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(54) Title: HUMANIZED ANTIBODIES AGAINST NECTIN-2 AND DRUG CONJUGATES THEREOF

(57) Abstract: The present disclosure provides humanized monoclonal antibodies that recognize human Nectin-2 with high affinity and specificity and inhibit its binding to CD 112R. These antibodies carry cytotoxic payload and do not interact with Fc gamma receptors. The present disclosure further provides pharmaceutical compositions comprising the antibodies and methods for their use in cancer immunotherapy.

HUMANIZED ANTIBODIES AGAINST NECTIN-2 AND DRUG CONJUGATES THEREOF

FIELD OF THE INVENTION

The invention is in the field of immunotherapy and relates to anti-Nectin-2 antibodies and antibody-conjugates and to therapeutic and diagnostic compositions comprising them, for treating diseases, particularly cancer.

BACKGROUND OF THE INVENTION

Cancer immunotherapy is utilized for generating and augmenting an anti-tumor immune response, e.g., by treatment with antibodies specific to antigens on tumor cells, or by specific activation of anti-tumor T cells. The ability of recruiting immune cells (e.g., T cells) against tumor cells in a patient provides a therapeutic modality of fighting cancer types and metastasis that are otherwise considered incurable.

T cell mediated immune responses include multiple sequential steps regulated by a balance between co-stimulatory and co-inhibitory signals that control the magnitude of the immune response. The inhibitory signals, referred to as immune checkpoints, are crucial for the maintenance of self-tolerance and for the limitation of immune-mediated collateral tissue damage. These inhibitory signals affect the response of T cells and re-shape the immune response.

Nectin-2, which was also named Poliovirus Receptor-Related Protein-2, Poliovirus Receptor-Like 2, CD112, or PRR-2, is a single pass transmembrane glycoprotein with two Ig-like C2-type domains and an Ig-like V-type domain. Nectin-2 is involved in mediating cell adhesion to extracellular matrix molecules, serving as one of the plasma membrane components of adherent junctions. It also serves as an entry receptor for certain mutant strains of herpes simplex virus and pseudorabies virus, and it is involved in cell to cell spreading of these viruses. Variations in this gene have been associated with differences in the severity of multiple sclerosis. Importantly, Nectin-2 can also serve as a modulator of T-cell signaling. It can be either a co-stimulator, or a co-inhibitor of T-cell functions, depending on the receptor it binds on these target cells: upon binding to CD226 (DNAM-1), it stimulates T-cell proliferation and cytokine production, including that of IL-2, and IFNγ, while upon interaction with PVRIG

(CD112R), and/or TIGIT (T-cell immunoreceptor with immunoglobulin and ITIM domains) it inhibits T-cell proliferation and activation. These contradictory interactions are competitive.

Nectin-2 was shown to be overexpressed in various tumors, including breast and ovarian cancers (Oshima et al. Molecular Cancer, 2013, 12:60). The presence of Nectin-2 on tumor cells leads to poor prognosis and reduced activity of T cells (Stamm et al. Oncogene (2018) 37:5269–5280).

US patent application No. 2017/0037133 discloses inhibitors (e.g., antibodies) against CD112 (Nectin-2, PVRL2), CD155 (PVR), Galectin-9, TIM-3 and/or TIGIT for use in treatment of a blood-borne cancer, in particular acute myeloid leukemia (AML).

International patent application No. WO 2020/144697 discloses monoclonal antibodies (mAbs) that recognize human Nectin-2 and block the interactions with TIGIT and CD112R, for use treatment of cancer.

Antibody–drug conjugates (ADCs) are a promising tool for both direct tumor cell killing and for the consequent activation of bystander immune cells. These therapeutic entities are composed of mAbs linked to cytotoxic drugs (payloads), and are designed, in principle, to widen the therapeutic window of those drugs by limiting their delivery specifically to cells that express the target antigen, and thus to reduce their systemic exposure and toxicity.

An example of a possible payload is Auristatin, a microtubule-destroying drug. It was derived from marine shell-less mollusk Dolabella auricularia called dolastatins. Various derivatives of auristatin have been synthesized, such as monomethyl auristatin E (MMAE) and monomethyl auristatin F (MMAF). MMAE and MMAF were developed by Seattle Genetics and used as payloads for ADCs. MMAF and MMAE have their advantages and disadvantages. MMAE is more membrane-permeable and has a lower IC50 than MMAF. However, MMAF is more hydrophilic and has a lower aggregation tendency to show lower systemic toxicity than MMAE (park et al. Molecules 2019, 24, 2754).

