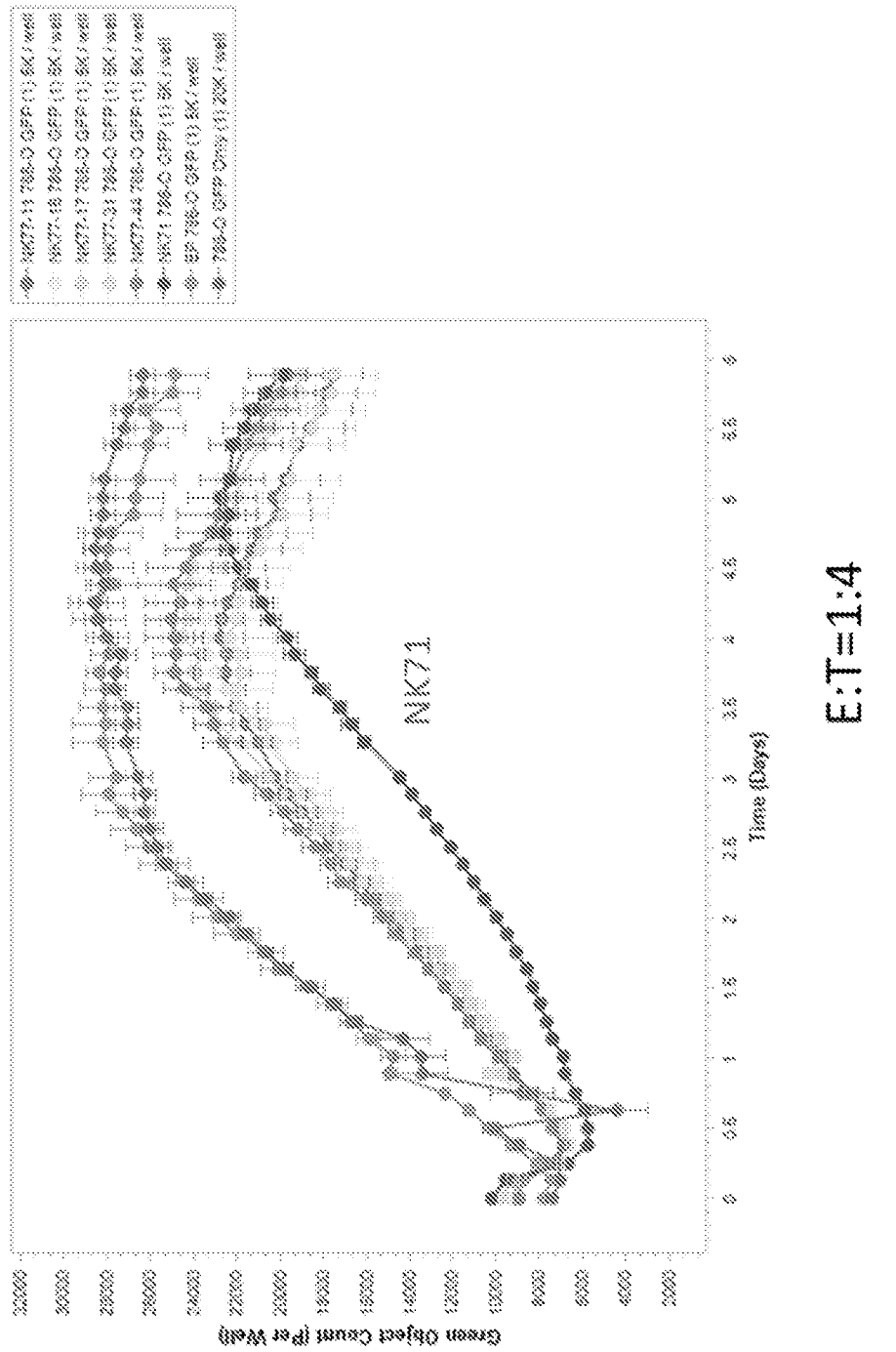
Figure 55J



E:T=1:4

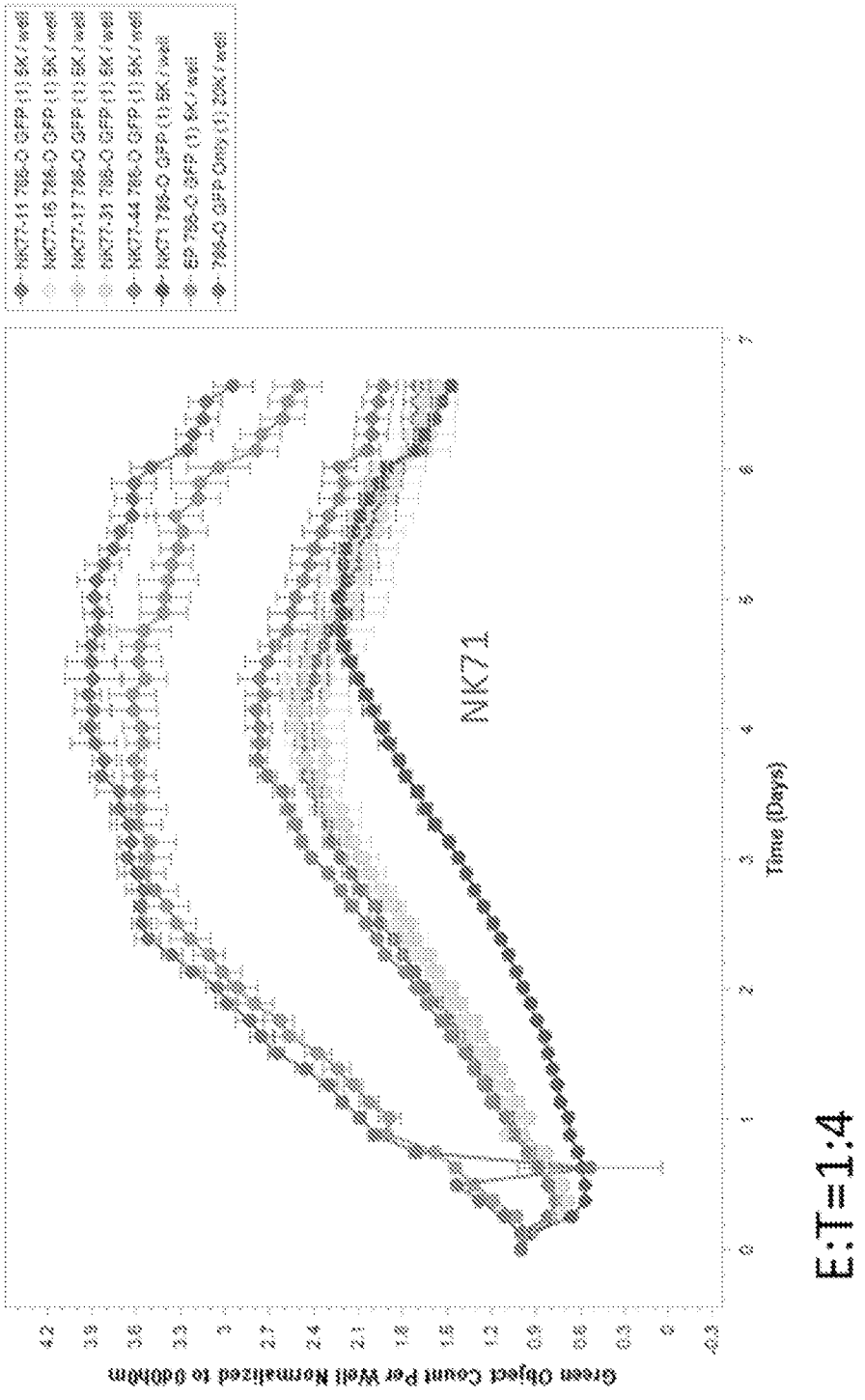
Figure 55K

K



E:T=1:4

Figure 55L

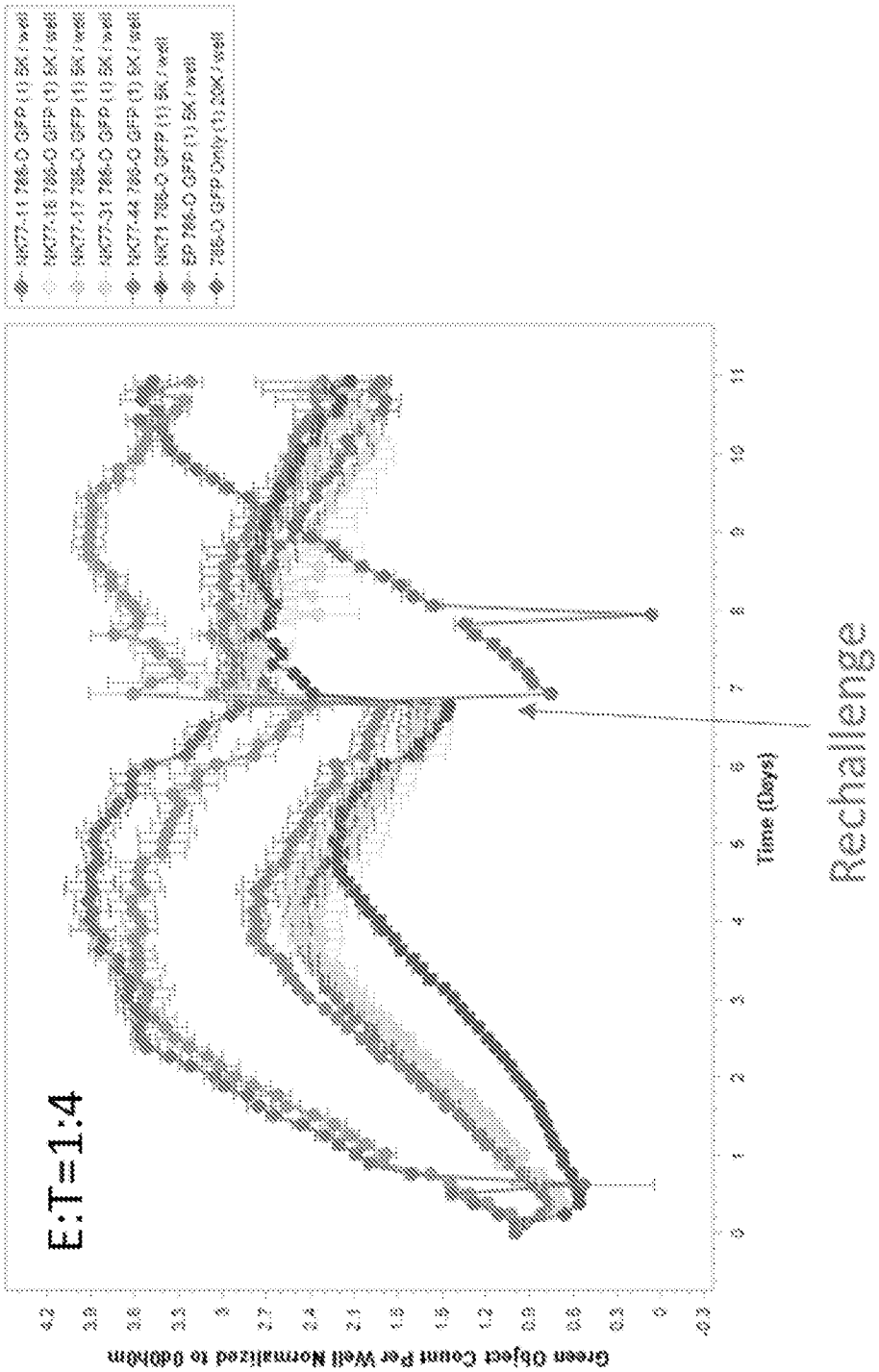


L

E:T=1:4

Figure 55M

M


YF 200723 Dnr451 CD70KO NK77-11-44 NK71 786-O-GFP - Mean vs Time
E:T=1:4
Green Object Count Per Well Normalized to 0dMin
Time (Days)
Rechallenge

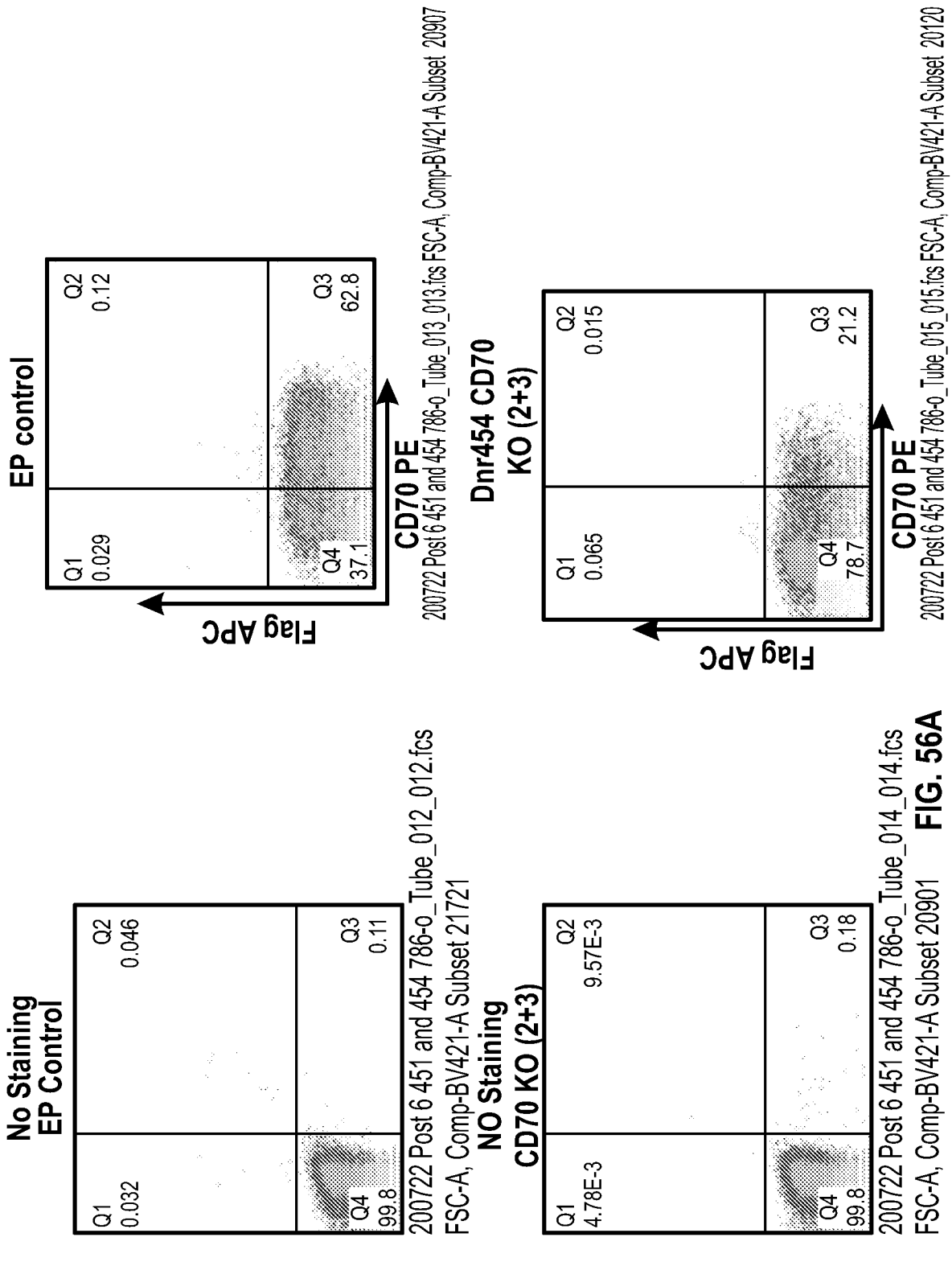
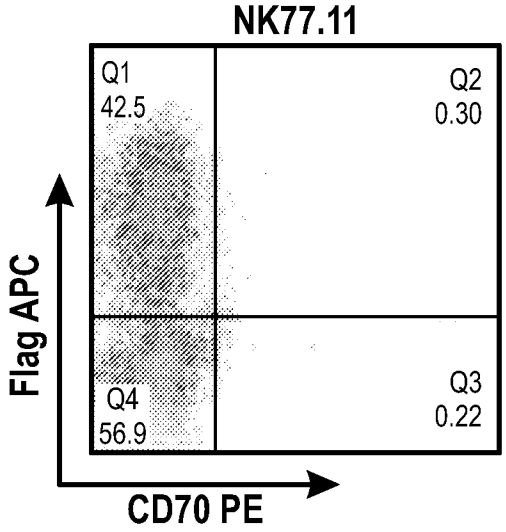
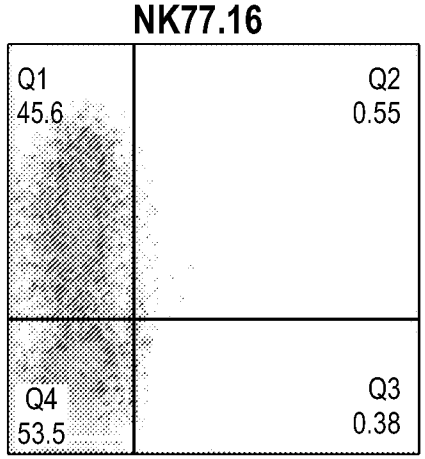

No Staining
EP Control
Q1
0.032
Q2
0.046
Q4
99.8
Q3
0.11
200722 Post 6 451 and 454 786-o_Tube_012_012.fcs
FSC-A, Comp-BV421-A Subset 21721
NO Staining
CD70 KO (2+3)
Q1
4.78E-3
Q2
9.57E-3
Q4
99.8
Q3
0.18
200722 Post 6 451 and 454 786-o_Tube_014_014.fcs
FSC-A, Comp-BV421-A Subset 20901
EP control
Q1
0.029
Q2
0.12
Q4
37.1
Q3
62.8
Flag APC
CD70 PE
200722 Post 6 451 and 454 786-o_Tube_013_013.fcs FSC-A, Comp-BV421-A Subset 20907
Dnr454 CD70
KO (2+3)
Q1
0.065
Q2
0.015
Q4
78.7
Q3
21.2
Flag APC
CD70 PE
200722 Post 6 451 and 454 786-o_Tube_015_015.fcs FSC-A, Comp-BV421-A Subset 20120

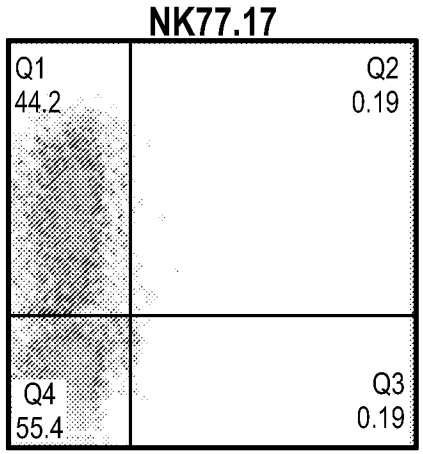
FIG. 56A



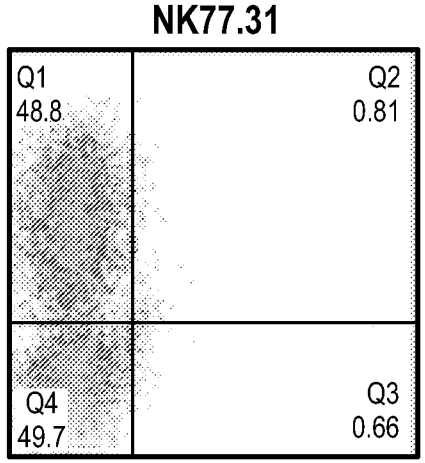
200722 Post 6 451 and 454 786-o_Tube_016_016.fcs FSC-A, Comp-BV421-A Subset 16899



200722 Post 6 451 and 454 786-o_Tube_017_017.fcs FSC-A, Comp-BV421-A Subset 17196



200722 Post 6 451 and 454 786-o_Tube_018_018.fcs FSC-A, Comp-BV421-A Subset 16697



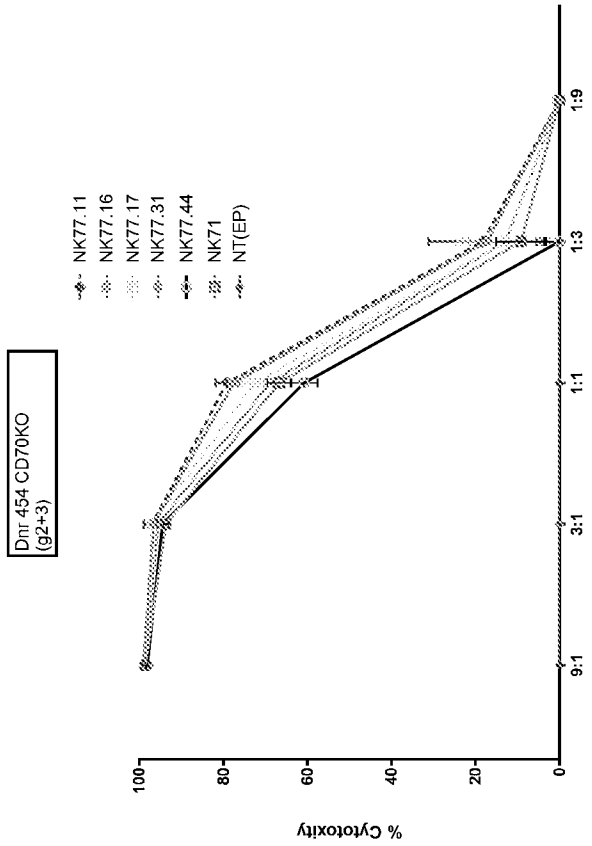
200722 Post 6 451 and 454 786-o_Tube_019_019.fcs FSC-A, Comp-BV421-A Subset 16086

FIG. 56A (Continued)

FIG. 56A
(Continued)

Figure 56B-56C

B

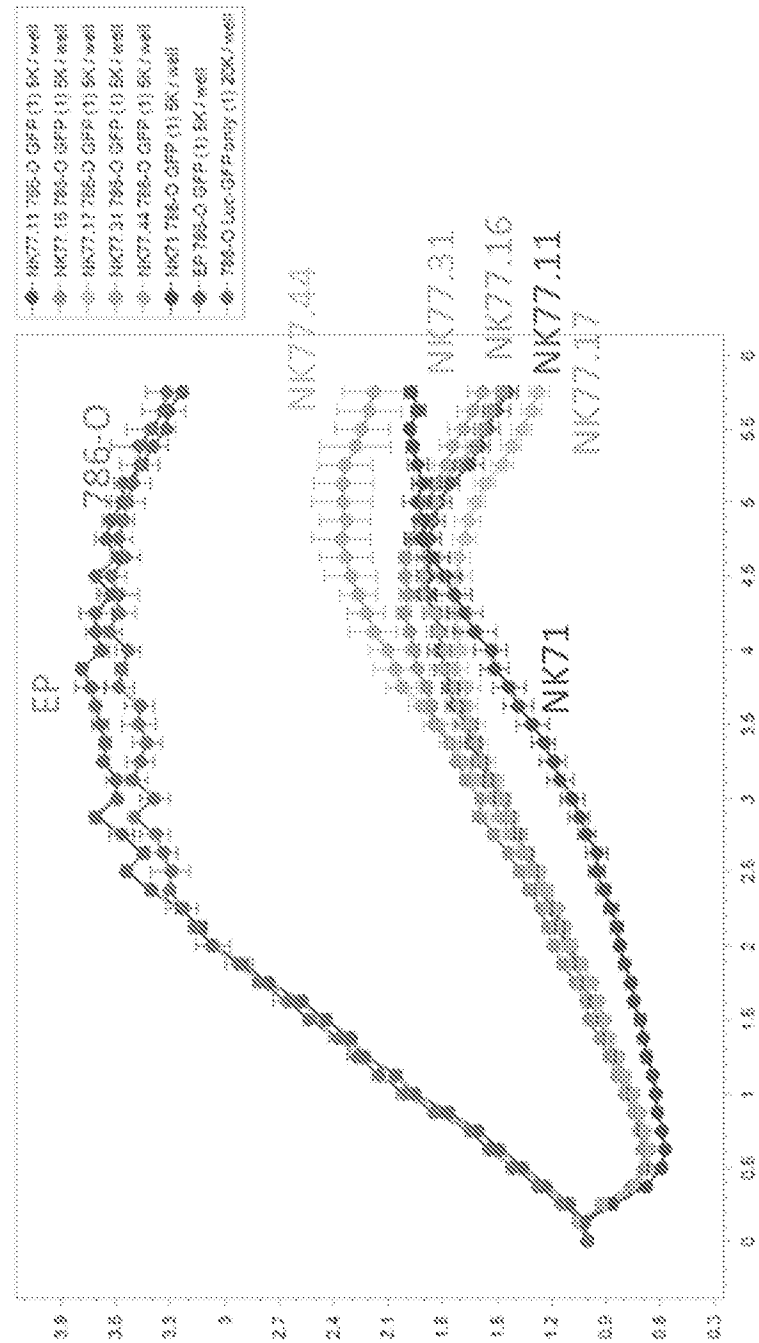


C

Construct	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)	EC_{50}
NK77.11	2.85E+06	0.22%	41.6%	0.6067
NK77.16	3.15E+06	0.3%	44.4%	0.7273
NK77.17	2.88E+06	0.19%	42.9%	0.6941
NK77.31	3.51E+06	0.66%	48.4%	0.6193
NK77.44	3.57E+06	0.70%	45.3%	0.9637
EPNT	-	62.8%	-	-
NK71	1.20E+06	0.28%	36.4%	0.786

Figure 56D

D



E:T=1:2

Figure 56E

E

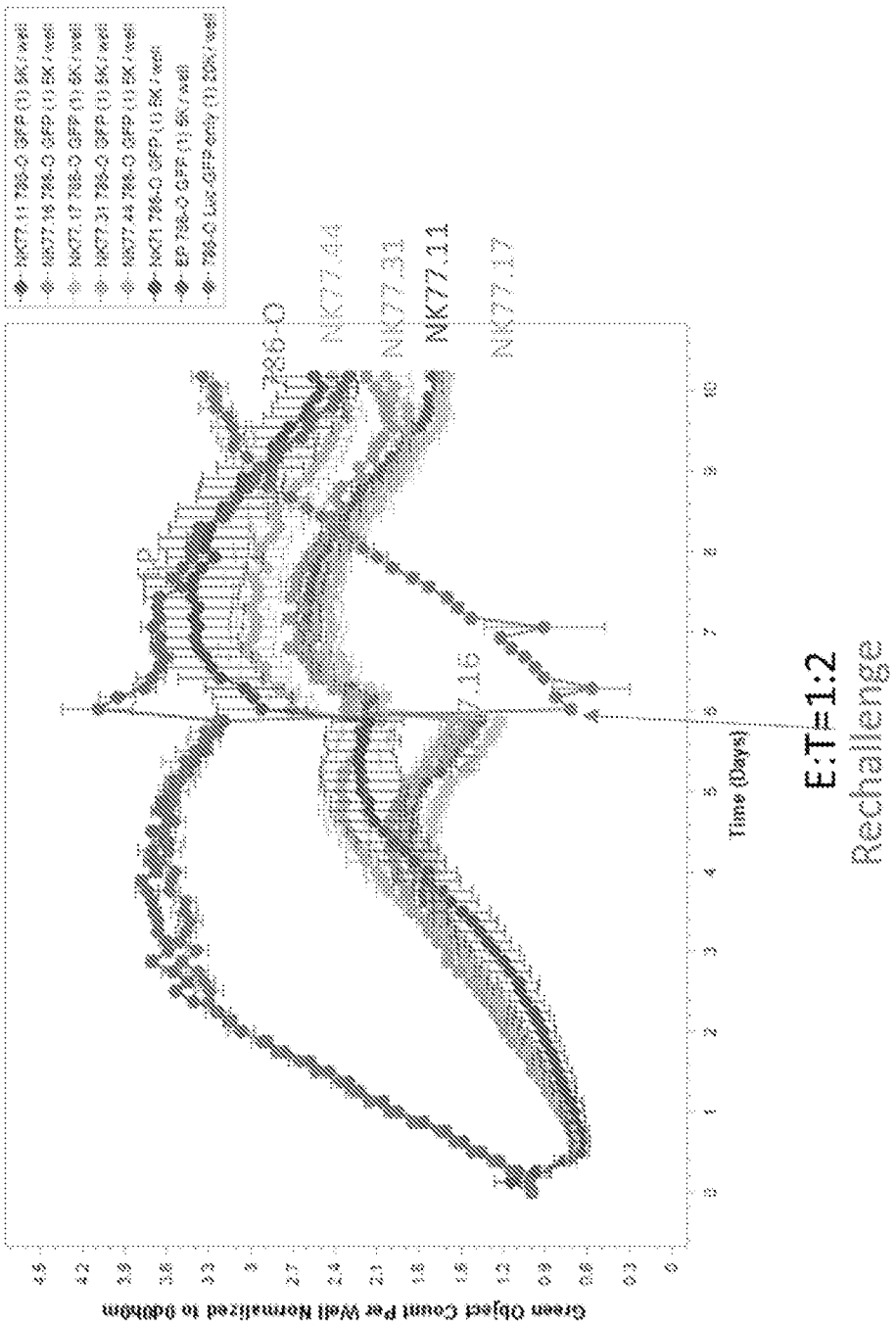
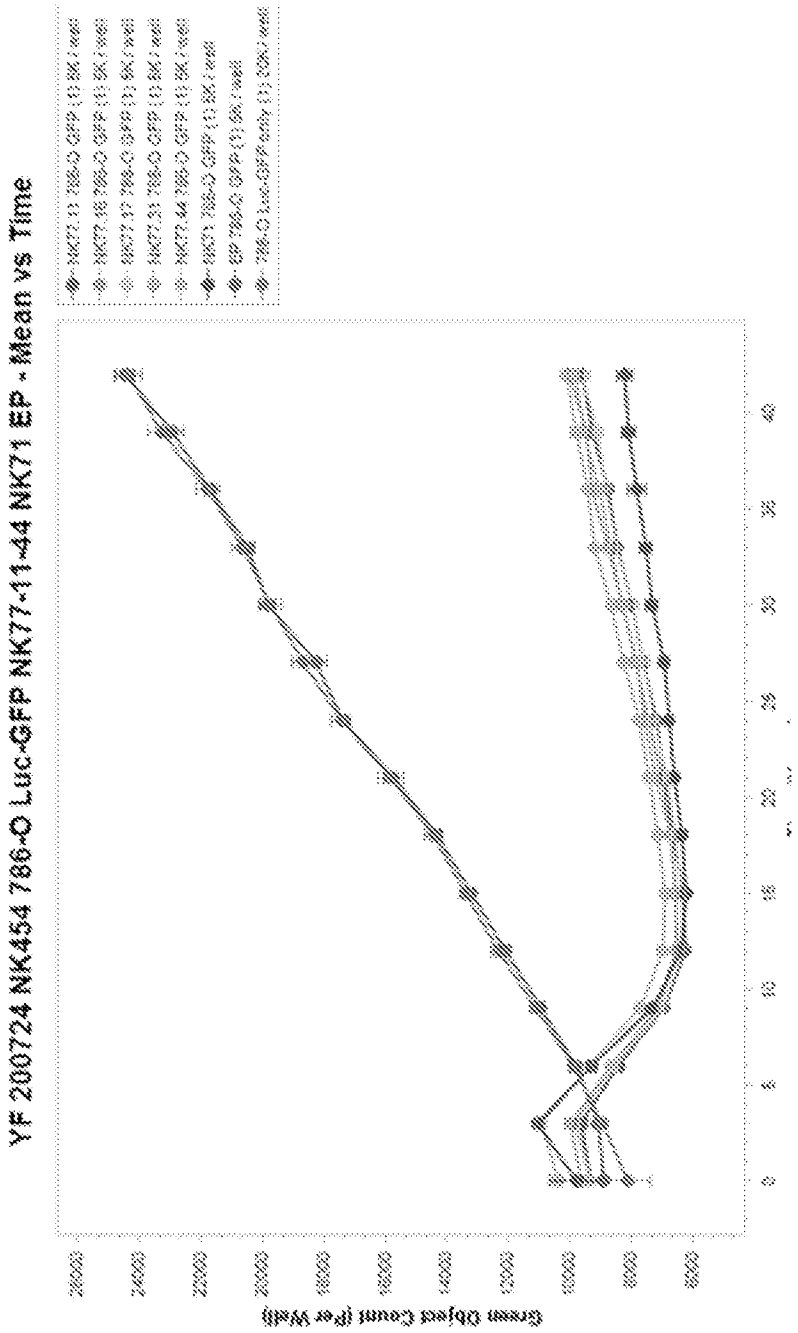

YF 200724 NK454 786-O Luc-GFP NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to baseline
Time (Days)
786-O
NK77.44
NK77.31
NK77.11
NK77.17
NK77.16
E:T=1:2
Rechallenge

Figure 56F

F



E:T=1:4

Figure 56G

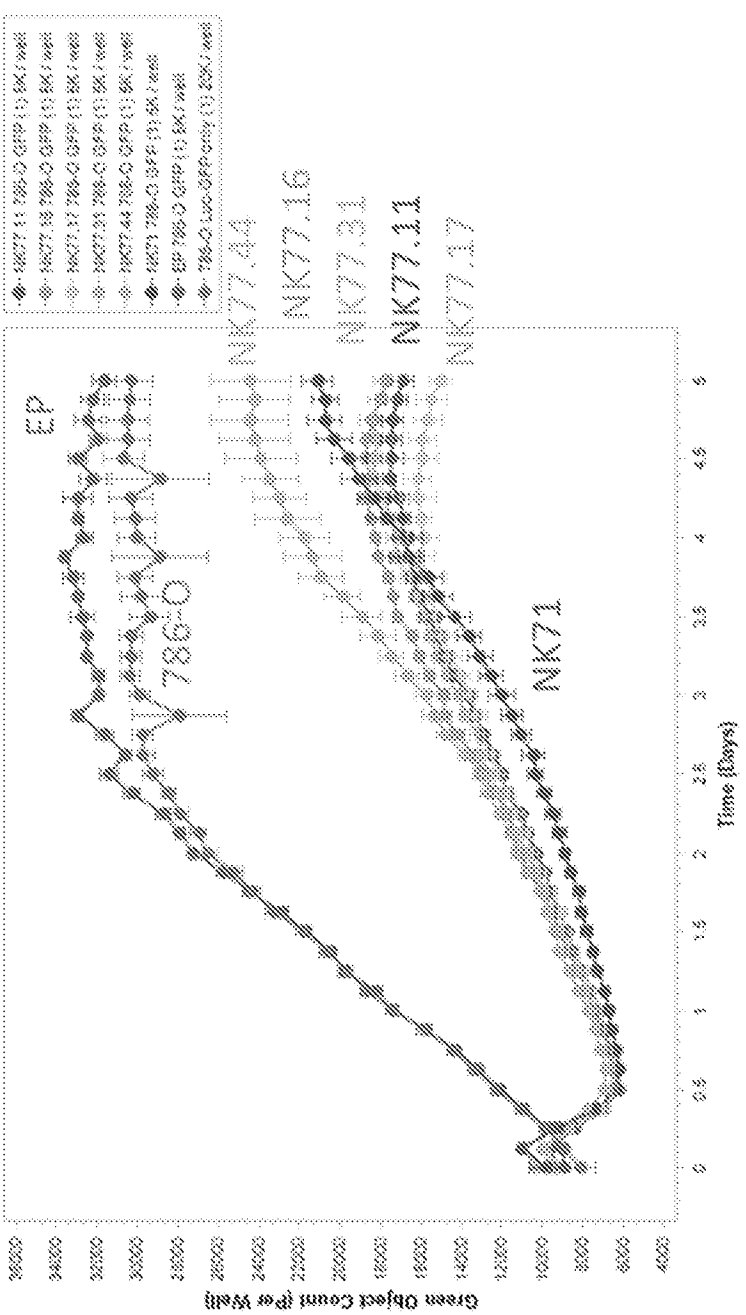

G
YF 200724 NK454 786-O Luc-GFP NK77-11-44 NK71 EP - Mean vs Time
Green Object Count (Per Well)
Time (Days)
EP
786-O
NK77.44
NK77.16
NK77.31
NK77.11
NK77.17
NK71
E:T=1:4

Figure 56H

H

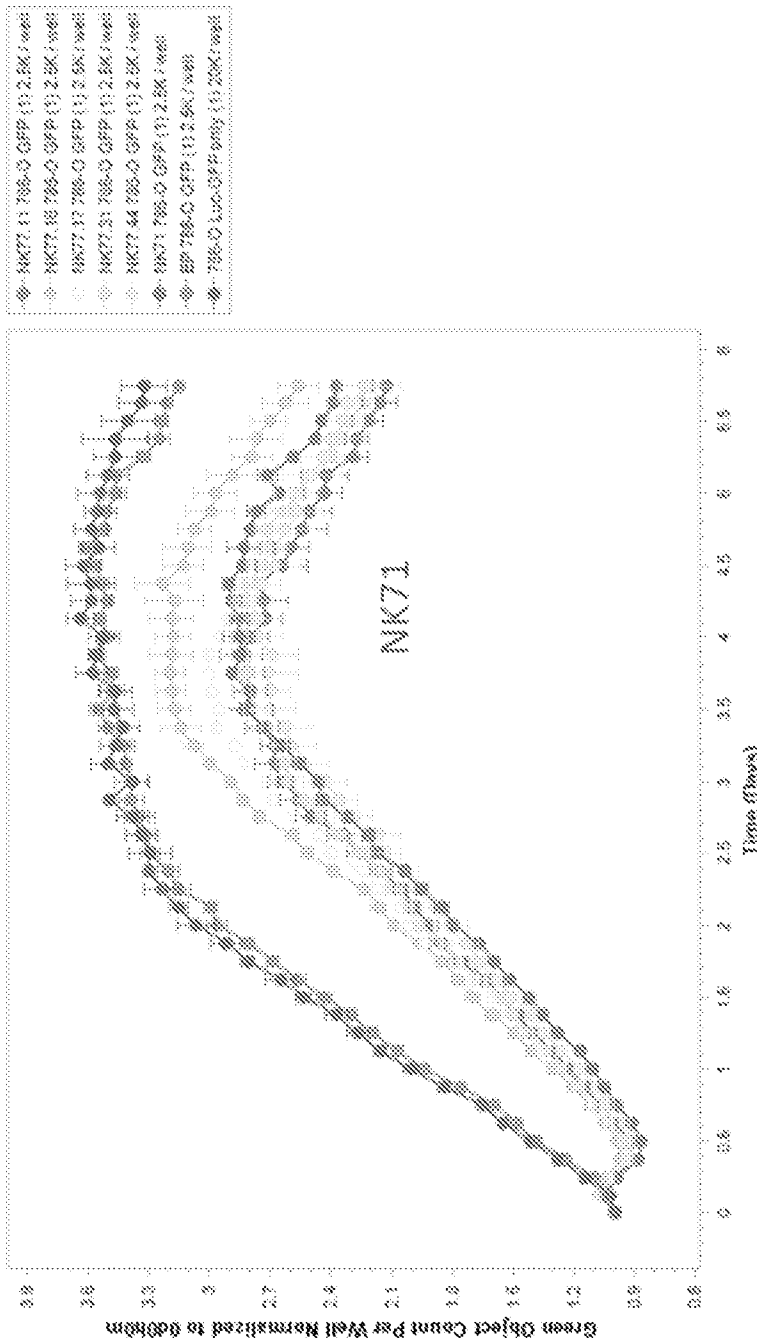
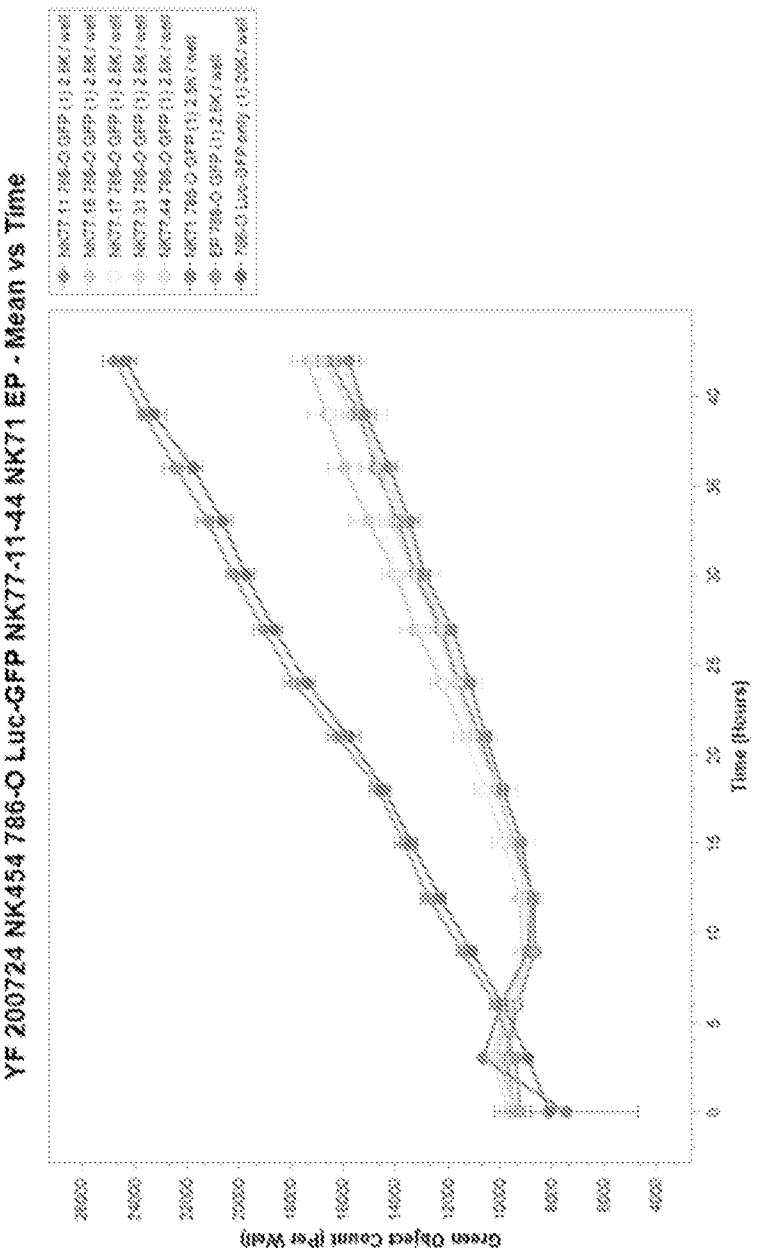
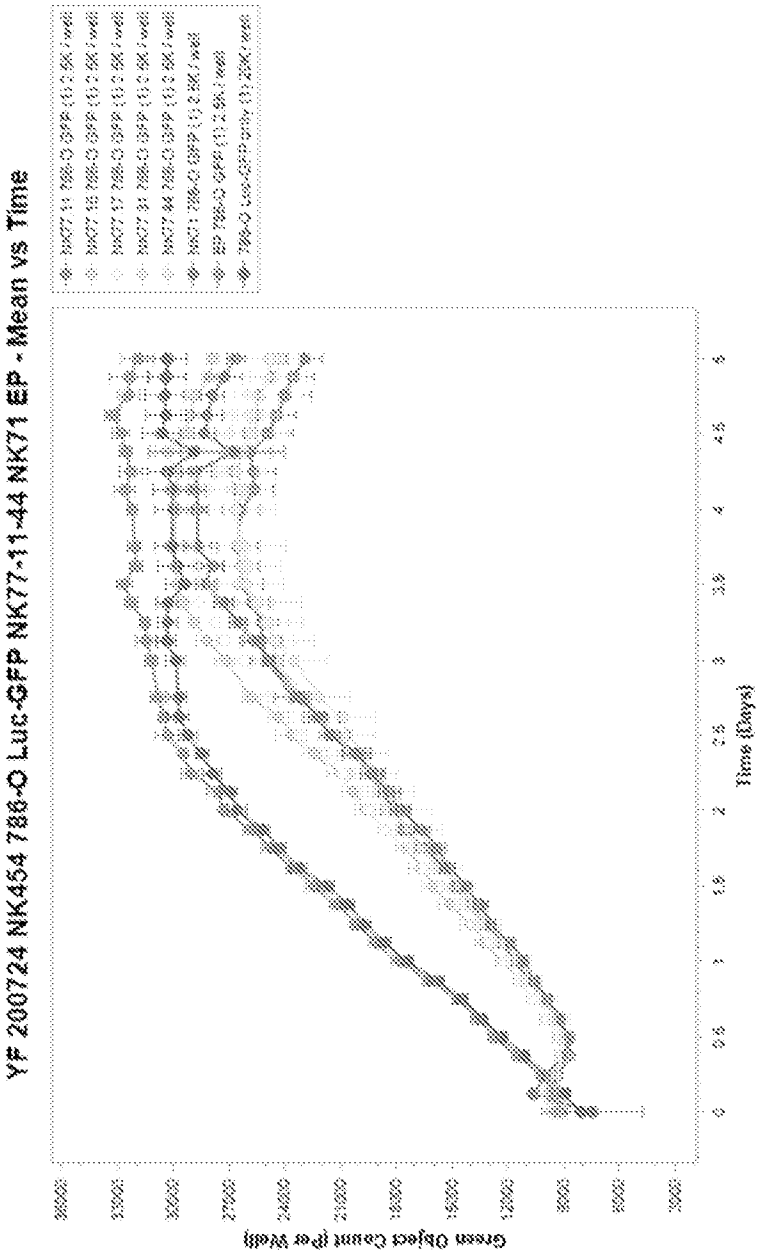

YF 200724 NK454 786-O Luc-GFP NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to Baseline
Time (Hours)
NK71
E:T=1:4

Figure 56I



E:T=1:8

Figure 56J



E:T=1:8

Figure 57A

A

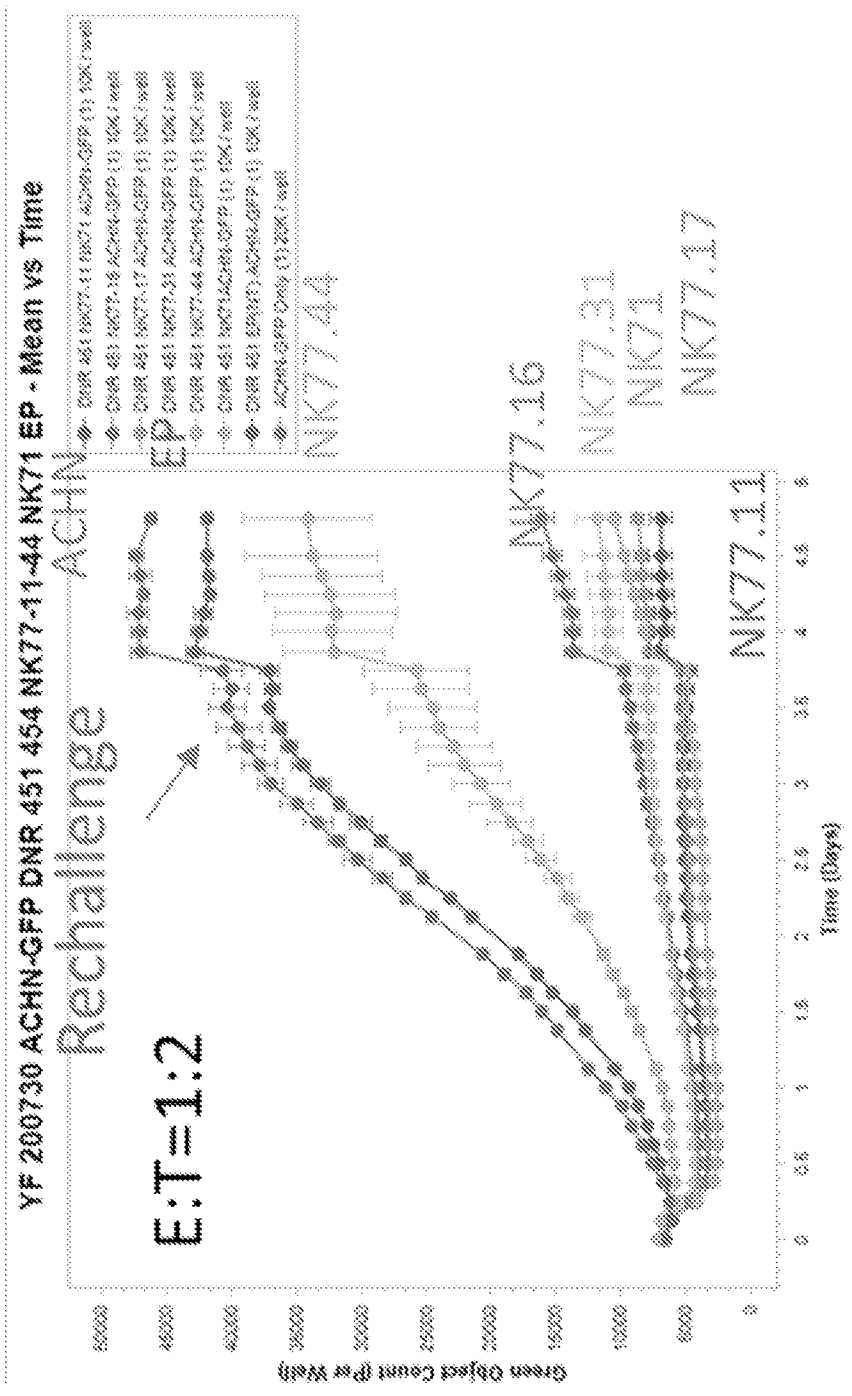

RAW count
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Rechallenge
ACHN
E:T=1:2
NK77.16
NK77.31
NK71
NK77.17
NK77.11
NK77.44
Green Object Count (Per Well)
Time (Days)

Figure 57B

B

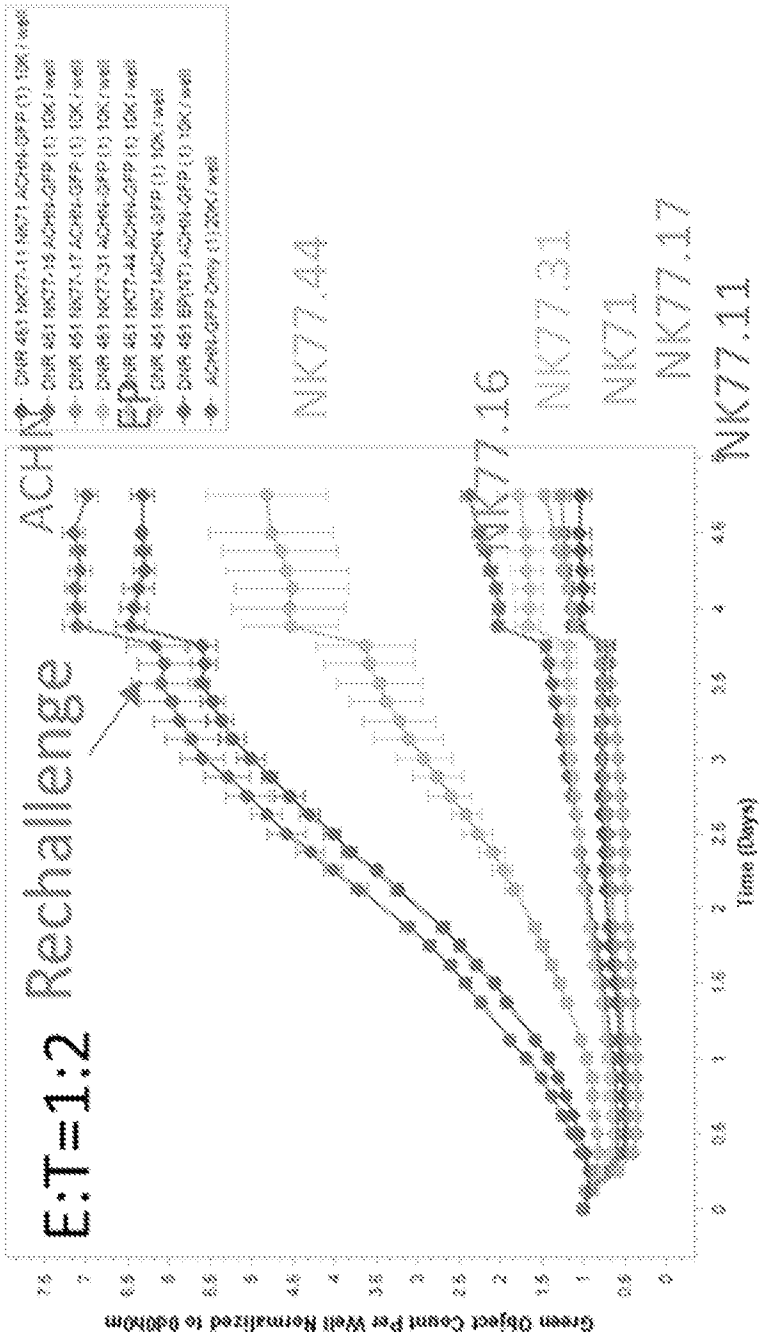

Count normalized to Day0
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
E:T=1:2
Rechallenge
ACHN
NK77.44
NK77.16
NK77.31
NK71
NK77.17
NK77.11
Green Object Count Per Well Normalized to Baseline
Time (Days)

Figure 57C

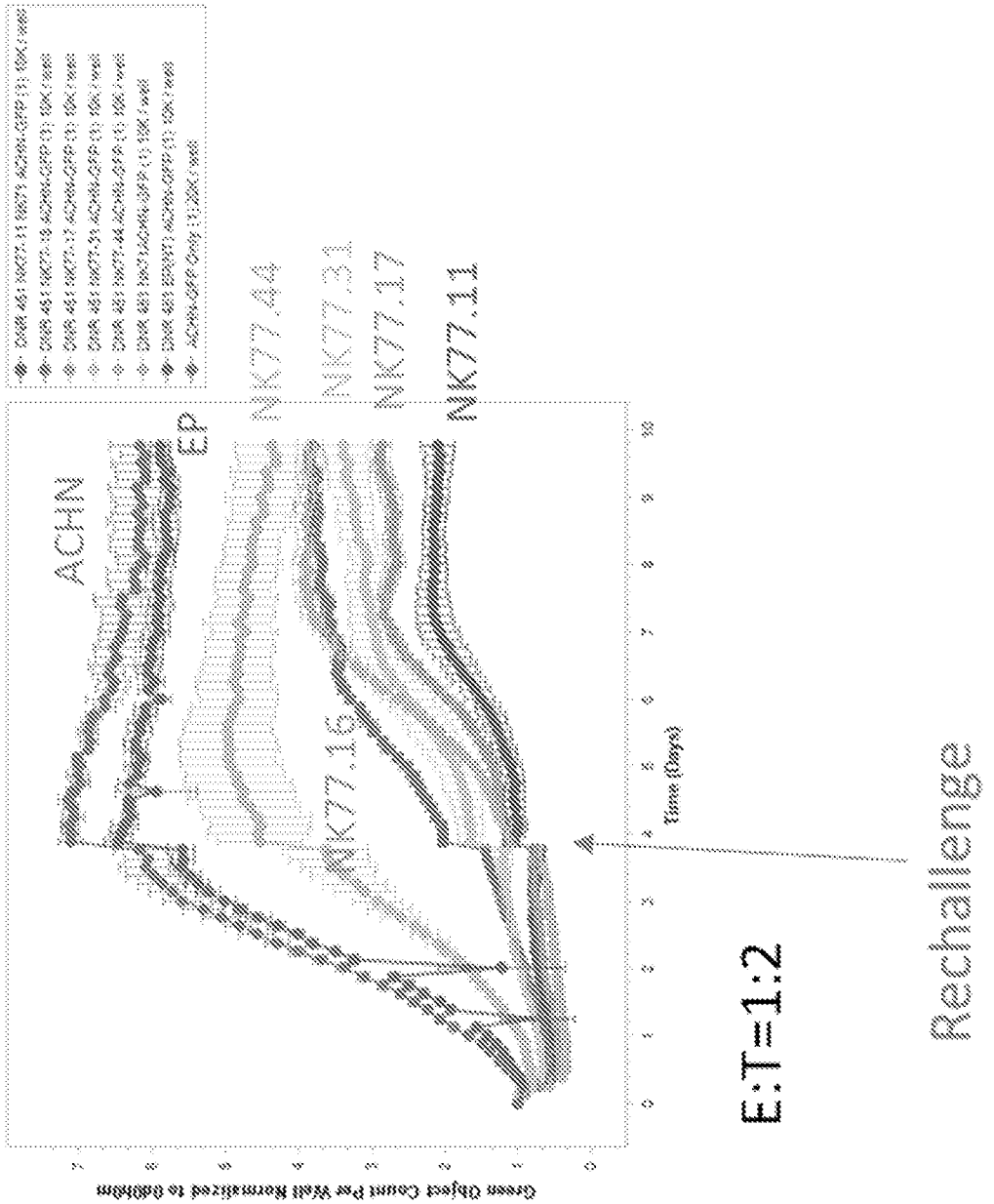

c
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to Baseline
Time (Days)
ACHN
EP
NK77.44
NK77.31
NK77.17
NK77.11
E:T=1:2
Rechallenge

Figure 57D

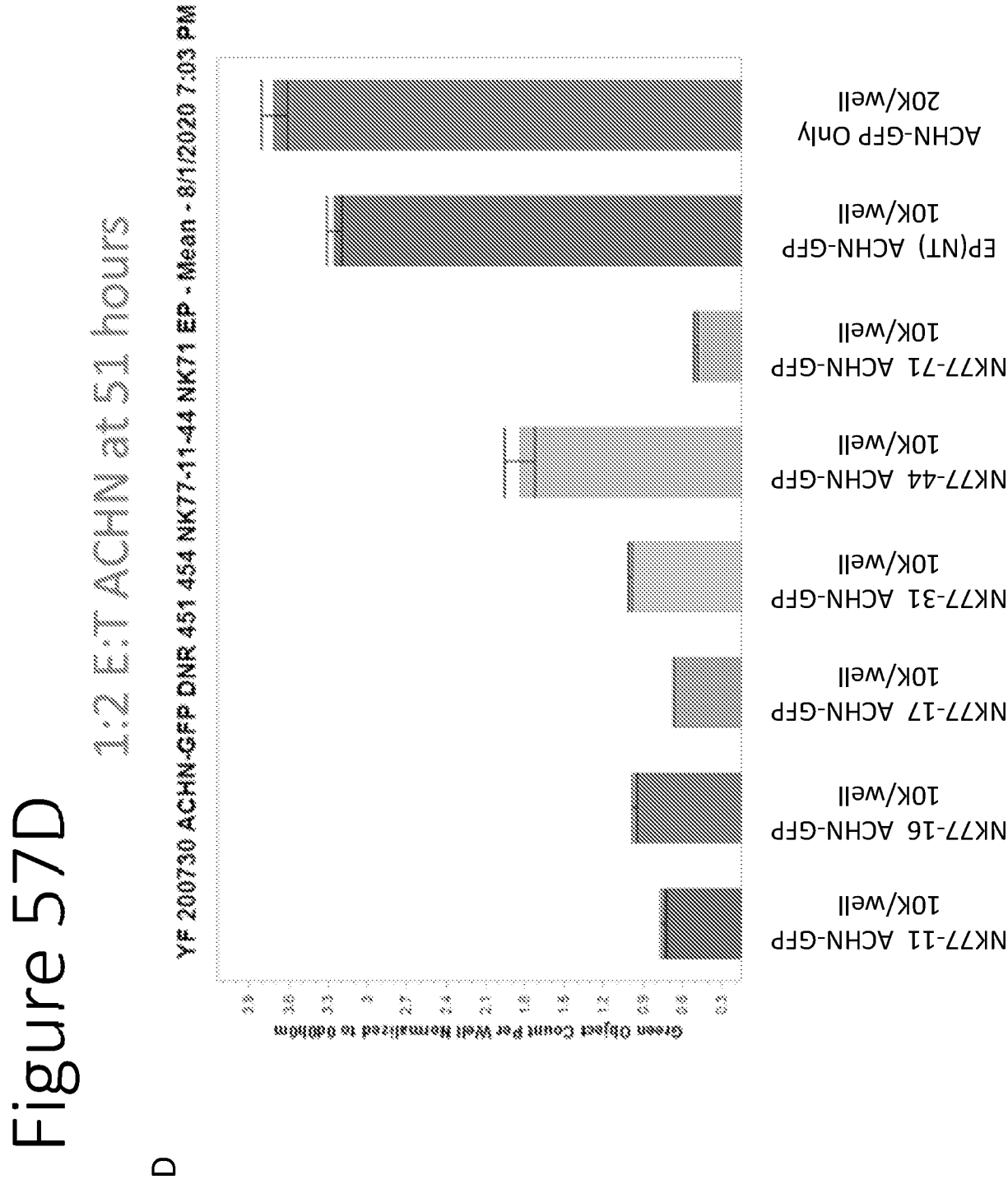

D
1:2 E:T ACHN at 51 hours
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean - 8/11/2020 7:03 PM
Green Object Count Per Well Normalized to Baseline
NK77-11 ACHN-GFP 10K/well
NK77-16 ACHN-GFP 10K/well
NK77-17 ACHN-GFP 10K/well
NK77-31 ACHN-GFP 10K/well
NK77-44 ACHN-GFP 10K/well
NK77-71 ACHN-GFP 10K/well
EP(NT) ACHN-GFP 10K/well
ACHN-GFP Only 20K/well

Figure 57E

E

1:2 E:T ACHN at 66 hours

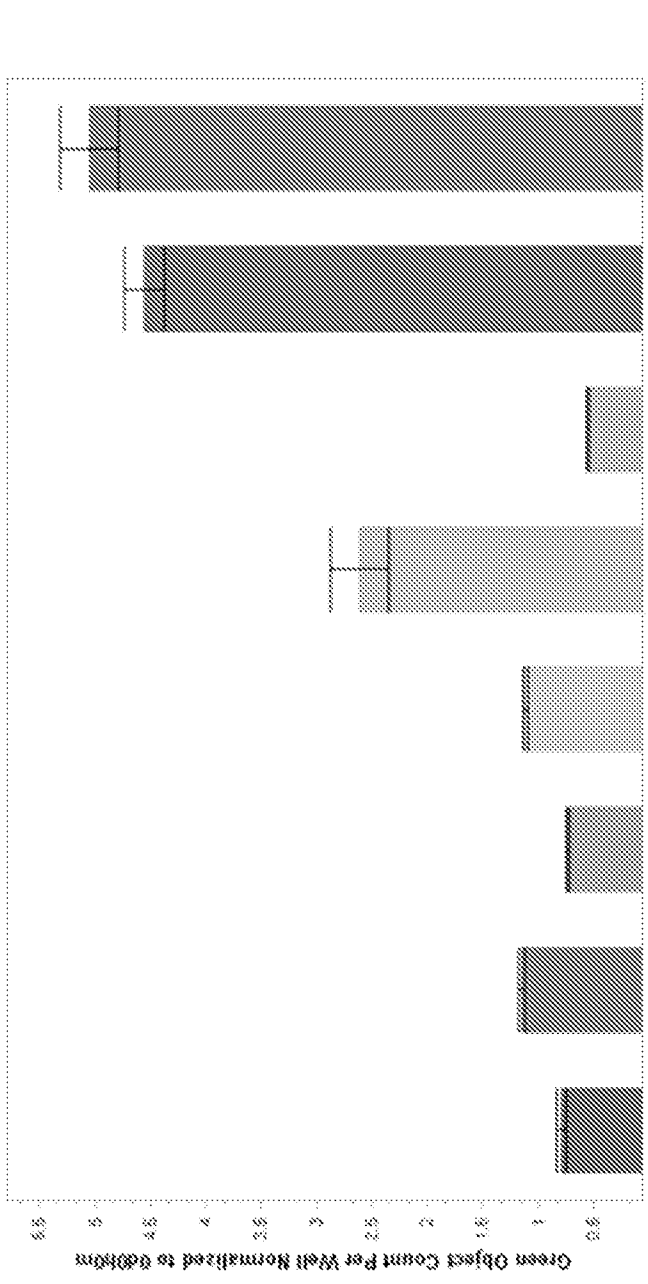


Figure 57F

F

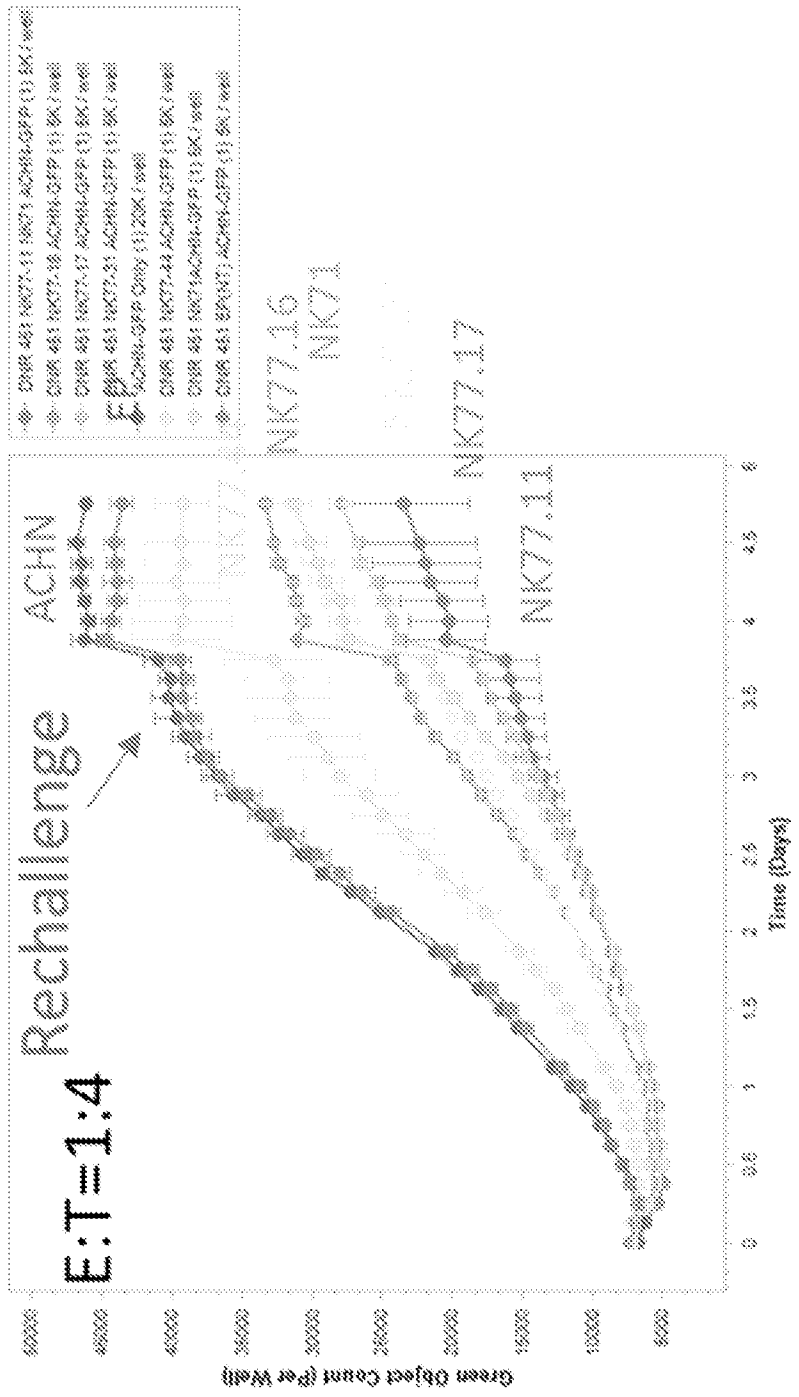

RAW count
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Rechallenge
E:T=1:4
ACHN
NK77
NK77.16
NK71
NK77.17
NK77.11
Green Object Count (Per Well)
Time (Days)

Figure 57G

G

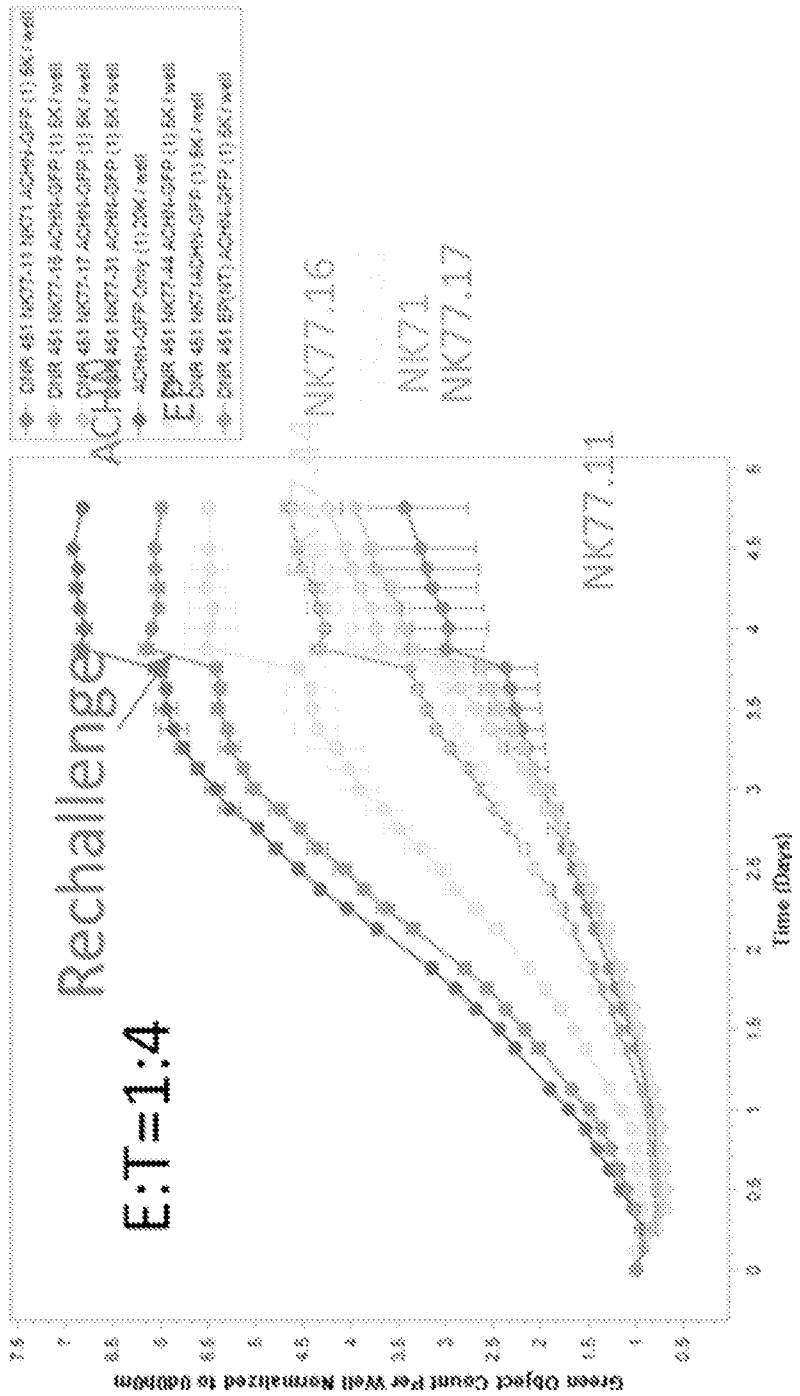

YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Count normalized to Day0
Green Object Count Per Well Normalized to Untreated
Time (Days)
E:T=1:4
Rechallenge
ACHN
EP
NK77.16
NK71
NK77.17
NK77.11

Figure 57H

H

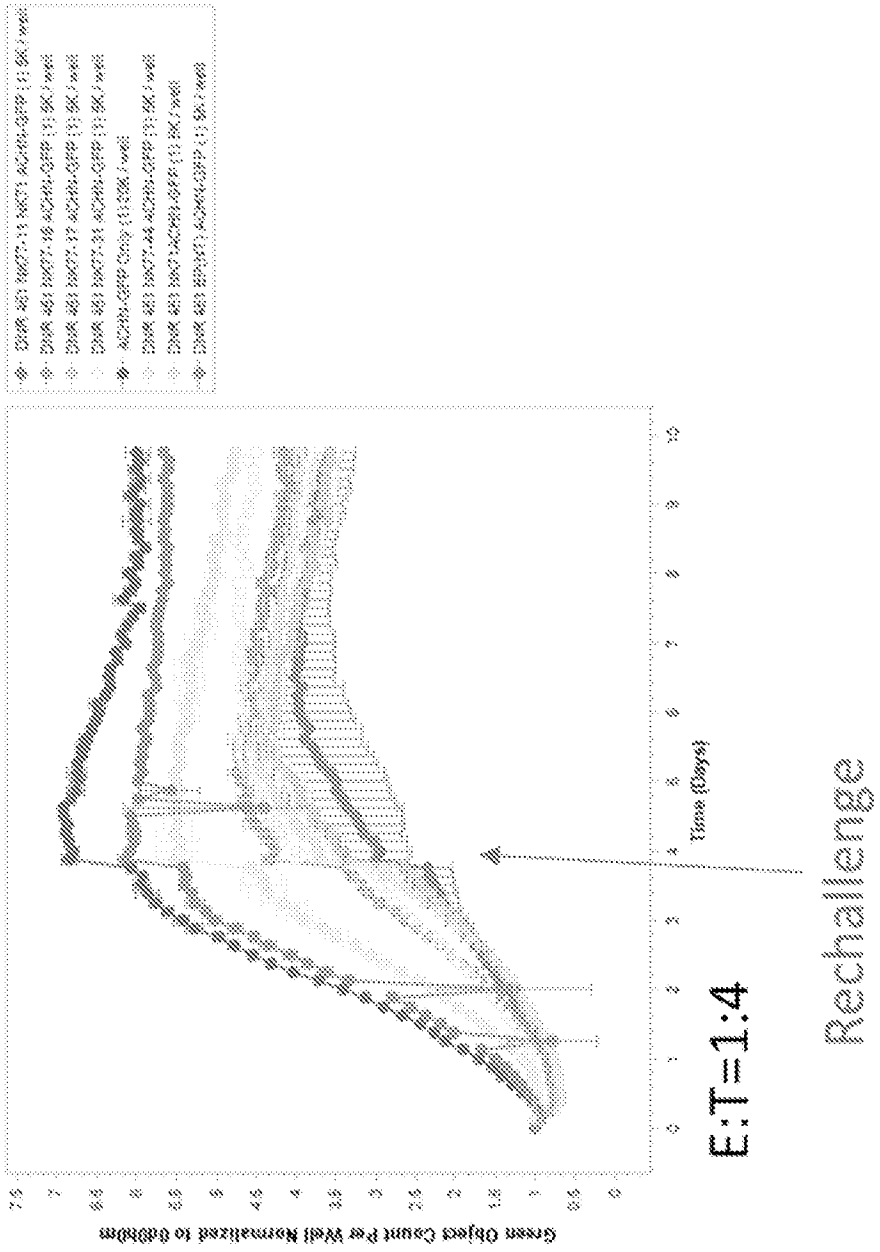

YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to Baseline
Time (Days)
E:T=1:4
Rechallenge

Figure 58A

A

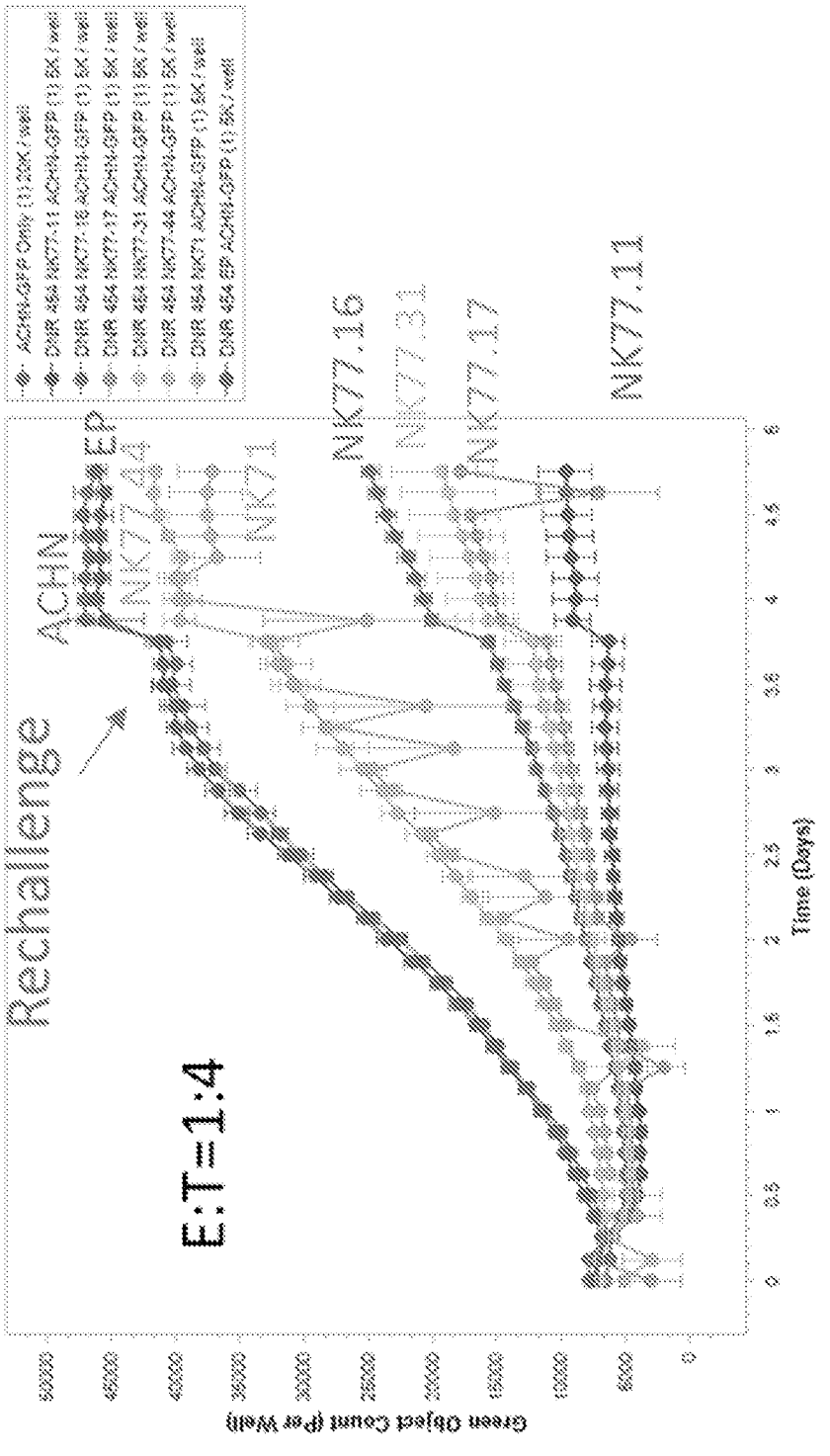

RAW count
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
ACHN-GFP Only (1.33K / well)
DNR 454 NK77-11 ACHN-GFP (1) 5K / well
DNR 454 NK77-16 ACHN-GFP (1) 5K / well
DNR 454 NK77-17 ACHN-GFP (1) 5K / well
DNR 454 NK77-31 ACHN-GFP (1) 5K / well
DNR 454 NK77-44 ACHN-GFP (1) 5K / well
DNR 454 NK71 ACHN-GFP (1) 5K / well
DNR 454 EP ACHN-GFP (1) 5K / well
Rechallenge
ACHN
NK77.44
NK71
NK77.16
NK77.31
NK77.17
NK77.11
E:T=1:4
Green Object Count (Per Well)
Time (Days)

Figure 58B

B

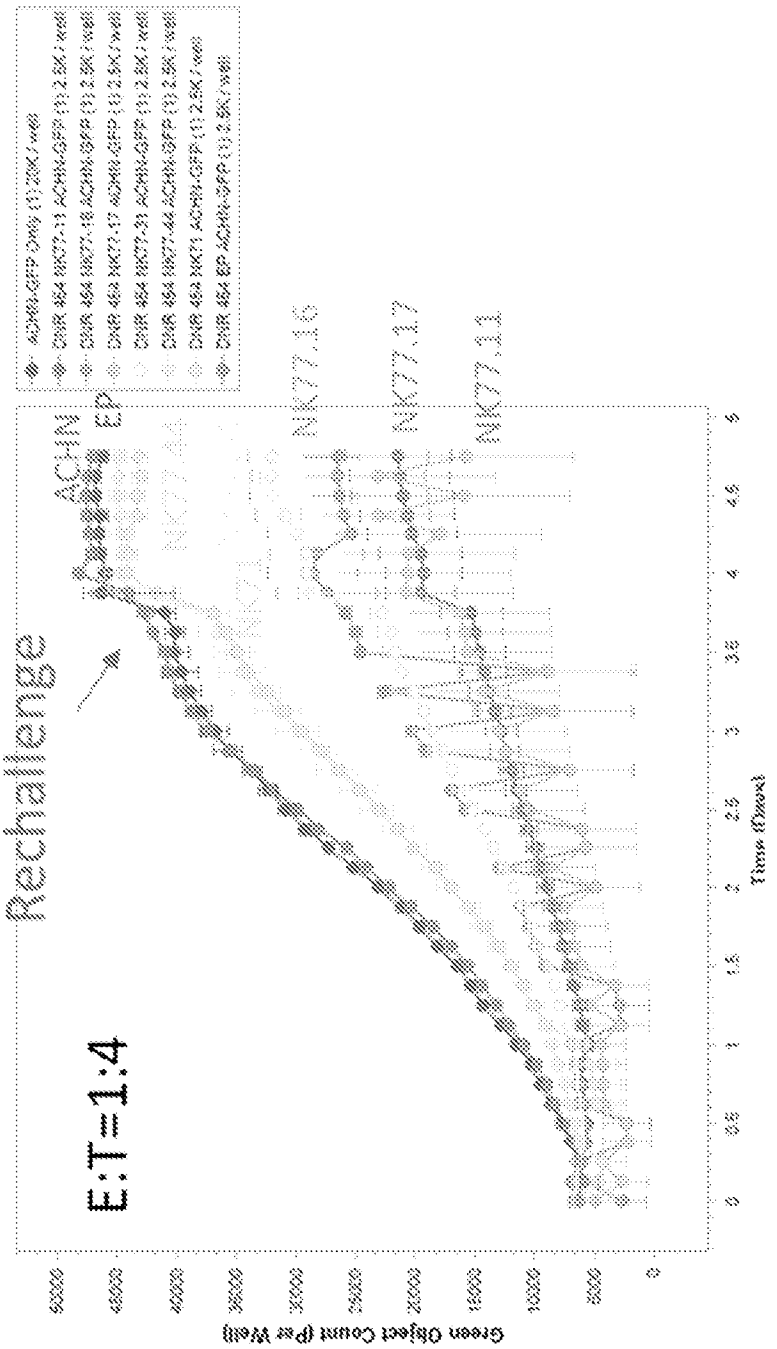

YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Rechallenge
E:T=1:4
ACHN
EP
NK77.16
NK77.17
NK77.11
Green Object Count (Per Well)
Time (Days)

Figure 58C

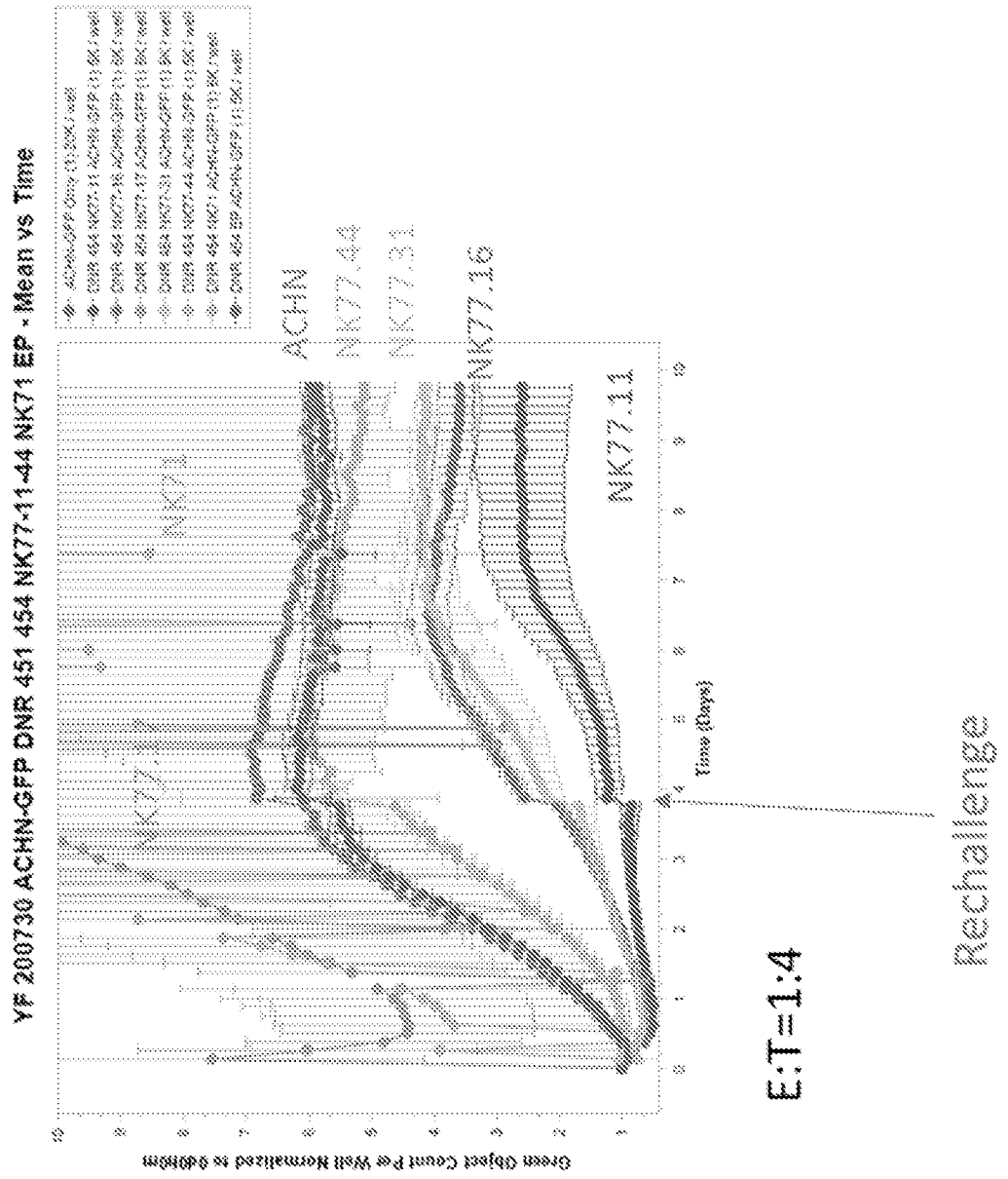

C
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to 0 Hour
Time (Days)
ACHN
NK77.44
NK77.31
NK77.16
NK77.11
NK71
E:T=1:4
Rechallenge

Figure 58D

D

1:4 E:T ACHN at 51 hours

* Incucyte errors at 51 hours

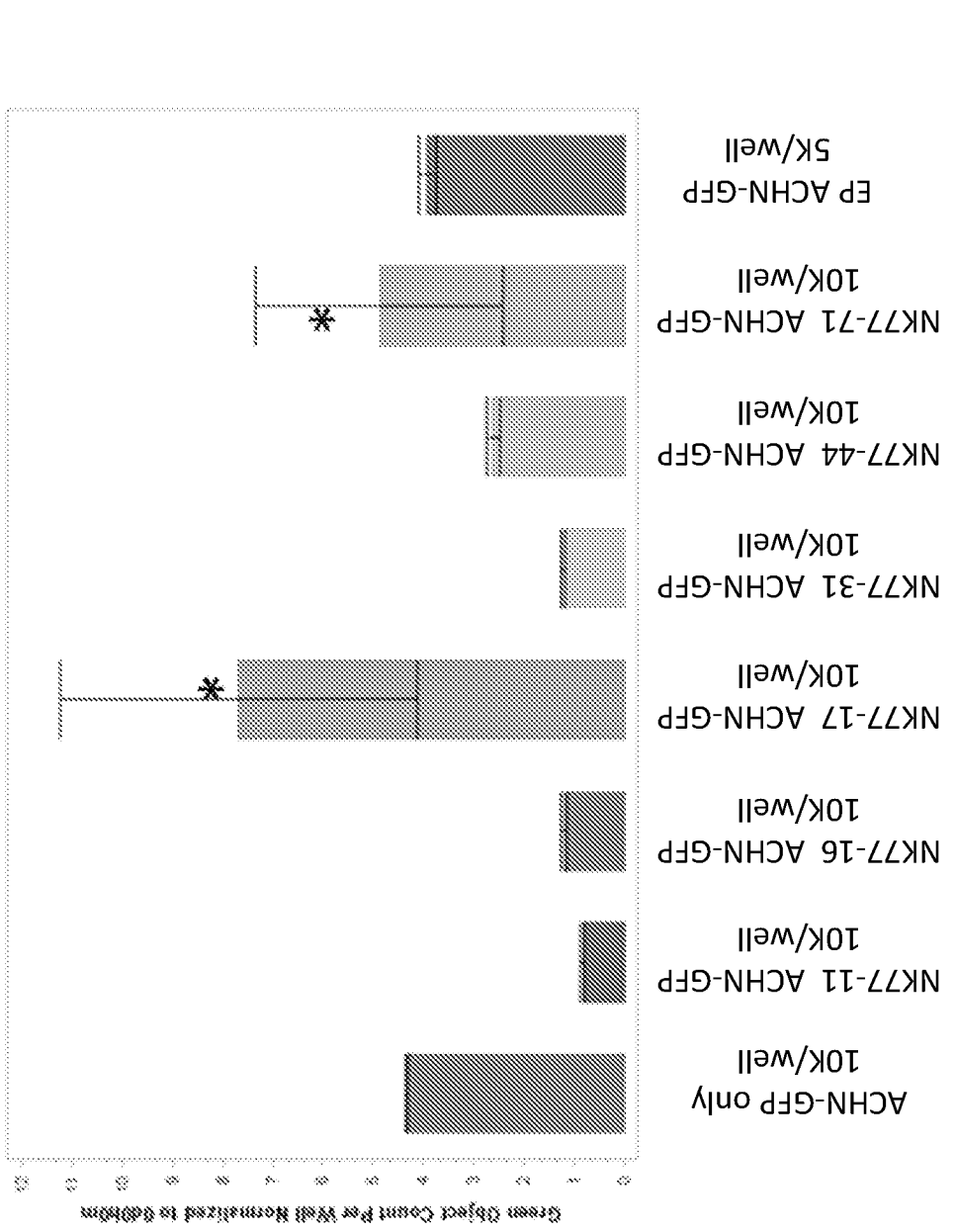


Figure 58E

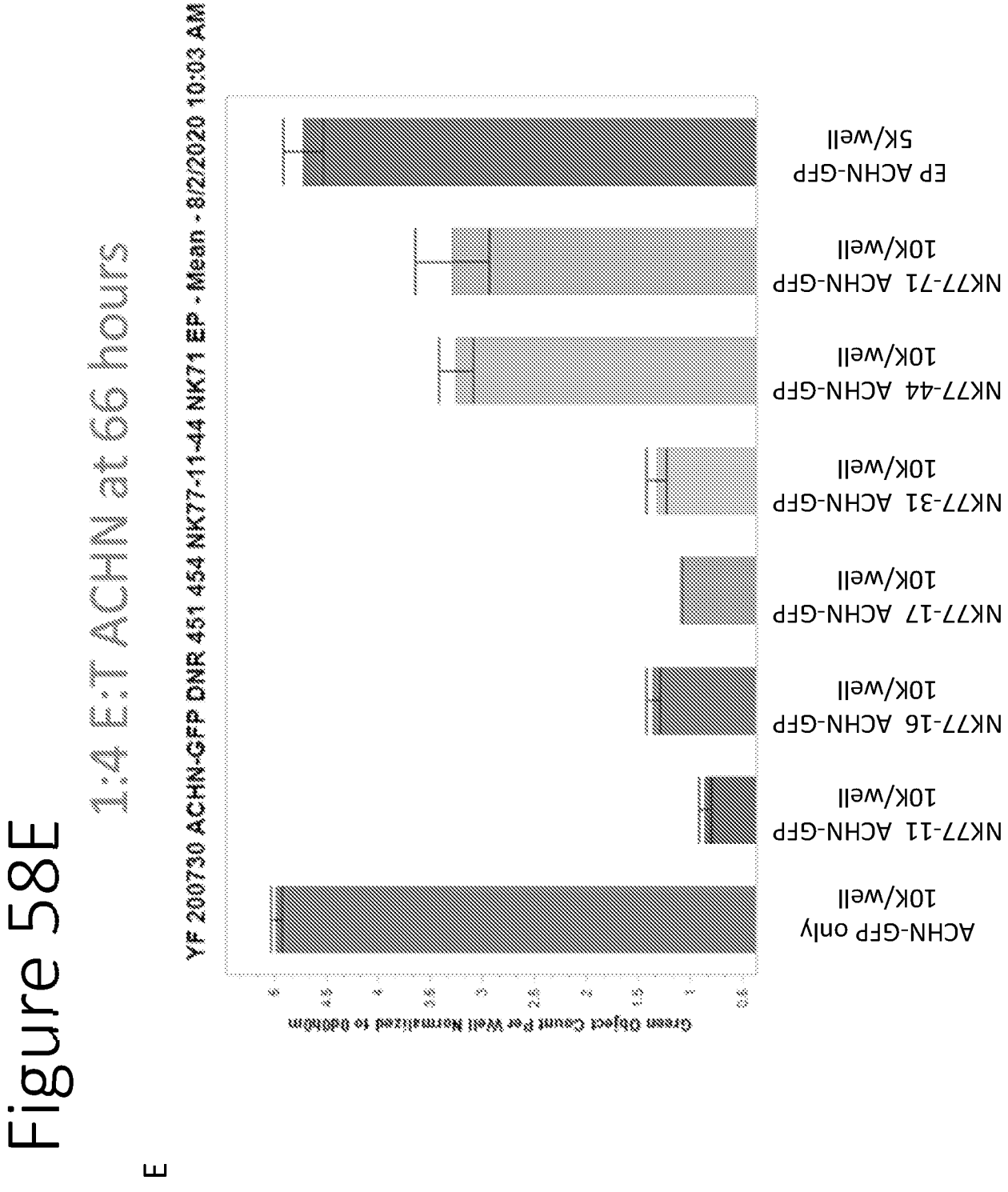

E
1:4 E:T ACHN at 66 hours
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean - 8/2/2020 10:03 AM
Green Object Count Per Well Normalized to Baseline
ACHN-GFP only 10K/well
NK77-11 ACHN-GFP 10K/well
NK77-16 ACHN-GFP 10K/well
NK77-17 ACHN-GFP 10K/well
NK77-31 ACHN-GFP 10K/well
NK77-44 ACHN-GFP 10K/well
NK77-71 ACHN-GFP 10K/well
EP ACHN-GFP 5K/well