There is an unmet need to provide humanized antibodies recognizing human Nectin-2 that are safe and potent and can be used, either alone or as a targeting tool, for diagnostically and therapeutically uses in diseases involving Nectin-2 expression, e.g., as ADCs in cancer.

SUMMARY OF THE INVENTION

The present invention provides humanized antibodies that specifically bind Nectin-2. The humanized antibodies of the present invention, selected from a larger collection of antibody clones, have improved properties compared to other anti-Nectin-2 antibodies. The present invention further provides, according to some embodiments, conjugates comprising the antibodies and diagnostic or therapeutic agents. In some embodiments, the conjugates comprise a cytotoxic moiety that is targeted by said humanized antibodies to tumor cells presenting the Nectin-2 receptor on their surface.

A large collection of humanized antibodies was produced by combining specific sets of complementarity determining regions (CDR) sequences and human framework (FW) sequences and introducing specific mutations in these sequences to produce antibodies with modified variable regions and improved properties. Advantageously, the newly designed humanized variable regions described herein preserve the residues critical for the maintenance of the antibody's conformation and binding affinity, while having lower incidence of potential T cell epitopes, thus minimizing the risk of adverse immune response towards the antibodies. The antibodies disclosed herein were designed based on factors including homology, T-cell epitopes, key residues, and predicted structures. Unexpectedly, the humanized antibodies disclosed herein show improved biostability compared with the parental chimeric antibody.

The humanized antibodies disclosed herein were found to be highly suitable for use as targeted anti-cancer therapy with therapeutic toxins. It is now disclosed that the anti-Nectin-2 monoclonal humanized antibody described herein, conjugated to a cytotoxic moiety, exhibit robust killing of various tumor cell lines. The direct targeting of toxins using the antibodies described herein has the potential to increase the anti-tumor efficacy of these toxins, reducing their systemic toxicity, and thus improving the survival of cancer patients.

Human Fc receptors (FcγRs) activate Fc-effector functions such as antibody-dependent cellular cytotoxicity (ADCC) and antibody dependent cellular phagocytosis (ADCP). Some of the ADCs of the present invention comprise one or more Fc mutations that significantly reduce their binding by FcγR that are expressed on immune cells, thereby increasing their safety and specificity. It is now disclosed that ADCs comprising anti-Nectin-2 monoclonal humanized antibody having specific Fc mutations and linked to toxins are highly effective and safe, suitable for anti-cancer therapy.

The inventors of the present invention have shown for the first time that ADCs targeted to Nectin-2 are highly useful for treating cancer, in particular solid tumors.

According to a first aspect, the present invention provides a humanized antibody that specifically binds human Nectin-2, or a fragment thereof comprising at least the antigen binding site, wherein the antibody or a fragment thereof comprises a heavy chain (HC) and a light chain (LC), wherein the heavy chain comprises a variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and wherein the light chain comprises a variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20.

According to some embodiments, the humanized antibody or a fragment thereof comprises a heavy chain and a light chain, wherein the heavy chain comprises a variable region having an amino acid sequence at least about 90% identical to SEQ ID NO: 11, and the light chain comprises a variable region having an amino acid sequence at least about 90% identical to SEQ ID NO: 12.

According to some embodiments, the humanized antibody or a fragment thereof comprises a heavy chain and a light chain, wherein the heavy-chain variable region comprises the sequence set forth in SEQ ID NO: 11, and the light-chain variable region comprises the sequence set forth in SEQ ID NO: 12.

There are several methods known in the art for determining the CDR sequences of a given antibody molecule, but there is no standard unequivocal method. Determination of CDR sequences from antibody heavy and light chain variable regions can be made according to any method known in the art, including but not limited to the methods known as KABAT, Chothia and IMGT. A selected set of CDRs may include sequences identified by more than one method, namely, some CDR sequences may be determined using KABAT and some using IMGT, for example. According to some embodiments, the CDR sequences of the mAb variable regions are determined using the IMGT method.

According to some embodiments, the humanized antibody or a fragment thereof comprises a set of six CDR sequences, wherein heavy-chain CDR1 comprising the sequence SYW, heavy-chain CDR2 comprising the sequence VYPGNSDS (SEQ ID NO: 8), heavy-

chain CDR3 comprising the sequence LVGTFDY (SEQ ID NO: 3), light-chain CDR1 comprising the sequence QNVGIN (SEQ ID NO: 10), light-chain CDR2 comprising the sequence SAS, and light-chain CDR3 comprising the sequence QQYNTNPFT (SEQ ID NO: 6).

According to some embodiments, the humanized antibody or a fragment thereof comprises a set of six CDR sequences, wherein heavy-chain CDR1 comprising the sequence SYWIH (SEQ ID NO: 1), heavy-chain CDR2 comprising the sequence AVYPGNSDSNYNQKF(KA/QG) (SEQ ID NO: 2), heavy-chain CDR3 comprising the sequence LVGTFDY (SEQ ID NO: 3), light-chain CDR1 comprising the sequence (K/R)ASQNVGINV(V/A) (SEQ ID NO: 4), light-chain CDR2 comprising the sequence SASYRYS (SEQ ID NO: 5), and light-chain CDR3 comprising the sequence QQYNTNPFT (SEQ ID NO: 6).

According to some embodiments, the heavy-chain CDR2 comprises the sequence AVYPGNSDSNYNQKFKA (SEQ ID NO: 41) or AVYPGNSDSNYNQKFQG (SEQ ID NO: 42). According to certain embodiments, the light-chain CDR1 comprises a sequence selected from the group consisting of KASQNVGINVV (SEQ ID NO: 43), KASQNVGINVA (SEQ ID NO: 44), RASQNVGINVV (SEQ ID NO: 45) and RASQNVGINVA (SEQ ID NO: 46).

According to some embodiments, the humanized antibody or a fragment thereof comprises a set of six CDR sequences set forth in SEQ ID NOs: 1, 2, 3, 4, 5, and 6. According to additional exemplary embodiments, the humanized antibody or a fragment thereof comprises a set of six CDR sequences set forth in SEQ ID NOs: 7, 8, 9, 10, (SAS), and 6. According to additional embodiments, the humanized antibody or a fragment thereof comprises a set of six CDR sequences set forth in SEQ ID NOs: 1, 41, 3, 43, 5, and 6.

According to some embodiments, the humanized antibody or antigen binding fragment thereof comprises a heavy chain variable region, comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 1-3; and
ii. a set of four heavy chain framework (FR) sequences, wherein FR-H1 is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22; FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; and FR-H4 is SEQ ID NO: 24.

According to some embodiments, the humanized antibody or antigen binding fragment thereof comprising a light chain variable region, comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 4-6; and

ii. a set of four light chain framework (FR) sequences, wherein FR-L1 is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.

According to some embodiments, the humanized antibody or antigen binding fragment thereof comprising a heavy chain variable region and a light chain variable region, the heavy chain variable region comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 1-3; and

ii. a set of four heavy chain framework sequences, wherein FR-H1 is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22; FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; FR-H4 is SEQ ID NO: 24;

and the light chain variable region comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 4-6; and

ii. a set of four light chain framework sequences, wherein FR-L1 is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.

According to some embodiments, the humanized antibody or antigen binding fragment thereof comprising a heavy chain variable region and a light chain variable region, the heavy chain variable region comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 7-9; and

ii. a set of four heavy chain framework sequences, wherein: FR-H1 is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22; FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; FR-H4 is SEQ ID NO: 24;

and the light chain variable region comprising:

i. a set of three CDR sequences comprising the sequences set forth in SEQ ID NO: 10, the sequence SAS, and SEQ ID NO: 6; and

ii. a set of four light chain framework sequences, wherein: FR-L1 is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.

According to some embodiments, the heavy chain variable region of the humanized monoclonal antibody comprises an amino acid sequence at least about 95% identical to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and the light chain variable region comprises an amino acid sequence at least about 95% identical to a sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 20. In certain embodiments, the heavy chain variable region of the humanized monoclonal antibody comprises an amino acid sequence at least about 97% identical to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and the light chain variable region comprises an amino acid sequence at least about 97% identical to a sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 20. In certain embodiments, the heavy chain variable region of the humanized monoclonal antibody comprises an amino acid sequence selected from the group consisting of

SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16, and the light chain variable region comprises an amino acid sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19, and SEQ ID NO: 20.

According to some embodiments, the humanized antibody or fragment thereof is a monoclonal antibody, Fab, $F(ab)_2$, a single-domain antibody, or a single chain variable fragment (scFv).

According to some embodiments, the humanized antibody or fragment thereof is an IgG monoclonal antibody. According to some embodiments, the humanized monoclonal antibody comprises a heavy chain constant region selected from IgG4, IgG1, and IgG2. In certain embodiments, the humanized antibody or fragment thereof is an IgG4 subclass. In certain embodiments, the humanized antibody or antigen binding fragment thereof is an IgG1 subclass.

According to some embodiments, the humanized monoclonal antibody comprises a kappa light chain constant region.

According to some embodiments, the humanized monoclonal antibody is IgG1, having a heavy chain comprising an amino acid sequence at least about 90%, 95%, or 98% identical to the sequence set forth in SEQ ID NO: 47. According to certain exemplary embodiments, the humanized monoclonal antibody is IgG1, having a heavy chain comprising the amino acid sequence set forth in SEQ ID NO: 47.