Figure 58F

F

RAW count

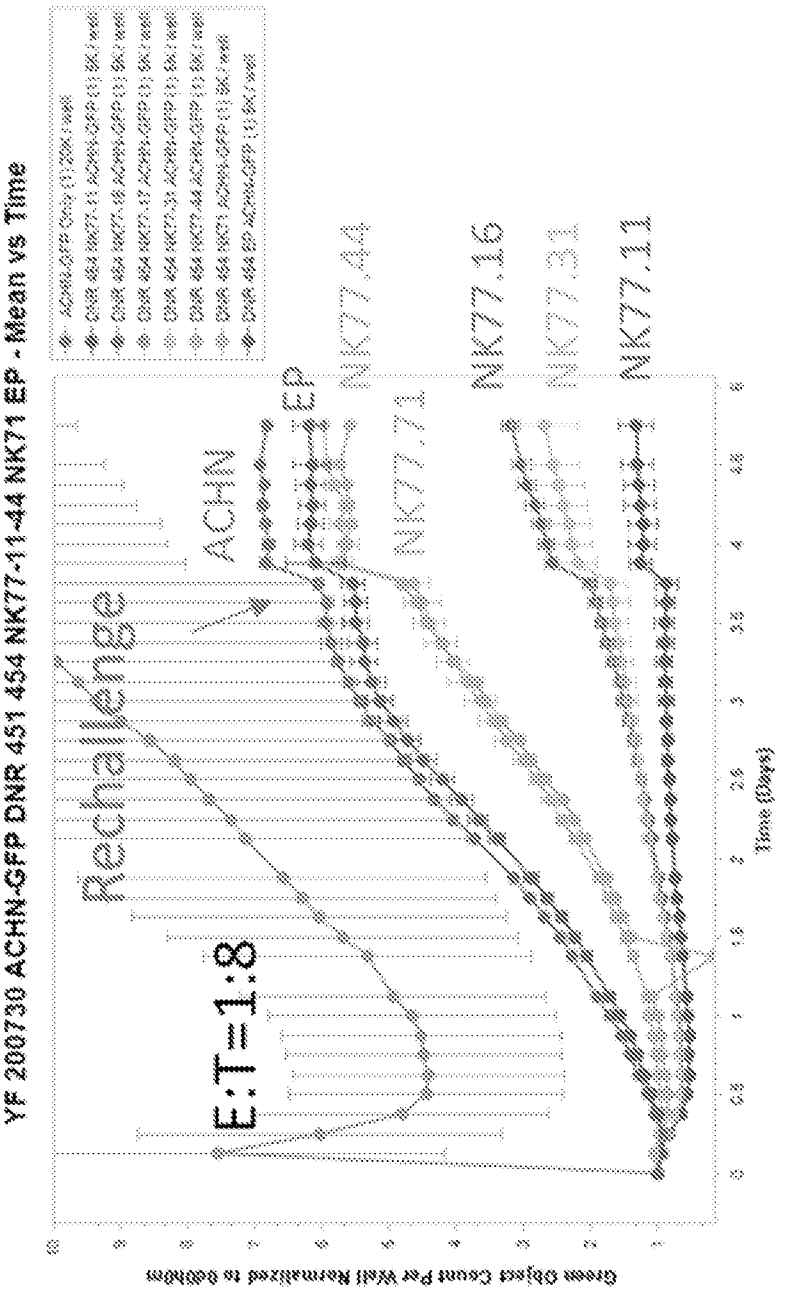


Figure 58G

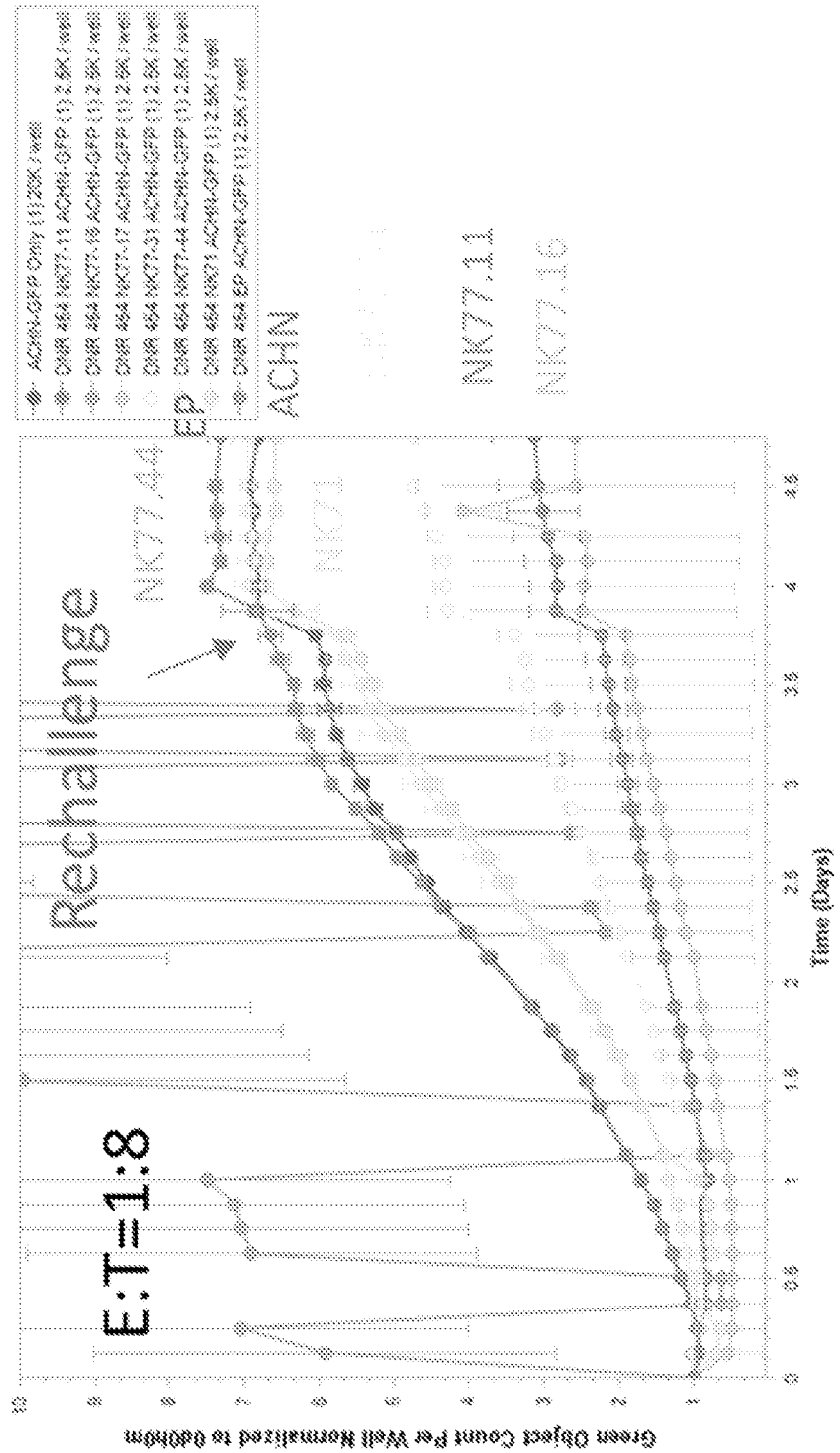
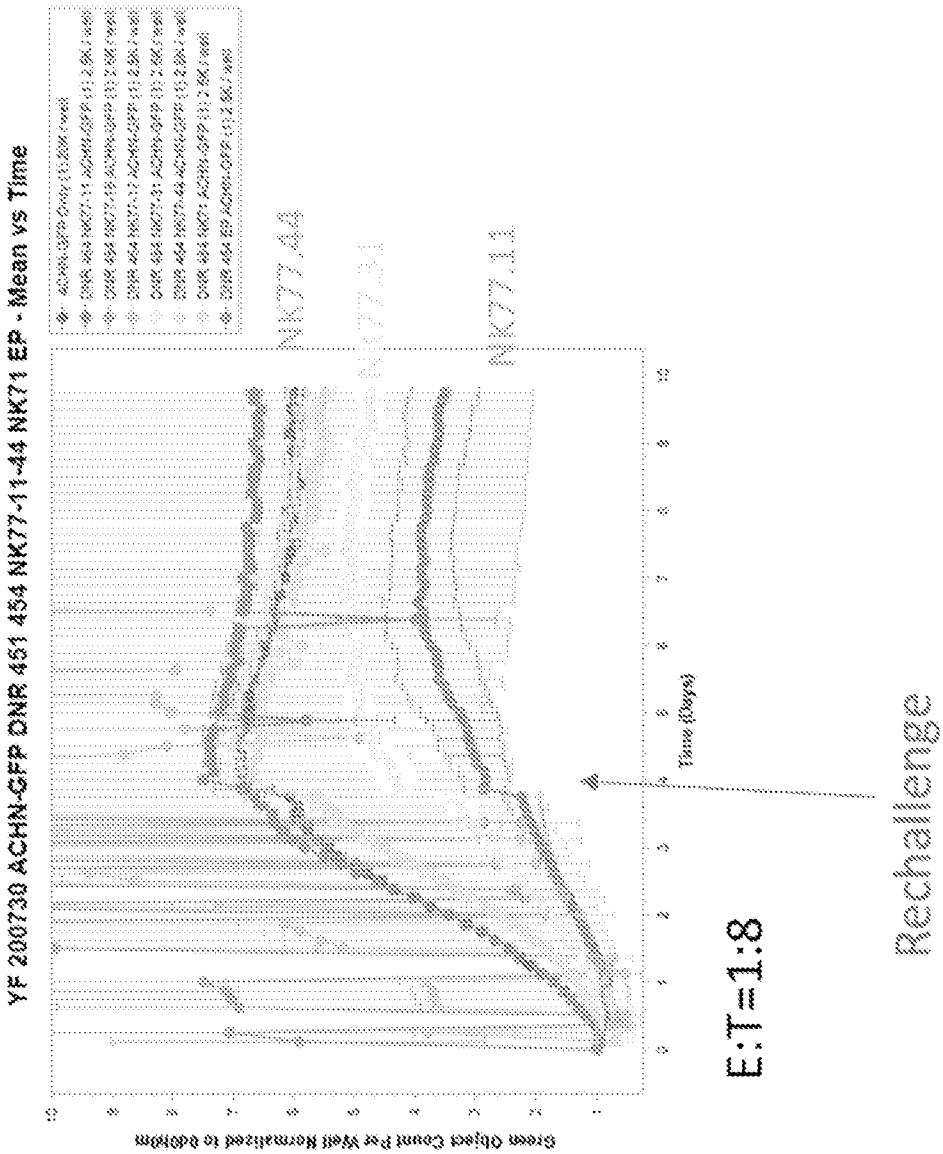

G
YF 200730 ACHN-GFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
ACHN-GFP Only (1) 2K / well
DNR 454 NK77-11 ACHN-GFP (1) 2.5K / well
DNR 454 NK77-16 ACHN-GFP (1) 2.5K / well
DNR 454 NK77-17 ACHN-GFP (1) 2.5K / well
DNR 454 NK77-31 ACHN-GFP (1) 2.5K / well
DNR 454 NK77-44 ACHN-GFP (1) 2.5K / well
DNR 454 NK71 ACHN-GFP (1) 2.5K / well
DNR 454 EP ACHN-GFP (1) 2.5K / well
Rechallenge
E:T=1:8
NK77.44
NK71
NK77.11
NK77.16
EP
ACHN
Green Object Count Per Well Normalized to 0d0hm
Time (Days)
0
0.5
1
1.5
2
2.5
3
3.5
4
4.5
1
2
3
4
5
6
7
8
9
10

Figure 58H

H


YF 200730 ACHN-CFP DNR 451 454 NK77-11-44 NK71 EP - Mean vs Time
Green Object Count Per Well Normalized to 0 Min
Time (Days)
NK77 44
NK77 01
NK77 11
E:T=1:8
Rechallenge

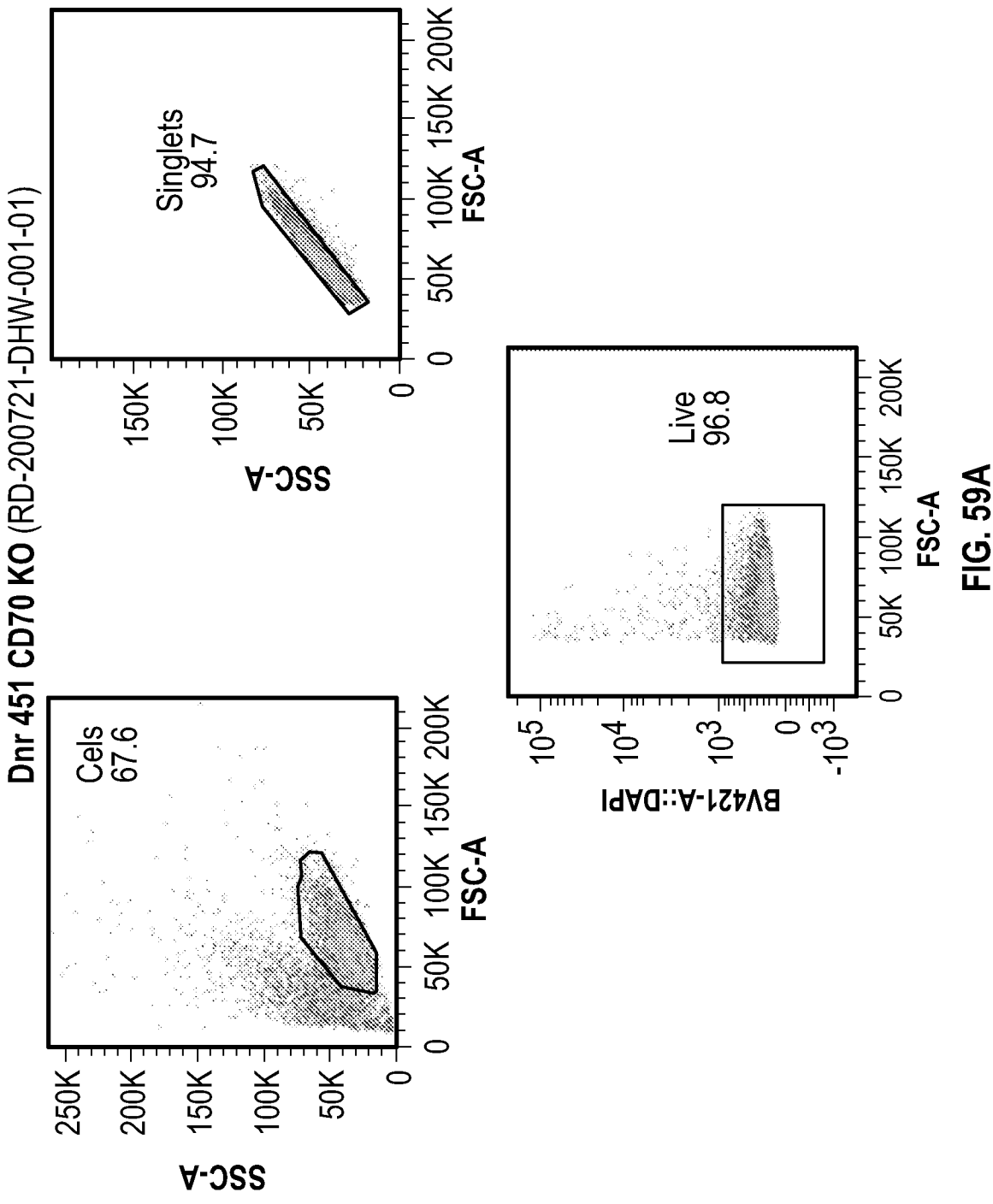

Dnr 451 CD70 KO (RD-200721-DHW-001-01)
Cels
67.6
SSC-A
FSC-A
Singlets
94.7
SSC-A
FSC-A
Live
96.8
BV421-A::DAPI
FSC-A

FIG. 59A

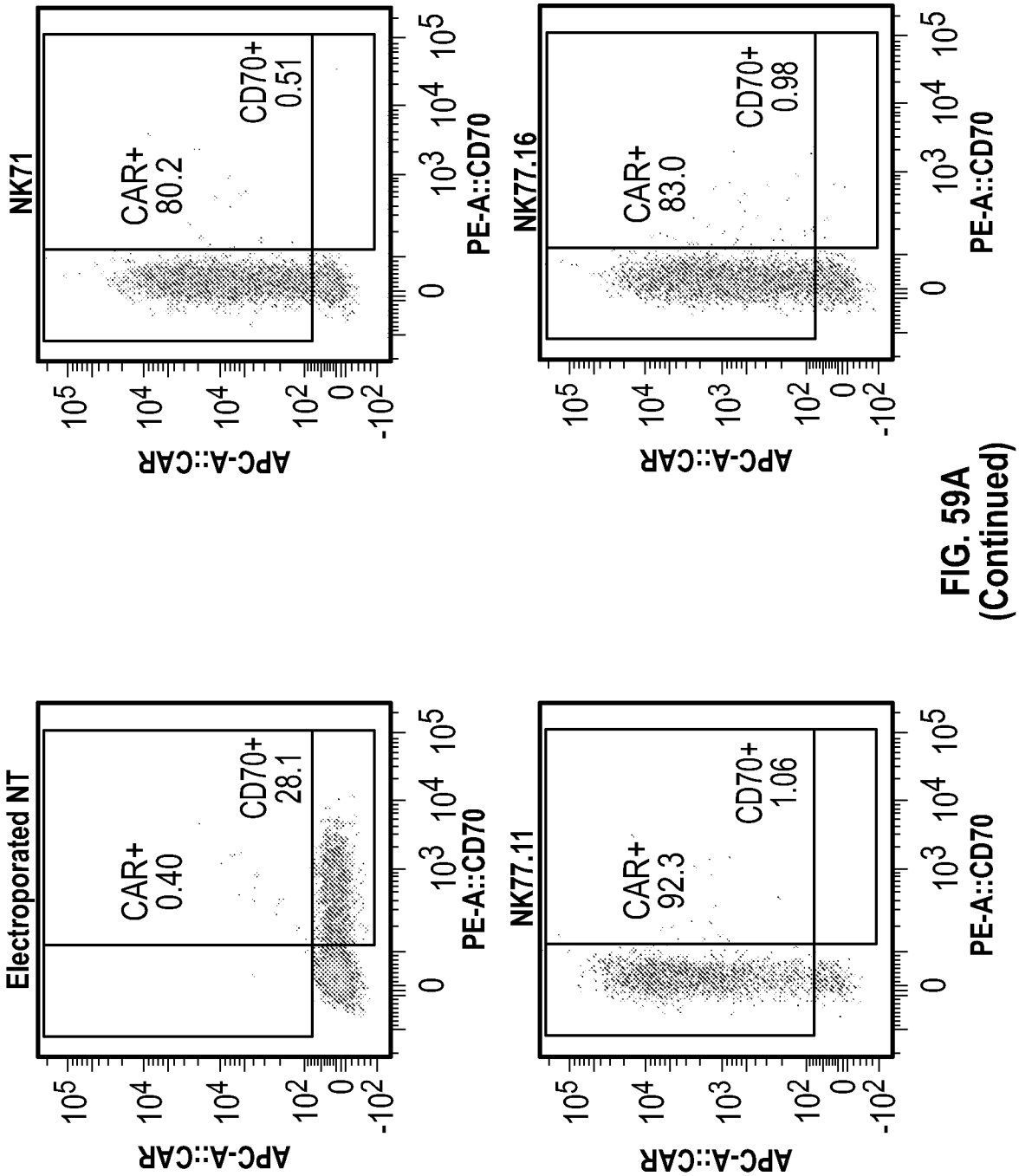


FIG. 59A (Continued)

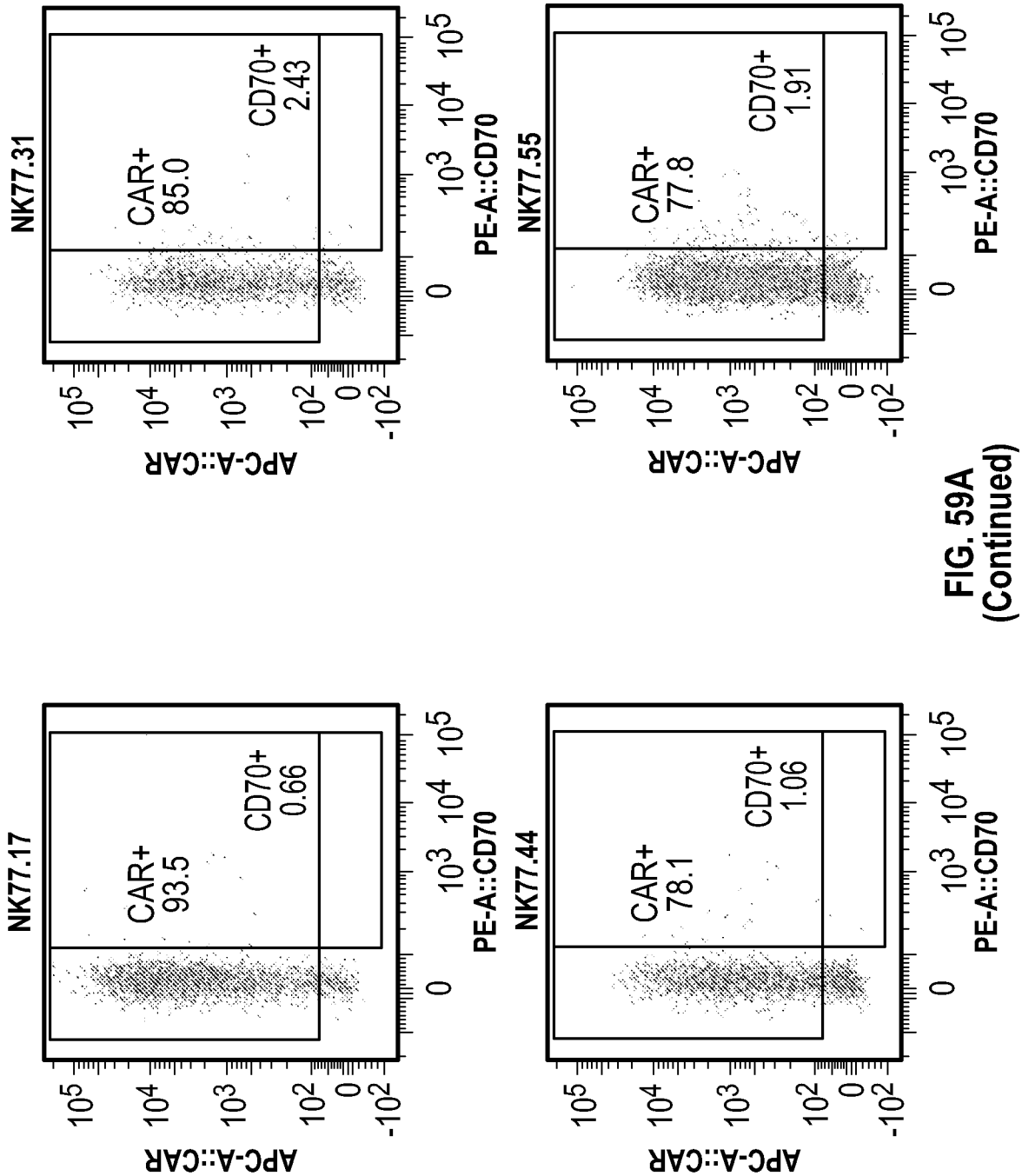


FIG. 59A
(Continued)

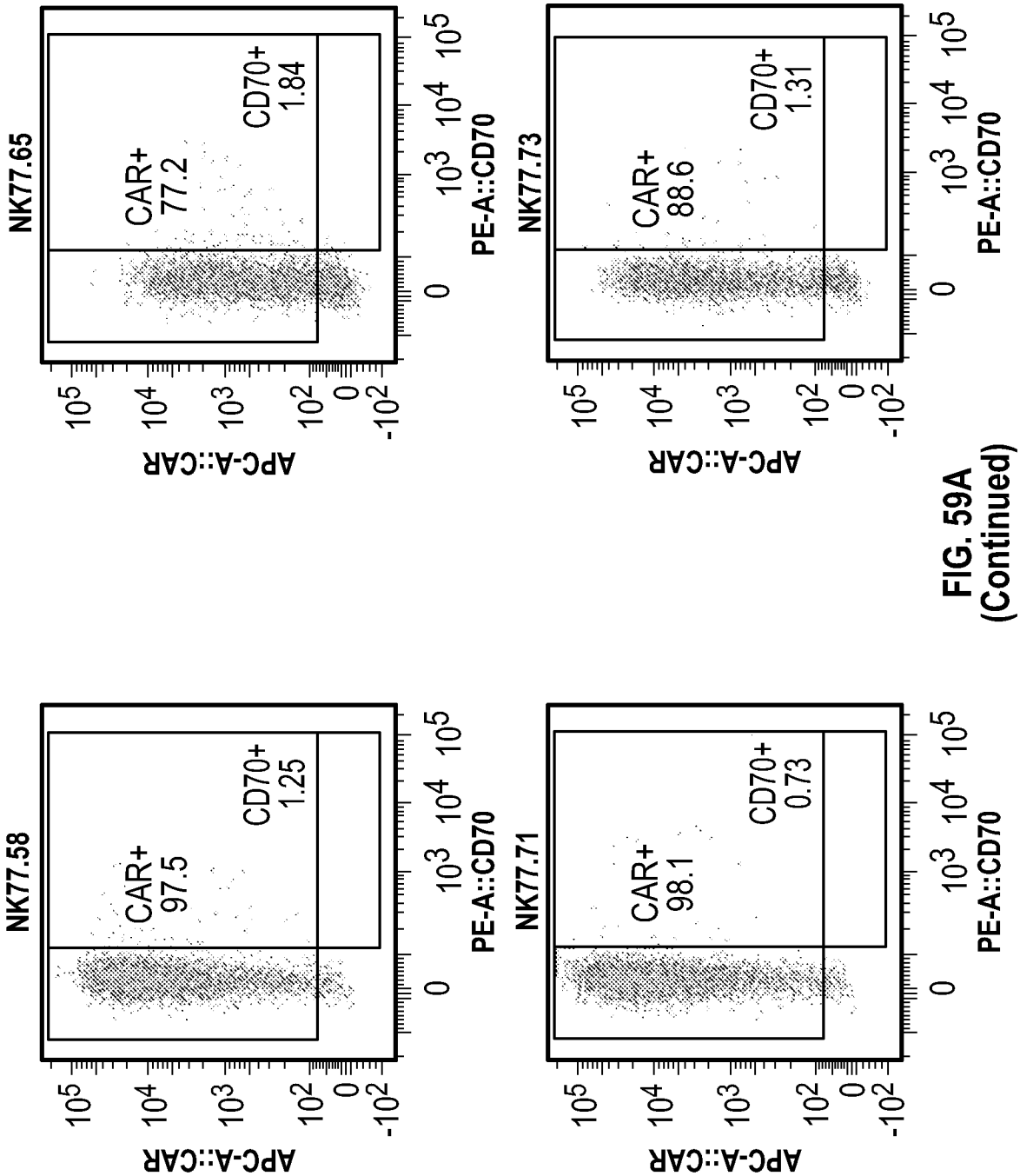


FIG. 59A
(Continued)

Figure 59B-59C

B

Construct	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)
EPNT	-	26.1%	-
NK71	1.20E+06	0.51%	80.2%
NK77.11	2.85E+06	1.06%	92.3%
NK77.16	3.15E+06	0.98%	83.0%
NK77.17	2.88E+06	0.66%	93.5%
NK77.31	3.51E+06	2.43%	85.0%
NK77.44	3.57E+06	1.06%	78.1%
NK77.55	1.03E+06	1.91%	77.8%
NK77.58	1.40E+06	1.25%	97.5%
NK77.65	5.95E+05	1.84%	77.2%
NK77.71	1.50E+06	0.73%	98.1%
NK77.73	9.17E+05	1.31%	88.6%

C

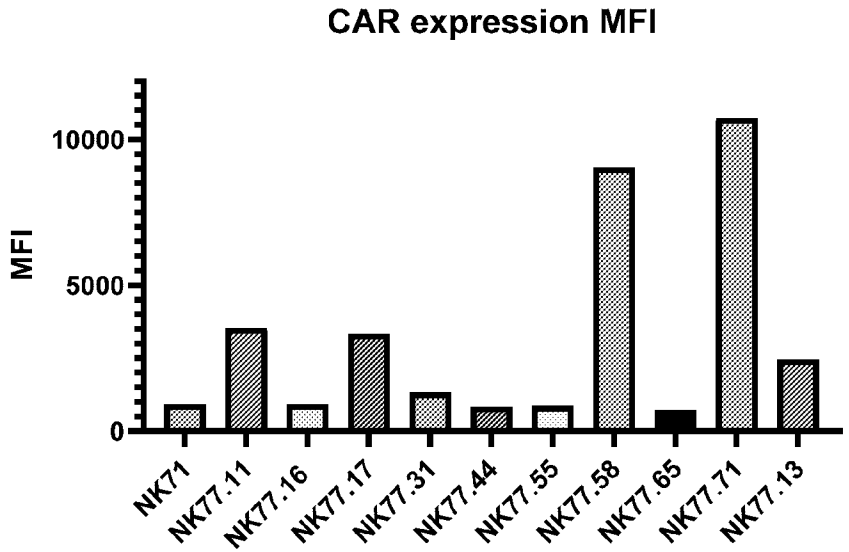
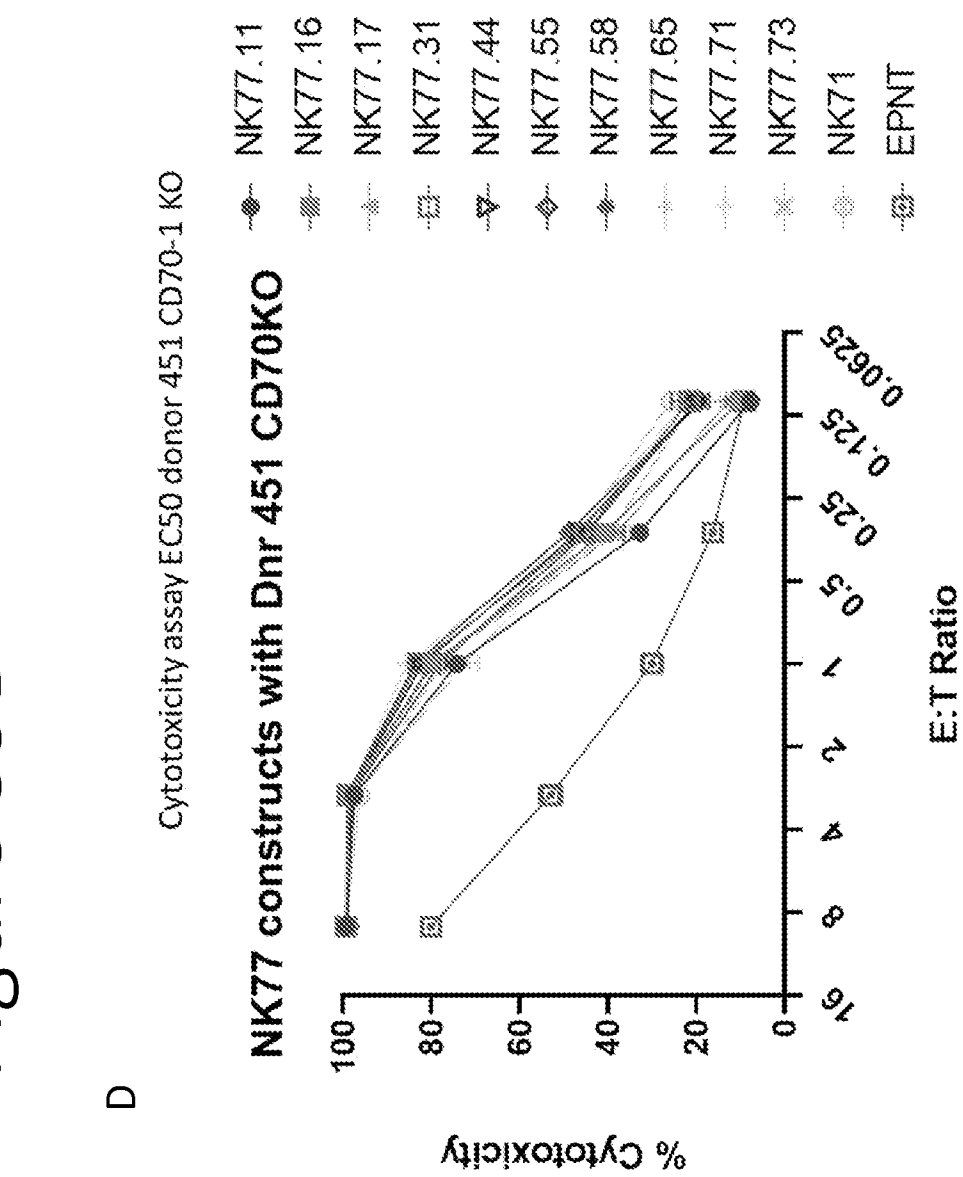


Figure 59D

D



Construct	%CAR+	EC50
NK77.11	92.3	0.5146
NK77.16	83	0.4203
NK77.17	93.5	0.4342
NK77.31	85	0.3428
NK77.44	78.1	0.3438
NK77.55	77.8	0.3677
NK77.58	97.5	0.3292
NK77.65	77.2	0.3914
NK77.71	98.1	0.3022
NK77.73	88.6	0.3703
NK71	80.2	0.3233
EPNT		2.343

Figure 60A

A

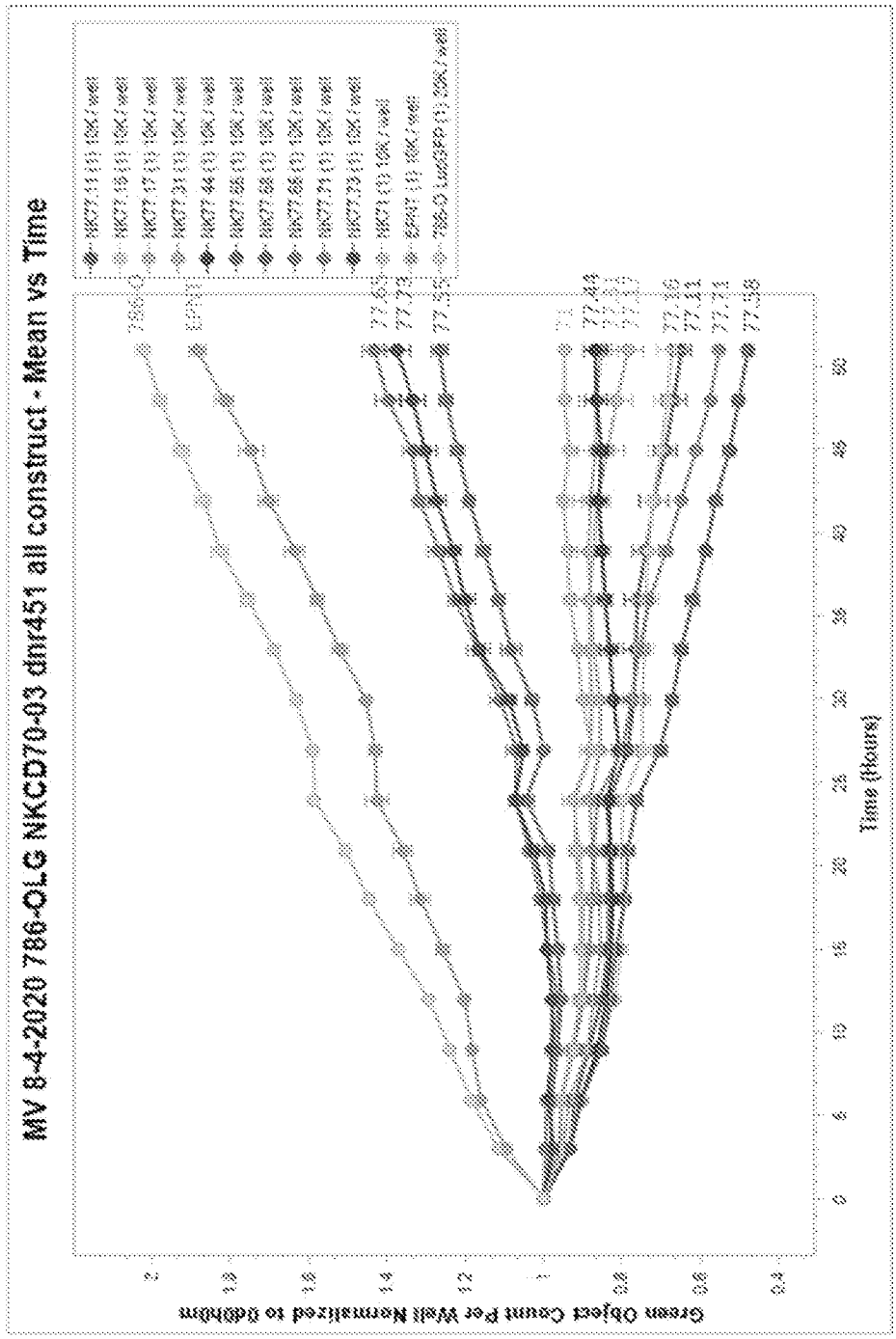

1:2 E:T 786-O
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean vs Time
Green Object Count Per Well Normalized to Bilirubin
Time (Hours)
786-O
Effort
77.63
77.73
77.55
77.44
77.11
77.16
77.11
77.71
77.58

Figure 60B

B

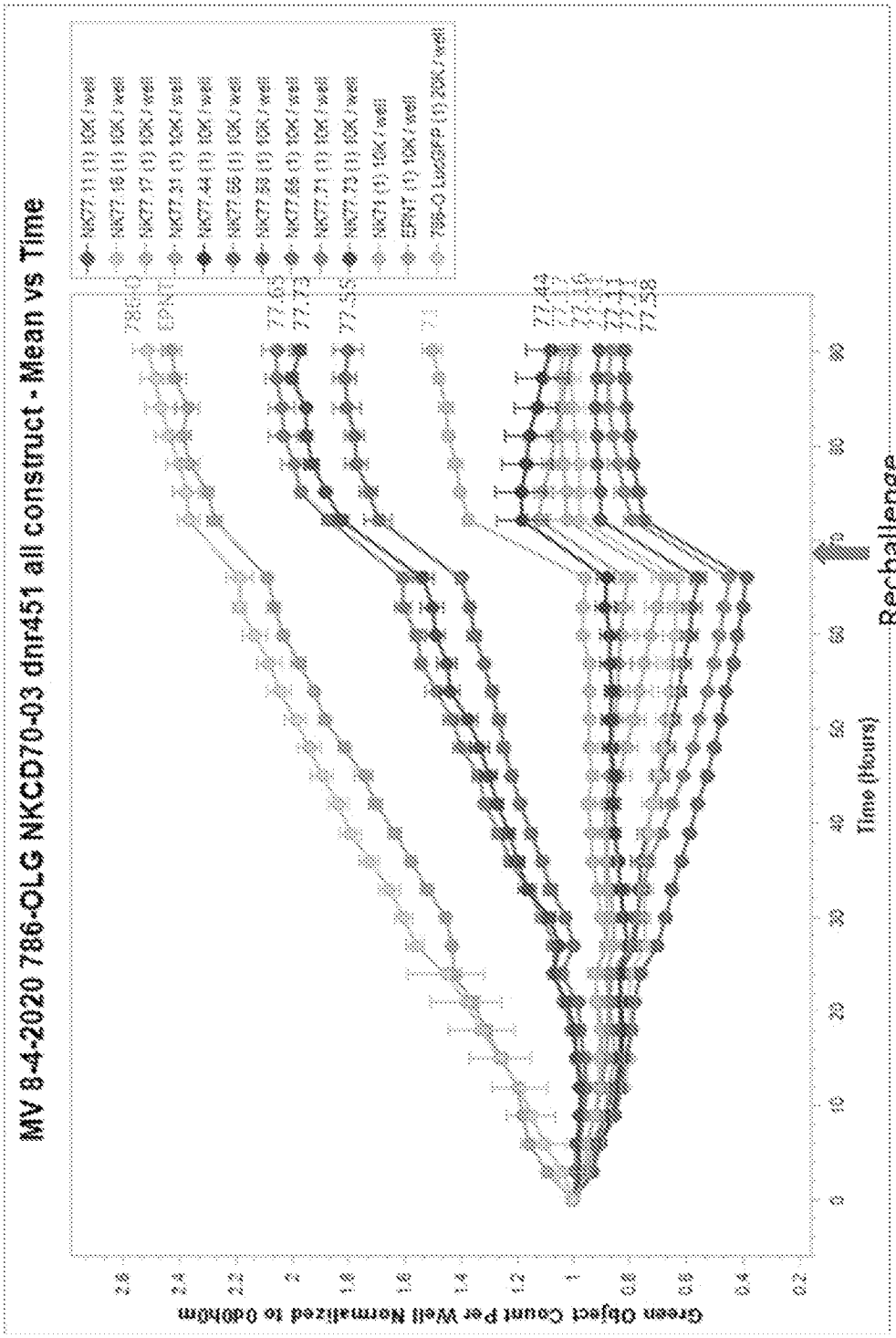
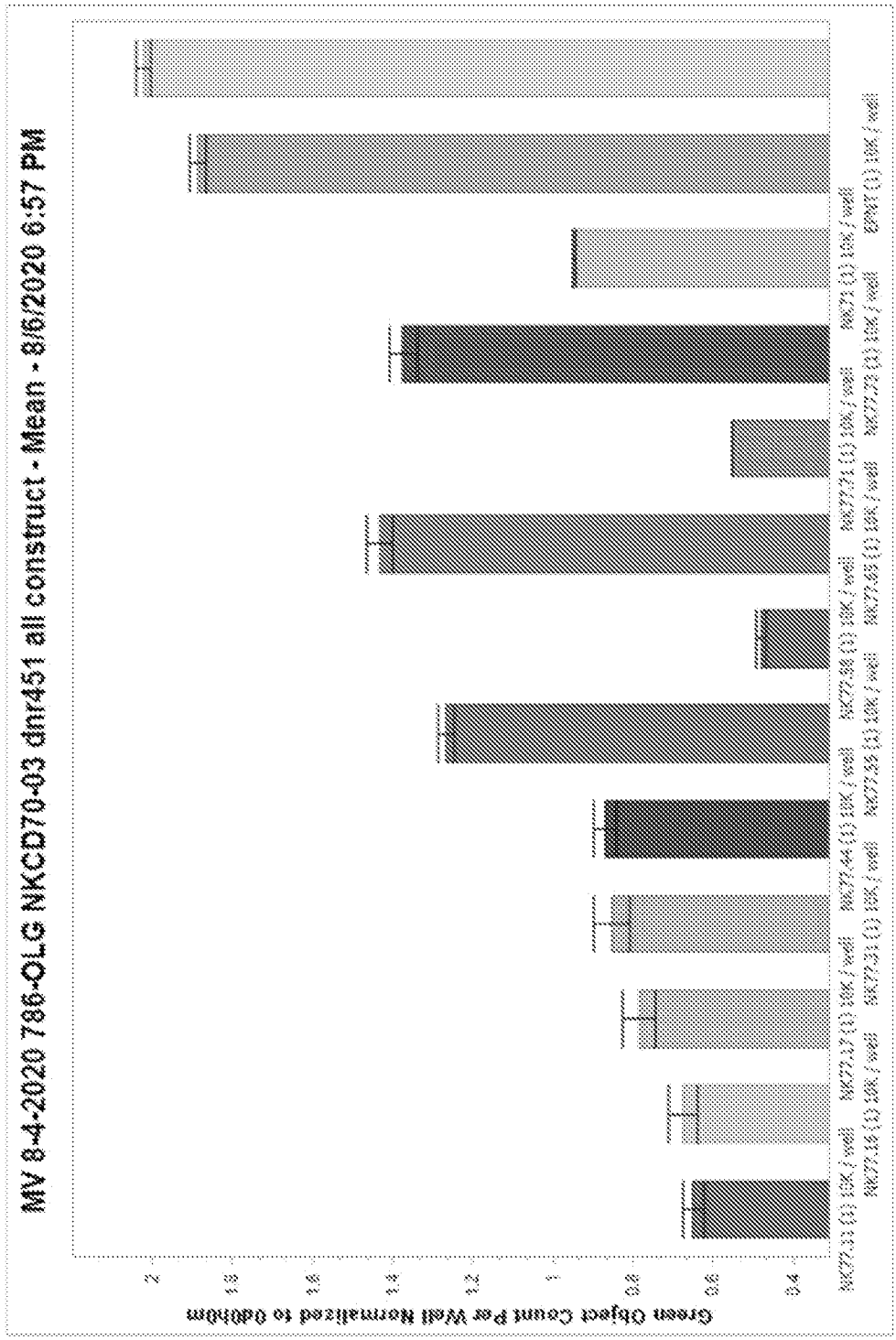

1:2 E:T 786-O
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean vs Time
Green Object Count Per Well Normalized to 0 Hour
Time (Hours)
Rechallenge
786-O
DMSO
77.55
77.73
77.55
77.44
77.47
77.46
77.41
77.58

Figure 60C


1:2 E:T 786-O at 51 hours
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean - 8/6/2020 6:57 PM
Green Object Count Per Well Normalized to 0dnhm
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
NKC72.33 (1) 10K / well
NKC72.16 (1) 10K / well
NKC72.17 (1) 10K / well
NKC72.31 (1) 10K / well
NKC72.44 (1) 10K / well
NKC72.36 (1) 10K / well
NKC72.56 (1) 10K / well
NKC72.68 (1) 10K / well
NKC72.71 (1) 10K / well
NKC72.73 (1) 10K / well
NKC71 (1) 10K / well
EPNT (1) 10K / well

C

Figure 60D

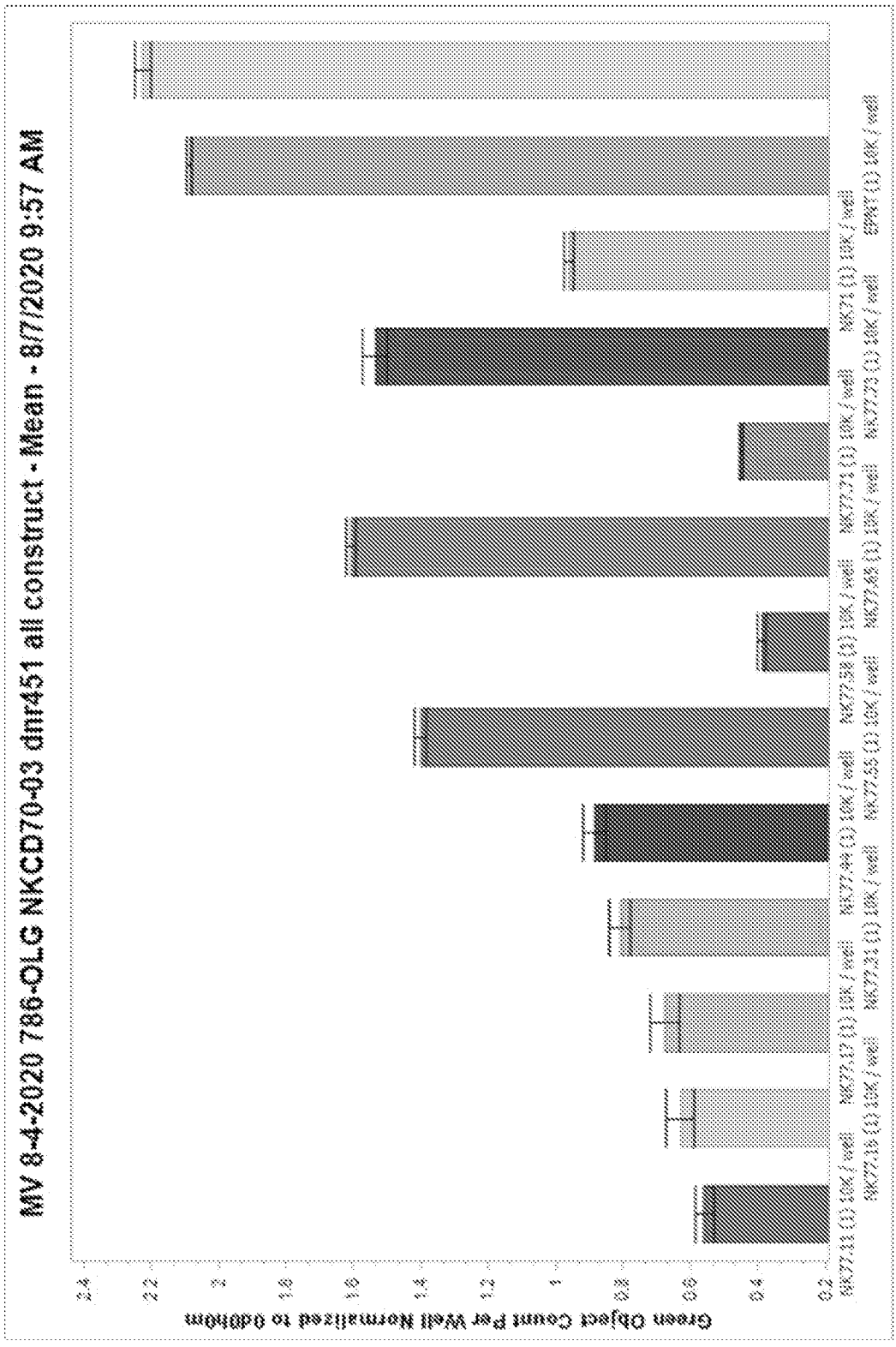

D
1:2 E:T 786-O at 66 hours
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean - 8/7/2020 9:57 AM
Green Object Count Per Well Normalized to 0dilnm
2.4
2.2
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
NK77.31 (1) 10K / well
NK77.16 (1) 10K / well
NK77.17 (1) 10K / well
NK77.23 (1) 10K / well
NK77.44 (1) 10K / well
NK77.55 (1) 10K / well
NK77.58 (1) 10K / well
NK77.63 (1) 10K / well
NK77.74 (1) 10K / well
NK77.78 (1) 10K / well
NK71 (1) 10K / well
EPRT (1) 10K / well

Figure 60E

E

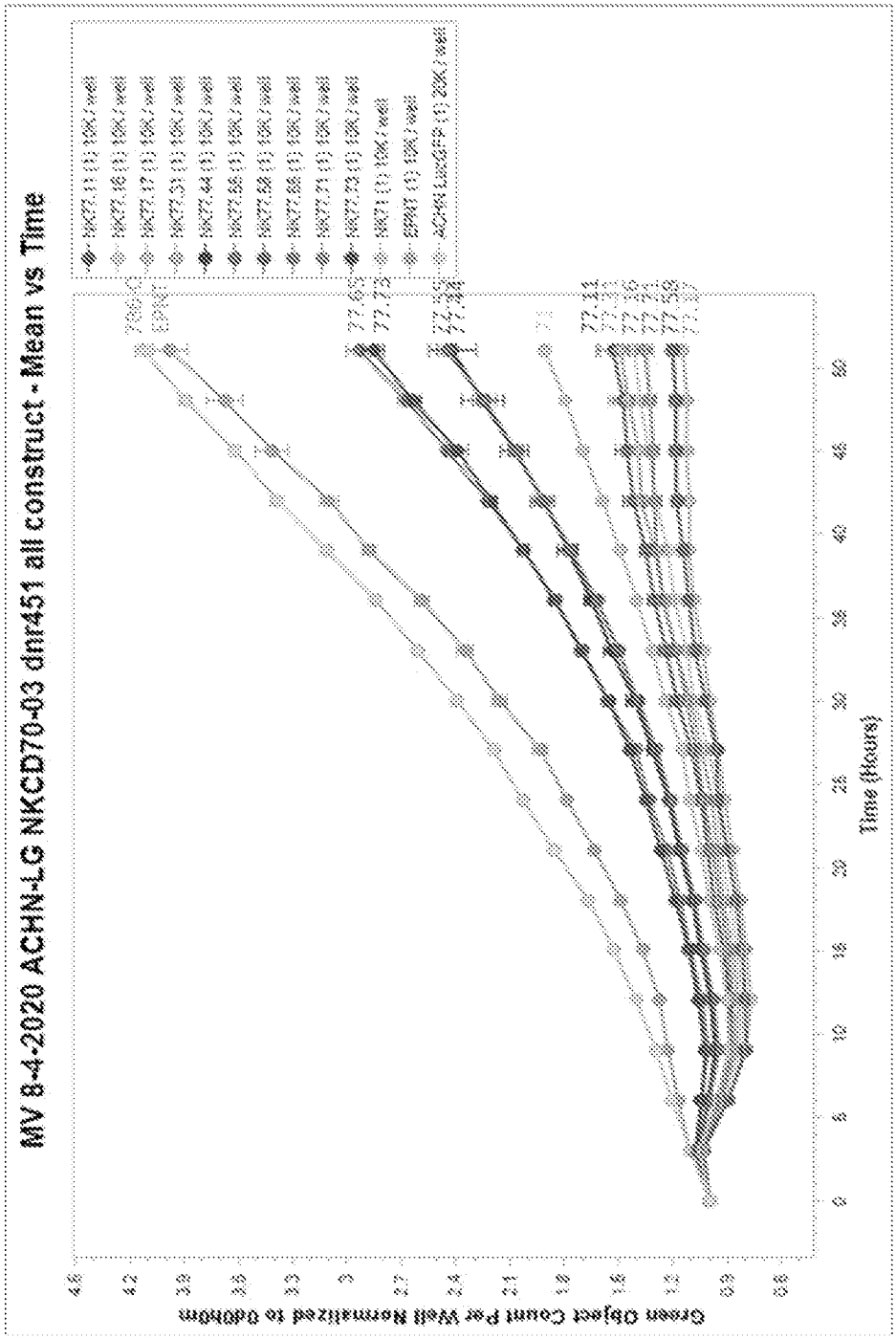

1:2 E:T ACHN
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean vs Time
Green Object Count Per Well Normalized to 0dhhm
Time (Hours)
4.6
4.2
3.8
3.5
3
2.7
2.4
2.1
1.8
1.5
1.2
0.9
0.6
0
5
10
15
20
25
30
35
40
45
50
77.44
77.41
77.16
77.21
77.58
77.07
77.66
77.73
77.34
77.33

Figure 60F

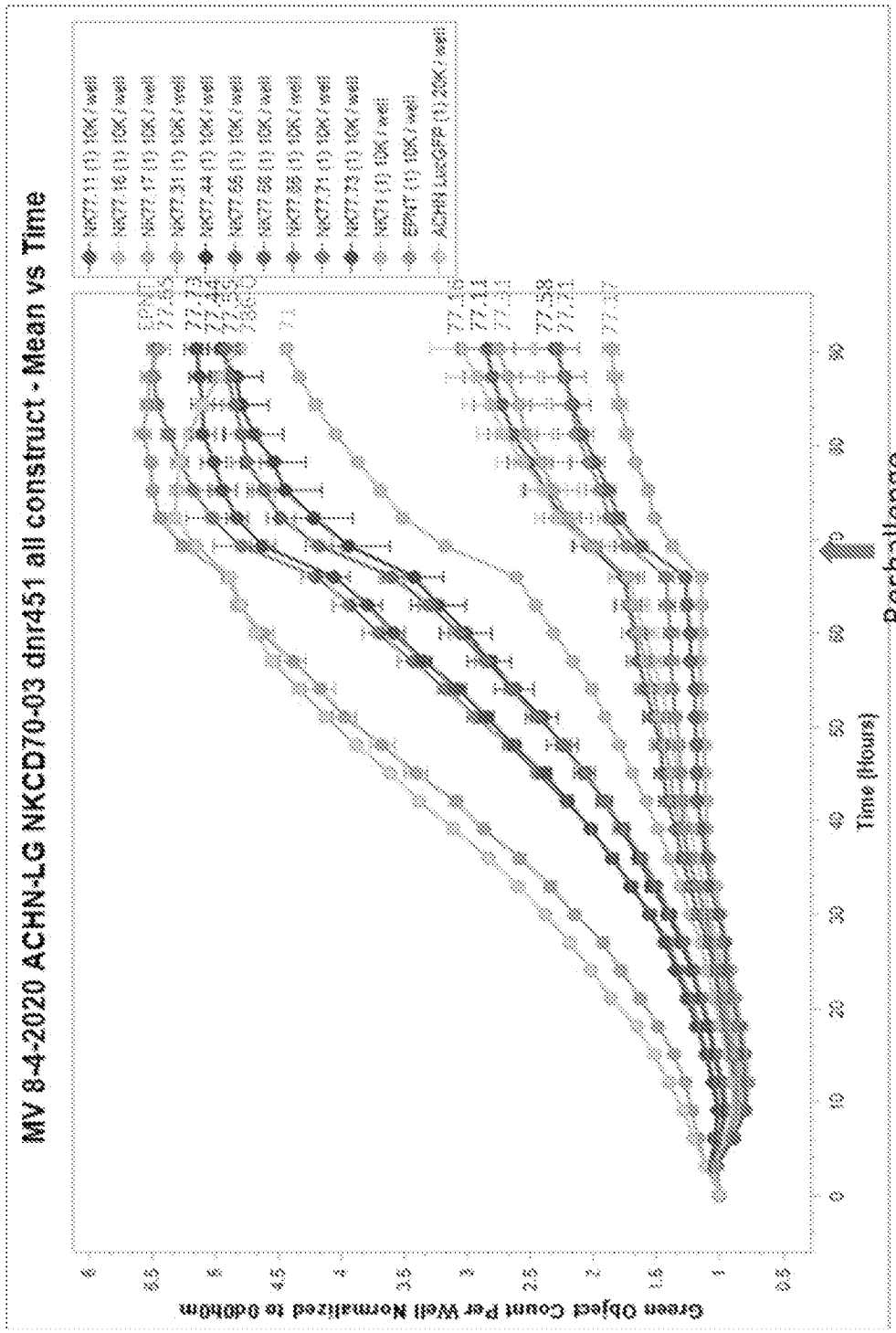
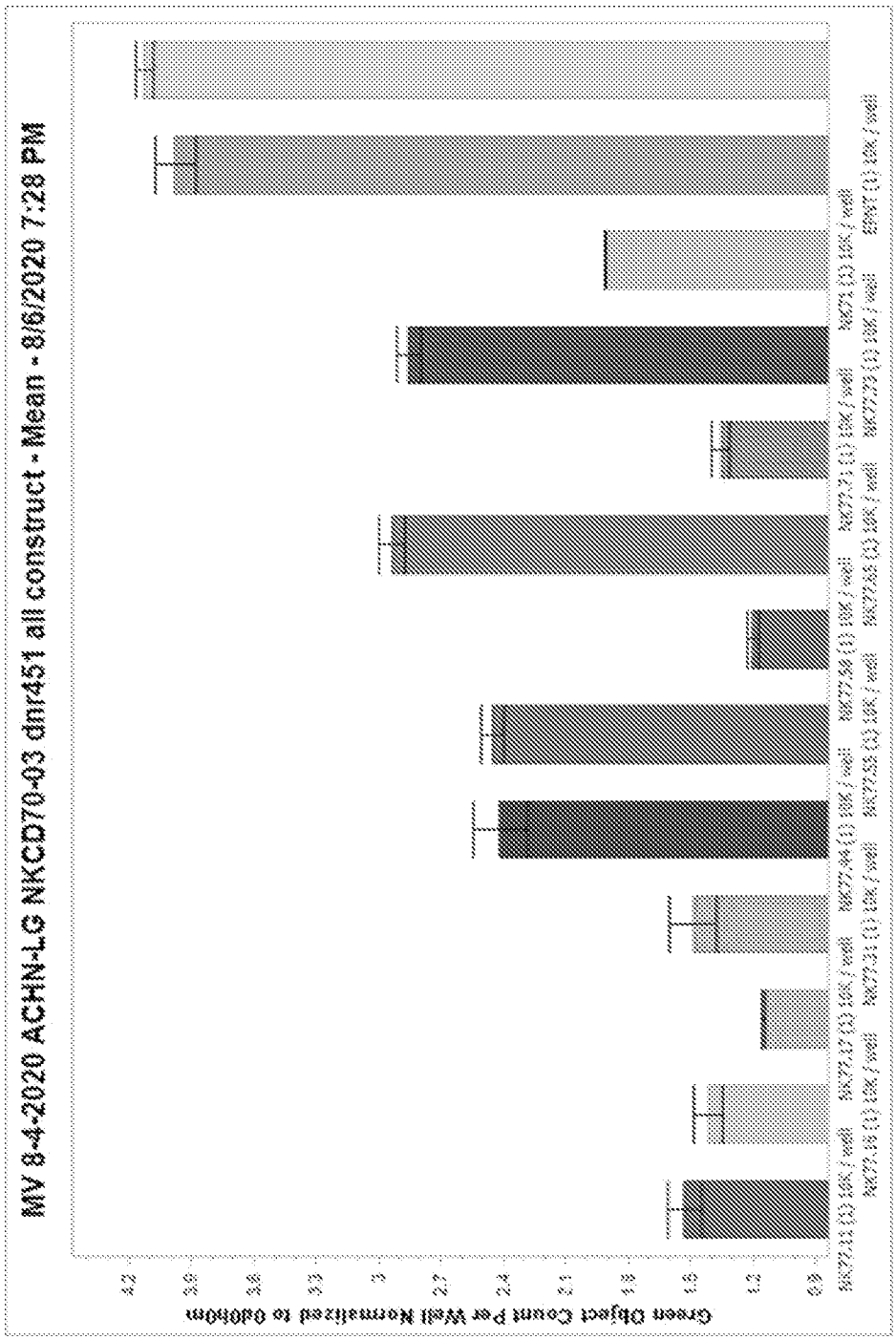

F
1:2 E:T ACHN
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean vs Time
Green Object Count Per Well Normalized to 0dnbm
Time (Hours)
Rechallenge

Figure 60G


1:2 E:T ACHN at 51 hours
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean - 8/6/2020 7:28 PM
Green Object Count Per Well Normalized to 0 Hour
4.2
3.9
3.6
3.3
3
2.7
2.4
2.1
1.8
1.5
1.2
0.9

G

Figure 60H

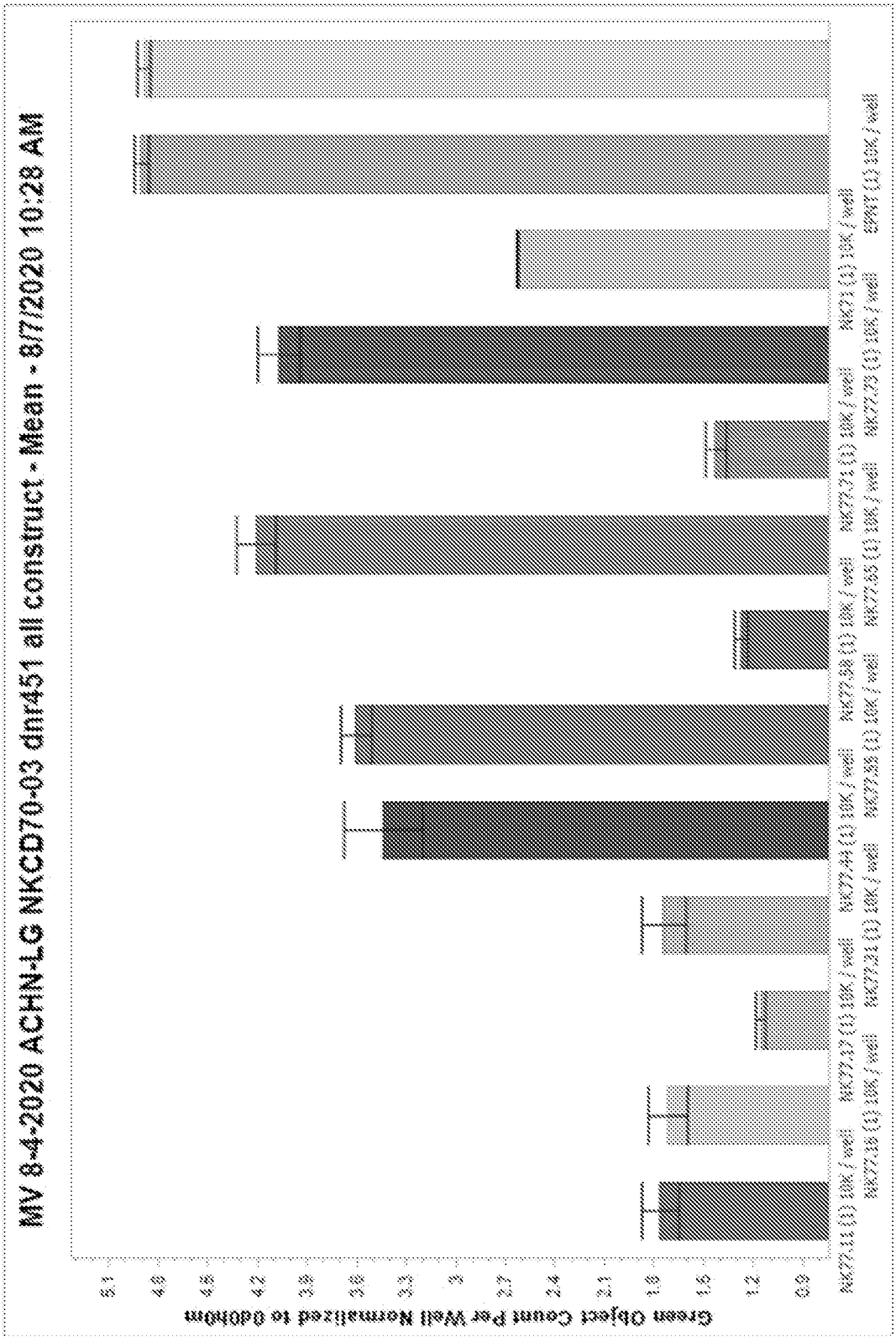

1:2 E:T ACHN at 66 hours
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean - 8/7/2020 10:28 AM
Green Object Count Per Well Normalized to 0dnr0m
8.1
6.6
5.4
4.2
3.9
3.6
3.3
3
2.7
2.4
2.1
1.8
1.5
1.2
0.9
NK77-11 (1) 10K / well
NK77-17 (1) 10K / well
NK77-18 (1) 10K / well
NK77-21 (1) 10K / well
NK77-44 (1) 10K / well
NK77-55 (1) 10K / well
NK77-58 (1) 10K / well
NK77-65 (1) 10K / well
NK77-74 (1) 10K / well
NK77-75 (1) 10K / well
NK21 (1) 10K / well
EPNT (1) 10K / well

Figure 60I

1:4 E:T 786-O

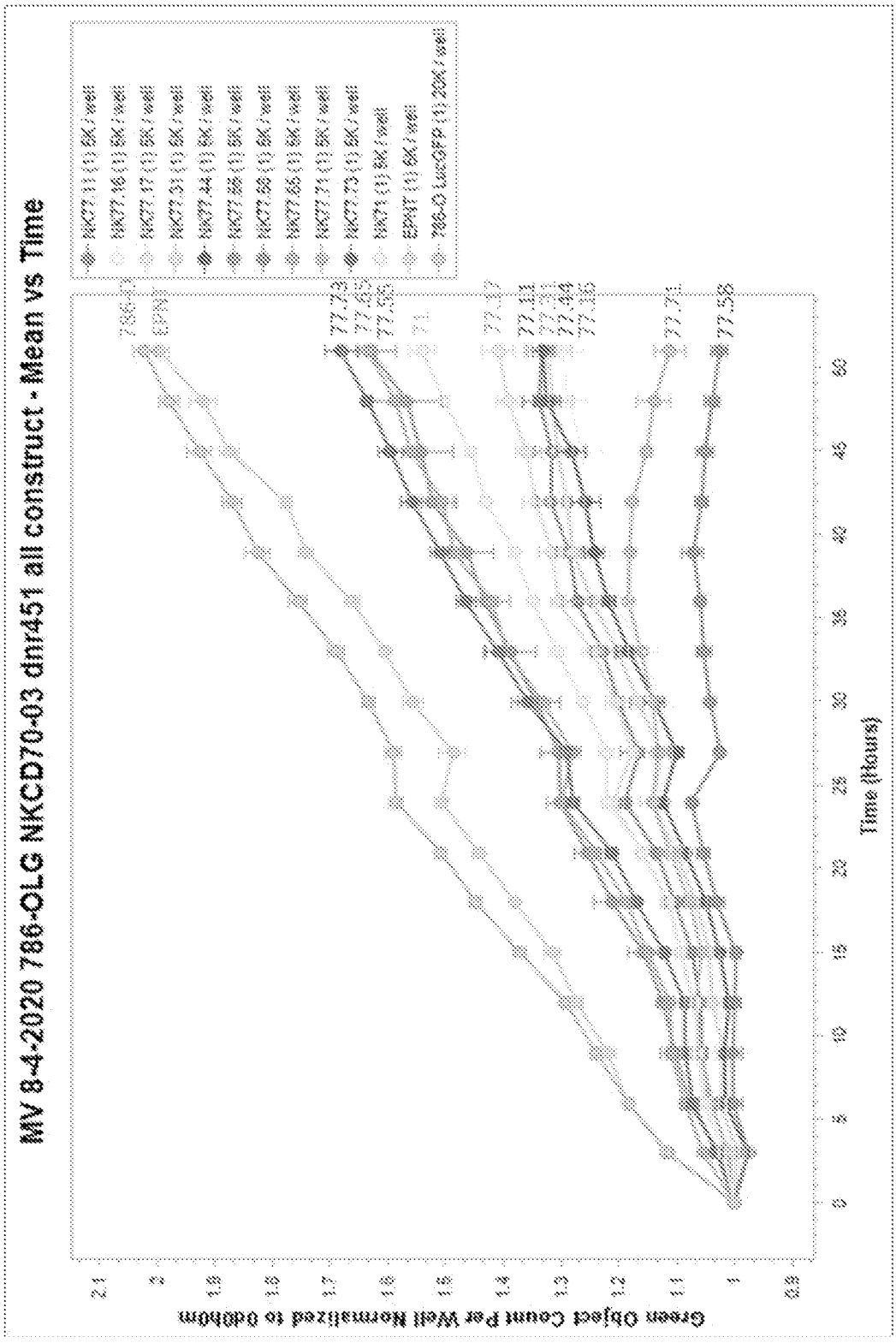
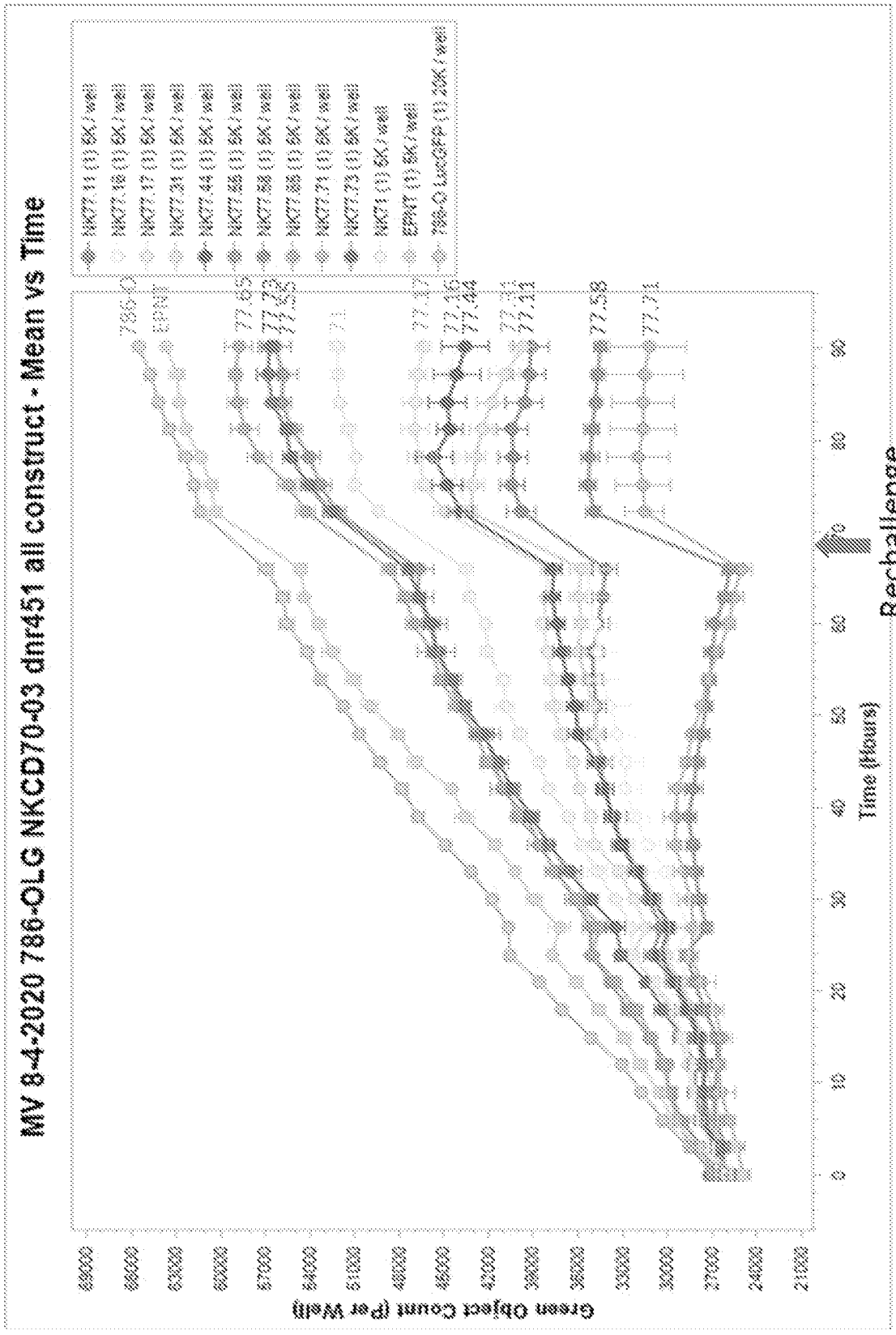


Figure 60J

1:4 E:T 786-O



J

Figure 60K

K

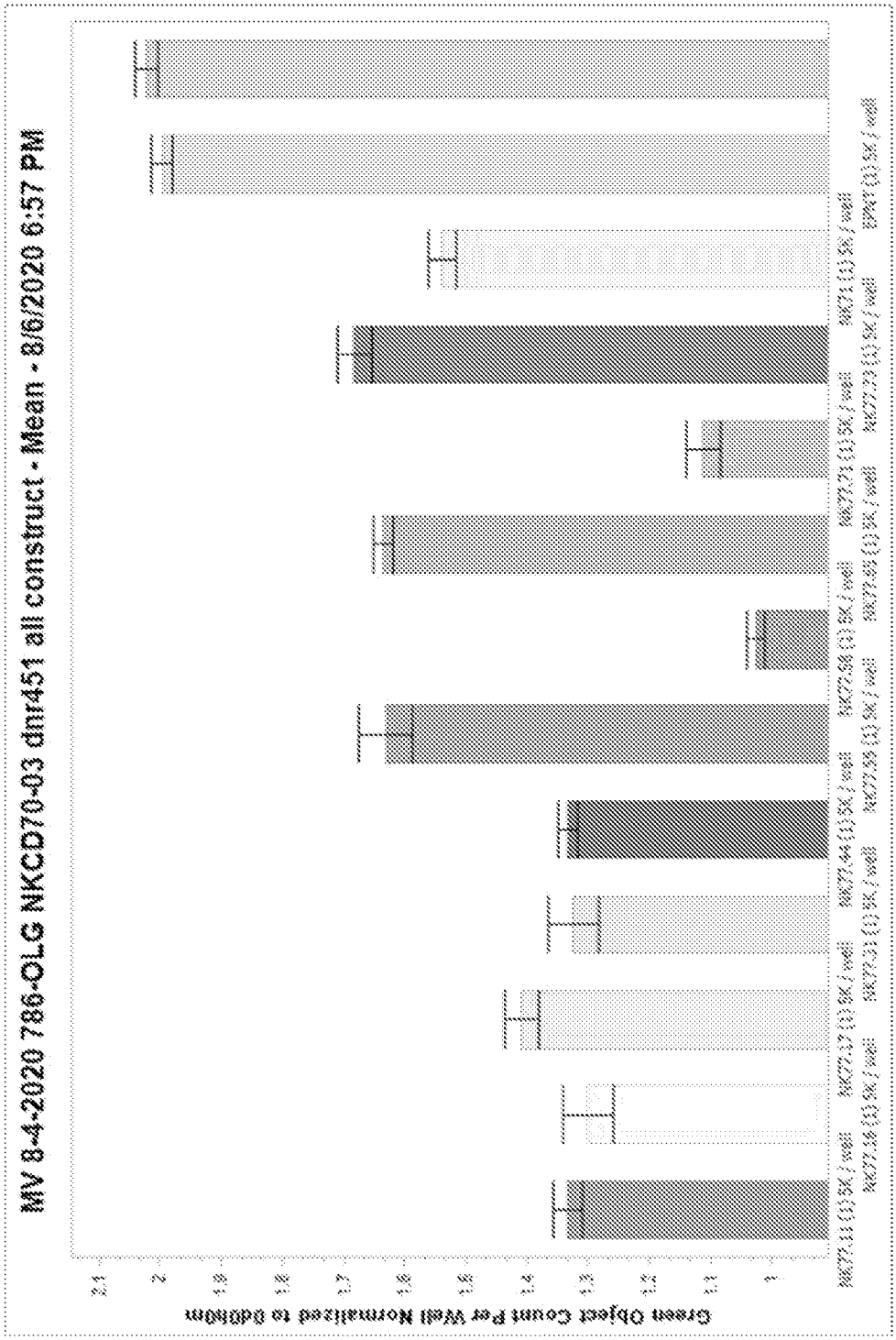

1:4 E:T 786-O at 51 hours
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean - 8/6/2020 6:57 PM
Green Object Count Per Well Normalized to 0dNkm
2.1
2
1.9
1.8
1.7
1.6
1.5
1.4
1.3
1.2
1.1
1
NKZ211 (1) 5K / well
NKZ216 (1) 5K / well
NKZ27 (1) 5K / well
NKZ231 (1) 5K / well
NKZ41 (1) 5K / well
NKZ59 (1) 5K / well
NKZ258 (1) 5K / well
NKZ451 (1) 5K / well
NKZ271 (1) 5K / well
NKZ272 (1) 5K / well
NKZ1 (1) 5K / well
EPAS (1) 5K / well

Figure 60L

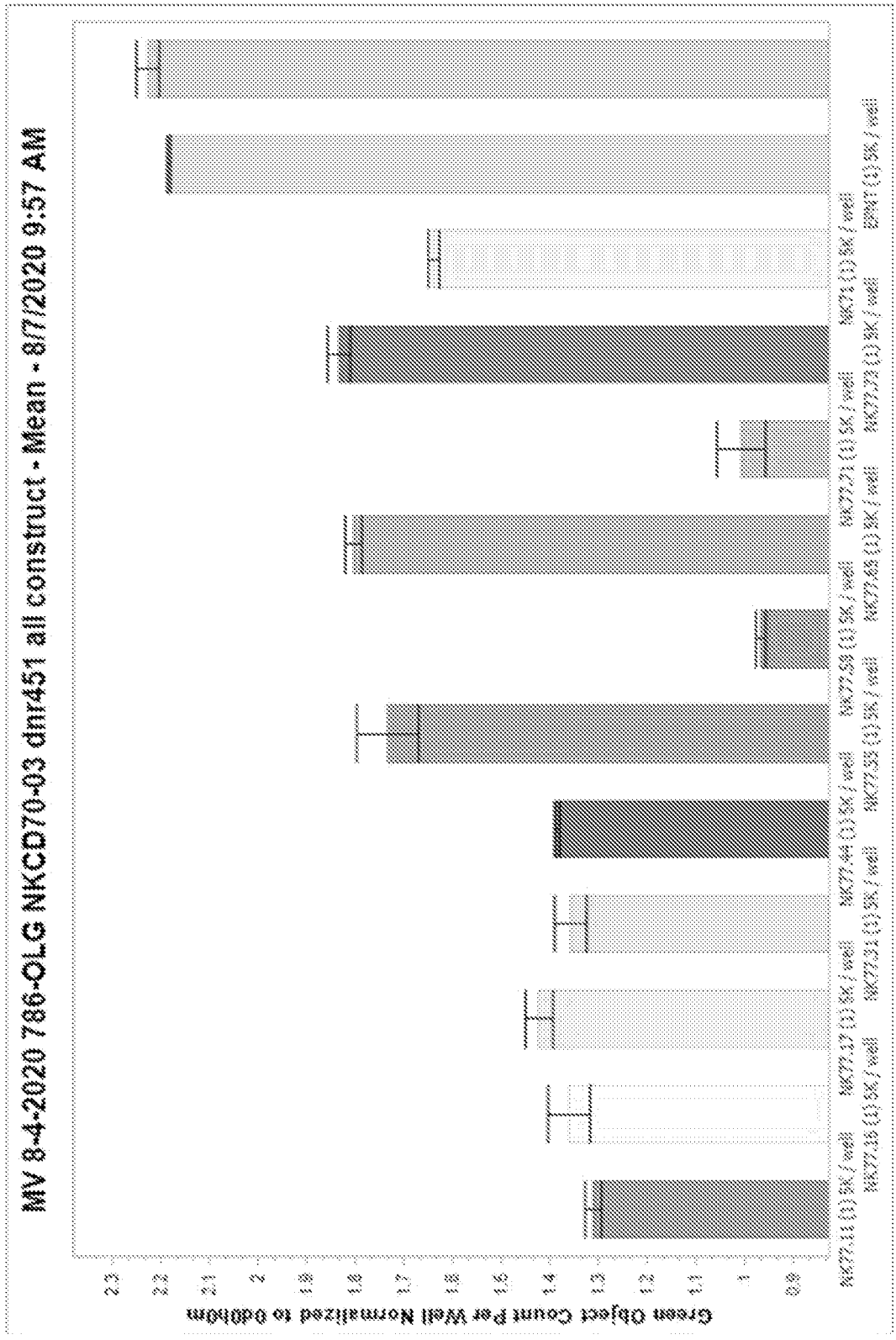

1:4 E:T 786-O at 66 hours
MV 8-4-2020 786-OLG NKCD70-03 dnr451 all construct - Mean - 8/7/2020 9:57 AM
Green Object Count Per Well Normalized to 0dilnm
2.3
2.2
2.1
2
1.9
1.8
1.7
1.6
1.5
1.4
1.3
1.2
1.1
1
0.9
NK77.11 (1) 5K / well
NK77.16 (1) 5K / well
NK77.17 (1) 5K / well
NK77.31 (1) 5K / well
NK77.44 (1) 5K / well
NK77.53 (1) 5K / well
NK77.59 (1) 5K / well
NK77.65 (1) 5K / well
NK77.71 (1) 5K / well
NK77.72 (1) 5K / well
NK71 (1) 5K / well
BSNT (1) 5K / well

Figure 60M

1:4 E:T ACHN

M

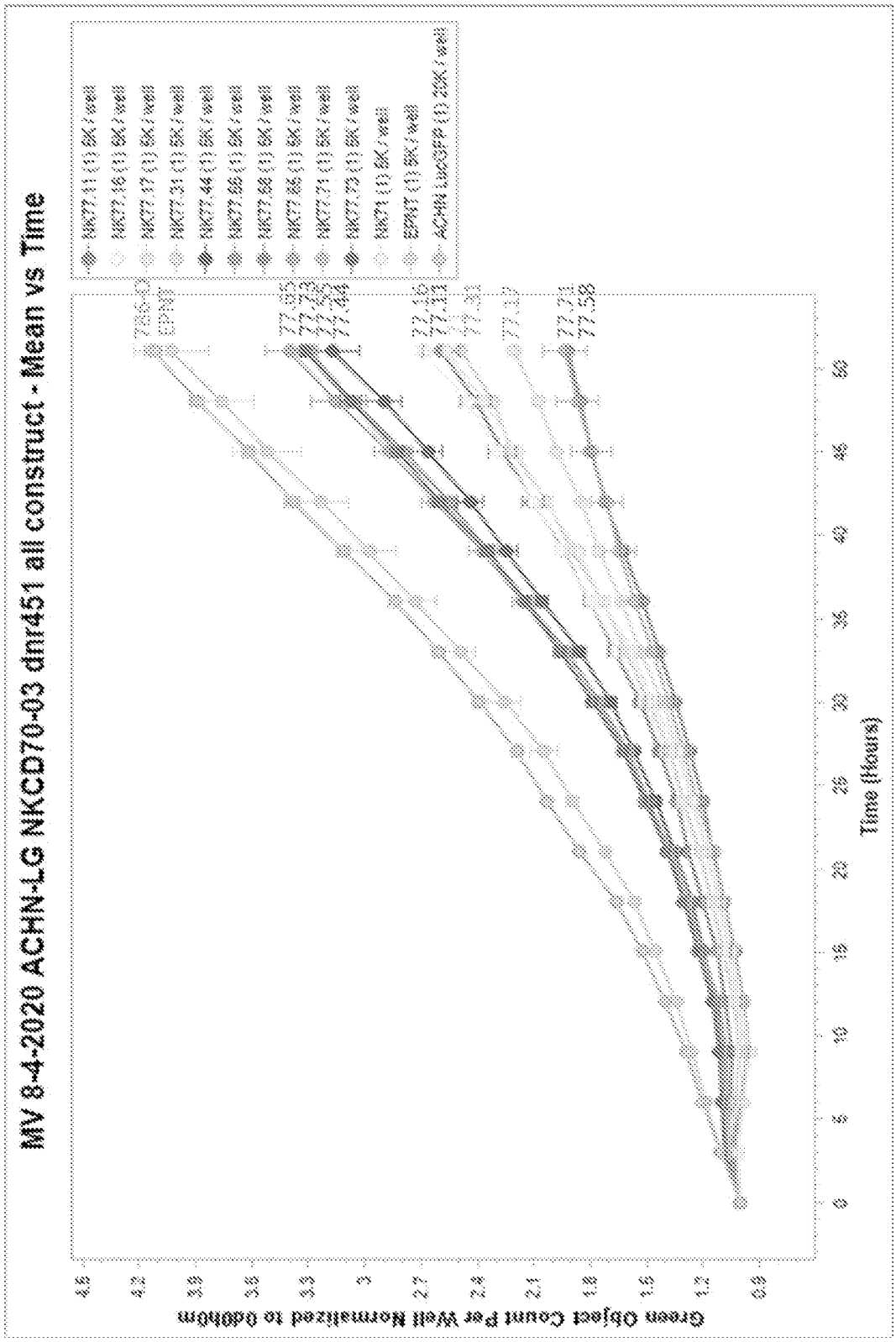
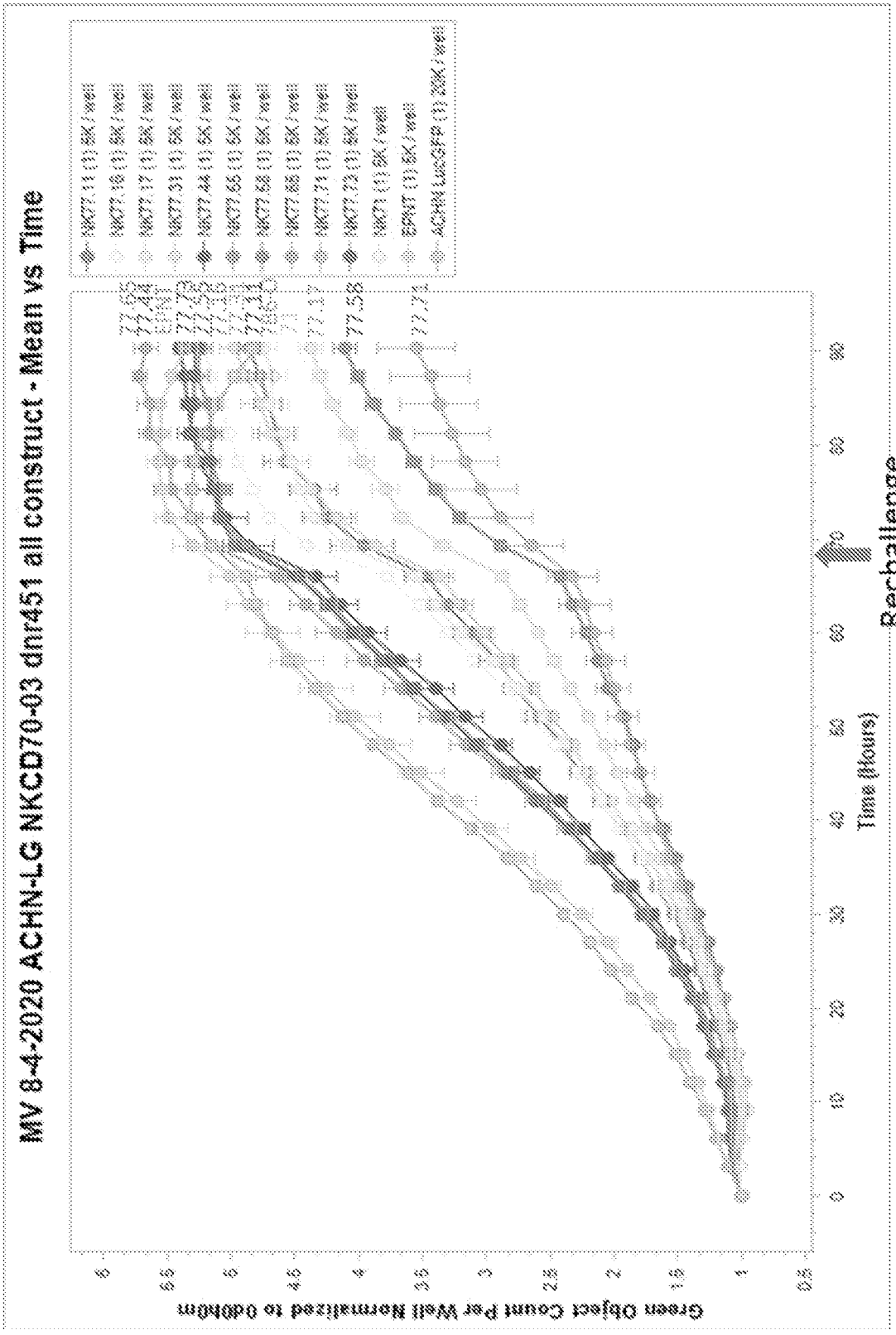


Figure 60N

1:4 E:T ACHN



N

Figure 60O

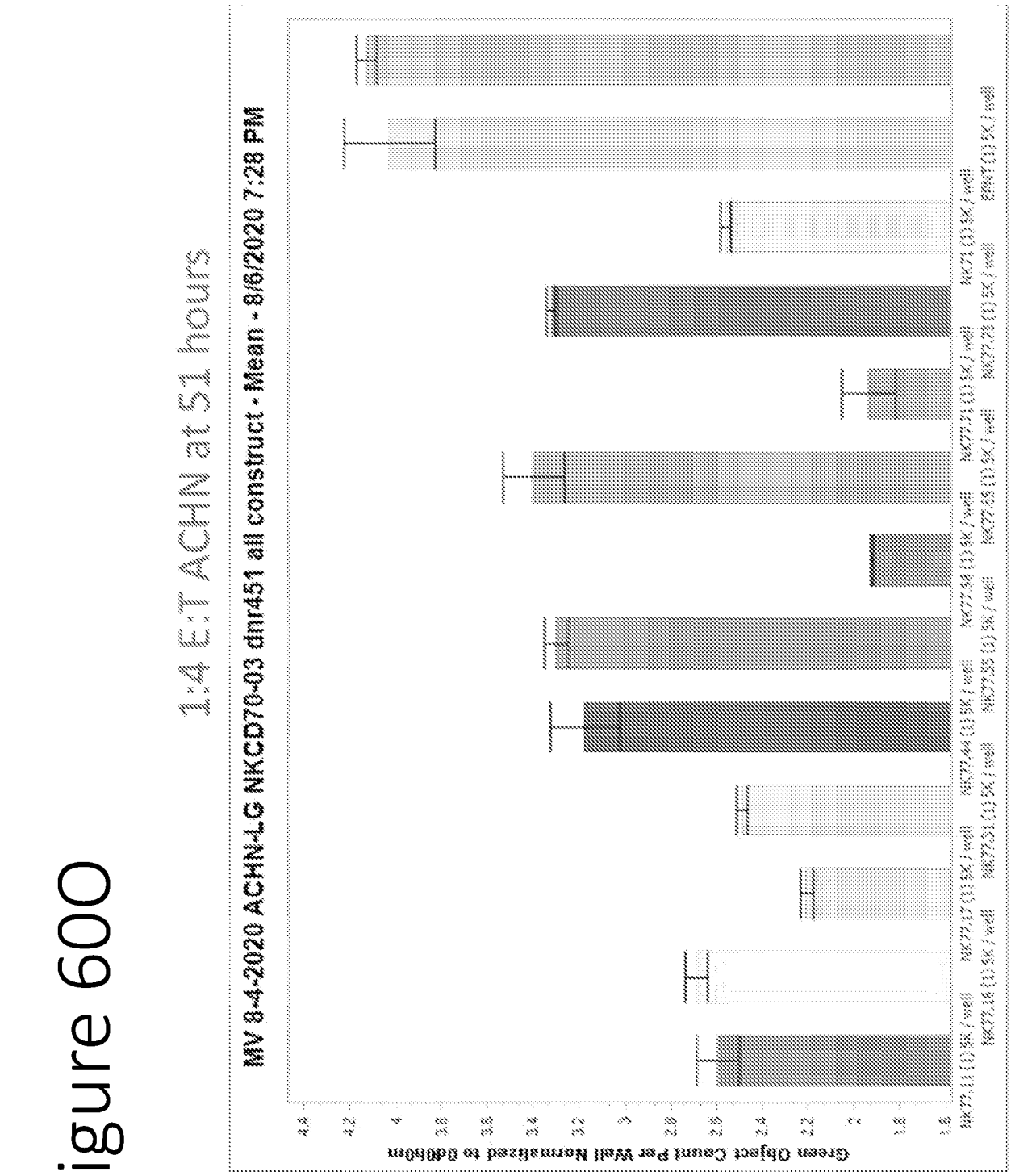
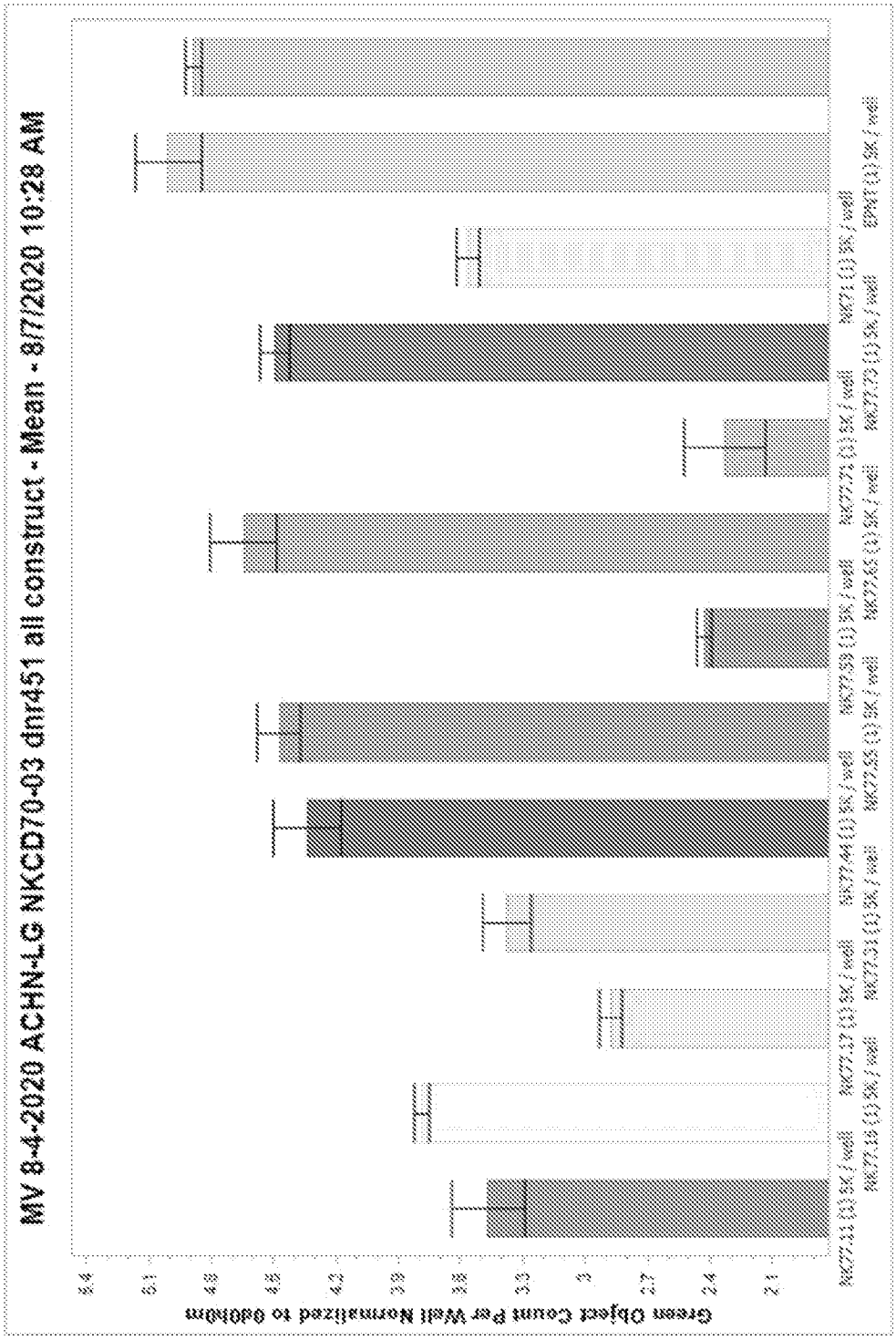

1:4 E:T ACHN at 51 hours
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean - 8/6/2020 7:28 PM
Green Object Count Per Well Normalized to Edbhom
4.4
4.2
4
3.8
3.6
3.4
3.2
3
2.8
2.6
2.4
2.2
2
1.8
1.6
NKT27.11 (1) 5K / well
NKT27.18 (1) 5K / well
NKT27.17 (1) 5K / well
NKT27.31 (1) 5K / well
NKT27.44 (1) 5K / well
NKT27.55 (1) 5K / well
NKT27.56 (1) 5K / well
NKT27.65 (1) 5K / well
NKT27.71 (1) 5K / well
NKT27.73 (1) 5K / well
NKT1 (1) 5K / well
EPNT (1) 5K / well

Figure 60P


1:4 E:T ACHN at 66 hours
MV 8-4-2020 ACHN-LG NKCD70-03 dnr451 all construct - Mean - 8/7/2020 10:28 AM
Green Object Count Per Well Normalized to dotolum
6.4
6.1
4.8
4.5
4.2
3.9
3.6
3.3
3
2.7
2.4
2.1
NK77.11 (1) 5K / well
NK77.19 (1) 5K / well
NK77.27 (1) 5K / well
NK77.31 (1) 5K / well
NK77.44 (1) 5K / well
NK77.55 (1) 5K / well
NK77.59 (1) 5K / well
NK77.65 (1) 5K / well
NK77.71 (1) 5K / well
NK77.79 (1) 5K / well
NK71 (1) 5K / well
EPNT (1) 5K / well

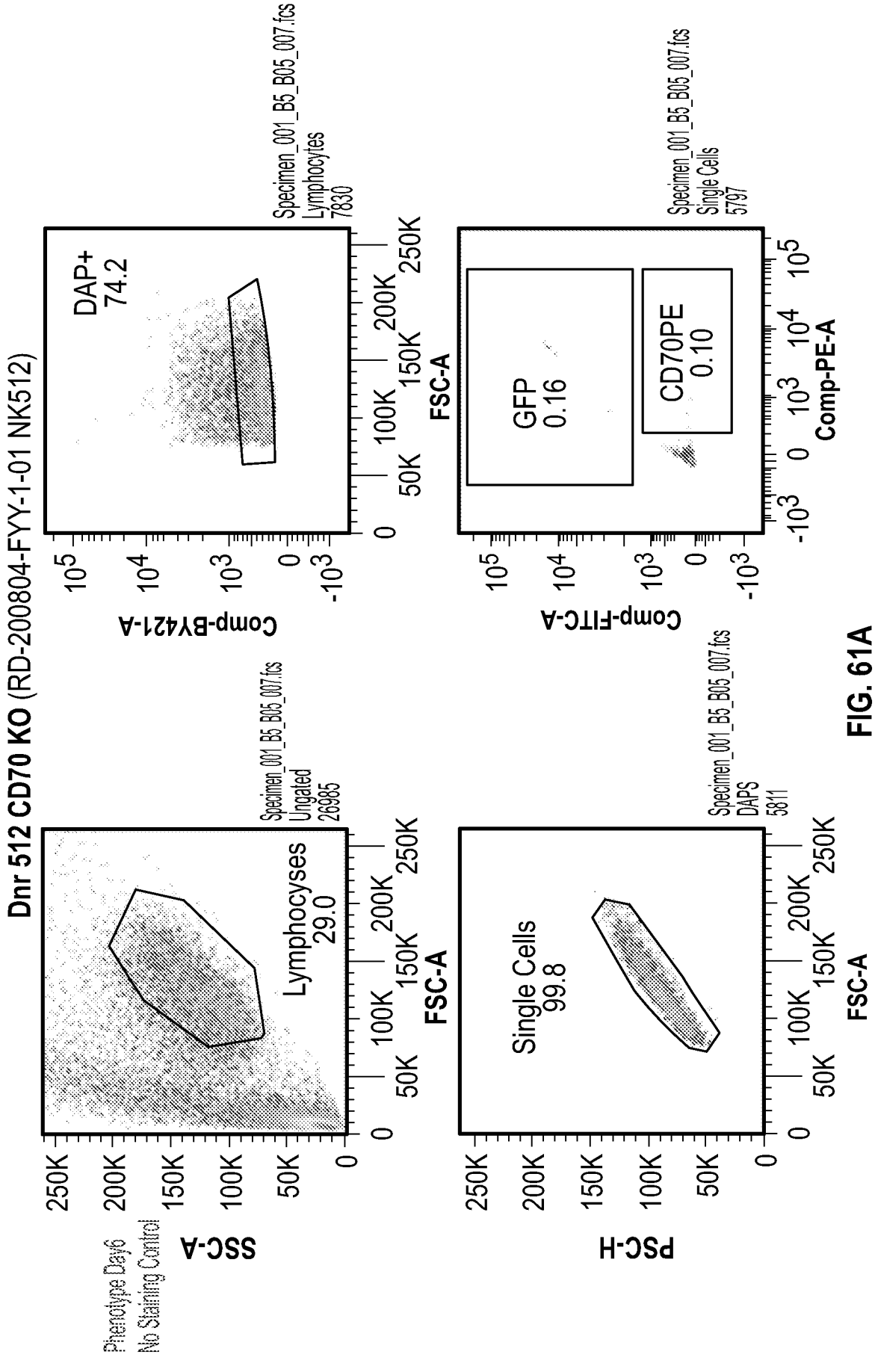

Dnr 512 CD70 KO (RD-200804-FYY-1-01 NK512)
Phenotype Day6
No Staining Control
SSC-A
FSC-A
Specimen_001_B5_B05_007.fcs
Ungated
26985
Lymphocyses
29.0
Comp-BY421-A
Specimen_001_B5_B05_007.fcs
Lymphocytes
7830
DAP+
74.2
PSC-H
Specimen_001_B5_B05_007.fcs
DAPS
5811
Single Cells
99.8
Comp-FITC-A
Specimen_001_B5_B05_007.fcs
Single Cells
5797
GFP
0.16
CD70PE
0.10
Comp-PE-A

FIG. 61A

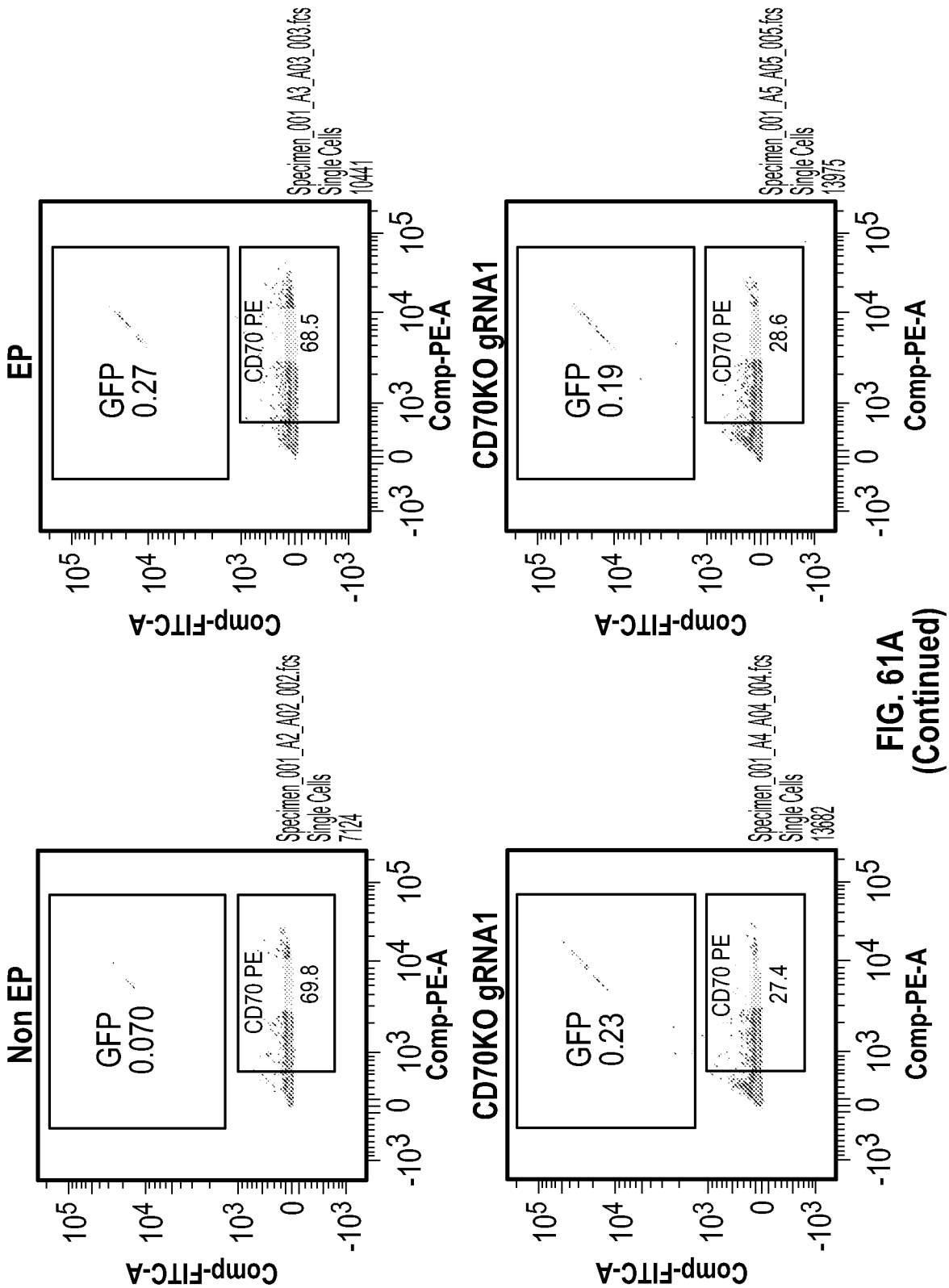


FIG. 61A
(Continued)

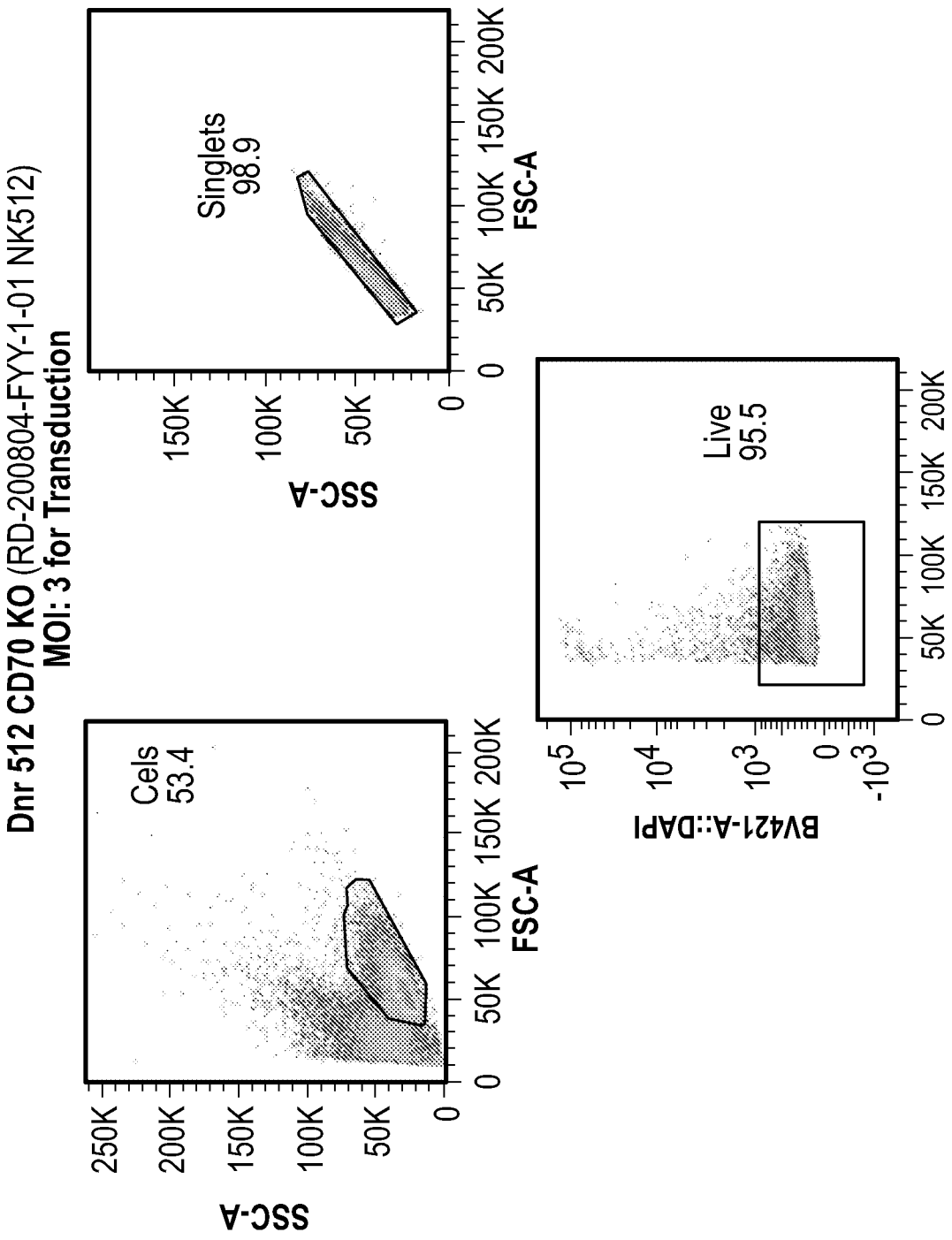

Dnr 512 CD70 KO (RD-200804-FYY-1-01 NK512)
MOI: 3 for Transduction
Cels
53.4
SSC-A
FSC-A
Singlets
98.9
SSC-A
FSC-A
Live
95.5
BV421-A::DAPI
FSC-A

FIG. 61B

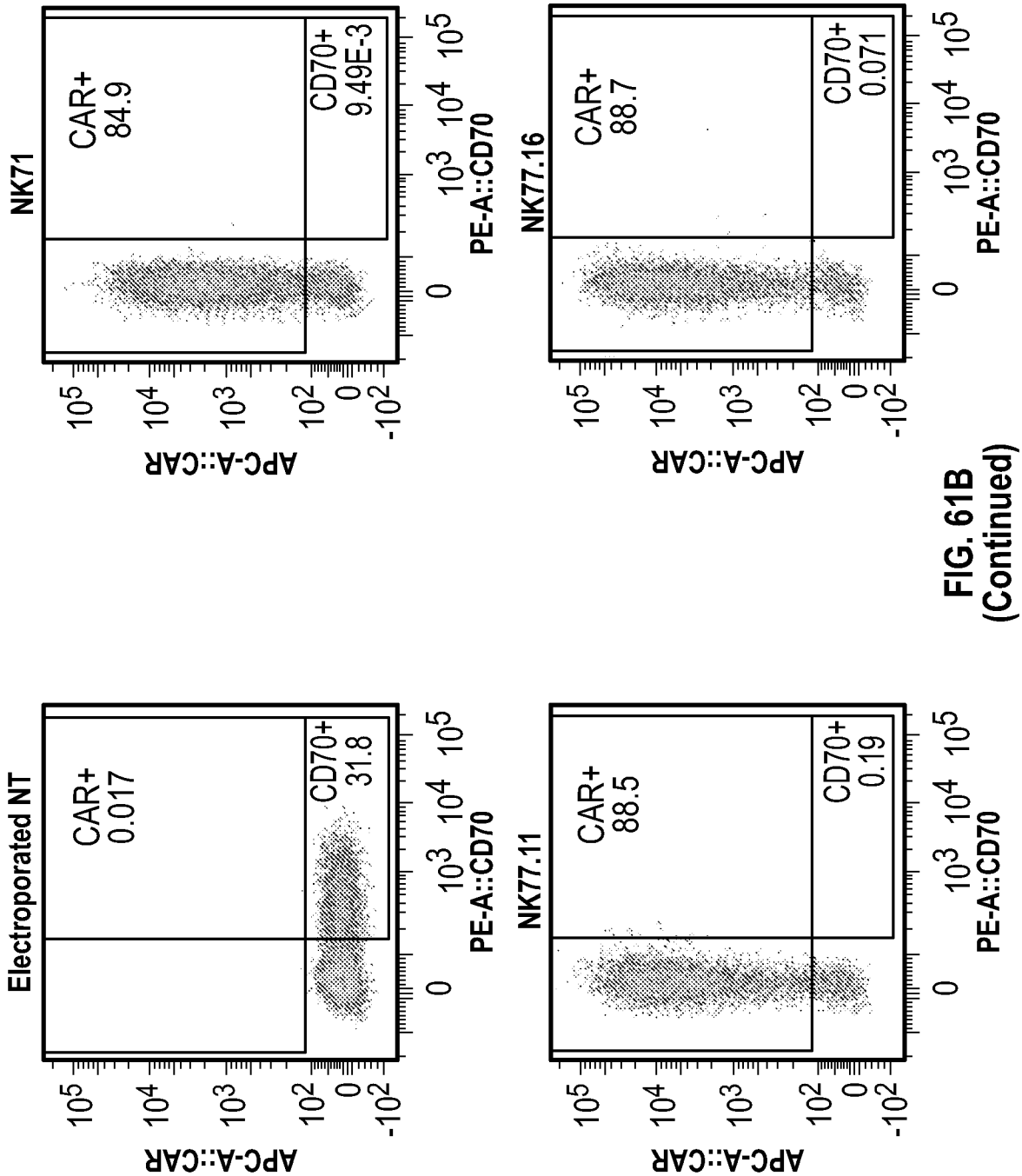


FIG. 61B
(Continued)

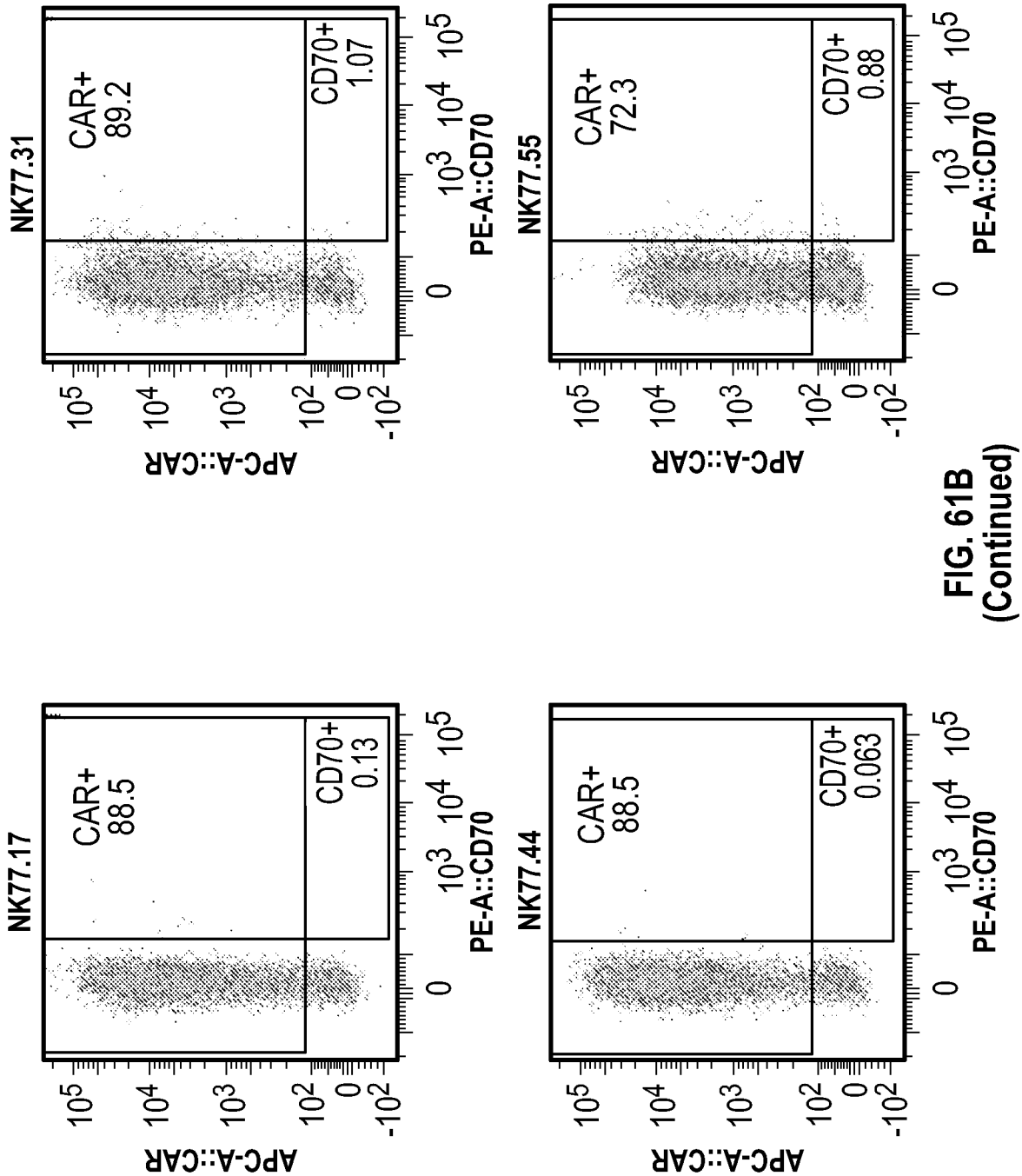


FIG. 61B
(Continued)

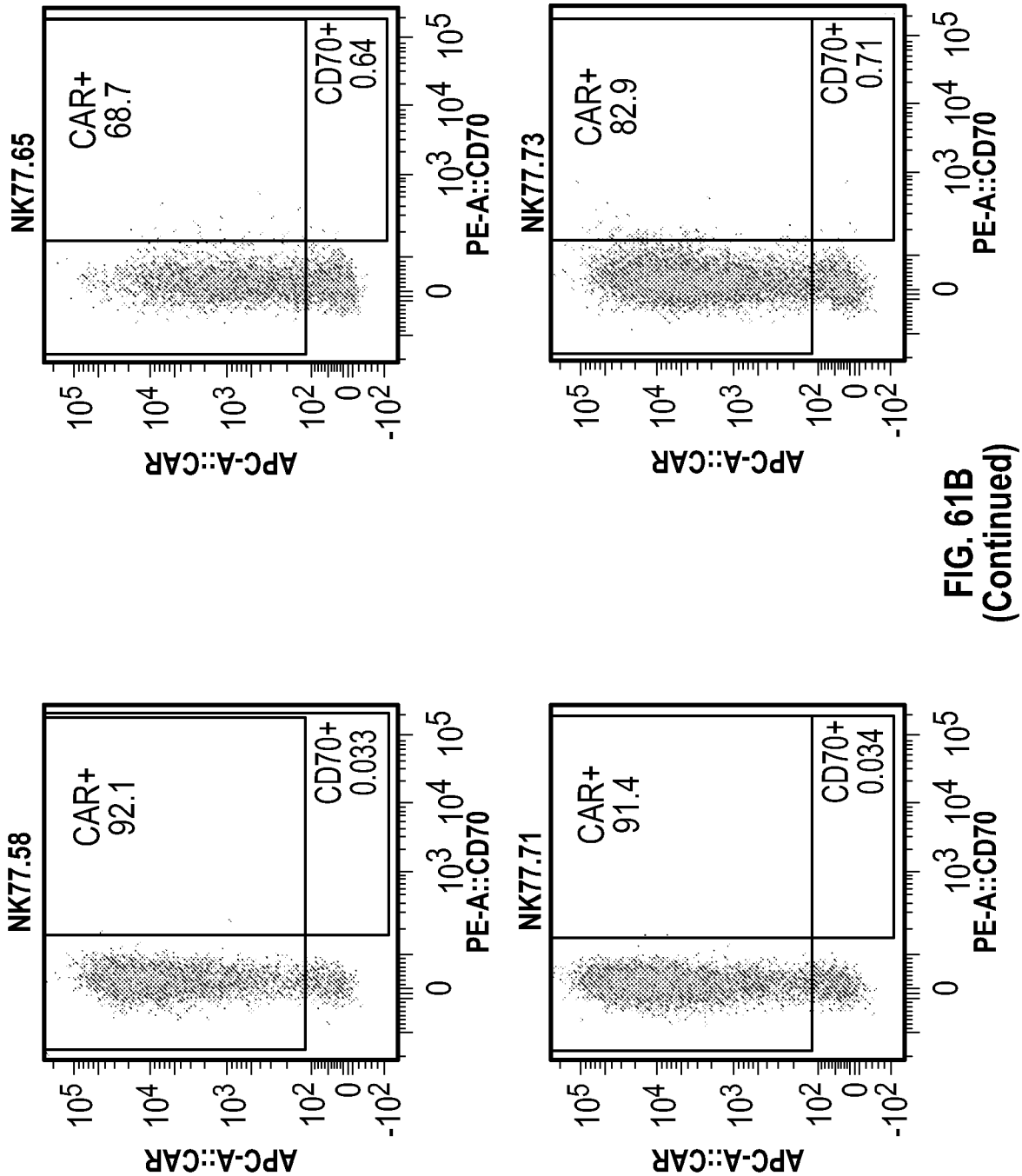


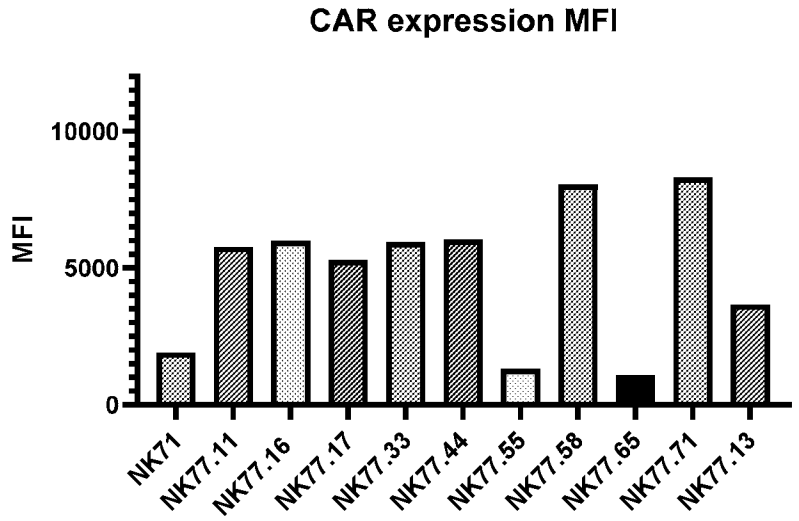
FIG. 61B
(Continued)

Figure 61C-61D

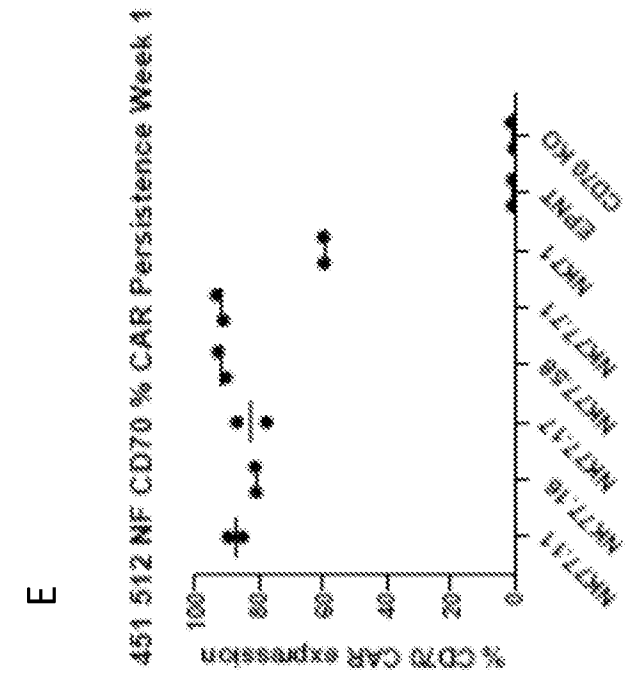
C

Construct	Titer	CD70 expression (Day 10)	CAR Expression (Day 10)
EPNT	-	31.8%	-
NK71	1.20E+06	0.009%	84.9%
NK77.11	2.85E+06	0.19%	88.5%
NK77.16	3.15E+06	0.07%	88.7%
NK77.17	2.88E+06	0.13%	88.5%
NK77.31	3.51E+06	1.07%	89.2%
NK77.44	3.57E+06	0.06%	88.5%
NK77.55	1.03E+06	0.86%	72.3%
NK77.58	1.40E+06	0.03%	92.1%
NK77.65	5.95E+05	0.64%	68.7%
NK77.71	1.50E+06	0.03%	91.4%
NK77.73	9.17E+05	0.71%	82.9%

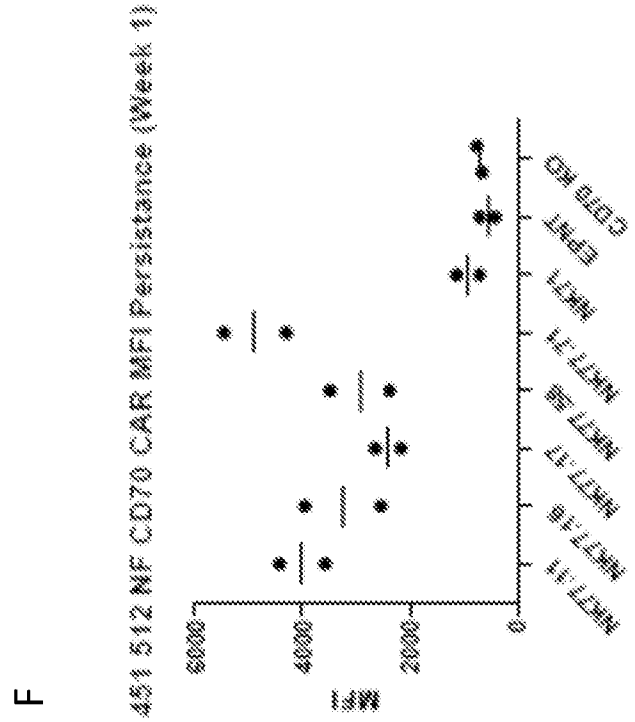
D



Figures 61E-61F

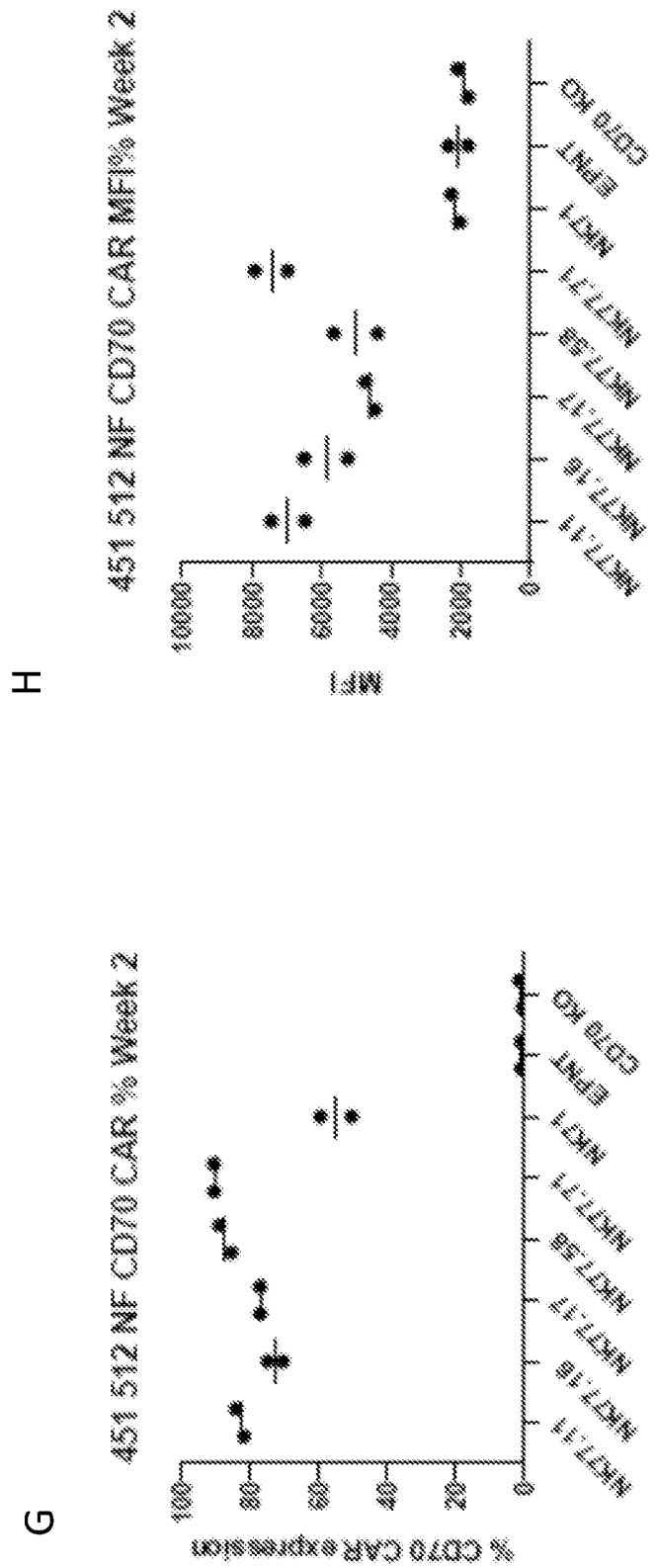


CAR% Week 1

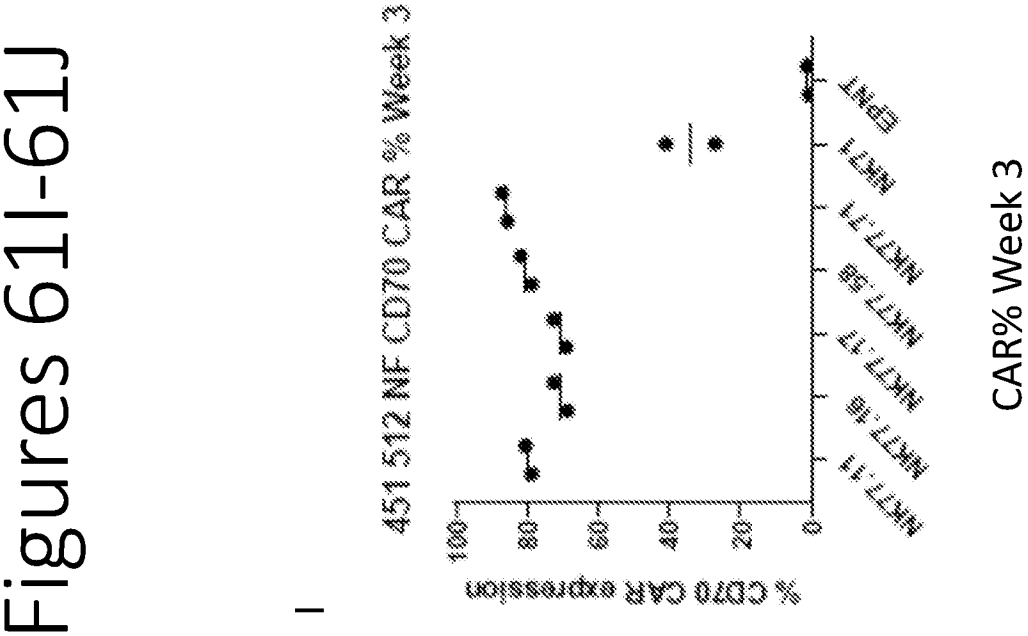


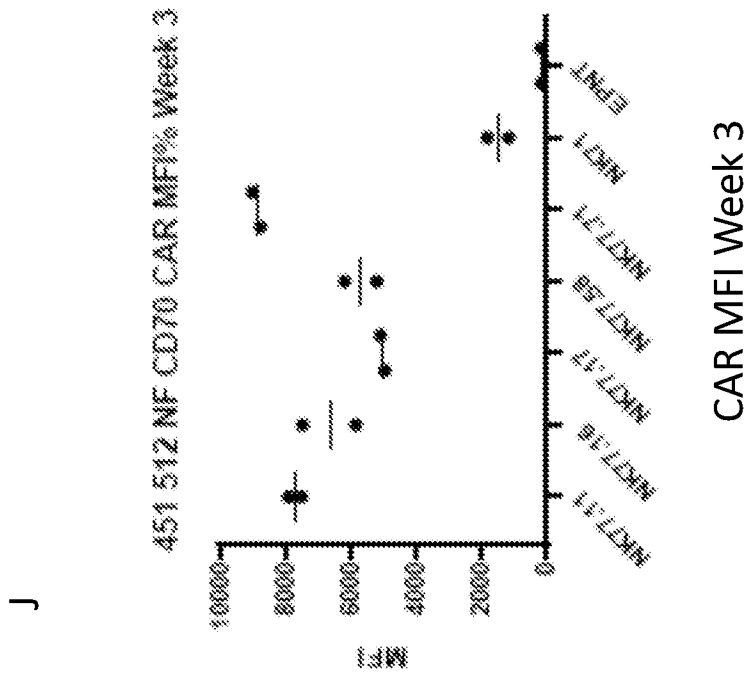
CAR MFI Week 1

Figures 61G-61H

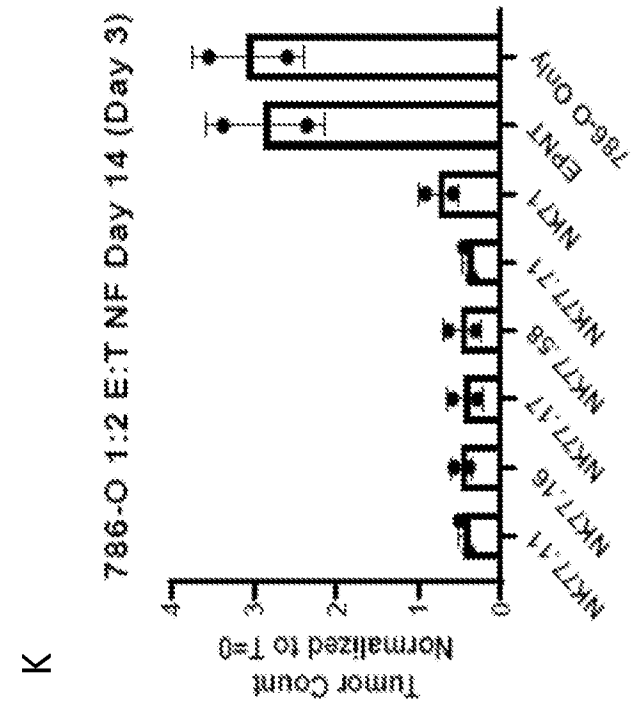


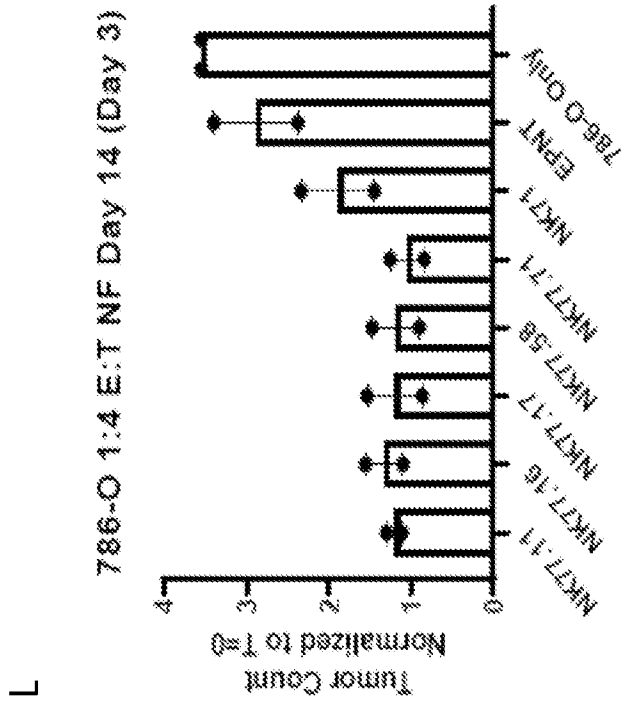
Figures 61I-61J





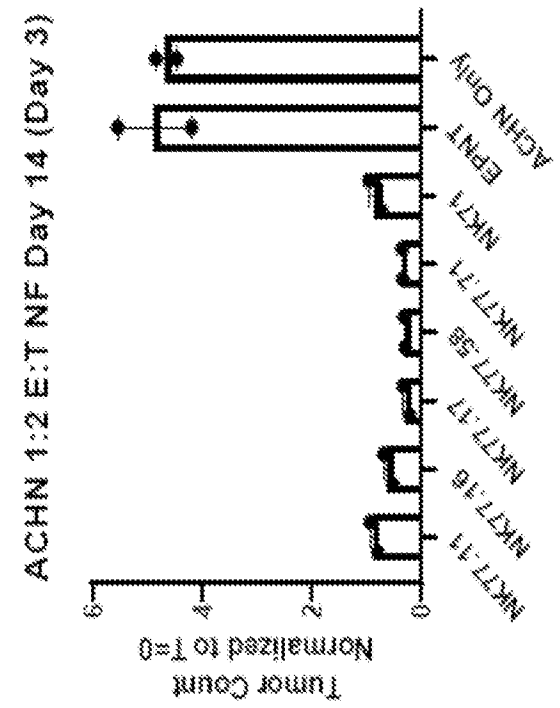
Figures 61K-61L





Figures 61M-61N

M



N

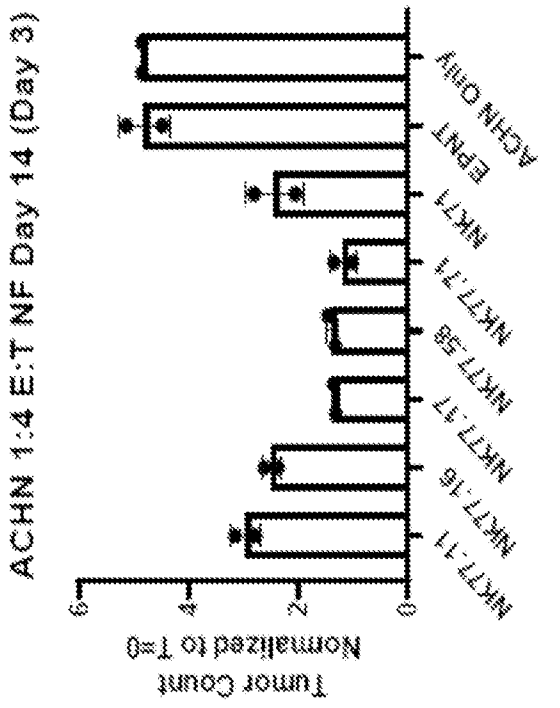


Figure 62A

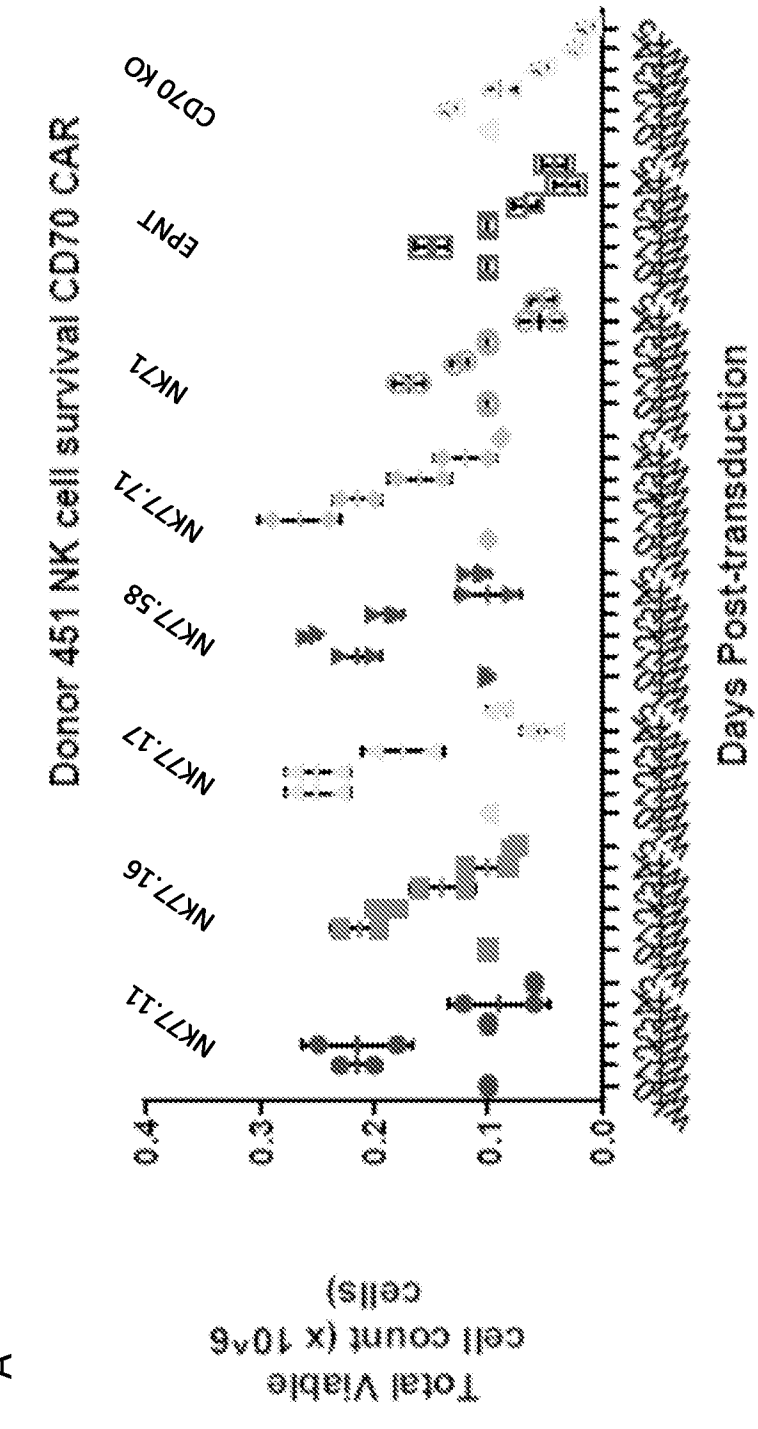

A
Donor 451 NK cell survival CD70 CAR
Total Viable cell count (x 10^6 cells)
Days Post-transduction
NK77.11
NK77.16
NK77.17
NK77.58
NK77.71
NK71
EPNT
CD70 KO

Figure 62B

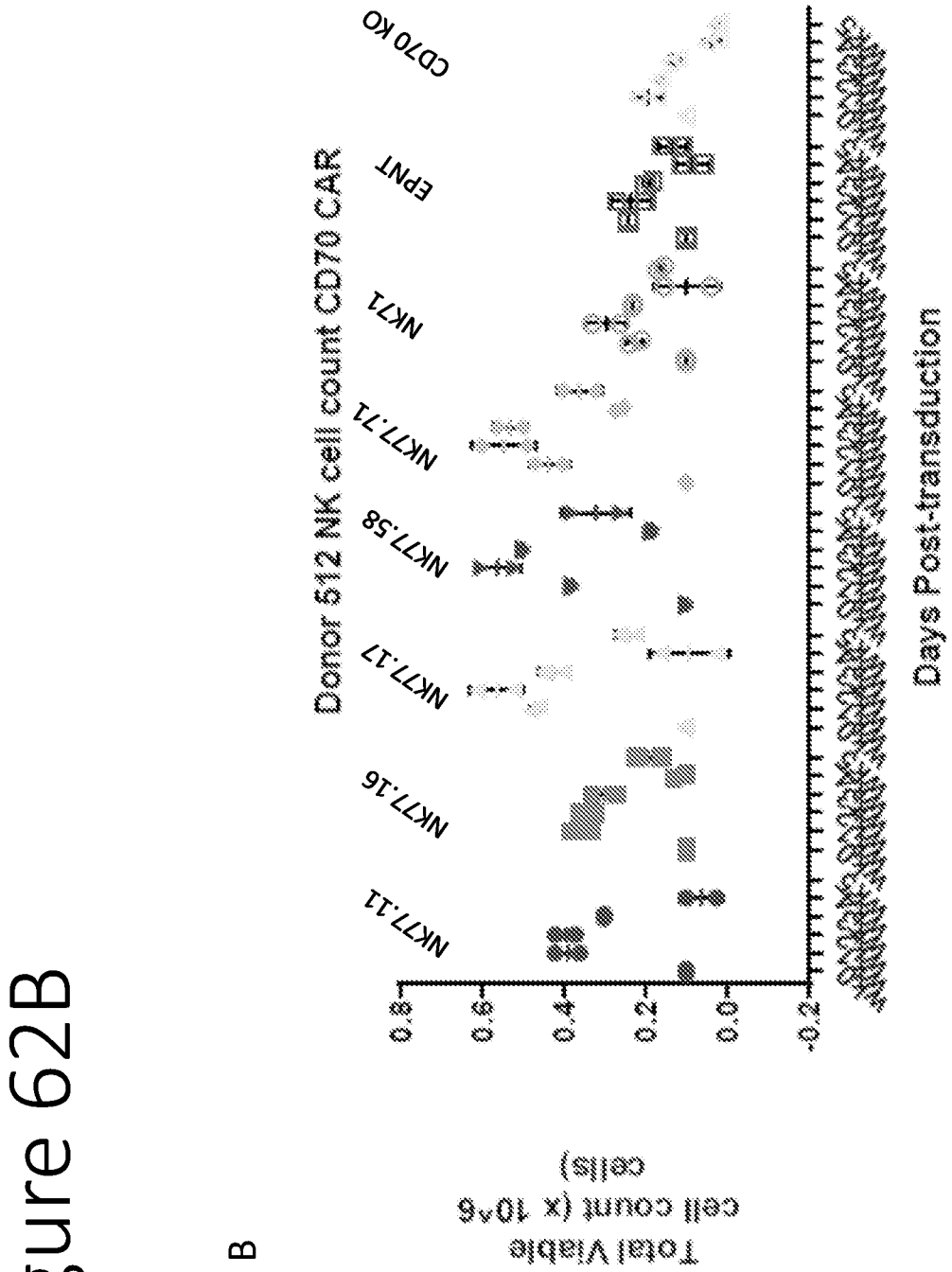
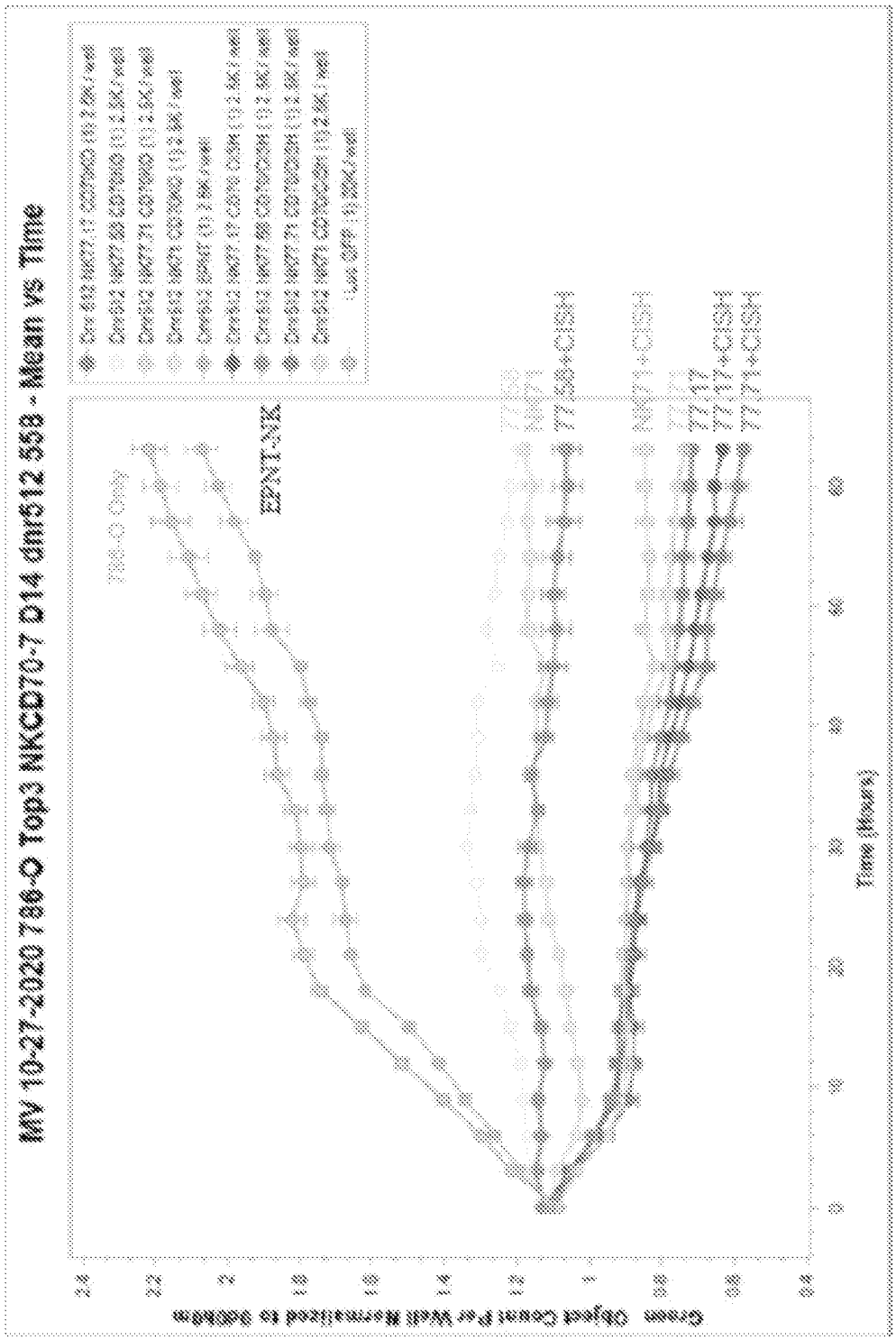

B
Total Viable cell count (x 10^6 cells)
Donor 612 NK cell count CD70 CAR
NK77.11
NK77.16
NK77.17
NK77.58
NK77.71
NK71
EPNT
CD70 KO
0.8
0.6
0.4
0.2
0.0
-0.2
Days Post-transduction

Figure 63A

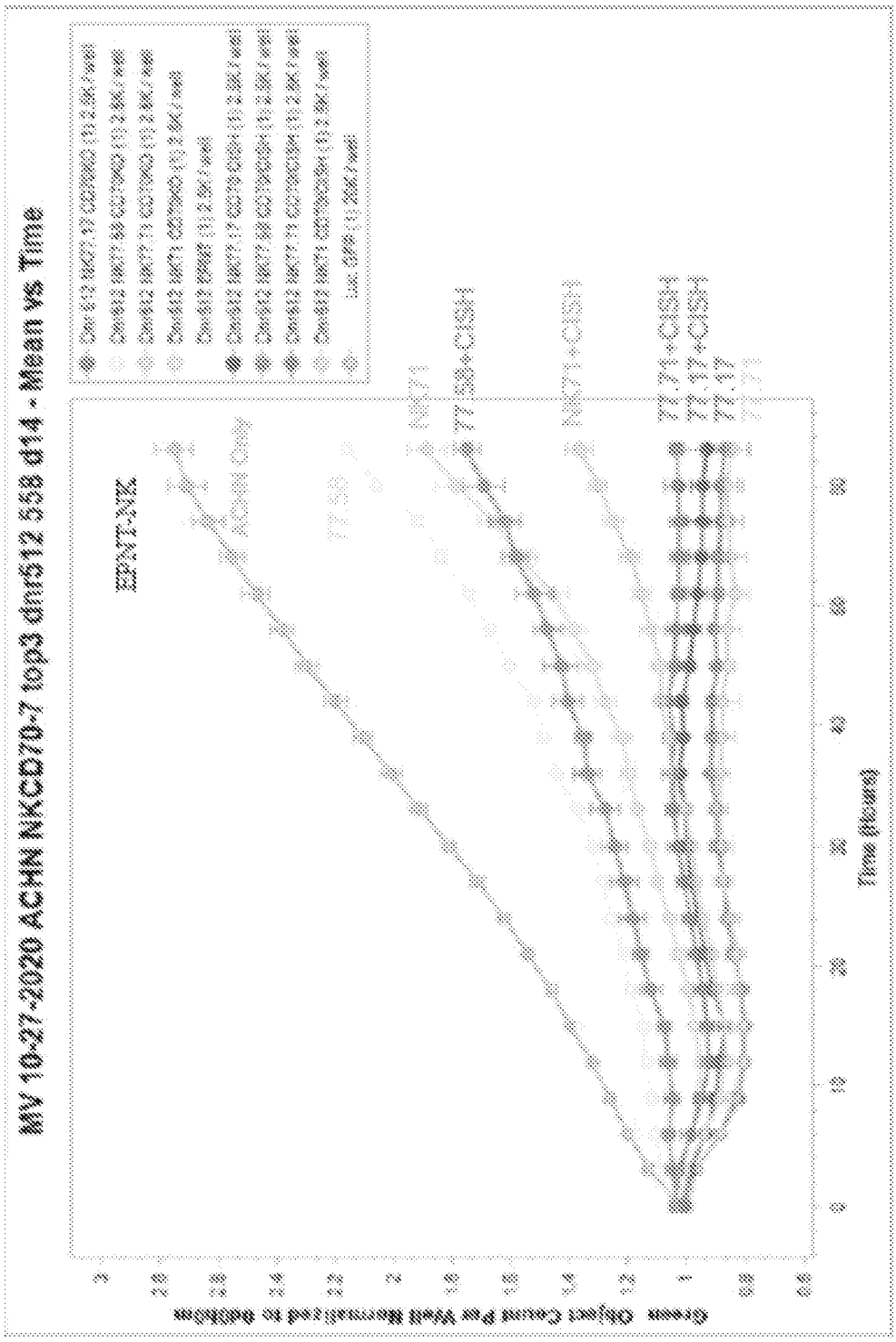
A



786-O 1:8 E:T

Figure 63B

B



ACHN 1:8 E:T

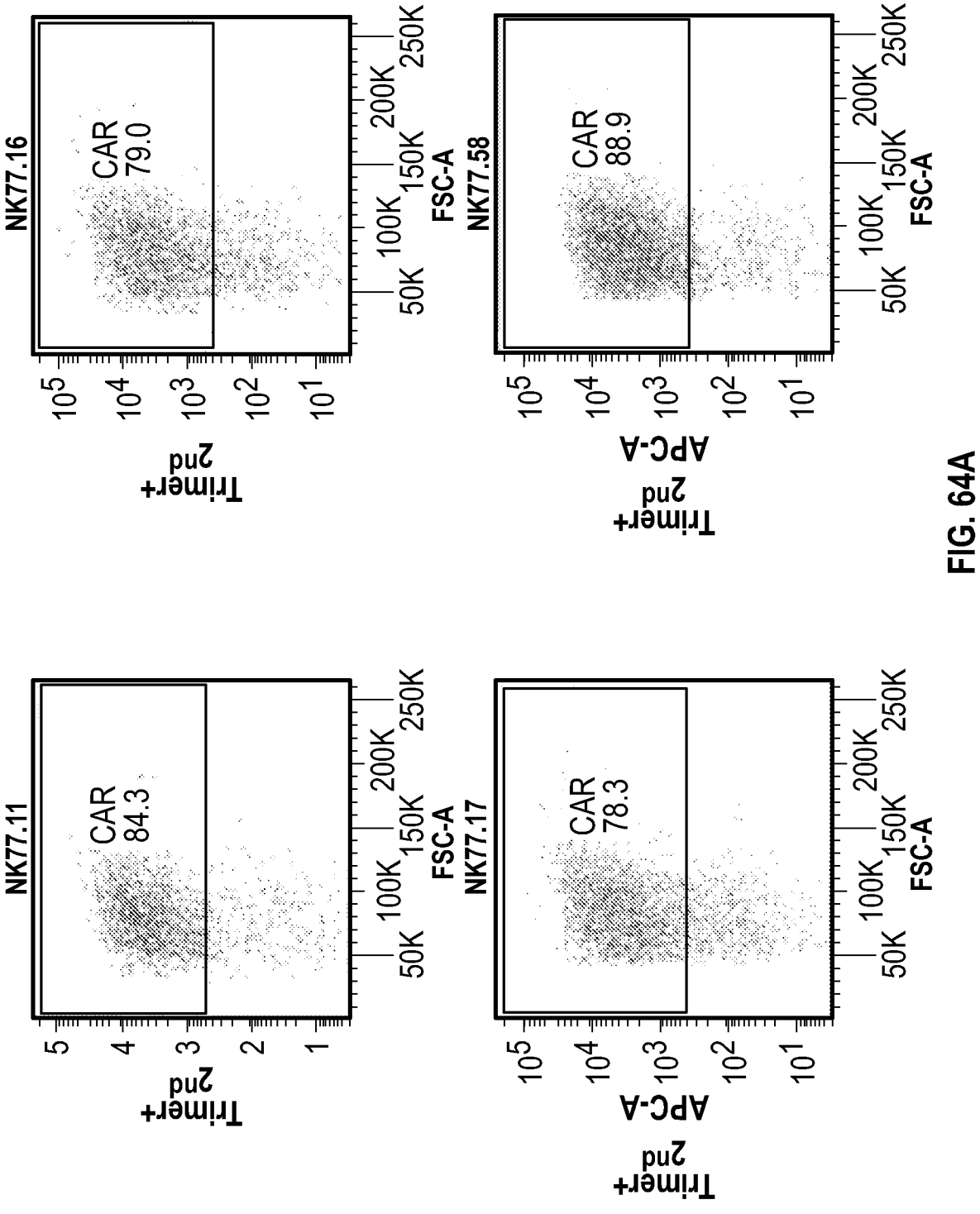

NK77.16
CAR
79.0
Trimer+
2nd
FSC-A
NK77.58
CAR
88.9
APC-A
NK77.11
CAR
84.3
NK77.17
CAR
78.3
50K
100K
150K
200K
250K

FIG. 64A

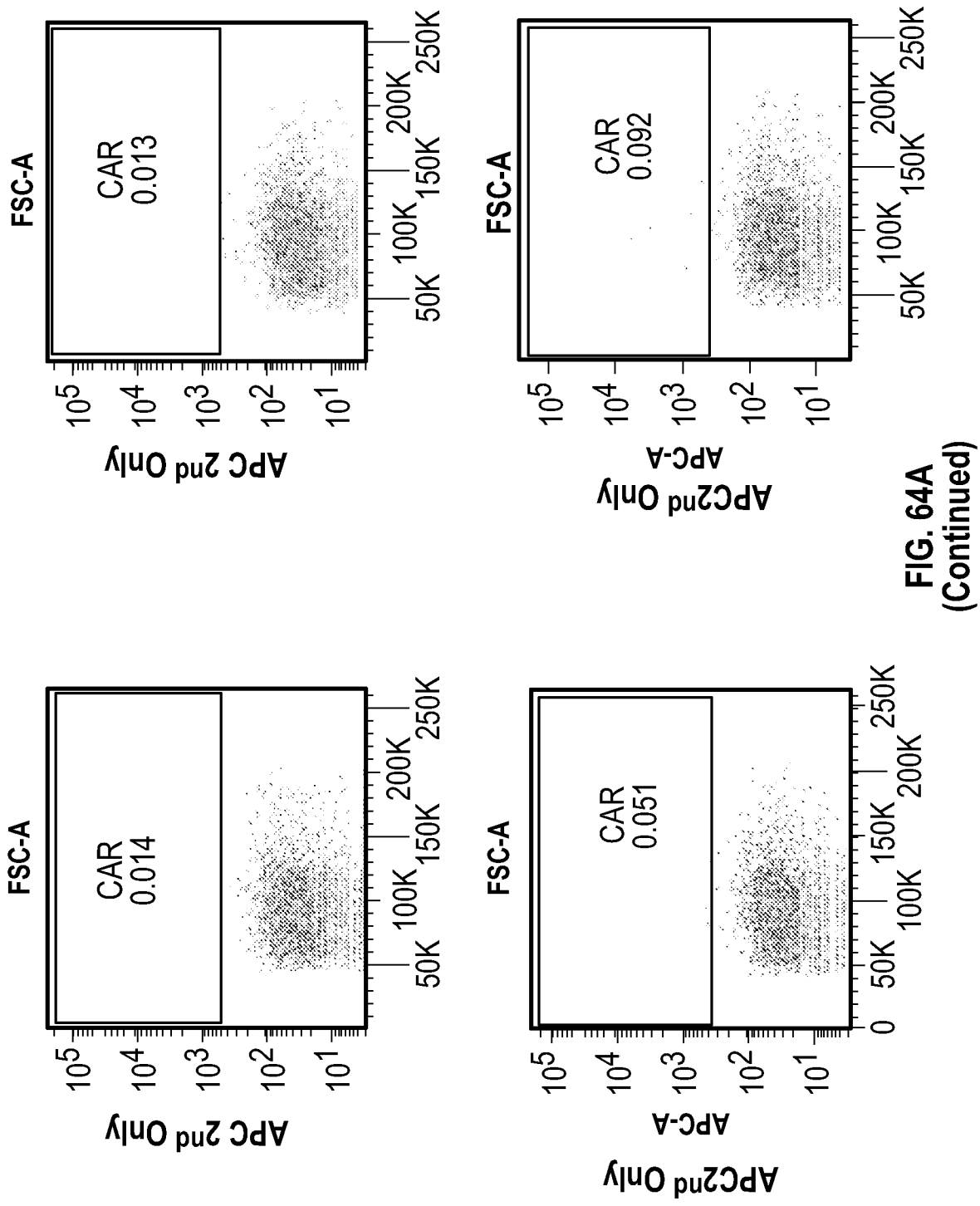


FIG. 64A
(Continued)

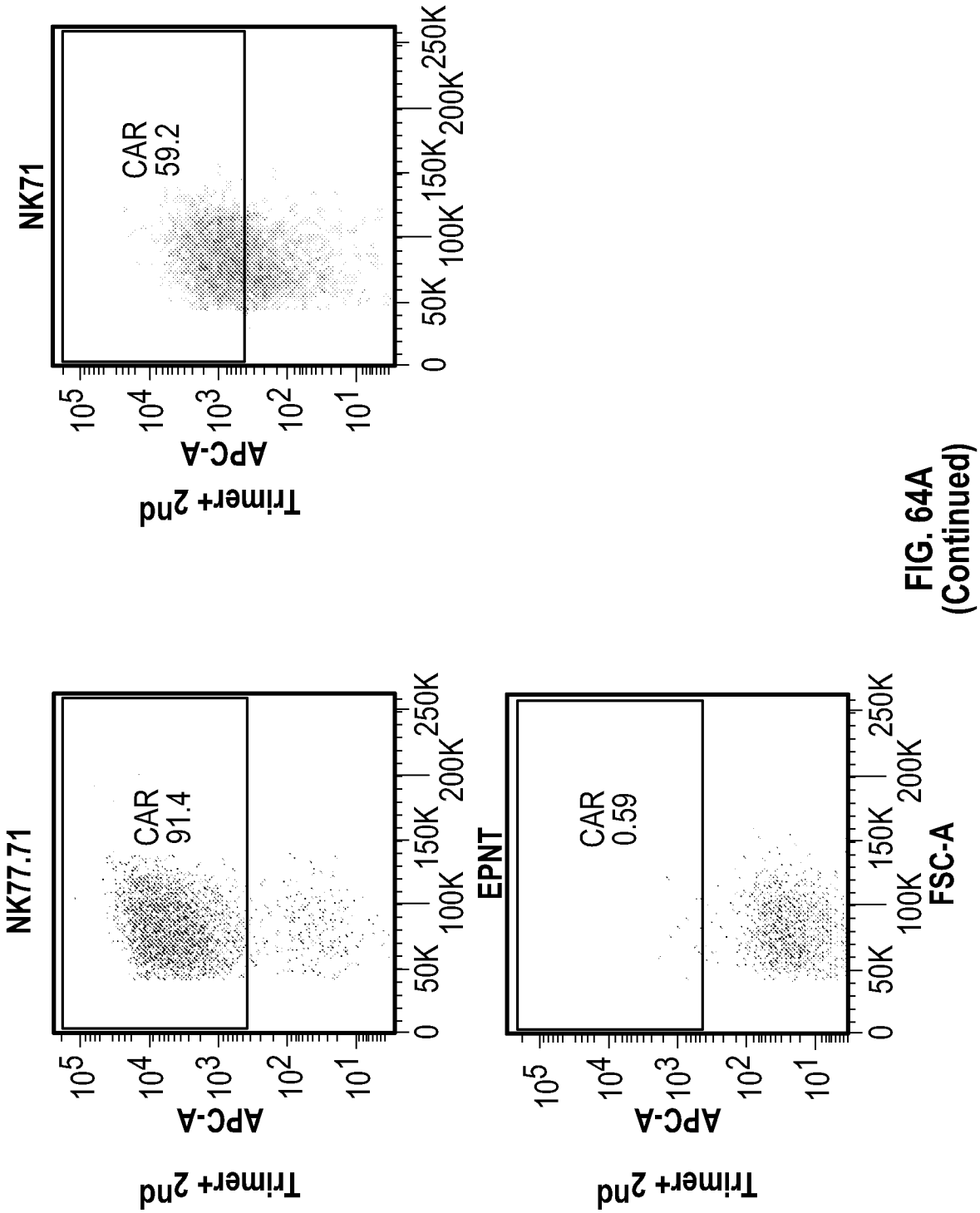
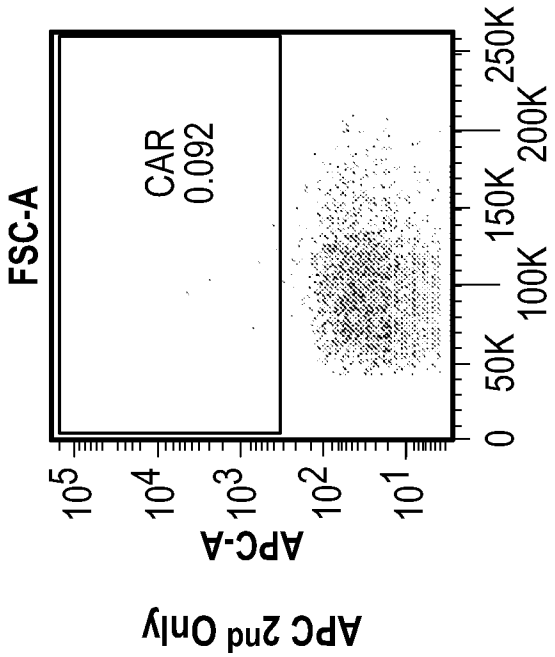
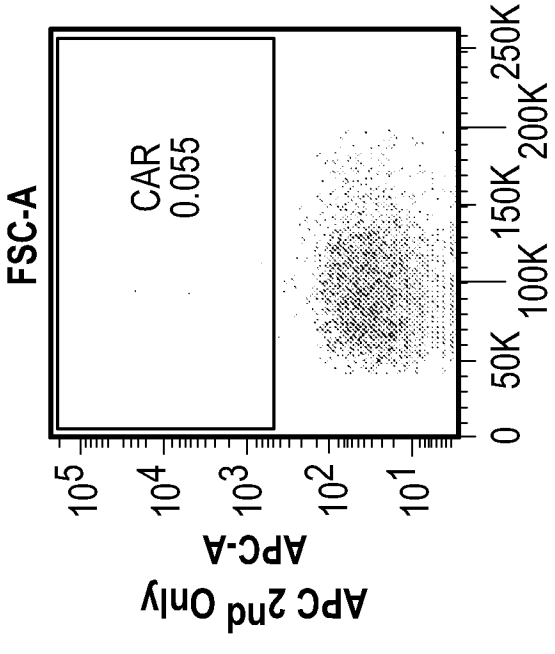
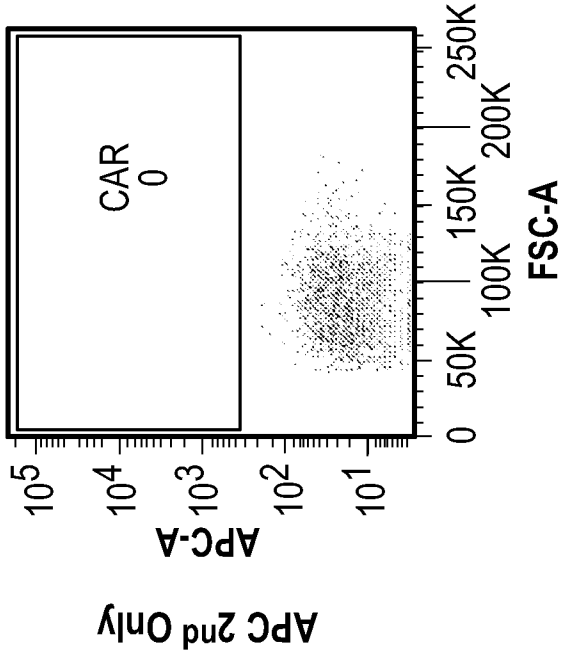


FIG. 64A
(Continued)







Donor 451 Week 1 Post Transduction

FIG. 64A (Continued)

Figure 64B

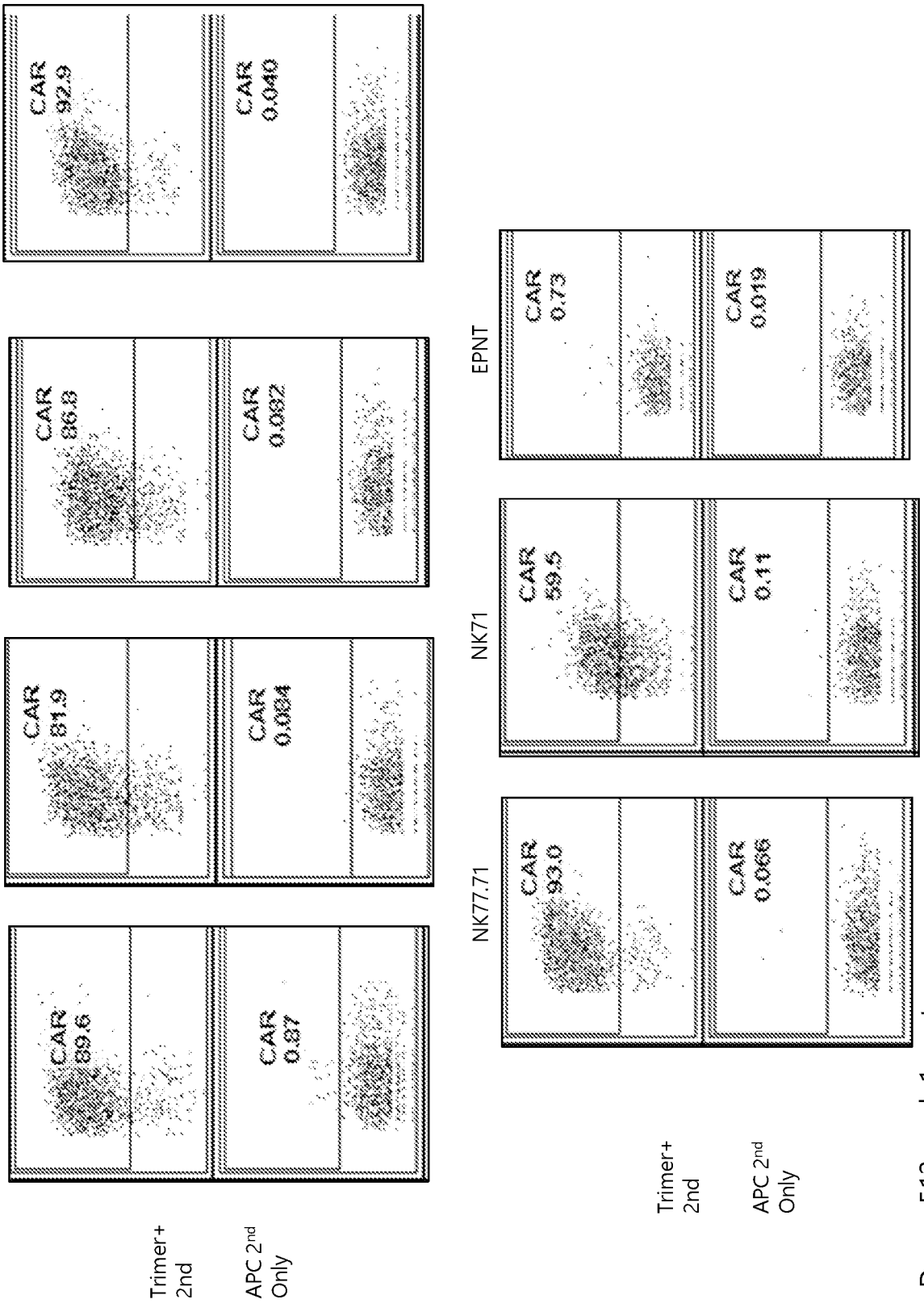

NK77.11
NK77.16
NK77.17
NK77.58
EPNT
NK71
NK77.71
CAR 89.6
CAR 0.87
CAR 81.9
CAR 0.084
CAR 86.8
CAR 0.092
CAR 92.9
CAR 0.040
CAR 0.73
CAR 0.019
CAR 59.5
CAR 0.11
CAR 93.0
CAR 0.066
Trimer+ 2nd
APC 2nd Only
Donor 512 week 1 post transduction

FIG. 64C

Dnr 451

	CAR%	MFI
NK77.11 trimer	84.3	4303
NK77.11 trimer-1	86.8	4644
NK7.16 trimer-1	79	3832
NK77.16 trimer	79.6	3865
NK77.17 trimer	76.7	2608
NK77.17 trimer-1	79.3	2715
NK77.58 trimer	87.7	3274
NK77.58 trimer-1	88.9	3309
NK77.71 trimer	90.9	5190
NK77.71 trimer-1	91.4	5039
NK71 trimer	59.2	1220
NK71 trimer-1	56.5	1225
EPNT	0.39	832
	0.58	960

FIG. 64D

Dnr 512

	CAR%	MFI
NK77.11 trimer	89.4 %	3415
NK77.11 trimer-1	89.6 %	3763
NK7.16 trimer-1	81.9 %	2620
NK77.16 trimer	80.5 %	2473
NK77.17 trimer	86.9 %	2040
NK77.17 trimer-1	86.8 %	2305
NK77.58 trimer	92.9 %	2205
NK77.58 trimer-1	92.6 %	2557
NK77.71 trimer	93.0 %	4187
NK77.71 trimer-1	93.5 %	4441
NK71 trimer	59.5 %	700
NK71 trimer-1	59.7 %	713
EPNT	0.73 %	669
CD70KO	0.31 %	684
EPNT-1	0.71 %	746
CD70KO-1	0.25 %	833

Week1 post transduction

FIG. 64F

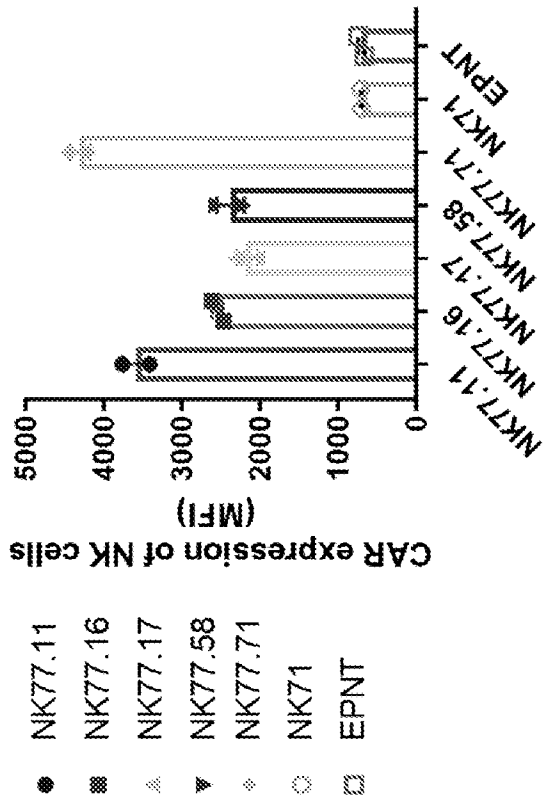
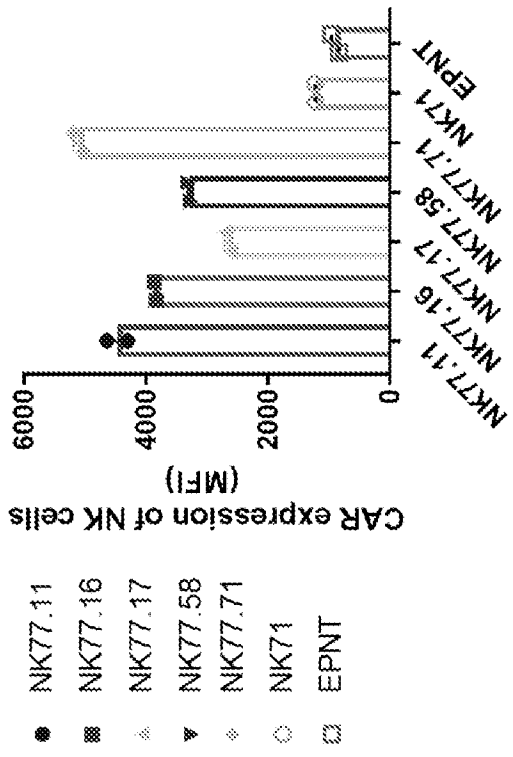


FIG. 64E



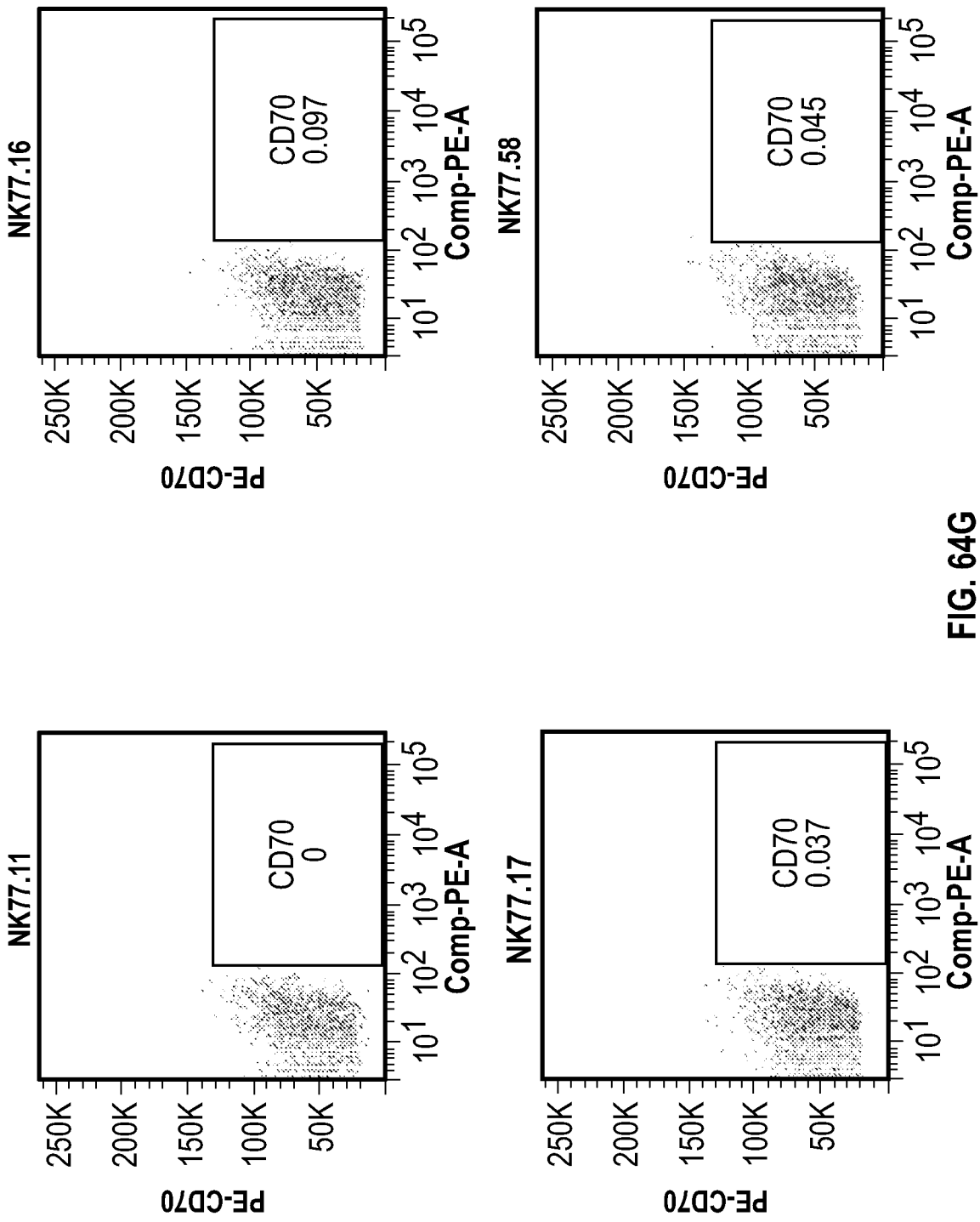
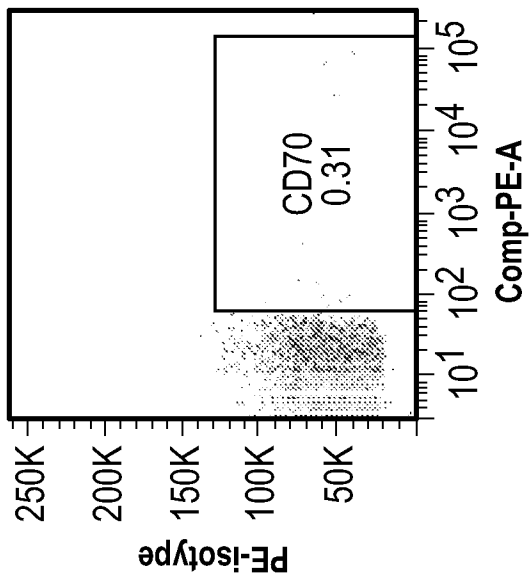
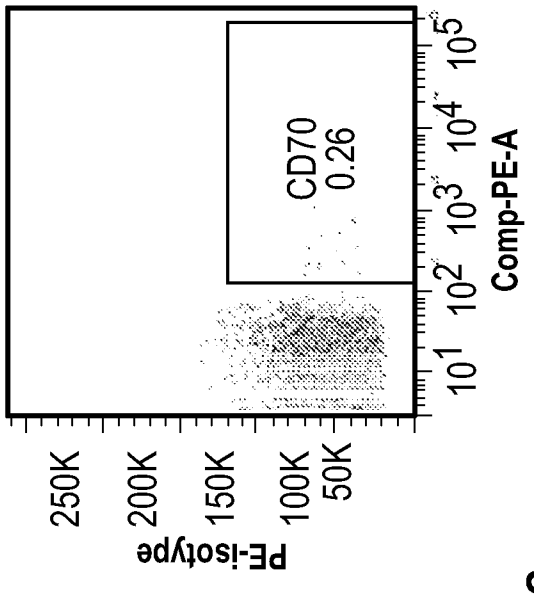
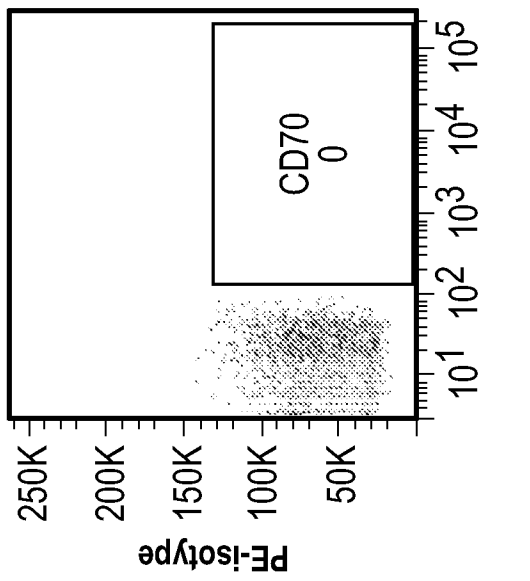

NK77.16
CD70
0.097
NK77.58
CD70
0.045
NK77.11
CD70
0
NK77.17
CD70
0.037
PE-CD70
Comp-PE-A
250K
200K
150K
100K
50K
10^1
10^2
10^3
10^4
10^5

FIG. 64G







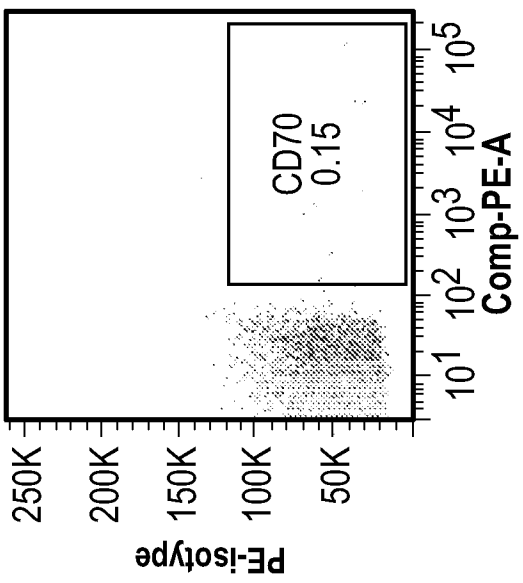


FIG. 64G
(Continued)

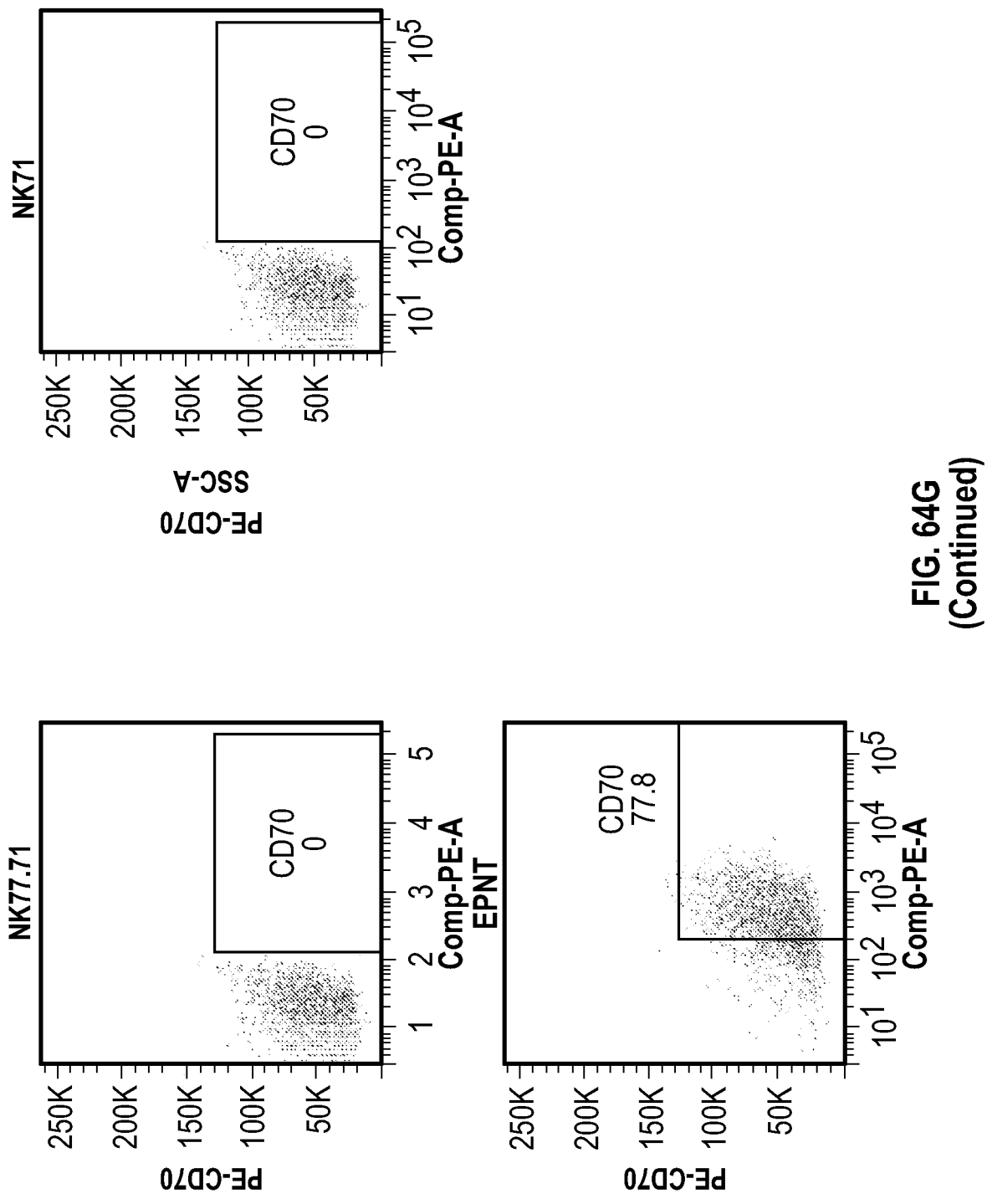
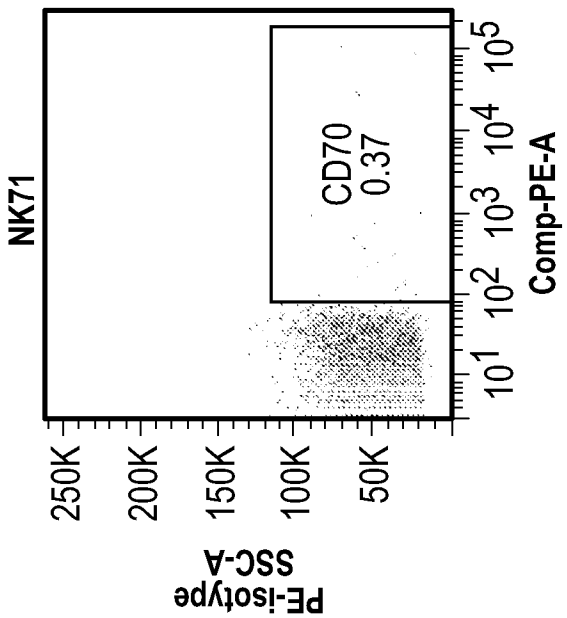
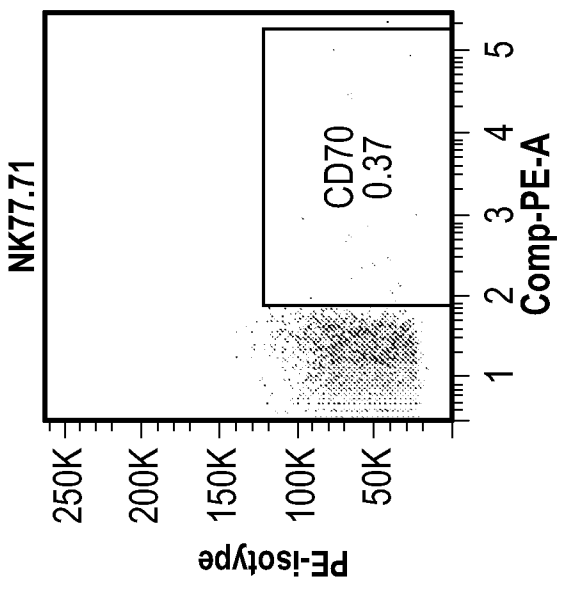


FIG. 64G
(Continued)



Donor 451 Week 1 Post Transduction



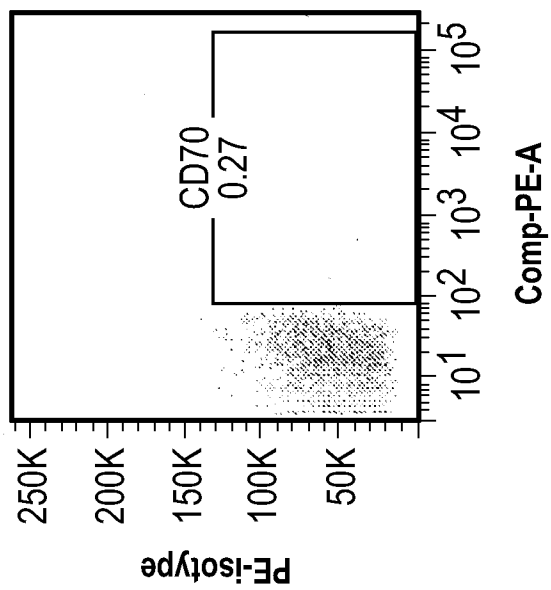
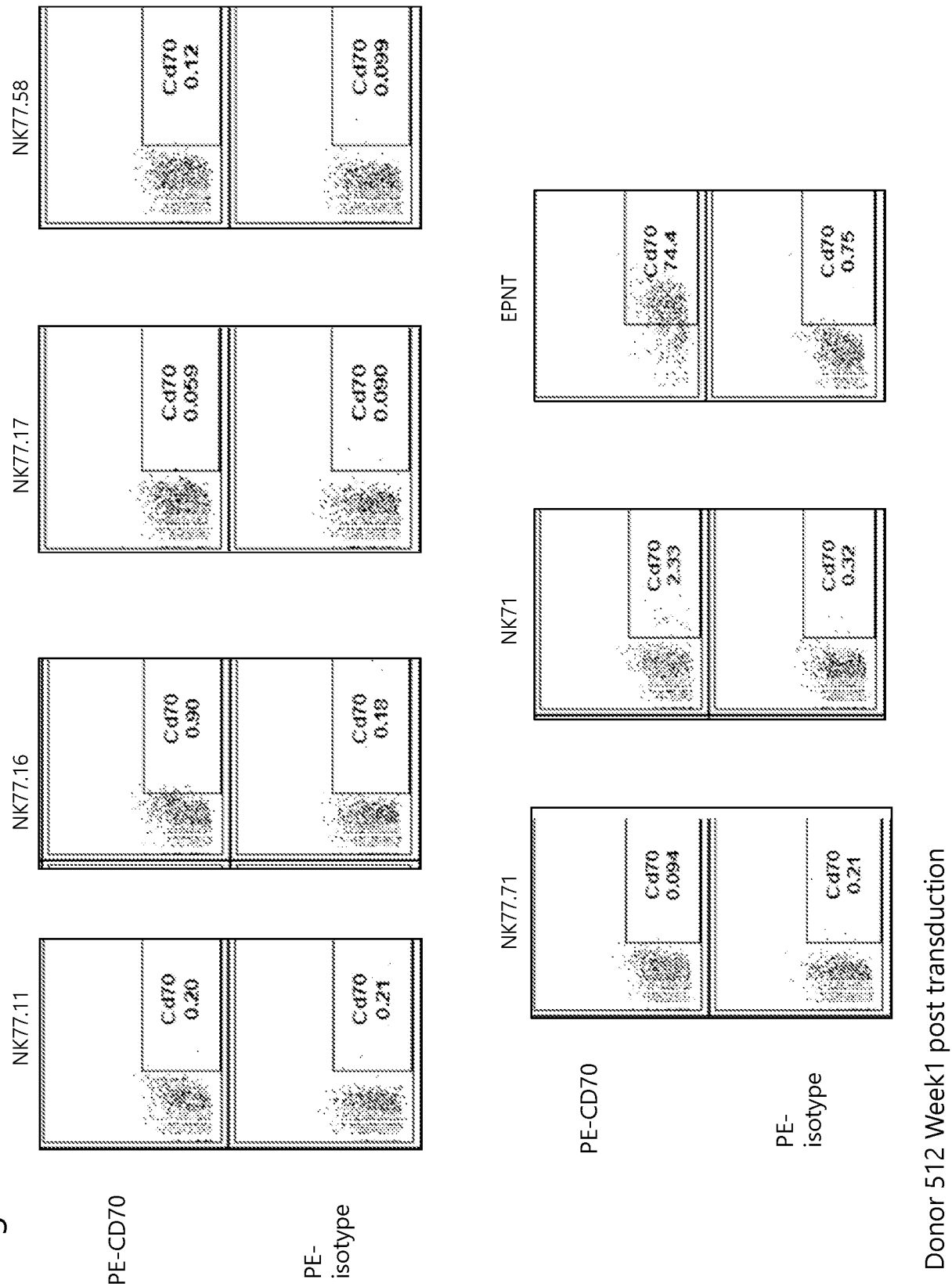


FIG. 64G (Continued)

Figure 64H



Donor 512 Week1 post transduction

FIG. 64I

Dnr 451

	CD70%	MFI
Nk77.11 CD70	0	0
NK77.11 CD70-1	0.052	669
NK77.16 CD70	0.097	307
NK77.16 CD70-1	0.078	137
Nk77.17 CD70	0.037	153
NK77.17 CD70-1	0.33	163
NK77.58 CD70	0.045	165
NK77.58 CD70-1	0.029	133
NK77.71 CD70	0	0
NK77.71 CD70-1	0.03	144
NK71 CD70	0	0
NK71CD70-1	0.086	171
EPNTCD70	77.8	534
EPNT Cd70-1	69.6	615

FIG. 64J

Dnr 512

	CD70%	MFI
Nk77.11 CD70	0.72 %	99.7
NK77.11 CD70-1	0.20 %	199
NK77.16 CD70	0.90 %	95.3
NK77.16 CD70-1	0.70 %	97.4
Nk77.17 CD70	0.079 %	187
NK77.17 CD70-1	0.059 %	121
NK77.58 CD70	0.12 %	129
NK77.58 CD70-1	0.12 %	125
NK77.71 CD70	0.094 %	224
NK77.71 CD70-1	0.041 %	274
NK71 CD70	2.33 %	347
NK71CD70-1	0.11 %	148
EPNTCD70	74.4 %	331
EPNT Cd70-1	82.6 %	331

Week1 post transduction

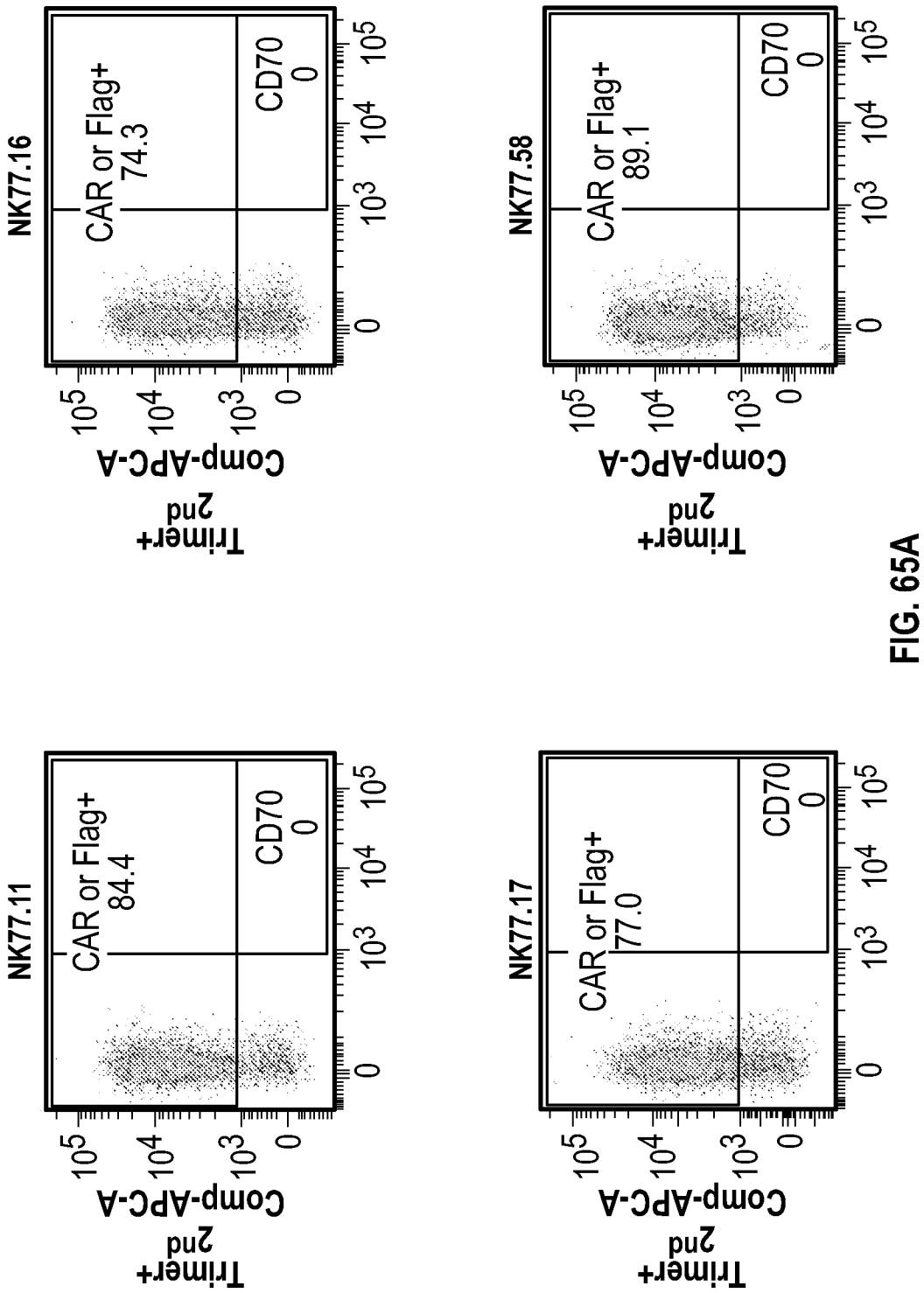

NK77.16
CAR or Flag+
74.3
CD70
0
NK77.58
CAR or Flag+
89.1
CD70
0
NK77.11
CAR or Flag+
84.4
CD70
0
NK77.17
CAR or Flag+
77.0
CD70
0
Trimer+
2nd
Comp-APC-A
0
10^3
10^4
10^5