According to some embodiments, the humanized monoclonal antibody has a kappa light chain comprising an amino acid sequence at least about 90%, 95%, or 98% identical to the sequence set forth in SEQ ID NO: 49. According to certain exemplary embodiments, the humanized monoclonal antibody has a kappa light chain comprising the amino acid sequence set forth in SEQ ID NO: 49.

According to some embodiments, the humanized antibody has a mutated Fc domain that prevents FcγR-mediated internalization.

According to some embodiments, the humanized antibody comprises a Fc null domain. According to certain embodiments, the Fc domain is null for binding to Fcγ receptors found on

immune cells. According to certain exemplary embodiments, the Fc domain is null for binding to CD64, CD32a, CD32b, CD16a, and/or CD16b.

According to some embodiments, the humanized antibody comprises a IgG1 Fc domain. According to certain embodiments, the IgG1 Fc domain is null for binding to Fcγ receptors. According to additional embodiments, the IgG1 Fc domain is null for binding to one or more Fcγ receptors. According to certain exemplary embodiments, the IgG1 Fc domain is null for binding to CD64, CD32a, CD32b, CD16a, and/or CD16b.

According to some embodiments, the humanized antibody comprises a human IgG selected from the group consisting of: (i) a human IgG1 having the mutation L235S; (ii) a human IgG1 having the mutations L235S and E272K; (iii) a human IgG1 having the mutation G237I; (iv) a human IgG1 having the mutations G237I and E272I; (v) a human IgG1 having the mutations G237I and V264R; (vi) a human IgG1 having the mutations V215A, E269R and K322A; (vii) a human IgG1 having the mutations L234A, L235A and P329G; (viii) a human IgG4 having the mutations S228P, L235P and V264R; (ix) a human IgG2 having the mutation P238H; or (x) a human IgG2 having the mutations P238H and V264R. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the humanized antibody comprises a heavy chain sequence selected from the group consisting of SEQ ID NOs: 61-70. Each possibility represents a separate embodiment of the invention.

According to some embodiments, a conjugate comprising the humanized antibody or fragment thereof described above is provided.

Antibodies or fragments thereof according to the present invention are attached, according to some embodiments, to a cytotoxic moiety, a radioactive moiety, or an affinity or labeling tag.

Antibody-drug conjugates (ADCs) according to the present invention comprises the humanized antibodies as described herein, an optional linker, and a toxin.

According to some embodiments, the humanized antibody or fragment thereof is conjugated directly or through a linker, to a toxin (payload).

According to some embodiments, the toxin is selected from the group consisting of microtubule inhibitor, DNA synthesis inhibitor, topoisomerase inhibitor and RNA polymerase inhibitor.

According to certain embodiments, the toxin is a microtubule-destroying drug. According to certain exemplary embodiments, the toxin is auristatin or a derivative thereof. According to certain embodiments, the auristatin derivative is monomethyl auristatin E (MMAE) or monomethyl auristatin F (MMAF).

According to some embodiments, the toxin is saporin.

According to some embodiments, the toxin is a maytansine derivative. According to certain embodiments, the maytansine derivative is DM4 or DM1.

According to some embodiments, the toxin is quinoline alkaloid. According to certain embodiments, the quinoline alkaloid is SN-38.

According to some embodiments, the toxin is a DNA topoisomerase I (TOP1) inhibitor. According to some embodiments, DNA topoisomerase I (TOP1) inhibitor is Exatecan or Exatecan derivative According to certain embodiments, the DNA topoisomerase I (TOP1) inhibitor is DXd.

According to some embodiments, the toxin is directly connected to the antibody. According to other embodiments, the antibody and the toxin are connected through a linker or a spacer. According to some embodiments, the toxin is covalently connected to the humanized antibody directly or through a linker or a spacer. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the linker is cleavable. According to other embodiments, the linker is not cleavable. According to some embodiments, the linker is an enzymatic cleavable linker. According to certain embodiments, the linker is a pH-sensitive linker. According to some embodiments, the linker is a reducible linker (sulfo-SPDB).

According to some embodiments, the linker is selected from the group consisting of Maleimidocaproyl (MC), Maleimidocaproyl-Valine-Citrulline- p-amino-benzyloxycarbonyl (MC-VC-PAB), Maleimidomethyl cyclohexane-1-carboxylate (SMCC), N-succinimidyl-4-(2-

pyridyldithio)butanoate (SPDB) and Lys-PAB-CO (Lysine- ρ-aminobenzyl -C=O). Each possibility represents a separate embodiment of the invention.

According to some embodiments, polynucleotide sequences encoding the amino acid sequences of heavy chain variable region and light chain variable region described above are provided.