FIG. 65A

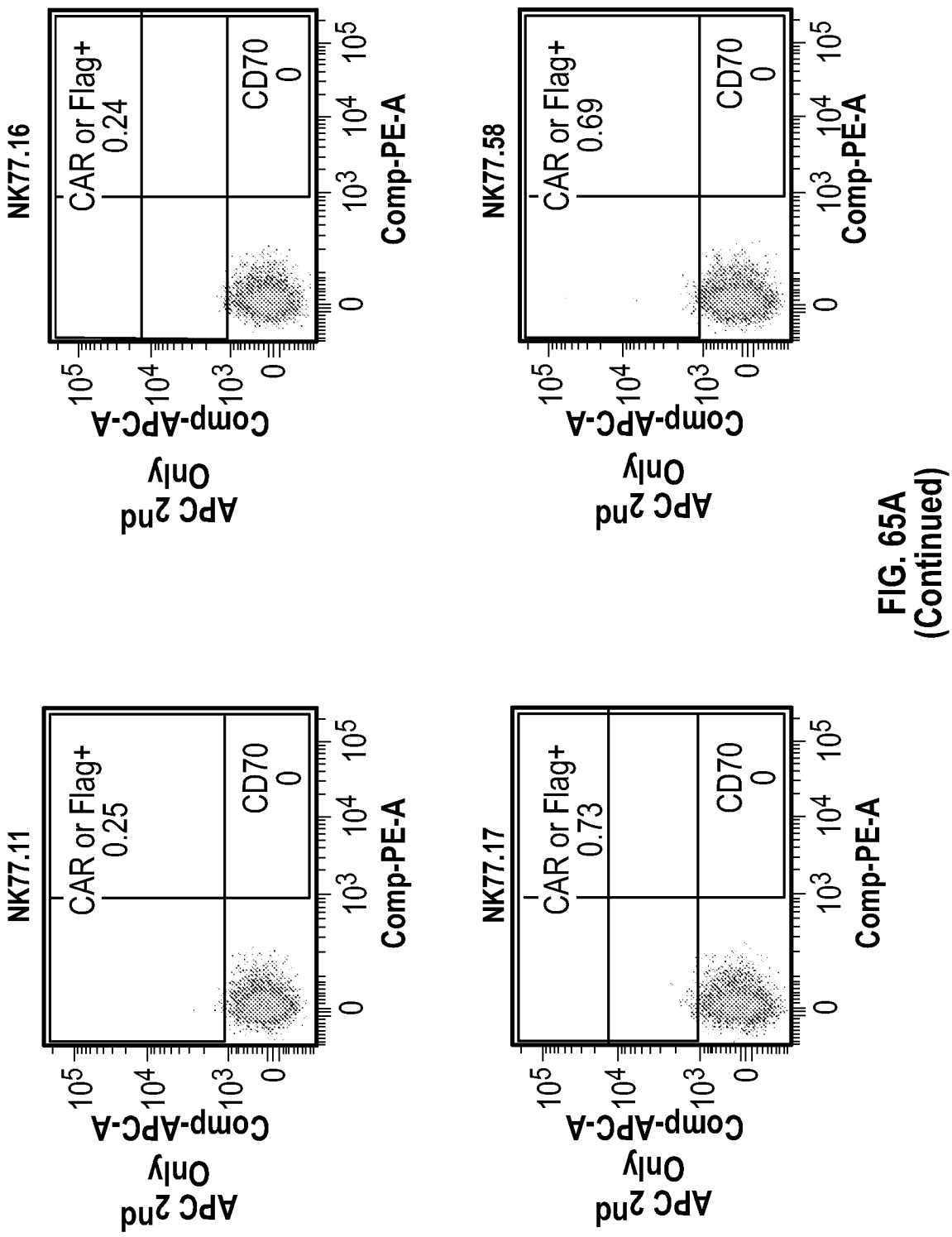
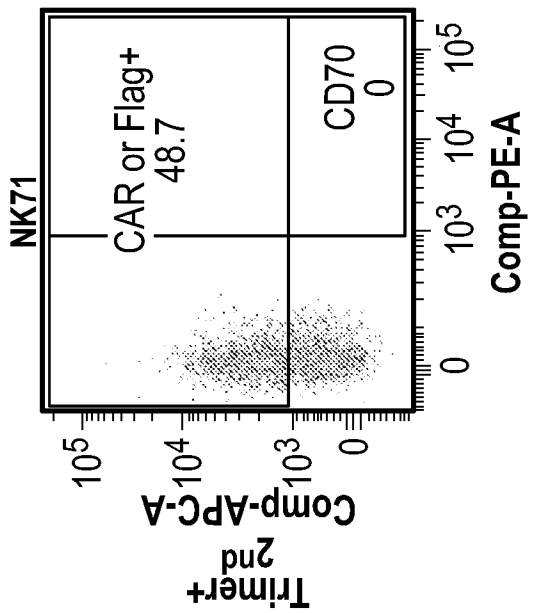
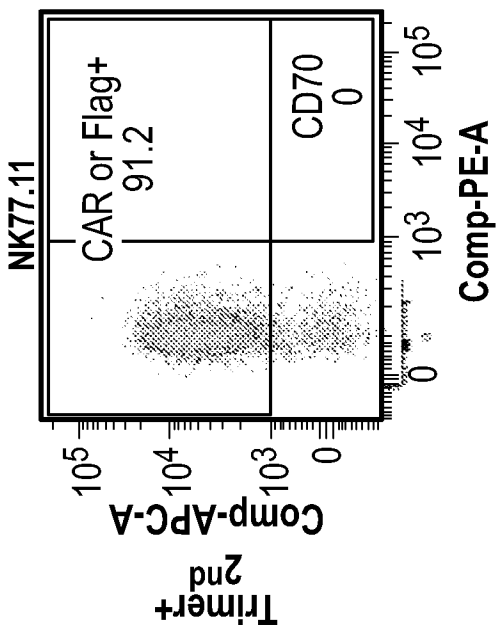


FIG. 65A
(Continued)





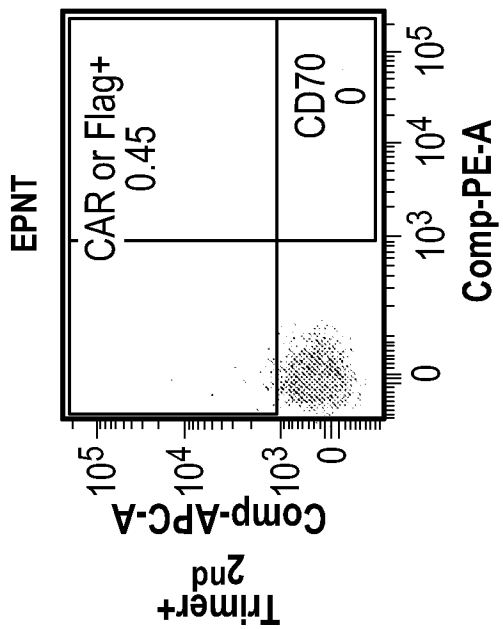
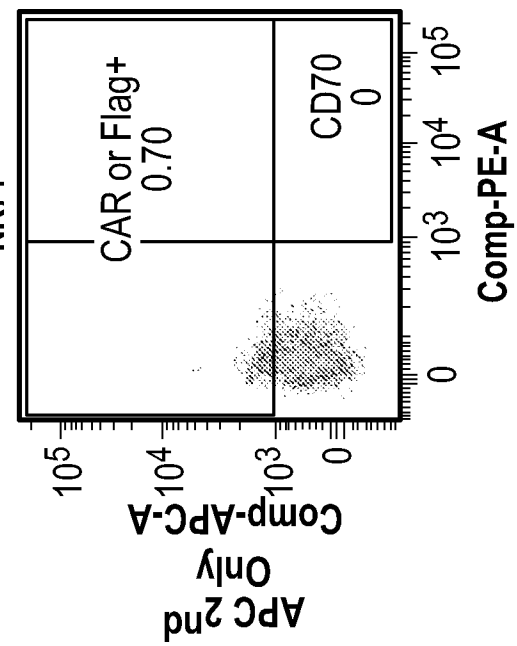
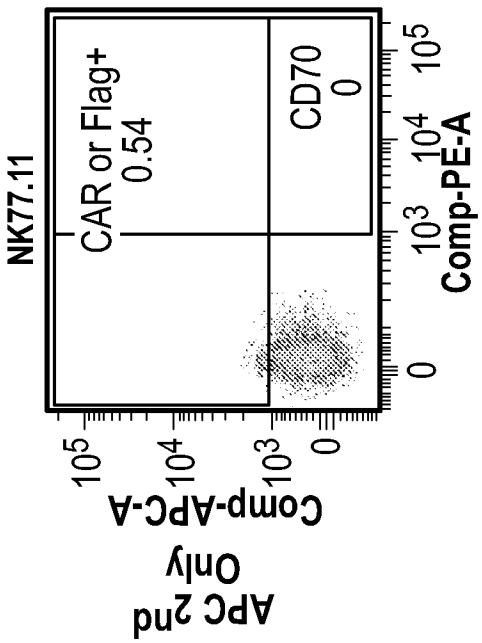


FIG. 65A
(Continued)



Donor 451 Week 2 Post Transduction



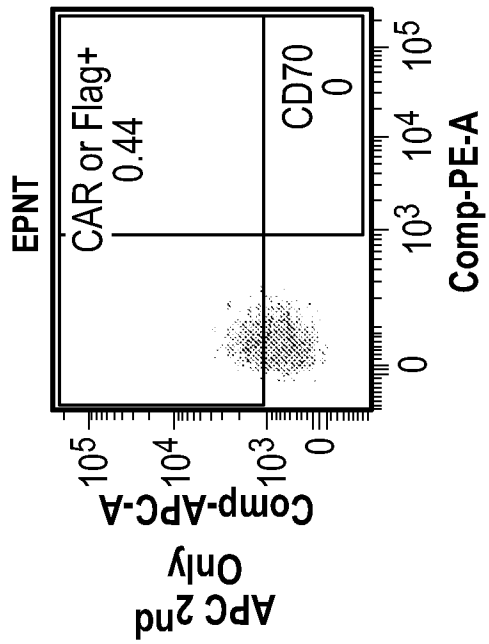


FIG. 65A (Continued)

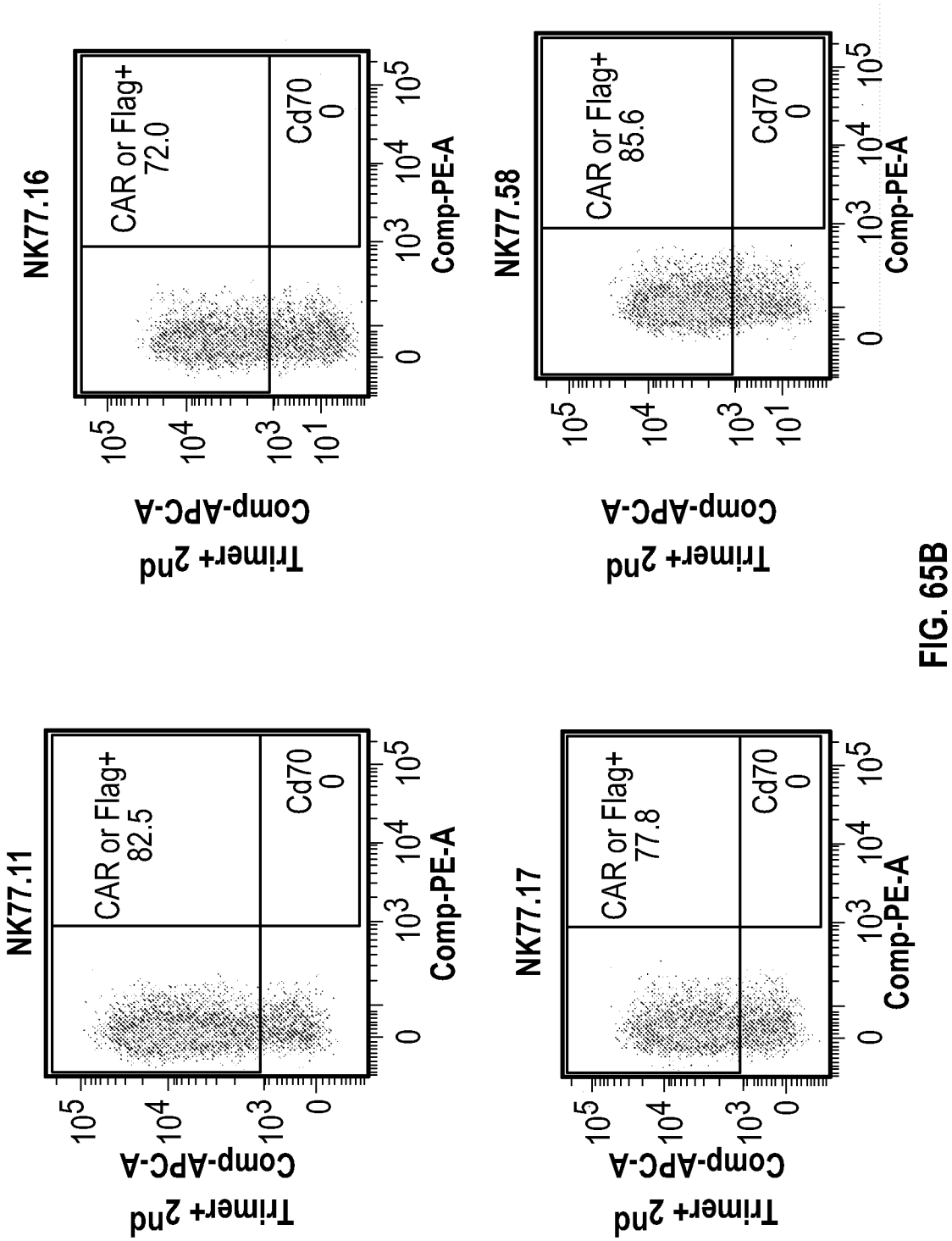

NK77.16
CAR or Flag+
72.0
Cd70
0
Trimer+ 2nd
Comp-APC-A
Comp-PE-A
NK77.58
CAR or Flag+
85.6
Cd70
0
Trimer+ 2nd
Comp-APC-A
Comp-PE-A
NK77.11
CAR or Flag+
82.5
Cd70
0
Trimer+ 2nd
Comp-APC-A
Comp-PE-A
NK77.17
CAR or Flag+
77.8
Cd70
0
Trimer+ 2nd
Comp-APC-A
Comp-PE-A

FIG. 65B

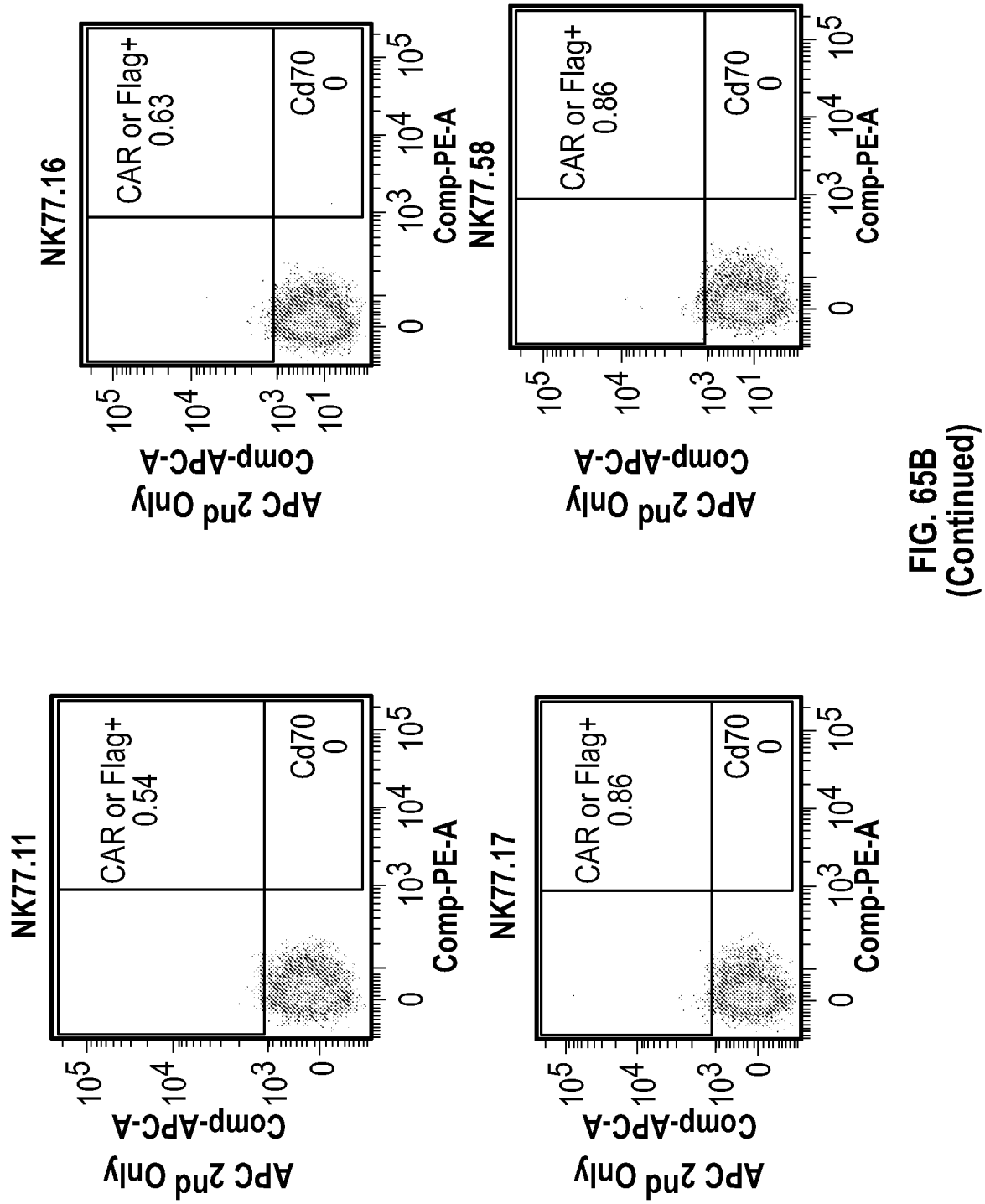


FIG. 65B
(Continued)

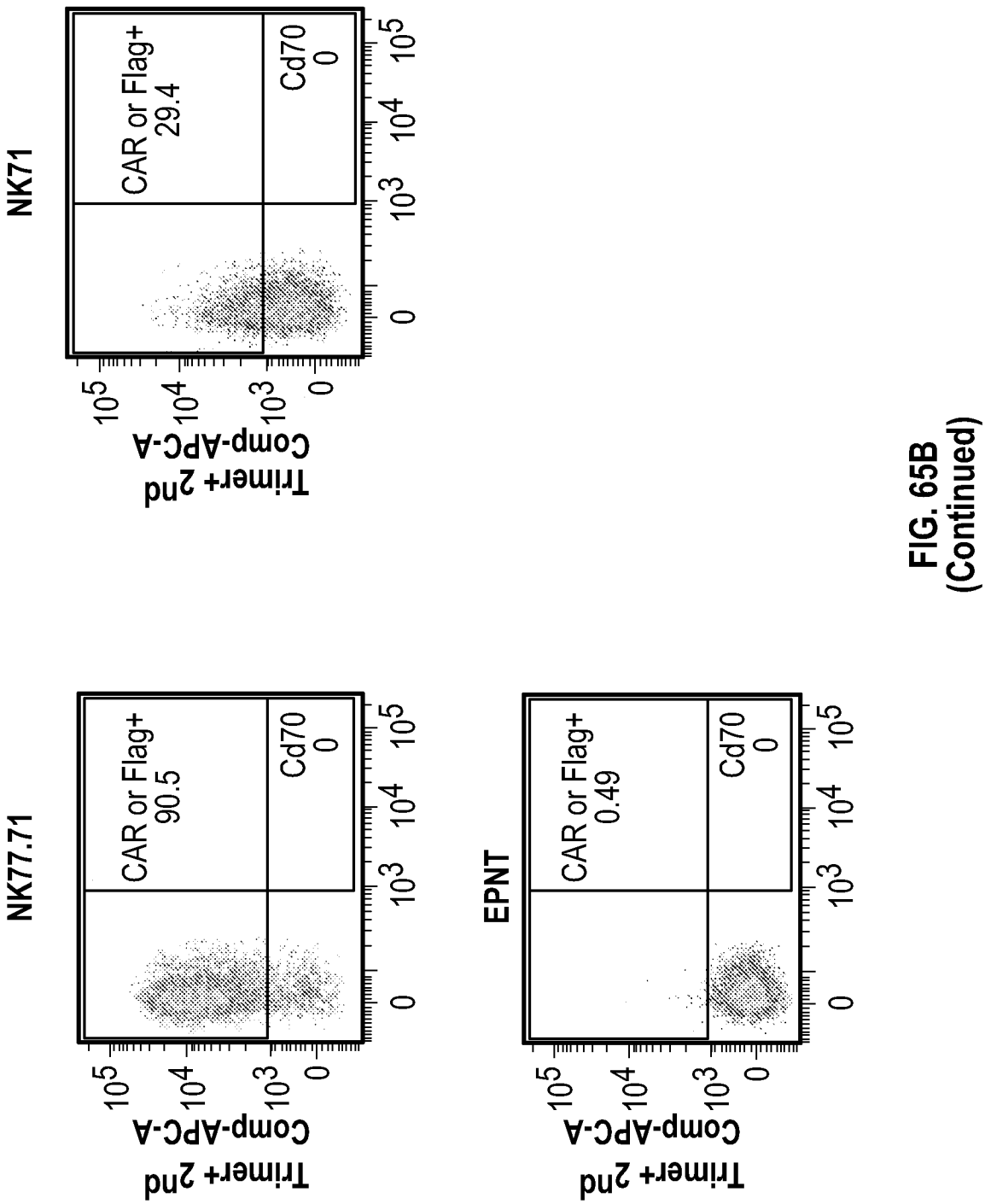


FIG. 65B
(Continued)

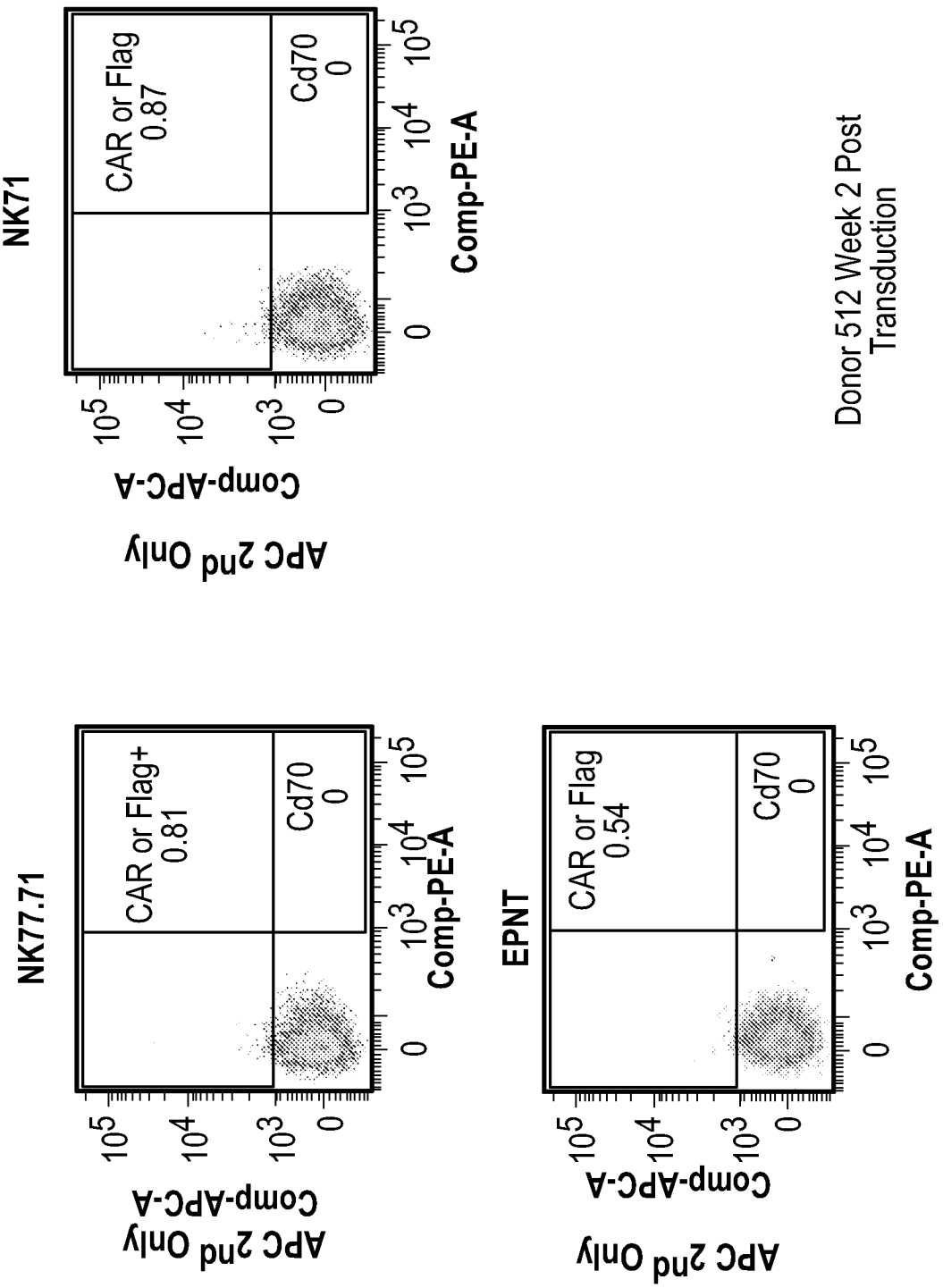


FIG. 65B
(Continued)

FIG. 65C

Dnr451 Construct	Titer	CAR (MFI)		CAR(%)	
EPNT	-	2033	2671	0.45	0.65
CD70KO NT	-	2661	1509	0.27	0.44
NK71	1.20E+06	2245	2298	48.7	52.2
NK77.11	2.32E+06	7359	7530	84.4	84.4
NK77.16	1.38E+06	6371	6637	74.3	75.981
NK77.17	2.31E+06	4652	4862	77	77.6
NK77.58	1.81E+06	5562	5738	89.1	89.4
NK77.71	2.25E+06	7843	7984	91.2	90.5

FIG. 65D

Dnr512 Construct	Titer	CAR (MFI)		CAR(%)	
EPNT	-	1712	1885	0.0049	0.004
CD70KO NT	-	1604	1966	0.00093	0.0023
NK71	1.20E+06	1989	2072	0.294	0.345
NK77.11	2.32E+06	6435	6525	0.825	0.814
NK77.16	1.38E+06	5259	5257	0.72	0.692
NK77.17	2.31E+06	4428	4489	0.778	0.766
NK77.58	1.81E+06	4280	4515	0.856	0.856
NK77.71	2.25E+06	6731	7229	0.905	0.911

Week 2 post transduction

FIG. 65E

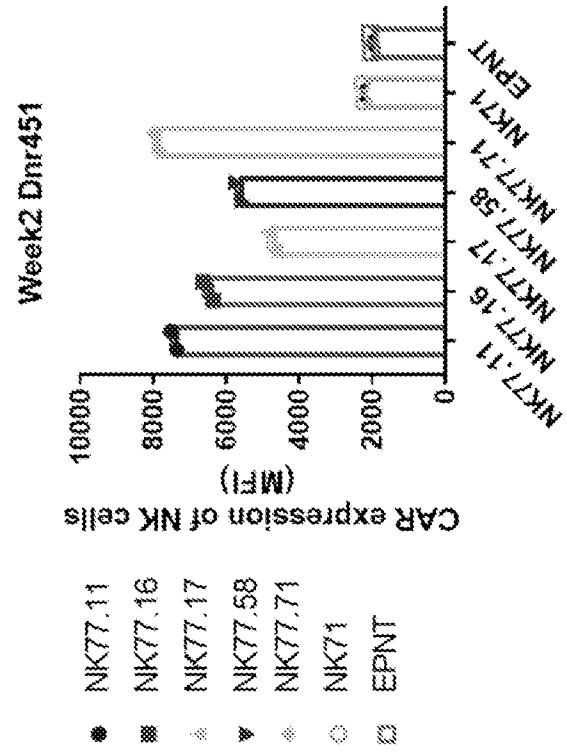
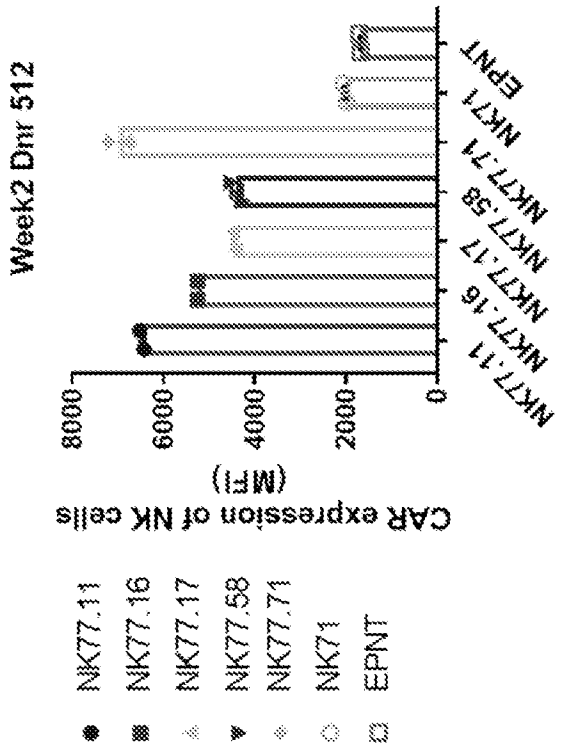


FIG. 65F



Week 2 post transduction

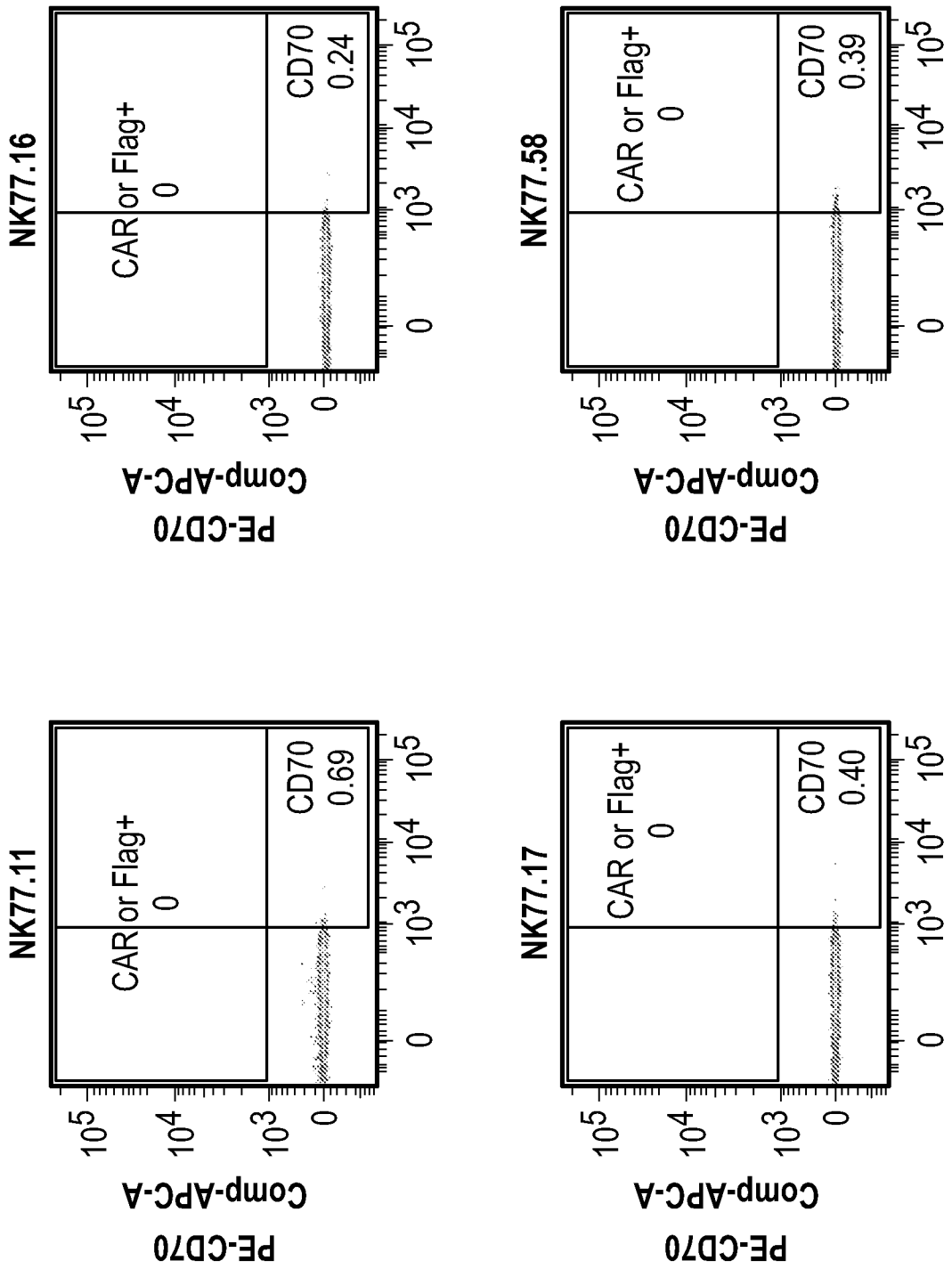

NK77.16
CAR or Flag+
0
CD70
0.24
NK77.58
CAR or Flag+
0
CD70
0.39
NK77.11
CAR or Flag+
0
CD70
0.69
NK77.17
CAR or Flag+
0
CD70
0.40
PE-CD70
Comp-APC-A
0
10^3
10^4
10^5

FIG. 65G

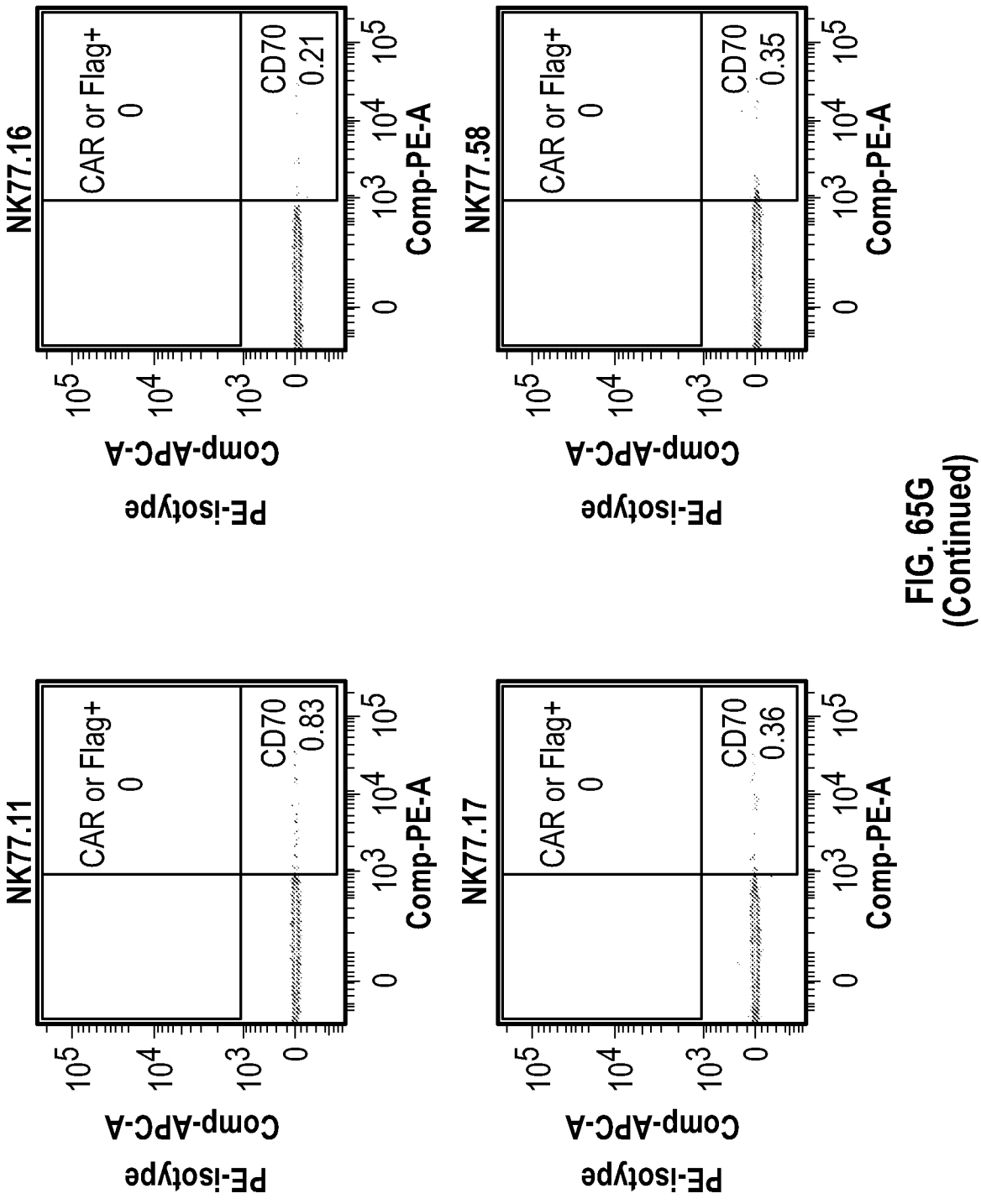
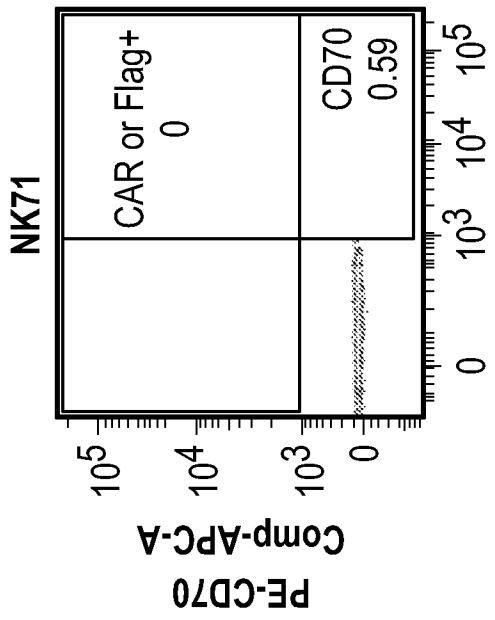
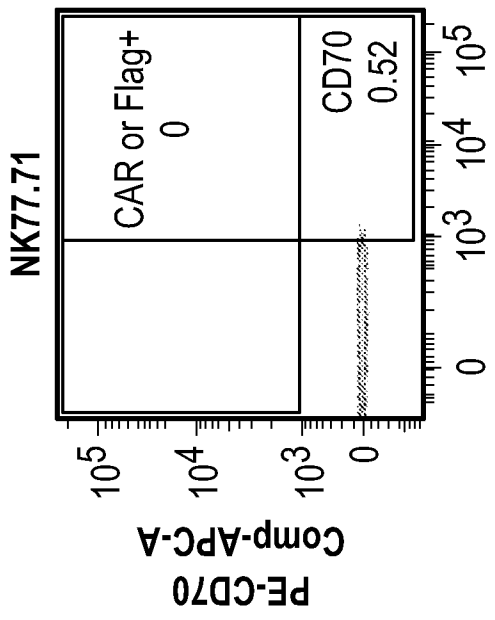


FIG. 65G
(Continued)





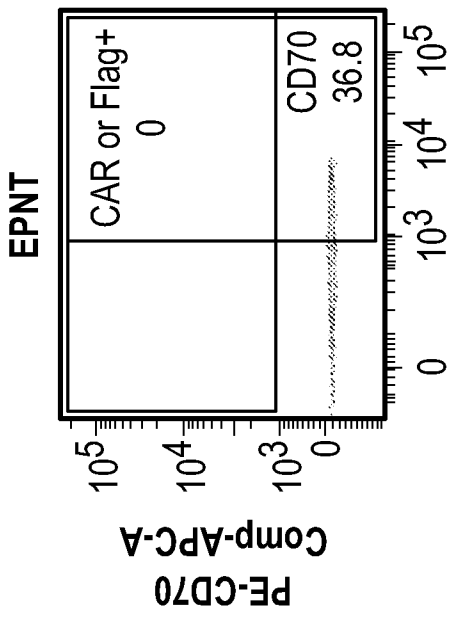


FIG. 65G
(Continued)

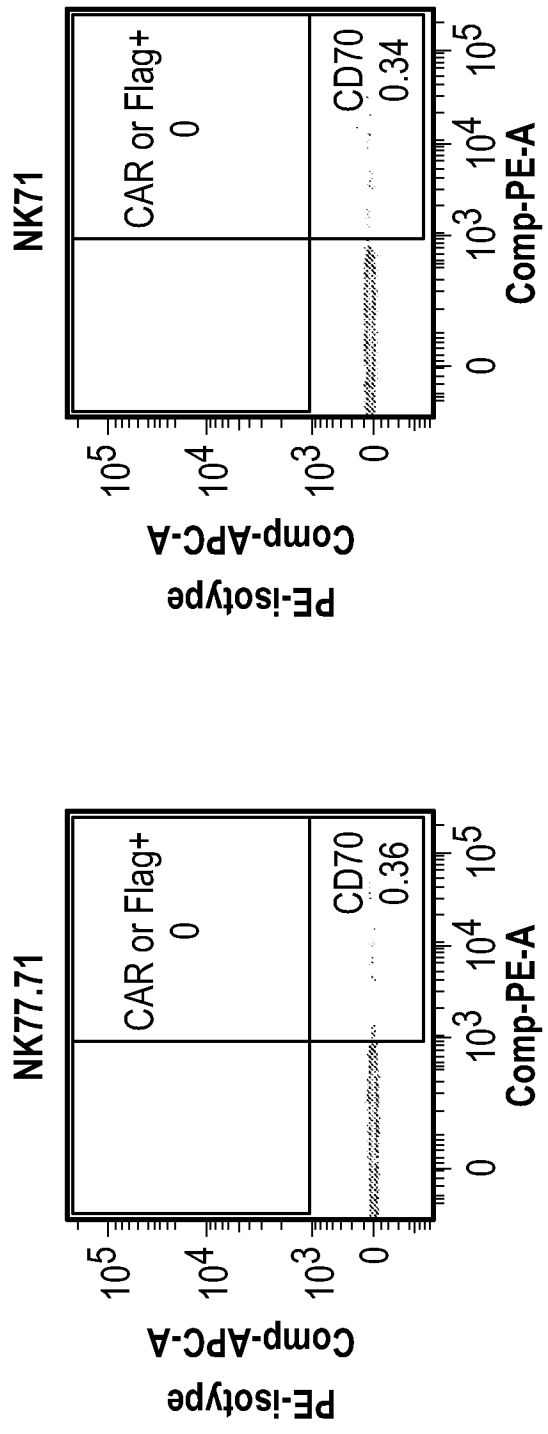


FIG. 65G
(Continued)

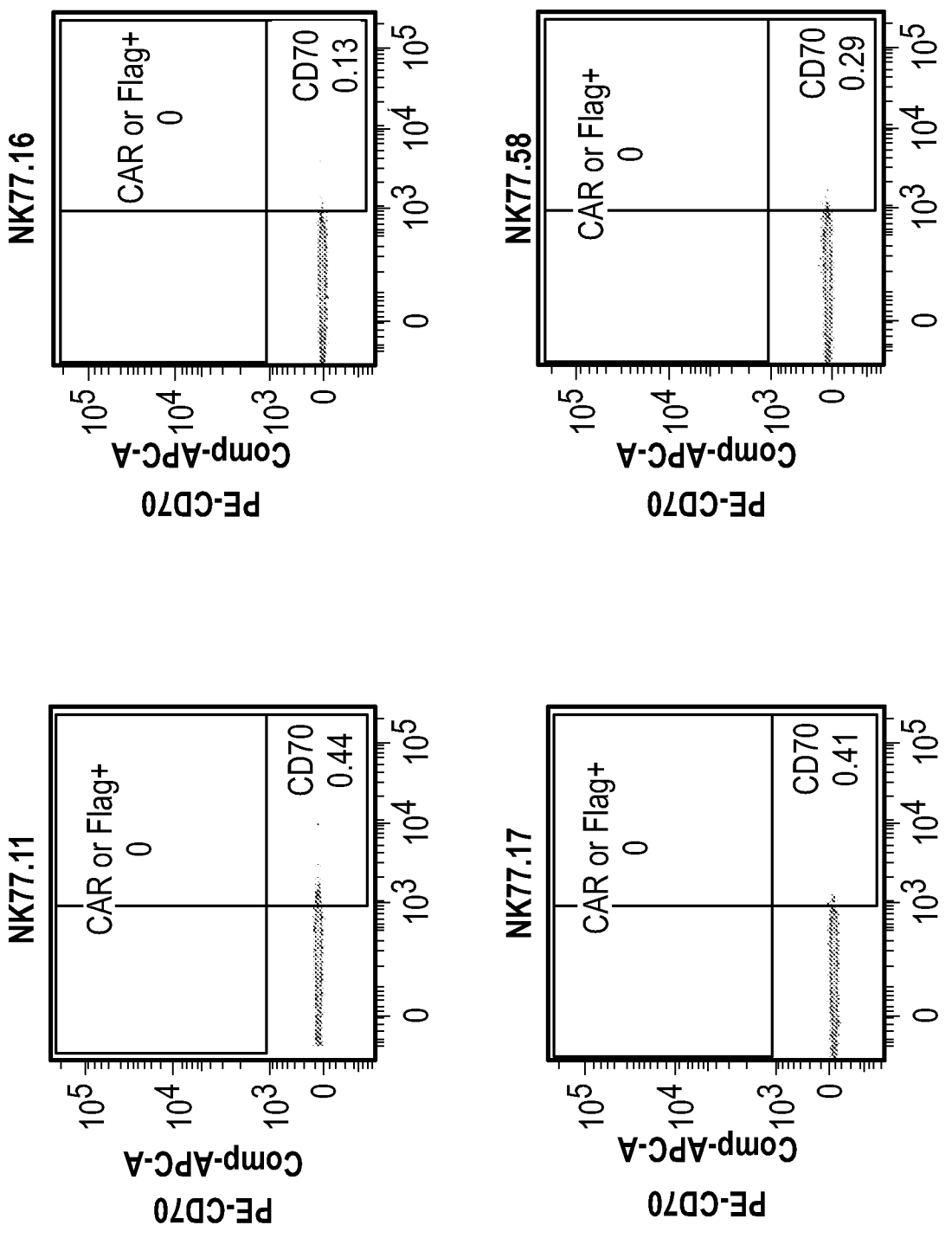
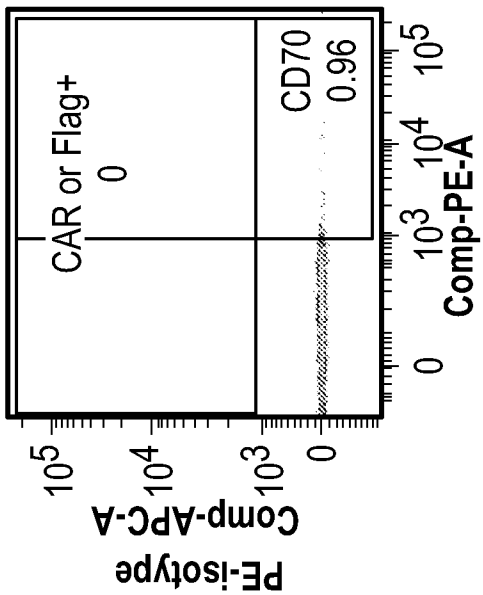
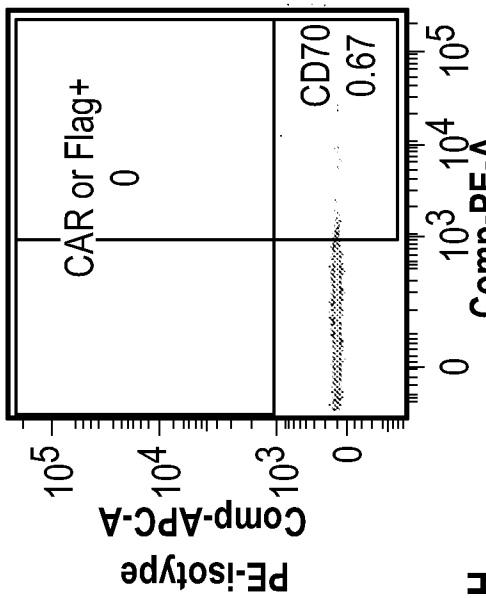
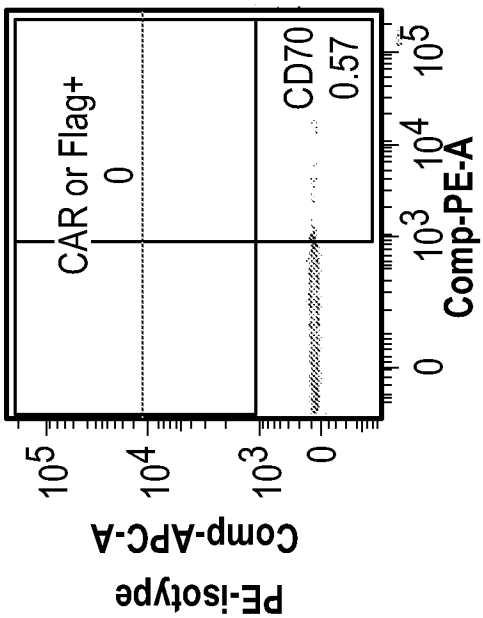

NK77.16
CAR or Flag+
0
CD70
0.13
NK77.58
CAR or Flag+
0
CD70
0.29
NK77.11
CAR or Flag+
0
CD70
0.44
NK77.17
CAR or Flag+
0
CD70
0.41
PE-CD70
Comp-APC-A
0
10^3
10^4
10^5

FIG. 65H







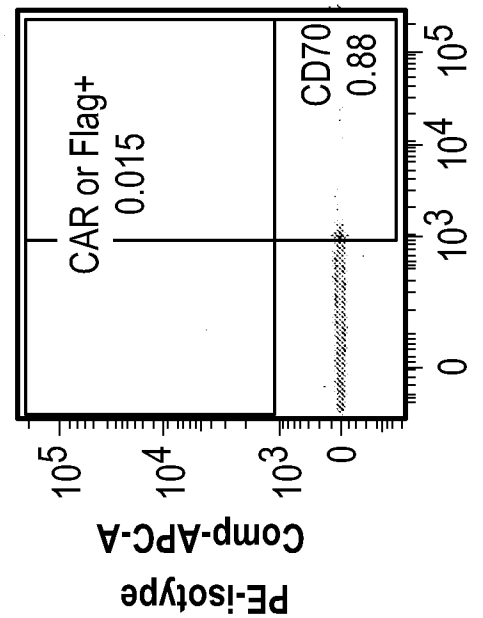


FIG. 65H
(Continued)

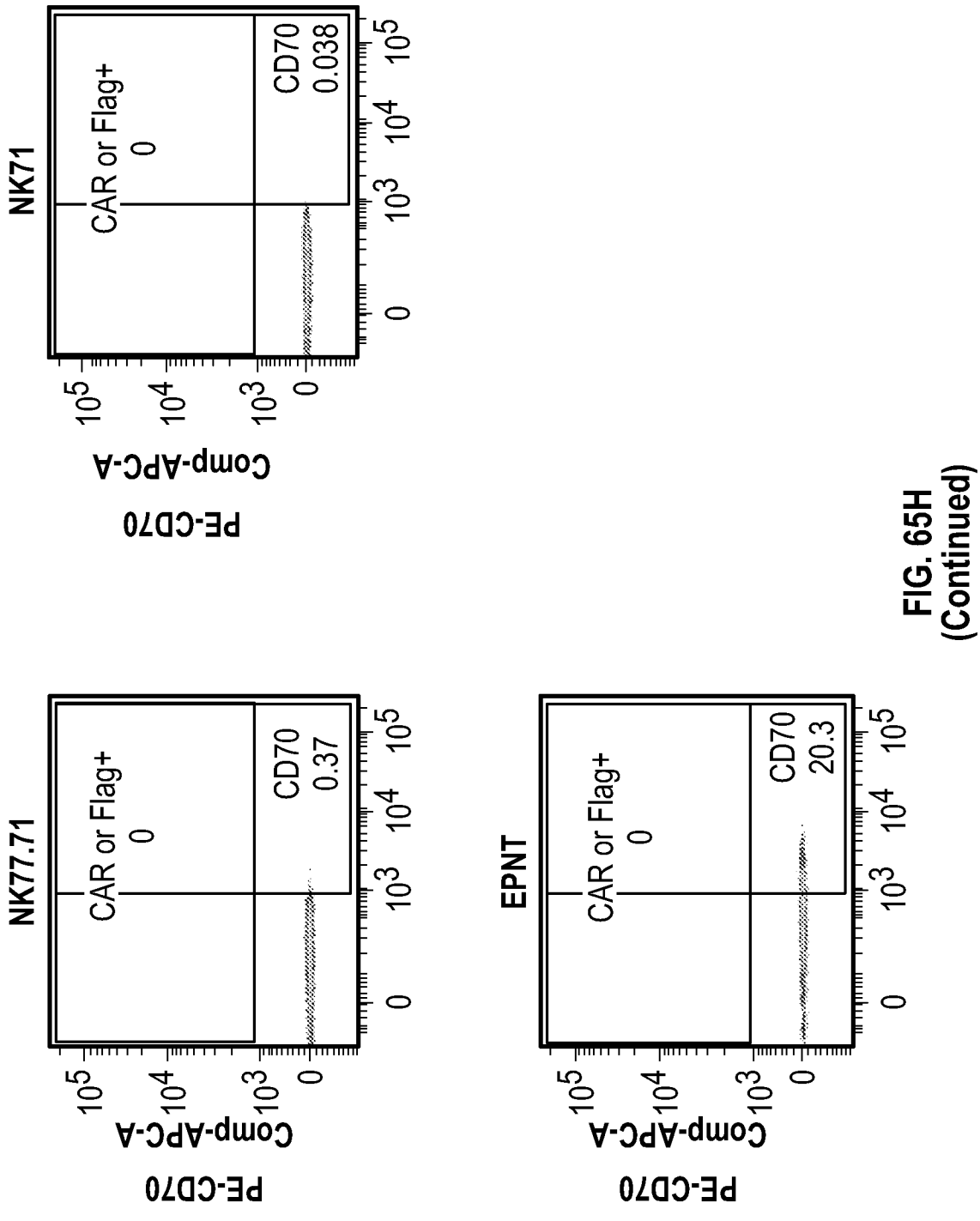
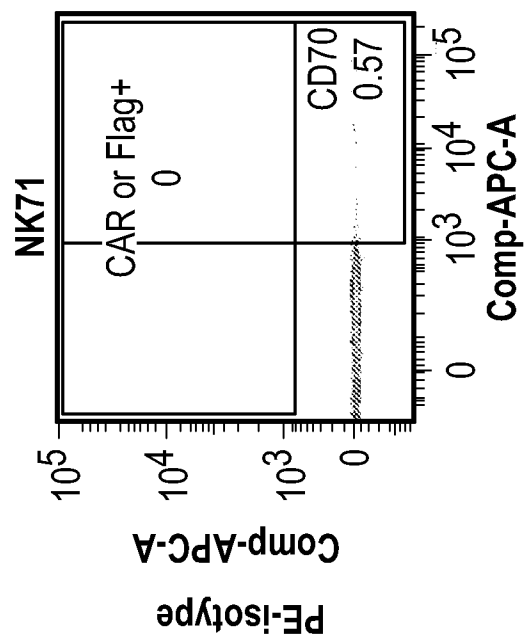
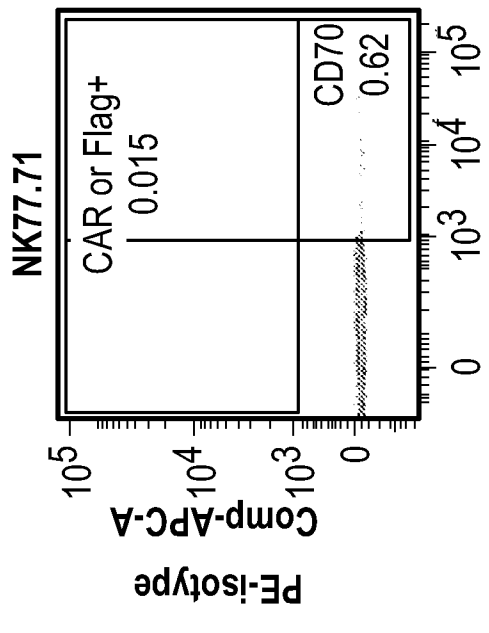
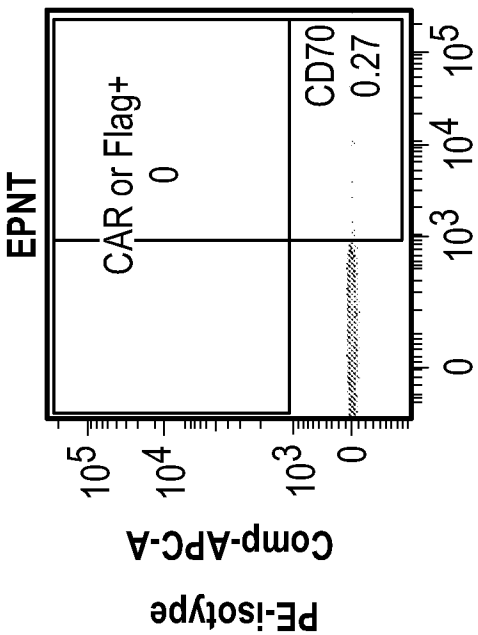


FIG. 65H
(Continued)







Donor 512 Week
2 Post Transduction

FIG. 65H
(Continued)

FIG. 65I

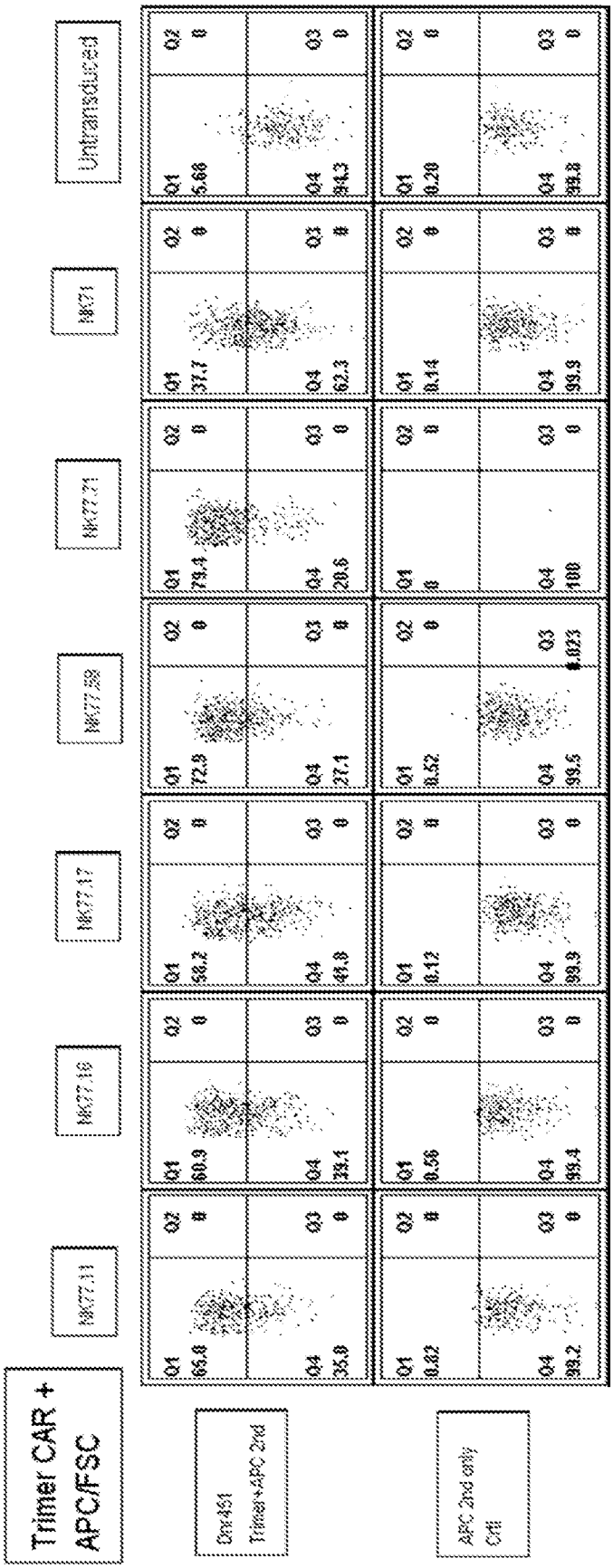
Dnr451 Construct	CD70 MFI (Day 29)		CD70 Expression (D29)	
EPNT	1604	1491	36.8	38
NK71	921	967	0.059	0.99
NK77.11	1004	1004	0.88	0.69
NK77.16	1101	967	0.24	0.19
NK77.17	1054	993	0.4	0.89
NK77.58	1011	1022	0.39	0.54
NK77.71	989	1086	0.52	0.38

FIG. 65J

Dnr512 Construct	CD70 MFI (Day 29)		CD70 Expression (D29)	
EPNT	1354	1405	20.3	24.5
NK71	932	989	0.038	1.58
NK77.11	967	1069	0.34	0.44
NK77.16	1142	966	0.13	0.12
NK77.17	982	959	0.41	0.28
NK77.58	1058	976	0.29	0.33
NK77.71	1021	962	0.37	0.24

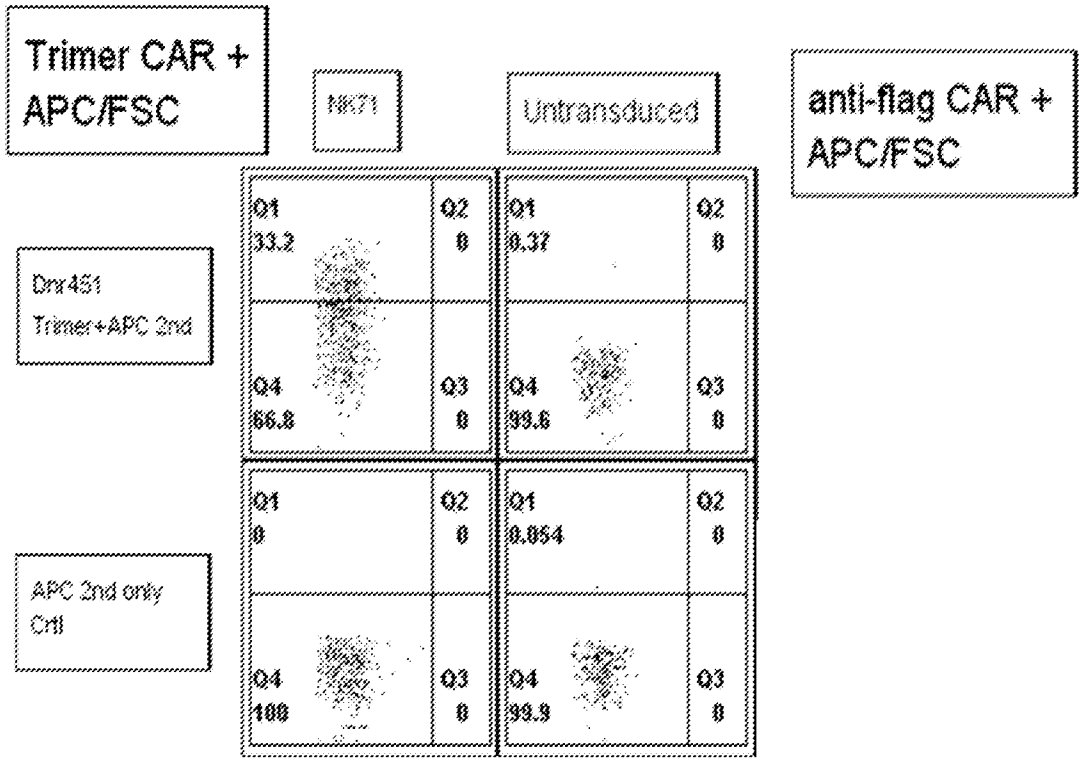
Week 2 post transduction

Figure 66A



Donor 451 week 3 post-transduction

Figure 66A Cont.



Donor 451 week 3 post-transduction

Figure 66B

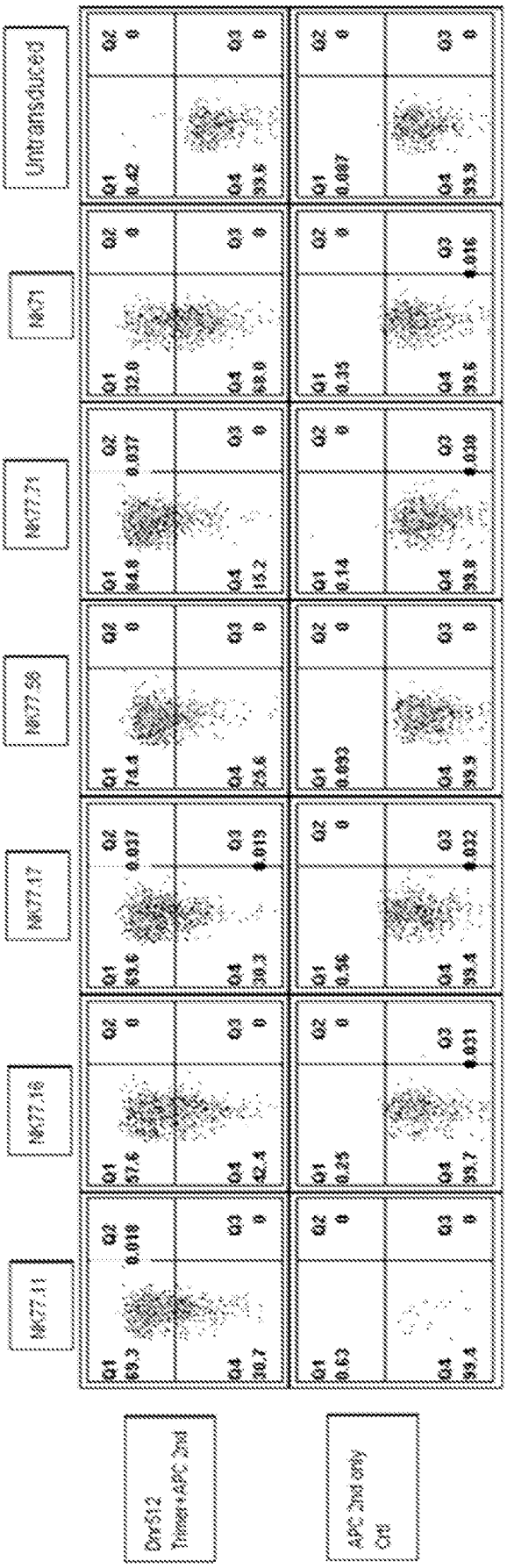
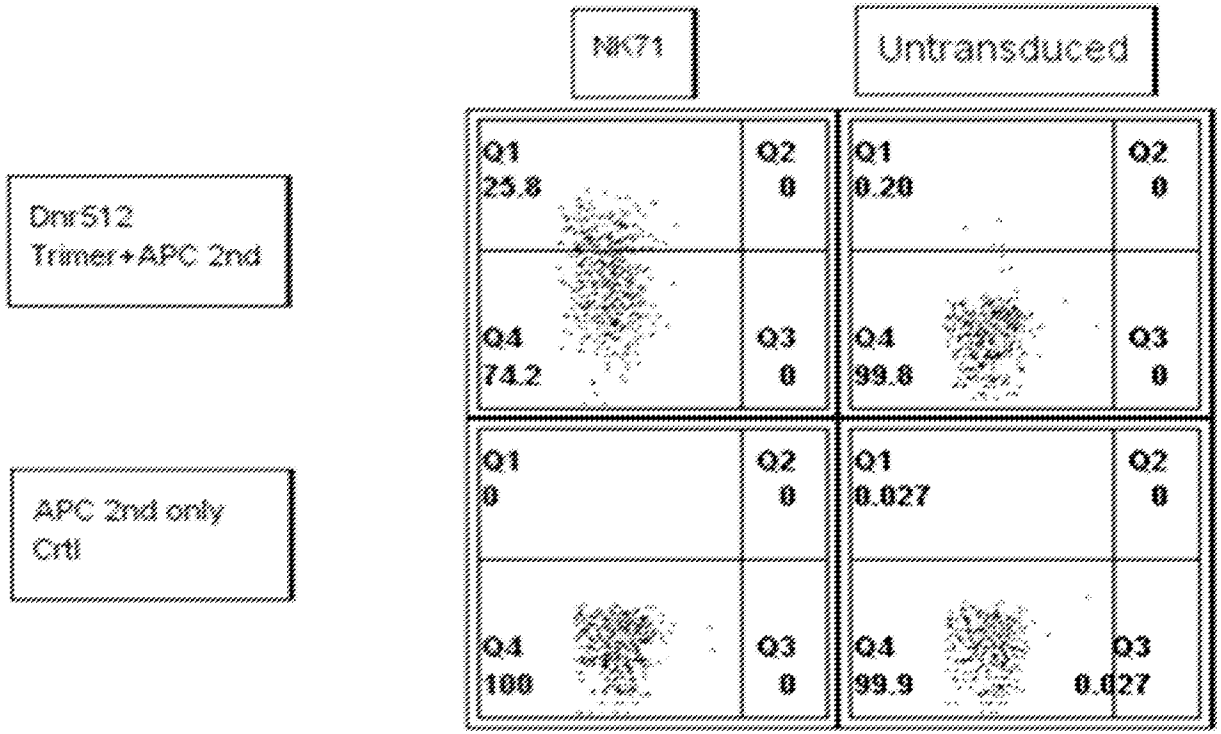

Untransduced
MK77.71
MK77.71
MK77.55
MK77.17
MK77.16
MK77.11
Donor 512 week 3 post-transduction

Figure 66B Cont.



Donor 512 week 3 post-transduction

Figure 66C

C

Dnr451		Titer	CAR %	MFI	CAR %	MFI
	NK77.11	2.32E+06	78.9	7609	79.1	7438
	NK77.16	1.38E+06	72.5	7895	73	7078
	NK77.17	2.31E+06	68.6	4882	70.2	5043
	NK77.58	1.81E+06	83.3	6336	81.1	6063
	NK77.71	2.25E+06	87	9402	84.7	8676
	NK71	1.20E+06	38.7	1653	43.5	1942
	EPNT	-	1.24	135	1.22	123
Dnr 512		Titer	CAR %	MFI	CAR %	MFI
	NK77.11	2.32E+06	80	7647	81.5	8198
	NK77.16	1.38E+06	68.4	5975	69.5	5718
	NK77.17	2.31E+06	74.4	5269	71.4	4921
	NK77.58	1.81E+06	79.8	5283	78.2	5147
	NK77.71	2.25E+06	87.7	9054	87	8522
	NK71	1.20E+06	24.2	1114	30.1	1184
	EPNT	-	0.46	143	0.86	144

Week 3 post-transduction

FIG. 66D

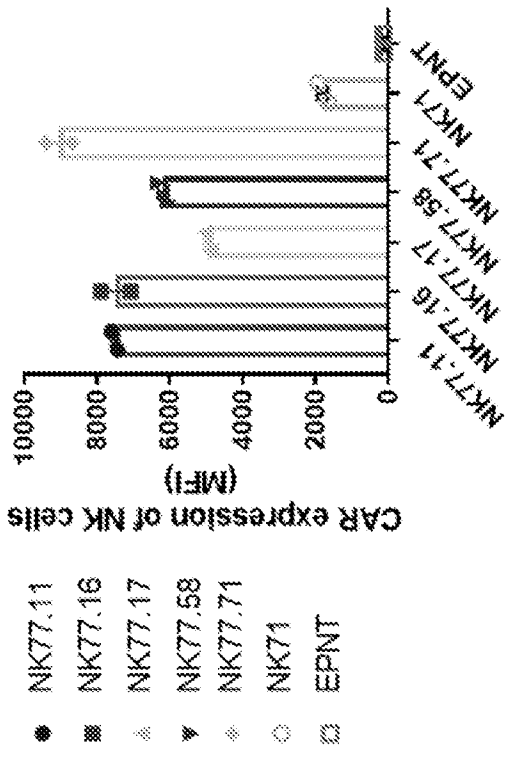


FIG. 66E

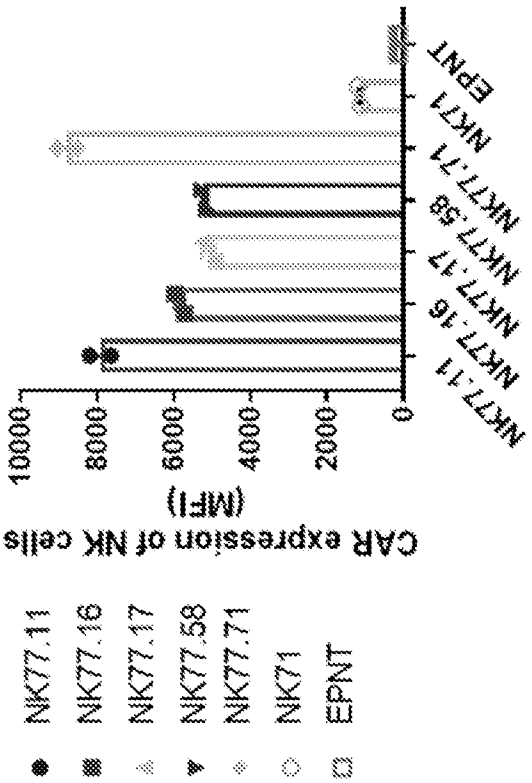
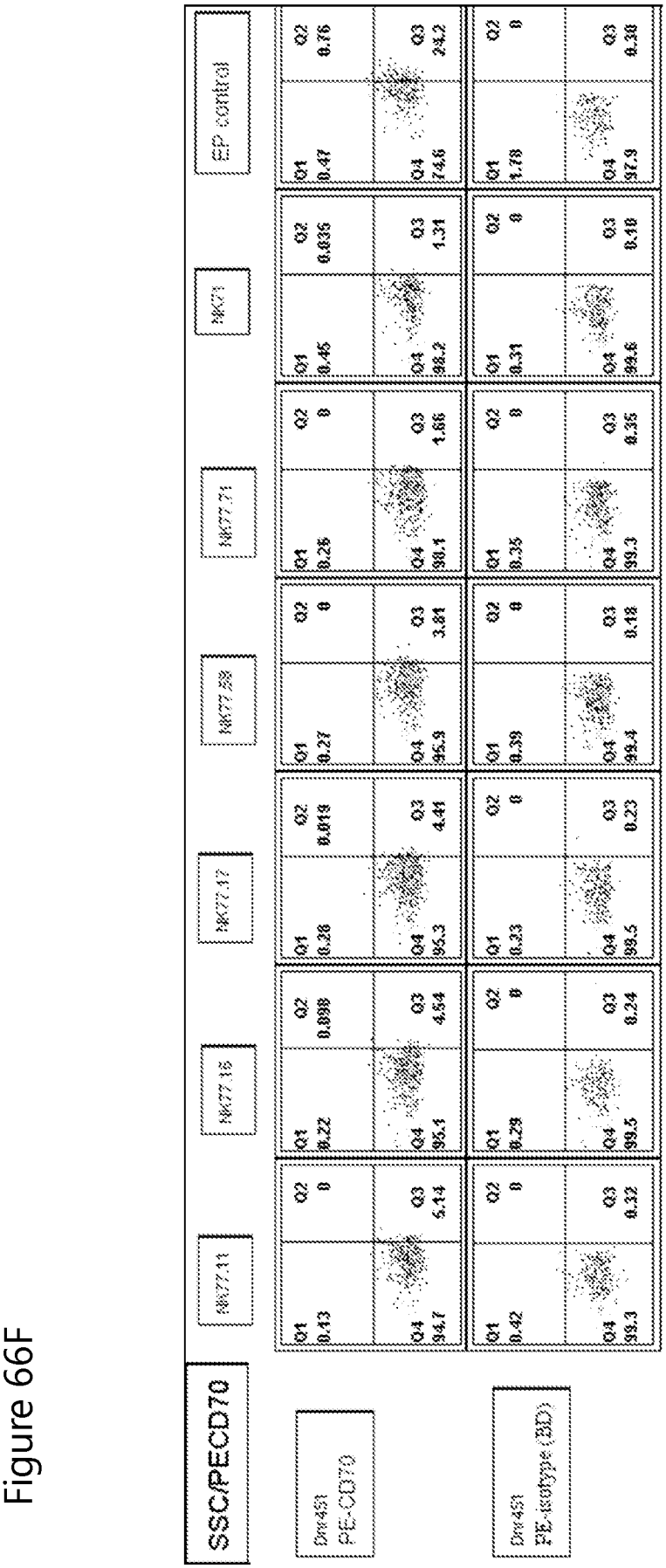
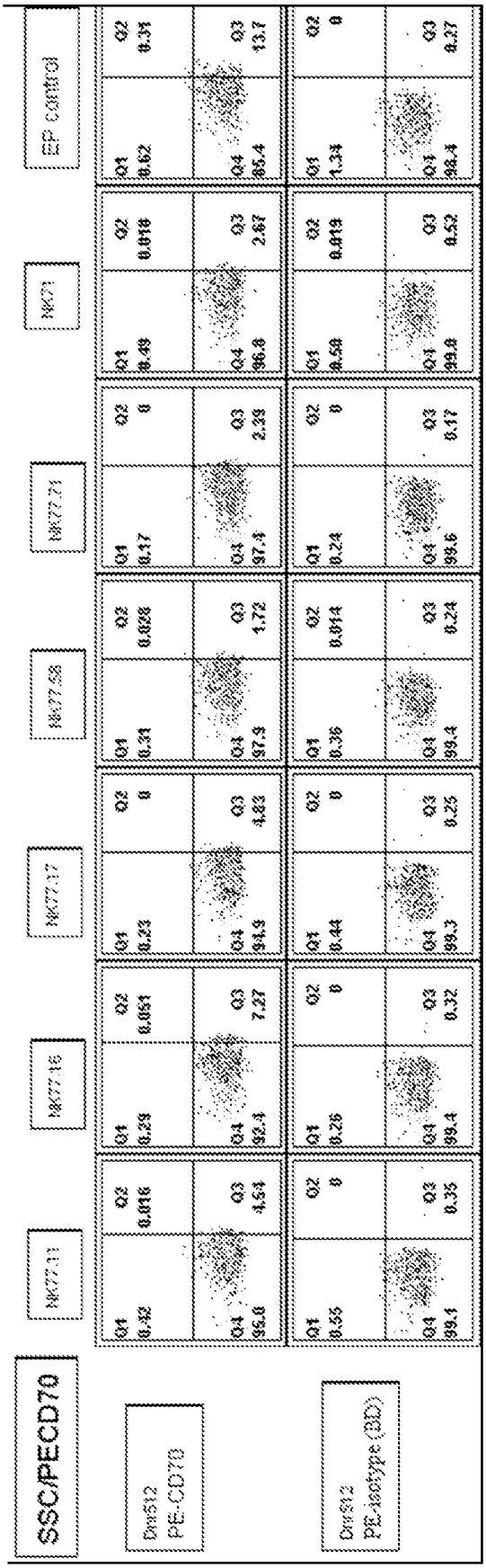


Figure 66F



Donor 451 week 3 post-transduction

Figure 66G



Donor 512 week 3 post-transduction

FIG. 66H

	viabiliy	CD70 %	MFI	viability	CD70 %	MFI
NK77.11	95.9	5.14	519	96.2	6.27	557
NK77.16	97.8	4.54	517	96.7	8.95	624
NK77.17	98.1	4.41	484	97.9	5.48	516
NK77.58	96.4	3.81	458	97	7.98	567
NK77.71	97.9	1.66	382	97	6.88	541
NK71	96.4	1.31	373	95.7	6.82	542
EPNT	93.6	24.2	1321	93.5	25.3	1356

Donor 451

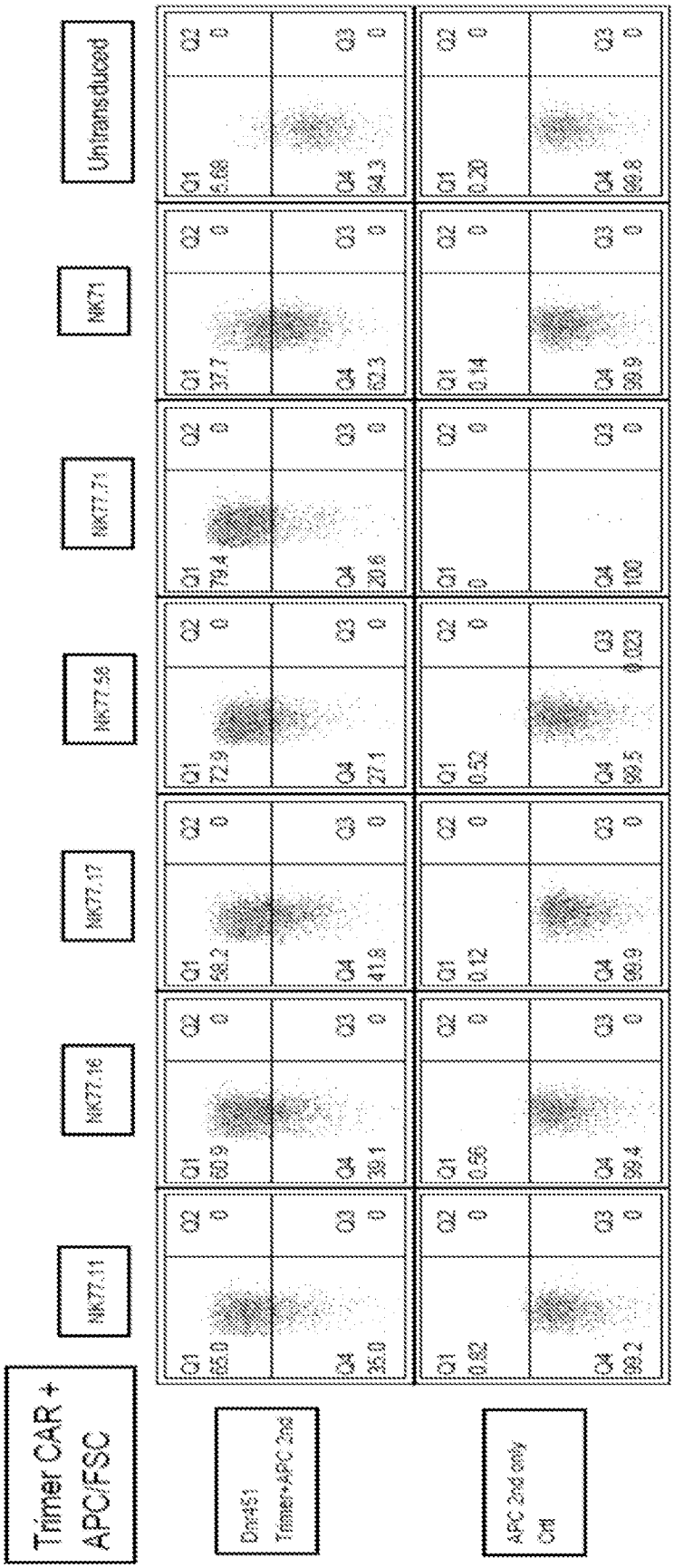
FIG. 66I

	viabiliy	CD70 %	MFI	viability	CD70 %	MFI
NK77.11	98.6	4.54	578	97.8	9.88	633
NK77.16	98.9	7.27	640	98	8.08	592
NK77.17	99	4.83	504	97.6	9.04	590
NK77.58	98.6	1.72	406	97.8	6.53	522
NK77.71	98.5	2.39	395	98	1.94	381
NK71	98.1	2.67	419	96.6	3.61	449
EPNT	98.1	13.7	935	97.3	18.7	1052

Donor 512

Week 3 Post-transduction

Figure 67A



Donor 451 week 4 Post-transduction

Figure 67A Cont.

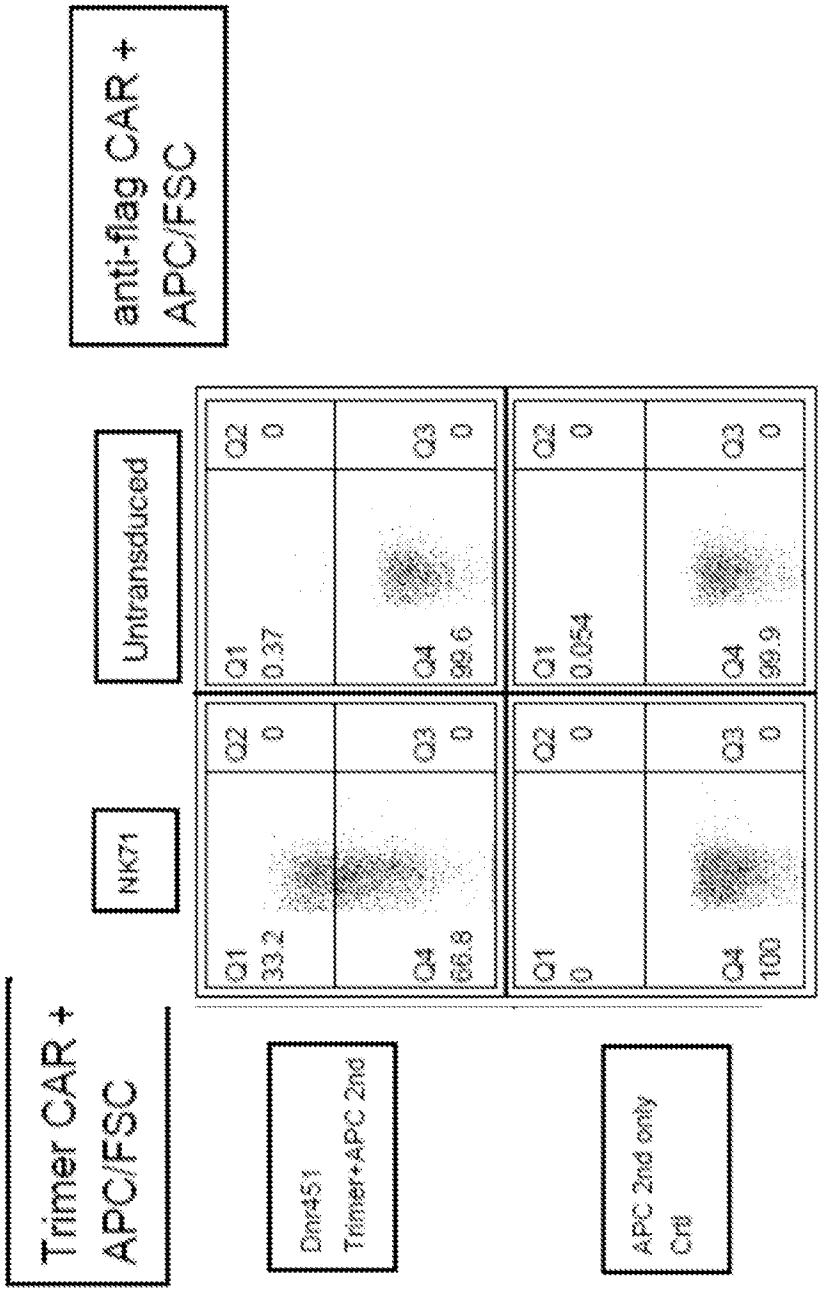


Figure 67B

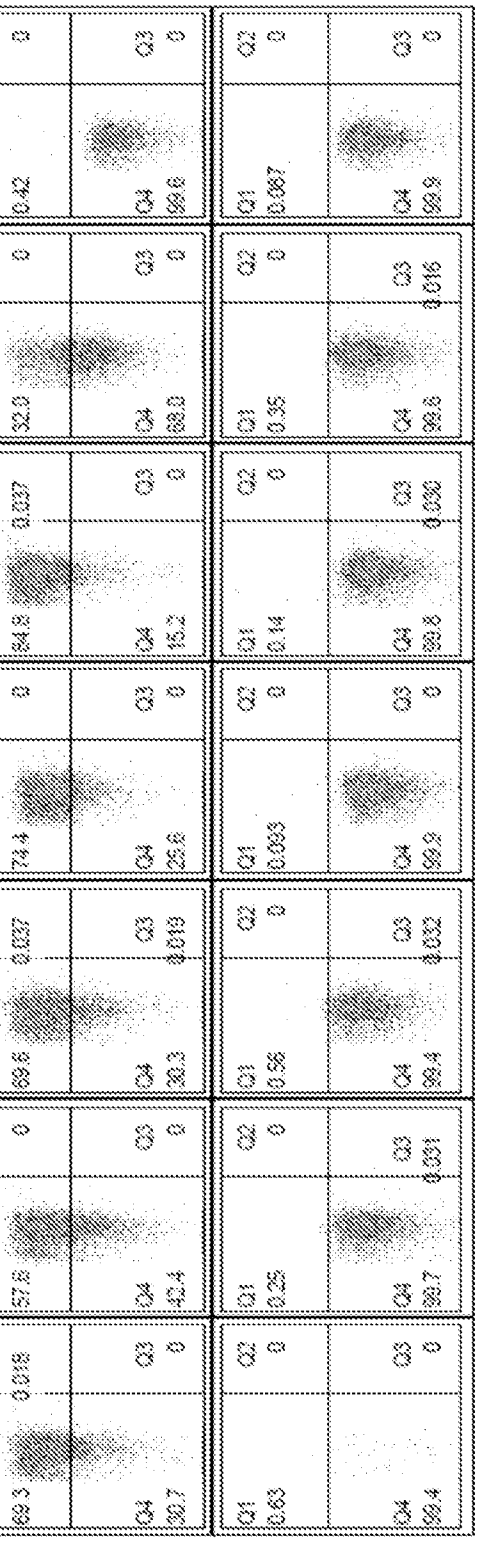
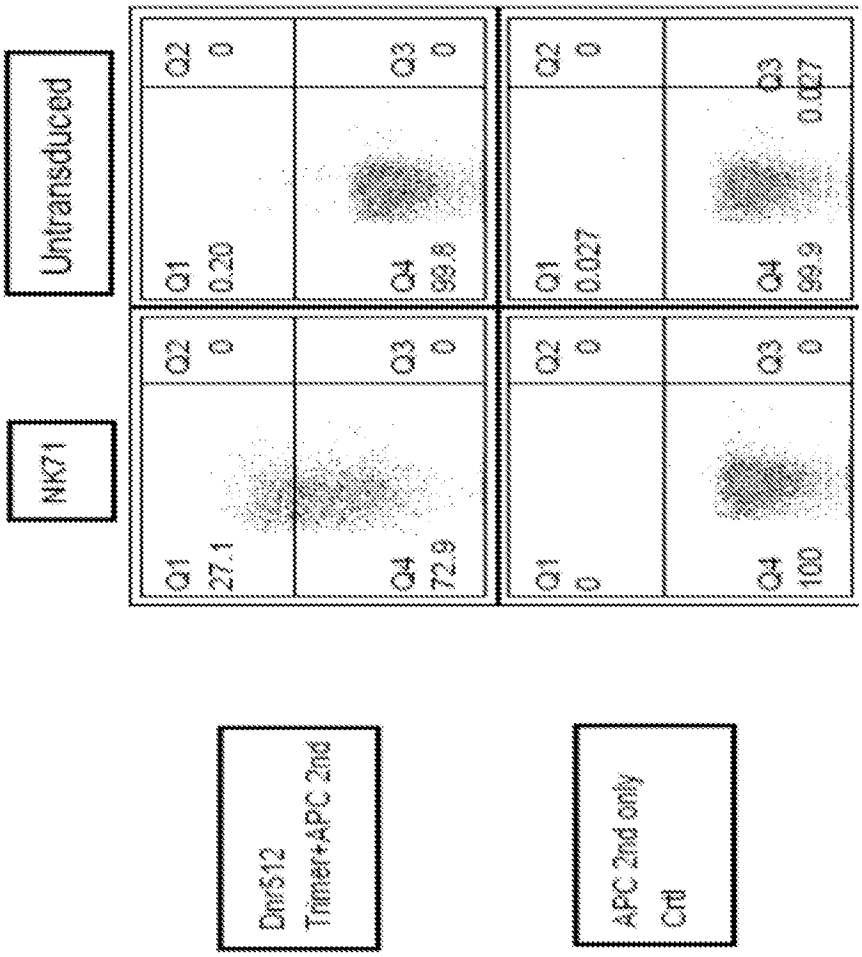

Untransduced
NK77.71
NK77.71
NK77.58
NK77.17
NK77.16
NK77.11
Donor 512 week 4 Post-transduction
Donor 512 Tetramer+APC 2nd
APC 2nd only Ctrl

Figure 67B Cont.



Donor 512 week 4 Post-transduction

FIG. 67C

Dnr451 Construct	Viability	Titer	CAR MFI	CAR (%)
NK77.11	88.80%	2.32E+06	5255	65
NK77.16	90%	1.38E+06	5032	60.9
NK77.17	91%	2.31E+06	4094	58.2
NK77.58	90.40%	1.81E+06	5621	72.9
NK77.71	90.10%	2.25E+06	7437	79.4
NK71	89.40%	1.20E+06	2459	37.7
EPNT	83.40%	-	389	5.68

FIG. 67D

Dnr512 Construct		Titer	CAR MFI	CAR (%)
NK77.11	88.90%	2.32E+06	5201	69.3
NK77.16	88.40%	1.38E+06	4533	57.6
NK77.17	87.20%	2.31E+06	5585	69.6
NK77.58	88.90%	1.81E+06	4847	74.4
NK77.71	89.40%	2.25E+06	8003	84.8
NK71	85.50%	1.20E+06	2575	32
EPNT	83.40%	-	187	0.42

Week 4 Post-transduction

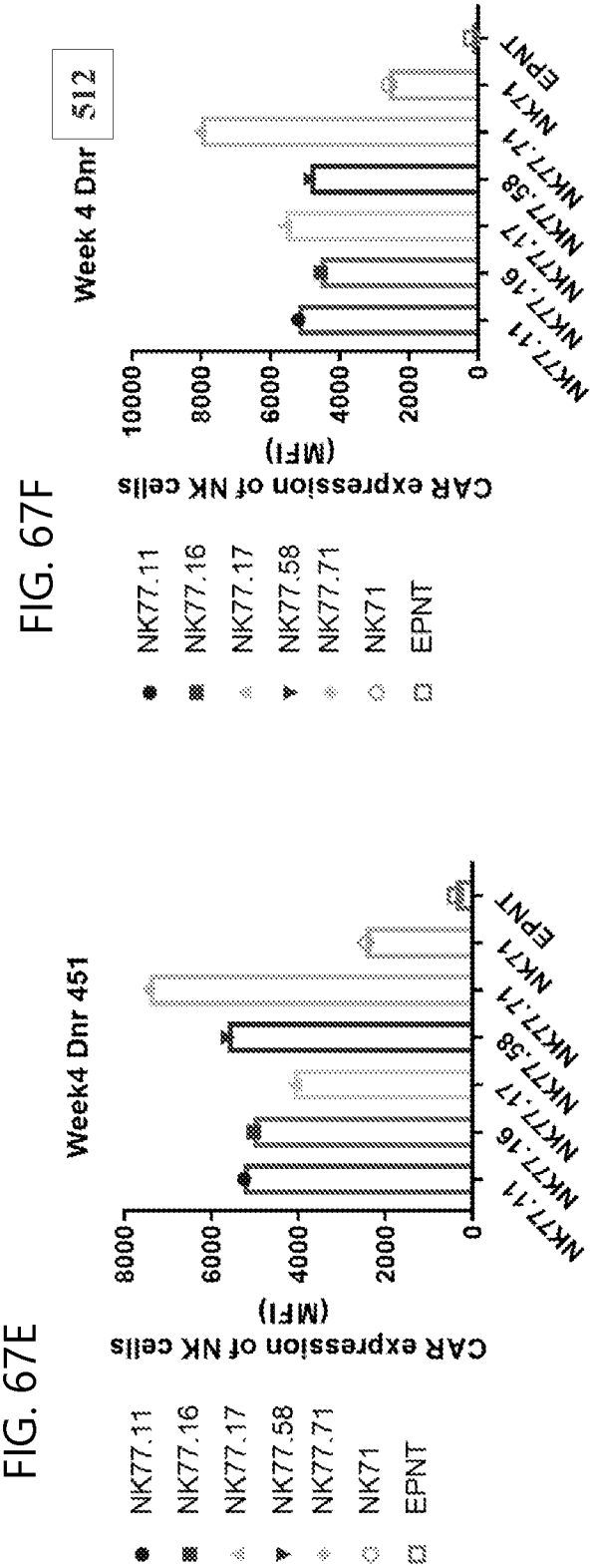
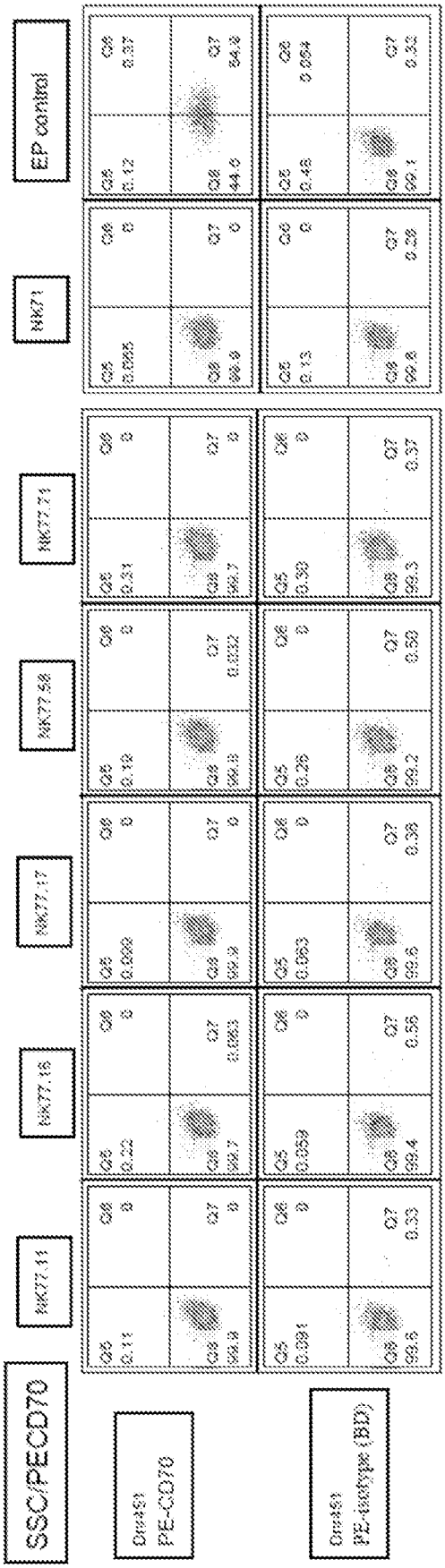


FIG. 67E

FIG. 67F

Week 4 Post-transduction

Figure 67G



Donor 451 week 4 post-transduction

Figure 67H

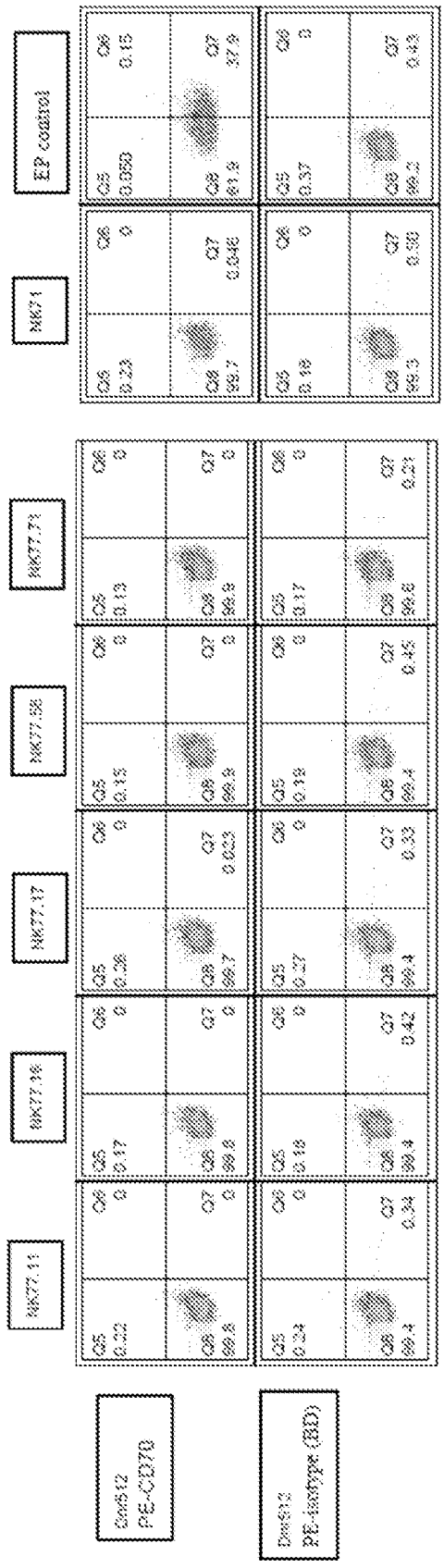


FIG. 67I

Dnr451		
Construct	CD70 MFI	CD70 (%)
NK77.11	74.4	0
NK77.16	73.4	0
NK77.17	84.1	0
NK77.58	91.8	0
NK77.71	83.7	0
NK71	94.1	0
EPNT	741	54.9

FIG. 67J

Dnr512		
Construct	CD70 MFI	CD70 (%)
NK77.11	71.2	0
NK77.16	74.2	0
NK77.17	84.7	0
NK77.58	81.8	0
NK77.71	81.2	0
NK71	32.6	0
EPNT	560	37.9

Week 4 post-transduction

Figure 68A

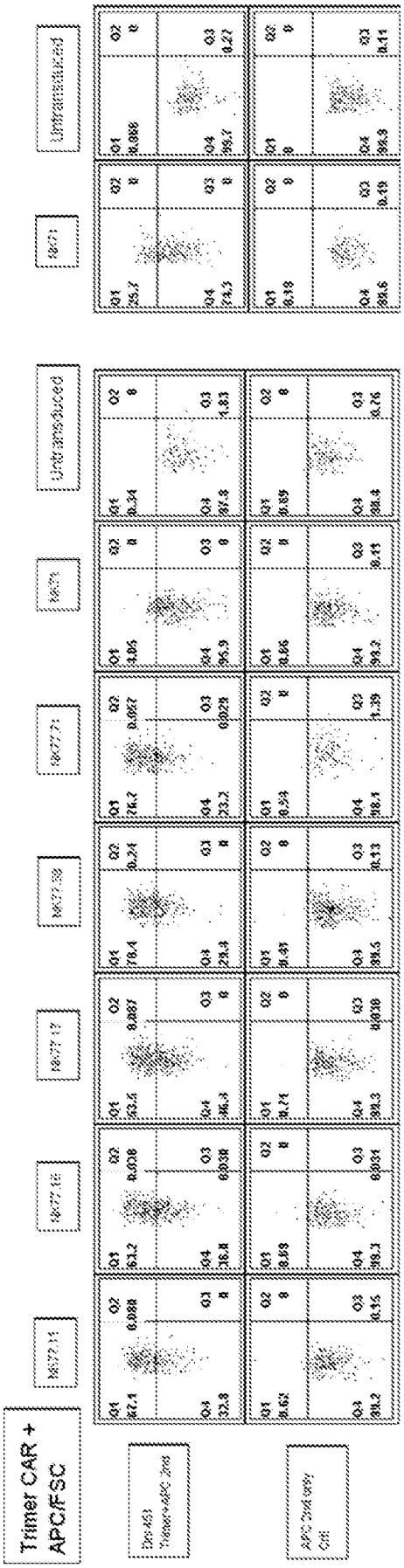
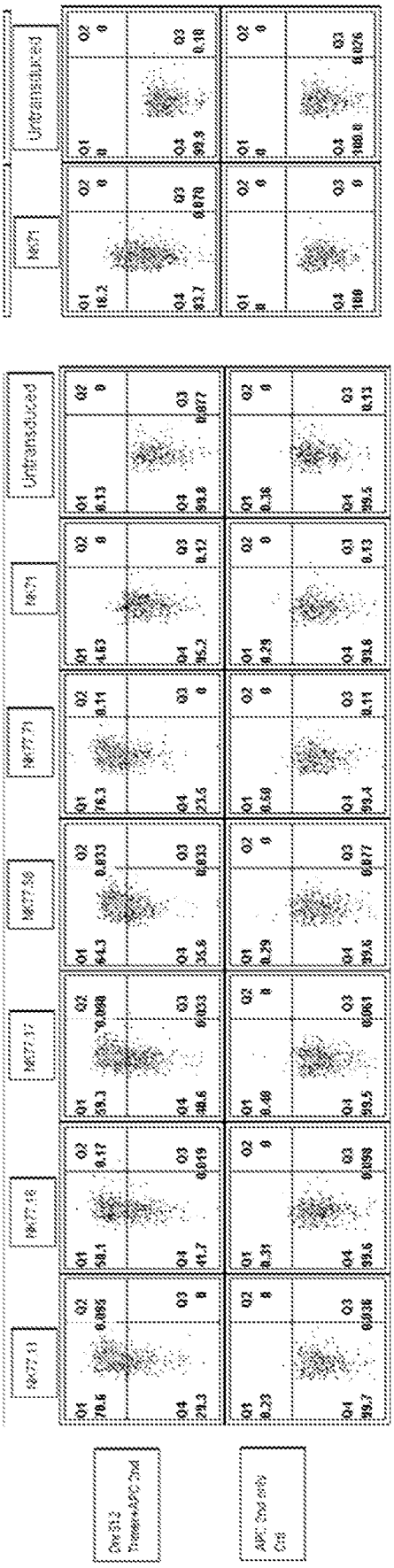


Figure 68B



Week 5 post-transduction

FIG. 68C

Dnr451	CAR %	MFI
NK77.11	67.1	7730
NK77.16	63.2	7615
NK77.17	53.5	5145
NK77.58	70.4	6370
NK77.71	76.7	8643
NK71	4.05	782
EPNT	0.34	345

FIG. 68D

Dnr512	CAR %	MFI
NK77.11	70.6	7569
NK77.16	58.1	6297
NK77.17	59.3	5659
NK77.58	64.3	4842
NK77.71	76.3	7910
NK71	4.63	845
EPNT	0.13	281

Week 5 post-transduction

FIG. 68E

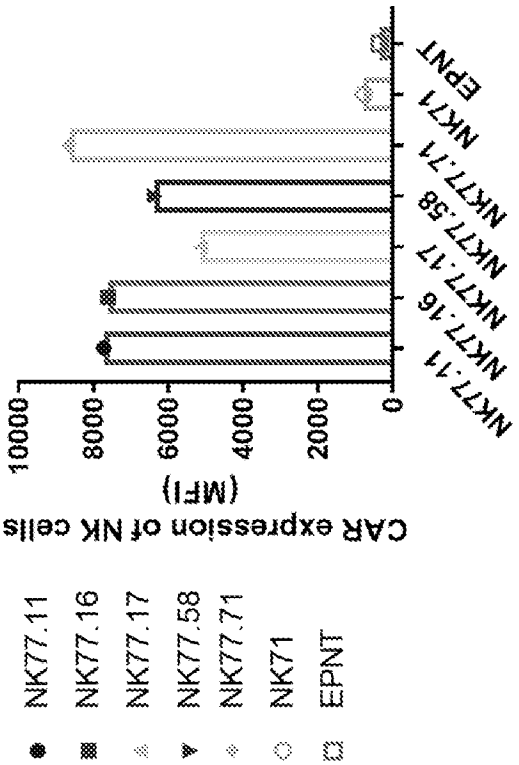
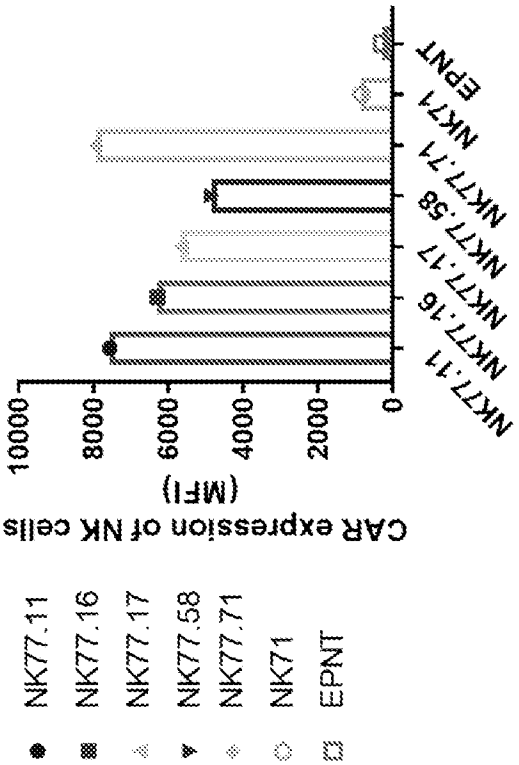


FIG. 68F



Week 5 post-transduction

Figure 68G

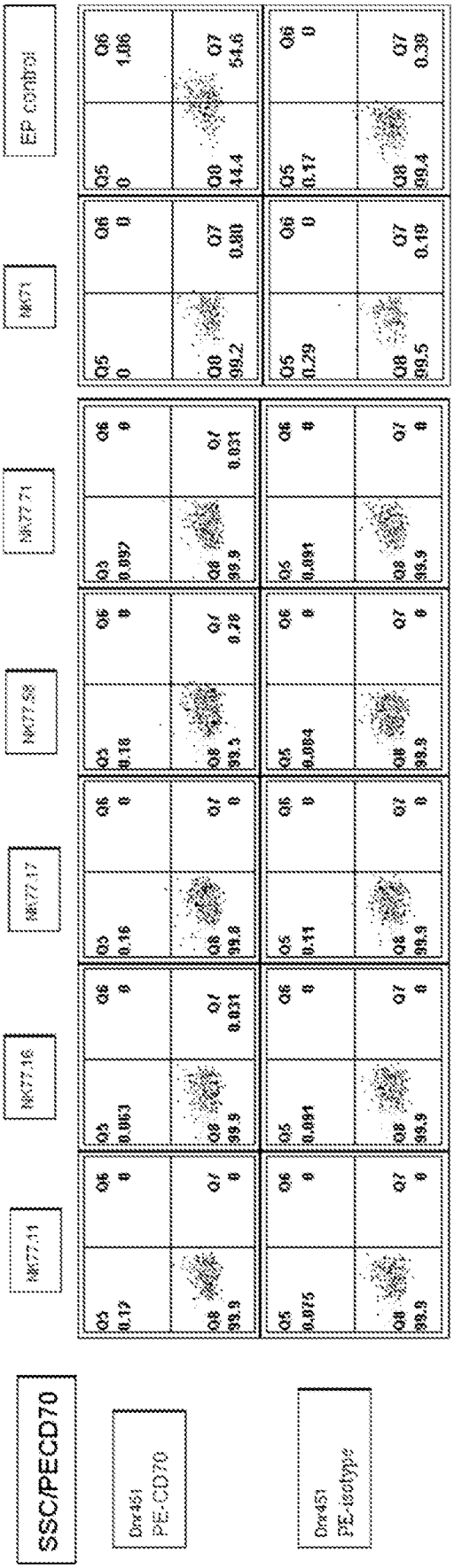
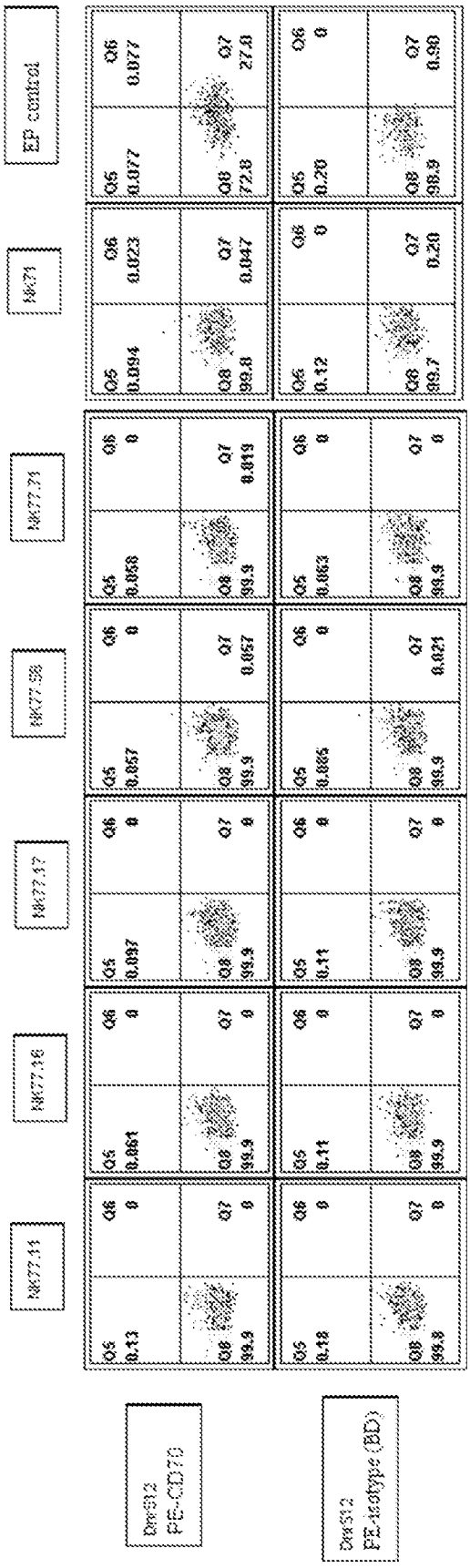

SSC/PECD70
NK77.11
NK77.16
NK77.17
NK77.68
NK77.71
NK71
EP control
Dnr451
PE-CD70
Dnr451
PE-isotype
Week 5 post-transduction

Figure 68H



Week 5 post-transduction

Figure 68I

Donor 451

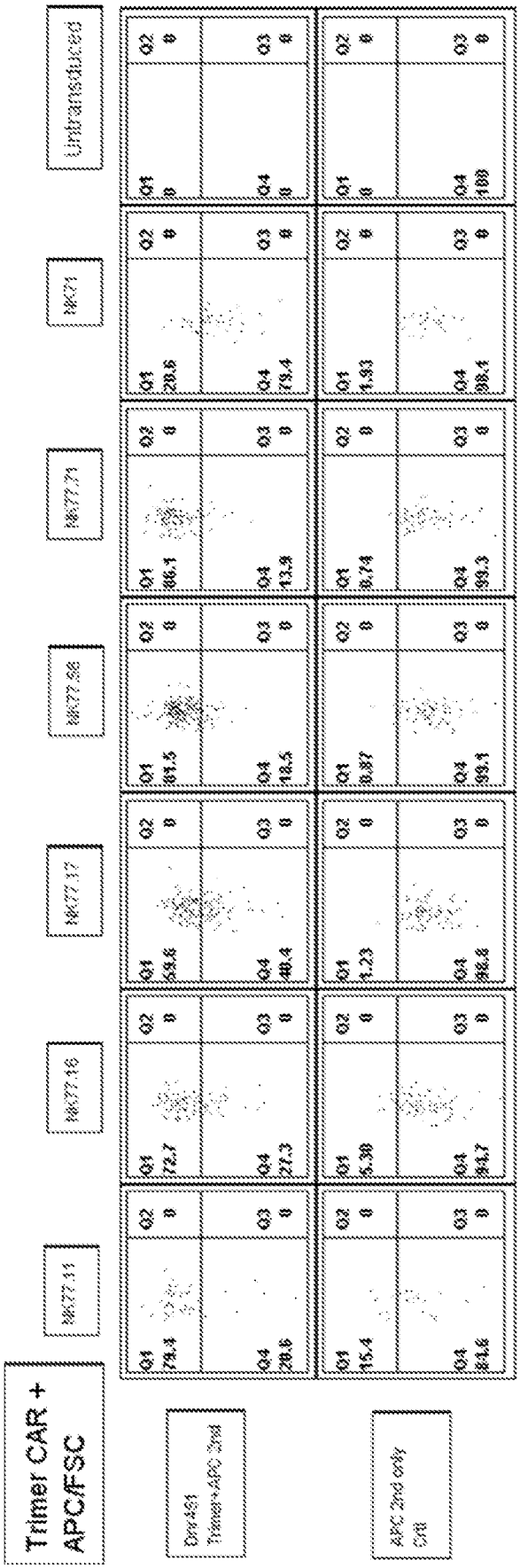
	CD70 %	MFI
NK77.11	0.019	114
NK77.16	0	115
NK77.17	0	107
NK77.58	0	105
NK77.71	0.057	109
NK71	0.047	148
EPNT	27	652

Donor 512

	CD70 %	MFI
NK77.11	0	121
NK77.16	0.031	116
NK77.17	0	113
NK77.58	0.28	114
NK77.71	0.031	129
NK71	0.8	192
EPNT	54.6	1201

Week 5 post-transduction

Figures 69A



Week 7 post-transduction

Figures 69B

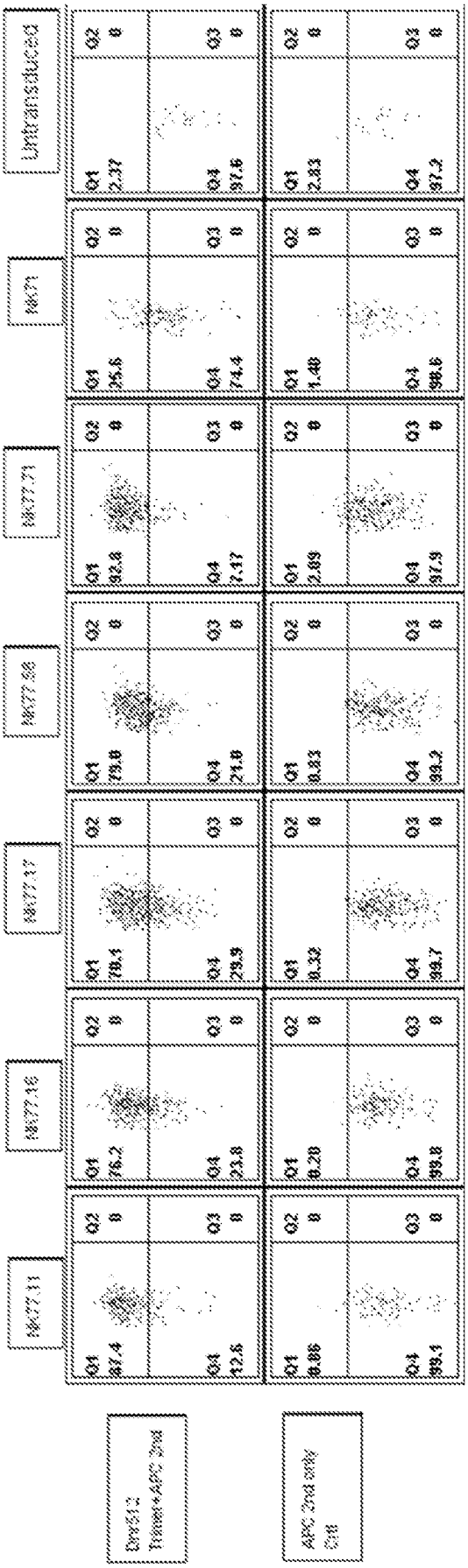

Untransduced
MK77.71
MK77.66
MK77.17
MK77.16
MK77.11
Q1 2.37
Q4 97.6
Q1 1.48
Q4 98.6
Q1 2.89
Q4 97.9
Q1 0.83
Q4 99.2
Q1 0.32
Q4 99.7
Q1 0.20
Q4 99.8
Q1 0.86
Q4 99.1
Week 7 post-transduction

FIG. 69C

Dnr451	viability %	CAR%	MFI
NK77.11	3.06	79.4	15878
NK77.16	9.98	72.7	11274
NK77.17	15.8	59.6	6430
NK77.58	19.9	81	9414
NK77.71	11.3	86.1	17051
NK71	4.91	20.6	792
EPNT	0	0	0
Dnr 512			
NK77.11	27.5	87.4	10774
NK77.16	33.8	76.2	8595
NK77.17	63	70.1	7270
NK77.58	59.2	79	6404
NK77.71	51.3	92.8	12061
NK71	5.14	25.6	511
EPNT	0.26	2.37	164

FIG. 69D

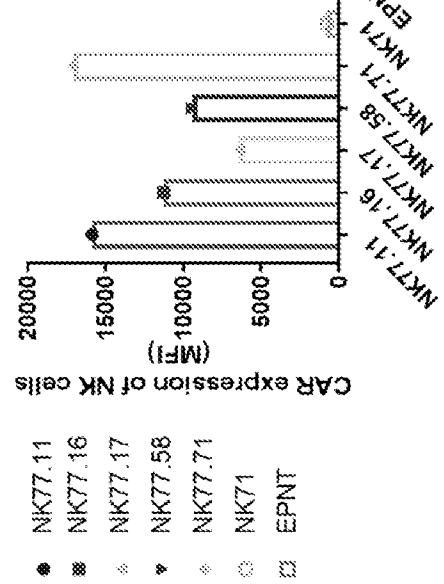
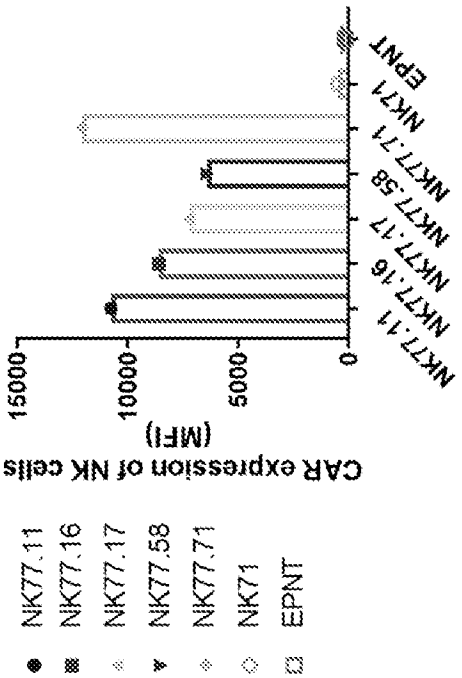
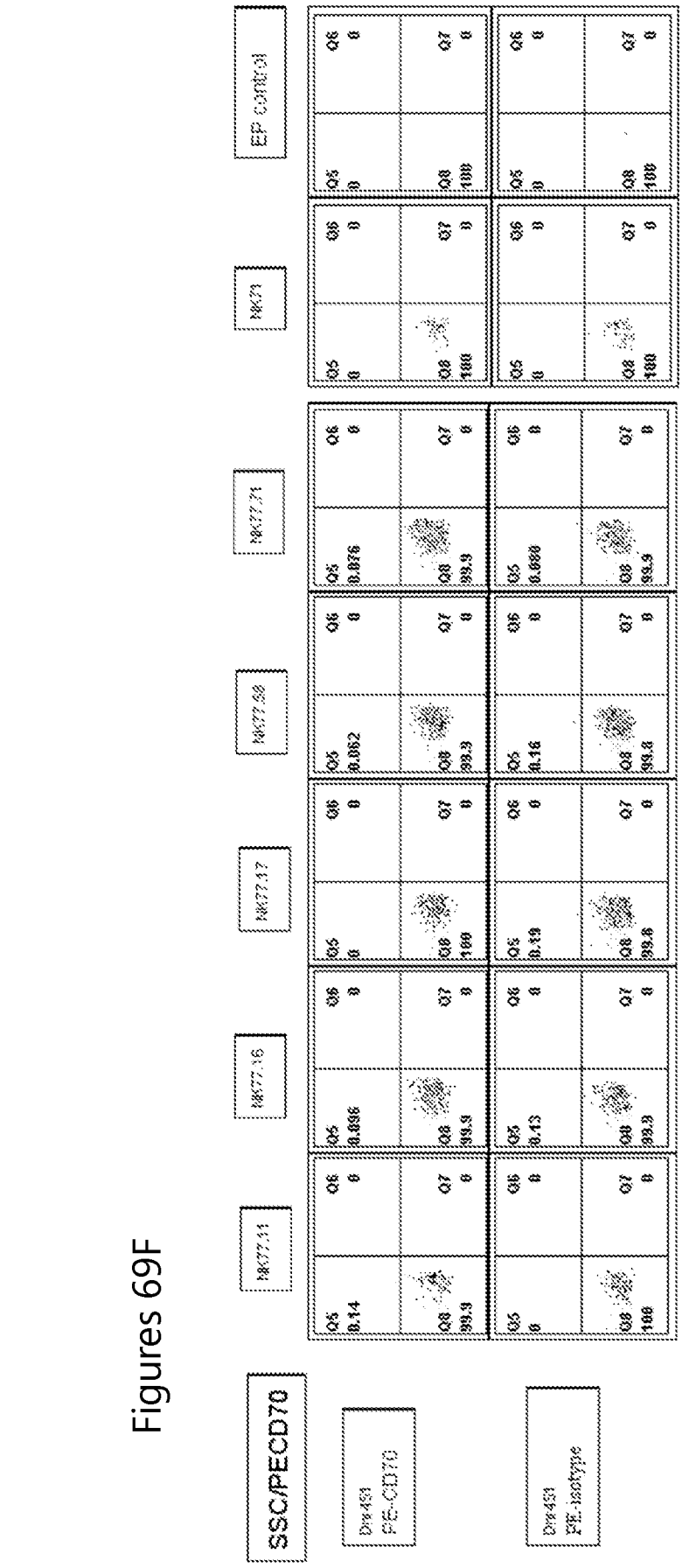


FIG. 69E



Week 7 post-transduction

Figures 69F


SSC/PECD70
Dm451
PE-CD70
Dm451
PE-isotype
NK77.11
NK77.16
NK77.17
NK77.69
NK77.71
NK73
EP control
Week 7 post-transduction

Figures 69G

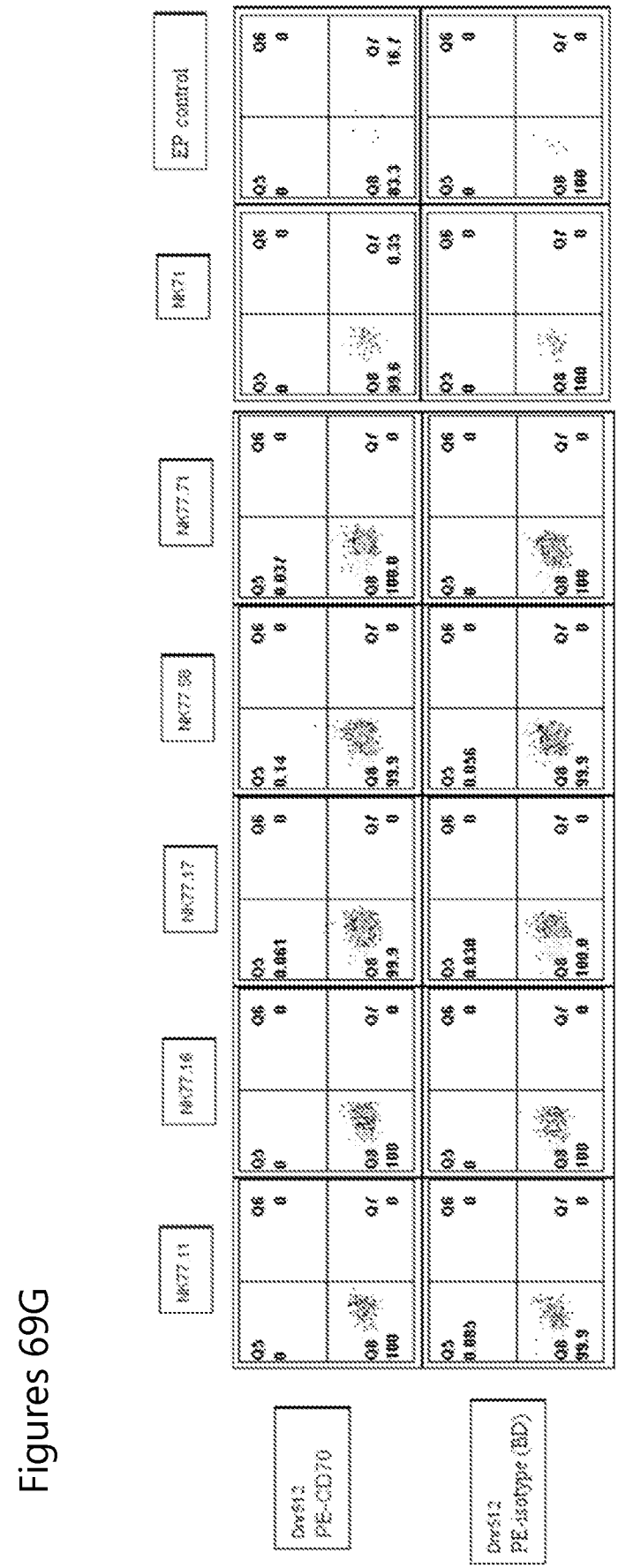


Figure 69H

Dnr451	CD70%	MFI
NK77.11	0	87.9
NK77.16	0	96.6
NK77.17	0	97.6
NK77.58	0	98.1
NK77.71	0	93.6
NK71	0	86.9
EPNT	0	45.4
Dnr 512		
NK77.11	0	82.9
NK77.16	0	91.3
NK77.17	0	87.8
NK77.58	0	88.3
NK77.71	0	88.4
NK71	0.35	115
EPNT	16.7	295

Week 7 post-transduction

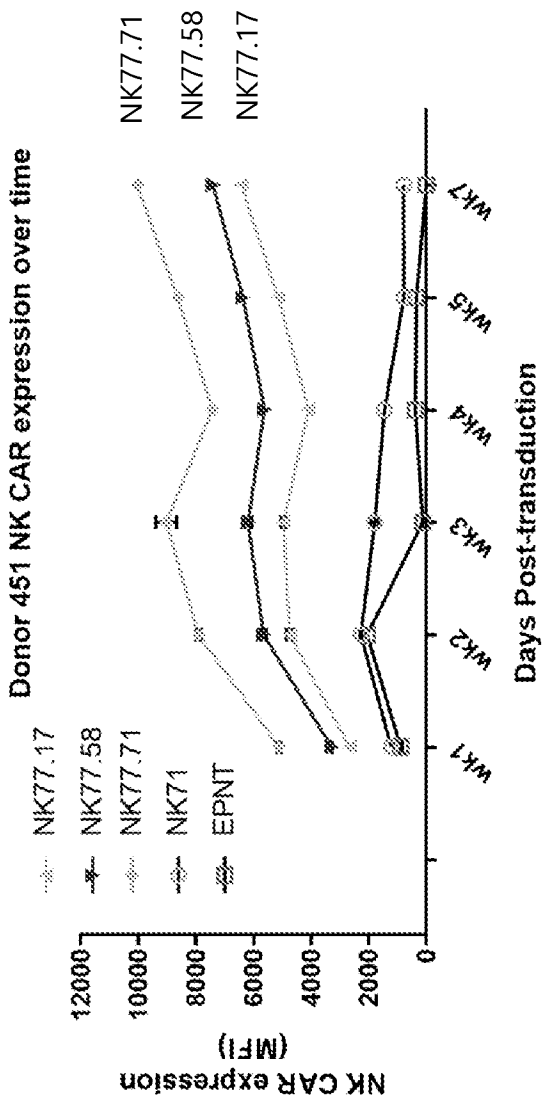


FIG. 70A

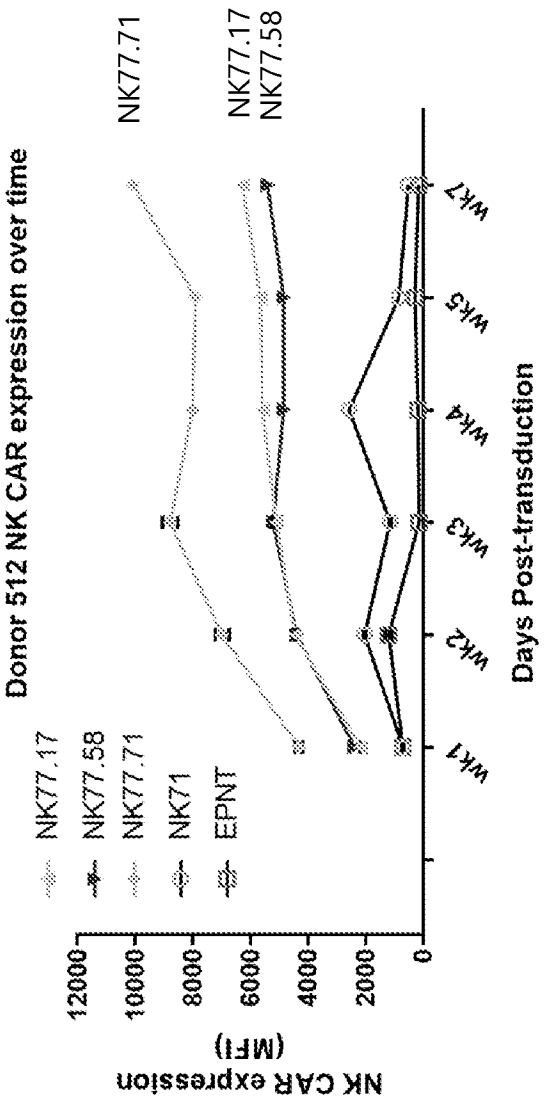


FIG. 70B

FIG. 71A

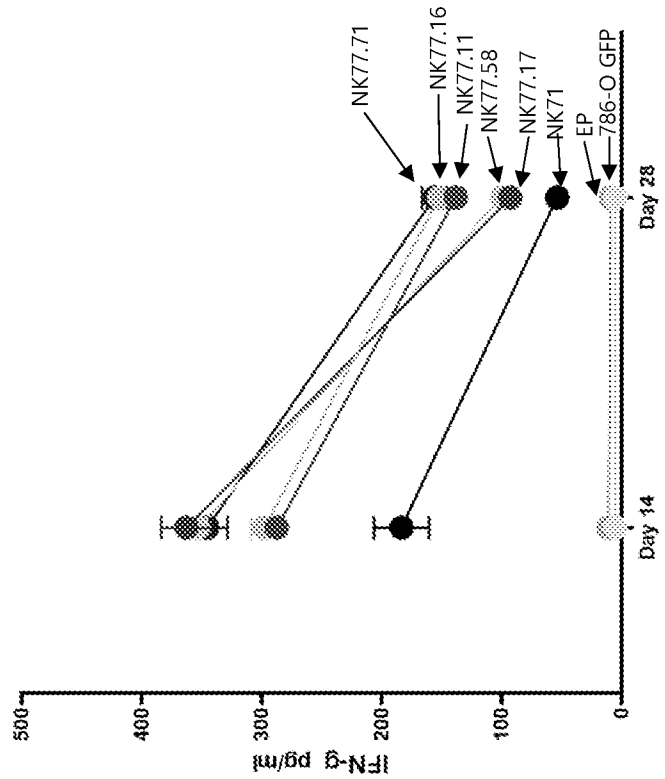


FIG. 71B

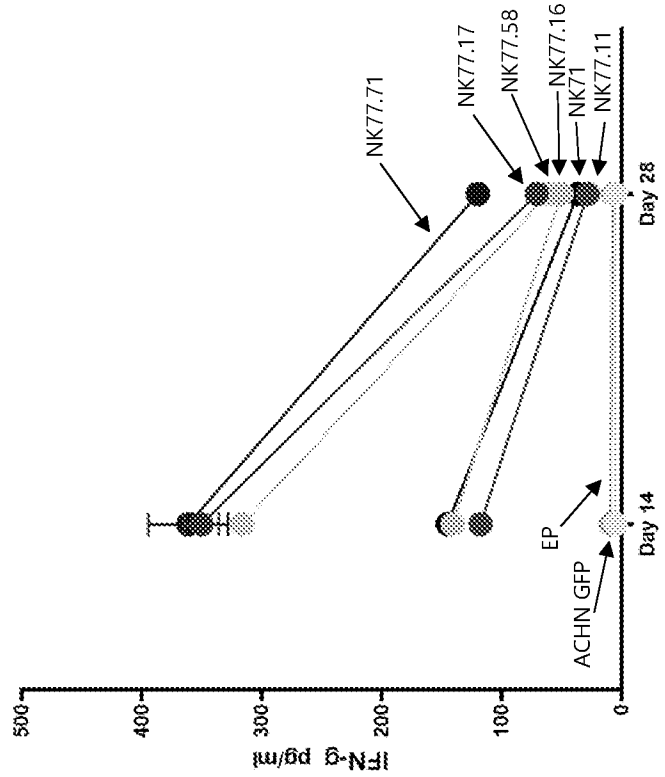


FIG. 71C

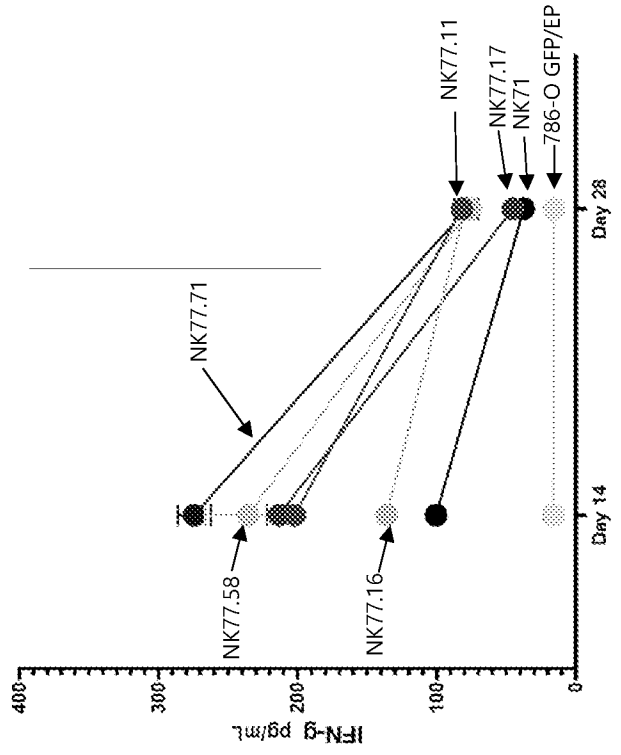


FIG. 71D

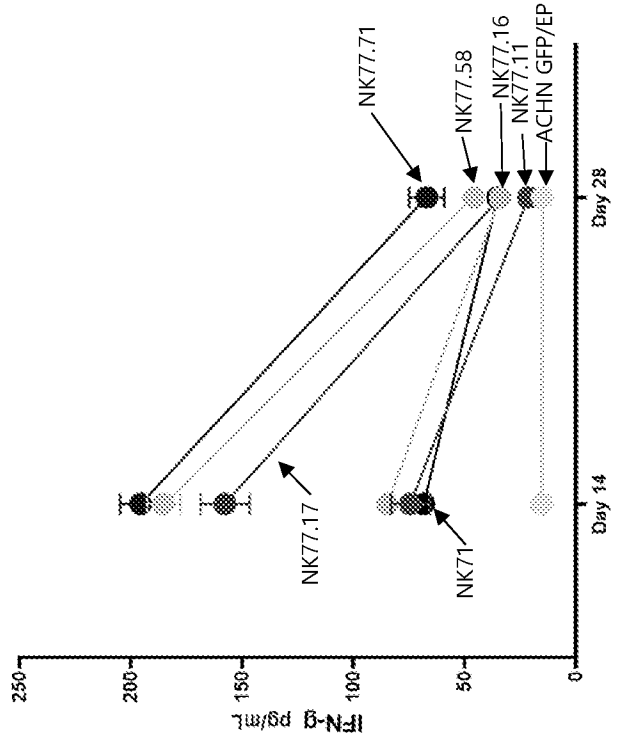


FIG. 71E

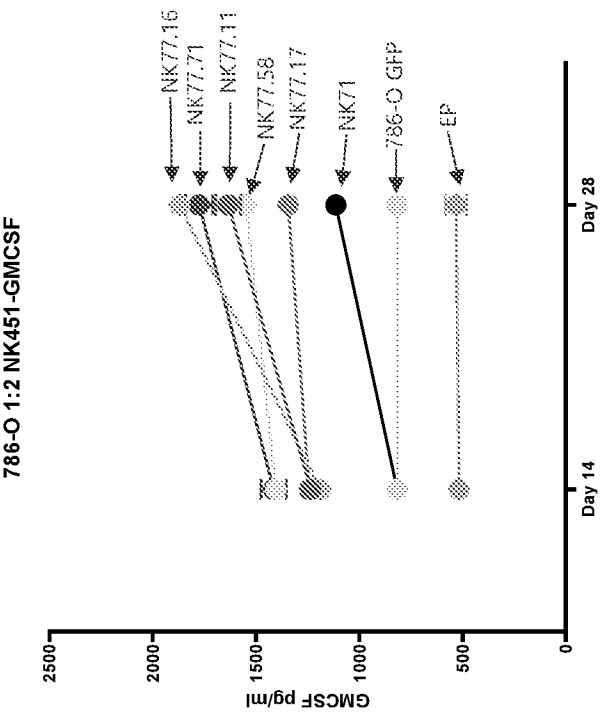


FIG. 71F

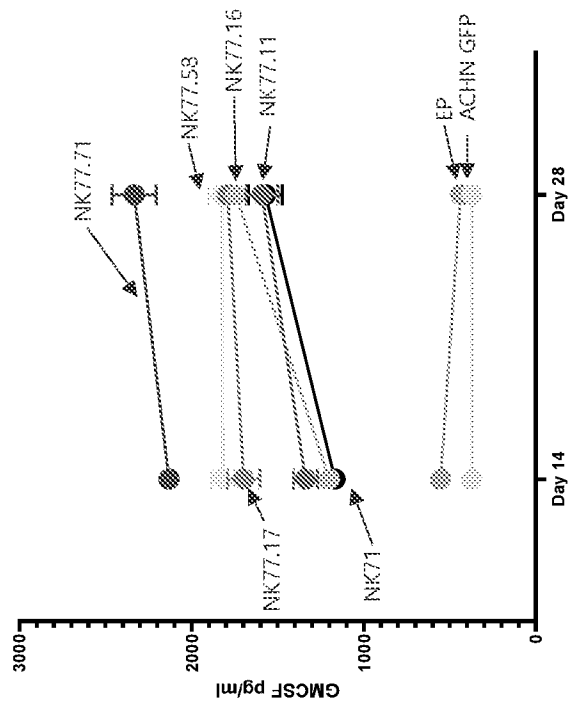


FIG. 71G

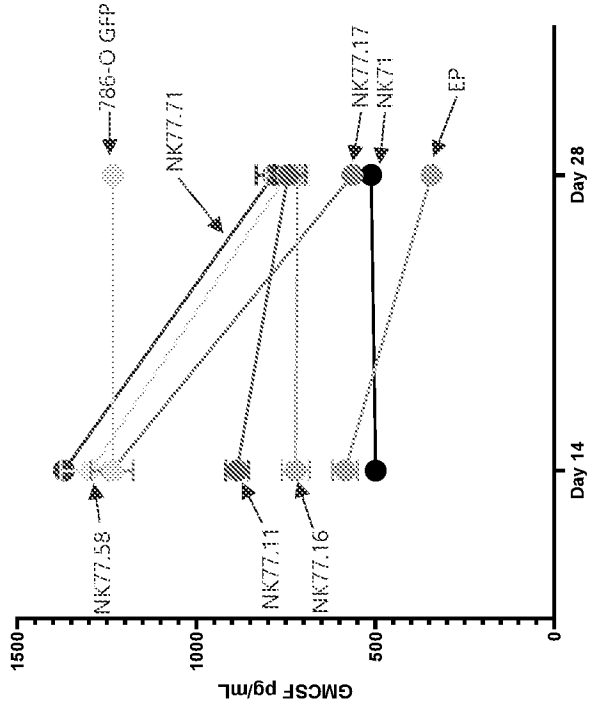
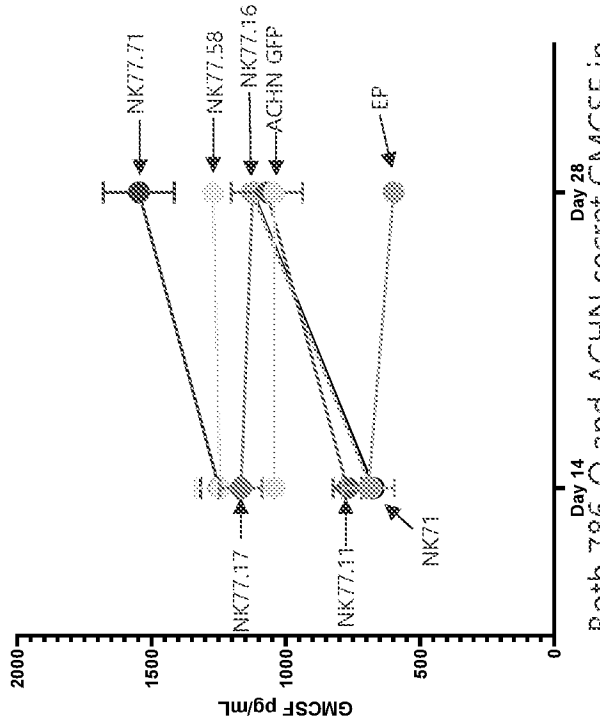


FIG. 71H



Both 786-O and ACHN secret GMCSF in vitro.

GMCSF secretion of NK451 increased slightly from day14 to day 28 while it decreased in the co-culture of NK512 and 786-O.

Nk77.71, 58 and 17 CAR NK cells are the top 3 producing GMCSF at day3 during co-culture with 786-O or ACHN

FIG. 71I

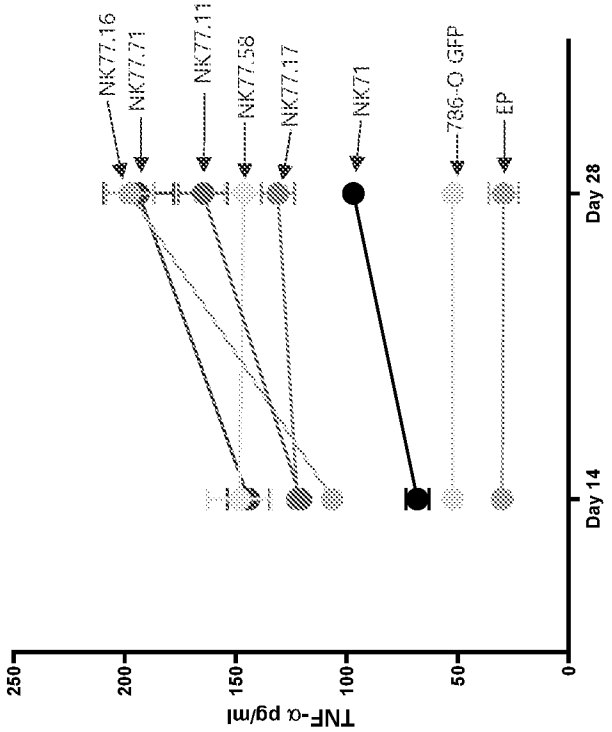
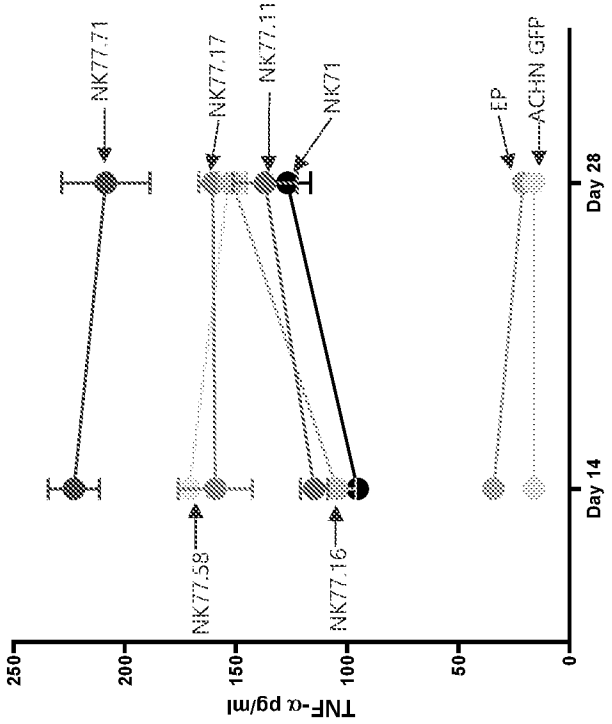


FIG. 71J



Both 786-O and ACHN secret TNF-a in vitro.

TNF-a secretion of NK451 was stable or increased slightly from day14 to day 28 while it decreased in the co-culture of NK512 and 786-O.

NK77.71, 58 and 17 CAR NK cells are the top 3 producing TNF-a at day3 during co-culture with 786-O or ACHN

FIG. 71K

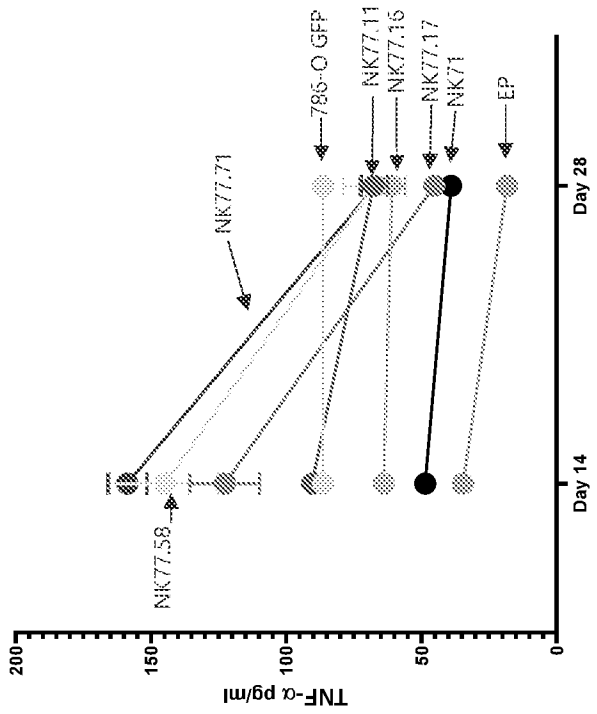


FIG. 71L

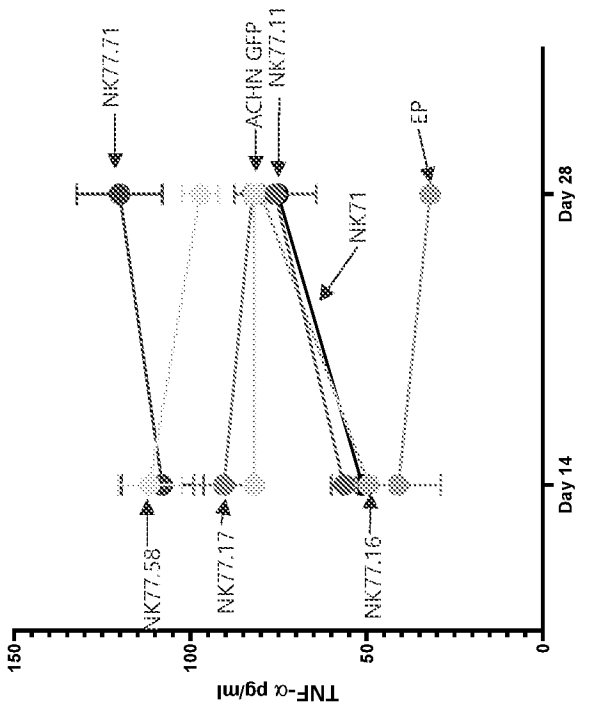


FIG. 71N

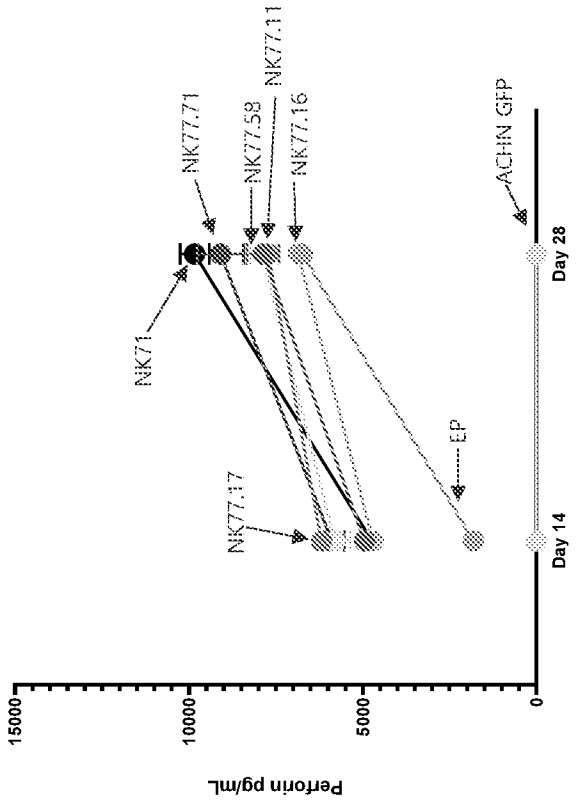


FIG. 71M

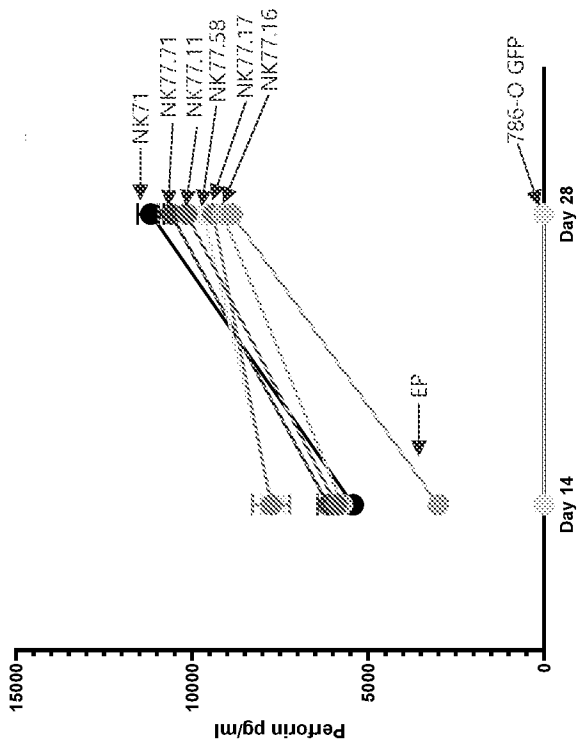


FIG. 71O

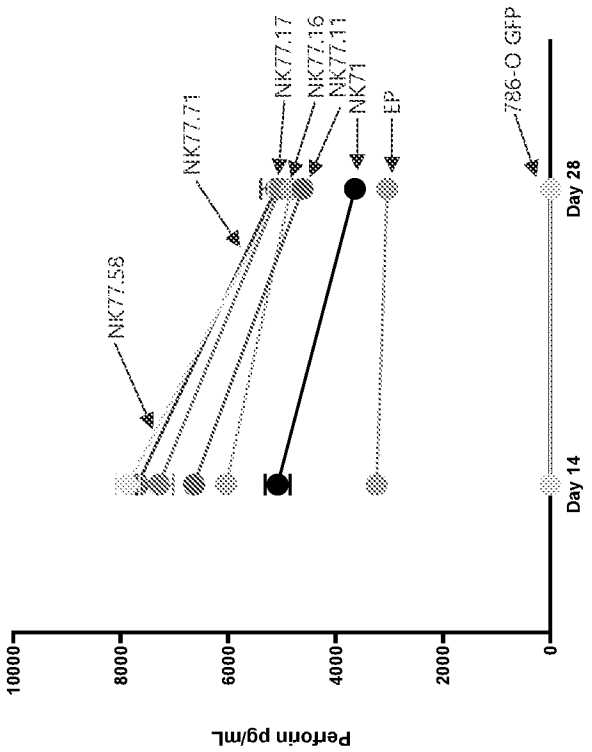


FIG. 71P

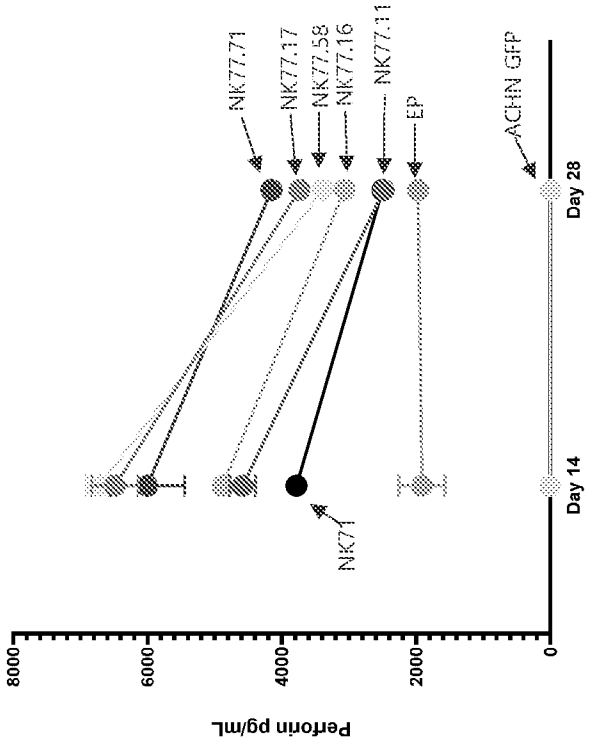


FIG. 71R

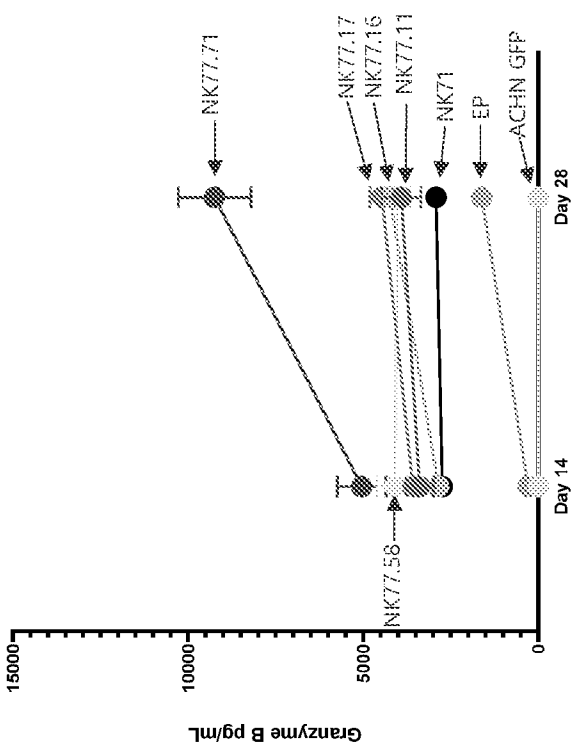


FIG. 71Q

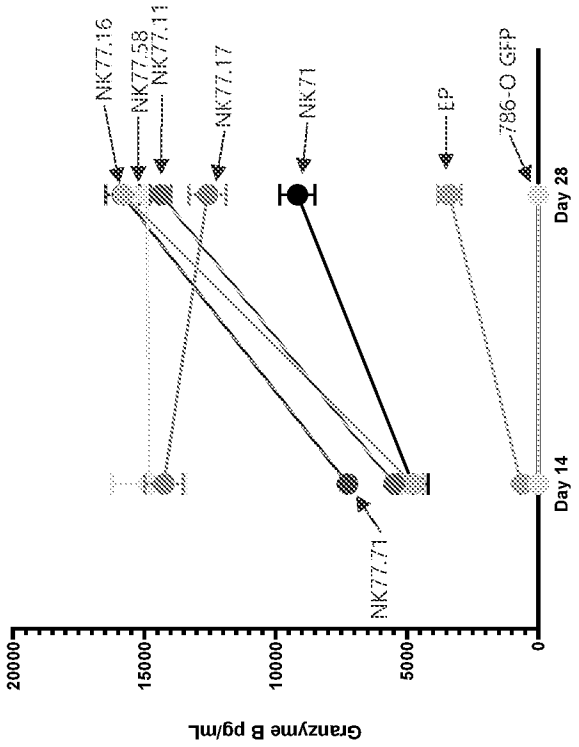


FIG. 71S

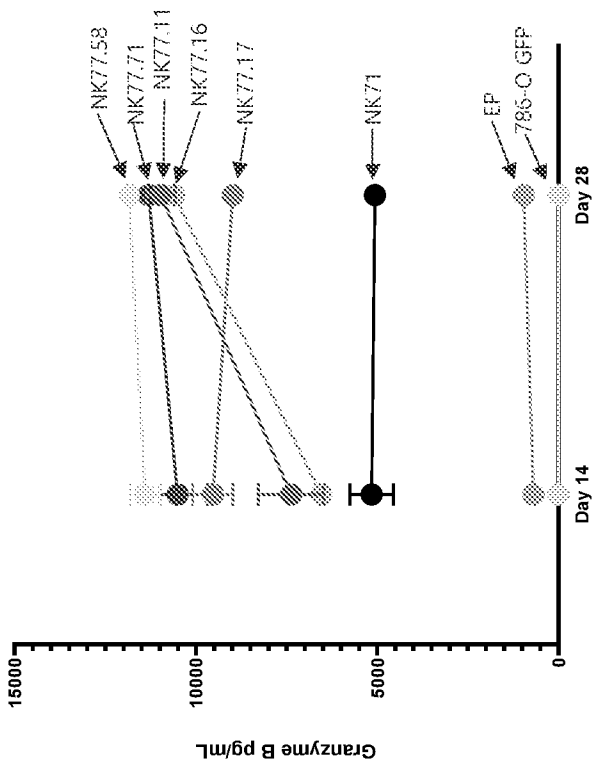
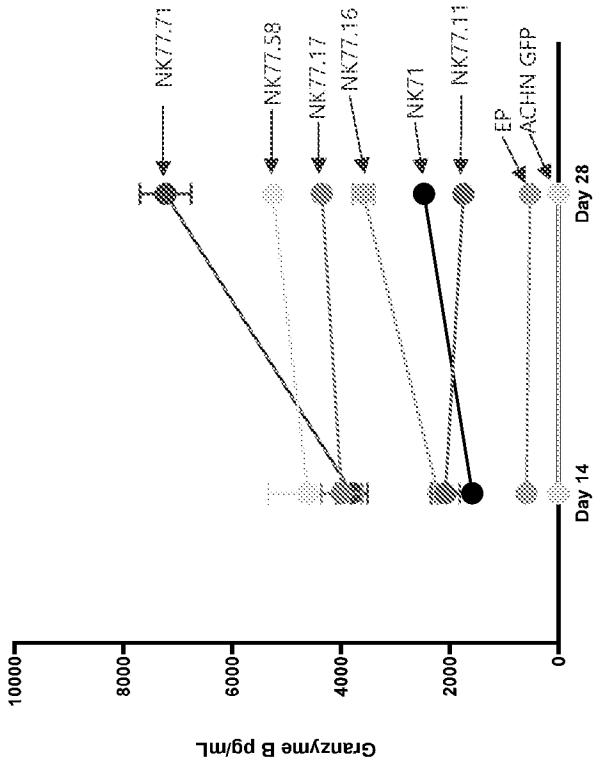


FIG. 71T



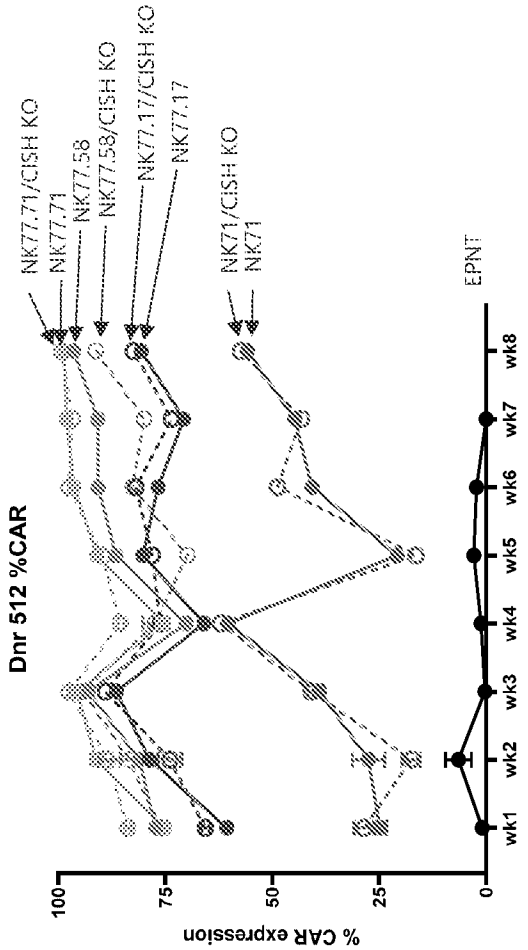


FIG. 72A

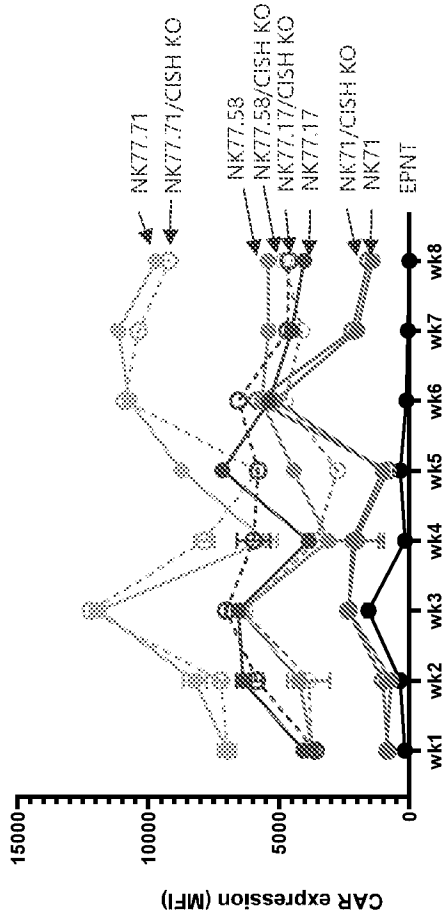


FIG. 72B

Figure 72C

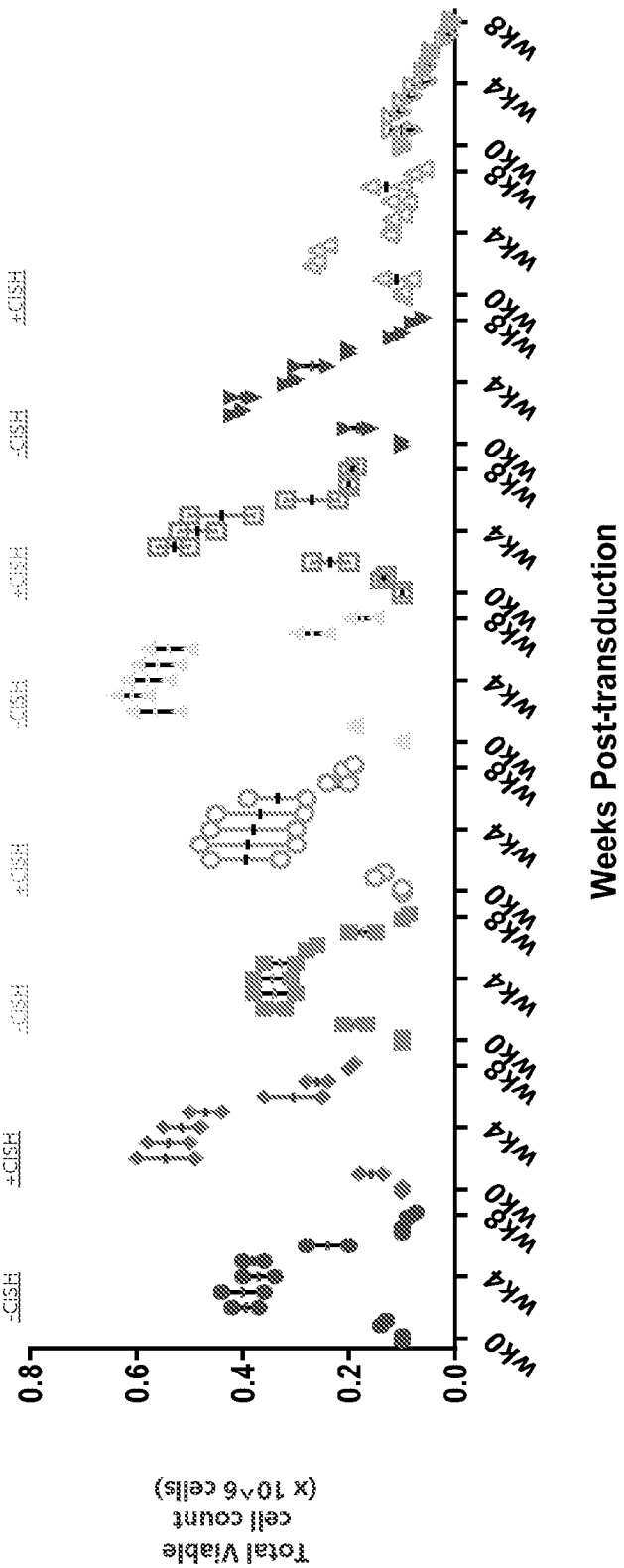
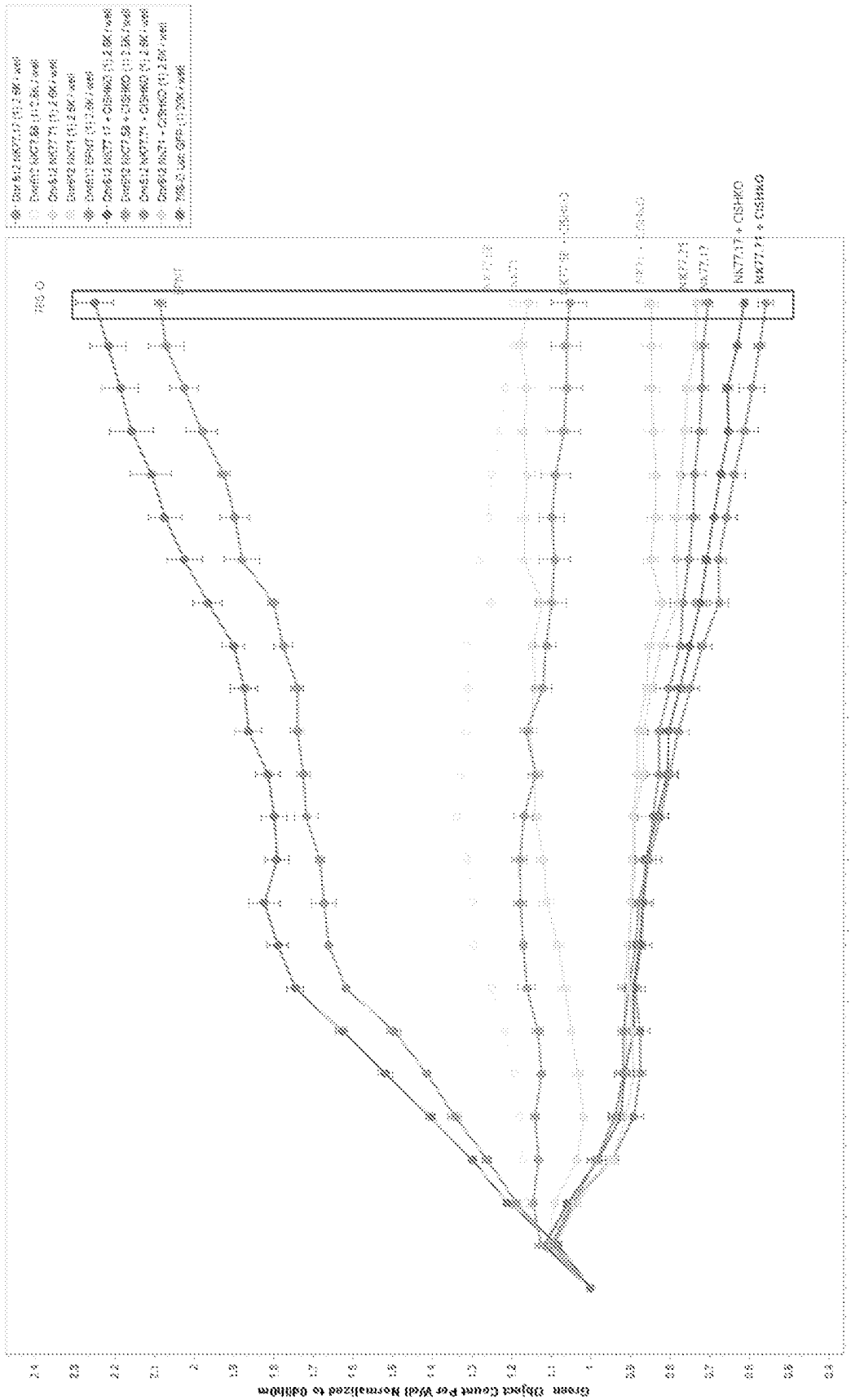
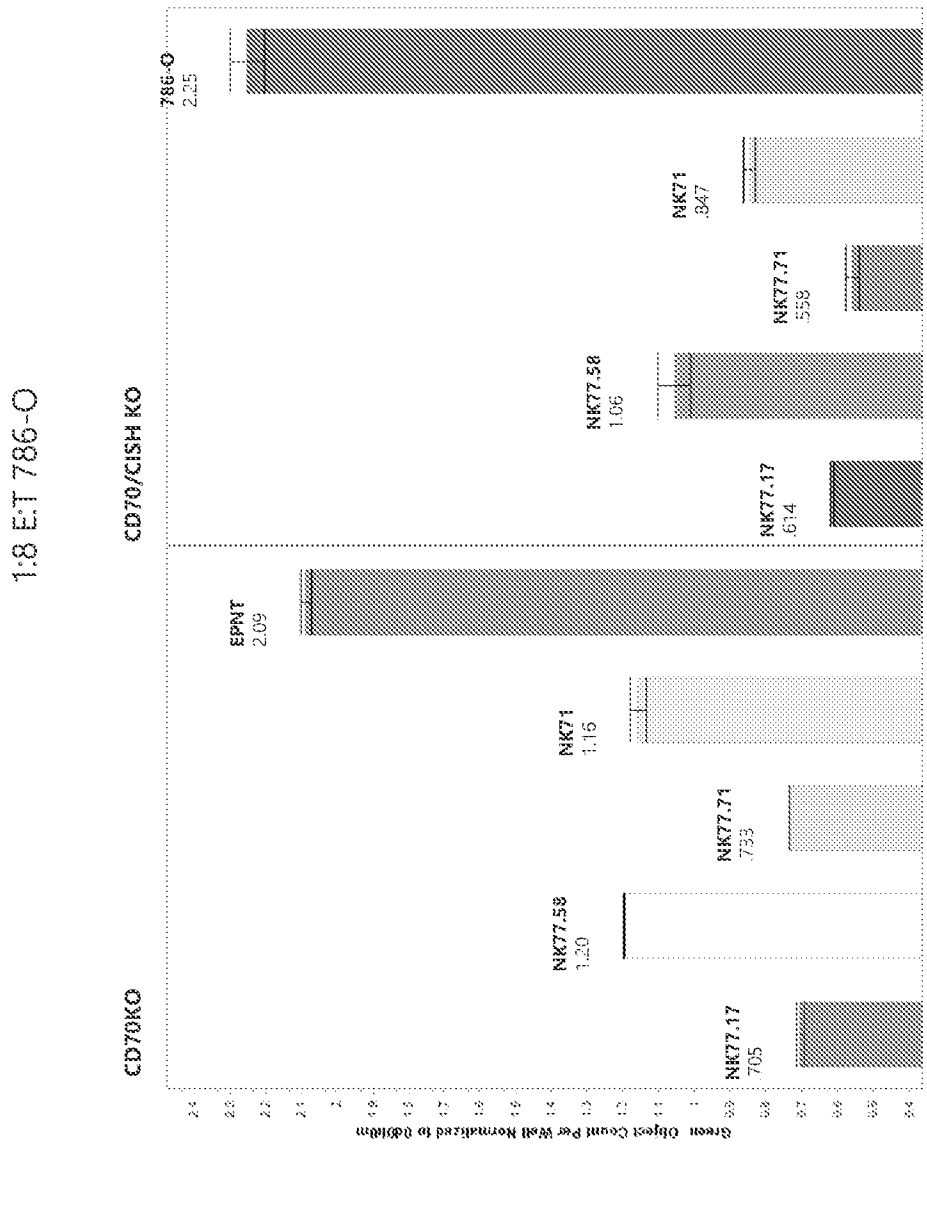

Donor 512 NK cell count CD70 CAR
NK77.17
-CISH
±CISH
NK77.58
-CISH
±CISH
NK77.71
-CISH
±CISH
NK71
-CISH
±CISH
EPNT
Total Viable cell count (x 10^6 cells)
0.0
0.2
0.4
0.6
0.8
Wk0
Wk4
Wk8
Weeks Post-transduction

Figure 72D



Dnr512
Normalized to 100% CAR
Day 14

Figure 72E



Dnr512
Normalized to 100% CAR
Day 14

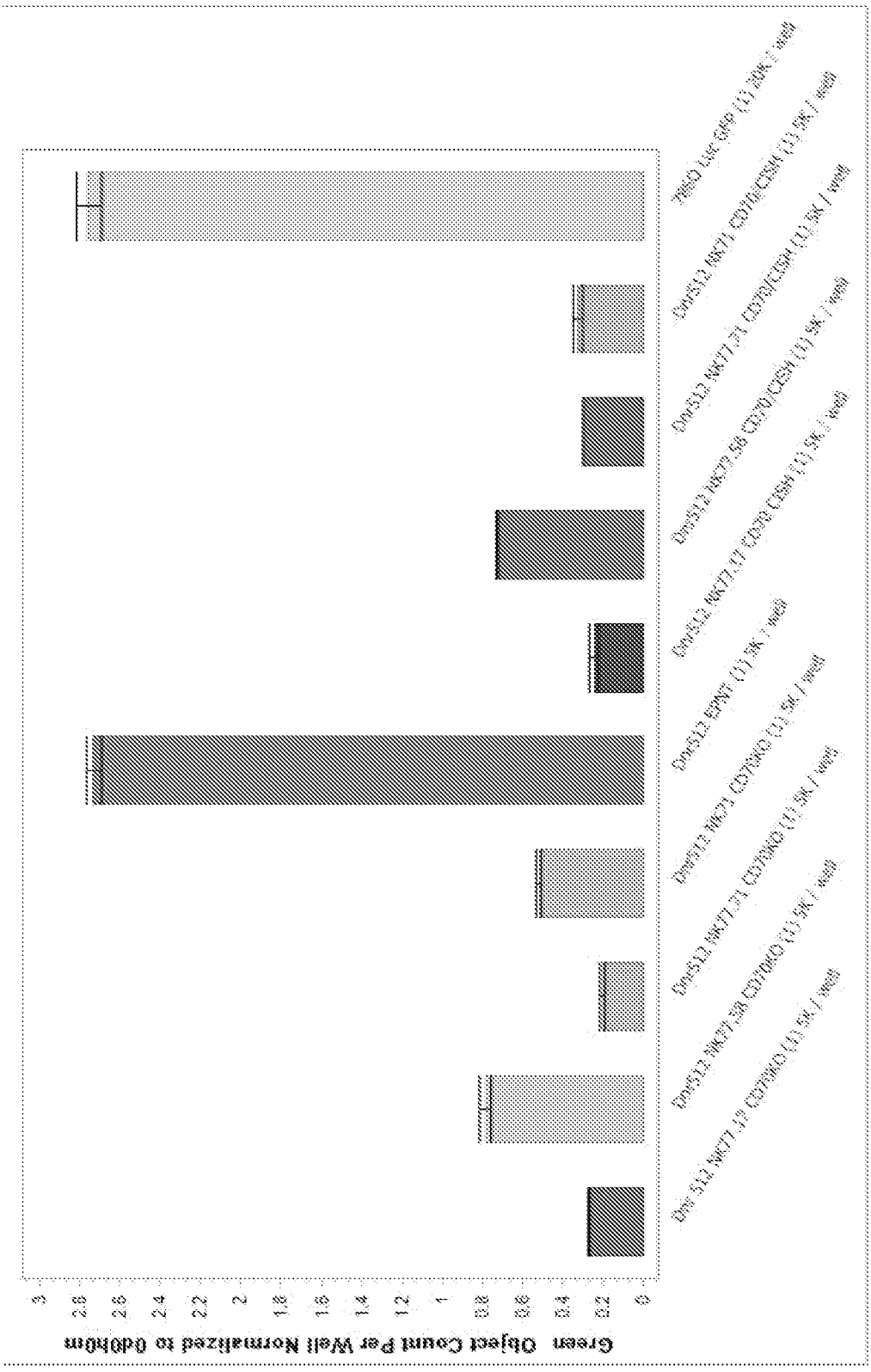
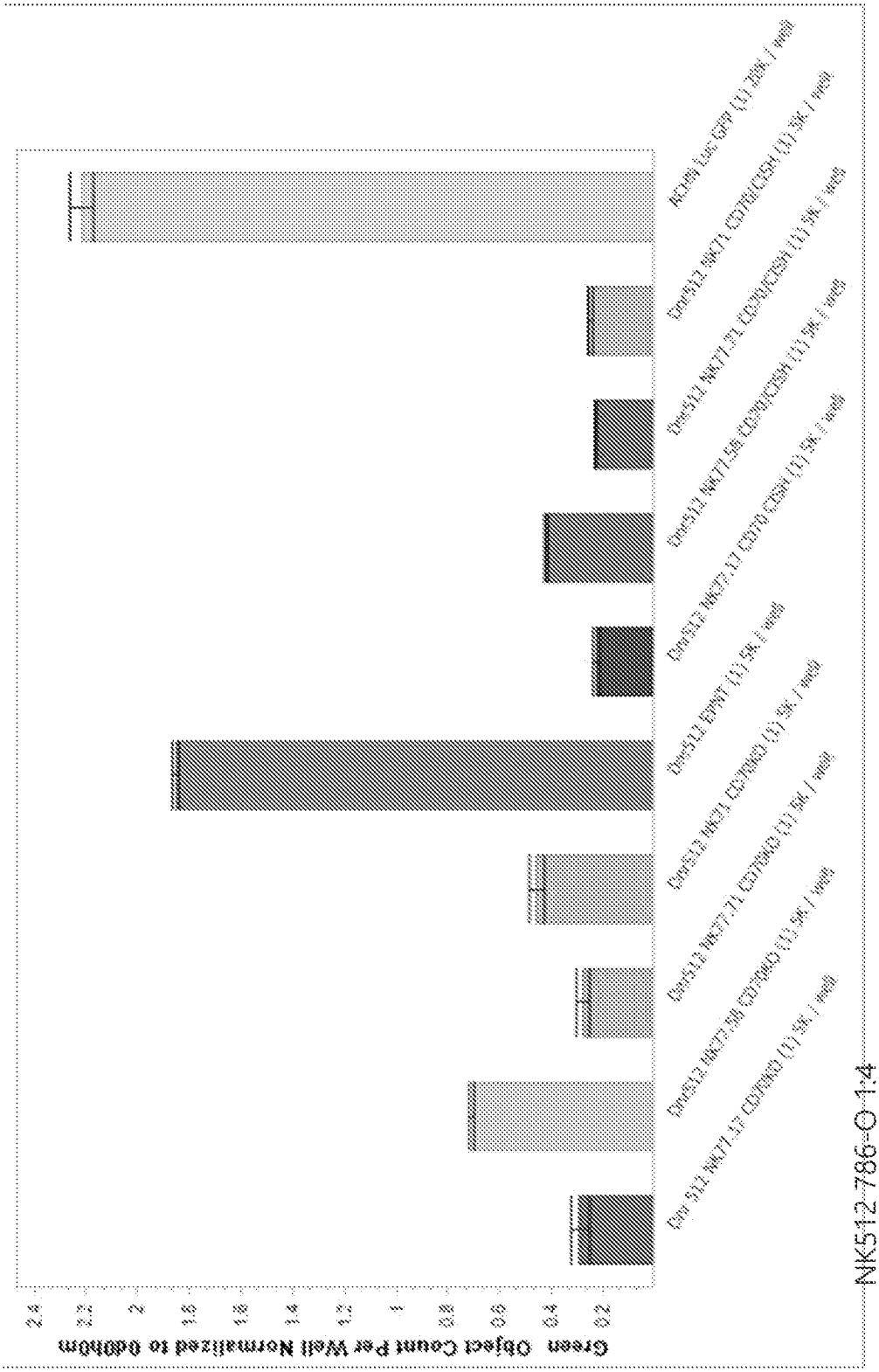


Figure 72F

NK512 ACHN-O 1:4

Figure 72G


Green Object Count Per Well Normalized to 0dnbm
2.4
2.2
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
Dnr 513 NK71.17 CD70KO (1) 5K / well
Dnr513 NK27.58 CD70KO (1) 5K / well
Dnr513 NK27.71 CD70KO (1) 5K / well
Dnr513 NK21 CD70KO (1) 5K / well
Dnr513 EPNT (1) 5K / well
Dnr513 NK27.17 CD70 CISH (1) 5K / well
Dnr513 NK27.58 CD30 CISH (1) 5K / well
Dnr513 NK27.71 CD30/CISH (1) 5K / well
Dnr513 NK71.71 CD70/CISH (1) 5K / well
NC196 Luc GFP (1) 75K / well
NK512 786-O 1:4

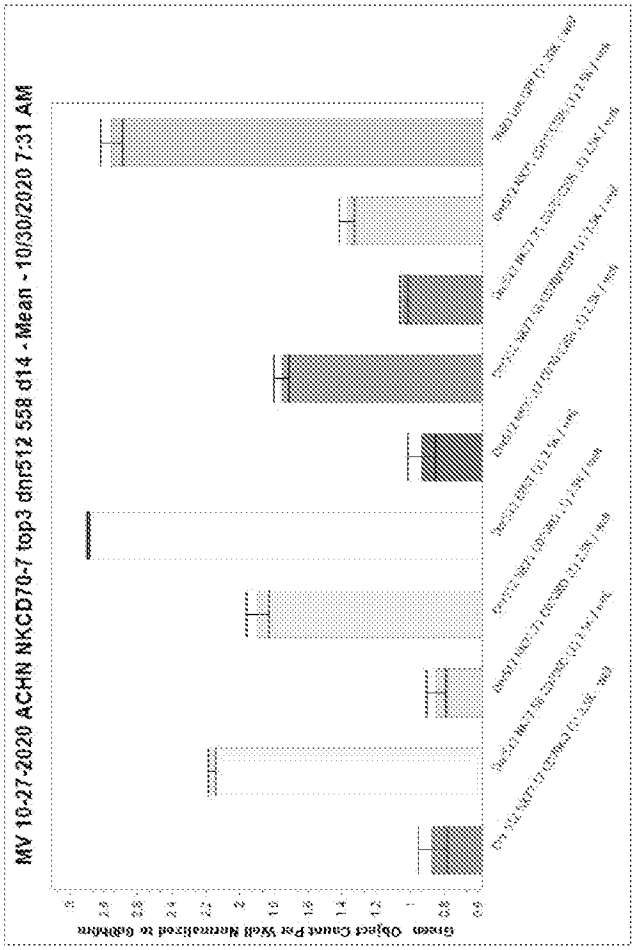


FIG. 72H

NK512 ACHN 1:8

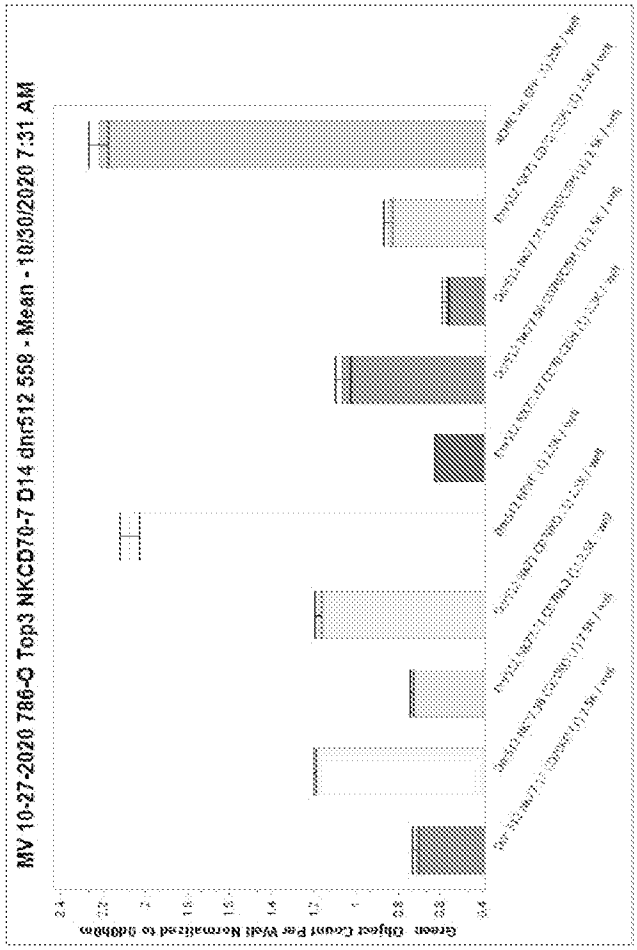


FIG. 72I

NK512 786-O 1:8

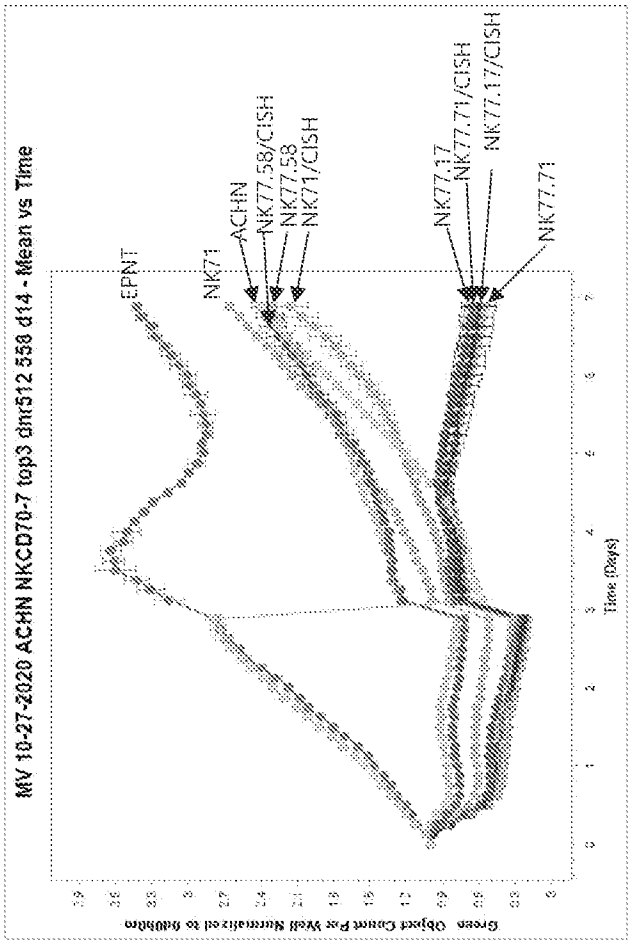


FIG. 72J

NK512 ACHN-O 1:4

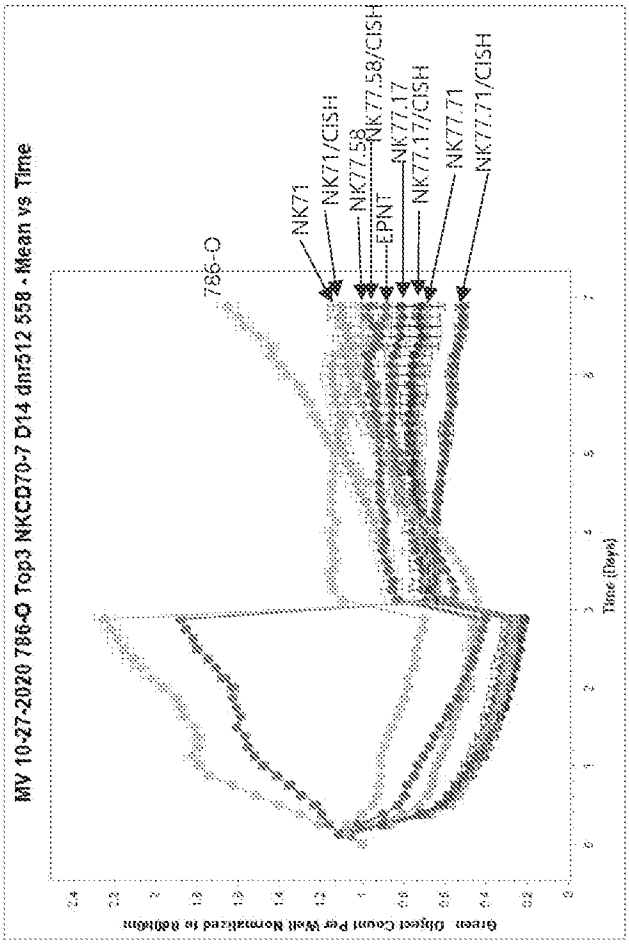


FIG. 72K

NK512 786-O 1:4

5K cells/well
for all Tx and
EPNP
20K for tumor
alone

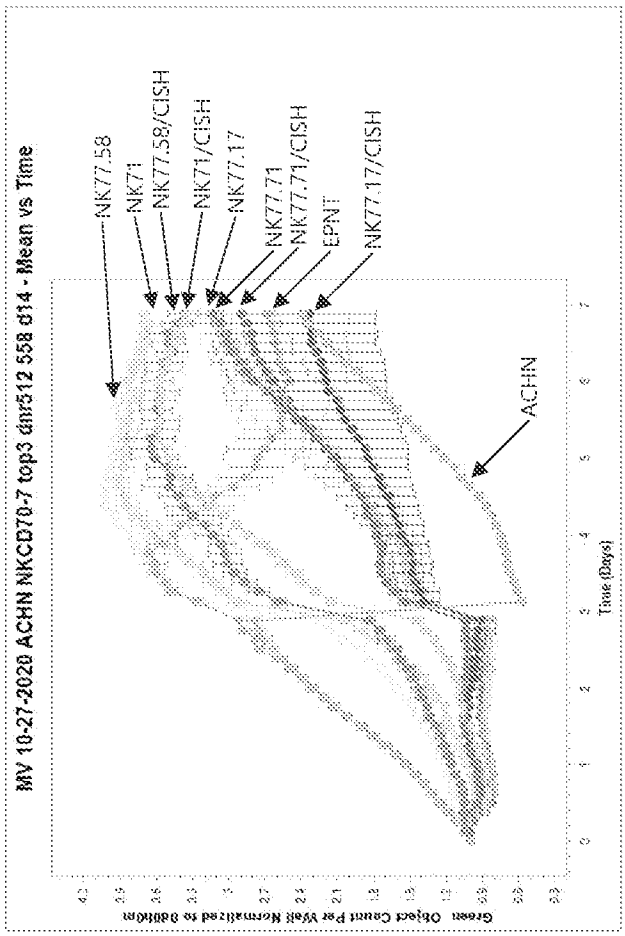


FIG. 72L

NK512 ACHN 1:8

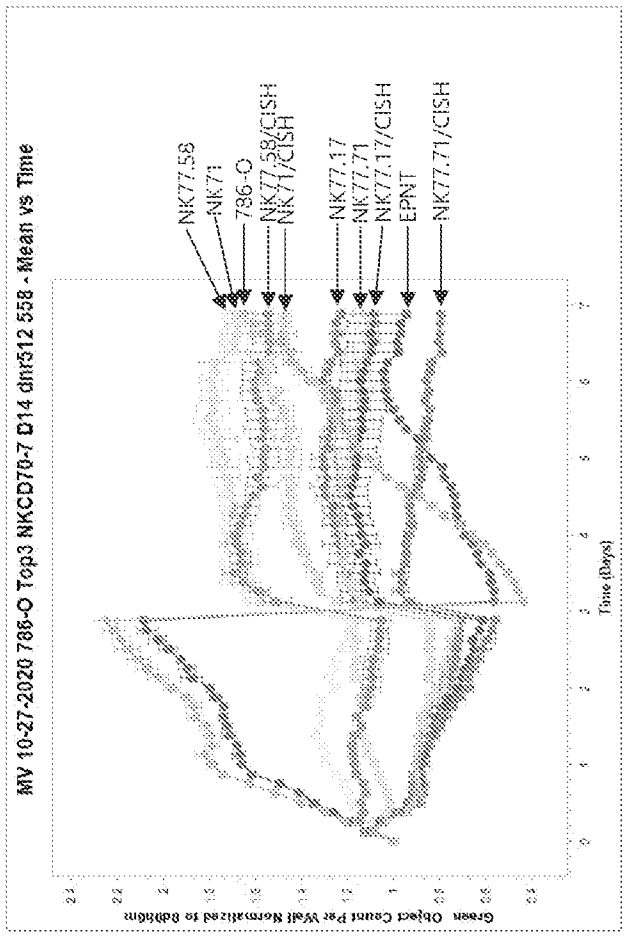


FIG. 72M

NK512 786-O 1:8

2.5K cells/well
for all Tx and
EPNP
20K for tumor
alone

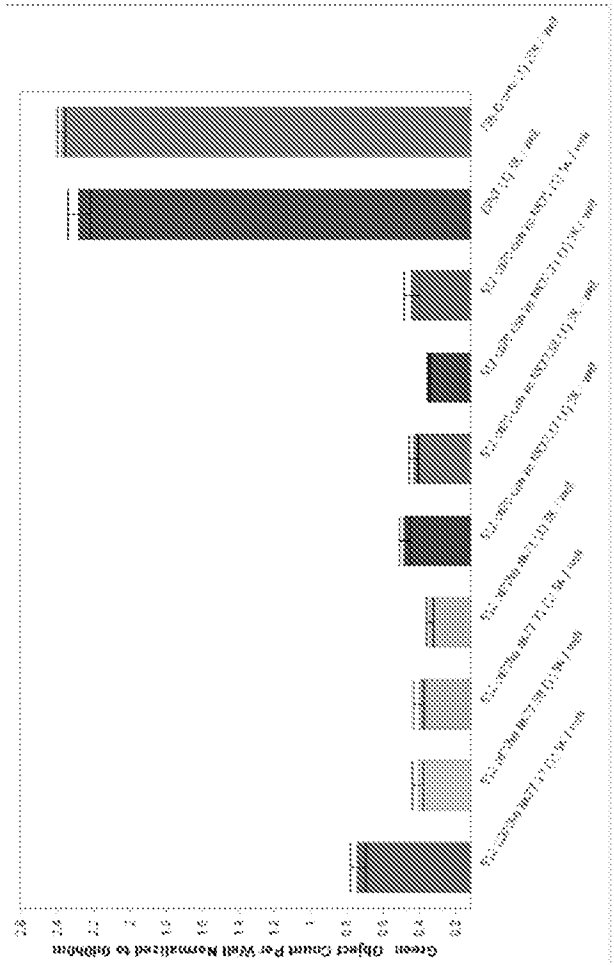


FIG. 73A

D21 786-O

72h 1 to 4 (prior to rechallenge)