According to some embodiments, the polynucleotide sequence encodes a humanized antibody heavy chain variable region, the polynucleotide comprise a sequence selected from the group consisting of SEQ ID NOs: 51-55 or a variant thereof having at least 80% sequence identity. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the polynucleotide sequence encodes a humanized antibody light chain variable region, the polynucleotide comprise a sequence selected from the group consisting of SEQ ID NOs: 56-60 or a variant thereof having at least 80% sequence identity. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the polynucleotide sequence encodes a humanized antibody heavy chain variable region, the polynucleotide comprise a sequence selected from the group consisting of SEQ ID NOs: 51-55. According to some embodiments, the polynucleotide sequence encodes a humanized antibody light chain variable region, the polynucleotide comprise a sequence selected from the group consisting of SEQ ID NOs: 56-60.

According to some embodiments, the polynucleotide sequence encodes a humanized antibody heavy chain variable region, said polynucleotide comprise a sequence set forth in SEQ ID NO: 51. According to some embodiments, said polynucleotide sequence encodes a humanized antibody light chain variable region, the polynucleotide comprise a sequence set forth in SEQ ID NO: 56.

According to some embodiments, polynucleotide sequences encoding the amino acid sequences of humanized antibody heavy chain and light chain described above are provided.

According to some embodiments, the polynucleotide sequence encoding the humanized antibody heavy chain comprises a sequence set forth in SEQ ID NO: 48 or a variant thereof having at least 80% sequence identity. According to some embodiments, the polynucleotide

sequence encoding the humanized antibody light chain comprises a sequence set forth in SEQ ID NO: 50 or a variant thereof having at least 80% sequence identity.

According to some embodiments, the DNA sequence encoding the amino acid chain of a humanized antibody as described herein comprises a leader sequence. According to certain exemplary embodiments, the DNA sequence encodes a leader peptide sequence set forth in SEQ ID NO: 71.

In a further aspect, the present invention provides a nucleic acid construct comprising a nucleic acid molecule encoding at least one humanized antibody chain or fragment thereof as described herein. According to some embodiments the nucleic acid construct is a plasmid.

Also described is a cell line comprising the nucleic acids encoding the antibodies of the present invention. The cell line is for expression of the humanized antibody or fragment thereof as described herein. In certain embodiments, the cell line is a mammalian cell line such as a Chinese Hamster Ovary (CHO) cell line.

The present invention provides, according to another aspect, a pharmaceutical composition comprising the humanized antibody or antigen binding fragment described herein or a conjugate comprising the antibody and a pharmaceutically acceptable excipient, carrier, or diluent.

According to some embodiments, the pharmaceutical composition is for use in treating cancer.

Any administration mode may be used to deliver the compositions of the present invention to a subject in need thereof, including parenteral and enteral administration modes.

According to some embodiments, the pharmaceutical composition is formulated for injection or infusion. According to some embodiments, the pharmaceutical composition is formulated for intravenous administration. In certain embodiments, the pharmaceutical composition is formulated for intratumoral administration.

According to yet another aspect, the present invention provides a method of treating cancer comprising administering to a subject in need thereof, a therapeutically effective amount of at least one humanized antibody or its conjugate as described herein.

According to some embodiments, the cancer is characterized by overexpression of Nectin-2.

In certain embodiments, the cancer comprises a solid tumor.

In certain embodiments, the cancer is selected from the group consisting of prostate cancer, colorectal cancer, liver cancer, ovarian cancer, endometrial cancer, stomach cancer, thyroid cancer, carcinoid tumor, head and neck cancer, breast cancer, pancreatic cancer, testis cancer, urothelial cancer, cervical cancer, melanoma, lymphoma and lung cancer. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the cancer is breast cancer. According to some embodiments, the cancer is colorectal adenocarcinoma or lung adenocarcinoma.

According to other embodiments, the cancer is a hematological cancer. According to some embodiments, the hematological cancer is selected from leukemia including acute myeloid leukemia (AML), chronic myeloid leukemia (CML), acute lymphocytic leukemia (ALL), and chronic lymphocytic leukemia (CLL); lymphoma, including Hodgkin disease, and non-Hodgkin lymphoma; and multiple myeloma.

According to some embodiments, the subject is human.

According to some embodiments, the method of treating cancer comprises administering or performing at least one additional anti-cancer therapy. According to certain embodiments, the additional anticancer therapy is surgery, chemotherapy, radiotherapy, or immunotherapy.

According to some embodiments, the method of treating cancer comprises administration of the humanized antibody described herein and an additional anti-cancer agent. According to some embodiments, the additional anti-cancer agent is selected from the group consisting of: immune-modulator, activated lymphocyte cell, kinase inhibitor and chemotherapeutic agent.

According to other embodiments, the additional immune-modulator is an antibody, antibody fragment or antibody conjugate that binds to an antigen other than human Nectin-2.

According to some embodiments, the additional immune-modulator is an antibody against an immune checkpoint molecule. According to some embodiments, the additional immune modulator is an antibody against an immune checkpoint molecule selected from the

group consisting of human programmed cell death protein 1 (PD-1), PD-L1 and PD-L2, carcinoembryonic antigen-related cell adhesion molecule 1 (CEACAM1), lymphocyte activation gene 3 (LAG3), CD137, OX40 (also referred to as CD134), killer cell immunoglobulin-like receptors (KIR), TIGIT, PVR, CTLA-4, NKG2A, GITR, and any other checkpoint molecule or a combination thereof. Each possibility represents a separate embodiment of the invention. According to certain embodiments, the additional immune modulator is an antibody against PD-1. According to some embodiments, the additional immune modulator is an antibody against CTLA-4.

According to some embodiments, the anti-cancer agent is selected from the group consisting of: erbitux, cytarabine, fludarabine, fluorouracil, mercaptopurine, methotrexate, thioguanine, gemcitabine, vincristine, vinblastine, vinorelbine, carmustine, lomustine, chlorambucil, cyclophosphamide, cisplatin, carboplatin, ifosfamide, mechlorethamine, melphalan, thiotepa, dacarbazine, bleomycin, dactinomycin, daunorubicin, doxorubicin, idarubicin, mitomycin, mitoxantrone, plicamycin, etoposide, teniposide and any combination thereof. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the method of treating cancer involves preventing or reducing formation, growth or spread of metastases in a subject.

According to an additional aspect, the present invention provides an antibody-drug conjugates comprising a humanized antibody that specifically binds human Nectin-2 and a toxin, for use in treating cancer.

The cancer and the toxin are as described above.

According to some embodiments, the humanized antibody comprises a mutated Fc domain.

The present invention further provides, according to an aspect, a method of diagnosing or prognosing cancer in a subject, the method comprises determining the expression level of Nectin-2 in a biological sample of said subject using at least one humanized antibody, fragment or conjugate as described herein.

The present invention further provides, according to another aspect, a method of determining or quantifying the expression of Nectin-2, the method comprising contacting a

biological sample with an antibody or antibody fragment as described herein, and measuring the level of complex formation.

According to some embodiments, the method for detecting or quantifying the expression of Nectin-2 comprises the steps of:

i. incubating a sample with the antibody specific to Nectin-2 or an antibody fragment thereof comprising at least an antigen-binding portion;
ii. detecting the bound Nectin-2 using a detectable probe.

According to some embodiments, the method further comprises the steps of:

iii. comparing the amount of (ii) to a standard curve obtained from a reference sample containing a known amount of Nectin-2; and
iv. calculating the amount of the Nectin-2 in the sample from the standard curve.

According to some particular embodiments, the sample is a body fluid or solid tissue. In some embodiments, the method is performed in-vitro or ex-vivo.

A kit for measuring the expression of Nectin-2 in biological sample is also provided comprising at least one antibody or antibody fragment as described herein and means for measuring Nectin-2 expression. In some embodiment, the kit further comprising instruction material directing the use of the kit.

Further embodiments and the full scope of applicability of the present invention will become apparent from the detailed description given hereinafter. However, it should be understood that the detailed description and specific examples, while indicating preferred embodiments of the invention, are given by way of illustration only, since various changes and modifications within the spirit and scope of the invention will become apparent to those skilled in the art from this detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A-1C depict the correlation of Nectin-2 mRNA levels (high or low as indicated) with survival probability of Low-grade glioma (Figure 1A), Kidney Renal Clear Cell Carcinoma (Figure 1B) and lung adenocarcinoma (Figure 1C) patients. Data sets were obtained from the

TCGA site and analyzed using oncolnc.org site (https://doi.org/10.7717/peerj-cs.67). N depicts number of patients included at the analysis.

Figure 2 is a schematic illustration of receptors expressed on immune cells and their respective affinities to Nectin-2 (CD112), which is expressed by tumors or on antigen presenting cells (APCs). TIGIT is a co-inhibitory receptor on many immune cells (e.g., T and NK cells); DNAM-1 (also termed CD226) is an activating receptor on many immune cells (e.g., T cells), and CD112R (also termed PVRIG) and TIGIT are co-inhibitory receptors on lymphoid immune cells (e.g., T and NK cells); Nectin-2 acts as an inhibitory ligand for immune cells, mainly via its high-affinity binding to CD112R (rectangle).