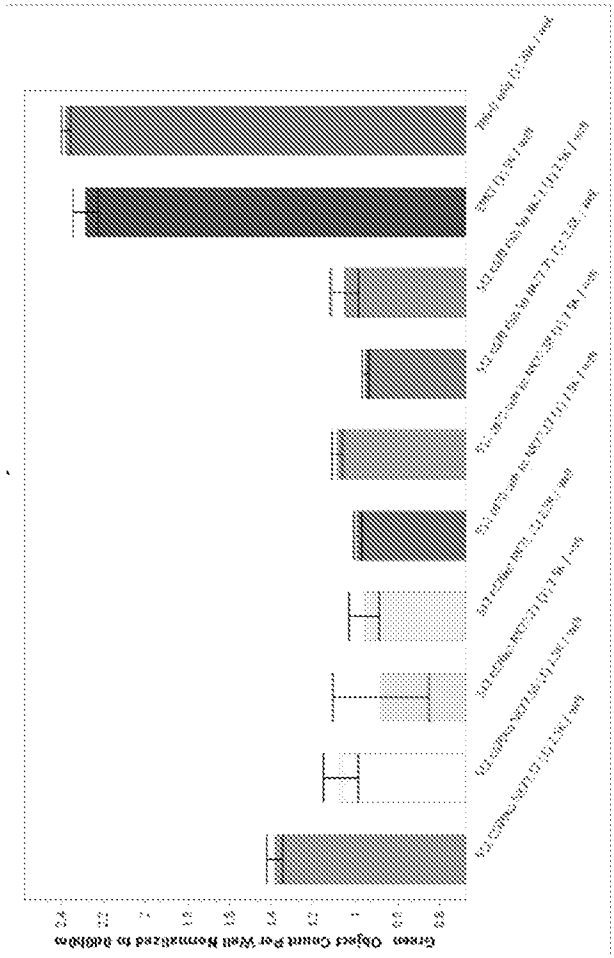


FIG. 73B

72h 1 to 8 (prior to rechallenge)

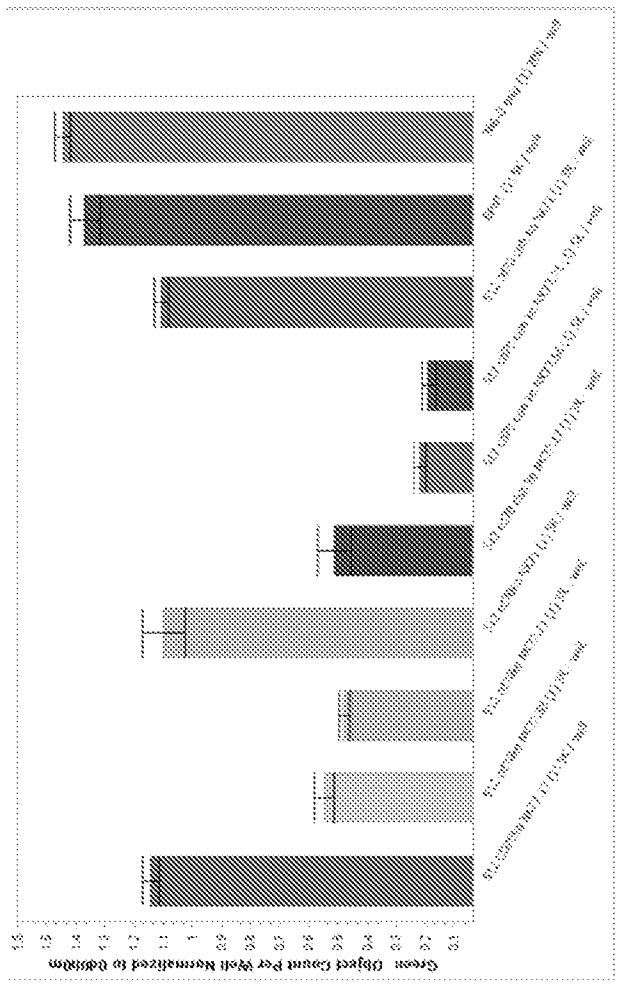


FIG. 73C

D21 786-O

Post rechallenge D6 1 to 4

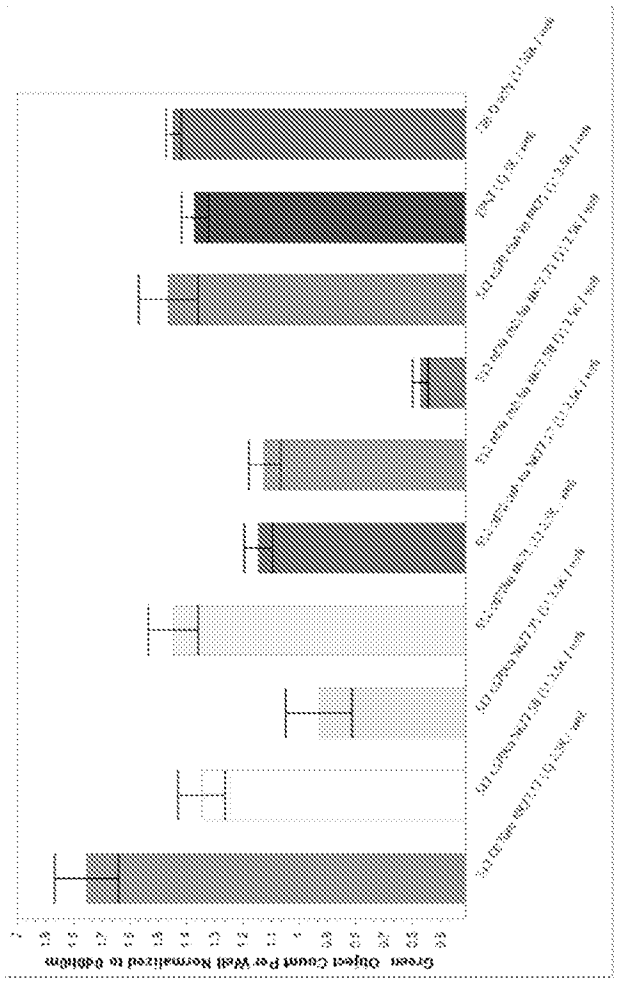


FIG. 73D

Post rechallenge D6 1 to 8

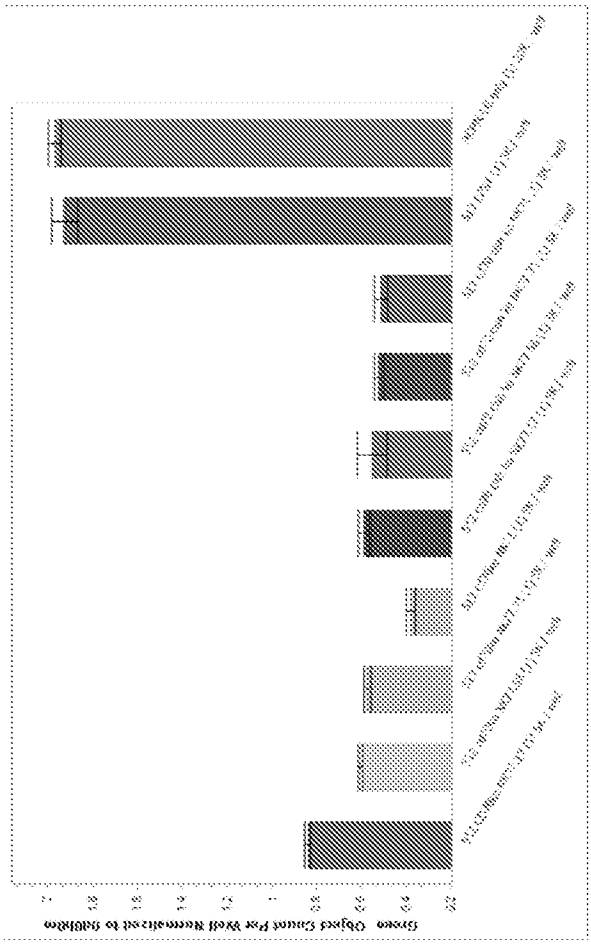


FIG. 73E

D21 ACHN

72h 1 to 4 (prior to rechallenge)

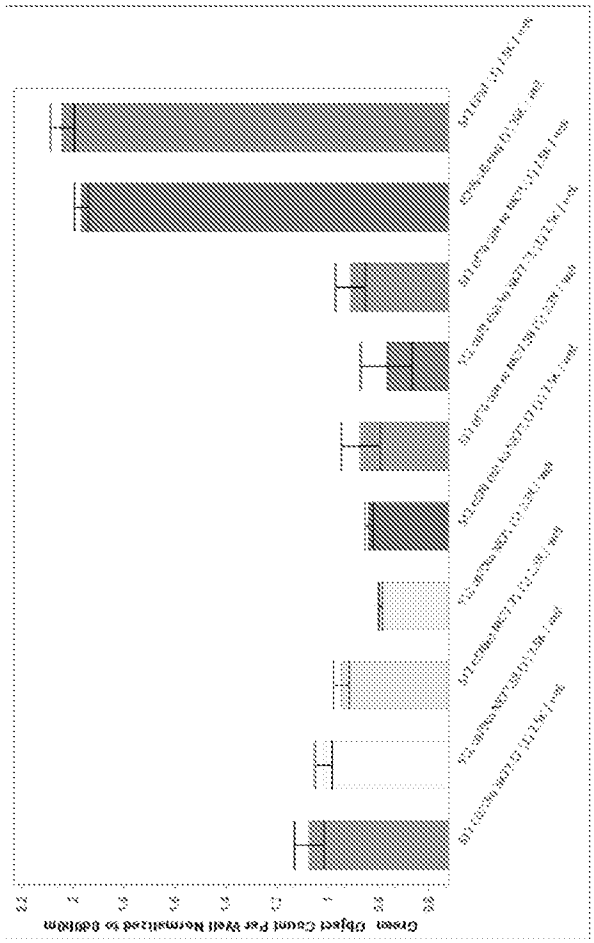


FIG. 73F

72h 1 to 8 (prior to rechallenge)

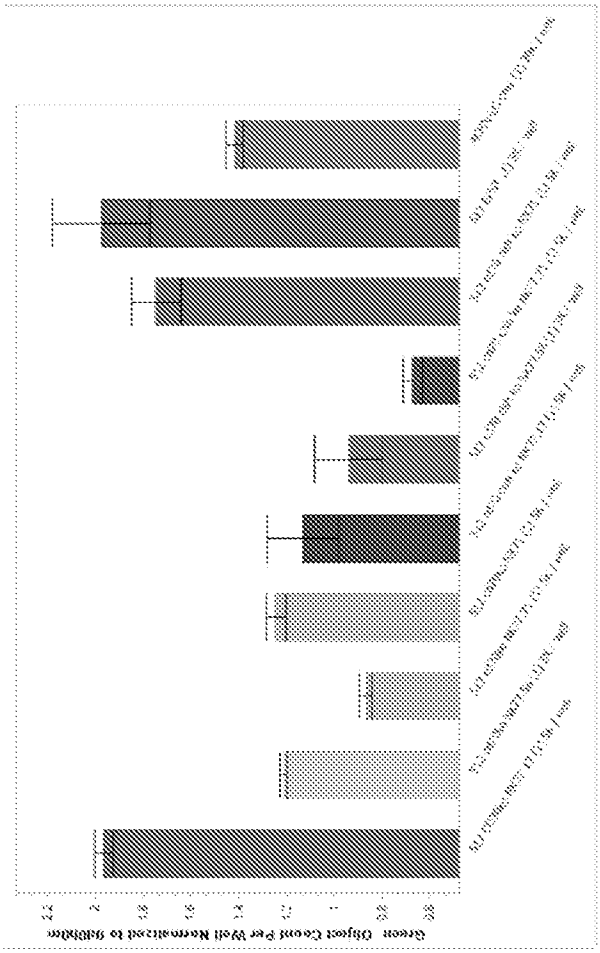


FIG. 73G

D21 ACHN

Post rechallenge
D6 1 to 4

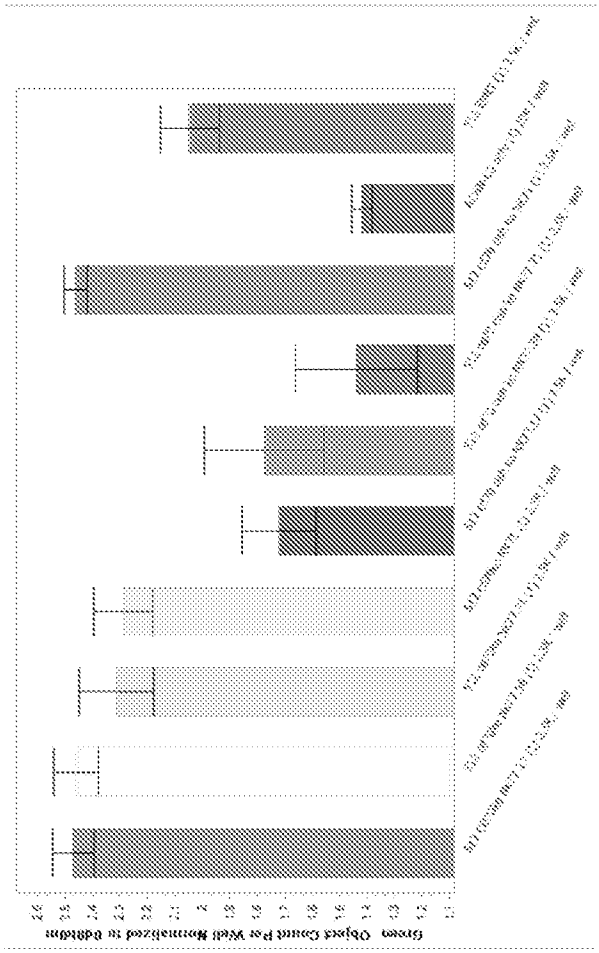


FIG. 73H

Post rechallenge
D6 1 to 8

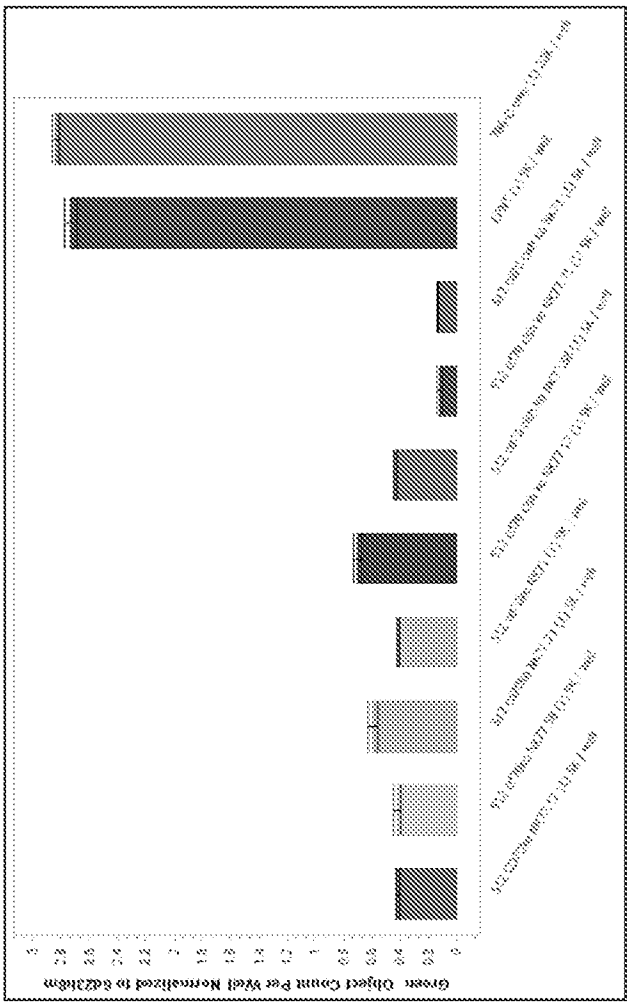


FIG. 74A

D28 786-O

72h 1 to 4
(prior to
rechallenge)

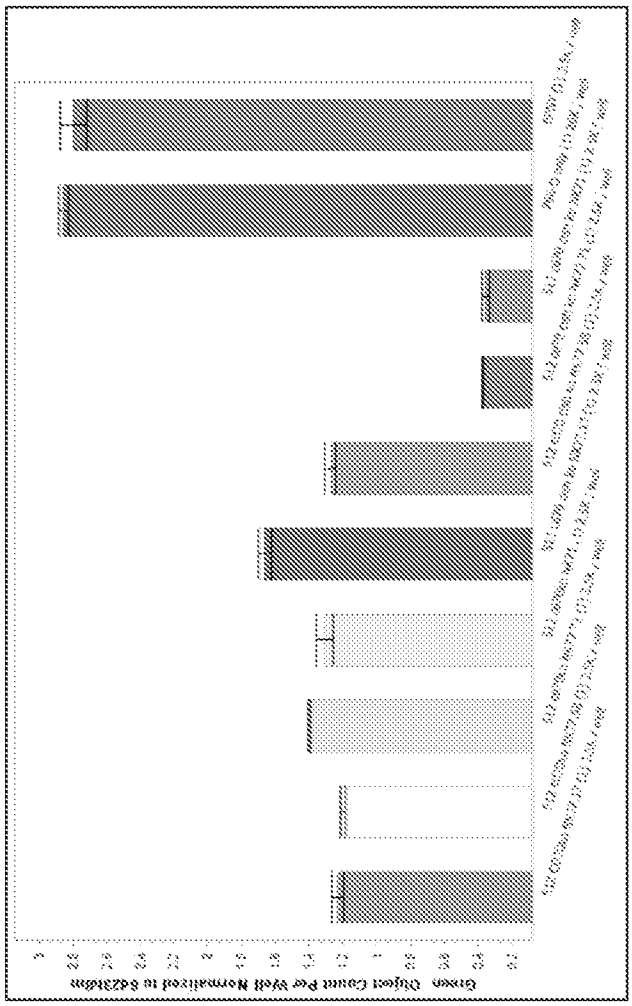


FIG. 74B

72h 1 to 8
(prior to
rechallenge)

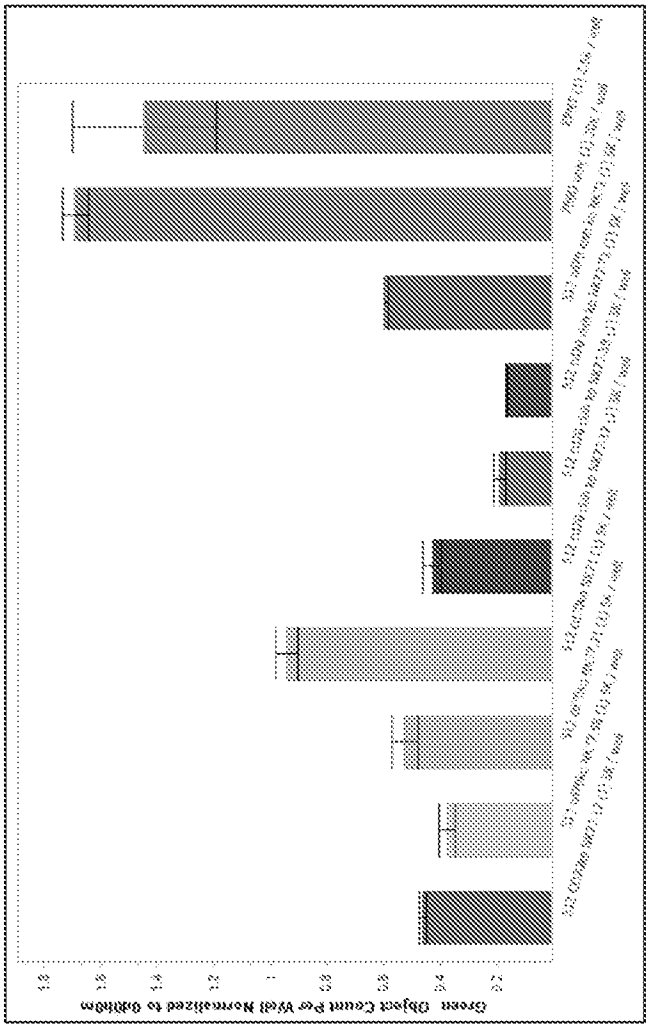


FIG. 74C

D28 786-O

Post rechallenge
D6 1 to 4

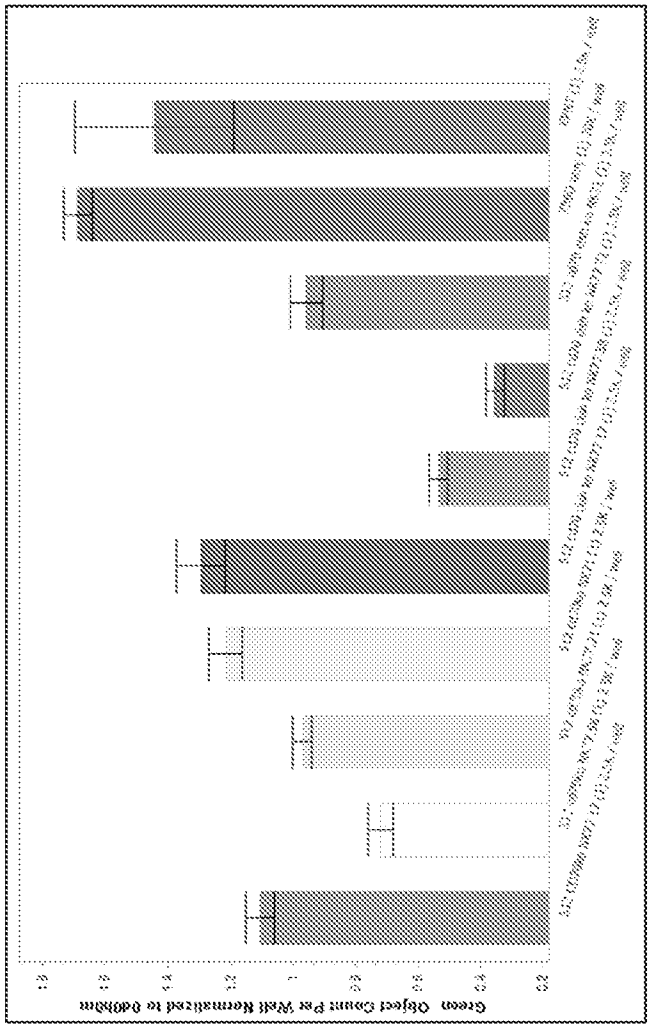


FIG. 74D

Post rechallenge
D6 1 to 8

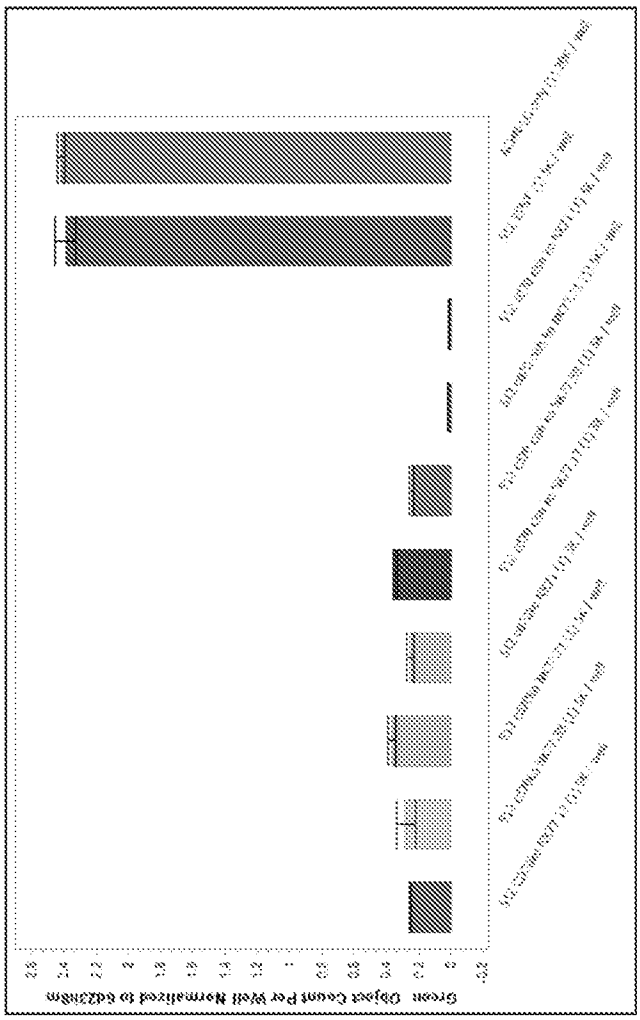


FIG. 74E

D28 ACHN

72h 1 to 4 (prior to rechallenge)

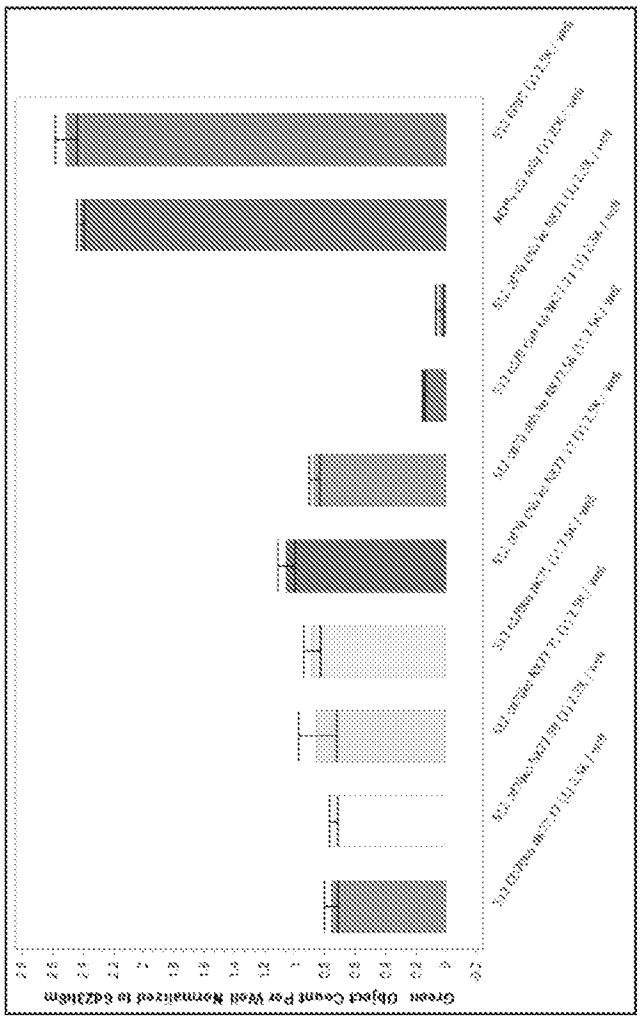


FIG. 74F

72h 1 to 8 (prior to rechallenge)

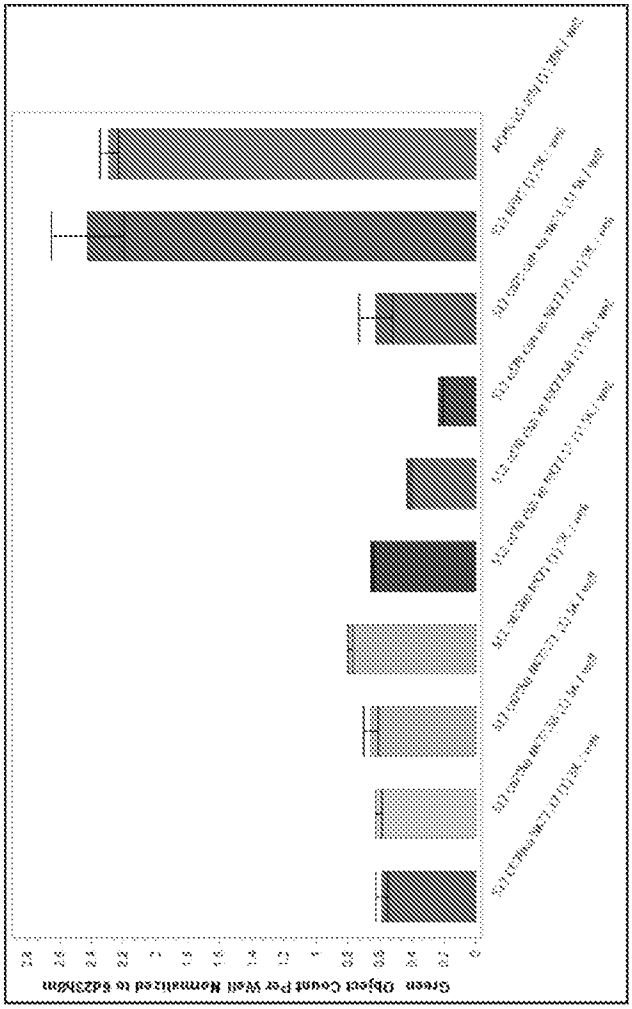


FIG. 74G

D28 ACHN

Post rechallenge
D6 1 to 4

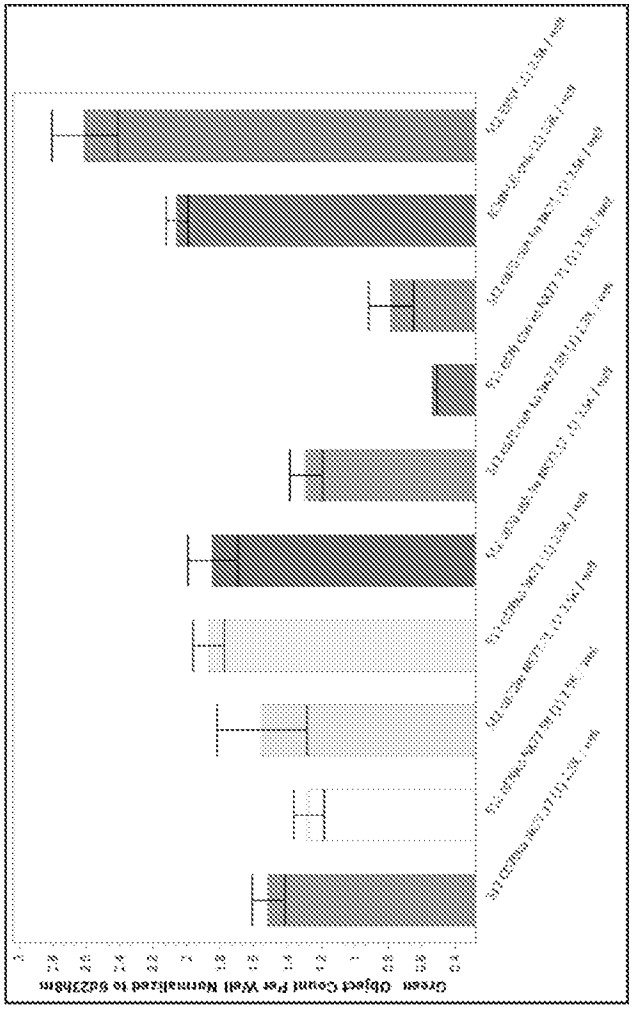


FIG. 74H

Post rechallenge
D6 1 to 8

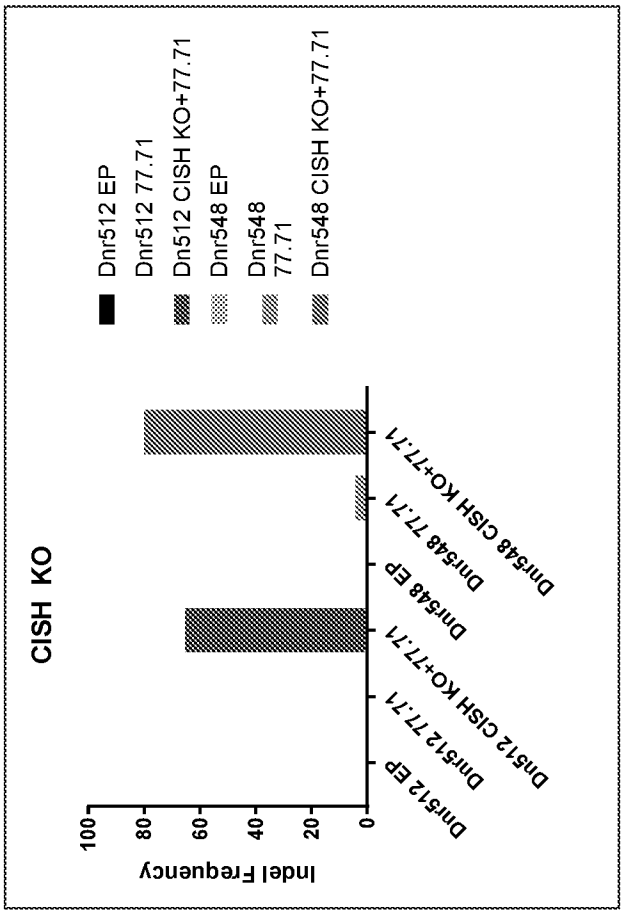


FIG. 75A

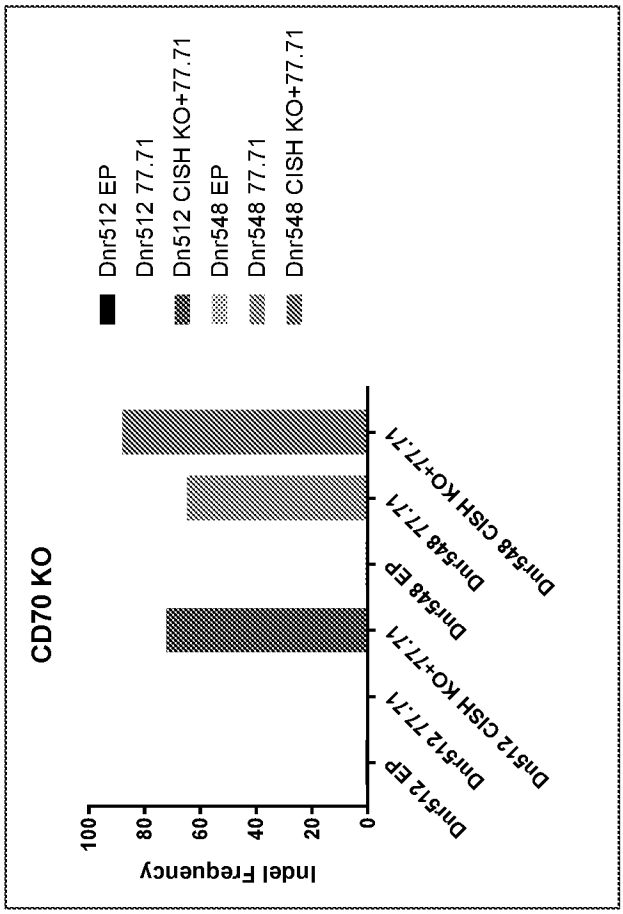
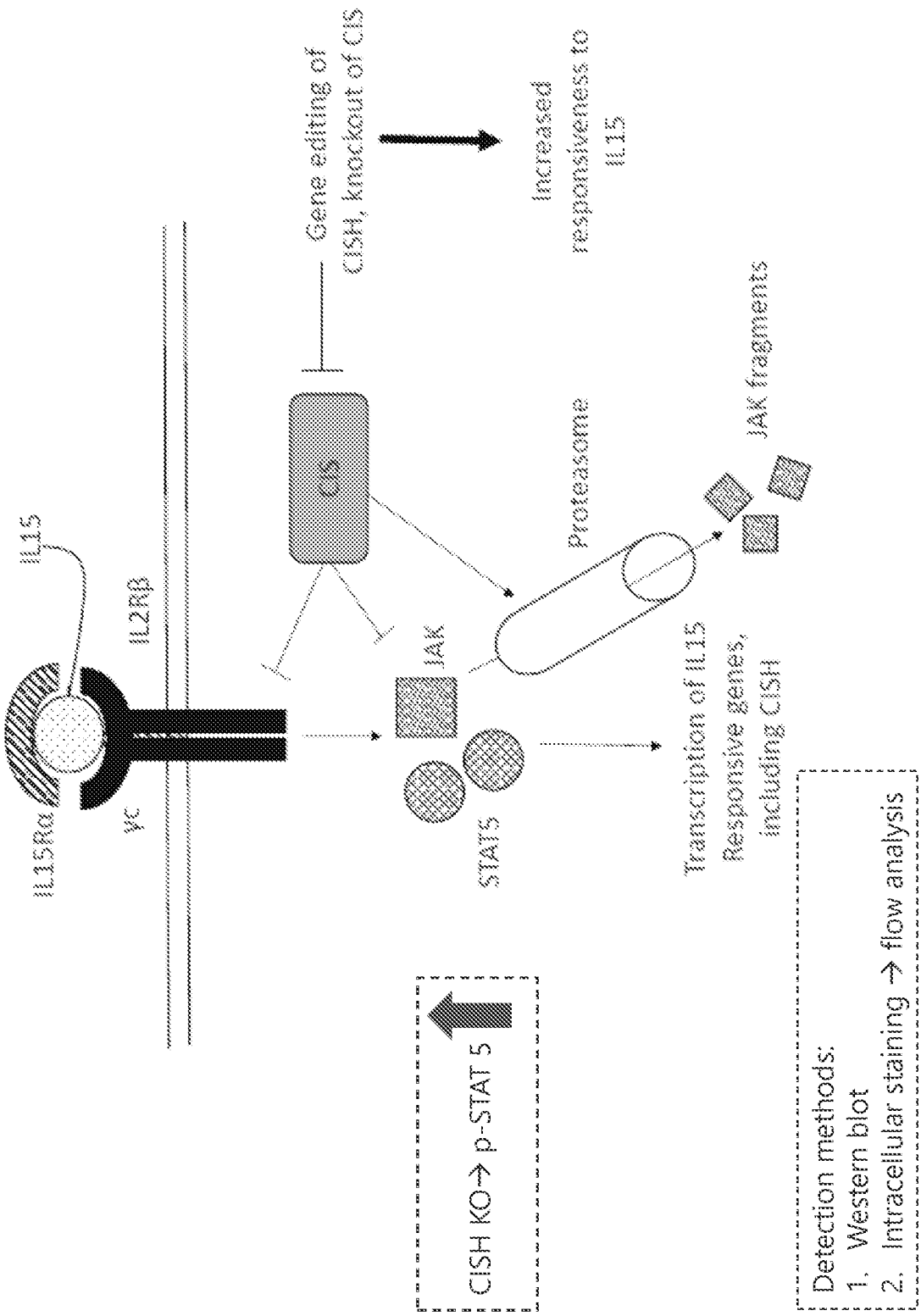
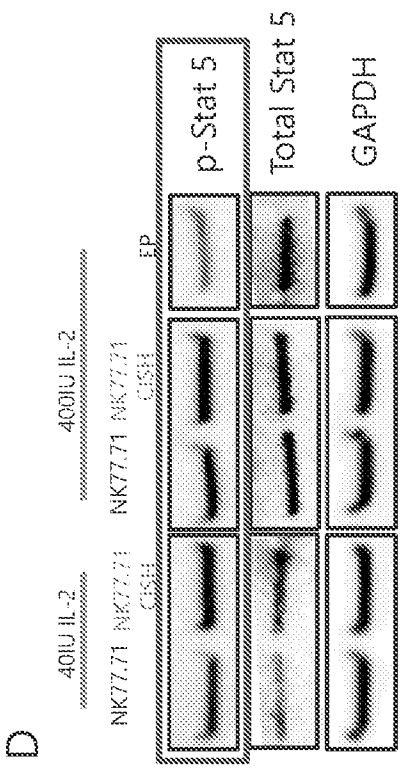


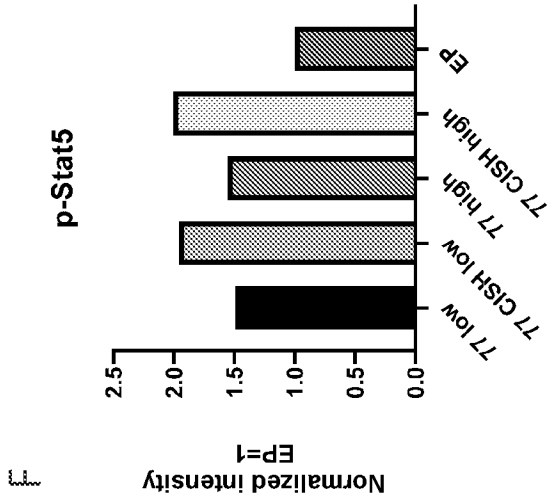
FIG. 75B

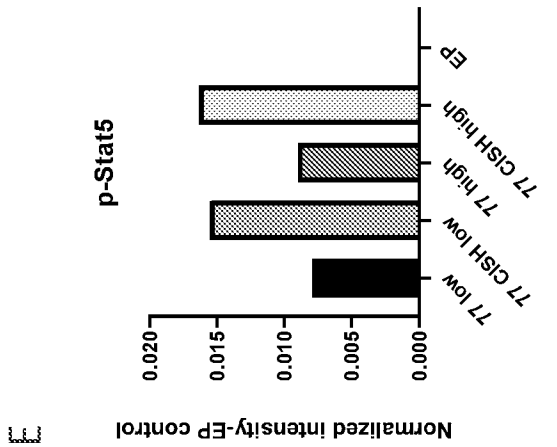
Figure 75C


IL15
IL2Rβ
IL15Rα
γc
JAK
STAT5
CIS
Gene editing of CISH, knockout of CIS
Increased responsiveness to IL15
Proteasome
JAK fragments
Transcription of IL15 Responsive genes, including CISH
CISH KO→ p-STAT 5
Detection methods:
1. Western blot
2. Intracellular staining → flow analysis

Figures 75D-75F







SEQUENCE LISTING

<110> Nkarta, Inc.

<120> GENETICALLY MODIFIED NATURAL KILLER CELLS FOR CD70-DIRECTED CANCER IMMUNOTHERAPY

<130> NKT.056WO

<150> 63/038645
<151> 2020-06-12

<150> 63/090041
<151> 2020-10-09

<150> 63/141411
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<150> 63/201490
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tccctgcgcc agaggcgtg ccggccagcg gcgggggcg cagtgcacac gagggggctg 120

gacttcgcct gtgat 135

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<212> PRT
<213> Homo sapiens

<220>
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<400> 2

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
35 40 45

<210> 3
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<212> DNA
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acc 63

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<211> 21
<212> PRT
<213> Homo sapiens

<220>
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Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
1 5 10 15

Ser Leu Val Ile Thr
20

<210> 5
<211> 111
<212> DNA
<213> Homo sapiens

<220>
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<223> OX40 - DNA

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acccccatcc aagaggagca ggccgacgcc cactccaccc tggccaagat c 111

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<211> 37
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<213> Homo sapiens

<220>
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<223> OX40 - protein

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Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
1   5   10   15

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
            20   25   30

Thr Leu Ala Lys Ile
        35

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<211> 336
<212> DNA
<213> Homo sapiens

<220>
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tataacgagc tcaatctagg acgaagagag gagtacgatg ttttggacaa gagacgtggc 120

cgggaccctg agatgggggg aaagccgaga aggaagaacc ctcaggaagg cctgtacaat 180

gaactgcaga aagataagat ggcggaggcc tacagtgaga ttgggatgaa aggcgagcgc 240

cggaggggca aggggcacga tggcctttac cagggtctca gtacagccac caaggacacc 300

tacgacgccc ttcacatgca ggccctgccc cctcgc 336

<210> 8
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> CD3zeta - protein

<400> 8

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
1 5 10 15

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
20 25 30

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
35 40 45

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
50 55 60

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65 70 75 80

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
85 90 95

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
100 105 110

<210> 9
<211> 63
<212> DNA
<213> Homo sapiens

<220>
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<400> 9
ggctctggcg agggaagggg ttccctgctt acttgcggcg acgtcgaaga gaatcccggt 60

ccg 63

<210> 10
<211> 21
<212> PRT
<213> Homo sapiens

<220>
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<223> T2A - protein

<400> 10

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
1 5 10 15

Glu Asn Pro Gly Pro
20

<210> 11
<211> 342
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
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attgacgcta cactgtatac tgagagtgat gtacacccgt cctgtaaggt aacggccatg 120

aaatgctttc ttctggagct ccaggtcatc agcttggagt ctggggacgc aagcatccac 180

gatacggttg aaaacctcat catccttgcg aacaactctc tctcatctaa tggaaacgtt 240

acagagagtg ggtgtaagga gtgcgaagag ttggaagaaa aaaacatcaa agaatttctt 300

caatccttcg ttcacatagt gcaaatgttc attaacacgt cc 342

<210> 12
<211> 114
<212> PRT

<213> Homo sapiens

<220>
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<223> Homo sapiens native IL15 - protein

<400> 12

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
1 5 10 15

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
20 25 30

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
35 40 45

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
50 55 60

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
85 90 95

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
100 105 110

Thr Ser

<210> 13
<211> 207
<212> DNA
<213> Homo sapiens

<220>
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<400> 13
actaccacac ccgccccgag gccacctacg ccggcaccga ctatcgccag tcaacccctc 60

tctctgcgcc ccgaggcttg ccggcctgcg gctggtgggg cggtccacac ccggggcctg 120

gattttgcgt gcgatatata catctgggca cctcttgccg gcacctgcgg agtgctgctt 180

ctctcactcg ttattacgct gtactgc 207

<210> 14
<211> 66
<212> PRT
<213> Homo sapiens

<220>
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<223> CD8hinge/TM - protein

<400> 14

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
1 5 10 15

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
20 25 30

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
35 40 45

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
50 55 60

Ile Thr
65

<210> 15
<211> 30
<212> DNA
<213> Homo sapiens

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<400> 15
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<220>
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<400> 16

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 17
<211> 30
<212> DNA
<213> Homo sapiens

<220>
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<400> 17
ggccaggccg gctccggagg aggaggatcc 30

<210> 18
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<220>
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Gly Gln Ala Gly Ser Gly Gly Gly Gly Ser
1 5 10

<210> 19
<211> 12
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<400> 19
ggccaggccg gc 12

<210> 20
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<400> 20

Gly Gln Ala Gly
1

<210> 21
<211> 33
<212> DNA
<213> Homo sapiens

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<223> Misc Linker - DNA

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<211> 11
<212> PRT
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Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10

<210> 23
<211> 18
<212> DNA

<213> Homo sapiens

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<400> 23
ggccaggccg gctccgga 18

<210> 24
<211> 6
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<213> Homo sapiens

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Gly Gln Ala Gly Ser Gly
1 5

<210> 25
<211> 405
<212> DNA
<213> Homo sapiens

<220>
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aactggatat gttacaaaaa taactgctac caatttttg atgagagtaa aaactggtat 120

gagagccagg cttcttgtat gtctcaaaat gccagccttc tgaaagtata cagcaaagag 180

gaccaggatt tacttaaact ggtgaagtca tatcattgga tgggactagt acacattcca 240

acaaatggat cttggcagtg ggaagatggc tccattctct cacccaacct actaacaata 300

attgaaatgc agaagggaga ctgtgcactc tatgcctcga gctttaaagg ctatatagaa 360

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<210> 26

<211> 135
<212> PRT
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<220>
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<223> NKG2D Extracellular Fragment - protein

<400> 26

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1 5 10 15

Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn Asn Cys Tyr Gln Phe
20 25 30

Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln Ala Ser Cys Met Ser
35 40 45

Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys Glu Asp Gln Asp Leu
50 55 60

Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly Leu Val His Ile Pro
65 70 75 80

Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser Ile Leu Ser Pro Asn
85 90 95

Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp Cys Ala Leu Tyr Ala
100 105 110

Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser Thr Pro Asn Thr Tyr
115 120 125

Ile Cys Met Gln Arg Thr Val
130 135

<210> 27
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<221> misc_feature
<223> Full Human NKG2D - DNA

<400> 27
gggtggattc gtggtcggag gtctcgacac agctgggaga tgagtgaatt tcataattat 60

aacttggatc tgaagaagag tgatttttca acacgatggc aaaagcaaag atgtccagta 120

gtcaaaagca aatgtagaga aaatgcatct ccatttttt tctgctgctt catcgctgta 180

gccatgggaa tccgtttcat tattatggta acaatatgga gtgctgtatt cctaaactca 240

ttattcaacc aagaagttca aattcccttg accgaaagtt actgtggccc atgtcctaaa 300

aactggatat gttacaaaaa taactgctac caatttttg atgagagtaa aaactggtat 360

gagagccagg cttcttgtat gtctcaaaat gccagccttc tgaaagtata cagcaaagag 420

gaccaggatt tacttaaact ggtgaagtca tatcattgga tgggactagt acacattcca 480

acaaatggat cttggcagtg ggaagatggc tccattctct cacccaacct actaacaata 540

attgaaatgc agaagggaga ctgtgcactc tatgcctcga gctttaaagg ctatatagaa 600

aactgttcaa ctccaaatac gtacatctgc atgcaaagga ctgtg 645

<210> 28
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> Codon optimized human NKG2D fragment - DNA

<400> 28
ctgttcaatc aggaagtcca gatccccctg acagagtctt actgcggccc atgtcccaag 60

aactggatct gctacaagaa caattgttat cagttctttg acgagagcaa gaactggtat 120

gagtcccagg cctcttgcat gagccagaat gcctctctgc tgaaggtgta cagcaaggag 180

gaccaggatc tgctgaagct ggtgaagtcc tatcactgga tgggcctggt gcacatccct 240

acaaacggct cttggcagtg ggaggacggc tccatcctgt ctccaaatct gctgaccatc 300

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aactgctcca cacccaatac ctacatctgt atgcagagga ccgtg 405

<210> 29

<211> 126
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> 4-1BB

<400> 29
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actactcaag aggaagatgg ctgtagctgc cgatttccag aagaagaaga aggaggatgt 120

gaactg 126

<210> 30
<211> 29
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Amino Acid Sequence CD28 Transmembrane domain

<400> 30

Phe Trp Val Leu Val Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu
1 5 10 15

Leu Val Thr Val Ala Phe Ile Ile Phe Trp Val Arg Ser
20 25

<210> 31
<211> 39
<212> PRT
<213> Homo sapiens

<220>
<221> MISC_FEATURE
<223> Amino Acid Sequence CD28 IC domain

<400> 31

Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn Met Thr Pro Arg
1 5 10 15

Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr Ala Pro Pro Arg

20 25 30

Asp Phe Ala Ala Tyr Arg Ser
35

<210> 32
<211> 1122
<212> DNA
<213> Artificial Sequence

<220>
<223> NKG2D-Ox40-CD3z (without mbIL15)

<400> 32
atggccttac cagtgaccgc cttgctcctg ccgctggcct tgctgctcca cgccgccagg 60

ccgttattca accaagaagt tcaaattccc ttgaccgaaa gttactgtgg cccatgtcct 120

aaaaactgga tatgttacaa aaataactgc taccaatttt ttgatgagag taaaaactgg 180

tatgagagcc aggcttcttg tatgtctcaa aatgccagcc ttctgaaagt atacagcaaa 240

gaggaccagg atttacttaa actggtgaag tcatatcatt ggatgggact agtacacatt 300

ccaacaaatg gatcttggca gtgggaagat ggctccattc tctcacccaa cctactaaca 360

ataattgaaa tgcagaaggg agactgtgca ctctatgcct cgagctttaa aggctatata 420

gaaaactgtt caactccaaa tacgtacatc tgcatgcaaa ggactgtgac cacgacgcca 480

gcgccgcgac caccaacacc ggcgcccacc atcgcgtcgc agcccctgtc cctgcgccca 540

gaggcgtgcc ggccagcggc gggggggcgca gtgcacacga gggggctgga cttcgcctgt 600

gatatctaca tctgggcgcc cttggccggg acttgtgggg tccttctcct gtcactggtt 660

atcacccttt actgccggag ggaccagagg ctgcccccg atgcccacaa gccccctggg 720

ggaggcagtt tccggacccc catccaagag gagcaggccg acgcccactc caccctggcc 780

aagatcagag tgaagttcag caggagcgca gacgcccccg cgtaccagca gggccagaac 840

cagctctata acgagctcaa tctaggacga agagaggagt acgatgtttt ggacaagaga 900

cgtggccggg accctgagat gggggggaaag ccgagaagga agaaccctca ggaaggcctg 960

tacaatgaac tgcagaaaga taagatggcg gaggcctaca gtgagattgg gatgaaaggc 1020

gagcgccgga ggggcaaggg gcacgatggc ctttaccagg gtctcagtac agccaccaag 1080

gacacctacg acgcccttca catgcaggcc ctgccccctc gc 1122

<210> 33
<211> 374
<212> PRT
<213> Artificial Sequence

<220>
<223> NKG2D-CD8a hinge/tm-OX40-CD3z (NKX101)

<400> 33

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Leu Phe Asn Gln Glu Val Gln Ile Pro Leu Thr
20 25 30

Glu Ser Tyr Cys Gly Pro Cys Pro Lys Asn Trp Ile Cys Tyr Lys Asn
35 40 45

Asn Cys Tyr Gln Phe Phe Asp Glu Ser Lys Asn Trp Tyr Glu Ser Gln
50 55 60

Ala Ser Cys Met Ser Gln Asn Ala Ser Leu Leu Lys Val Tyr Ser Lys
65 70 75 80

Glu Asp Gln Asp Leu Leu Lys Leu Val Lys Ser Tyr His Trp Met Gly
85 90 95

Leu Val His Ile Pro Thr Asn Gly Ser Trp Gln Trp Glu Asp Gly Ser
100 105 110

Ile Leu Ser Pro Asn Leu Leu Thr Ile Ile Glu Met Gln Lys Gly Asp
115 120 125

Cys Ala Leu Tyr Ala Ser Ser Phe Lys Gly Tyr Ile Glu Asn Cys Ser
130 135 140

Thr Pro Asn Thr Tyr Ile Cys Met Gln Arg Thr Val Thr Thr Thr Pro
145 150 155 160

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
165 170 175

```
Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
            180                 185                 190

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
        195                 200                 205

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
    210                 215                 220

Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
225                 230                 235                 240

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
                245                 250                 255

Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
            260                 265                 270

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
        275                 280                 285

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
    290                 295                 300

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
305                 310                 315                 320

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
                325                 330                 335

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
            340                 345                 350

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
        355                 360                 365

Gln Ala Leu Pro Pro Arg
    370
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<210> 34

<211> 2150
<212> DNA
<213> Artificial Sequence

<220>
<223> NK19H-NF-2 -NKX019 (includes T2A and mbIL15)

<400> 34
gaattcgccg ccaccatggc cttaccagtg accgccttgc tcctgccgct ggccttgctg 60

ctccacgccg ccaggccgga tattcagatg acccagagcc cgagcagcct gagcgcgagc 120

gtgggcgatc gcgtgaccat tacctgccgc gcgagccagg atattagcaa atatctgaac 180

tggtatcagc agaaaccggg cggcaccgtg aaactgctga tttatcatac cagccgcctg 240

catagcggcg tgccgagccg ctttagcggc agcggcagcg gcaccgattt taccctgacc 300

attagcagcc tgcagccgga agatattgcg acctattttt gccagcaggg caacaccctg 360

ccgtatacct ttggcggcgg caccaaactg gaaattaccg gtggcggtgg ctcgggcggt 420

ggtgggtcgg gtggcggcgg atctcaggtg cagctgcagg aaagcggccc gggcctggtg 480

aaaccgagcc agaccctgag cctgacctgc accgtgagcg gcgtgagcct gccggattat 540

ggcgtgagct ggattcgcca gccgccgggc aaaggcctgg aatggattgg cgtgatttgg 600

ggcagcgaaa ccacctatta taacagcgcg ctgaaaagcc gcctgaccat tagcaaagat 660

aacagcaaaa accaggtgag cctgaaactg agcagcgtga ccgcggcgga taccgcggtg 720

tattattgcg cgaaacatta ttattatggc ggcagctatg cgatggatta ttggggccag 780

ggcaccagcg tgaccgtgag cagcaccacg acgccagcgc cgcgaccacc aacaccggcg 840

cccaccatcg cgtcgcagcc cctgtccctg cgcccagagg cgtgccggcc agcggcgggg 900

ggcgcagtgc acacgagggg gctggacttc gcctgtgata tctacatctg ggcgcccttg 960

gccgggactt gtggggtcct tctcctgtca ctggttatca ccctttactg ccggagggac 1020

cagaggctgc cccccgatgc ccacaagccc cctgggggag gcagtttccg gacccccatc 1080

caagaggagc aggccgacgc ccactccacc ctggccaaga tcagagtgaa gttcagcagg 1140

agcgcagacg cccccgcgta ccagcagggc cagaaccagc tctataacga gctcaatcta 1200

ggacgaagag aggagtacga tgttttggac aagagacgtg gccgggaccc tgagatgggg 1260

ggaaagccga gaaggaagaa ccctcaggaa ggcctgtaca atgaactgca gaaagataag 1320

atggcggagg cctacagtga gattgggatg aaaggcgagc gccggagggg caaggggcac 1380

gatggccttt accagggtct cagtacagcc accaaggaca cctacgacgc ccttcacatg 1440

caggccctgc cccctcgcgg ctctggcgag ggaaggggtt ccctgcttac ttgcggcgac 1500

gtcgaagaga atcccggtcc gatggccctc ccagtaactg ccctcctttt gcccctcgca 1560

ctccttcttc atgccgctcg ccccaactgg gtcaacgtga ttagcgattt gaagaaaatc 1620

gaggacctta tacagtctat gcatattgac gctacactgt atactgagag tgatgtacac 1680

ccgtcctgta aggtaacggc catgaaatgc tttcttctgg agctccaggt catcagcttg 1740

gagtctgggg acgcaagcat ccacgatacg gttgaaaacc tcatcatcct tgcgaacaac 1800

tctctctcat ctaatggaaa cgttacagag agtgggtgta aggagtgcga agagttggaa 1860

gaaaaaaaca tcaaagaatt tcttcaatcc ttcgttcaca tagtgcaaat gttcattaac 1920

acgtccacta ccacacccgc cccgaggcca cctacgccgg caccgactat cgccagtcaa 1980

cccctctctc tgcgccccga ggcttgccgg cctgcggctg gtggggcggt ccacacccgg 2040

ggcctggatt ttgcgtgcga tatatacatc tgggcacctc ttgccggcac ctgcggagtg 2100

ctgcttctct cactcgttat tacgctgtac tgctaagcgg ccgcgtcgac 2150

<210> 35
<211> 706
<212> PRT
<213> Artificial Sequence

<220>
<223> NK19H-NF-2

<400> 35

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
20 25 30

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
35 40 45

Asp Ile Ser Lys Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Thr
50 55 60

Val Lys Leu Leu Ile Tyr His Thr Ser Arg Leu His Ser Gly Val Pro

```
65                  70                  75                  80

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                85                  90                  95

Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly
            100                 105                 110

Asn Thr Leu Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Thr
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
    130                 135                 140

Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln Thr
145                 150                 155                 160

Leu Ser Leu Thr Cys Thr Val Ser Gly Val Ser Leu Pro Asp Tyr Gly
                165                 170                 175

Val Ser Trp Ile Arg Gln Pro Pro Gly Lys Gly Leu Glu Trp Ile Gly
            180                 185                 190

Val Ile Trp Gly Ser Glu Thr Thr Tyr Tyr Asn Ser Ala Leu Lys Ser
        195                 200                 205

Arg Leu Thr Ile Ser Lys Asp Asn Ser Lys Asn Gln Val Ser Leu Lys
    210                 215                 220

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Tyr Cys Ala Lys
225                 230                 235                 240

His Tyr Tyr Tyr Gly Gly Ser Tyr Ala Met Asp Tyr Trp Gly Gln Gly
                245                 250                 255

Thr Ser Val Thr Val Ser Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            260                 265                 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        275                 280                 285
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Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    290                 295                 300

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
305                 310                 315                 320

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
                325                 330                 335

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
            340                 345                 350

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
        355                 360                 365

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
    370                 375                 380

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
385                 390                 395                 400

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
                405                 410                 415

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
            420                 425                 430

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
        435                 440                 445

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
    450                 455                 460

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
465                 470                 475                 480

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
                485                 490                 495

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
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            500                 505                 510

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
        515                 520                 525

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
    530                 535                 540

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
545                 550                 555                 560

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
                565                 570                 575

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
            580                 585                 590

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
        595                 600                 605

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
    610                 615                 620

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
625                 630                 635                 640

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
                645                 650                 655

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
            660                 665                 670

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
        675                 680                 685

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
    690                 695                 700

Tyr Cys
705
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<210> 36
<211> 735
<212> DNA
<213> Artificial Sequence

<220>
<223> NK71 anti-CD70 scFv

<400> 36
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acctgcaccg tctctgggtt ctcactcagt aatgctagaa tgggtgtgac ctggatccgt 120

cagcccccag ggaaggccct ggagtggctt gcacacattt tttcgaatga cgaaaaatcc 180

tacagtacat ctctgaagag caggctcacc atctccaagg acacttccaa aacccaggtg 240

gtccttacca tgaccaacat ggaccctgtg gacacagcca catattactg tgcacggata 300

cgagattact atgacattag tagttattat gactactggg gccagggaac cctggtcagc 360

gtctcctcag gcggtggtgg ctctggtggt ggcggcagcg gcggtggtgg ctctgacatc 420

cagatgaccc agtctccatc tgccatgtct gcatctgtag gagacagagt caccatcact 480

tgtcgggcga gtcaggacat tagcaattat ttagcctggt ttcagcagaa accagggaaa 540

gtccctaagc gcctgatcta tgctgcatcc agtttgcaaa gtggggtccc atcaaggttc 600

agcggcagtg gatcggggac agagttcact ctcacaatca gcagcctgct gcctgaagat 660

tttgcaactt attactgtct acagcttaat agtttcccgt tcacttttgg cggagggacc 720

aaggtggaga tcaac 735

<210> 37
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> NK72 anti-CD70 scFv

<400> 37
gaagtgcagc ttgtccagag cggagccgaa gtgaagaagc ctggcgagag cctgaagatc 60

agctgcaagg gctcaggtta cggattcaca agttattgga taggttgggt gcgccagatg 120

cctggtaagg gactggaatg gatgggtatc attcatcccg atgatagcga caccaaatac 180

agcccaagct ttcagggcca ggtcacaatc agcgctgaca agagcatcag caccgcctac 240

cttcagtggt cgtctctgaa ggccagcgac accgcaatgt actactgtgc ctctagctat 300

ttgcgtggct tgtggggagg ctattttgac tattggggcc aaggtacact ggtcaccgtc 360

agcagcggcg gtggtggctc tggtggtggc ggcagcggcg gtggtggctc tgagctccag 420

agcgtgctga cccagcctcc tagcgcaagc ggcacccctg gacagcgtgt gacaattagc 480

tgtagcggat caagctcaaa cattggctca aattatgtga attggtatca gcaattgccc 540

ggtacagcac ccaaactgct catttatgga gattatcaac gacctagcgg agtgcctgat 600

cgttttagcg gtagcaaaag cggcaccagc gcatcactgg caatttcagg cctgcgtagc 660

gaagatgagg cggattatta ctgtgctacc cgcgacgatt cgttatctgg gtctgtcgtt 720

tttggcaccg gtacaaaact gaccgtgctg 750

<210> 38
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03 scFv

<400> 38
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtc 60

tcctgcaagg cttctggata caccttcacc ggccattatt tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccactag cacagtgtac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgt tagaggaagc 300

ggttggtatg acctggacta ctggggccaa gggaccctgg tcaccgtctc ctcaggtgga 360

ggcggttcag gcggaggtgg ctctggcggt ggcggatcgg acatccagat gacccagtct 420

ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgccg ggcaagtcag 480

aatattggca catatttagc ttggtatcag cagaaaccag ggaaagcccc taagctcctg 540

atctatgacg catccaactt ggagactggg gtcccatcaa ggttcagtgg cagtggatct 600

gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660

tgtcaacaga gttacagaat ccctctcacc ttcggccaag ggacacgact ggagattaaa 720

<210> 39

<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02 scFv

<400> 39
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggata caccttcacc aactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtgggag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaacta 300

ggagtcgccg ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctcaggt 360

ggaggcggtt caggcggagg tggctctggc ggtggcggat cggacatcca gatgacccag 420

tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccgggcgagt 480

cagaggatta gcaattggtt agcctggtat cagcagaaac cagggaaagc ccctaagctc 540

ctgatctatg atgcatccaa cttggaaacc ggggtcccat ccaggttcag tggcagtgga 600

tctgggacgg attttactct caccatcagc agcctgcagc ctgaagattt tgcaacttat 660

tactgtcaac agacctatag tcctcccccc actttggcc aggggaccaa gctggagatc 720

aaa 723

<210> 40
<211> 750
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06 scFv

<400> 40
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tcctgcaagg catctggata caccttcacc ggttactata tccactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggaag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagacctg 300

tcagggatcg acggatatat tggtttcttt gactactggg gccaagggac cctggtcacc 360

gtctcctcag gtggaggcgg ttcaggcgga ggtggctctg gcggtggcgg atcggatatt 420

gtgatgactc agtctccact ctccctgccc gtcacccctg gagagccggc ctccatctcc 480

tgcaggtcta gtcagagcct cctgcactct aacggataca actatttgga ttggtacctg 540

cagaagccag ggcagtctcc acagctcctg atctatgcag cctcttcatt acaatccggg 600

gtccctgaca ggttcagtgg cagtggatca ggcacagatt ttacactgaa aatcagcaga 660

gtggaggctg aggatgttgg ggtttattac tgcatgcaag ctctacaaac tcctatcacc 720

ttcggccaag ggacacgact ggagattaaa 750

<210> 41
<211> 723
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04 scFv

<400> 41
caggtgcagc tggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgaaggtt 60

tcctgcaagg catctggagg aaccttcaga agccatgtca tatcctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcgatccta gtggtggcag cacaagctac 180

gcacagaggt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc taaagattac 300

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caggacattg acacctattt agcctggtat cagcagaaac cagggaaagc ccctaagctc 540

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tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 660

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aaa 723

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<220>
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ggaggcggtt caggcggagg tggctctggc ggtggcggat cggacatcca gatgacccag 420

tctccatcct ccctgtctgc atctgtagga gacagagtca ccatcacttg ccaggcaagt 480

caggacatta gcaactattt aaattggtat cagcagaaac cagggaaagc ccctaagctc 540

ctgatctatg atgcatccag tttggaaagt ggggtcccat caaggttcag tggcagtgga 600

tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 660

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aaa 723

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gacattagca actatttaaa ttggtatcag cagaaaccag ggaaagcccc taagctcctg 540

atctacgatg catccaattt ggaaacaggg gtcccatcaa ggttcagtgg aagtggatct 600

gggacagatt ttactttgac catcagcagc ctgcagcctg aagattttgc aacatattac 660

tgtcaacagg cttataggtg gcctatcacc ttcggccaag ggacacgact ggagattaaa 720

<210> 44
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<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11 scFv

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tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 660

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aaa 723

<210> 45
<211> 744
<212> DNA

<213> Artificial Sequence

<220>
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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

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tcaaggttca gtggaagtgg atctgggaca gattttactc tcaccatcag cagcctgcag 660

cctgaagatt ttgcaacata ttactgtcaa cagagctatt ccacccctct cactttcggc 720

caggggacca aggtggagat caaa 744

<210> 46
<211> 738
<212> DNA
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<220>
<223> NK77.10_CD70_DB02_A04 scFv

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cagagcctcc tgcattccaa cggatacaac tatttggatt ggtacctgca gaagccaggg 540

cagtctccac agctcctgat ctatcaggca tctagcctgg agtccggggt ccctgacagg 600

ttcagtggca gtggatcagg cacagatttt acactgaaaa tcagcagagt ggaggctgag 660

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accaaggtgg agatcaaa 738

<210> 47
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<220>
<223> NK77.11_CD70_DB02_A05 scFv

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ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

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aaa 723

<210> 48
<211> 726
<212> DNA

<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06 scFv

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cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccaggcg 480

agtcaggaca ttagcaacta tttaaattgg tatcagcaga aaccagggaa agcccctaag 540

ctcctgatct acgatgcatc caatttggaa acaggggtcc catcaaggtt cagtggaagt 600

ggatctggga cagattttac tctgaccatc agcagcctgc agcctgaaga ttttgcaaca 660

tattactgtc aacagtctta cagtacgcct cctacgttcg gccaagggac caaggtggaa 720

atcaaa 726

<210> 49
<211> 726
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07 scFv

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cagtctccat cctccctgtc tgcatctgta ggagacagag tcaccatcac ttgccgggca 480

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ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgcaact 660

tactactgtc aacagagtta cgatagtcct cccacttttg gccaggggac caagctggag 720

atcaaa 726

<210> 50
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08 scFv

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attagcaact atttaaattg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 540

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acagatttta ctttgaccat cagcagcctg cagcctgaag attttgcaac atattactgt 660

caacagtcct atagcacccc tctcactttc ggcggaggga ccaaggtgga gatcaaa 717

<210> 51
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09 scFv

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attagcaact atttaaattg gtatcagcag aaaccaggga aagcccctaa gctcctgatc 540

tacgatgtgt ccaatttgga aacaggggtc ccatcaaggt tcagtggaag tggatctggg 600

acagatttta ctctcaccat cagcagcctg cagcctgaag attttgcaac atattactgt 660

caacaggcta attccttccc tctcactttc ggcggaggga ccaaggtgga gatcaaa 717

<210> 52
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11 scFv

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atctatgacg catccagttt ggaaagtggg gtcccatcaa ggttcagtgg cagtggatct 600

gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660

tgtcaacagg caatcagttt tcctctcact ttcggcggag ggaccaaggt ggagatcaaa 720

<210> 53
<211> 732
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06 scFv

<400> 53
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cctggacaag ggcttgagtg gatgggaata atcaacccta atagtggtgg aacaaattac 180

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagatttt 300

agtgtgtatg ctgctgcaga tggcatggat gtctggggcc aagggacatt ggtcaccgtc 360

tcttcaggtg gaggcggttc aggcggaggt ggctctggcg gtggcggatc ggacatccag 420

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cgggcaagtc agagcattag cagctattta aattggtatc agcagaaacc agggaaagcc 540

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ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

gcaacttact actgtcaaca gagtgatagt tcacctctca ctttcggcca agggaccaag 720

gtggagatca aa 732

<210> 54
<211> 729
<212> DNA
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<220>
<223> NK77.18_CD70_DB02_B09 scFv

<400> 54

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agtggatctg ggacagattt cactctcacc atcagcagtc tgcaacctga agattttgca 660

acttactact gtcaacaggc ggatagtttt ccttacactt ttggccaggg gaccaagctg 720

gagatcaaa 729

<210> 55
<211> 720
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03 scFv

<400> 55
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actattgaca tctatttaaa ttggtatcag cagaaaccag ggaaagcccc taagctcctg 540

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gggacagatt ttactttgac catcagcagc ctgcagcctg aagattttgc aacatattac 660

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<210> 56
<211> 747
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04 scFv

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aaaccaggga aagcccctaa gctcctgatc tatgctgcat ccagtttgca cagtggggtc 600

ccatcaaggt tcagcggcag tggatctggg acagatttca ctctcactat cagcagcctg 660

cagcctgaag attttgcaac ttactattgt caacaggctg atgctttccc tctcactttc 720

ggcggaggga ccaaggtgga gatcaaa 747

<210> 57
<211> 735
<212> DNA
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<220>
<223> NK77.22_CD70_DB02_C07 scFv

<400> 57
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tttgcaactt actactgtca acagagttac accaccccta ttacgttcgg ccaagggacc 720

aaggtggaaa tcaaa 735

<210> 58
<211> 723
<212> DNA
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<220>
<223> NK77.24_CD70_DB02_D02 scFv

<400> 58
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ggcagtggat ctgggacaga tttcactctc accatcagca gtctgcaacc tgaagatttt 660

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aaa 723

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aaa 723

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acacgactgg agattaaa 738

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<210> 84
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<220>
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attaaa 726

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tctgggacag atttcactct caccatcagc agtctgcaac ctgaagattt tgcaacttac 660

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aaa 723

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tcaggcacag attttacact gaaaatcagc agagtggagg ctgaggatgt tggggtttat 660

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aaa 723

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ggaagtggat ctgggacaga ttttactctt accatcagca gcctgcagcc tgaagatttt 660

gcaacatatt acctgagcac agatctgcag accaccgctc acttcggcca agggaccaag 720

gtggaaatca aa 732

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aaa 723

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acagatttca ctctcaccat cagcagtctg caacctgaag attttgcaac ttactactgt 660

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cagatgaccc agtctccatc ctccctgtct gcatctgtag gagacagagt caccatcact 1260

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agtggaagtg gatctgggac agattttact ctcaccatca gcagcctgca gcctgaagat 1440

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cctggacaag ggcttgagtg gatgggatgg atcaacccga acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccactag cacagtgtac 240

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ccatcctccc tgtctgcatc tgtaggagac agagtcacca tcacttgccg ggcaagtcag 480

agcgttagca gatatttaaa ttggtatcag cagaaaccag ggaaagcccc taagctcctg 540

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gggacagatt tcactctcac catcagcagt ctgcaacctg aagattttgc aacttactac 660

tgtcaacagg ccgacagttt ccctgtgact tttggccagg ggaccaagct ggagatcaaa 720

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ggacaagggc ttgagtggat gggatggatc aaccctaaca gtggtggcac aaactatgca 300

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tcacagagcc tcctgcattc aaatggctat aactacctgg actggtacct ccagaagcct 1320

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aggttttcag gctccgggtc gggcaccgat ttcaccctca agatctctcg cgtggaggct 1440

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<211> 1485
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.78_65-65 scFv codon optimized

<400> 223
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gcccagaaat ttcagggccg cgttacaatg acccgcgaca cgtccacgag caccgtctac 240

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ggtactgatt tcaccctgac catctcgtcc ctgcagccag aagattttgc cacctattac 660

tgtcagcagg cggacagctt ccccgtgacc ttcggccagg ggaccaagct ggaaattaag 720

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<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.79_38-67 scFv codon optimized

<400> 224
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ccggggcagg gcctggagtg gatgggcatc atcaatccat cagggggggac aacgagctat 180

gcgcagaaat ttcagggtcg cgtcactatg actcgcgaca catcaacctc caccgtgtac 240

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acctgccgag cctcccagga tatccgccac tacctggcgt ggtaccagca gaagccgggt 540

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gactttgcta cctactactg tcaacagacc tacgacgcac ctatcacttt cggtcagggc 720

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gcgccaggcc agggtttgga gtggatgggt ggcatcacgc cgatgtttgg cacgacggac 960

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gtggaggccg aagatgtggg cgtctactac tgcatgcagg gcacccactg gccccctacc 1500

ttcggccagg gcaccaaggt ggagatcaag 1530

<210> 225
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.80_38-68 scFv codon optimized

<400> 225
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gcacagaagt tccagggtag agttaccatg actcgcgaca cctctacctc caccgtgtac 240

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aaggccccca aattattgat ctacgacgct tcgtccctcc agtcgggcgt gccttcccgt 600

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tcacaggtgc agctggtgca aagtggagcg gaagtgaaga agccgggcgc gagcgtcaag 840

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gccccgggac agggcctgga gtggatgggc attatcaatc catccgatgg cggcacatcg 960

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cgtctggaga tcaag 1515

<210> 226
<211> 1530
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.81_64-67 scFv codon optimized

<400> 226
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<210> 227
<211> 1515
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.82_64-68 scFv codon optimized

<400> 227
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cgcctggaga ttaag 1515

<210> 228
<211> 1512
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.83_65-67 scFv codon optimized

<400> 228
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gtggagatca aa 1512

<210> 229
<211> 1497
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.84_65-68 scFv codon optimized

<400> 229

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<210> 230
<211> 240
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03 scFv

<400> 230

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            20                  25                  30


Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Val Arg Gly Ser Gly Trp Tyr Asp Leu Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160


Asn Ile Gly Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175


Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190
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Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
210 215 220

Tyr Arg Ile Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
225 230 235 240

<210> 231
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02 scFv

<400> 231

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
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Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Gly Val Ala Gly Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

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Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Arg Ile Ser Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Thr Tyr Ser Pro Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
225                 230                 235                 240

Lys
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<210> 232
<211> 250
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06 scFv

<400> 232

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Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Ser Gly Ile Asp Gly Tyr Ile Gly Phe Phe Asp Tyr
            100                 105                 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
    130                 135                 140

Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
145                 150                 155                 160

Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu
                165                 170                 175

Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
            180                 185                 190

Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
        195                 200                 205

Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
    210                 215                 220

Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Thr Pro Ile Thr
225                 230                 235                 240

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
                245                 250
```

<210> 233

<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04 scFv

<400> 233

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Ser His
20 25 30

Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asp Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Arg Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Tyr Thr Gly Leu Leu Gly Met Asp Val Trp Gly Gln Gly
100 105 110

Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145 150 155 160

Gln Asp Ile Asp Thr Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val

180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Ser Tyr Thr Thr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 234
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05 scFv

<400> 234

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Leu Ser Gly Tyr Asp Leu Asp Asp Tyr Trp Gly Gln Gly

100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
145 150 155 160

Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
165 170 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val
180 185 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Ser Tyr Arg Ser Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 235
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07 scFv

<400> 235

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

```
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala His Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Leu Ser Gly Tyr Asp Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln
145                 150                 155                 160

Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
    210                 215                 220

Tyr Arg Trp Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
225                 230                 235                 240
```

<210> 236
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11 scFv

<400> 236

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Thr Asp Val Tyr Gly Asp Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160


Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175
```

```
Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Tyr Leu Glu Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Thr Ile Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys
```

<210> 237
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03 scFv

<400> 237

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Glu Gly Gly Thr Ala Met Ala Thr Gly Tyr Tyr Tyr Tyr Gly
            100                 105                 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
    130                 135                 140

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
145                 150                 155                 160

Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp
                165                 170                 175

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
            180                 185                 190

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
    210                 215                 220

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 238
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04 scFv

<400> 238

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Ser Asn Gly Gly Tyr Thr Gly Tyr Ala Leu Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Ser Asn Tyr Gly Gly His Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140

Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145                 150                 155                 160

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
                165                 170                 175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Gln Ala Ser Ser
            180                 185                 190

Leu Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gly Gly
```

225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 239
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05 scFv

<400> 239

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Met Gly Ala Trp Ala Ala Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala

145 150 155 160

Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Thr Ser Thr Leu Ala Asn Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
225 230 235 240

Lys

<210> 240
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06 scFv

<400> 240

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Val Asn Asp Tyr Gly Asp Tyr Asp Gly Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
145 150 155 160

Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
165 170 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly
180 185 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
195 200 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
210 215 220

Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
225 230 235 240

Ile Lys

<210> 241
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07 scFv

<400> 241

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Tyr Gly Asp Tyr Asp Ala Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160


Ser Gln Ser Ile Asp Asn Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175


Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly
            180                 185                 190


Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205
```

```
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Asp Ser Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 242
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08 scFv

<400> 242

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ile Tyr Ala Gln Asn Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Val Lys Glu Glu Ala Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125
```

```
Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
    130                 135                 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp
145                 150                 155                 160

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
                165                 170                 175

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
    210                 215                 220

Ser Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235
```

<210> 243
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09 scFv

<400> 243

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asp Asn Gly Asp Thr Gly Tyr Ala Gln Met Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Gly Asp Tyr Tyr Asp Ile Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
    130                 135                 140


Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp
145                 150                 155                 160


Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
                165                 170                 175


Lys Leu Leu Ile Tyr Asp Val Ser Asn Leu Glu Thr Gly Val Pro Ser
            180                 185                 190


Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
        195                 200                 205


Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn
    210                 215                 220


Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225                 230                 235


<210>  244
<211>  240
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.16_CD70_DB02_A11 scFv

<400>  244
```

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asn Ser Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Pro Ser Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

Thr Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
```

210 215 220

Ile Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 245
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06 scFv

<400> 245

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Phe Ser Val Tyr Ala Ala Ala Asp Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

145 150 155 160

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Ala
180 185 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Ser Asp Ser Ser Pro Leu Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Val Glu Ile Lys

<210> 246
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09 scFv

<400> 246

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asp Gly Gly Thr Ile Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Gly Glu Ser Ala Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
130 135 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln
145 150 155 160

Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
165 170 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Thr Thr Leu Gln Ser
180 185 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
195 200 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
210 215 220

Gln Gln Ala Asp Ser Phe Pro Tyr Thr Phe Gly Gln Gly Thr Lys Leu
225 230 235 240

Glu Ile Lys

<210> 247
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03 scFv

<400> 247

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ala Gly Thr Glu Ile Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125


Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160


Thr Ile Asp Ile Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175


Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205
```

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
210 215 220

Asp Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 248
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04 scFv

<400> 248

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Asp Gly Ala Thr Thr Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Glu Leu Leu His Phe Ala Thr Asn Tyr Tyr Tyr Tyr
100 105 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
130 135 140

```
Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
145                 150                 155                 160


Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
                165                 170                 175


Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
            180                 185                 190


Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
        195                 200                 205


Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
    210                 215                 220


Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ala Phe Pro Leu Thr Phe
225                 230                 235                 240


Gly Gly Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 249
<211> 245
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07 scFv

<400> 249

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Asn
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Pro Asp Asn Gly Val Thr Asn Tyr Ala Gln Asn Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Thr Gln Gly Ser Ser Ser Trp Tyr Gln Trp Tyr Phe Asp Leu
            100                 105                 110

Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Arg Ala Ser Gln Ser Ile Gly Thr Trp Leu Ala Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ile Thr Phe Gly Gln Gly Thr
225                 230                 235                 240

Lys Val Glu Ile Lys
                245
```

<210> 250
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.24_CD70_DB02_D02 scFv

<400> 250

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asp Pro Gly Ser Gly Asp Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ser Asn Trp Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser Pro Ala Thr
    130                 135                 140


Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser
145                 150                 155                 160


Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
                165                 170                 175


Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile
            180                 185                 190


Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr
```

195 200 205

Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln
210 215 220

Tyr Asp Ser Tyr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 251
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04 scFv

<400> 251

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Arg Leu Ser Asp His
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ser Ser Tyr Tyr Gly Asp Tyr Val Leu Val Asn Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

```
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
145                 150                 155                 160

Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Glu Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln
    210                 215                 220

Asp Tyr Asp Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
225                 230                 235                 240

Lys
```

<210> 252
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10 scFv

<400> 252

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

```
        35                  40                  45

Gly Trp Ile Asn Pro Asn Thr Gly Gly Thr Ser Phe Ala Gln Asn Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Gly Gln Trp Leu Gly Glu Ile Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Thr Ile Tyr Lys Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ala Asn Ser Phe Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp
225                 230                 235                 240

Ile Lys
```

<210> 253
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11 scFv

<400> 253

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Thr Asp Tyr Phe Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45


Glu Trp Met Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala
    50                  55                  60


Gln Glu Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
65                  70                  75                  80


Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                85                  90                  95


Tyr Tyr Cys Ala Arg Gly Pro Tyr Ser Ser Ser Trp Tyr Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140


Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160


Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175
```

```
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
            180                 185                 190


Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205


Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220


Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Pro Thr Phe Gly Gln Gly
225                 230                 235                 240


Thr Lys Val Glu Ile Lys
                245
```

<210> 254
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.28_CD70_DB02_E04 scFv

<400> 254

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Leu Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Glu Gly Val Gly Ala Met Gly Val Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Thr Ser Ile Ser Asp Tyr Val His Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Asp Ser Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 255
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06 scFv

<400> 255

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Ala Tyr Asn Gly Lys Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Thr Ile Tyr Tyr Asp Phe Trp Ser Gly Tyr Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Ala Ser Thr Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg
```

225 230 235 240

Leu Glu Ile Lys

<210> 256
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08 scFv

<400> 256

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ala Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Arg Gly Asp Tyr Tyr Gly Ser Gly Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
130 135 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys

145 150 155 160

Arg Ala Ser Gln Thr Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
165 170 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Thr Leu Glu
180 185 190

Ala Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
195 200 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
210 215 220

Cys Gln Gln Ser Tyr Asn Pro Pro Tyr Thr Phe Gly Gln Gly Thr Lys
225 230 235 240

Leu Glu Ile Lys

<210> 257
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07 scFv

<400> 257

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Phe Asp His Ala Phe Asp Ile Trp Gly Gln Gly Thr
100 105 110

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145 150 155 160

Ser Ile Ser Thr Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Ile Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
210 215 220

Asp Ser Ser Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 258
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04 scFv

<400> 258

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

```
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Ile Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Asp Ser Ser Ser Trp Tyr Asp Tyr Tyr Tyr Tyr Met Asp
            100                 105                 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220
```

Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu Thr Phe Gly Gly Gly
225 230 235 240

Thr Lys Val Glu Ile Lys
245

<210> 259
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05 scFv

<400> 259

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Thr His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Asp Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Met Glu Trp Leu Gly Gln Val Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

```
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160


Gln Asp Ile Arg Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175


Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205


Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220


Ser Tyr Ser Ala Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
225                 230                 235                 240


Lys
```

<210> 260
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08 scFv

<400> 260

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Arg Ile Asn Pro Asn Gly Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly His Arg Gly Gly Gly Gly Ile Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Glu Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Gln Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Ser Thr Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
225                 230                 235                 240

Lys
```

<210> 261
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.36_CD70_DB03_A06 scFv

<400> 261

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Ser Pro Asn Ser Gly Asp Thr His Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Trp Gly Ser Gly Trp Tyr Val Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser
145                 150                 155                 160


Gln Asp Ile Ser Asp Ser Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175


Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Ser Leu Gln Ser Gly Val
            180                 185                 190


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
```

195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Ser Phe Thr Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 262
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07 scFv

<400> 262

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asn Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Thr Tyr Gly Asp Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly

```
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Asn Phe Ser Pro Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
225                 230                 235                 240

Lys
```

<210> 263
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.38_CD70_DB03_A08 scFv

<400> 263

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

```
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Arg Leu Glu Ile Lys
                245
```

<210> 264
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.39_CD70_DB03_A09 scFv

<400> 264

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Thr Pro Asn Ser Gly Tyr Thr Tyr Tyr Ala Gln Asn Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asn Thr Asp Cys Tyr Gly Asp Phe Leu Gly Leu Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser
    130                 135                 140


Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile Asn Cys
145                 150                 155                 160


Arg Ala Ser Ser Ser Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175
```

```
Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
            180                 185                 190


Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205


Thr Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
    210                 215                 220


Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240


Val Glu Ile Lys
```

<210> 265
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11 scFv

<400> 265

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
            20                  25                  30


Leu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Val Asn Pro Ser Asp Gly Ser Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Lys Asp Thr Gly Leu Arg Tyr Phe Asp Trp Leu Leu Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Thr Asn Phe Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Gly Ala Pro Leu Thr Phe Gly Gln Gly Thr Arg
225                 230                 235                 240

Leu Glu Ile Lys
```

<210> 266
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12 scFv

<400> 266

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asp Pro Ser Gly Gly Arg Thr Ile Tyr Ala Gln Arg Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg His Glu Ala Gly Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln
145                 150                 155                 160

Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Ser Ala Ser Thr Leu Gln Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
    210                 215                 220

Tyr Ser Ser Pro Tyr Arg Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
```

225 230 235 240

<210> 267
<211> 248
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01 scFv

<400> 267

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Ser
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Gly Ile Ile Pro Met Ala Gly Ile Pro Ala Tyr Ala Glu Glu Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Asp Asp Tyr Gly Gly Asn Trp Tyr Phe Asp Leu Trp Gly
100 105 110

Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
130 135 140

Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg
145 150 155 160

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp

```
                165                 170                 175

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Ala Ala
            180                 185                 190

Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
        195                 200                 205

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val
    210                 215                 220

Gly Val Tyr Tyr Cys Met Gln Gly Ala His Trp Pro Pro Thr Phe Gly
225                 230                 235                 240

Gln Gly Thr Lys Leu Glu Ile Lys
                245
```

<210> 268
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.43_CD70_DB03_B04 scFv

<400> 268

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95

Ala Arg Asp Ser Gly Trp Tyr Glu Ser Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Asp Ile Arg Asp Gly Leu Gly Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Gly Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 269
<211> 243
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.44_CD70_DB03_B06 scFv

<400> 269

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
```

```
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Ile Val Gly Ala Thr Glu Asp Trp Tyr Phe Asp Leu Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val Met Thr Gln Ser
    130                 135                 140

Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala Thr Leu Ser Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala Ser Thr Arg Ala
            180                 185                 190

Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr
    210                 215                 220
```

Cys Gln Gln Tyr Asp Ser Ser Pro Thr Phe Gly Gln Gly Thr Lys Val
225 230 235 240

Glu Ile Lys

<210> 270
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09 scFv

<400> 270

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Asn Asn Gly Gly Thr Ile Tyr Ala Gln Thr Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Gly Gly Tyr Val Leu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
130 135 140

```
Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160


Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175


Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190


Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205


Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220


Ser His Ser Ala Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
225                 230                 235                 240


Lys
```

<210> 271
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.46_CD70_DB03_C05 scFv

<400> 271

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Met Ile Asn Pro Arg Gly Gly Ser Thr Thr Tyr Ala Gln Ser Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Leu Gly Asp Tyr Gly Asp Tyr Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Thr Asn Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Tyr Leu Glu Ala Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Ser Thr Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile
225                 230                 235                 240

Lys
```

<210> 272
<211> 252
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11 scFv

<400> 272

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ser
            20                  25                  30


Asp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ser Ala Ile Ser Gly Gly Gly Asp Thr Leu Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Met Ala Ser Ala Leu Asp Ser Ser Gly Asp Asn Glu Ala Phe Asp
            100                 105                 110


Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
    130                 135                 140


Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly Glu Arg Ala Thr Ile
145                 150                 155                 160


Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ser Asn Asn Lys Asn
                165                 170                 175


Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu
            180                 185                 190


Ile Tyr Trp Ala Ser Thr Arg Asp Ser Gly Val Pro Asp Arg Phe Ser
```

195 200 205

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
210 215 220

Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Gly Phe Pro
225 230 235 240

Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
245 250

<210> 273
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01 scFv

<400> 273

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Glu Asp Asp Phe Trp Ser Gly Pro Ser Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly

```
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Gln Ala Ser His Asp Ile Ser Lys Phe Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Gln
            180                 185                 190

Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Thr Tyr Ser Phe Pro Phe Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240

Leu Glu Ile Lys
```

<210> 274
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03 scFv

<400> 274

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Thr Asn Tyr
            20                  25                  30

Ala Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
```

```
        35                  40                  45

Gly Gly Ile Ile Pro Ile Ser Gly Ala Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Gly Leu Asp Asp Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110

Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140

Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145                 150                 155                 160

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
                165                 170                 175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Met Gln Ala Arg Gln Thr Pro Leu Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Arg Leu Glu Ile Lys
                245
```

<210> 275
<211> 256
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09 scFv

<400> 275

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Gly Arg Ile Asp Tyr Gly Asp Tyr Asp Asp Tyr Tyr Tyr
            100                 105                 110


Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
        115                 120                 125


Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140


Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
145                 150                 155                 160


Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
                165                 170                 175
```

```
Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
            180                 185                 190

Pro Gln Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Gly Gly Val Pro
        195                 200                 205

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
    210                 215                 220

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
225                 230                 235                 240

Leu Glu Ser Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                245                 250                 255
```

<210> 276
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02 scFv

<400> 276

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Thr Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg Asp Gln Gly Leu Trp Phe Thr Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Ser Asn Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Arg Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Asp Gly Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 277
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05 scFv

<400> 277

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
            20                  25                  30

His Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Gly Asp Gly Ala Thr Gly Tyr Ala Gln Asn Leu
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Gly Glu Gly Ile Ser Gly Ser Asp Ala Phe Asp Ile Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu
    210                 215                 220

Gln Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu
```

225 230 235 240

Ile Lys

<210> 278
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06 scFv

<400> 278

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Trp Gly Val Asp Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln

145 150 155 160

Ser Ile Asn Arg Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala
165 170 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
180 185 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
195 200 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
210 215 220

Tyr Ile Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
225 230 235 240

<210> 279
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09 scFv

<400> 279

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys

```
                85                  90                  95

Ala Arg Asp Val Gly Glu Thr Thr Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln
145                 150                 155                 160

Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr
    210                 215                 220

Asn Ser Phe Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
225                 230                 235                 240


<210>  280
<211>  245
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.55_CD70_DB03_F12 scFv

<400>  280

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
```

```
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Val Arg Gly Trp Asp Tyr Tyr Tyr Gly Met Gly Val
            100                 105                 110

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
    130                 135                 140

Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145                 150                 155                 160

Cys Gln Ala Ser Gln Asp Ile Arg Asn Phe Leu Asn Trp Tyr Gln Gln
                165                 170                 175

Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu
            180                 185                 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
        195                 200                 205

Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr
    210                 215                 220

Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Ser Thr Phe Gly Gln Gly Thr
225                 230                 235                 240
```

Lys Leu Glu Ile Lys
245

<210> 281
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.56_CD70_DB03_G06 scFv

<400> 281

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro His Ser Gly Asn Ser Asp Asn Ala Pro Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Tyr Ser Gly Tyr Asp Leu Thr Ala Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145 150 155 160

```
Ser Gln Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 282
<211> 251
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11 scFv

<400> 282

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Gln
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Thr Gly Asp Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Val Phe Glu Val Glu Gly Gly Thr Asp Tyr Tyr Tyr
            100                 105                 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
    130                 135                 140

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
145                 150                 155                 160

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Thr Ile Ser Gly Trp
                165                 170                 175

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
            180                 185                 190

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
        195                 200                 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
    210                 215                 220

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp
225                 230                 235                 240

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
                245                 250
```

<210> 283
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.58_CD70_DB03_H08 scFv

<400> 283

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Val Ile Asn Pro Ser Gly Gly Gly Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Tyr Ser Gly Tyr Asp Trp Val Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Gly Ile Gly Ser Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
```

210 215 220

Ser Tyr Ser Thr Pro Trp Thr Phe Gly Pro Gly Thr Lys Val Asp Ile
225 230 235 240

Lys

<210> 284
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.59_CD70_DB03_H10 scFv

<400> 284

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Ser Tyr Phe Gly Trp Phe Asp Pro Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser

```
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Ser Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Asn Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 285
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.60_CD70_DB04_A05 scFv

<400> 285

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Thr Gly Gly Ser Thr Tyr Tyr Ala Gln Lys Phe
```

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Gly Asn Tyr Gln Gly Ile Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
145                 150                 155                 160

Ser Gln Gly Ile Gly Gly Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Asp Ser Pro Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu
225                 230                 235                 240

Ile Lys
```

<210> 286
<211> 241
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.61_CD70_DB04_A07 scFv

<400> 286

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Asn Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Val Ser Gly Tyr Asp Leu Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140


Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160


Gln Ser Val Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175


Ala Pro Lys Leu Leu Ile Tyr Asp Thr Ser Asn Leu Glu Thr Gly Val
            180                 185                 190
```

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
195 200 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
210 215 220

Ala His Ser Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 287
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.62_CD70_DB04_A10 scFv

<400> 287

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Lys His Asp Gly Ser Glu Gln Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ser Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

```
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
    130                 135                 140


Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His
145                 150                 155                 160


Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
                165                 170                 175


Ser Pro Gln Leu Leu Ile Tyr Leu Gly Ser Thr Arg Ala Ser Gly Val
            180                 185                 190


Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
        195                 200                 205


Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
    210                 215                 220


Ala Leu Asp Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
225                 230                 235                 240


Lys
```

<210> 288
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.63_CD70_DB04_A11 scFv

<400> 288

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
            20                  25                  30
```

```
Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45

Gly Ile Ile Asp Pro Thr Gly Ala Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Tyr Ser Tyr Gly Met Asp Tyr Tyr Gly Met Asp Val Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Thr Ser Asn Leu Gln
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Leu Ser Thr Asp Leu Gln Thr Thr Ala His Phe Gly Gln Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 289
<211> 246
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.64_CD70_DB04_B03 scFv