Figure 3 is a graph showing percent of tumors positive for Nectin-2 expression. Data obtained from proteinatlas.com using the HPA012759 mAb (anti Nectin-2; Sigma-Aldrich®). In 17/20 indications moderate-high membranous expression of Nectin-2 is seen.

Figures 4A-4C depict improved on-cell binding of the humanized variants of the parental (chimeric) anti-Nectin2 mAb. Nectin-2 expressing cells were analyzed by FACS analysis for binding of serially diluted mAb humanized variants. EC-50 values were calculated for each variant and are reported relative to the EC-50 value of the chimeric Ab (H0K0), which was set as 1. Figure 4A - fold change EC-50 binding to 293T cells expressing human Nectin-2. Figure 4B - fold change EC-50 binding to Vero cells derived from African green monkey (AFG, Chlorocebus) and naturally expressing Nectin-2 (XP_007995342.1). Figure 4C - results of CD112R blocking by the different humanized mAb variants, as assessed by FACS analysis of CD112R-Fc binding to CHO(K)1 cells overexpressing human Nectin-2, in presence of the anti-Nectin-2 humanized clones in concentrations from 66-0.81nM. Variants maintaining >70% blocking capacity at the lowest dose were considered superior.

Figures 5A-5C depict the killing effect of humanized anti-Nectin-2 ADC variants. ADC was based on Saporin (ZAP) and the A549 target cells (lung adenocarcinoma) were confirmed to express Nectin-2. Figure 5A shows the superior killing effect of the lead clone H3K3, compared to other humanized variants tested at two concentrations. Figure 5B depicts comparable levels of ADC activity between the humanized H3K3 and H4K2 variants. Figure 5C - comparable levels of ADC activity between the chimeric mAb (H0K0), and the humanized H3K3 variant at three concentrations. H3K3 was also tested when grafted on IgG2-P238H, which has an FcgR-null Fc, and which had no effect on the potency of this variant. All killing results are significant ($p<0.001$, two-way t-test), unless indicated by NS (not significant).

Figures 6A-6C demonstrate that humanized H3K3-FcgR^{null} anti-Nectin-2 ADCs, conjugated to various toxins, lead to robust killing of various solid tumor cell lines. The Figures show significant killing activity of the H3K3-FcgR^{null} ADCs, at different ADC concentrations and across different cancer targets after 72 hours of incubation. Figure 6A depicts killing of RKO cells (colorectal adenocarcinoma). Figure 6B depicts killing of MDA-MB-231 cells (triple negative breast cancer). Figure 6C depicts killing of A549 cells (lung adenocarcinoma). Killing of target cells was significant ($p<0.001$), unless indicated by NS (not significant). While all ADCs had a toxic effect, its magnitude varied pending the conjugated toxin and nature of target cells. Still, the ADCs containing either MMAE or MMAF were superior to all others across all target cells.

Figure 7 demonstrates that humanized H3K3-FcgR^{null} anti-Nectin-2 ADCs are not internalized via interaction with the high affinity FcgR - CD64. CHO-K1 cells or CHO-K1 cells overexpressing human CD64 (hCD64), but not Nectin-2, were incubated with two versions of H3K3-FcgR^{null} ADCs (conjugated to either MMAE or DM4), or with control irrelevant ADCs that have either hIgG4 (S228P) or hIgG1 Fc (both conjugated to DM4), at 12ug/ml for 72 hours. Specific increased killing was seen for the CD64 positive cells when either hIgG4 or hIgG1 was used, but not when the FcgR^{null} Fc H3K3 ADC variants were used. Note that background, non-specific killing was induced by DM4, regardless of either Nectin-2 or CD64 expression by the target cells.

Figure 8 demonstrates that humanized H3K3-FcgR^{null} anti-Nectin-2 ADCs lead to robust killing of a hematological cell line. H3K3-FcgR^{null} Abs, with the indicated linker-payload combinations, were incubated at concentration from 9-1 μg/ml, for 72 hours with HL-60 cells (an AML model). All linker-payload combinations, except DM1, resulted in >90% killing at the high dose and significant killing at all doses tested ($p< 0.001$).

Figures 9A-9B depict in-vivo efficacy of the humanized H3K3-FcgR^{null} anti-Nectin-2 ADCs against the hematological tumor cells line, HL-60 implanted s.c. to Nude female mice. Figure 9A compares the effect of treatment with different combinations of linker payloads (LP). Two of the LP combinations had a significant effect: DM4 resulted in significant tumor growth inhibition (TGI, $p<0.05$), while complete tumor regression was seen for MMAE. The effect of the MMAE-based ADC is shown in Figure 9B without including the other treatments.