<400> 289

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125


Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140


Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145                 150                 155                 160


Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
```

```
                165                 170                 175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys
                245
```

<210> 290
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.65_CD70_DB04_B05 scFv

<400> 290

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
```

```
                85                  90                  95

Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

Ser Val Ser Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
    210                 215                 220

Asp Ser Phe Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225                 230                 235                 240


<210>  291
<211>  243
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.66_CD70_DB04_B07 scFv

<400>  291

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
```

```
            20                  25                  30

Tyr Ile Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Asp Gly Ala Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Asn Asp Tyr Tyr Tyr Tyr Phe Met Asp Tyr Trp Gly
            100                 105                 110

Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
    130                 135                 140

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg
145                 150                 155                 160

Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn Trp Tyr Gln Gln Lys Pro
                165                 170                 175

Gly Lys Ala Pro Lys Leu Leu Ile Tyr His Ala Ser Asn Leu Glu Thr
            180                 185                 190

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
        195                 200                 205

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
    210                 215                 220

Gln Gln Ser Tyr Asp Gly Pro Met Thr Phe Gly Gln Gly Thr Lys Leu
225                 230                 235                 240
```

Glu Ile Lys

<210> 292
<211> 249
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.67_CD70_DB04_C01 scFv

<400> 292

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20                  25                  30


Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Gly Ile Thr Pro Met Phe Gly Thr Thr Asp Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile Trp
            100                 105                 110


Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125


Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser
    130                 135                 140


Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys
145                 150                 155                 160
```

```
Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
                165                 170                 175

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp
            180                 185                 190

Ala Ser Asn Leu Glu Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
        195                 200                 205

Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
    210                 215                 220

Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe
225                 230                 235                 240

Gly Gln Gly Thr Lys Val Glu Ile Lys
                245
```

<210> 293
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04 scFv

<400> 293

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser Tyr Ala Asp Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Asp Gly Pro Ile Thr Phe Gly Gln Gly Thr Arg
225                 230                 235                 240

Leu Glu Ile Lys
```

<210> 294
<211> 241
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.69_CD70_DB04_C06 scFv

<400> 294

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Ser Ser Gly Val Thr Asn Phe Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Ser Asp Gln Gly Asp Trp Ser Asp Pro Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
```

210 215 220

Ser Tyr Asn Thr Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile
225 230 235 240

Lys

<210> 295
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07 scFv

<400> 295

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Met Asn Pro Asn Thr Gly Asp Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Asp Phe Gly Glu Leu Ala Pro Ala Thr Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
115 120 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser

```
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Gly Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Leu Gln Asp Ala Ala Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg
225                 230                 235                 240

Leu Glu Ile Lys
```

<210> 296
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02 scFv

<400> 296

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Val Ile Ser Pro Ser Gly Gly Gly Thr Ser Tyr Ala Gln Lys Phe
```

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Tyr Tyr Gly Gly Asn Pro Glu Gly Trp Tyr Phe Asp Leu Trp
            100                 105                 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Ser Ile Gly Asn Trp Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asp Leu Glu
            180                 185                 190

Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser Tyr Thr Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 297
<211> 259
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05 scFv

<400> 297

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                  10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Val Phe Asp Asp Tyr
            20                  25                  30


Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Pro Gln Tyr Tyr Gly Ser Gly Thr Asp Pro Leu Glu Val
            100                 105                 110


Arg Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
        115                 120                 125


Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
    130                 135                 140


Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val
145                 150                 155                 160


Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu
                165                 170                 175


Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro
            180                 185                 190
```

Gly Gln Ser Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser
        195   200   205

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    210   215   220

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys
225   230   235   240

Met Lys Gly Leu Gln Thr Pro Leu Thr Phe Gly Pro Gly Thr Lys Val
                245   250   255

Asp Ile Lys

<210> 298
<211> 244
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.73_CD70_DB04_D07 scFv

<400> 298

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Asn Tyr
            20   25   30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

```
Ala Arg Asp His Ser Ala Gly Thr His His Asp Ala Phe Asp Ile Trp
            100                 105                 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser
    130                 135                 140

Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys
145                 150                 155                 160

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala Trp Tyr Gln Gln Lys
                165                 170                 175

Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln
            180                 185                 190

Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
        195                 200                 205

Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
    210                 215                 220

Cys Gln Gln Ser His Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys
225                 230                 235                 240

Val Glu Ile Lys
```

<210> 299
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.74_CD70_DB04_D08 scFv

<400> 299

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15
```

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asn Ser Gly Asn Ala Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Tyr Trp Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
    130                 135                 140

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly
145                 150                 155                 160

Ile Ser Asn Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
                165                 170                 175

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser
            180                 185                 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
        195                 200                 205

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
    210                 215                 220

Ser Thr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
```

225 230 235

<210> 300
<211> 240
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10 scFv

<400> 300

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asp Pro Ser Asp Gly Ser Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Pro Leu Tyr Ala Ser Asp Leu Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
130 135 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145 150 155 160

Asp Ile Gly Asn Asp Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala

```
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp
    210                 215                 220

Tyr Asp Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
225                 230                 235                 240


<210>  301
<211>  241
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.85_CD70_DB03_B02 scFv

<400>  301

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asp Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Ser Ser Ser Trp Pro Asp Phe Asp Leu Trp Gly Arg Gly
```

```
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser
    130                 135                 140

Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser
145                 150                 155                 160

Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
                165                 170                 175

Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val
            180                 185                 190

Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
        195                 200                 205

Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
    210                 215                 220

Ser Tyr Asn Thr Pro Tyr Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
225                 230                 235                 240

Lys
```

<210> 302
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06 scFv

<400> 302

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
```

```
            20                  25                  30

Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45

Gly Ile Ile Asn Pro Ser Ser Gly Ser Ala Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Arg Gly Ala Tyr Ser Ser Thr Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Thr
145                 150                 155                 160

Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Leu
    210                 215                 220

Gln Asp Tyr Ser Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu
225                 230                 235                 240
```

Ile Lys

<210> 303
<211> 242
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09 scFv

<400> 303

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Val Ile Asn Pro Ser Asp Gly Thr Ala His Tyr Ala Gln Arg Leu
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Gly Ser Tyr Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        115                 120                 125


Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
    130                 135                 140


Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala
145                 150                 155                 160
```

```
Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly
                165                 170                 175

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly
            180                 185                 190

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
        195                 200                 205

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
    210                 215                 220

Gln Ser Tyr Ser Thr Pro Pro Ala Phe Gly Gln Gly Thr Lys Val Glu
225                 230                 235                 240

Ile Lys
```

<210> 304
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.76_38-38 scFv

<400> 304

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Arg Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            260                 265                 270

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
        275                 280                 285

Ser Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
```

```
    290                 295                 300

Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser
305                 310                 315                 320

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
                325                 330                 335

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350

Ala Val Tyr Tyr Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp
        355                 360                 365

Trp Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
    370                 375                 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
385                 390                 395                 400

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
                405                 410                 415

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr
            420                 425                 430

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        435                 440                 445

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    450                 455                 460

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
465                 470                 475                 480

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile
                485                 490                 495

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            500                 505
```

<210> 305
<211> 507
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.77_64-64 scFv

<400> 305

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
130 135 140

Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145 150 155 160

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
165 170 175

```
Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            260                 265                 270

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
        275                 280                 285

Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
    290                 295                 300

Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn
305                 310                 315                 320

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
                325                 330                 335

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350

Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp
        355                 360                 365

Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
    370                 375                 380

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr
```

385 390 395 400

Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile
405 410 415

Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr
420 425 430

Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile
435 440 445

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly
450 455 460

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
465 470 475 480

Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro
485 490 495

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
500 505

<210> 306
<211> 495
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.78_65-65 scFv

<400> 306

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
20 25 30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

Ser Val Ser Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
    210                 215                 220

Asp Ser Phe Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
            260                 265                 270
```

```
Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn Glu
        275                 280                 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
    290                 295                 300

Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe Gln
305                 310                 315                 320

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
                325                 330                 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            340                 345                 350

Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu
        355                 360                 365

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
    370                 375                 380

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
385                 390                 395                 400

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser
                405                 410                 415

Val Ser Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
            420                 425                 430

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser
        435                 440                 445

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
    450                 455                 460

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp
465                 470                 475                 480

Ser Phe Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
```

485 490 495

<210> 307
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.79_38-67 scFv

<400> 307

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp
100 105 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
130 135 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145 150 155 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr Leu Ala Trp Tyr Gln

```
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Arg Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            260                 265                 270

Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
        275                 280                 285

Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
    290                 295                 300

Gly Leu Glu Trp Met Gly Gly Ile Thr Pro Met Phe Gly Thr Thr Asp
305                 310                 315                 320

Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
                325                 330                 335

Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350

Ala Val Tyr Tyr Cys Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val
        355                 360                 365

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
    370                 375                 380
```

```
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
385                 390                 395                 400


Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro
                405                 410                 415


Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
            420                 425                 430


Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
        435                 440                 445


Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Asp Arg
    450                 455                 460


Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
465                 470                 475                 480


Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His
                485                 490                 495


Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            500                 505                 510


<210>  308
<211>  505
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.80_38-68 scFv

<400>  308

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp
            100                 105                 110

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
    130                 135                 140

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
145                 150                 155                 160

Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr Leu Ala Trp Tyr Gln
                165                 170                 175

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
    210                 215                 220

Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile Thr Phe Gly Gln Gly
225                 230                 235                 240

Thr Arg Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
```

```
            260                 265                 270

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
        275                 280                 285

Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
    290                 295                 300

Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser
305                 310                 315                 320

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
                325                 330                 335

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350

Ala Val Tyr Tyr Cys Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp
        355                 360                 365

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
385                 390                 395                 400

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                405                 410                 415

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
            420                 425                 430

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        435                 440                 445

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
    450                 455                 460

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
465                 470                 475                 480
```

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile Thr Phe
485 490 495

Gly Gln Gly Thr Arg Leu Glu Ile Lys
500 505

<210> 309
<211> 510
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.81_64-67 scFv

<400> 309

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
130 135 140

```
Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145                 150                 155                 160


Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
                165                 170                 175


Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190


Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205


Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220


Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly
225                 230                 235                 240


Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255


Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            260                 265                 270


Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly
        275                 280                 285


Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln
    290                 295                 300


Gly Leu Glu Trp Met Gly Gly Ile Thr Pro Met Phe Gly Thr Thr Asp
305                 310                 315                 320


Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser
                325                 330                 335


Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350


Ala Val Tyr Tyr Cys Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val
```

```
        355                 360                 365

Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
385                 390                 395                 400

Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro
                405                 410                 415

Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly
            420                 425                 430

Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln
        435                 440                 445

Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Asp Arg
    450                 455                 460

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg
465                 470                 475                 480

Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His
                485                 490                 495

Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            500                 505                 510


<210>  310
<211>  505
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.82_64-68 scFv

<400>  310

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
```

```
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
        115                 120                 125

Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser
    130                 135                 140

Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser
145                 150                 155                 160

Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu
                165                 170                 175

Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser
            180                 185                 190

Leu Gln Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr
        195                 200                 205

Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val
    210                 215                 220

Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly
225                 230                 235                 240
```

```
Thr Lys Val Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                245                 250                 255

Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val
            260                 265                 270

Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr
        275                 280                 285

Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln
    290                 295                 300

Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser
305                 310                 315                 320

Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser
                325                 330                 335

Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
            340                 345                 350

Ala Val Tyr Tyr Cys Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp
        355                 360                 365

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly
    370                 375                 380

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
385                 390                 395                 400

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
                405                 410                 415

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
            420                 425                 430

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
        435                 440                 445

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
```

```
    450                 455                 460

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
465                 470                 475                 480

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile Thr Phe
                485                 490                 495

Gly Gln Gly Thr Arg Leu Glu Ile Lys
            500                 505

<210>  311
<211>  504
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.83_65-67 scFv

<400>  311

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
```

```
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

Ser Val Ser Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
    210                 215                 220

Asp Ser Phe Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser
            260                 265                 270

Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala
        275                 280                 285

Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
    290                 295                 300

Gly Ile Thr Pro Met Phe Gly Thr Thr Asp Tyr Ala Gln Lys Phe Gln
305                 310                 315                 320

Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met
                325                 330                 335
```

```
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            340                 345                 350

Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile Trp Gly
        355                 360                 365

Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
    370                 375                 380

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
385                 390                 395                 400

Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg
                405                 410                 415

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
            420                 425                 430

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala
        435                 440                 445

Ser Asn Leu Glu Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
    450                 455                 460

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val
465                 470                 475                 480

Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly
                485                 490                 495

Gln Gly Thr Lys Val Glu Ile Lys
            500
```

<210> 312
<211> 499
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.84_65-68 scFv

<400> 312

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
        115                 120                 125

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
    130                 135                 140

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
145                 150                 155                 160

Ser Val Ser Arg Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
                165                 170                 175

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
            180                 185                 190

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
        195                 200                 205

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
```

```
    210                 215                 220

Asp Ser Phe Pro Val Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
225                 230                 235                 240

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln
                245                 250                 255

Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser
            260                 265                 270

Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr
        275                 280                 285

Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly
    290                 295                 300

Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser Tyr Ala Asp Lys Phe Gln
305                 310                 315                 320

Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
                325                 330                 335

Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala
            340                 345                 350

Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val Trp Gly
        355                 360                 365

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
    370                 375                 380

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
385                 390                 395                 400

Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln
                405                 410                 415

Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro
            420                 425                 430
```

```
Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr
        435                 440                 445

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
    450                 455                 460

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
465                 470                 475                 480

Gln Gln Ser Tyr Asp Gly Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu
                485                 490                 495

Glu Ile Lys
```

<210> 313
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03 construct

<400> 313

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Gly His Tyr Leu His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
                85                  90                  95
```

```
Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Val Arg Gly Ser Gly Trp Tyr Asp Leu
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Thr Tyr Leu Ala Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ile Pro Leu Thr Phe Gly Gln
            260                 265                 270

Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
```

```
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525
```

```
Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys
```

<210> 314

<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02 construct

<400> 314

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asn Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
85 90 95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Leu Gly Val Ala Gly Tyr
130 135 140

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
165 170 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val

```
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Asn Trp Leu Ala Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Pro Pro Pro Thr Phe Gly
            260                 265                 270

Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400
```

```
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
```

610 615 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625 630 635 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
645 650 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
660 665 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
675 680 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 315
<211> 732
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06 construct

<400> 315

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser

```
    50                  55                  60

Gly Tyr Thr Phe Thr Gly Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Ser Gly Ile Asp Gly
    130                 135                 140

Tyr Ile Gly Phe Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
145                 150                 155                 160

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                165                 170                 175

Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
            180                 185                 190

Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His
        195                 200                 205

Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln
    210                 215                 220

Ser Pro Gln Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val
225                 230                 235                 240

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
                245                 250                 255

Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln
            260                 265                 270
```

```
Ala Leu Gln Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
        275                 280                 285

Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
    290                 295                 300

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
305                 310                 315                 320

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
                325                 330                 335

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
            340                 345                 350

Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala
        355                 360                 365

His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu
    370                 375                 380

Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser
385                 390                 395                 400

Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
                405                 410                 415

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys
            420                 425                 430

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
        435                 440                 445

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
    450                 455                 460

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
465                 470                 475                 480

His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
```

```
                485                 490                 495

Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly
            500                 505                 510

Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro
        515                 520                 525

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
    530                 535                 540

His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys
545                 550                 555                 560

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
                565                 570                 575

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
            580                 585                 590

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
        595                 600                 605

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
    610                 615                 620

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
625                 630                 635                 640

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
                645                 650                 655

Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
            660                 665                 670

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
        675                 680                 685

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
    690                 695                 700
```

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
705 710 715 720

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
725 730

<210> 316
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04 construct

<400> 316

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Gly Thr Phe Arg Ser His Val Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asp Pro Ser Gly Gly Ser
85 90 95

Thr Ser Tyr Ala Gln Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Tyr Thr Gly Leu Leu Gly
130 135 140

```
Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190


Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Thr Tyr Leu Ala Trp
        195                 200                 205


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
    210                 215                 220


Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Phe Thr Phe Gly
            260                 265                 270


Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285


Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300


Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320


Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335


Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350


Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
```

```
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575
```

```
Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 317
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05 construct

<400> 317

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Ile Asp Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn
                85                  90                  95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Leu Ser Gly Tyr Asp Leu
    130                 135                 140

Asp Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
```

```
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ser Pro Leu Thr Phe Gly
            260                 265                 270

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445
```

```
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
```

660 665 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
675 680 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 318
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07 construct

<400> 318

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
85 90 95

Thr Lys Tyr Ala His Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp

```
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Leu Ser Gly Tyr Asp Phe
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Tyr Arg Trp Pro Ile Thr Phe Gly Gln
            260                 265                 270

Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320
```

```
Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
```

```
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys


<210>  319
<211>  723
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11 construct

<400> 319

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn
                85                  90                  95


Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Thr Asp Val Tyr Gly Asp
    130                 135                 140


Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160


Gly Gly Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190
```

```
Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Tyr Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Ile Pro Pro Thr Phe Gly
            260                 265                 270

Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
```

```
               405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620
```

```
Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640


Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655


Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670


Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685


Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700


Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720


Leu Tyr Cys
```

<210> 320
<211> 730
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03 construct

<400> 320

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60
```

```
Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
                85                  90                  95

Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Gly Thr Ala Met Ala
    130                 135                 140

Thr Gly Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr
145                 150                 155                 160

Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
                165                 170                 175

Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
            180                 185                 190

Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp
        195                 200                 205

Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro
    210                 215                 220

Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser
225                 230                 235                 240

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser
                245                 250                 255

Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr
            260                 265                 270

Ser Thr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr
```

```
        275                 280                 285

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
    290                 295                 300

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
305                 310                 315                 320

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
                325                 330                 335

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
            340                 345                 350

Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys
        355                 360                 365

Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala
    370                 375                 380

Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser
385                 390                 395                 400

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
                405                 410                 415

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
            420                 425                 430

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
        435                 440                 445

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
    450                 455                 460

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
465                 470                 475                 480

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
                485                 490                 495
```

```
Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly
            500                 505                 510

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
        515                 520                 525

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
    530                 535                 540

Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
            660                 665                 670

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
        675                 680                 685

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
    690                 695                 700

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
```

705 710 715 720

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
725 730

<210> 321
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04 construct

<400> 321

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Ser Asn Gly Gly Tyr
85 90 95

Thr Gly Tyr Ala Leu Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Ser Asn Tyr Gly Gly His
130 135 140

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly

```
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
                165                 170                 175

Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220

Leu Ile Tyr Gln Ala Ser Ser Leu Glu Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp
            260                 265                 270

Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
    290                 295                 300

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365
```

```
Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
385                 390                 395                 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
```

```
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655

Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            660                 665                 670

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        675                 680                 685

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    690                 695                 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705                 710                 715                 720

Ser Leu Val Ile Thr Leu Tyr Cys
                725
```

<210> 322
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05 construct

<400> 322

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
```

```
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Met Gly Ala Trp Ala Ala
    130                 135                 140

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
    210                 215                 220

Thr Ser Thr Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240
```

```
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr Phe Gly
            260                 265                 270

Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
```

```
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670
```

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
675 680 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 323
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06 construct

<400> 323

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Asp
85 90 95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

```
Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Val Asn Asp Tyr Gly Asp
    130                 135                 140

Tyr Asp Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe
            260                 265                 270

Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
```

```
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540
```

```
Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 324
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07 construct

<400> 324

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95


Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Gly Asp Tyr Asp Ala
    130                 135                 140


Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175


Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190


Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Asn Trp Leu Ala
```

```
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
    210                 215                 220

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ser Pro Pro Thr Phe
            260                 265                 270

Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415
```

```
Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
```

625 630 635 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
645 650 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
660 665 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
675 680 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 325
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08 construct

<400> 325

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro

```
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Asp Gly Ser
                85                  90                  95

Thr Ile Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Val Lys Glu Glu Ala Trp Tyr Phe Asp
    130                 135                 140

Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
                165                 170                 175

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
            180                 185                 190

Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
    210                 215                 220

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
                245                 250                 255

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe Gly Gly Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
        275                 280                 285
```

```
Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
    290                 295                 300

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
305                 310                 315                 320

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
                325                 330                 335

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg
            340                 345                 350

Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr
        355                 360                 365

Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            420                 425                 430

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465                 470                 475                 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490                 495

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
```

```
            500                 505                 510

Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro
        515                 520                 525

Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile
    530                 535                 540

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
545                 550                 555                 560

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
                565                 570                 575

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
            580                 585                 590

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
        595                 600                 605

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
    610                 615                 620

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
625                 630                 635                 640

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro
                645                 650                 655

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
            660                 665                 670

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
        675                 680                 685

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
    690                 695                 700

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
705                 710                 715                 720
```

Cys

<210> 326
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09 construct

<400> 326

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asp Asn Gly Asp
                85                  90                  95


Thr Gly Tyr Ala Gln Met Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Ser Gly Asp Tyr Tyr Asp Ile Leu
    130                 135                 140


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160
```

```
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
                165                 170                 175

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
            180                 185                 190

Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Val Ser Asn
    210                 215                 220

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
                245                 250                 255

Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu Thr Phe Gly Gly Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
        275                 280                 285

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
    290                 295                 300

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
305                 310                 315                 320

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
                325                 330                 335

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg
            340                 345                 350

Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr
        355                 360                 365

Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
```

```
    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            420                 425                 430

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465                 470                 475                 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490                 495

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
            500                 505                 510

Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro
        515                 520                 525

Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile
    530                 535                 540

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
545                 550                 555                 560

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
                565                 570                 575

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
            580                 585                 590
```

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
595 600 605

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
610 615 620

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
625 630 635 640

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro
645 650 655

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
660 665 670

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
675 680 685

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
690 695 700

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
705 710 715 720

Cys

<210> 327
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11 construct

<400> 327

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

```
Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asp
                85                  90                  95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Ser Gly Tyr Glu Phe
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
```

```
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Ile Ser Phe Pro Leu Thr Phe Gly Gly
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460
```

```
Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
```

675 680 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
690 695 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705 710 715 720

Tyr Cys

<210> 328
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06 construct

<400> 328

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Asn Ser Gly Gly
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu

```
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Phe Ser Val Tyr Ala Ala
    130                 135                 140

Ala Asp Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Asp Ala Ser Asn Leu Ala Thr Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Ser Pro Leu
            260                 265                 270

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335
```

```
Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
```

545 550 555 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
565 570 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
580 585 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
595 600 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
610 615 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625 630 635 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
645 650 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 329
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09 construct

<400> 329

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Gly Asp Gly Gly
                85                  90                  95

Thr Ile Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Phe Gly Glu Ser Ala Pro
    130                 135                 140

Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                165                 170                 175

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
            180                 185                 190

Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu
        195                 200                 205
```

```
Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
    210                 215                 220

Gly Ala Thr Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
225                 230                 235                 240

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
                245                 250                 255

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Tyr Thr
            260                 265                 270

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
        275                 280                 285

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
    290                 295                 300

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
305                 310                 315                 320

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
                325                 330                 335

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
            340                 345                 350

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly
        355                 360                 365

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr
    370                 375                 380

Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
385                 390                 395                 400

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
                405                 410                 415

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
```

```
            420                 425                 430

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
        435                 440                 445

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
    450                 455                 460

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
465                 470                 475                 480

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
                485                 490                 495

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
            500                 505                 510

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
        515                 520                 525

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp
    530                 535                 540

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
545                 550                 555                 560

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
                565                 570                 575

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
            580                 585                 590

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
        595                 600                 605

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
    610                 615                 620

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
625                 630                 635                 640
```

```
Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
                645                 650                 655

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
            660                 665                 670

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
        675                 680                 685

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
    690                 695                 700

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
705                 710                 715                 720

Ile Thr Leu Tyr Cys
                725
```

<210> 330
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03 construct

<400> 330

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80
```

```
Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Ala Gly Thr Glu Ile Tyr Tyr Met
    130                 135                 140

Asp Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Thr Ile Asp Ile Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Leu Thr Phe Gly Gly
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
```

```
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510
```

```
Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys
```

<210> 331
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04 construct

<400> 331

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20   25   30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35   40   45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50   55   60

Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro
65   70   75   80

Gly Gln Gly Leu Glu Trp Met Gly Met Ile Asn Pro Ser Asp Gly Ala
                85   90   95

Thr Thr Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100   105   110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115   120   125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Glu Leu Leu His Phe
    130   135   140

Ala Thr Asn Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr
145   150   155   160

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser

```
                165                 170                 175

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
            180                 185                 190

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln
        195                 200                 205

Gly Ile Ser Asn Asn Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
    210                 215                 220

Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro
225                 230                 235                 240

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
                245                 250                 255

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala
            260                 265                 270

Asp Ala Phe Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
        275                 280                 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
    290                 295                 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
305                 310                 315                 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
                325                 330                 335

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
            340                 345                 350

Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His
        355                 360                 365

Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln
    370                 375                 380
```

```
Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg
385                 390                 395                 400

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
                405                 410                 415

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            420                 425                 430

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
        435                 440                 445

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
    450                 455                 460

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
465                 470                 475                 480

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
                485                 490                 495

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
            500                 505                 510

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
        515                 520                 525

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
    530                 535                 540

Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
545                 550                 555                 560

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
                565                 570                 575

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
            580                 585                 590

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
```

595 600 605

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
610 615 620

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
625 630 635 640

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
645 650 655

Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
660 665 670

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
675 680 685

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
690 695 700

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
705 710 715 720

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
725 730

<210> 332
<211> 727
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07 construct

<400> 332

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala

```
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Arg Asn Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Ser Pro Asp Asn Gly Val
                85                  90                  95

Thr Asn Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Thr Gln Gly Ser Ser Ser Trp
    130                 135                 140

Tyr Gln Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val
145                 150                 155                 160

Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                165                 170                 175

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
            180                 185                 190

Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr
        195                 200                 205

Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
    210                 215                 220

Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
225                 230                 235                 240

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
                245                 250                 255
```

```
Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro
            260                 265                 270

Ile Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro
        275                 280                 285

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
    290                 295                 300

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
305                 310                 315                 320

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
                325                 330                 335

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
            340                 345                 350

Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
        355                 360                 365

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
    370                 375                 380

Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
385                 390                 395                 400

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
                405                 410                 415

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
            420                 425                 430

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
        435                 440                 445

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
    450                 455                 460

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
```

```
465                 470                 475                 480

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
                485                 490                 495

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
            500                 505                 510

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val
        515                 520                 525

Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro
    530                 535                 540

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
545                 550                 555                 560

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
                565                 570                 575

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
            580                 585                 590

Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
        595                 600                 605

Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
    610                 615                 620

Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
625                 630                 635                 640

Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
                645                 650                 655

Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
            660                 665                 670

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
        675                 680                 685
```

```
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
    690                 695                 700


Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
705                 710                 715                 720


Leu Val Ile Thr Leu Tyr Cys
                725


<210>  333
<211>  723
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.24_CD70_DB02_D02 construct

<400>  333

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asp Pro Gly Ser Gly Asp
                85                  90                  95


Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125
```

```
Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Asn Trp Tyr Asp Tyr
    130                 135                 140

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Ile Val
                165                 170                 175

Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly Glu Arg Ala
            180                 185                 190

Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr Gly Ala
    210                 215                 220

Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe
                245                 250                 255

Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Tyr Pro Pro Thr Phe Gly
            260                 265                 270

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
```

```
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560
```

```
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 334
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04 construct

<400> 334

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Arg Leu Ser Asp His Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Thr Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Ser Ser Tyr Tyr Gly Asp Tyr Val
    130                 135                 140

Leu Val Asn Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
```

```
    210                 215                 220

Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asp Tyr Pro Leu Thr Phe Gly
            260                 265                 270

Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430
```

```
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
```

```
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 335
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10 construct

<400> 335

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Val His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Thr Gly Gly
```

```
                85                  90                  95

Thr Ser Phe Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Gln Trp Leu Gly
    130                 135                 140

Glu Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Tyr Lys Trp Leu Ala
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe Thr Phe
            260                 265                 270

Gly Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300
```

```
Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
```

```
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 336
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11 construct

<400> 336

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20   25   30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35   40   45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50   55   60

Gly Tyr Thr Phe Thr Asp Tyr Thr Asp Tyr Phe Val His Trp Val Arg
65   70   75   80

Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Phe Asn Pro Ser
                85   90   95

Asp Gly Ser Thr Ser Tyr Ala Gln Glu Phe Gln Gly Arg Val Thr Met
            100   105   110

Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu
        115   120   125

Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Pro Tyr Ser
    130   135   140

Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
145   150   155   160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165   170   175

```
Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            180                 185                 190

Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser
        195                 200                 205

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe
            260                 265                 270

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
    290                 295                 300

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365

Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
```

```
385                 390                 395                 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605
```

```
Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655

Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            660                 665                 670

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        675                 680                 685

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    690                 695                 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705                 710                 715                 720

Ser Leu Val Ile Thr Leu Tyr Cys
                725
```

<210> 337
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.28_CD70_DB02_E04 construct

<400> 337

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45
```

```
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Ile Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Asp
                85                  90                  95

Thr Leu Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Val Gly Ala Met Gly
    130                 135                 140

Val Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Thr Ser Ile Ser Asp Tyr Val His
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Thr Pro Pro Thr Phe
```

```
            260                 265                 270

Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480
```

```
Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
```

690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 338
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06 construct

<400> 338

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asp His Tyr Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Lys
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Thr Ile Tyr Tyr Asp Phe

```
    130                 135                 140

Trp Ser Gly Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile
            260                 265                 270

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350
```

```
Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
```

565 570 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
580 585 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
595 600 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
610 615 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625 630 635 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
645 650 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 339
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08 construct

<400> 339

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ala
                85                  90                  95

Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Arg Gly Asp Tyr Tyr Gly
    130                 135                 140

Ser Gly Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220
```

```
Tyr Asp Ala Ser Thr Leu Glu Ala Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Pro Pro Tyr
            260                 265                 270


Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285


Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300


Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320


Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335


Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350


Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365


Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380


Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400


Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415


Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430


Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
```

```
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655
```

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 340
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07 construct

<400> 340

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
85 90 95

```
Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Phe Asp His Ala Phe
    130                 135                 140

Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Ile Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Ser Pro Leu Thr Phe Gly Gln
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
```

```
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525
```

```
Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys
```

<210> 341

<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04 construct

<400> 341

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Asp
85 90 95

Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Asp Ser Ser Ser Trp Tyr
130 135 140

Asp Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr Val Thr
145 150 155 160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
165 170 175

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser

```
            180                 185                 190

Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser
        195                 200                 205

Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr
            260                 265                 270

Pro Leu Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
    290                 295                 300

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365

Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
385                 390                 395                 400
```

```
Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
```

610 615 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625 630 635 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
645 650 655

Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
660 665 670

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
675 680 685

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
690 695 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705 710 715 720

Ser Leu Val Ile Thr Leu Tyr Cys
725

<210> 342
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05 construct

<400> 342

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser

```
    50                  55                  60

Gly Tyr Thr Phe Thr Asp Tyr Phe Thr His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Thr Tyr Asp Gly Asn
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Met Glu Trp Leu Gly Gln
    130                 135                 140

Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp Leu Gly Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Phe Thr Phe Gly
            260                 265                 270
```

```
Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
```

```
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700
```

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 343
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08 construct

<400> 343

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Arg Ile Asn Pro Asn Gly Gly Gly
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly His Arg Gly Gly Gly Gly
130 135 140

```
Ile Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175


Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190


Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Ser Asn Tyr Leu Ala Trp
        195                 200                 205


Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220


Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240


Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255


Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe Thr Phe Gly
            260                 265                 270


Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285


Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300


Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320


Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335


Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350


Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
```

```
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575
```

```
Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 344
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.36_CD70_DB03_A06 construct

<400> 344

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15
```

```
His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Ser Pro Asn Ser Gly Asp
                85                  90                  95

Thr His Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Trp Gly Ser Gly Trp Tyr
    130                 135                 140

Val Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Ser Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala
    210                 215                 220

Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
```

```
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Tyr Thr Phe Gly
            260                 265                 270

Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445
```

```
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
```

660 665 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
675 680 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 345
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07 construct

<400> 345

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Gly Thr Phe Asn Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
85 90 95

Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp

```
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Thr Tyr Gly Asp Asp Ala
    130                 135                 140

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Asn Phe Ser Pro Pro Leu Thr Phe Gly
            260                 265                 270

Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320
```

```
Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
```

```
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys


<210>  346
<211>  728
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> NK77.38_CD70_DB03_A08 construct

<400> 346

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Thr
                85                  90                  95


Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser
    130                 135                 140


Ser Trp Trp Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
145                 150                 155                 160


Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175


Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            180                 185                 190
```

```
Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg
        195                 200                 205

His Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala
            260                 265                 270

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
    290                 295                 300

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365

Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
385                 390                 395                 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
```

```
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620
```

```
Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640


Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655


Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            660                 665                 670


Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        675                 680                 685


Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    690                 695                 700


Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705                 710                 715                 720


Ser Leu Val Ile Thr Leu Tyr Cys
                725
```

<210> 347
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.39_CD70_DB03_A09 construct

<400> 347

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60
```

```
Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Thr Pro Asn Ser Gly Tyr
                85                  90                  95

Thr Tyr Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asn Thr Asp Cys Tyr Gly Asp
    130                 135                 140

Phe Leu Gly Leu Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
            180                 185                 190

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Ser Ser Ile Ser Asn Tyr
        195                 200                 205

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Gly Ala Ser Thr Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
                245                 250                 255

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
            260                 265                 270

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
```

```
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495
```

```
Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
            660                 665                 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
        675                 680                 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
    690                 695                 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
```

705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 348
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11 construct

<400> 348

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Asn Gly Tyr Leu Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Val Asn Pro Ser Asp Gly Ser
85 90 95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Thr Gly Leu Arg Tyr Phe
130 135 140

Asp Trp Leu Leu Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser

```
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Asn Phe
        195                 200                 205

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Gly Ala Pro Leu
            260                 265                 270

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365
```

```
Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
```

```
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
            660                 665                 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
        675                 680                 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
    690                 695                 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705                 710                 715                 720

Val Ile Thr Leu Tyr Cys
                725


<210>  349
<211>  722
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.41_CD70_DB03_A12 construct

<400>  349

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
```

```
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asp Pro Ser Gly Gly Arg
                85                  90                  95

Thr Ile Tyr Ala Gln Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg His Glu Ala Gly Gly Ile Phe
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser
    210                 215                 220

Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240
```

```
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Tyr Arg Phe Gly Gln
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
```

```
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670
```

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
675 680 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
690 695 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705 710 715 720

Tyr Cys

<210> 350
<211> 730
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01 construct

<400> 350

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Ser Asp Ser Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Val Gly Gly Ile Ile Pro Met Ala Gly Ile
85 90 95

Pro Ala Tyr Ala Glu Glu Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
100 105 110

```
Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Asp Asp Tyr Gly Gly Asn
    130                 135                 140

Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                165                 170                 175

Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu
            180                 185                 190

Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
        195                 200                 205

Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
    210                 215                 220

Gln Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Asp
225                 230                 235                 240

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
                245                 250                 255

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Ala
            260                 265                 270

His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr
        275                 280                 285

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
    290                 295                 300

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
305                 310                 315                 320

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
```

```
                325                 330                 335

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
            340                 345                 350

Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys
        355                 360                 365

Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala
    370                 375                 380

Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser
385                 390                 395                 400

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
                405                 410                 415

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
            420                 425                 430

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
        435                 440                 445

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
    450                 455                 460

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
465                 470                 475                 480

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
                485                 490                 495

Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly
            500                 505                 510

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
        515                 520                 525

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
    530                 535                 540
```

```
Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
545                 550                 555                 560

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
                565                 570                 575

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
            580                 585                 590

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
        595                 600                 605

Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
    610                 615                 620

Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
625                 630                 635                 640

Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
                645                 650                 655

Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
            660                 665                 670

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
        675                 680                 685

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
    690                 695                 700

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
705                 710                 715                 720

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                725                 730
```

<210> 351
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.43_CD70_DB03_B04 construct

<400> 351

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Ile Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95


Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Trp Tyr Glu Ser
    130                 135                 140


Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160


Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175


Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190


Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Gly Leu Gly
```

```
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
    210                 215                 220

Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Gly Thr Pro Pro Thr Phe
            260                 265                 270

Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415
```

```
Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
```

625 630 635 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
645 650 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
660 665 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
675 680 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 352
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.44_CD70_DB03_B06 construct

<400> 352

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Leu His Trp Val Arg Gln Ala Pro

```
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly Asn
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Ile Val Gly Ala Thr Glu
    130                 135                 140

Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
            180                 185                 190

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
        195                 200                 205

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
    210                 215                 220

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
                245                 250                 255

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Ser Pro Thr
            260                 265                 270

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro
        275                 280                 285
```

```
Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
    290                 295                 300

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
305                 310                 315                 320

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
                325                 330                 335

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
            340                 345                 350

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly
        355                 360                 365

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr
    370                 375                 380

Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
385                 390                 395                 400

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
                405                 410                 415

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
            420                 425                 430

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
        435                 440                 445

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
    450                 455                 460

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
465                 470                 475                 480

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
                485                 490                 495

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
```

```
            500                 505                 510

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
        515                 520                 525

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp
    530                 535                 540

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
545                 550                 555                 560

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
                565                 570                 575

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
            580                 585                 590

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
        595                 600                 605

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
    610                 615                 620

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
625                 630                 635                 640

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
                645                 650                 655

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
            660                 665                 670

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
        675                 680                 685

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
    690                 695                 700

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
705                 710                 715                 720
```

Ile Thr Leu Tyr Cys
725

<210> 353
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09 construct

<400> 353

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ala Tyr Tyr Leu His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Met Ile Asn Pro Asn Asn Gly Gly
85 90 95

Thr Ile Tyr Ala Gln Thr Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Gly Tyr Val Leu
130 135 140

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145 150 155 160

```
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Ile Thr Phe Gly
            260                 265                 270

Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
```

```
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590
```

```
Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605


Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620


Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640


Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655


Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670


Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685


Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700


Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720


Leu Tyr Cys
```

<210> 354
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.46_CD70_DB03_C05 construct

<400> 354

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30
```

```
Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Met Ile Asn Pro Arg Gly Gly Ser
                85                  90                  95

Thr Thr Tyr Ala Gln Ser Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Leu Gly Asp Tyr Gly Asp
    130                 135                 140

Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Asn Leu Ala Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Tyr Leu Glu Ala Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
```

```
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Thr Phe Gly
            260                 265                 270

Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460
```

```
Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
```

675 680 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 355
<211> 734
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11 construct

<400> 355

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
35 40 45

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
50 55 60

Gly Phe Thr Phe Ser Asn Ser Asp Met Asn Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Ser Gly Gly Gly Asp Thr
85 90 95

Leu Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
100 105 110

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu

```
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Met Ala Ser Ala Leu Asp Ser Ser
    130                 135                 140

Gly Asp Asn Glu Ala Phe Asp Ile Trp Gly Gln Gly Thr Thr Val Thr
145                 150                 155                 160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser
            180                 185                 190

Leu Gly Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu
        195                 200                 205

Tyr Ser Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro
    210                 215                 220

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Asp Ser
225                 230                 235                 240

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
                245                 250                 255

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys
            260                 265                 270

Gln Gln Tyr Tyr Gly Phe Pro Pro Thr Phe Gly Gln Gly Thr Arg Leu
        275                 280                 285

Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
    290                 295                 300

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
305                 310                 315                 320

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
                325                 330                 335
```

```
Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
            340                 345                 350

Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro
        355                 360                 365

Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln
    370                 375                 380

Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys
385                 390                 395                 400

Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln
                405                 410                 415

Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu
            420                 425                 430

Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg
        435                 440                 445

Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met
    450                 455                 460

Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly
465                 470                 475                 480

Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp
                485                 490                 495

Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly
            500                 505                 510

Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro
        515                 520                 525

Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu
    530                 535                 540

Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu
```

```
545                 550                 555                 560

Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu
                565                 570                 575

Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys
            580                 585                 590

Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala
        595                 600                 605

Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser
    610                 615                 620

Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu
625                 630                 635                 640

Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His
                645                 650                 655

Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg
            660                 665                 670

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
        675                 680                 685

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
    690                 695                 700

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
705                 710                 715                 720

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
                725                 730
```

<210> 356
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01 construct

<400> 356

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Asn Gly Gly
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Val Glu Asp Asp Phe Trp Ser
    130                 135                 140

Gly Pro Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Asp Ile Ser Lys Phe
        195                 200                 205
```

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Asp Ala Ser Asn Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Phe Pro Phe
            260                 265                 270

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
```

```
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640
```

```
Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
            660                 665                 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
        675                 680                 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
    690                 695                 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705                 710                 715                 720

Val Ile Thr Leu Tyr Cys
                725
```

<210> 357
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03 construct

<400> 357

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Gly Thr Phe Thr Asn Tyr Ala Phe Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80
```

```
Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Ser Gly Ala
                85                  90                  95

Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Gly Leu Asp Asp Ala
    130                 135                 140

Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
                165                 170                 175

Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala Arg Gln Thr
            260                 265                 270

Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
```

```
    290                 295                 300

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365

Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
385                 390                 395                 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510
```

```
Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655

Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            660                 665                 670

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        675                 680                 685

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    690                 695                 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705                 710                 715                 720

Ser Leu Val Ile Thr Leu Tyr Cys
```

725

<210> 358
<211> 738
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09 construct

<400> 358

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ala Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn
85 90 95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Arg Ile Asp Tyr Gly
130 135 140

Asp Tyr Asp Asp Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
145 150 155 160

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly

```
                165                 170                 175

Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu
            180                 185                 190

Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser
        195                 200                 205

Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr
    210                 215                 220

Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Ala Ala Ser
225                 230                 235                 240

Asn Leu Gln Gly Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly
                245                 250                 255

Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly
            260                 265                 270

Val Tyr Tyr Cys Met Gln Thr Leu Glu Ser Pro Val Thr Phe Gly Gly
        275                 280                 285

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
    290                 295                 300

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
305                 310                 315                 320

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
                325                 330                 335

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
            340                 345                 350

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
        355                 360                 365

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
    370                 375                 380
```

```
Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
385                 390                 395                 400

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
                405                 410                 415

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
            420                 425                 430

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
        435                 440                 445

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
    450                 455                 460

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
465                 470                 475                 480

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
                485                 490                 495

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
            500                 505                 510

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
        515                 520                 525

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
    530                 535                 540

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
545                 550                 555                 560

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
                565                 570                 575

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
            580                 585                 590

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
```

595 600 605

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
610 615 620

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
625 630 635 640

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
645 650 655

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
660 665 670

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
675 680 685

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
690 695 700

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
705 710 715 720

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
725 730 735

Tyr Cys

<210> 359
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02 construct

<400> 359

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly

```
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Val His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Thr Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Gln Gly Leu Trp Phe Thr
    130                 135                 140

Gly Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Asn Leu Glu Arg Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240
```

```
Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile Thr Phe
            260                 265                 270

Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
```

```
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670
```

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
675 680 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 360
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05 construct

<400> 360

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ala Tyr His Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Gly Asp Gly Ala
85 90 95

Thr Gly Tyr Ala Gln Asn Leu Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

```
Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Gly Glu Gly Ile Ser Gly Ser Asp
    130                 135                 140

Ala Phe Asp Ile Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala
    210                 215                 220

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Ser Tyr Pro Leu Thr Phe
            260                 265                 270

Gly Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
```

```
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540
```

```
Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 361
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06 construct

<400> 361

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn
                85                  90                  95


Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110


Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Trp Gly Val Asp Pro Tyr Tyr Phe
    130                 135                 140


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175


Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190


Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Arg Trp Leu Ala Trp Tyr
```

```
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Leu Thr Phe Gly Gly
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415
```

```
Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
```

625 630 635 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
645 650 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
660 665 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
675 680 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
690 695 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705 710 715 720

Tyr Cys

<210> 362
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09 construct

<400> 362

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro

```
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Phe Asn Pro Ser Asp Gly Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Val Gly Glu Thr Thr Phe
    130                 135                 140

Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Thr Asn Ser Phe Pro Ile Thr Phe Gly Gln
            260                 265                 270

Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285
```

```
Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
```

```
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605

Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720
```

Tyr Cys

<210> 363
<211> 727
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.55_CD70_DB03_F12 construct

<400> 363

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Ser Ala Tyr Asn Gly His
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Val Arg Gly Trp Asp
    130                 135                 140

Tyr Tyr Tyr Gly Met Gly Val Trp Gly Gln Gly Thr Thr Val Thr Val
145                 150                 155                 160
```

```
Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
                165                 170                 175

Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
            180                 185                 190

Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Asn
        195                 200                 205

Phe Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu
    210                 215                 220

Ile Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser
225                 230                 235                 240

Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln
                245                 250                 255

Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro
            260                 265                 270

Ser Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro
        275                 280                 285

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
    290                 295                 300

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
305                 310                 315                 320

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
                325                 330                 335

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
            340                 345                 350

Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly
        355                 360                 365

Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His
```

```
    370                 375                 380

Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala
385                 390                 395                 400

Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu
                405                 410                 415

Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp
            420                 425                 430

Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu
        435                 440                 445

Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile
    450                 455                 460

Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr
465                 470                 475                 480

Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met
                485                 490                 495

Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu
            500                 505                 510

Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val
        515                 520                 525

Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro
    530                 535                 540

Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile
545                 550                 555                 560

Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His
                565                 570                 575

Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln
            580                 585                 590
```

```
Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu
        595                 600                 605


Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
    610                 615                 620


Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile
625                 630                 635                 640


Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn
                645                 650                 655


Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
            660                 665                 670


Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
        675                 680                 685


Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
    690                 695                 700


Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
705                 710                 715                 720


Leu Val Ile Thr Leu Tyr Cys
                725


<210>  364
<211>  724
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.56_CD70_DB03_G06 construct

<400>  364

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30
```

```
Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Ile Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro His Ser Gly Asn
                85                  90                  95

Ser Asp Asn Ala Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Tyr Ser Gly Tyr Asp Leu
    130                 135                 140

Thr Ala Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
```

```
               245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile Thr Phe
            260                 265                 270

Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
               325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
               405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460
```

```
Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
```

675 680 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 365
<211> 733
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11 construct

<400> 365

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Gly Gln Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Thr Gly Asp
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu

```
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Val Phe Glu Val Glu
    130                 135                 140

Gly Gly Thr Asp Tyr Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln
145                 150                 155                 160

Gly Thr Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
            180                 185                 190

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
        195                 200                 205

Ser Glu Thr Ile Ser Gly Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly
    210                 215                 220

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly
225                 230                 235                 240

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
                245                 250                 255

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
            260                 265                 270

Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly Gln Gly Thr Lys Leu Glu
        275                 280                 285

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
    290                 295                 300

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
305                 310                 315                 320

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
                325                 330                 335
```

```
Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
            340                 345                 350

Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp
        355                 360                 365

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu
    370                 375                 380

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe
385                 390                 395                 400

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
                405                 410                 415

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
            420                 425                 430

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
        435                 440                 445

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
    450                 455                 460

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
465                 470                 475                 480

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
                485                 490                 495

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
            500                 505                 510

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
        515                 520                 525

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
    530                 535                 540

Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys
```

545 550 555 560

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
565 570 575

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
580 585 590

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
595 600 605

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
610 615 620

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
625 630 635 640

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
645 650 655

Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro
660 665 670

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
675 680 685

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
690 695 700

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
705 710 715 720

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
725 730

<210> 366
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.58_CD70_DB03_H08 construct

<400> 366

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Ser Gly Gly Gly
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Ser Gly Tyr Asp Trp Val
    130                 135                 140

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Ser Trp Leu Ala Trp
        195                 200                 205
```

```
Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala
    210                 215                 220

Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp Thr Phe Gly
            260                 265                 270

Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
```

```
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640
```

```
Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 367
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.59_CD70_DB03_H10 construct

<400> 367

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Ala Asn Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80
```

```
Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Ser Tyr Phe Gly
    130                 135                 140

Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser Leu Ala
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro Thr Phe
            260                 265                 270

Gly Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
```

```
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510
```

```
Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 368
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.60_CD70_DB04_A05 construct

<400> 368

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1   5   10   15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20   25   30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35   40   45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50   55   60

Gly Tyr Thr Phe Thr Thr Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65   70   75   80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Thr Gly Gly Ser
                85   90   95

Thr Tyr Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100   105   110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115   120   125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Asn Tyr Gln Gly
    130   135   140

Ile Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145   150   155   160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile

```
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Gly Tyr Leu Ala
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ser Pro Pro Thr Phe
            260                 265                 270

Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380
```

```
Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400


Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415


Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430


Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445


Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460


Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480


Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495


Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510


Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525


Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540


Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560


His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575


Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590


Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
```

```
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 369
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.61_CD70_DB04_A07 construct

<400> 369

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
```

```
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Asn Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Asp
                85                  90                  95

Thr Asn Tyr Ala Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Val Ser Gly Tyr Asp Leu
    130                 135                 140

Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Thr
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255
```

```
Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Leu Thr Phe Gly
            260                 265                 270

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
```

```
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685
```

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 370
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.62_CD70_DB04_A10 construct

<400> 370

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Val Glu Ser Gly Gly
35 40 45

Gly Leu Val Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
50 55 60

Gly Phe Thr Phe Ser Ser Tyr Gly Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Lys Gly Leu Glu Trp Val Ala Ser Ile Lys His Asp Gly Ser Glu
85 90 95

Gln Tyr Tyr Val Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
100 105 110

Asp Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu
115 120 125

```
Asp Thr Ala Val Tyr Tyr Cys Ala Ala Ser Gly Val Asp Val Trp Gly
    130                 135                 140

Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro
                165                 170                 175

Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg
            180                 185                 190

Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp
        195                 200                 205

Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Leu Gly
    210                 215                 220

Ser Thr Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val
                245                 250                 255

Gly Val Tyr Tyr Cys Met Gln Ala Leu Asp Thr Pro Leu Thr Phe Gly
            260                 265                 270

Gly Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
```

```
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560
```

```
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 371
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.63_CD70_DB04_A11 construct

<400> 371

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Gly Thr Phe Ser Arg Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Val Gly Ile Ile Asp Pro Thr Gly Ala Ser
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Tyr Ser Tyr Gly Met Asp
    130                 135                 140

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
```

```
    210                 215                 220

Tyr Asp Thr Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Leu Ser Thr Asp Leu Gln Thr Thr Ala
            260                 265                 270

His Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430
```

```
Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
```

645 650 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 372
<211> 728
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.64_CD70_DB04_B03 construct

<400> 372

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr

```
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Gly Asp Gly Tyr
    130                 135                 140

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
                165                 170                 175

Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp
            260                 265                 270

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr
        275                 280                 285

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
    290                 295                 300
```

```
Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
305                 310                 315                 320

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
                325                 330                 335

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
            340                 345                 350

Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro
        355                 360                 365

Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala
    370                 375                 380

His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp
385                 390                 395                 400

Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn
                405                 410                 415

Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg
            420                 425                 430

Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly
        435                 440                 445

Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu
    450                 455                 460

Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu
465                 470                 475                 480

Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His
                485                 490                 495

Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu
            500                 505                 510

Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro
```

```
        515                 520                 525

Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg
    530                 535                 540

Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu
545                 550                 555                 560

Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val
                565                 570                 575

His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu
            580                 585                 590

Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val
        595                 600                 605

Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn
    610                 615                 620

Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn
625                 630                 635                 640

Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile
                645                 650                 655

Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro
            660                 665                 670

Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro
        675                 680                 685

Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp
    690                 695                 700

Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu
705                 710                 715                 720

Ser Leu Val Ile Thr Leu Tyr Cys
                725
```

<210> 373
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.65_CD70_DB04_B05 construct

<400> 373

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
                85                  90                  95


Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe
    130                 135                 140


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175
```

```
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe Gly Gln
            260                 265                 270

Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
```

```
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605
```

```
Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys
```

<210> 374
<211> 725
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.66_CD70_DB04_B07 construct

<400> 374

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45
```

```
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asn Tyr Tyr Ile Tyr Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Asp Gly Ala
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Gly Asn Asp Tyr Tyr Tyr
    130                 135                 140

Tyr Phe Met Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
145                 150                 155                 160

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
                165                 170                 175

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
            180                 185                 190

Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu
        195                 200                 205

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
    210                 215                 220

His Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser
225                 230                 235                 240

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
                245                 250                 255

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Met Thr
```

```
            260                 265                 270

Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
        275                 280                 285

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
    290                 295                 300

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
305                 310                 315                 320

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
                325                 330                 335

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
            340                 345                 350

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly
        355                 360                 365

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr
    370                 375                 380

Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
385                 390                 395                 400

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
                405                 410                 415

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
            420                 425                 430

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
        435                 440                 445

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
    450                 455                 460

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
465                 470                 475                 480
```

```
Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
                485                 490                 495

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
            500                 505                 510

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
        515                 520                 525

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp
    530                 535                 540

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
545                 550                 555                 560

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
                565                 570                 575

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
            580                 585                 590

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
        595                 600                 605

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
    610                 615                 620

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
625                 630                 635                 640

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
                645                 650                 655

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
            660                 665                 670

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
        675                 680                 685

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
```

690 695 700

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
705 710 715 720

Ile Thr Leu Tyr Cys
725

<210> 375
<211> 731
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.67_CD70_DB04_C01 construct

<400> 375

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Thr Pro Met Phe Gly Thr
85 90 95

Thr Asp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
100 105 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Glu Arg Asp Gly Tyr Ala

```
    130                 135                 140

Thr Val Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
            180                 185                 190

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
        195                 200                 205

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
    210                 215                 220

Pro Gln Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
225                 230                 235                 240

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
                245                 250                 255

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
            260                 265                 270

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
        275                 280                 285

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
    290                 295                 300

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
305                 310                 315                 320

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
                325                 330                 335

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
            340                 345                 350
```

```
Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His
        355                 360                 365

Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln
    370                 375                 380

Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg
385                 390                 395                 400

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
                405                 410                 415

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
            420                 425                 430

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
        435                 440                 445

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
    450                 455                 460

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
465                 470                 475                 480

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
                485                 490                 495

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
            500                 505                 510

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
        515                 520                 525

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
    530                 535                 540

Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
545                 550                 555                 560

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
```

565 570 575

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
580 585 590

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
595 600 605

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
610 615 620

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
625 630 635 640

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
645 650 655

Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
660 665 670

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
675 680 685

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
690 695 700

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
705 710 715 720

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
725 730

<210> 376
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04 construct

<400> 376

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu

```
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Asp Gly Gly
                85                  90                  95

Thr Ser Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Ala Pro Leu Gly Trp
    130                 135                 140

Gly Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220
```

```
Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile
            260                 265                 270

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
```

```
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655
```

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 377
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.69_CD70_DB04_C06 construct

<400> 377

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Ser Ser Gly Val
85 90 95

```
Thr Asn Phe Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Gly Ser Asp Gln Gly Asp Trp
    130                 135                 140

Ser Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro Thr Phe Gly
            260                 265                 270

Gly Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
```

```
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480

Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525
```

```
Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
    690                 695                 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr
705                 710                 715                 720

Leu Tyr Cys
```

<210> 378

<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07 construct

<400> 378

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Asp Ser Tyr Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Ile Gly Trp Met Asn Pro Asn Thr Gly Asp
85 90 95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Lys Asp Asp Phe Gly Glu Leu Ala
130 135 140

Pro Ala Thr Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr Val Ser
145 150 155 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
165 170 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

```
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
        195                 200                 205

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ala Ala Thr Pro Ile
            260                 265                 270

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400
```

```
Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
```

610 615 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625 630 635 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
645 650 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 379
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02 construct

<400> 379

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser

```
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Asp Ile Asn Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Val Ile Ser Pro Ser Gly Gly Gly
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Tyr Tyr Gly Gly Asn Pro Glu
    130                 135                 140

Gly Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Asn Trp
        195                 200                 205

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    210                 215                 220

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Trp
            260                 265                 270
```

```
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430

Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
```

```
               485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
                645                 650                 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
            660                 665                 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
        675                 680                 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
    690                 695                 700
```

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 380
<211> 741
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05 construct

<400> 380

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Glu Val Gln Leu Leu Glu Ser Gly Gly
35 40 45

Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser
50 55 60

Gly Phe Val Phe Asp Asp Tyr Ala Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Lys Gly Leu Glu Trp Val Ala Ala Ile Ser Tyr Asp Gly Ser Asn
85 90 95

Lys Tyr Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp
100 105 110

Asn Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Pro Gln Tyr Tyr Gly Ser
130 135 140

```
Gly Thr Asp Pro Leu Glu Val Arg Tyr Tyr Tyr Tyr Gly Met Asp Val
145                 150                 155                 160


Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser
                165                 170                 175


Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
            180                 185                 190


Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
        195                 200                 205


Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu
    210                 215                 220


Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
225                 230                 235                 240


Glu Val Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
                245                 250                 255


Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu
            260                 265                 270


Asp Val Gly Val Tyr Tyr Cys Met Lys Gly Leu Gln Thr Pro Leu Thr
        275                 280                 285


Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Thr Thr Thr Pro Ala Pro
    290                 295                 300


Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
305                 310                 315                 320


Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
                325                 330                 335


Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
            340                 345                 350


Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
```

```
        355                 360                 365

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly
    370                 375                 380

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr
385                 390                 395                 400

Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
                405                 410                 415

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
            420                 425                 430

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
        435                 440                 445

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
    450                 455                 460

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
465                 470                 475                 480

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
                485                 490                 495

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
            500                 505                 510

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
        515                 520                 525

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
    530                 535                 540

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp
545                 550                 555                 560

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                565                 570                 575
```

```
Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            580                 585                 590

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
        595                 600                 605

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
    610                 615                 620

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
625                 630                 635                 640

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
                645                 650                 655

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            660                 665                 670

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
        675                 680                 685

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
    690                 695                 700

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
705                 710                 715                 720

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
                725                 730                 735

Ile Thr Leu Tyr Cys
            740
```

<210> 381
<211> 726
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.73_CD70_DB04_D07 construct

<400> 381

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Gly Thr Phe Arg Asn Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
                85                  90                  95

Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Ala Gly Thr His
    130                 135                 140

His Asp Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
                165                 170                 175

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
            180                 185                 190

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
        195                 200                 205

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
```

```
    210                 215                 220

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
225                 230                 235                 240

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
                245                 250                 255

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Thr Pro Leu
            260                 265                 270

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala
        275                 280                 285

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    290                 295                 300

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
305                 310                 315                 320

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                325                 330                 335

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            340                 345                 350

Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly
        355                 360                 365

Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser
    370                 375                 380

Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro
385                 390                 395                 400

Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly
                405                 410                 415

Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro
            420                 425                 430
```

```
Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr
        435                 440                 445

Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly
    450                 455                 460

Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln
465                 470                 475                 480

Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln
                485                 490                 495

Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr
            500                 505                 510

Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr
        515                 520                 525

Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn
    530                 535                 540

Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln
545                 550                 555                 560

Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro
                565                 570                 575

Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val
            580                 585                 590

Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn
        595                 600                 605

Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr
    610                 615                 620

Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys
625                 630                 635                 640

Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr
```

645 650 655

Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile
660 665 670

Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala
675 680 685

Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr
690 695 700

Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu
705 710 715 720

Val Ile Thr Leu Tyr Cys
725

<210> 382
<211> 721
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.74_CD70_DB04_D08 construct

<400> 382

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Tyr Ile His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asn Ser Gly Asn

```
                85                  90                  95

Ala Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Tyr Trp Gly Ser Phe Asp
    130                 135                 140

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
145                 150                 155                 160

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
                165                 170                 175

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
            180                 185                 190

Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn Trp Tyr Gln
        195                 200                 205

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
    210                 215                 220

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225                 230                 235                 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
                245                 250                 255

Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr Thr Phe Gly Gln Gly
            260                 265                 270

Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
        275                 280                 285

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
    290                 295                 300
```

```
Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
305                 310                 315                 320

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
                325                 330                 335

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg
            340                 345                 350

Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr
        355                 360                 365

Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
    370                 375                 380

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
385                 390                 395                 400

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
                405                 410                 415

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            420                 425                 430

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        435                 440                 445

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
    450                 455                 460

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
465                 470                 475                 480

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                485                 490                 495

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
            500                 505                 510

Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro
```

```
        515                 520                 525

Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile
    530                 535                 540

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
545                 550                 555                 560

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
                565                 570                 575

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
            580                 585                 590

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
        595                 600                 605

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
    610                 615                 620

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
625                 630                 635                 640

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro
                645                 650                 655

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
            660                 665                 670

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
        675                 680                 685

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
    690                 695                 700

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
705                 710                 715                 720

Cys
```

<210> 383
<211> 722
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10 construct

<400> 383

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Gly Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Met Ile Asp Pro Ser Asp Gly Ser
                85                  90                  95


Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Pro Leu Tyr Ala Ser
    130                 135                 140


Asp Leu Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175
```

```
Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Asp Leu Gly Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser
    210                 215                 220

Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Leu Gln Asp Tyr Asp Tyr Pro Leu Thr Phe Gly Gln
            260                 265                 270

Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro
        275                 280                 285

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
    290                 295                 300

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
305                 310                 315                 320

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
                325                 330                 335

Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln
            340                 345                 350

Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg
        355                 360                 365

Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys
    370                 375                 380

Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln
```

```
385                 390                 395                 400

Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu
                405                 410                 415

Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly
            420                 425                 430

Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln
        435                 440                 445

Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu
    450                 455                 460

Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr
465                 470                 475                 480

Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro
                485                 490                 495

Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val
            500                 505                 510

Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu
        515                 520                 525

Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val
    530                 535                 540

Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile
545                 550                 555                 560

Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val
                565                 570                 575

Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu
            580                 585                 590

Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu
        595                 600                 605
```

```
Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys
    610                 615                 620

Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln
625                 630                 635                 640

Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr
                645                 650                 655

Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro
            660                 665                 670

Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val
        675                 680                 685

His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro
    690                 695                 700

Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu
705                 710                 715                 720

Tyr Cys
```

<210> 384
<211> 723
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02 construct

<400> 384

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45
```

```
Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asn Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Met Asn Pro Asp Ser Gly Asn
                85                  90                  95

Thr Gly Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ser Ser Ser Ser Trp Pro Asp
    130                 135                 140

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln
                165                 170                 175

Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val
            180                 185                 190

Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn Trp
        195                 200                 205

Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala
    210                 215                 220

Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser
225                 230                 235                 240

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe
                245                 250                 255

Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Tyr Ser Phe Gly
```

```
            260                 265                 270

Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro
        275                 280                 285

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    290                 295                 300

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
305                 310                 315                 320

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
                325                 330                 335

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp
            340                 345                 350

Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe
        355                 360                 365

Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala
    370                 375                 380

Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln
385                 390                 395                 400

Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu
                405                 410                 415

Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly
            420                 425                 430

Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu
        435                 440                 445

Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly
    450                 455                 460

Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser
465                 470                 475                 480
```

```
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro
                485                 490                 495

Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp
            500                 505                 510

Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu
        515                 520                 525

Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn
    530                 535                 540

Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
545                 550                 555                 560

Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys
                565                 570                 575

Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu
            580                 585                 590

Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile
        595                 600                 605

Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly
    610                 615                 620

Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
625                 630                 635                 640

Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr
                645                 650                 655

Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln
            660                 665                 670

Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala
        675                 680                 685

Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala
```

690 695 700

Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Ser Leu Val Ile Thr
705 710 715 720

Leu Tyr Cys

<210> 385
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06 construct

<400> 385

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Ser Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Val Gly Ile Ile Asn Pro Ser Ser Gly Ser
85 90 95

Ala Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
100 105 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Glu Arg Gly Ala Tyr Ser Ser

```
    130                 135                 140

Thr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220

Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Ser Tyr Pro Leu Thr Phe
            260                 265                 270

Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350
```

```
Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
```

```
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
            660                 665                 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
        675                 680                 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
    690                 695                 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705                 710                 715                 720

Thr Leu Tyr Cys
```

<210> 386
<211> 724
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09 construct

<400> 386

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
```

```
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Asp Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Val Ile Asn Pro Ser Asp Gly Thr
                85                  90                  95

Ala His Tyr Ala Gln Arg Leu Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Ser Gly Ser Tyr Tyr Ala
    130                 135                 140

Asp Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly
145                 150                 155                 160

Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile
                165                 170                 175

Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
            180                 185                 190

Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
        195                 200                 205

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp
    210                 215                 220
```

```
Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly
225                 230                 235                 240

Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp
                245                 250                 255

Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro Ala Phe
            260                 265                 270

Gly Gln Gly Thr Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg
        275                 280                 285

Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg
    290                 295                 300

Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly
305                 310                 315                 320

Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr
                325                 330                 335

Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg
            340                 345                 350

Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser
        355                 360                 365

Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu
    370                 375                 380

Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr
385                 390                 395                 400

Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg
                405                 410                 415

Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met
            420                 425                 430

Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu
```

```
        435                 440                 445

Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys
    450                 455                 460

Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu
465                 470                 475                 480

Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu
                485                 490                 495

Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly
            500                 505                 510

Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu
        515                 520                 525

Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val
    530                 535                 540

Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met
545                 550                 555                 560

His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys
                565                 570                 575

Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser
            580                 585                 590

Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile
        595                 600                 605

Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser
    610                 615                 620

Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe
625                 630                 635                 640

Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr
                645                 650                 655
```

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
660 665 670

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
675 680 685

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
690 695 700

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
705 710 715 720

Thr Leu Tyr Cys

<210> 387
<211> 989
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.76_38-38 construct

<400> 387

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Thr
85 90 95

```
Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser
    130                 135                 140

Ser Trp Trp Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
145                 150                 155                 160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            180                 185                 190

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg
        195                 200                 205

His Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala
            260                 265                 270

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly Gly
        275                 280                 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
```

```
305                 310                 315                 320

Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His Trp
                325                 330                 335

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
            340                 345                 350

Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val
        355                 360                 365

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
    370                 375                 380

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn
385                 390                 395                 400

Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp Tyr Trp Gly Gln
                405                 410                 415

Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
            420                 425                 430

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
        435                 440                 445

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
    450                 455                 460

Ser Gln Asp Ile Arg His Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly
465                 470                 475                 480

Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly
                485                 490                 495

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            500                 505                 510

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln
        515                 520                 525
```

```
Gln Thr Tyr Asp Ala Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu
    530                 535                 540

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
545                 550                 555                 560

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
                565                 570                 575

Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
            580                 585                 590

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
        595                 600                 605

Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp
    610                 615                 620

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu
625                 630                 635                 640

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe
                645                 650                 655

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
            660                 665                 670

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
        675                 680                 685

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
    690                 695                 700

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
705                 710                 715                 720

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                725                 730                 735

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
```

```
            740                 745                 750

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
        755                 760                 765

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
    770                 775                 780

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
785                 790                 795                 800

Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys
                805                 810                 815

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
            820                 825                 830

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
        835                 840                 845

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
    850                 855                 860

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
865                 870                 875                 880

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
                885                 890                 895

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
            900                 905                 910

Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro
        915                 920                 925

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
    930                 935                 940

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
945                 950                 955                 960
```

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
965 970 975

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
980 985

<210> 388
<211> 989
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.77_64-64 construct

<400> 388

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
100 105 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Gly Asp Gly Tyr
130 135 140

```
Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160


Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
                165                 170                 175


Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190


Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205


Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220


Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240


Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255


Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp
            260                 265                 270


Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly
        275                 280                 285


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300


Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
305                 310                 315                 320


Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp
                325                 330                 335


Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile
            340                 345                 350


Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val
```

```
        355                 360                 365

Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
    370                 375                 380

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His
385                 390                 395                 400

Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr
                405                 410                 415

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
            420                 425                 430

Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr
        435                 440                 445

Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu
    450                 455                 460

His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly
465                 470                 475                 480

Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly
                485                 490                 495

Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
            500                 505                 510

Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met
        515                 520                 525

Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu
    530                 535                 540

Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr
545                 550                 555                 560

Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala
                565                 570                 575
```

```
Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile
            580                 585                 590

Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser
        595                 600                 605

Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp
    610                 615                 620

Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu
625                 630                 635                 640

Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe
                645                 650                 655

Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu
            660                 665                 670

Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp
        675                 680                 685

Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys
    690                 695                 700

Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala
705                 710                 715                 720

Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys
                725                 730                 735

Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr
            740                 745                 750

Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu
        755                 760                 765

Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly
    770                 775                 780

Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu
```

785 790 795 800

Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys
805 810 815

Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr
820 825 830

Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys
835 840 845

Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser
850 855 860

Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu
865 870 875 880

Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu
885 890 895

Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile
900 905 910

Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro
915 920 925

Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro
930 935 940

Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu
945 950 955 960

Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys
965 970 975

Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
980 985

<210> 389
<211> 977
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.78_65-65 construct

<400> 389

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45


Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60


Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80


Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
                85                  90                  95


Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110


Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125


Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe
    130                 135                 140


Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160


Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175


Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190
```

```
Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe Gly Gln
            260                 265                 270

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275                 280                 285

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
    290                 295                 300

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
305                 310                 315                 320

Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro Gly
                325                 330                 335

Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr
            340                 345                 350

Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
        355                 360                 365

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
    370                 375                 380

Thr Ala Val Tyr Tyr Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp
385                 390                 395                 400

Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly
```

```
                405                 410                 415

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr
            420                 425                 430

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
        435                 440                 445

Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn Trp Tyr Gln
    450                 455                 460

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn
465                 470                 475                 480

Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
                485                 490                 495

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
            500                 505                 510

Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe Gly Gln Gly
        515                 520                 525

Thr Lys Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
    530                 535                 540

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
545                 550                 555                 560

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
                565                 570                 575

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
            580                 585                 590

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg
        595                 600                 605

Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr
    610                 615                 620
```

```
Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile
625                 630                 635                 640

Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly
                645                 650                 655

Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr
            660                 665                 670

Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
        675                 680                 685

Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
    690                 695                 700

Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
705                 710                 715                 720

Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                725                 730                 735

Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
            740                 745                 750

Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu
        755                 760                 765

Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro
    770                 775                 780

Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile
785                 790                 795                 800

Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp
                805                 810                 815

Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr
            820                 825                 830

Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser
```

```
        835                 840                 845

Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala
    850                 855                 860

Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys
865                 870                 875                 880

Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser
                885                 890                 895

Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro
            900                 905                 910

Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu
        915                 920                 925

Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His
    930                 935                 940

Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu
945                 950                 955                 960

Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr
                965                 970                 975

Cys
```

<210> 390
<211> 992
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.79_38-67 construct

<400> 390

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
```

```
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Thr
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser
    130                 135                 140

Ser Trp Trp Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
145                 150                 155                 160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            180                 185                 190

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg
        195                 200                 205

His Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
225                 230                 235                 240
```

```
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala
            260                 265                 270

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly Gly
        275                 280                 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
305                 310                 315                 320

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp
                325                 330                 335

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Thr
            340                 345                 350

Pro Met Phe Gly Thr Thr Asp Tyr Ala Gln Lys Phe Gln Gly Arg Val
        355                 360                 365

Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
    370                 375                 380

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Glu
385                 390                 395                 400

Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile Trp Gly Gln Gly Thr
                405                 410                 415

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu
        435                 440                 445

Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln
```

```
    450                 455                 460

Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln
465                 470                 475                 480

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Asn Leu
                485                 490                 495

Glu Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            500                 505                 510

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
        515                 520                 525

Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr
    530                 535                 540

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
545                 550                 555                 560

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
                565                 570                 575

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
            580                 585                 590

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
        595                 600                 605

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu
    610                 615                 620

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
625                 630                 635                 640

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
                645                 650                 655

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
            660                 665                 670
```

```
Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
        675                 680                 685

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
    690                 695                 700

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
705                 710                 715                 720

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
                725                 730                 735

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
            740                 745                 750

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
        755                 760                 765

Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
    770                 775                 780

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
785                 790                 795                 800

Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser
                805                 810                 815

Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala
            820                 825                 830

Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala
        835                 840                 845

Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly
    850                 855                 860

Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn
865                 870                 875                 880

Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu
```

885 890 895

Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe
900 905 910

Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala
915 920 925

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
930 935 940

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
945 950 955 960

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
965 970 975

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
980 985 990

<210> 391
<211> 987
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.80_38-68 construct

<400> 391

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Ser Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro

```
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Gly Gly Thr
                85                  90                  95

Thr Ser Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser
    130                 135                 140

Ser Trp Trp Asp Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr
145                 150                 155                 160

Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly
                165                 170                 175

Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser
            180                 185                 190

Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg
        195                 200                 205

His Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
                245                 250                 255

Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala
            260                 265                 270

Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Gly Gly Gly
        275                 280                 285
```

```
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
305                 310                 315                 320

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp
                325                 330                 335

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
            340                 345                 350

Pro Ser Asp Gly Gly Thr Ser Tyr Ala Asp Lys Phe Gln Gly Arg Val
        355                 360                 365

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
    370                 375                 380

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu
385                 390                 395                 400

Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val Trp Gly Gln Gly Thr
                405                 410                 415

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430

Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
        435                 440                 445

Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln
    450                 455                 460

Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
465                 470                 475                 480

Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
                485                 490                 495

Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
```

```
            500                 505                 510

Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
        515                 520                 525

Tyr Asp Gly Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
    530                 535                 540

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
545                 550                 555                 560

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
                565                 570                 575

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
            580                 585                 590

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
        595                 600                 605

Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His
    610                 615                 620

Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln
625                 630                 635                 640

Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg
                645                 650                 655

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
            660                 665                 670

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
        675                 680                 685

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
    690                 695                 700

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
705                 710                 715                 720
```

```
Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
                725                 730                 735

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
            740                 745                 750

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
        755                 760                 765

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
    770                 775                 780

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
785                 790                 795                 800

Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
                805                 810                 815

Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
            820                 825                 830

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
        835                 840                 845

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
    850                 855                 860

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
865                 870                 875                 880

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
                885                 890                 895

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
            900                 905                 910

Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
        915                 920                 925

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
```

```
    930                 935                 940

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
945                 950                 955                 960

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
                965                 970                 975

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            980                 985
```

<210> 392
<211> 992
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.81_64-67 construct

<400> 392

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
            100                 105                 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
```

```
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Gly Asp Gly Tyr
    130                 135                 140

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145                 150                 155                 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val
                165                 170                 175

Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp
            260                 265                 270

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly
        275                 280                 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val
305                 310                 315                 320

Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp
                325                 330                 335
```

```
Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Thr
            340                 345                 350

Pro Met Phe Gly Thr Thr Asp Tyr Ala Gln Lys Phe Gln Gly Arg Val
        355                 360                 365

Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser
    370                 375                 380

Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp Glu
385                 390                 395                 400

Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile Trp Gly Gln Gly Thr
                405                 410                 415

Met Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430

Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu
        435                 440                 445

Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln
    450                 455                 460

Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln
465                 470                 475                 480

Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr Asp Ala Ser Asn Leu
                485                 490                 495

Glu Thr Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
            500                 505                 510

Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr
        515                 520                 525

Tyr Cys Met Gln Gly Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr
    530                 535                 540

Lys Val Glu Ile Lys Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
```

```
545                 550                 555                 560

Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
                565                 570                 575

Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
            580                 585                 590

Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
        595                 600                 605

Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu
    610                 615                 620

Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro
625                 630                 635                 640

Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg
                645                 650                 655

Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln
            660                 665                 670

Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp
        675                 680                 685

Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro
    690                 695                 700

Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp
705                 710                 715                 720

Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg
                725                 730                 735

Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr
            740                 745                 750

Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly
        755                 760                 765
```

```
Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu
    770                 775                 780

Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu
785                 790                 795                 800

Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser
                805                 810                 815

Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala
            820                 825                 830

Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala
        835                 840                 845

Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly
    850                 855                 860

Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn
865                 870                 875                 880

Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu
                885                 890                 895

Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe
            900                 905                 910

Val His Ile Val Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala
        915                 920                 925

Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser
    930                 935                 940

Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr
945                 950                 955                 960

Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala
                965                 970                 975

Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
```

980 985 990

<210> 393
<211> 987
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.82_64-68 construct

<400> 393

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1 5 10 15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
20 25 30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
35 40 45

Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser
50 55 60

Gly Tyr Thr Phe Thr Ser Tyr Gly Ile Ser Trp Val Arg Gln Ala Pro
65 70 75 80

Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr
85 90 95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp
100 105 110

Glu Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
115 120 125

Asp Thr Ala Val Tyr Tyr Cys Ala Arg Asp His Ser Gly Asp Gly Tyr
130 135 140

Phe Asp Leu Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser Gly Gly
145 150 155 160

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Val

```
                165                 170                 175

Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala
            180                 185                 190

Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr
        195                 200                 205

Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu
    210                 215                 220

Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Asp Arg Phe
225                 230                 235                 240

Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val
                245                 250                 255

Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr His Trp
            260                 265                 270

Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Gly Gly Gly
        275                 280                 285

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
    290                 295                 300

Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
305                 310                 315                 320

Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp
                325                 330                 335

Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met Gly Ile Ile Asn
            340                 345                 350

Pro Ser Asp Gly Gly Thr Ser Tyr Ala Asp Lys Phe Gln Gly Arg Val
        355                 360                 365

Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
    370                 375                 380
```

```
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu
385                 390                 395                 400


Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val Trp Gly Gln Gly Thr
                405                 410                 415


Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
            420                 425                 430


Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu
        435                 440                 445


Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln
    450                 455                 460


Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala
465                 470                 475                 480


Pro Lys Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro
                485                 490                 495


Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
            500                 505                 510


Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser
        515                 520                 525


Tyr Asp Gly Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
    530                 535                 540


Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
545                 550                 555                 560


Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
                565                 570                 575


Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
            580                 585                 590


Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
```

```
        595                 600                 605

Ile Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His
    610                 615                 620

Lys Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln
625                 630                 635                 640

Ala Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg
                645                 650                 655

Ser Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn
            660                 665                 670

Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg
        675                 680                 685

Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro
    690                 695                 700

Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala
705                 710                 715                 720

Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His
                725                 730                 735

Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp
            740                 745                 750

Ala Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg
        755                 760                 765

Gly Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met
    770                 775                 780

Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His
785                 790                 795                 800

Ala Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile
                805                 810                 815
```

```
Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu
            820                 825                 830

Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu
        835                 840                 845

Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
    850                 855                 860

Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser
865                 870                 875                 880

Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu
                885                 890                 895

Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln
            900                 905                 910

Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr
        915                 920                 925

Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala
    930                 935                 940

Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe
945                 950                 955                 960

Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val
                965                 970                 975

Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            980                 985
```

<210> 394
<211> 986
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.83_65-67 construct

<400> 394

```
Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                  10                  15

His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30

Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45

Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
```

```
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe Gly Gln
            260                 265                 270

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275                 280                 285

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
    290                 295                 300

Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly
305                 310                 315                 320

Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly
                325                 330                 335

Gln Gly Leu Glu Trp Met Gly Gly Ile Thr Pro Met Phe Gly Thr Thr
            340                 345                 350

Asp Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu
        355                 360                 365

Ser Thr Ser Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
    370                 375                 380

Thr Ala Val Tyr Tyr Cys Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr
385                 390                 395                 400

Val Ala Phe Asp Ile Trp Gly Gln Gly Thr Met Val Thr Val Ser Ser
                405                 410                 415

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
            420                 425                 430
```

```
Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu
        435                 440                 445

Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser Asn
    450                 455                 460

Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
465                 470                 475                 480

Gln Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Asp
                485                 490                 495

Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
            500                 505                 510

Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly Thr
        515                 520                 525

His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Thr
    530                 535                 540

Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser
545                 550                 555                 560

Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly
                565                 570                 575

Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp
            580                 585                 590

Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile
        595                 600                 605

Thr Leu Tyr Cys Arg Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys
    610                 615                 620

Pro Pro Gly Gly Gly Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala
625                 630                 635                 640

Asp Ala His Ser Thr Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser
```

```
                645                 650                 655

Ala Asp Ala Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu
            660                 665                 670

Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg
        675                 680                 685

Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln
    690                 695                 700

Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr
705                 710                 715                 720

Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp
                725                 730                 735

Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala
            740                 745                 750

Leu His Met Gln Ala Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly
        755                 760                 765

Ser Leu Leu Thr Cys Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala
    770                 775                 780

Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala
785                 790                 795                 800

Ala Arg Pro Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu
                805                 810                 815

Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser
            820                 825                 830

Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu
        835                 840                 845

Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp
    850                 855                 860
```

```
Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn
865                 870                 875                 880


Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu
                885                 890                 895


Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val Gln Met
            900                 905                 910


Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro
        915                 920                 925


Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys
    930                 935                 940


Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala
945                 950                 955                 960


Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu
                965                 970                 975


Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
            980                 985


<210>  395
<211>  981
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.84_65-68 construct

<400>  395

Met Ala Leu Pro Val Thr Ala Leu Leu Leu Pro Leu Ala Leu Leu Leu
1               5                   10                  15


His Ala Ala Arg Pro Asp Tyr Lys Asp Asp Asp Asp Lys Gly Gly Gly
            20                  25                  30


Gly Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala
        35                  40                  45
```

```
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser
    50                  55                  60

Gly Tyr Thr Phe Thr Glu Asn Glu Met His Trp Val Arg Gln Ala Pro
65                  70                  75                  80

Gly Gln Gly Leu Glu Trp Met Gly Trp Ile Asn Pro Asn Ser Gly Gly
                85                  90                  95

Thr Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp
            100                 105                 110

Thr Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu
        115                 120                 125

Asp Thr Ala Val Tyr Tyr Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe
    130                 135                 140

Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly
145                 150                 155                 160

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met
                165                 170                 175

Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr
            180                 185                 190

Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn Trp Tyr
        195                 200                 205

Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Asp Ala Ser
    210                 215                 220

Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
225                 230                 235                 240

Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala
                245                 250                 255

Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe Gly Gln
```

```
            260                 265                 270

Gly Thr Lys Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Gly
        275                 280                 285

Ser Gly Gly Gly Gly Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu
    290                 295                 300

Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Ala Ser Gly
305                 310                 315                 320

Tyr Thr Phe Thr Ser Tyr Tyr Met His Trp Val Arg Gln Ala Pro Gly
                325                 330                 335

Gln Gly Leu Glu Trp Met Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr
            340                 345                 350

Ser Tyr Ala Asp Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr
        355                 360                 365

Ser Thr Ser Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp
    370                 375                 380

Thr Ala Val Tyr Tyr Cys Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly
385                 390                 395                 400

Asp Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
                405                 410                 415

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp
            420                 425                 430

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
        435                 440                 445

Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu
    450                 455                 460

Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
465                 470                 475                 480
```

```
Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly Ser
                485                 490                 495

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
            500                 505                 510

Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile Thr
        515                 520                 525

Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Thr Thr Thr Pro Ala Pro
    530                 535                 540

Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu
545                 550                 555                 560

Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg
                565                 570                 575

Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly
            580                 585                 590

Thr Cys Gly Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys Arg
        595                 600                 605

Arg Asp Gln Arg Leu Pro Pro Asp Ala His Lys Pro Pro Gly Gly Gly
    610                 615                 620

Ser Phe Arg Thr Pro Ile Gln Glu Glu Gln Ala Asp Ala His Ser Thr
625                 630                 635                 640

Leu Ala Lys Ile Arg Val Lys Phe Ser Arg Ser Ala Asp Ala Pro Ala
                645                 650                 655

Tyr Gln Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg
            660                 665                 670

Arg Glu Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu
        675                 680                 685

Met Gly Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn
```

```
    690                 695                 700

Glu Leu Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met
705                 710                 715                 720

Lys Gly Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly
                725                 730                 735

Leu Ser Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala
            740                 745                 750

Leu Pro Pro Arg Gly Ser Gly Glu Gly Arg Gly Ser Leu Leu Thr Cys
        755                 760                 765

Gly Asp Val Glu Glu Asn Pro Gly Pro Met Ala Leu Pro Val Thr Ala
    770                 775                 780

Leu Leu Leu Pro Leu Ala Leu Leu Leu His Ala Ala Arg Pro Asn Trp
785                 790                 795                 800

Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser
                805                 810                 815

Met His Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser
            820                 825                 830

Cys Lys Val Thr Ala Met Lys Cys Phe Leu Leu Glu Leu Gln Val Ile
        835                 840                 845

Ser Leu Glu Ser Gly Asp Ala Ser Ile His Asp Thr Val Glu Asn Leu
    850                 855                 860

Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val Thr Glu
865                 870                 875                 880

Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu
                885                 890                 895

Phe Leu Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
            900                 905                 910
```

Thr Thr Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala
915 920 925

Ser Gln Pro Leu Ser Leu Arg Pro Glu Ala Cys Arg Pro Ala Ala Gly
930 935 940

Gly Ala Val His Thr Arg Gly Leu Asp Phe Ala Cys Asp Ile Tyr Ile
945 950 955 960

Trp Ala Pro Leu Ala Gly Thr Cys Gly Val Leu Leu Leu Ser Leu Val
965 970 975

Ile Thr Leu Tyr Cys
980

<210> 396
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A2AR-1 guide RNA

<400> 396
cgaggagccc atgatgggca 20

<210> 397
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A2AR-2 guide RNA

<400> 397
gggcaatgtg ctggtgtgct 20

<210> 398
<211> 20
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<223> A2AR-3 guide RNA

<400> 398
cagtgacacc acaaagtagt 20

<210> 399
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H1_1

<400> 399

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly
20 25

<210> 400
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H1_2

<400> 400

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly
20 25

<210> 401
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H1_3

<400> 401

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
            20   25

<210> 402
<211> 26
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H1_4

<400> 402

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1   5   10   15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly
            20   25

<210> 403
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H2_1

<400> 403

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1   5   10

<210> 404
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H2_2

<400> 404

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
1   5   10

<210> 405
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H2_3

<400> 405

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
1   5   10

<210> 406
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H2_4

<400> 406

Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
1   5   10

<210> 407
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H3_1

<400> 407

Gln Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1   5   10   15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            20   25   30

Tyr Tyr

<210> 408
<211> 34
<212> PRT

<213> Artificial Sequence

<220>
<223> FW-H3_2

<400> 408

Gln Arg Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 409
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H3_3

<400> 409

His Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 410
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<400> 410

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
1 5 10 15

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 411
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-H3_5

<400> 411

Leu Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 412
<211> 34
<212> PRT
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<220>
<223> FW-H3_6

<400> 412

Gln Asn Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 413

<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<400> 413

Gln Met Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1   5   10   15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            20   25   30

Tyr Tyr

<210> 414
<211> 34
<212> PRT
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<220>
<223> FW-H3_8

<400> 414

Gln Glu Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1   5   10   15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
            20   25   30

Tyr Tyr

<210> 415
<211> 34
<212> PRT
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<220>
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<400> 415

Glu Glu Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser

1 5 10 15

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 416
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<220>
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<400> 416

Gln Thr Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 417
<211> 34
<212> PRT
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<220>
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<400> 417

Gln Ser Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 418
<211> 34
<212> PRT
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<220>
<223> FW-H3_12

<400> 418

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn
1 5 10 15

Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 419
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
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<400> 419

Gln Asn Leu Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 420
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<220>
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<400> 420

Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser
1 5 10 15

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 421
<211> 34
<212> PRT
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<220>
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<400> 421

Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn
1 5 10 15

Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 422
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<220>
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<400> 422

Asp Lys Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
1 5 10 15

Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
20 25 30

Tyr Tyr

<210> 423
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<400> 423

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
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<210> 424
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<220>
<223> FW-H4_2

<400> 424

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
1   5   10

<210> 425
<211> 10
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<400> 425

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
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<210> 426
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<220>
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<400> 426

Gly Gln Gly Thr Met Val Thr Val Ser Ser
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<210> 427
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<212> PRT
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<220>
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<400> 427

Gly Lys Gly Thr Thr Val Thr Val Ser Ser
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<210> 428
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<220>
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<400> 428

Tyr Thr Phe Thr Gly His Tyr Leu His
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<210> 429
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<400> 429

Tyr Thr Phe Thr Asn Tyr Tyr Met His
1 5

<210> 430
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<220>
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<400> 430

Tyr Thr Phe Thr Gly Tyr Tyr Ile His
1 5

<210> 431
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<400> 431

Gly Thr Phe Arg Ser His Val Ile Ser
1 5

<210> 432
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<400> 432

Tyr Thr Phe Ile Asp Tyr Tyr Ile His
1 5

<210> 433
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<400> 433

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5

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<400> 434

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1   5

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<400> 435

Tyr Thr Phe Thr Glu Asn Glu Met His
1   5

<210> 436
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<400> 436

Tyr Thr Phe Thr Glu Asn Glu Met His
1   5

<210> 437
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<400> 437

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1   5

<210> 438
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<220>
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<400> 438

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5

<210> 439
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<220>
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<400> 439

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5

<210> 440
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<400> 440

Tyr Thr Phe Thr Ser Tyr Asp Ile Asn
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Tyr Thr Phe Thr Ser Tyr Tyr Met His
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Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5

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Tyr Thr Phe Thr Asp Tyr Tyr Met His
1 5

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<400> 444

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5

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<400> 445

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5

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<400> 446

Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1   5

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<400> 447

Tyr Thr Phe Thr Arg Asn Tyr Met His
1   5

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<400> 448

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1   5

<210> 449
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<212> PRT
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<220>
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<400> 449

Tyr Arg Leu Ser Asp His Tyr Met His

1 5

<210> 450
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Tyr Thr Phe Thr Asp Tyr Tyr Val His
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<400> 451

Tyr Thr Phe Thr Asp Tyr Thr Asp Tyr Phe Val His
1 5 10

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<400> 452

Tyr Ile Phe Thr Asp Tyr Tyr Met His
1 5

<210> 453
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<400> 453

Tyr Thr Phe Thr Asp His Tyr Ile His
1   5

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<400> 454

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1   5

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<400> 455

Tyr Thr Phe Thr Asp Tyr Tyr Met His
1   5

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<400> 456

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1   5

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<400> 457

Tyr Thr Phe Thr Asp Tyr Phe Thr His
1 5

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<400> 458

Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

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<400> 459

Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1 5

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<400> 460

Gly Thr Phe Asn Ser Tyr Gly Ile Ser
1 5

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Tyr Ser Phe Thr Ser Tyr Tyr Met His
1   5

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<400> 462

Tyr Thr Phe Thr Asp Tyr Tyr Ile His
1   5

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<400> 463

Tyr Thr Phe Asn Gly Tyr Leu Met His
1   5

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<400> 464

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1   5

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<400> 465

Tyr Thr Phe Ser Asp Ser Tyr Met His
1 5

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<400> 466

Tyr Ile Phe Thr Asp Tyr Tyr Met His
1 5

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<400> 467

Tyr Thr Phe Thr Asp Tyr Tyr Leu His
1 5

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<400> 468

Tyr Thr Phe Thr Ala Tyr Tyr Leu His
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<400> 469

Tyr Thr Phe Thr Asp Tyr Tyr Ile His
1 5

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<400> 470

Phe Thr Phe Ser Asn Ser Asp Met Asn
1 5

<210> 471
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<400> 471

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5

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<212> PRT
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<400> 472

Gly Thr Phe Thr Asn Tyr Ala Phe Ser
1 5

<210> 473
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<212> PRT
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<400> 473

Tyr Thr Phe Thr Ala Tyr Tyr Met His
1   5

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<400> 474

Tyr Thr Phe Thr Asp Tyr Tyr Val His
1   5

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<400> 475

Tyr Thr Phe Thr Ala Tyr His Met His
1   5

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<400> 476

Gly Thr Phe Ser Ser Tyr Ala Ile Ser

1 5

<210> 477
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<400> 477

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1 5

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<400> 478

Tyr Thr Phe Thr Ser Tyr Gly Ile Ser
1 5

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<400> 479

Tyr Thr Phe Ile Asp Tyr Tyr Met His
1 5

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<400> 480

Tyr Thr Phe Thr Gly Gln Tyr Met His
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<210> 481
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<400> 481

Tyr Thr Phe Thr Ser Tyr Asp Ile Asn
1   5

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<400> 482

Tyr Thr Phe Ala Asn Tyr Tyr Met His
1   5

<210> 483
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<400> 483

Tyr Thr Phe Thr Thr Tyr Tyr Met His
1   5

<210> 484
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<400> 484

Asn Thr Phe Thr Ser Tyr Tyr Met His
1 5

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<212> PRT
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<400> 485

Phe Thr Phe Ser Ser Tyr Gly Met His
1 5

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<212> PRT
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<400> 486

Gly Thr Phe Ser Arg Tyr Asp Ile Asn
1 5

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<400> 487

Tyr Thr Phe Thr Ser Tyr Gly Ile Ser
1 5

<210> 488
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<212> PRT
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<400> 488

Tyr Thr Phe Thr Glu Asn Glu Met His
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<400> 489

Tyr Thr Phe Thr Asn Tyr Tyr Ile Tyr
1   5

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<212> PRT
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<220>
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<400> 490

Gly Thr Phe Ser Ser Tyr Ala Ile Ser
1   5

<210> 491
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<220>
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<400> 491

Tyr Thr Phe Thr Ser Tyr Tyr Met His
1   5

<210> 492
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<400> 492

Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

<210> 493
<211> 9
<212> PRT
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<220>
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<400> 493

Tyr Thr Phe Thr Asp Ser Tyr Ile His
1 5

<210> 494
<211> 9
<212> PRT
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<400> 494

Tyr Thr Phe Thr Ser Tyr Asp Ile Asn
1 5

<210> 495
<211> 9
<212> PRT
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<220>
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<400> 495

Phe Val Phe Asp Asp Tyr Ala Ile His
1 5

<210> 496

<211> 9
<212> PRT
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<400> 496

Gly Thr Phe Arg Asn Tyr Ala Ile Ser
1 5

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<400> 497

Tyr Thr Phe Thr Ser Tyr Tyr Ile His
1 5

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<212> PRT
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<400> 498

Tyr Thr Phe Thr Gly Tyr Tyr Met His
1 5

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<400> 499

Tyr Thr Phe Thr Asn Tyr Tyr Met His
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<400> 500

Tyr Thr Phe Thr Ser Tyr Ser Met His
1   5

<210> 501
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<212> PRT
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<220>
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<400> 501

Tyr Thr Phe Thr Asp Tyr Tyr Met His
1   5

<210> 502
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<212> PRT
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<220>
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<400> 502

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
1   5   10

<210> 503
<211> 13
<212> PRT
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<220>
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<400> 503

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala

1 5 10

<210> 504
<211> 13
<212> PRT
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<220>
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<400> 504

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
1 5 10

<210> 505
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<212> PRT
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<220>
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<400> 505

Gly Ile Ile Asp Pro Ser Gly Gly Ser Thr Ser Tyr Ala
1 5 10

<210> 506
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<212> PRT
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<220>
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<400> 506

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala
1 5 10

<210> 507
<211> 13
<212> PRT
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<400> 507

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala
1 5 10

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Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
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Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ile Tyr Ala
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Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Gly Tyr Ala
1 5 10

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1   5   10

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Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala
1 5 10

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Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Leu Tyr Ala
1 5 10

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Gly Trp Ile Ser Ala Tyr Asn Gly Lys Thr Asn Tyr Ala
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<220>
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<400> 528

Gly Ile Ile Asn Pro Ser Gly Gly Ala Thr Ile Tyr Ala
1   5   10

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Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
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<220>
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<400> 530

Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Ile Tyr Ala

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<212> PRT
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<220>
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Gly Trp Ile Asn Thr Tyr Asp Gly Asn Thr Asn Tyr Ala
1 5 10

<210> 532
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1 5 10

<210> 533
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<212> PRT
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<220>
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Gly Trp Ile Ser Pro Asn Ser Gly Asp Thr His Tyr Ala
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<210> 534
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<220>
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<400> 534

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
1 5 10

<210> 535
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1 5 10

<210> 536
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<220>
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<210> 537
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<212> PRT
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<220>
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<400> 537

Gly Ile Val Asn Pro Ser Asp Gly Ser Thr Gly Tyr Ala
1 5 10

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<220>
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Gly Ile Ile Asp Pro Ser Gly Gly Arg Thr Ile Tyr Ala
1 5 10

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<220>
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<400> 539

Gly Gly Ile Ile Pro Met Ala Gly Ile Pro Ala Tyr Ala
1 5 10

<210> 540
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<220>
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Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
1 5 10

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<220>
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<400> 541

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala
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<210> 542
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<220>
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<400> 542

Gly Met Ile Asn Pro Asn Asn Gly Gly Thr Ile Tyr Ala
1   5   10

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<400> 543

Gly Met Ile Asn Pro Arg Gly Gly Ser Thr Thr Tyr Ala
1   5   10

<210> 544
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<220>
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<400> 544

Ser Ala Ile Ser Gly Gly Gly Asp Thr Leu Tyr Tyr Ala
1   5   10

<210> 545
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<220>
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<400> 545

Gly Trp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala
1   5   10

<210> 546
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<213> Artificial Sequence

<220>
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<400> 546

Gly Gly Ile Ile Pro Ile Ser Gly Ala Ala Asn Tyr Ala
1 5 10

<210> 547
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<220>
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<400> 547

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala
1 5 10

<210> 548
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<212> PRT
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<220>
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<400> 548

Gly Thr Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
1 5 10

<210> 549
<211> 13
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<220>
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<400> 549

Gly Ile Ile Asn Pro Gly Asp Gly Ala Thr Gly Tyr Ala
1 5 10

<210> 550

<211> 13
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<220>
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<400> 550

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala
1 5 10

<210> 551
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<400> 551

Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala
1 5 10

<210> 552
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<220>
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<400> 552

Gly Trp Ile Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala
1 5 10

<210> 553
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<212> PRT
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<220>
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<400> 553

Gly Trp Met Asn Pro His Ser Gly Asn Ser Asp Asn Ala
1 5 10

<210> 554
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<220>
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<400> 554

Gly Trp Ile Asn Pro Asn Thr Gly Asp Thr Asn Tyr Ala
1   5   10

<210> 555
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<220>
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<400> 555

Gly Val Ile Asn Pro Ser Gly Gly Gly Thr Ser Tyr Ala
1   5   10

<210> 556
<211> 13
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<220>
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<400> 556

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala
1   5   10

<210> 557
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<220>
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<400> 557

Gly Ile Ile Asn Pro Thr Gly Gly Ser Thr Tyr Tyr Ala

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<210> 558
<211> 13
<212> PRT
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<220>
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<400> 558

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<210> 559
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<220>
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<400> 559

Ala Ser Ile Lys His Asp Gly Ser Glu Gln Tyr Tyr Val
1 5 10

<210> 560
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<220>
<223> NK77.63_CD70_DB04_A11_CDR-H2

<400> 560

Gly Ile Ile Asp Pro Thr Gly Ala Ser Thr Ser Tyr Ala
1 5 10

<210> 561
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<220>
<223> NK77.64_CD70_DB04_B03_CDR-H2

<400> 561

Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala
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<220>
<223> NK77.65_CD70_DB04_B05_CDR-H2

<400> 562

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala
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<210> 563
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<220>
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<400> 563

Gly Trp Ile Asn Pro Asn Asp Gly Ala Thr Asn Tyr Ala
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<210> 564
<211> 13
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<220>
<223> NK77.67_CD70_DB04_C01_CDR-H2

<400> 564

Gly Gly Ile Thr Pro Met Phe Gly Thr Thr Asp Tyr Ala
1 5 10

<210> 565
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<212> PRT
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<220>
<223> NK77.68_CD70_DB04_C04_CDR-H2

<400> 565

Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser Tyr Ala
1 5 10

<210> 566
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<220>
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<400> 566

Gly Trp Met Asn Pro Ser Ser Gly Val Thr Asn Phe Ala
1 5 10

<210> 567
<211> 13
<212> PRT
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<220>
<223> NK77.70_CD70_DB04_C07_CDR-H2

<400> 567

Gly Trp Met Asn Pro Asn Thr Gly Asp Thr Gly Tyr Ala
1 5 10

<210> 568
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02_CDR-H2

<400> 568

Gly Val Ile Ser Pro Ser Gly Gly Gly Thr Ser Tyr Ala
1 5 10

<210> 569
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05_CDR-H2

<400> 569

Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala
1   5   10

<210> 570
<211> 13
<212> PRT
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<220>
<223> NK77.73_CD70_DB04_D07_CDR-H2

<400> 570

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala
1   5   10

<210> 571
<211> 13
<212> PRT
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<220>
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<400> 571

Gly Trp Met Asn Pro Asn Ser Gly Asn Ala Gly Tyr Ala
1   5   10

<210> 572
<211> 13
<212> PRT
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<220>
<223> NK77.75_CD70_DB04_D10_CDR-H2

<400> 572

Gly Met Ile Asp Pro Ser Asp Gly Ser Thr Ile Tyr Ala
1   5   10

<210> 573
<211> 13
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_CDR-H2

<400> 573

Gly Trp Met Asn Pro Asp Ser Gly Asn Thr Gly Tyr Ala
1 5 10

<210> 574
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_CDR-H2

<400> 574

Gly Ile Ile Asn Pro Ser Ser Gly Ser Ala Ser Tyr Ala
1 5 10

<210> 575
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_CDR-H2

<400> 575

Gly Val Ile Asn Pro Ser Asp Gly Thr Ala His Tyr Ala
1 5 10

<210> 576
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_CDR-H3

<400> 576

Cys Val Arg Gly Ser Gly Trp Tyr Asp Leu Asp Tyr Trp
1 5 10

<210> 577

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 577

Cys Ala Arg Glu Leu Gly Val Ala Gly Tyr Phe Asp Leu Trp
1 5 10

<210> 578
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06_CDR-H3

<400> 578

Cys Ala Arg Asp Leu Ser Gly Ile Asp Gly Tyr Ile Gly Phe Phe Asp
1 5 10 15

Tyr Trp

<210> 579
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
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<400> 579

Cys Ala Lys Asp Tyr Thr Gly Leu Leu Gly Met Asp Val Trp
1 5 10

<210> 580
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05_CDR-H3

<400> 580

Cys Ala Arg Gly Leu Ser Gly Tyr Asp Leu Asp Asp Tyr Trp
1   5   10

<210> 581
<211> 13
<212> PRT
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<220>
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<400> 581

Cys Ala Arg Gly Leu Ser Gly Tyr Asp Phe Asp Tyr Trp
1   5   10

<210> 582
<211> 14
<212> PRT
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<220>
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<400> 582

Cys Ala Arg Gly Thr Asp Val Tyr Gly Asp Phe Asp Tyr Trp
1   5   10

<210> 583
<211> 21
<212> PRT
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<220>
<223> NK77.9_CD70_DB02_A03_CDR-H3

<400> 583

Cys Ala Arg Glu Gly Gly Thr Ala Met Ala Thr Gly Tyr Tyr Tyr Tyr
1   5   10   15

Gly Met Asp Val Trp
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<210> 584
<211> 14
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_CDR-H3

<400> 584

Cys Ala Arg Ala Ser Asn Tyr Gly Gly His Phe Asp Tyr Trp
1 5 10

<210> 585
<211> 15
<212> PRT
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<220>
<223> NK77.11_CD70_DB02_A05_CDR-H3

<400> 585

Cys Ala Lys Asp Met Gly Ala Trp Ala Ala Gly Phe Asp Tyr Trp
1 5 10 15

<210> 586
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<212> PRT
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<220>
<223> NK77.12_CD70_DB02_A06_CDR-H3

<400> 586

Cys Ala Arg Ser Val Asn Asp Tyr Gly Asp Tyr Asp Gly Tyr Trp
1 5 10 15

<210> 587
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<220>
<223> NK77.13_CD70_DB02_A07_CDR-H3

<400> 587

Cys Ala Arg Asp Tyr Gly Asp Tyr Asp Ala Ser Phe Asp Tyr Trp
1 5 10 15

<210> 588

<211> 12
<212> PRT
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<220>
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<400> 588

Cys Val Lys Glu Glu Ala Trp Tyr Phe Asp Leu Trp
1 5 10

<210> 589
<211> 12
<212> PRT
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<220>
<223> NK77.15_CD70_DB02_A09_CDR-H3

<400> 589

Cys Ala Ser Gly Asp Tyr Tyr Asp Ile Leu Tyr Trp
1 5 10

<210> 590
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11_CDR-H3

<400> 590

Cys Ala Arg Gly Pro Ser Gly Tyr Glu Phe Asp Tyr Trp
1 5 10

<210> 591
<211> 17
<212> PRT
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<220>
<223> NK77.17_CD70_DB02_B06_CDR-H3

<400> 591

Cys Ala Arg Asp Phe Ser Val Tyr Ala Ala Ala Asp Gly Met Asp Val
1 5 10 15

Trp

<210> 592
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09_CDR-H3

<400> 592

Cys Ala Arg Gly Phe Gly Glu Ser Ala Pro Asp Ala Phe Asp Ile Trp
1 5 10 15

<210> 593
<211> 13
<212> PRT
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<220>
<223> NK77.19_CD70_DB02_C03_CDR-H3

<400> 593

Cys Ala Ala Gly Thr Glu Ile Tyr Tyr Met Asp Val Trp
1 5 10

<210> 594
<211> 22
<212> PRT
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<220>
<223> NK77.20_CD70_DB02_C04_CDR-H3

<400> 594

Cys Ala Arg Glu Arg Glu Leu Leu His Phe Ala Thr Asn Tyr Tyr Tyr
1 5 10 15

Tyr Gly Met Asp Val Trp
20

<210> 595
<211> 18
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07_CDR-H3

<400> 595

Cys Ala Lys Thr Gln Gly Ser Ser Ser Trp Tyr Gln Trp Tyr Phe Asp
1 5 10 15

Leu Trp

<210> 596
<211> 14
<212> PRT
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<220>
<223> NK77.24_CD70_DB02_D02_CDR-H3

<400> 596

Cys Ala Arg Gly Ser Asn Trp Tyr Asp Tyr Phe Asp Tyr Trp
1 5 10

<210> 597
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<220>
<223> NK77.25_CD70_DB02_D04_CDR-H3

<400> 597

Cys Ala Ser Ser Tyr Tyr Gly Asp Tyr Val Leu Val Asn Trp
1 5 10

<210> 598
<211> 15
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<220>
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<400> 598

Cys Ala Arg Asp Leu Gly Gln Trp Leu Gly Glu Ile Asp Tyr Trp

1 5 10 15

<210> 599
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
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<400> 599

Cys Ala Arg Gly Pro Tyr Ser Ser Ser Trp Tyr Tyr Phe Asp Tyr Trp
1 5 10 15

<210> 600
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
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<400> 600

Cys Ala Arg Glu Gly Val Gly Ala Met Gly Val Phe Asp Tyr Trp
1 5 10 15

<210> 601
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06_CDR-H3

<400> 601

Cys Ala Arg Asp Thr Ile Tyr Tyr Asp Phe Trp Ser Gly Tyr Asp Tyr
1 5 10 15

Trp

<210> 602
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08_CDR-H3

<400> 602

Cys Ala Arg Ser Arg Gly Asp Tyr Tyr Gly Ser Gly Asp Phe Asp Tyr
1   5   10   15

Trp

<210> 603
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07_CDR-H3

<400> 603

Cys Ala Arg Gly Tyr Phe Asp His Ala Phe Asp Ile Trp
1   5   10

<210> 604
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04_CDR-H3

<400> 604

Cys Ala Arg Gly Asp Ser Ser Ser Trp Tyr Asp Tyr Tyr Tyr Tyr Met
1   5   10   15

Asp Val Trp

<210> 605
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05_CDR-H3

<400> 605

Cys Ala Arg Glu Met Glu Trp Leu Gly Gln Val Asp Tyr Trp
1 5 10

<210> 606
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08_CDR-H3

<400> 606

Cys Ala Arg Gly His Arg Gly Gly Gly Gly Ile Asp Tyr Trp
1 5 10

<210> 607
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.36_CD70_DB03_A06_CDR-H3

<400> 607

Cys Ala Arg Asp Trp Gly Ser Gly Trp Tyr Val Asp Tyr Trp
1 5 10

<210> 608
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07_CDR-H3

<400> 608

Cys Ala Arg Asp Thr Tyr Gly Asp Asp Ala Phe Asp Ile Trp
1 5 10

<210> 609
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.38_CD70_DB03_A08_CDR-H3

<400> 609

Cys Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe
1 5 10 15

Asp Tyr Trp

<210> 610
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.39_CD70_DB03_A09_CDR-H3

<400> 610

Cys Ala Arg Asn Thr Asp Cys Tyr Gly Asp Phe Leu Gly Leu Asp Val
1 5 10 15

Trp

<210> 611
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11_CDR-H3

<400> 611

Cys Ala Lys Asp Thr Gly Leu Arg Tyr Phe Asp Trp Leu Leu Asp Tyr
1 5 10 15

Trp

<210> 612
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12_CDR-H3

<400> 612

Cys Ala Arg His Glu Ala Gly Gly Ile Phe Asp Tyr Trp
1 5 10

<210> 613
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01_CDR-H3

<400> 613

Cys Ala Arg Ala Asp Asp Tyr Gly Gly Asn Trp Tyr Phe Asp Leu Trp
1 5 10 15

<210> 614
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.43_CD70_DB03_B04_CDR-H3

<400> 614

Cys Ala Arg Asp Ser Gly Trp Tyr Glu Ser Trp Phe Asp Pro Trp
1 5 10 15

<210> 615
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.44_CD70_DB03_B06_CDR-H3

<400> 615

Cys Ala Arg Glu Ile Val Gly Ala Thr Glu Asp Trp Tyr Phe Asp Leu
1 5 10 15

Trp

<210> 616

<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09_CDR-H3

<400> 616

Cys Ala Arg Asp Leu Gly Gly Tyr Val Leu Phe Asp Tyr Trp
1 5 10

<210> 617
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.46_CD70_DB03_C05_CDR-H3

<400> 617

Cys Ala Arg Asp Leu Gly Asp Tyr Gly Asp Tyr Asp Tyr Trp
1 5 10

<210> 618
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11_CDR-H3

<400> 618

Cys Ala Met Ala Ser Ala Leu Asp Ser Ser Gly Asp Asn Glu Ala Phe
1 5 10 15

Asp Ile Trp

<210> 619
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01_CDR-H3

<400> 619

Cys Ala Arg Val Glu Asp Asp Phe Trp Ser Gly Pro Ser Phe Asp Tyr
1   5   10   15

Trp

<210> 620
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03_CDR-H3

<400> 620

Cys Ala Arg Gly Ser Gly Leu Asp Asp Ala Phe Asp Ile Trp
1   5   10

<210> 621
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09_CDR-H3

<400> 621

Cys Ala Arg Glu Gly Arg Ile Asp Tyr Gly Asp Tyr Asp Asp Tyr Tyr
1   5   10   15

Tyr Tyr Tyr Gly Met Asp Val Trp
            20

<210> 622
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02_CDR-H3

<400> 622

Cys Ala Arg Asp Gln Gly Leu Trp Phe Thr Gly Phe Asp Tyr Trp
1   5   10   15

<210> 623
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05_CDR-H3

<400> 623

Cys Ala Gly Glu Gly Ile Ser Gly Ser Asp Ala Phe Asp Ile Trp
1 5 10 15

<210> 624
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06_CDR-H3

<400> 624

Cys Ala Trp Gly Val Asp Pro Tyr Tyr Phe Asp Tyr Trp
1 5 10

<210> 625
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09_CDR-H3

<400> 625

Cys Ala Arg Asp Val Gly Glu Thr Thr Phe Asp Pro Trp
1 5 10

<210> 626
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.55_CD70_DB03_F12_CDR-H3

<400> 626

Cys Ala Arg Asp Ser Val Arg Gly Trp Asp Tyr Tyr Tyr Gly Met Gly

1 5 10 15

Val Trp

<210> 627
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.56_CD70_DB03_G06_CDR-H3

<400> 627

Cys Ala Arg Gly Tyr Ser Gly Tyr Asp Leu Thr Ala Asp Tyr Trp
1 5 10 15

<210> 628
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11_CDR-H3

<400> 628

Cys Ala Arg Asp Ser Val Phe Glu Val Glu Gly Gly Thr Asp Tyr Tyr
1 5 10 15

Tyr Tyr Tyr Gly Met Asp Val Trp
20

<210> 629
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.58_CD70_DB03_H08_CDR-H3

<400> 629

Cys Ala Arg Tyr Ser Gly Tyr Asp Trp Val Phe Asp Tyr Trp
1 5 10

<210> 630

<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.59_CD70_DB03_H10_CDR-H3

<400> 630

Cys Ala Arg Asp Ser Gly Ser Tyr Phe Gly Trp Phe Asp Pro Trp
1 5 10 15

<210> 631
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.60_CD70_DB04_A05_CDR-H3

<400> 631

Cys Ala Arg Asp Ser Gly Asn Tyr Gln Gly Ile Phe Asp Tyr Trp
1 5 10 15

<210> 632
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.61_CD70_DB04_A07_CDR-H3

<400> 632

Cys Ala Arg Gly Val Ser Gly Tyr Asp Leu Phe Asp Tyr Trp
1 5 10

<210> 633
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.62_CD70_DB04_A10_CDR-H3

<400> 633

Cys Ala Ala Ser Gly Val Asp Val Trp
1 5

<210> 634
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.63_CD70_DB04_A11_CDR-H3

<400> 634

Cys Ala Arg Asp Tyr Ser Tyr Gly Met Asp Tyr Tyr Gly Met Asp Val
1   5   10   15

Trp

<210> 635
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.64_CD70_DB04_B03_CDR-H3

<400> 635

Cys Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp
1   5   10

<210> 636
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.65_CD70_DB04_B05_CDR-H3

<400> 636

Cys Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp
1   5   10

<210> 637
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.66_CD70_DB04_B07_CDR-H3

<400> 637

Cys Ala Arg Glu Gly Asn Asp Tyr Tyr Tyr Tyr Phe Met Asp Tyr Trp
1 5 10 15

<210> 638
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.67_CD70_DB04_C01_CDR-H3

<400> 638

Cys Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile
1 5 10 15

Trp

<210> 639
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04_CDR-H3

<400> 639

Cys Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val
1 5 10 15

Trp

<210> 640
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.69_CD70_DB04_C06_CDR-H3

<400> 640

Cys Ala Arg Gly Ser Asp Gln Gly Asp Trp Ser Asp Pro Trp

1 5 10

<210> 641
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07_CDR-H3

<400> 641

Cys Ala Lys Asp Asp Phe Gly Glu Leu Ala Pro Ala Thr Phe Asp Pro
1 5 10 15

Trp

<210> 642
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02_CDR-H3

<400> 642

Cys Ala Arg Tyr Tyr Gly Gly Asn Pro Glu Gly Trp Tyr Phe Asp Leu
1 5 10 15

Trp

<210> 643
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05_CDR-H3

<400> 643

Cys Ala Arg Ala Pro Gln Tyr Tyr Gly Ser Gly Thr Asp Pro Leu Glu
1 5 10 15

Val Arg Tyr Tyr Tyr Tyr Gly Met Asp Val Trp

20 25

<210> 644
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.73_CD70_DB04_D07_CDR-H3

<400> 644

Cys Ala Arg Asp His Ser Ala Gly Thr His His Asp Ala Phe Asp Ile
1 5 10 15

Trp

<210> 645
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.74_CD70_DB04_D08_CDR-H3

<400> 645

Cys Ala Arg Glu Tyr Trp Gly Ser Phe Asp Tyr Trp
1 5 10

<210> 646
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10_CDR-H3

<400> 646

Cys Ala Arg Glu Arg Pro Leu Tyr Ala Ser Asp Leu Trp
1 5 10

<210> 647
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_CDR-H3

<400> 647

Cys Ala Arg Ser Ser Ser Ser Trp Pro Asp Phe Asp Leu Trp
1   5   10

<210> 648
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_CDR-H3

<400> 648

Cys Ala Arg Glu Arg Gly Ala Tyr Ser Ser Thr Phe Asp Tyr Trp
1   5   10   15

<210> 649
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_CDR-H3

<400> 649

Cys Ala Arg Asp Ser Gly Ser Tyr Tyr Ala Asp Phe Asp Tyr Trp
1   5   10   15

<210> 650
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L1_1

<400> 650

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys
            20

<210> 651
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L1_2

<400> 651

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1   5   10   15

Glu Pro Ala Ser Ile Ser Cys
            20

<210> 652
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L1_3

<400> 652

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1   5   10   15

Glu Arg Ala Thr Leu Ser Cys
            20

<210> 653
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L1_4

<400> 653

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1   5   10   15

Glu Arg Ala Thr Ile Asn Cys
            20

<210> 654
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L2_1

<400> 654

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 655
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L2_2

<400> 655

Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Gln Leu Leu Ile Tyr
1 5 10 15

<210> 656
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L2_3

<400> 656

Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile Tyr
1 5 10 15

<210> 657
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L2_4

<400> 657

Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr

1 5 10 15

<210> 658
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L3_1

<400> 658

Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr
20 25 30

<210> 659
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L3_2

<400> 659

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
20 25 30

<210> 660
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L3_3

<400> 660

Gly Ile Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ser Glu Asp Phe Ala Val Tyr Tyr

20 25 30

<210> 661
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L3_4

<400> 661

Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr
20 25 30

<210> 662
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_1

<400> 662

Gly Gln Gly Thr Arg Leu Glu Ile Lys
1 5

<210> 663
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_2

<400> 663

Gly Gln Gly Thr Lys Leu Glu Ile Lys
1 5

<210> 664
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_3

<400> 664

Gly Gln Gly Thr Lys Val Glu Ile Lys
1   5

<210> 665
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_4

<400> 665

Gly Gly Gly Thr Lys Val Glu Ile Lys
1   5

<210> 666
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_5

<400> 666

Gly Pro Gly Thr Lys Val Asp Ile Lys
1   5

<210> 667
<211> 9
<212> PRT
<213> Artificial Sequence

<220>
<223> FW-L4_6

<400> 667

Gly Gly Gly Thr Lys Leu Glu Ile Lys
1   5

<210> 668
<211> 11
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_CDR-L1

<400> 668

Arg Ala Ser Gln Asn Ile Gly Thr Tyr Leu Ala
1 5 10

<210> 669
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02_CDR-L1

<400> 669

Arg Ala Ser Gln Arg Ile Ser Asn Trp Leu Ala
1 5 10

<210> 670
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06_CDR-L1

<400> 670

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 671
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04_CDR-L1

<400> 671

Arg Ala Ser Gln Asp Ile Asp Thr Tyr Leu Ala
1 5 10

<210> 672

<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05_CDR-L1

<400> 672

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 673
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07_CDR-L1

<400> 673

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 674
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11_CDR-L1

<400> 674

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 675
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03_CDR-L1

<400> 675

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 676
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_CDR-L1

<400> 676

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 677
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05_CDR-L1

<400> 677

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 678
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06_CDR-L1

<400> 678

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 679
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07_CDR-L1

<400> 679

Arg Ala Ser Gln Ser Ile Asp Asn Trp Leu Ala

1 5 10

<210> 680
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08_CDR-L1

<400> 680

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 681
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09_CDR-L1

<400> 681

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 682
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11_CDR-L1

<400> 682

Arg Ala Ser Gln Thr Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 683
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06_CDR-L1

<400> 683

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1   5   10

<210> 684
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09_CDR-L1

<400> 684

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1   5   10

<210> 685
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03_CDR-L1

<400> 685

Arg Ala Ser Gln Thr Ile Asp Ile Tyr Leu Asn
1   5   10

<210> 686
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04_CDR-L1

<400> 686

Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
1   5   10

<210> 687
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07_CDR-L1

<400> 687

Arg Ala Ser Gln Ser Ile Gly Thr Trp Leu Ala
1 5 10

<210> 688
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.24_CD70_DB02_D02_CDR-L1

<400> 688

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 689
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04_CDR-L1

<400> 689

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 690
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10_CDR-L1

<400> 690

Arg Ala Ser Gln Thr Ile Tyr Lys Trp Leu Ala
1 5 10

<210> 691
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11_CDR-L1

<400> 691

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1   5   10

<210> 692
<211> 11
<212> PRT
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<220>
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Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
1   5   10

<210> 694
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1   5   10

<210> 695
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<400> 695

Arg Ala Ser Gln Ser Ile Ser Thr Tyr Leu Asn
1 5 10

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<400> 696

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 697
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1 5 10

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1 5 10

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Gln Ala Ser Gln Asp Ile Ser Asp Ser Leu Asn
1   5   10

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Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1   5   10

<210> 701
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<400> 701

Arg Ala Ser Gln Asp Ile Arg His Tyr Leu Ala
1   5   10

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Arg Ala Ser Ser Ser Ile Ser Asn Tyr Leu Ala
1   5   10

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1 5 10

<210> 704
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<212> PRT
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<220>
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Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 705
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<220>
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<400> 705

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 706
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<220>
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<400> 706

Arg Ala Ser Gln Asp Ile Arg Asp Gly Leu Gly

1 5 10

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<220>
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Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Ala
1 5 10

<210> 708
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1 5 10

<210> 709
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<220>
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Arg Ala Ser Gln Ser Ile Ser Thr Asn Leu Ala
1 5 10

<210> 710
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<220>
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1   5   10   15

Ala

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<220>
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Gln Ala Ser His Asp Ile Ser Lys Phe Leu Asn
1   5   10

<210> 712
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<400> 712

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1   5   10   15

<210> 713
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<220>
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1   5   10   15

<210> 714
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<220>
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<210> 715
<211> 11
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<220>
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<400> 715

Arg Ala Ser Gln Ser Ile Ser Ser Trp Leu Ala
1 5 10

<210> 716
<211> 11
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<220>
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<400> 716

Arg Ala Ser Gln Ser Ile Asn Arg Trp Leu Ala
1 5 10

<210> 717
<211> 11
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<400> 717

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 718

<211> 11
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<220>
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<400> 718

Gln Ala Ser Gln Asp Ile Arg Asn Phe Leu Asn
1 5 10

<210> 719
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<220>
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<400> 719

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1 5 10

<210> 720
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1 5 10

<210> 721
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<220>
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Arg Ala Ser Gln Gly Ile Gly Ser Trp Leu Ala
1 5 10

<210> 722
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<220>
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<400> 722

Arg Ala Ser Gln Ser Ile Ser Ser Ser Leu Ala
1 5 10

<210> 723
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<220>
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<400> 723

Arg Ala Ser Gln Gly Ile Gly Gly Tyr Leu Ala
1 5 10

<210> 724
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<220>
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<400> 724

Arg Ala Ser Gln Ser Val Ser Ser Tyr Leu Asn
1 5 10

<210> 725
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<220>
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<400> 725

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp

1 5 10 15

<210> 726
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<220>
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<400> 726

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 727
<211> 16
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<220>
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<400> 727

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 728
<211> 11
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<220>
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<400> 728

Arg Ala Ser Gln Ser Val Ser Arg Tyr Leu Asn
1 5 10

<210> 729
<211> 11
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<400> 729

Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
1 5 10

<210> 730
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<220>
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<400> 730

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 731
<211> 11
<212> PRT
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<220>
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<400> 731

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 732
<211> 11
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<220>
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<400> 732

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1 5 10

<210> 733
<211> 11
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<220>
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<400> 733

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

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<220>
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<400> 734

Arg Ala Ser Gln Ser Ile Gly Asn Trp Leu Ala
1 5 10

<210> 735
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<220>
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<400> 735

Arg Ser Ser Gln Ser Leu Leu His Ser Asn Gly Tyr Asn Tyr Leu Asp
1 5 10 15

<210> 736
<211> 11
<212> PRT
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<220>
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<400> 736

Arg Ala Ser Gln Gly Ile Ser Asn Tyr Leu Ala
1 5 10

<210> 737
<211> 11
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<220>
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<400> 737

Arg Ala Ser Gln Gly Ile Ser Asn Asn Leu Asn
1   5   10

<210> 738
<211> 11
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<400> 738

Arg Ala Ser Gln Asp Ile Gly Asn Asp Leu Gly
1   5   10

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<400> 739

Arg Ala Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1   5   10

<210> 740
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<400> 740

Arg Thr Ser Gln Ser Ile Ser Ser Tyr Leu Asn
1   5   10

<210> 741
<211> 11
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<220>
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<400> 741

Gln Ala Ser Gln Asp Ile Ser Asn Tyr Leu Asn
1 5 10

<210> 742
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<220>
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<400> 742

Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 743
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<212> PRT
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<220>
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Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 744
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<212> PRT
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<220>
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<400> 744

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 745

<211> 7
<212> PRT
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<220>
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<400> 745

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 746
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<220>
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Asp Ala Ser Ser Leu Glu Ser
1 5

<210> 747
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<400> 747

Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 748
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<212> PRT
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<400> 748

Asp Ala Ser Tyr Leu Glu Thr
1 5

<210> 749
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<220>
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<400> 749

Asp Ala Ser Asn Leu Glu Thr
1   5

<210> 750
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<212> PRT
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<400> 750

Gln Ala Ser Ser Leu Glu Ser
1   5

<210> 751
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<212> PRT
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<400> 751

Ala Thr Ser Thr Leu Ala Asn
1   5

<210> 752
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<220>
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1 5

<210> 753
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<220>
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<400> 753

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 754
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<220>
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<400> 754

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1 5

<210> 755
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<212> PRT
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<220>
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<400> 755

Asp Val Ser Asn Leu Glu Thr
1 5

<210> 756
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Asp Ala Ser Ser Leu Glu Ser
1   5

<210> 757
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<400> 757

Asp Ala Ser Asn Leu Ala Thr
1   5

<210> 758
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<220>
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<400> 758

Gly Ala Thr Thr Leu Gln Ser
1   5

<210> 759
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<212> PRT
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<220>
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<400> 759

Asp Ala Ser Asn Leu Glu Thr
1   5

<210> 760
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<212> PRT
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<220>
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<400> 760

Ala Ala Ser Ser Leu His Ser
1 5

<210> 761
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<212> PRT
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<220>
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<400> 761

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 762
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<212> PRT
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<400> 762

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 763
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<220>
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<400> 763

Ala Ala Ser Thr Leu Glu Ser
1 5

<210> 764
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<212> PRT
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<400> 764

Asp Ala Ser Ser Leu Glu Ser
1   5

<210> 765
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Asp Ala Ser Asn Leu Glu Thr
1   5

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<220>
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<400> 766

Asp Ala Ser Ser Leu Gln Ser
1   5

<210> 767
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<220>
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<400> 767

Tyr Ala Ser Thr Leu Gln Ser
1   5

<210> 768
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<212> PRT

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<220>
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<400> 768

Asp Ala Ser Thr Leu Glu Ala
1 5

<210> 769
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<220>
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<400> 769

Asp Ala Ser Asn Leu Glu Ile
1 5

<210> 770
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<212> PRT
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<220>
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<400> 770

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 771
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<400> 771

Ala Ala Ser Asn Leu Glu Thr
1 5

<210> 772

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<400> 772

Asp Ala Ser Asn Leu Gln Thr
1 5

<210> 773
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Ser Ala Ser Ser Leu Gln Ser
1 5

<210> 774
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<400> 774

Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 775
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<400> 775

Asp Ala Ser Ser Leu Gln Ser
1 5

<210> 776
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<400> 776

Gly Ala Ser Thr Arg Ala Ser
1   5

<210> 777
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<220>
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<400> 777

Asp Ala Ser Asn Leu Glu Thr
1   5

<210> 778
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<212> PRT
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<400> 778

Ser Ala Ser Thr Leu Gln Ser
1   5

<210> 779
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<220>
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<400> 779

Ala Ala Ser Ser Leu Gln Ser

1 5

<210> 780
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<400> 780

Ala Ala Ser Thr Leu Gln Ser
1 5

<210> 781
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<400> 781

Gly Ala Ser Thr Arg Ala Thr
1 5

<210> 782
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<220>
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<400> 782

Asp Ala Ser Asn Leu Glu Thr
1 5

<210> 783
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<400> 783

Asp Ala Ser Tyr Leu Glu Ala
1   5

<210> 784
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<400> 784

Trp Ala Ser Thr Arg Asp Ser
1   5

<210> 785
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<400> 785

Asp Ala Ser Asn Leu Gln Arg
1   5

<210> 786
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<400> 786

Asp Ala Ser Ser Leu Gln Ser
1   5

<210> 787
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<400> 787

Ala Ala Ser Asn Leu Gln Gly
1 5

<210> 788
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<400> 788

Asp Ala Ser Asn Leu Glu Arg
1 5

<210> 789
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<400> 789

Ala Ala Ser Ser Leu Gln Ser
1 5

<210> 790
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Ala Ala Ser Thr Leu Gln Ser
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Asp Thr Ser Asn Leu Glu Thr
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1   5

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Gly Ala Ser Ser Leu Gln Ser
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Asp Ala Ser Asn Leu Glu Thr
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Cys Met Gln Ala Leu Gln Thr Pro Ile Thr Phe
1   5   10

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1   5   10

<210> 820
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1   5   10

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Cys Gln Gln Ala Tyr Arg Trp Pro Ile Thr Phe
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Cys Gln Gln Ser Tyr Thr Ile Pro Pro Thr Phe
1 5 10

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Cys Gln Gln Ser Tyr Ser Thr Pro Leu Thr Phe
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1   5   10

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Cys Gln Gln Ser Asp Ser Ser Pro Leu Thr Phe
1   5   10

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<220>
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<400> 832

Cys Gln Gln Ala Asp Ser Phe Pro Tyr Thr Phe
1   5   10

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1 5 10

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1   5   10

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1   5   10

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<210> 862
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1 5 10

<210> 870
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1 5 10

<210> 871
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1 5 10

<210> 872
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Cys Met Gln Ala Leu Asp Thr Pro Leu Thr Phe
1   5   10

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1   5   10

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1   5   10

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<400> 876

Cys Gln Gln Ala Asp Ser Phe Pro Val Thr Phe
1 5 10

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<400> 879

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1 5 10

<210> 880

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1 5 10

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<400> 881

Cys Leu Gln Asp Ala Ala Thr Pro Ile Thr Phe
1 5 10

<210> 882
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<400> 882

Cys Gln Gln Ser Tyr Thr Thr Pro Trp Thr Phe
1 5 10

<210> 883
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<400> 883

Cys Met Lys Gly Leu Gln Thr Pro Leu Thr Phe
1 5 10

<210> 884
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<400> 884

Cys Gln Gln Ser His Ser Thr Pro Leu Thr Phe
1   5   10

<210> 885
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<400> 885

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1   5   10

<210> 886
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10_CDR-L3

<400> 886

Cys Leu Gln Asp Tyr Asp Tyr Pro Leu Thr Phe
1   5   10

<210> 887
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_CDR-L3

<400> 887

Cys Gln Gln Ser Tyr Asn Thr Pro Tyr Ser Phe

1 5 10

<210> 888
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_CDR-L3

<400> 888

Cys Leu Gln Asp Tyr Ser Tyr Pro Leu Thr Phe
1 5 10

<210> 889
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_CDR-L3

<400> 889

Cys Gln Gln Ser Tyr Ser Thr Pro Pro Ala Phe
1 5 10

<210> 890
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_VH

<400> 890

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly His
20 25 30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe

50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Val Arg Gly Ser Gly Trp Tyr Asp Leu Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 891
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02_VH

<400> 891

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Leu Gly Val Ala Gly Tyr Phe Asp Leu Trp Gly Arg Gly

```
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  892
<211>  123
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.3_CD70_DB01_E06_VH

<400>  892

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Ser Gly Ile Asp Gly Tyr Ile Gly Phe Phe Asp Tyr
            100                 105                 110


Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  893
<211>  119
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> NK77.4_CD70_DB01_G04_VH

<400> 893

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Ser His
            20   25   30

Val Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Ile Ile Asp Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Arg Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Lys Asp Tyr Thr Gly Leu Leu Gly Met Asp Val Trp Gly Gln Gly
            100   105   110

Thr Thr Val Thr Val Ser Ser
        115

<210> 894
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05_VH

<400> 894

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
            20   25   30

```
Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Leu Ser Gly Tyr Asp Leu Asp Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  895
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.6_CD70_DB01_G07_VH

<400>  895

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Lys Tyr Ala His Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Leu Ser Gly Tyr Asp Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110


Thr Val Thr Val Ser Ser
        115


<210>  896
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.7_CD70_DB01_G11_VH

<400>  896

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Thr Asp Val Tyr Gly Asp Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115
```

<210> 897
<211> 126
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03_VH

<400> 897

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
20 25 30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Gly Thr Ala Met Ala Thr Gly Tyr Tyr Tyr Tyr Gly
100 105 110

Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120 125

<210> 898
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_VH

<400> 898

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
20 25 30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Ser Asn Gly Gly Tyr Thr Gly Tyr Ala Leu Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ala Ser Asn Tyr Gly Gly His Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 899
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05_VH

<400> 899

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ile Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Asp Met Gly Ala Trp Ala Ala Gly Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 900
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06_VH

<400> 900

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ser Val Asn Asp Tyr Gly Asp Tyr Asp Gly Tyr Trp Gly Gln
```

```
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  901
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.13_CD70_DB02_A07_VH

<400>  901

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Tyr Gly Asp Tyr Asp Ala Ser Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  902
<211>  117
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> NK77.14_CD70_DB02_A08_VH

<400> 902

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Ile Ile Asn Pro Ser Asp Gly Ser Thr Ile Tyr Ala Gln Asn Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Val Lys Glu Glu Ala Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Leu
            100   105   110

Val Thr Val Ser Ser
        115

<210> 903
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09_VH

<400> 903

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

```
Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asp Asn Gly Asp Thr Gly Tyr Ala Gln Met Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Ser Gly Asp Tyr Tyr Asp Ile Leu Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  904
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.16_CD70_DB02_A11_VH

<400>  904

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro Asn Ser Gly Asp Thr Gly Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Pro Ser Gly Tyr Glu Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 905
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06_VH

<400> 905

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Phe Ser Val Tyr Ala Ala Ala Asp Gly Met Asp Val Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 906
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09_VH

<400> 906

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asp Gly Gly Thr Ile Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Phe Gly Glu Ser Ala Pro Asp Ala Phe Asp Ile Trp Gly
100 105 110

Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 907
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03_VH

<400> 907

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Gly Thr Glu Ile Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr
100 105 110

Thr Val Thr Val Ser Ser
115

<210> 908
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04_VH

<400> 908

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Met Ile Asn Pro Ser Asp Gly Ala Thr Thr Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Arg Glu Leu Leu His Phe Ala Thr Asn Tyr Tyr Tyr Tyr
            100                 105                 110

Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120                 125
```

<210> 909
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07_VH

<400> 909

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Arg Asn
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Pro Asp Asn Gly Val Thr Asn Tyr Ala Gln Asn Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Lys Thr Gln Gly Ser Ser Ser Trp Tyr Gln Trp Tyr Phe Asp Leu
```

```
            100                 105                 110


Trp Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  910
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.24_CD70_DB02_D02_VH

<400>  910

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asp Pro Gly Ser Gly Asp Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Ser Asn Trp Tyr Asp Tyr Phe Asp Tyr Trp Gly Gln Gly
            100                 105                 110


Thr Leu Val Thr Val Ser Ser
        115


<210>  911
<211>  119
<212>  PRT
<213>  Artificial Sequence
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<220>
<223> NK77.25_CD70_DB02_D04_VH

<400> 911

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Arg Leu Ser Asp His
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Thr Tyr Ala Gln Asn Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Ser Ser Tyr Tyr Gly Asp Tyr Val Leu Val Asn Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 912
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10_VH

<400> 912

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

```
Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Ile Asn Pro Asn Thr Gly Gly Thr Ser Phe Ala Gln Asn Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Leu Gly Gln Trp Leu Gly Glu Ile Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  913
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.27_CD70_DB02_D11_VH

<400>  913

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30


Thr Asp Tyr Phe Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu
        35                  40                  45


Glu Trp Met Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala
    50                  55                  60


Gln Glu Phe Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser
65                  70                  75                  80
```

```
Thr Val Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
                85                  90                  95


Tyr Tyr Cys Ala Arg Gly Pro Tyr Ser Ser Ser Trp Tyr Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  914
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.28_CD70_DB02_E04_VH

<400>  914

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Leu Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Gly Val Gly Ala Met Gly Val Phe Asp Tyr Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 915
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06_VH

<400> 915

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Ser Ala Tyr Asn Gly Lys Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Thr Ile Tyr Tyr Asp Phe Trp Ser Gly Tyr Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 916
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08_VH

<400> 916

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ala Thr Ile Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Arg Gly Asp Tyr Tyr Gly Ser Gly Asp Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 917
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07_VH

<400> 917

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Tyr Phe Asp His Ala Phe Asp Ile Trp Gly Gln Gly Thr
            100                 105                 110

Met Val Thr Val Ser Ser
        115
```

<210> 918
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04_VH

<400> 918

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Asp Thr Ile Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Gly Asp Ser Ser Ser Trp Tyr Asp Tyr Tyr Tyr Tyr Met Asp
```

100 105 110

Val Trp Gly Lys Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 919
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05_VH

<400> 919

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Phe Thr His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Thr Tyr Asp Gly Asn Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Met Glu Trp Leu Gly Gln Val Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 920
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08_VH

<400> 920

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Arg Ile Asn Pro Asn Gly Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Gly His Arg Gly Gly Gly Gly Ile Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 921
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.36_CD70_DB03_A06_VH

<400> 921

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
            20   25   30

```
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Pro Asn Ser Gly Asp Thr His Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Trp Gly Ser Gly Trp Tyr Val Asp Tyr Trp Gly Gln Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 922
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07_VH

<400> 922

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Asn Ser Tyr
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Thr Tyr Gly Asp Asp Ala Phe Asp Ile Trp Gly Gln Gly
            100                 105                 110


Thr Met Val Thr Val Ser Ser
        115


<210>  923
<211>  124
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.38_CD70_DB03_A08_VH

<400>  923

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ser Phe Thr Ser Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Thr Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Asn Ser Pro Tyr Ser Ser Ser Trp Trp Asp Tyr Phe Asp
            100                 105                 110


Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 924
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.39_CD70_DB03_A09_VH

<400> 924

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Thr Pro Asn Ser Gly Tyr Thr Tyr Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asn Thr Asp Cys Tyr Gly Asp Phe Leu Gly Leu Asp Val Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 925
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11_VH

<400> 925

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Asn Gly Tyr
20 25 30

Leu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Val Asn Pro Ser Asp Gly Ser Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Thr Gly Leu Arg Tyr Phe Asp Trp Leu Leu Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 926
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12_VH

<400> 926

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asp Pro Ser Gly Gly Arg Thr Ile Tyr Ala Gln Arg Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg His Glu Ala Gly Gly Ile Phe Asp Tyr Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 927
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01_VH

<400> 927

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ser Asp Ser
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45

Gly Gly Ile Ile Pro Met Ala Gly Ile Pro Ala Tyr Ala Glu Glu Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Asp Asp Tyr Gly Gly Asn Trp Tyr Phe Asp Leu Trp Gly
```

```
            100                 105                 110


Arg Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  928
<211>  120
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.43_CD70_DB03_B04_VH

<400>  928

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Ile Phe Thr Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Gly Trp Tyr Glu Ser Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110


Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  929
<211>  122
<212>  PRT
<213>  Artificial Sequence
```

<220>
<223> NK77.44_CD70_DB03_B06_VH

<400> 929

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Ser Ala Tyr Asn Gly Asn Thr Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Glu Ile Val Gly Ala Thr Glu Asp Trp Tyr Phe Asp Leu Trp
            100   105   110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 930
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09_VH

<400> 930

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
            20   25   30

Tyr Leu His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Met Ile Asn Pro Asn Asn Gly Gly Thr Ile Tyr Ala Gln Thr Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Leu Gly Gly Tyr Val Leu Phe Asp Tyr Trp Gly Gln Gly
            100   105   110

Thr Leu Val Thr Val Ser Ser
        115

<210> 931
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.46_CD70_DB03_C05_VH

<400> 931

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20   25   30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Met Ile Asn Pro Arg Gly Gly Ser Thr Thr Tyr Ala Gln Ser Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Leu Gly Asp Tyr Gly Asp Tyr Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 932
<211> 124
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11_VH

<400> 932

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Asn Ser
20 25 30

Asp Met Asn Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ser Ala Ile Ser Gly Gly Gly Asp Thr Leu Tyr Tyr Ala Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Met Ala Ser Ala Leu Asp Ser Ser Gly Asp Asn Glu Ala Phe Asp
100 105 110

Ile Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
115 120

<210> 933
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01_VH

<400> 933

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Asn Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Val Glu Asp Asp Phe Trp Ser Gly Pro Ser Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 934
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03_VH

<400> 934

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Thr Asn Tyr
20 25 30

Ala Phe Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Ile Pro Ile Ser Gly Ala Ala Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ser Gly Leu Asp Asp Ala Phe Asp Ile Trp Gly Gln Gly
100 105 110

Thr Met Val Thr Val Ser Ser
115

<210> 935
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09_VH

<400> 935

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Glu Gly Arg Ile Asp Tyr Gly Asp Tyr Asp Asp Tyr Tyr Tyr
            100                 105                 110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser
        115                 120                 125

Ser
```

<210> 936
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02_VH

<400> 936

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
            20                  25                  30

Tyr Val His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Thr Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
```

85 90 95

Ala Arg Asp Gln Gly Leu Trp Phe Thr Gly Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 937
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05_VH

<400> 937

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ala Tyr
20 25 30

His Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Ile Ile Asn Pro Gly Asp Gly Ala Thr Gly Tyr Ala Gln Asn Leu
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Gly Glu Gly Ile Ser Gly Ser Asp Ala Phe Asp Ile Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 938

<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06_VH

<400> 938

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asn Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Trp Gly Val Asp Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 939
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09_VH

<400> 939

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

```
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Phe Asn Pro Ser Asp Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Val Gly Glu Thr Thr Phe Asp Pro Trp Gly Gln Gly Thr
            100                 105                 110

Leu Val Thr Val Ser Ser
        115
```

<210> 940
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.55_CD70_DB03_F12_VH

<400> 940

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Ser Ala Tyr Asn Gly His Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60
```

```
Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Ser Val Arg Gly Trp Asp Tyr Tyr Tyr Gly Met Gly Val
            100                 105                 110


Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120
```

<210> 941
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.56_CD70_DB03_G06_VH

<400> 941

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ile Asp Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Trp Met Asn Pro His Ser Gly Asn Ser Asp Asn Ala Pro Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Gly Tyr Ser Gly Tyr Asp Leu Thr Ala Asp Tyr Trp Gly Gln
            100                 105                 110
```

Gly Thr Leu Val Thr Val Ser Ser
        115   120

<210> 942
<211> 129
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11_VH

<400> 942

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1   5   10   15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Gln
            20   25   30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35   40   45

Gly Trp Ile Asn Pro Asn Thr Gly Asp Thr Asn Tyr Ala Gln Lys Phe
    50   55   60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65   70   75   80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85   90   95

Ala Arg Asp Ser Val Phe Glu Val Glu Gly Gly Thr Asp Tyr Tyr Tyr
            100   105   110

Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Met Val Thr Val Ser
        115   120   125

Ser

<210> 943
<211> 119
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.58_CD70_DB03_H08_VH

<400> 943

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Ser Gly Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Ser Gly Tyr Asp Trp Val Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 944
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.59_CD70_DB03_H10_VH

<400> 944

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Ala Asn Tyr

```
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Gly Gly Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Gly Ser Tyr Phe Gly Trp Phe Asp Pro Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 945
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.60_CD70_DB04_A05_VH

<400> 945

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Thr Tyr
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Thr Gly Gly Ser Thr Tyr Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
```

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Ser Gly Asn Tyr Gln Gly Ile Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 946
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.61_CD70_DB04_A07_VH

<400> 946

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Asn Thr Phe Thr Ser Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Ser Gly Asp Thr Asn Tyr Ala Gln Asn Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Val Ser Gly Tyr Asp Leu Phe Asp Tyr Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser

115

<210> 947
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.62_CD70_DB04_A10_VH

<400> 947

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
20 25 30

Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Ser Ile Lys His Asp Gly Ser Glu Gln Tyr Tyr Val Asp Ser Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Asn Thr Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Ala Ser Gly Val Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val
100 105 110

Ser Ser

<210> 948
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.63_CD70_DB04_A11_VH

<400> 948

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Arg Tyr
            20                  25                  30


Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
        35                  40                  45


Gly Ile Ile Asp Pro Thr Gly Ala Ser Thr Ser Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Asp Tyr Ser Tyr Gly Met Asp Tyr Tyr Gly Met Asp Val Trp
            100                 105                 110


Gly Gln Gly Thr Leu Val Thr Val Ser Ser
        115                 120


<210>  949
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.64_CD70_DB04_B03_VH

<400>  949

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30


Gly Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45
```

```
Gly Gly Ile Ile Pro Ile Phe Gly Thr Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp His Ser Gly Asp Gly Tyr Phe Asp Leu Trp Gly Arg Gly
            100                 105                 110

Thr Leu Val Thr Val Ser Ser
        115
```

<210> 950
<211> 118
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.65_CD70_DB04_B05_VH

<400> 950

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Glu Asn
            20                  25                  30

Glu Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Ile Asn Pro Asn Ser Gly Gly Thr Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95
```

Ala Gly Ser Trp Gly Gly Tyr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr
100 105 110

Leu Val Thr Val Ser Ser
115

<210> 951
<211> 121
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.66_CD70_DB04_B07_VH

<400> 951

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Ile Tyr Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Ile Asn Pro Asn Asp Gly Ala Thr Asn Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Gly Asn Asp Tyr Tyr Tyr Tyr Phe Met Asp Tyr Trp Gly
100 105 110

Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 952
<211> 122
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.67_CD70_DB04_C01_VH

<400> 952

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Ser Ser Tyr
20 25 30

Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Gly Ile Thr Pro Met Phe Gly Thr Thr Asp Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Asp Glu Arg Asp Gly Tyr Ala Thr Val Ala Phe Asp Ile Trp
100 105 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
115 120

<210> 953
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04_VH

<400> 953

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr

```
            20                  25                  30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile Asn Pro Ser Asp Gly Gly Thr Ser Tyr Ala Asp Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Ala Leu Ala Pro Leu Gly Trp Gly Asp Gly Met Asp Val Trp
            100                 105                 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser
        115                 120


<210>  954
<211>  119
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.69_CD70_DB04_C06_VH

<400>  954

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Ser Ser Gly Val Thr Asn Phe Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
```

65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Gly Ser Asp Gln Gly Asp Trp Ser Asp Pro Trp Gly Gln Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 955
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07_VH

<400> 955

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Ser
20 25 30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Trp Met Asn Pro Asn Thr Gly Asp Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Lys Asp Asp Phe Gly Glu Leu Ala Pro Ala Thr Phe Asp Pro Trp
100 105 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser

115 120

<210> 956
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02_VH

<400> 956

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asp Ile Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Ser Pro Ser Gly Gly Gly Thr Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Tyr Tyr Gly Gly Asn Pro Glu Gly Trp Tyr Phe Asp Leu Trp
100 105 110

Gly Arg Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 957
<211> 132
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05_VH

<400> 957

```
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1               5                   10                  15


Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Val Phe Asp Asp Tyr
            20                  25                  30


Ala Ile His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45


Ala Ala Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val
    50                  55                  60


Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80


Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Ala Pro Gln Tyr Tyr Gly Ser Gly Thr Asp Pro Leu Glu Val
            100                 105                 110


Arg Tyr Tyr Tyr Tyr Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val
        115                 120                 125


Thr Val Ser Ser
    130


<210>  958
<211>  122
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.73_CD70_DB04_D07_VH

<400>  958

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe Arg Asn Tyr
            20                  25                  30
```

```
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp His Ser Ala Gly Thr His His Asp Ala Phe Asp Ile Trp
            100                 105                 110

Gly Gln Gly Thr Met Val Thr Val Ser Ser
        115                 120
```

<210> 959
<211> 117
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.74_CD70_DB04_D08_VH

<400> 959

```
Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
            20                  25                  30

Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45

Gly Trp Met Asn Pro Asn Ser Gly Asn Ala Gly Tyr Ala Gln Lys Phe
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80
```

```
Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Tyr Trp Gly Ser Phe Asp Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110


Val Thr Val Ser Ser
        115


<210>  960
<211>  118
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.75_CD70_DB04_D10_VH

<400>  960

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1               5                   10                  15


Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Gly Tyr
            20                  25                  30


Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
        35                  40                  45


Gly Met Ile Asp Pro Ser Asp Gly Ser Thr Ile Tyr Ala Gln Lys Phe
    50                  55                  60


Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80


Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95


Ala Arg Glu Arg Pro Leu Tyr Ala Ser Asp Leu Trp Gly Gln Gly Thr
            100                 105                 110


Leu Val Thr Val Ser Ser
        115
```

<210> 961
<211> 119
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_VH

<400> 961

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Trp Met Asn Pro Asp Ser Gly Asn Thr Gly Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser Ser Ser Ser Trp Pro Asp Phe Asp Leu Trp Gly Arg Gly
100 105 110

Thr Leu Val Thr Val Ser Ser
115

<210> 962
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_VH

<400> 962

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala

1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Ser Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Val
35 40 45

Gly Ile Ile Asn Pro Ser Ser Gly Ser Ala Ser Tyr Ala Gln Lys Phe
50 55 60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Glu Arg Gly Ala Tyr Ser Ser Thr Phe Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 963
<211> 120
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_VH

<400> 963

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr
20 25 30

Tyr Met His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
35 40 45

Gly Val Ile Asn Pro Ser Asp Gly Thr Ala His Tyr Ala Gln Arg Leu

```
    50                  55                  60

Gln Gly Arg Val Thr Met Thr Arg Asp Thr Ser Thr Ser Thr Val Tyr
65                  70                  75                  80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg Asp Ser Gly Ser Tyr Tyr Ala Asp Phe Asp Tyr Trp Gly Gln
            100                 105                 110

Gly Thr Leu Val Thr Val Ser Ser
        115                 120
```

<210> 964
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_VL

<400> 964

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asn Ile Gly Thr Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ile Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
```

100 105

<210> 965
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02_VL

<400> 965

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Arg Ile Ser Asn Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Pro Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 966
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.3_CD70_DB01_E06_VL

<400> 966

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Gln Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95

Leu Gln Thr Pro Ile Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
            100   105   110

Arg

<210> 967
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04_VL

<400> 967

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Asp Thr Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

```
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Phe
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210>  968
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.5_CD70_DB01_G05_VL

<400>  968

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Ser Pro Leu
                85                  90                  95


Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210>  969
<211>  108
<212>  PRT
```

<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07_VL

<400> 969

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Tyr Arg Trp Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 970
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11_VL

<400> 970

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```
        35                  40                  45

Tyr Asp Ala Ser Tyr Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Ile Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 971
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03_VL

<400> 971

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
```

100 105

<210> 972
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_VL

<400> 972

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Gln Ala Ser Ser Leu Glu Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
85 90 95

Thr His Trp Pro Pro Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 973
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05_VL

<400> 973

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Thr Ser Thr Leu Ala Asn Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Leu Thr
                85                  90                  95


Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105


<210>  974
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.12_CD70_DB02_A06_VL

<400>  974

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 975
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07_VL

<400> 975

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asp Asn Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ser Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 976
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08_VL

<400> 976

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 977
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09_VL

<400> 977

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```
        35                  40                  45

Tyr Asp Val Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
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<210> 978
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11_VL

<400> 978

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Ile Ser Phe Pro Leu
                85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
```

100 105

<210> 979
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06_VL

<400> 979

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Ala Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Ser Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 980
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09_VL

<400> 980

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Thr Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100                 105
```

<210> 981
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03_VL

<400> 981

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Asp Ile Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 982
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04_VL

<400> 982

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ala Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 983
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07_VL

<400> 983

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Thr Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Ile
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 984
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.24_CD70_DB02_D02_VL

<400> 984

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1   5   10   15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35   40   45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Tyr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 985
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04_VL

<400> 985

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asp Tyr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 986

<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10_VL

<400> 986

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Tyr Lys Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asn Ser Phe Pro Phe
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 987
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11_VL

<400> 987

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Pro
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 988
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.28_CD70_DB02_E04_VL

<400> 988

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Thr Ser Ile Ser Asp Tyr
            20                  25                  30

Val His Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Thr Pro Pro
                85                  90                  95
```

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 989
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06_VL

<400> 989

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 990
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08_VL

<400> 990

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Thr Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Thr Leu Glu Ala Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Pro Pro Tyr
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 991
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07_VL

<400> 991

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Ile Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Asp Ser Ser Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 992
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04_VL

<400> 992

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Arg Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 993
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05_VL

<400> 993

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asn Asp
            20   25   30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Phe
                85   90   95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
            100   105

<210> 994
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08_VL

<400> 994

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Glu Ile Ser Asn Tyr
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

```
Tyr Asp Ala Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Phe
                85                  90                  95


Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
            100                 105


<210>  995
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.36_CD70_DB03_A06_VL

<400>  995

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asp Ser
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Phe Thr Thr Pro Tyr
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 996
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07_VL

<400> 996

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Asn Phe Ser Pro Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 997
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.38_CD70_DB03_A08_VL

<400> 997

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg His Tyr

```
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Asp Ala Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105


<210>  998
<211>  107
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.39_CD70_DB03_A09_VL

<400>  998

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1               5                   10                  15

Glu Arg Ala Thr Ile Asn Cys Arg Ala Ser Ser Ser Ile Ser Asn Tyr
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Thr Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Ala
65                  70                  75                  80

Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Leu
```

85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 999
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11_VL

<400> 999

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Thr Asn Phe
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Gly Ala Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 1000
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12_VL

<400> 1000

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30


Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ser Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ser Pro Tyr
                85                  90                  95


Arg Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105


<210>  1001
<211>  113
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.42_CD70_DB03_B01_VL

<400>  1001

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1               5                   10                  15


Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20                  25                  30


Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35                  40                  45


Pro Gln Leu Leu Ile Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro
    50                  55                  60
```

```
Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80


Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95


Ala His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
            100                 105                 110


Arg
```

<210> 1002
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.43_CD70_DB03_B04_VL

<400> 1002

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15


Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Arg Asp Gly
            20                  25                  30


Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45


Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60


Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80


Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Gly Thr Pro Pro
                85                  90                  95


Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 1003
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.44_CD70_DB03_B06_VL

<400> 1003

Glu Ile Val Met Thr Gln Ser Pro Ala Thr Leu Ser Val Ser Pro Gly
1 5 10 15

Glu Arg Ala Thr Leu Ser Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Arg Leu Leu Ile
35 40 45

Tyr Gly Ala Ser Thr Arg Ala Thr Gly Ile Pro Ala Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Ser
65 70 75 80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Tyr Asp Ser Ser Pro Thr
85 90 95

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1004
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09_VL

<400> 1004

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr

```
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Ala Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105


<210>  1005
<211>  108
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  NK77.46_CD70_DB03_C05_VL

<400>  1005

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Thr Asn
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Tyr Leu Glu Ala Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
```

85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1006
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11_VL

<400> 1006

Asp Ile Val Met Thr Gln Ser Pro Asp Ser Leu Ala Val Ser Leu Gly
1 5 10 15

Glu Arg Ala Thr Ile Asn Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser
20 25 30

Ser Asn Asn Lys Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln
35 40 45

Pro Pro Lys Leu Leu Ile Tyr Trp Ala Ser Thr Arg Asp Ser Gly Val
50 55 60

Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
65 70 75 80

Ile Ser Ser Leu Gln Ala Glu Asp Val Ala Val Tyr Tyr Cys Gln Gln
85 90 95

Tyr Tyr Gly Phe Pro Pro Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile
100 105 110

Lys Arg

<210> 1007
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01_VL

<400> 1007

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser His Asp Ile Ser Lys Phe
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Ala Ser Asn Leu Gln Arg Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Tyr Ser Phe Pro Phe
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100   105

<210> 1008
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03_VL

<400> 1008

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1   5   10   15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
85 90 95

Arg Gln Thr Pro Leu Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys
100 105 110

Arg

<210> 1009
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09_VL

<400> 1009

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Ala Ala Ser Asn Leu Gln Gly Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Thr
85 90 95

Leu Glu Ser Pro Val Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 1010
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02_VL

<400> 1010

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Arg Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 1011
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05_VL

<400> 1011

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Ser Tyr Pro Leu
                85   90   95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 1012
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06_VL

<400> 1012

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Asn Arg Trp
            20   25   30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly

50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ile Thr Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1013
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09_VL

<400> 1013

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Glu Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Ser Phe Pro Ile
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 1014

<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.55_CD70_DB03_F12_VL

<400> 1014

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Arg Asn Phe
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Ala Pro Ser
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1015
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.56_CD70_DB03_G06_VL

<400> 1015

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Asn Tyr
20 25 30

```
Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105
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<210> 1016
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11_VL

<400> 1016

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Thr Ile Ser Gly Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp
                85                  90                  95
```

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1017
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.58_CD70_DB03_H08_VL

<400> 1017

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Ser Trp
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Thr Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Trp
85 90 95

Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys Arg
100 105

<210> 1018
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.59_CD70_DB03_H10_VL

<400> 1018

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly

1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Ser
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1019
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.60_CD70_DB04_A05_VL

<400> 1019

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Gly Gly Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ser Pro Pro
85 90 95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
100 105

<210> 1020
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.61_CD70_DB04_A07_VL

<400> 1020

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Thr Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala His Ser Phe Pro Leu
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1021
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.62_CD70_DB04_A10_VL

<400> 1021

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1   5   10   15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Thr Arg Ala Ser Gly Val Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala
                85   90   95

Leu Asp Thr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100   105   110

Arg

<210> 1022
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.63_CD70_DB04_A11_VL

<400> 1022

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr Asp Thr Ser Asn Leu Gln Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Leu Ser Thr Asp Leu Gln Thr Thr Ala
                85   90   95

His Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100   105

<210> 1023
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.64_CD70_DB04_B03_VL

<400> 1023

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1   5   10   15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Gln Leu Leu Ile Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro
    50   55   60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65   70   75   80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85   90   95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg

<210> 1024
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.65_CD70_DB04_B05_VL

<400> 1024

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Val Ser Arg Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ala Asp Ser Phe Pro Val
85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
100 105

<210> 1025
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.66_CD70_DB04_B07_VL

<400> 1025

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1   5   10   15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
            20   25   30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35   40   45

Tyr His Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50   55   60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65   70   75   80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Met
                85   90   95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg
            100   105

<210> 1026
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.67_CD70_DB04_C01_VL

<400> 1026

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1   5   10   15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
            20   25   30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
        35   40   45

Pro Gln Leu Leu Ile Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro

```
    50                  55                  60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65                  70                  75                  80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly
                85                  90                  95

Thr His Trp Pro Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
            100                 105                 110

Arg
```

<210> 1027
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04_VL

<400> 1027

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Gly Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
```

100 105

<210> 1028
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.69_CD70_DB04_C06_VL

<400> 1028

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Pro
85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1029
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07_VL

<400> 1029

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Gly Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Ala Ala Thr Pro Ile
                85                  90                  95

Thr Phe Gly Gln Gly Thr Arg Leu Glu Ile Lys Arg
            100                 105
```

<210> 1030
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02_VL

<400> 1030

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Gly Asn Trp
            20                  25                  30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asp Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Thr Thr Pro Trp
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1031
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05_VL

<400> 1031

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser
20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Glu Val Ser Asn Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Lys Gly
85 90 95

Leu Gln Thr Pro Leu Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys
100 105 110

Arg

<210> 1032
<211> 108
<212> PRT

<213> Artificial Sequence

<220>
<223> NK77.73_CD70_DB04_D07_VL

<400> 1032

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Tyr
20 25 30

Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser His Ser Thr Pro Leu
85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1033
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.74_CD70_DB04_D08_VL

<400> 1033

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Gly Ile Ser Asn Asn
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile

```
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Tyr
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 1034
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10_VL

<400> 1034

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ile Gly Asn Asp
            20                  25                  30

Leu Gly Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Ala Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Asp Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
```

100 105

<210> 1035
<211> 107
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_VL

<400> 1035

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser Ser Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asn Thr Pro Tyr
85 90 95

Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105

<210> 1036
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_VL

<400> 1036

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

```
Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Asn Leu Glu Thr Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80

Glu Asp Phe Ala Thr Tyr Tyr Cys Leu Gln Asp Tyr Ser Tyr Pro Leu
                85                  90                  95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
            100                 105
```

<210> 1037
<211> 108
<212> PRT
<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_VL

<400> 1037

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1               5                   10                  15

Asp Arg Val Thr Ile Thr Cys Gln Ala Ser Gln Asp Ile Ser Asn Tyr
            20                  25                  30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
        35                  40                  45

Tyr Asp Ala Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
65                  70                  75                  80
```

Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Ser Thr Pro Pro
85 90 95

Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
100 105

<210> 1038
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_VH_DNA

<400> 1038
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cctggacaag ggcttgagtg gatgggatgg atcaacccta acagtggtgg cacaaactat 180

gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccactag cacagtgtac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgt tagaggaagc 300

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<210> 1039
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02_VH_DNA

<400> 1039
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tcctgcaagg catctggata caccttcacc aactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtgggag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaacta 300

ggagtcgccg ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctca 357

<210> 1040

<211> 369
<212> DNA
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<220>
<223> NK77.3_CD70_DB01_E06_VH_DNA

<400> 1040
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cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggaag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagacctg 300

tcagggatcg acggatatat tggtttcttt gactactggg gccaagggac cctggtcacc 360

gtctcctca 369

<210> 1041
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.4_CD70_DB01_G04_VH_DNA

<400> 1041
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tcctgcaagg catctggagg aaccttcaga agccatgtca tatcctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcgatccta gtggtggcag cacaagctac 180

gcacagaggt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc taaagattac 300

actgggctgc ttggaatgga tgtctggggc caagggacaa ccgtcaccgt ctcttca 357

<210> 1042
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05_VH_DNA

<400> 1042

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cctggacaag ggcttgagtg gatgggatgg atgaacccca acagtggtaa cacaggctat 180

gcacagaagt tccagggcag agtcaccatg accagggaca cctccacaag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggcctt 300

tccggctacg acttggacga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1043
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07_VH_DNA

<400> 1043
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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccga acagtggtgg cacaaaatac 180

gcacataagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagaggactg 300

tcaggttacg attttgacta ctggggccaa gggaccacag tcaccgtctc ctca 354

<210> 1044
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11_VH_DNA

<400> 1044
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tcctgcaagg catctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atgaacccta atagtggtaa cacaggctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagggacc 300

gacgtgtatg gagactttga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1045
<211> 378
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03_VH_DNA

<400> 1045
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tcctgcaagg cttctggata caccttcaca gagaacgaaa tgcattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggc atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagaggga 300

ggaaccgcca tggccaccgg ttattactac tatgggatgg acgtgtgggg ccaagggacc 360

accgtcaccg tctcctca 378

<210> 1046
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_VH_DNA

<400> 1046
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tcctgcaagg catctggata caccttcacc gagaatgaaa tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaactcta atggtggcta cacagggtac 180

gcactgaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagccagt 300

aattacggag gacactttga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1047
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.11_CD70_DB02_A05_VH_DNA

<400> 1047
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cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtggcag cacaatatac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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ggagcgtggg cagctggttt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1048
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06_VH_DNA

<400> 1048
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tcctgcaagg catctggata caccttcacc gggtactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccaa atagtggtga tacagggtac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagatccgtc 300

aacgactacg gtgattacga cggttactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1049
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07_VH_DNA

<400> 1049
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tcctgcaagg catctggata caccttcacc ggatactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtggtgggag cacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagattac 300

ggtgattatg acgcctcgtt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1050
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.14_CD70_DB02_A08_VH_DNA

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tcctgcaagg catctggata caccttcacc agctacgata tcaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccct ccgatggtag cacaatctac 180

gcacagaact tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgt gaaggaagag 300

gcctggtact tcgatctctg gggccgtggc accctggtca ctgtctcctc a 351

<210> 1051
<211> 351
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.15_CD70_DB02_A09_VH_DNA

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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atgaaccctg ataacggtga tacagggtac 180

gcacagatgt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc ttcaggggat 300

tactatgaca tcttgtactg gggccaaggg accctggtca ccgtctcctc a 351

<210> 1052
<211> 354
<212> DNA

<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11_VH_DNA

<400> 1052
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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atgaacccca acagtggtga tacaggatac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagggccc 300

agcgggtacg aatttgacta ctggggccaa gggaccctgg tcaccgtctc ctca 354

<210> 1053
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.17_CD70_DB02_B06_VH_DNA

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tcctgcaagg catctggata caccttcacc gattactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta atagtggtgg aacaaattac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagatttt 300

agtgtgtatg ctgctgcaga tggcatggat gtctggggcc aagggacatt ggtcaccgtc 360

tcttca 366

<210> 1054
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.18_CD70_DB02_B09_VH_DNA

<400> 1054
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tcctgcaagg catctggata caccttcacc gggtactata tgcactgggt gcgacaggcc 120

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gcacagaatt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagaggattc 300

ggcgagtcag cccccgatgc ttttgatatc tggggccaag ggacaatggt caccgtctct 360

tca 363

<210> 1055
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03_VH_DNA

<400> 1055
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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tgccgggaca 300

gagatctact acatggacgt ctggggcaaa gggaccacgg tcaccgtctc ctca 354

<210> 1056
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.20_CD70_DB02_C04_VH_DNA

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tcttgtaaag ccagtggcgg cacatttagc tcttatgcga tatcatgggt tcgccaagca 120

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagagagg 300

gagctactac atttcgccac aaattattac tactatggta tggacgtgtg gggccaaggg 360

accaccgtca ccgtctcctc a 381

<210> 1057
<211> 369
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.22_CD70_DB02_C07_VH_DNA

<400> 1057
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tcctgcaagg catctggata caccttcacc cggaactata tgcactgggt gcgacaggcc 120

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ggctcatcca gctggtatca gtggtacttc gatctctggg gccgtggcac cctggtcact 360

gtctcctca 369

<210> 1058
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.24_CD70_DB02_D02_VH_DNA

<400> 1058
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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagggtcc 300

aactggtacg actactttga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1059
<211> 357
<212> DNA

<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04_VH_DNA

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tatggtgact acgtcttggt gaattggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1060
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.26_CD70_DB02_D10_VH_DNA

<400> 1060
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ggtcaatggt tgggagagat tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1061
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11_VH_DNA

<400> 1061
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agaggacctt acagtagtag ctggtattac tttgactact ggggccaagg gaccctggtc 360

accgtctcct ca 372

<210> 1062
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.28_CD70_DB02_E04_VH_DNA

<400> 1062
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gtaggagcta tgggcgtgtt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1063
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06_VH_DNA

<400> 1063
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cctggacaag ggcttgagtg gatgggatgg atcagtgcgt acaatggtaa aacaaattac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagacaca 300

atctactatg acttttggag tgggtacgac tactggggcc aagggaccct ggtcaccgtc 360

tcctca 366

<210> 1064
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08_VH_DNA

<400> 1064
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ggtgactact atggaagcgg ggattttgac tactggggcc aagggaccct ggtcaccgtc 360

tcctca 366

<210> 1065
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07_VH_DNA

<400> 1065
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tttgatcacg cattcgatat ctggggccaa gggacaatgg tcaccgtctc ttca 354

<210> 1066
<211> 372
<212> DNA
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<220>
<223> NK77.33_CD70_DB02_H04_VH_DNA

<400> 1066
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tcgtcttcat ggtacgacta ttactactac atggacgtct ggggcaaagg gaccacggtc 360

accgtctcct ca 372

<210> 1067
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.34_CD70_DB02_H05_VH_DNA

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaaatg 300

gagtggctcg gccaggtgga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1068
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08_VH_DNA

<400> 1068
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tcctgcaagg catctggata caccttcacc agctactata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggacga atcaacccta atggtggagg gacaaactac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagaggccac 300

agagggggtg gcgggattga ctactggggc caagggaccc tggtcaccgt ctcctca 357

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagactgg 300

gggtcaggct ggtacgtgga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1070
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<212> DNA
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<223> NK77.37_CD70_DB03_A07_VH_DNA

<400> 1070
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cctggacaag ggcttgagtg gatgggaggt atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatacc 300

tacggggatg acgcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 1071

<211> 372
<212> DNA
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<220>
<223> NK77.38_CD70_DB03_A08_VH_DNA

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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tccccgtata gctcaagctg gtgggactac tttgactact ggggccaagg gaccctggtc 360

accgtctcct ca 372

<210> 1072
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.39_CD70_DB03_A09_VH_DNA

<400> 1072
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gcacagaatt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagaaacaca 300

gactgttatg gggacttcct ggggctggat gtctggggcc aagggacaac ggtcaccgtc 360

tcttca 366

<210> 1073
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11_VH_DNA

<400> 1073
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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gaaggacaca 300

ggactccgct actttgactg gctacttgac tactggggcc aagggaccct ggtcaccgtc 360

tcctca 366

<210> 1074
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12_VH_DNA

<400> 1074
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cctggacaag ggcttgagtg gatgggaata atcgatccta gtggtggccg aacaatttac 180

gcacagcgct tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagacacgaa 300

gcaggcggaa tctttgacta ctggggccaa gggaccctgg tcaccgtctc ctca 354

<210> 1075
<211> 363
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01_VH_DNA

<400> 1075
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tcctgcaagg cttctggata taccttcagc gactcctaca tgcattgggt gcgacaggcc 120

cctggacaag ggcttgagtg ggtcggaggg atcatcccta tggcaggtat acccgcctac 180

gcagaggaat tccagggcag agtcacgatt accgcggacg agtccacgag cacagcctac 240

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gattatgggg gaaattggta cttcgatctc tggggccgtg gcaccctggt cactgtctcc 360

tca 363

<210> 1076
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.43_CD70_DB03_B04_VH_DNA

<400> 1076
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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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ggatggtatg agtcctggtt cgacccctgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 1077
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<212> DNA
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<220>
<223> NK77.44_CD70_DB03_B06_VH_DNA

<400> 1077
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gtgggtgcta cagaagattg gtacttcgat ctctggggcc gtggcaccct ggtcactgtc 360

tcctca 366

<210> 1078
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09_VH_DNA

<400> 1078
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ggcggctacg tcctgtttga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1079
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.46_CD70_DB03_C05_VH_DNA

<400> 1079
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cctggacaag ggcttgagtg gatgggaatg atcaacccta gaggaggtag cacaacttac 180

gcacagtcat tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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ggtgactatg gggactacga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1080
<211> 372
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.47_CD70_DB03_D11_VH_DNA

<400> 1080

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ccagggaagg ggctggagtg ggtctcagct attagtggtg gaggtgacac actctactac 180

gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240

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gctttggaca gtagcggtga caatgaggct tttgatatct ggggccaagg gacaacagtc 360

accgtctctt ca 372

<210> 1081
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01_VH_DNA

<400> 1081
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cctggacaag ggcttgagtg gatgggatgg atcaacccaa ataacggtgg tacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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gacgatttct ggagcggccc tagctttgac tactggggcc aagggaccct ggtcaccgtc 360

tcctca 366

<210> 1082
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.49_CD70_DB03_E03_VH_DNA

<400> 1082
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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagggtcc 300

ggactggacg atgcttttga tatctggggc caagggacaa tggtcaccgt ctcttca 357

<210> 1083
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09_VH_DNA

<400> 1083
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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagagggc 300

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caagggacca ctgtcaccgt ctcctca 387

<210> 1084
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.51_CD70_DB03_F02_VH_DNA

<400> 1084
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ggactctggt tcaccggttt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1085

<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.52_CD70_DB03_F05_VH_DNA

<400> 1085
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atttccggat cagatgcttt tgatatctgg ggccaaggga cattagtcac cgtctcttca 360

<210> 1086
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.53_CD70_DB03_F06_VH_DNA

<400> 1086
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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gtggggagtc 300

gatccgtact actttgacta ctggggccaa gggaccctgg tcaccgtctc ctca 354

<210> 1087
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.54_CD70_DB03_F09_VH_DNA

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ggtgagacca cgttcgaccc ctggggccag ggaaccctgg tcaccgtctc ctca 354

<210> 1088
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.55_CD70_DB03_F12_VH_DNA

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gtacggggtt gggactacta ctacggcatg ggggtctggg gccaagggac cactgtcacc 360

gtctcctca 369

<210> 1089
<211> 360
<212> DNA
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<220>
<223> NK77.56_CD70_DB03_G06_VH_DNA

<400> 1089
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tccggatacg atctgacggc tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1090
<211> 387
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.57_CD70_DB03_G11_VH_DNA

<400> 1090
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gttttcgagg ttgaaggggg tactgattat tattattact acggtatgga tgtctggggc 360

caagggacaa tggtcaccgt ctcttca 387

<210> 1091
<211> 357
<212> DNA
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<220>
<223> NK77.58_CD70_DB03_H08_VH_DNA

<400> 1091
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<220>
<223> NK77.59_CD70_DB03_H10_VH_DNA

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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ggctcctact ttggttggtt cgacccctgg ggccagggaa ccctggtcac cgtctcctca 360

<210> 1093
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<212> DNA
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<220>
<223> NK77.60_CD70_DB04_A05_VH_DNA

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atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagacagc 300

gggaactatc aagggatctt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1094
<211> 357
<212> DNA
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<220>
<223> NK77.61_CD70_DB04_A07_VH_DNA

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agcggttacg atctatttga ctactggggc caagggaccc tggtcaccgt ctcctca 357

<210> 1095
<211> 342
<212> DNA
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<220>
<223> NK77.62_CD70_DB04_A10_VH_DNA

<400> 1095
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gttgactccg tgaagggccg attcaccatc tccagagacg attccaagaa cacgctgtat 240

ctgcaaatga acagcctgaa aacggaggac acggctgtgt attactgtgc ggctagtgga 300

gtggatgtct ggggccaagg gacaaccgtc accgtctctt ca 342

<210> 1096
<211> 366
<212> DNA
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<223> NK77.63_CD70_DB04_A11_VH_DNA

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gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

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<210> 1097

<211> 357
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gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatcat 300

agcggcgatg ggtacttcga tctctggggc cgtggcaccc tggtcactgt ctcctca 357

<210> 1098
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<223> NK77.65_CD70_DB04_B05_VH_DNA

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gcacagaagt ttcagggcag ggtcaccatg accagggaca cgtccactag cacagtgtac 240

atggagctga gctctctgag atctgaagac acggccgtgt attactgtgc ggggagctgg 300

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<210> 1099
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<213> Artificial Sequence

<220>
<223> NK77.66_CD70_DB04_B07_VH_DNA

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tcctgcaagg catctggata caccttcacc aactactata tctactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atcaacccca atgacggtgc aacaaattac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagaaggc 300

aacgattact attattattt catggactac tggggccaag ggaccctggt caccgtctcc 360

tca 363

<210> 1100
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<212> DNA
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<220>
<223> NK77.67_CD70_DB04_C01_VH_DNA

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tcctgcaagg cttctggagg caccttcagc agctatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagga atcacaccaa tgtttggtac aacggactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatgag 300

cgggacggat acgccacagt ggcttttgat atctggggcc aagggacaat ggtcaccgtc 360

tcttca 366

<210> 1101
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.68_CD70_DB04_C04_VH_DNA

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tcctgcaagg catctggata caccttcacc agctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaata atcaacccta gtgacggagg aacaagctac 180

gcagacaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagcgctt 300

gccccctgg gatggggtga cggcatggat gtctggggcc aagggacaac agtcaccgtc 360

tcttca 366

<210> 1102
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.69_CD70_DB04_C06_VH_DNA

<400> 1102
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tcctgcaagg cttctggata caccttcact agctattaca tccactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atgaatccct cctcaggtgt tacgaacttc 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagaggttcg 300

gaccagggtg actggtctga cccctggggc cagggaaccc tggtcaccgt ctcctca 357

<210> 1103
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.70_CD70_DB04_C07_VH_DNA

<400> 1103
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tcctgcaagg catctggata caccttcacc gactcctata tacactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gattggatgg atgaacccta atacaggtga cacaggctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc taaggacgac 300

tttggagagc ttgctccagc caccttcgac ccctggggcc agggaaccct ggtcaccgtc 360

tcctca 366

<210> 1104

<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.71_CD70_DB04_D02_VH_DNA

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tcctgcaagg catctggata caccttcacc agctacgaca tcaattgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagtc atcagcccta gtggtggtgg aacaagctac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagatactac 300

ggcggcaacc ccgaagggtg gtacttcgat ctctggggcc gtggcaccct ggtcactgtc 360

tcctca 366

<210> 1105
<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.72_CD70_DB04_D05_VH_DNA

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tcctgtgcag cctctggatt cgttttcgat gactatgcta tccactgggt ccgccaggct 120

ccgggcaagg ggctagagtg ggtggcagcg atatcatatg atggaagtaa taaatactac 180

gcagactccg tgaagggccg attcaccatc tccagagaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgag agctgaggac acggctgtgt attactgtgc gagagctcca 300

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gtgtggggcc aagggaccac ggtcaccgtc tcctca 396

<210> 1106
<211> 366
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.73_CD70_DB04_D07_VH_DNA

<400> 1106
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tcctgcaagg cttctggagg caccttccgc aattatgcta tcagctgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaggt atcatcccta tctttggtac agcaaactac 180

gcacagaagt tccagggcag agtcacgatt accgcggacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagatcac 300

agtgctggga ctcaccacga cgcttttgat atctggggcc aagggacaat ggtcaccgtc 360

tcttca 366

<210> 1107
<211> 351
<212> DNA
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<220>
<223> NK77.74_CD70_DB04_D08_VH_DNA

<400> 1107
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tcctgcaagg cttctggata caccttcacc agttattata tccactgggt gcgacaggcc 120

ccgggacaag ggcttgagtg gatgggatgg atgaacccaa acagtggtaa cgccggctat 180

gcacagaagt tccagggcag agtcaccatg accagggata cctccacaag cacagtgtac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc gagagagtac 300

tgggggagct ttgactactg gggccaaggg accctggtca ccgtctcctc a 351

<210> 1108
<211> 354
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.75_CD70_DB04_D10_VH_DNA

<400> 1108
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tcctgcaagg catctggata caccttcacc ggctactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggaatg atcgatccaa gcgacggtag cacaatttac 180

gcacagaagt tccagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagagcgg 300

ccactgtacg cttccgacct gtggggccaa gggaccctgg tcaccgtctc ctca 354

<210> 1109
<211> 357
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.85_CD70_DB03_B02_VH_DNA

<400> 1109
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tcctgcaagg catctggata caccttcacc aactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggatgg atgaaccccg atagtggtaa tacagggtac 180

gcacagaagt tccagggcag agtcaccatc accgctgacg aatccacgag cacagcctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagaagtagc 300

agctcctggc ctgacttcga tctctggggc cgtggcaccc tggtcactgt ctcctca 357

<210> 1110
<211> 360
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.86_CD70_DB04_A06_VH_DNA

<400> 1110
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tcatgtaaag ctagcgggta tacatttaca tcctattcca tgcattgggt acgccaagct 120

ccaggccagg gcctggaatg ggtcggtatc attaatccca gttccggctc tgccagttat 180

gcgcaaaaat ttcaaggaag ggtgacaatg actcgagata ccagtacctc cactgtgtat 240

atggaactgt cctcactaag gagcgaagat actgctgtat actactgcgc acgcgaacgt 300

ggggcctata gtagtacctt cgactattgg ggtcagggca cgttagtgac agtgtcttcc 360

<210> 1111
<211> 360
<212> DNA

<213> Artificial Sequence

<220>
<223> NK77.87_CD70_DB04_A09_VH_DNA

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tcctgcaagg catctggata caccttcacc gactactata tgcactgggt gcgacaggcc 120

cctggacaag ggcttgagtg gatgggagtc atcaacccct ctgatggtac agctcattac 180

gcacagcggc tgcagggcag agtcaccatg accagggaca cgtccacgag cacagtctac 240

atggagctga gcagcctgag atctgaggac acggccgtgt attactgtgc tagagacagc 300

ggatcttact acgctgactt tgactactgg ggccaaggga ccctggtcac cgtctcctca 360

<210> 1112
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.1_CD70_DB01_C03_VL_DNA

<400> 1112
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atcacttgcc gggcaagtca gaatattggc acatatttag cttggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgac gcatccaact tggagactgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagaa tccctctcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1113
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.2_CD70_DB01_D02_VL_DNA

<400> 1113
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atcacttgcc gggcgagtca gaggattagc aattggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccaact tggaaaccgg ggtcccatcc 180

aggttcagtg gcagtggatc tgggacggat tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag acctatagtc ctccccctac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 1114
<211> 336
<212> DNA
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<220>
<223> NK77.3_CD70_DB01_E06_VL_DNA

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atctcctgca ggtctagtca gagcctcctg cactctaacg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atgcagcctc ttcattacaa 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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atcaccttcg gccaagggac acgactggag attaaa 336

<210> 1115
<211> 321
<212> DNA
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<220>
<223> NK77.4_CD70_DB01_G04_VL_DNA

<400> 1115
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atcacttgcc gggcaagtca ggacattgac acctatttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacacaa ccccttttcac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1116

<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.5_CD70_DB01_G05_VL_DNA

<400> 1116
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atcacttgcc aggcaagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccagtt tggaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttaccgat cacctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1117
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.6_CD70_DB01_G07_VL_DNA

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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttga ccatcagcag cctgcagcct 240

gaagattttg caacatatta ctgtcaacag gcttataggt ggcctatcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1118
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.7_CD70_DB01_G11_VL_DNA

<400> 1118
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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatcctact tggaaacagg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacacaa ttcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1119
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.9_CD70_DB02_A03_VL_DNA

<400> 1119
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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacatatta ctgtcaacag agctattcca cccctctcac tttcggccag 300

gggaccaagg tggagatcaa a 321

<210> 1120
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.10_CD70_DB02_A04_VL_DNA

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atctcctgca ggtctagtca gagcctcctg cattccaacg gatacaacta tttggattgg 120

tacctgcaga agccagggca gtctccacag ctcctgatct atcaggcatc tagcctggag 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

agcagagtgg aggctgagga tgttggggtt tattactgca tgcaaggaac gcactggcct 300

ccaactttcg gcggagggac caaggtggag atcaaa 336

<210> 1121
<211> 318
<212> DNA
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<220>
<223> NK77.11_CD70_DB02_A05_VL_DNA

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atcacttgcc aagcaagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct acctccacct tggctaacgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cgcttacctt cggccaaggg 300

acacgactgg agattaaa 318

<210> 1122
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.12_CD70_DB02_A06_VL_DNA

<400> 1122
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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactctga ccatcagcag cctgcagcct 240

gaagattttg caacatatta ctgtcaacag tcttacagta cgcctcctac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1123
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.13_CD70_DB02_A07_VL_DNA

<400> 1123

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atcacttgcc gggcaagtca gagcattgac aattggttag cgtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccacat tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacgata gtcctcccac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 1124
<211> 321
<212> DNA
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<220>
<223> NK77.14_CD70_DB02_A08_VL_DNA

<400> 1124
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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactttga ccatcagcag cctgcagcct 240

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gggaccaagg tggagatcaa a 321

<210> 1125
<211> 321
<212> DNA
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<220>
<223> NK77.15_CD70_DB02_A09_VL_DNA

<400> 1125
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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gtgtccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactctca ccatcagcag cctgcagcct 240

gaagattttg caacatatta ctgtcaacag gctaattcct tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1126
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.16_CD70_DB02_A11_VL_DNA

<400> 1126
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atcacttgcc gggcaagtca gaccattagc aattatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgac gcatccagtt tggaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggagatcaa a 321

<210> 1127
<211> 321
<212> DNA
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<220>
<223> NK77.17_CD70_DB02_B06_VL_DNA

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gggaaagccc ctaagctcct gatctatgac gcatccaatt tggccaccgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggagatcaa a 321

<210> 1128
<211> 321
<212> DNA
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<220>
<223> NK77.18_CD70_DB02_B09_VL_DNA

<400> 1128
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atcacttgcc aggcaagtca ggacattagc aattatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatggt gcaacgacat tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagc tggagatcaa a 321

<210> 1129
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.19_CD70_DB02_C03_VL_DNA

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aggttcagtg gaagtggatc tgggacagat tttactttga ccatcagcag cctgcagcct 240

gaagattttg caacatatta ctgtcaacag gcagattcct tccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcacagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ctatcagcag cctgcagcct 240

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gggaccaagg tggagatcaa a 321

<210> 1131
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<212> DNA
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<220>
<223> NK77.22_CD70_DB02_C07_VL_DNA

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atcacttgcc gggcaagtca gagcattgga acctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacacca cccctattac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1132
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.24_CD70_DB02_D02_VL_DNA

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ctctcctgca gggccagtca gagtgttagc agctacttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

gaagattttg cagtttatta ctgtcagcag tatgatagct atcctccaac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1133
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.25_CD70_DB02_D04_VL_DNA

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atcacttgcc aggcaagtca ggacattagc aattatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccacct tggaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcttcag gattacgact accctctgac ttttggccag 300

gggaccaagc tggagatcaa a 321

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<220>
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atcacttgtc gggcgagtca gacaatttat aagtggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgac gcatccagtt tggaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ctatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag gctaacagtt tccctttcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 1135
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.27_CD70_DB02_D11_VL_DNA

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atcacttgcc aggcgagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctacgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagtg gaagtggatc tgggacagat tttactctga ccatcagcag cctgcagcct 240

gaagatttcg caacatatta ctgtcaacag gcccactcgt ttcctcccac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1136
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.28_CD70_DB02_E04_VL_DNA

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atcacttgcc gggcaagtac cagcattagc gattatgtgc attggtatca gcagaaacca 120

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gaagattttg caacttacta ctgtcaacag agtgatagta cccctcccac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1137
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.29_CD70_DB02_F06_VL_DNA

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atcacttgcc gggcaagtca gggaattagc aataatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattac gcatccacct tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctatcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1138
<211> 321
<212> DNA

<213> Artificial Sequence

<220>
<223> NK77.31_CD70_DB02_F08_VL_DNA

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atcacttgcc gggcaagtca gacgattagc aattatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccacgt tggaagccgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagc tggagatcaa a 321

<210> 1139
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.32_CD70_DB02_G07_VL_DNA

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atcacttgcc gggcaagtca gagcattagc acttatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccaact tggagatcgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agtgacagtt caccactcac tttcggccag 300

gggaccaagg tggagatcaa a 321

<210> 1140
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.33_CD70_DB02_H04_VL_DNA

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atcacttgcc aagcaagtca ggatattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggagatcaa a 321

<210> 1141
<211> 321
<212> DNA
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<220>
<223> NK77.34_CD70_DB02_H05_VL_DNA

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atcacttgcc gggcaagtca ggatattcgc aacgatttag ggtggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgct gcatccaact tggagaccgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagtg cacctttcac tttcggccct 300

gggaccaaag tggatatcaa a 321

<210> 1142
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.35_CD70_DB02_H08_VL_DNA

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atcacttgcc gggcaagtca ggagattagc aactatttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccaact tgcaaactgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaaag tggatatcaa a 321

<210> 1143

<211> 321
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<220>
<223> NK77.36_CD70_DB03_A06_VL_DNA

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atcacttgcc aggcaagtca ggacattagc gattctttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattcc gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggaaatcaa a 321

<210> 1144
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.37_CD70_DB03_A07_VL_DNA

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atcacttgtc gggcgagtca gtctattagc agctggttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgat gcatccaatt tggaaacagg ggtcccatca 180

aggttcagcg gcagtggatc tgggacagat ttcactctca ctatcagcag cctgcagcct 240

gaagattttg caacttacta ttgtcaacag aatttcagtc ctcctctcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1145
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.38_CD70_DB03_A08_VL_DNA

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atcacttgcc gggcaagtca ggacattcgg cattatttag catggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgac gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggacacgac tggagattaa a 321

<210> 1146
<211> 321
<212> DNA
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<220>
<223> NK77.39_CD70_DB03_A09_VL_DNA

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atcaactgcc gggccagctc tagtatttcc aactacttag cttggtacca gcagaaacca 120

ggacagcctc ctaagctgct catttacggc gcatctaccc gggcttccgg ggtccctgac 180

cgattcagtg gcagcgggtc tgggacagat ttcactctca ccatcagcag cctgcaggct 240

gaagatgtgg cagtttatta ctgtcagcaa agctatagta ctcctctcac tttcggccag 300

gggaccaagg tggagatcaa a 321

<210> 1147
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.40_CD70_DB03_A11_VL_DNA

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atcacttgcc gggcgagtca gggcattacc aatttttag cctggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatatatgat gcatccaact tggaaaccgg ggtcccatcc 180

aggttcagtg gcagtggatc tgggacggat ttcactctca ccatcagcag cctgcagcct 240

gaagattttg caacttatta ctgtcaacag agctatgggg cccctcttac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1148
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.41_CD70_DB03_A12_VL_DNA

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atcacttgcc aagcaagtca ggacattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctattcc gcatccacct tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagtt ctccttatag attcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1149
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<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.42_CD70_DB03_B01_VL_DNA

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atctcctgca ggtctagtca gagcctcctc cactctaatg gctacaacta tttggattgg 120

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tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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ccgacttttg gccaggggac caagctggag atcaaa 336

<210> 1150
<211> 321
<212> DNA
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<220>
<223> NK77.43_CD70_DB03_B04_VL_DNA

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atcacttgcc gggcaagtca ggacattagg gatgggttag gctggtatca gcagaaacca 120

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gaagattttg caacttacta ctgtcaacag agttacggga cccctcctac gttcggccaa 300

gggaccaagg tggaaatcaa a 321

<210> 1151
<211> 318
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.44_CD70_DB03_B06_VL_DNA

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ctctcctgca gggccagtca gagtgttagc agctatttag cctggtacca gcagaaacct 120

ggccaggctc ccaggctcct catctatggt gcatccacca gggccactgg tatcccagcc 180

aggttcagtg gcagtgggtc tgggacagag ttcactctca ccatcagcag cctgcagtct 240

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accaaggtgg aaatcaaa 318

<210> 1152
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.45_CD70_DB03_B09_VL_DNA

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atcacttgcc gggcaagtca gagcattagc agctatttaa attggtatca gcagaaacca 120

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gaagattttg caacttacta ctgtcaacag agtcacagtg cgcctatcac cttcggccaa 300

gggacacgac tggagattaa a 321

<210> 1153
<211> 321
<212> DNA
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<220>
<223> NK77.46_CD70_DB03_C05_VL_DNA

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gggaccaagc tggagatcaa a 321

<210> 1154
<211> 339
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<220>
<223> NK77.47_CD70_DB03_D11_VL_DNA

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gattccgggg tccctgaccg attcagtggc agcgggtctg ggacagattt cactctcacc 240

atcagcagcc tgcaggctga agatgtggca gtttattact gtcagcaata ttatggcttc 300

cctcccacct tcggccaagg gacacgactg gagattaaa 339

<210> 1155
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.48_CD70_DB03_E01_VL_DNA

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gggaaagccc ctaagctcct gatctatgat gcatccaatt tgcaacgagg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag acctacagtt tccctttcac ttttggccag 300

gggaccaagc tggagatcaa a 321

<210> 1156
<211> 336
<212> DNA
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<220>
<223> NK77.49_CD70_DB03_E03_VL_DNA

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ctgaccttcg gccaagggac acgactggag attaaa 336

<210> 1157
<211> 336
<212> DNA
<213> Artificial Sequence

<220>
<223> NK77.50_CD70_DB03_E09_VL_DNA

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tacctgcaga agccagggca gtctccacag ctcctgatct atgctgcttc taatttacag 180

ggtggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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gtaactttcg gcggagggac caaggtggag atcaaa 336

<210> 1158
<211> 321
<212> DNA
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<220>
<223> NK77.51_CD70_DB03_F02_VL_DNA

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gggaaagccc ctaagctcct gatctatgat gcatccaact tggaacgtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggacacgac tggagattaa a 321

<210> 1159
<211> 321
<212> DNA
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<223> NK77.52_CD70_DB03_F05_VL_DNA

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gaagattttg caacttacta ctgtttgcag gactacagtt atcctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1160
<211> 321
<212> DNA
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<220>
<223> NK77.53_CD70_DB03_F06_VL_DNA

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gaagattttg caacttacta ctgtcaacag agttacatta cccctctcac tttcggcgga 300

gggaccaagg tggagatcaa a 321

<210> 1161
<211> 321
<212> DNA
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<223> NK77.54_CD70_DB03_F09_VL_DNA

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atcacttgcc aggcaagtca ggatattagc aactatttaa attggtatca gcagaaacca 120

gggaaagccc ctaagctcct gatctatgac gcatccagtt tggaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaaagccc ctaagctcct gatctatgct gcatccacgt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagtg cccctagcac ttttggccag 300

gggaccaagc tggagatcaa a 321

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gggaaagccc ctaagctcct gatctatgac gcatccaact tggagaccgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agttacagta cccctatcac cttcggccaa 300

gggacacgac tggagattaa a 321

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gggaaagccc ctaagctcct gatctatgac gcatccaact tggagactgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagc tggaaatcaa a 321

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<213> Artificial Sequence

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gggaaagccc ctaagctcct gatctatgct gcatccacat tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaaag tggatatcaa a 321

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<213> Artificial Sequence

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagc tggagatcaa a 321

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<212> DNA
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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggagatcaa a 321

<210> 1169
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<212> DNA
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<220>
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tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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<212> DNA
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<223> NK77.63_CD70_DB04_A11_VL_DNA

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gggaccaagg tggaaatcaa a 321

<210> 1171
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tacctgcaga agccagggca gtctccacag ctcctgatct atgatgcctc ttcacttcag 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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acaggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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aggttcagtg gaagtggatc tgggacagat tttactctca ccatcagcag cctgcagcct 240

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<223> NK77.69_CD70_DB04_C06_VL_DNA

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gggaaagccc ctaagctcct gatctatgac gcatccaact tggaaacggg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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<223> NK77.70_CD70_DB04_C07_VL_DNA

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gggaaagccc ctaagctcct gatctatggt gcatccagtt tgcaaagtgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggacacgac tggagattaa a 321

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<212> DNA
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<220>
<223> NK77.71_CD70_DB04_D02_VL_DNA

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gggaaagccc ctaagctcct gatctatgac gcatccgatt tggaaaccgg ggtcccatca 180

aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggaaatcaa a 321

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<212> DNA
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<220>
<223> NK77.72_CD70_DB04_D05_VL_DNA

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tacctgcaga agccagggca gtctccacag ctcctgatct atgaagtctc taatcgggcc 180

tccggggtcc ctgacaggtt cagtggcagt ggatcaggca cagattttac actgaaaatc 240

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg caacttacta ctgtcaacag agtcacagta cccctctcac tttcggccaa 300

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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<223> NK77.75_CD70_DB04_D10_VL_DNA

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gggaaagccc ctaagctcct gatctatgct gcatccagtt tacaaagtgg ggtcccatca 180

aggttcagcg gcagtggatc tggcacagat ttcactctca ccatcagcag cctgcagcct 240

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gaagattttg caacttacta ctgtcttcag gactacagtt accctctcac tttcggccaa 300

gggaccaagg tggagatcaa a 321

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aggttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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gggaccaagg tggaaatcaa a 321

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<220>
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<400> 1186

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20 25 30

Arg Met Gly Val Thr Trp Ile Arg Gln Pro Pro Gly Lys Ala Leu Glu
35 40 45

Trp Leu Ala His Ile Phe Ser Asn Asp Glu Lys Ser Tyr Ser Thr Ser
50 55 60

Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser Lys Thr Gln Val

65 70 75 80

Val Leu Thr Met Thr Asn Met Asp Pro Val Asp Thr Ala Thr Tyr Tyr
85 90 95

Cys Ala Arg Ile Arg Asp Tyr Tyr Asp Ile Ser Ser Tyr Tyr Asp Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Ser Val Ser Ser Gly Gly Gly Gly Ser
115 120 125

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln
130 135 140

Ser Pro Ser Ala Met Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr
145 150 155 160

Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr Leu Ala Trp Phe Gln Gln
165 170 175

Lys Pro Gly Lys Val Pro Lys Arg Leu Ile Tyr Ala Ala Ser Ser Leu
180 185 190

Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu
195 200 205

Phe Thr Leu Thr Ile Ser Ser Leu Leu Pro Glu Asp Phe Ala Thr Tyr
210 215 220

Tyr Cys Leu Gln Leu Asn Ser Phe Pro Phe Thr Phe Gly Gly Gly Thr
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Lys Val Glu Ile Asn
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<212> PRT
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<223> NK72 scFv peptide sequence

<400> 1187

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Trp Ile Gly Trp Val Arg Gln Met Pro Gly Lys Gly Leu Glu Trp Met
        35                  40                  45

Gly Ile Ile His Pro Asp Asp Ser Asp Thr Lys Tyr Ser Pro Ser Phe
    50                  55                  60

Gln Gly Gln Val Thr Ile Ser Ala Asp Lys Ser Ile Ser Thr Ala Tyr
65                  70                  75                  80

Leu Gln Trp Ser Ser Leu Lys Ala Ser Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

Ala Ser Ser Tyr Leu Arg Gly Leu Trp Gly Gly Tyr Phe Asp Tyr Trp
            100                 105                 110

Gly Gln Gly Thr Leu Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly
        115                 120                 125

Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Ser Val Leu Thr
    130                 135                 140

Gln Pro Pro Ser Ala Ser Gly Thr Pro Gly Gln Arg Val Thr Ile Ser
145                 150                 155                 160

Cys Ser Gly Ser Ser Ser Asn Ile Gly Ser Asn Tyr Val Asn Trp Tyr
                165                 170                 175

Gln Gln Leu Pro Gly Thr Ala Pro Lys Leu Leu Ile Tyr Gly Asp Tyr
            180                 185                 190

Gln Arg Pro Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Lys Ser Gly
        195                 200                 205
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Thr Ser Ala Ser Leu Ala Ile Ser Gly Leu Arg Ser Glu Asp Glu Ala
210 215 220

Asp Tyr Tyr Cys Ala Thr Arg Asp Asp Ser Leu Ser Gly Ser Val Val
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Phe Gly Thr Gly Thr Lys Leu Thr Val Leu
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catattgacg ctacactgta tactgagagt gatgtacacc cgtcctgtaa ggtaacggcc 180

atgaaatgct ttcttctgga gctccaggtc atcagcttgg agtctgggga cgcaagcatc 240

cacgatacgg ttgaaaacct catcatcctt gcgaacaact ctctctcatc taatggaaac 300

gttacagaga gtgggtgtaa ggagtgcgaa gagttggaag aaaaaaacat caaagaattt 360

cttcaatcct tcgttcacat agtgcaaatg ttcattaaca cgtccactac cacacccgcc 420

ccgaggccac ctacgccggc accgactatc gccagtcaac ccctctctct gcgccccgag 480

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<210> 1189
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<220>
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<400> 1189

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            20                  25                  30

Ile Glu Asp Leu Ile Gln Ser Met His Ile Asp Ala Thr Leu Tyr Thr
        35                  40                  45

Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met Lys Cys Phe
    50                  55                  60

Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile
65                  70                  75                  80

His Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser
                85                  90                  95

Ser Asn Gly Asn Val Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu
            100                 105                 110

Glu Glu Lys Asn Ile Lys Glu Phe Leu Gln Ser Phe Val His Ile Val
        115                 120                 125

Gln Met Phe Ile Asn Thr Ser Thr Thr Thr Pro Ala Pro Arg Pro Pro
    130                 135                 140

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
145                 150                 155                 160

Ala Cys Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
                165                 170                 175

Phe Ala Cys Asp Ile Tyr Ile Trp Ala Pro Leu Ala Gly Thr Cys Gly
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Val Leu Leu Leu Ser Leu Val Ile Thr Leu Tyr Cys
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<211> 20
<212> DNA
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<220>
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<210> 1191
<211> 20
<212> DNA
<213> Artificial Sequence

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