Figure 10 depicts in-vivo efficacy of the humanized H3K3-FcgR^{null} anti-Nectin-2 ADC (1107-MC-VC-MMAE) against the solid (colorectal adenocarcinoma) tumor cell line, RKO. An empty vehicle was used as control.

Figure 11 depicts in-vitro killing of MDA-MB-231 (triple negative breast cancer or TNBC) cells by the humanized H3K3-FcgR^{null} anti-Nectin-2 mAb (NTX1107) linked to Dxd, compared to Trodelvy (Sacituzumab govitecan), an approved ADC drug for TNBC. Both ADCs use the same class of cytotoxic payload (i.e., topoisomerase I (TOP1) inhibitors). MDA-MB-231 cells were incubated in presence of the indicated concentration of these ADCs. Killing was evaluated after 120 hours. Robust killing of target cells was induced by both ADCs with significant superiority of Trodelvy at both concentrations (***$p < 0.0005$).

Figure 12 depicts in-vivo efficacy of humanized H3K3-FcgR^{null} anti-Nectin-2 ADC (NTX1107), compared to Trodelvy, against MDA-MB-231 s.c. tumor model in Nude female mice. NTX1107-Dxd was able to significantly inhibit tumor growth, resulting in tumor stasis, while Trodelvy had no effect on tumor growth at the same treatment regimen.

Figure 13 compares the effect of in-vivo treatment with H3K3-FcgR^{null}-Dxd (NTX1107-Dxd) to that of H3K3-FcgR^{null} MMAE (NTX1107-MMAE) against MDA-MB-231 s.c. tumor model in Nude female mice. Complete tumor regression was seen for H NTX1107-MMAE with 7/7 mice having no measurable tumors at the end of the study. Tumor regression was seen for NTX1107-Dxd with 4/7 mice having no measurable tumors at the end of the study.

DETAILED DESCRIPTION OF THE INVENTION

The present invention provides humanized monoclonal antibodies that recognize Nectin-2. Advantageously, the antibodies of the invention are almost fully humanized, thus avoiding the risk of adverse immune response towards the antibodies and are therefore likely to be safe for use in humans. The antibodies of the invention are characterized by having unique CDR sequences and novel humanized framework sequences and design.

The present invention further provides in some embodiments antibody-drug conjugates, or ADCs, comprising the humanized antibodies described herein, which are useful in treating cancer.

In the following description, certain specific details are set forth in order to provide a thorough understanding of various embodiments. However, one skilled in the art will understand that the embodiments provided may be practiced without these details. Unless the context requires otherwise, throughout the specification and claims which follow, the word "comprise" and variations thereof, such as, "comprises" and "comprising" are to be construed in an open, inclusive sense, that is, as "including, but not limited to." As used in this specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the content clearly dictates otherwise. It should also be noted that the term "or" is generally employed in its sense including "and/or" unless the content clearly dictates otherwise. Further, headings provided herein are for convenience only and do not interpret the scope or meaning of the claimed embodiments.

As used herein the term "about" refers to an amount that is near the stated amount by 10% or less.

The term "Nectin-2" or "Nectin Cell Adhesion Molecule 2", as used herein refers to a human plasma membrane glycoprotein, also known as CD112, and PVRL2. The Nectin-2 protein is a single-pass type I membrane glycoprotein with two Ig-like C2-type domains and an Ig-like V-type domain. This protein is one of the plasma membrane components of adherent junctions. It also serves as an entry for certain mutant strains of herpes simplex virus and pseudorabies virus, and it is involved in cell to cell spreading of these viruses. An exemplary Nectin-2 according to the invention is set forth in SwissPort, UniPort and GenBank symbols or accession numbers: Gene ID: 5819, Q92692, I68093, NP_001036189.1, NP_002847.1, and # Q92692.

According to an aspect, the present invention provides a humanized antibody that specifically bind Nectin-2, or a fragment thereof comprising at least the antigen binding site, wherein the antibody or a fragment thereof comprises a heavy chain and a light chain, wherein the heavy chain comprises a variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and wherein the light chain comprises a variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20.

According to another aspect, the present invention provides a humanized antibody that specifically binds Nectin-2, or a fragment thereof comprising at least the antigen binding site, wherein the antibody, or a fragment thereof, comprises a heavy chain variable region and a light chain variable region, the heavy chain variable region comprising:

(i) a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 1-3; and

(ii) a set of four heavy chain framework sequences, wherein: FR-H1 (frame work heavy chain No. 1) is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22; FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; FR-H4 is SEQ ID NO: 24;

and the light chain variable region comprising:

(i) a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 4-6; and

(ii) a set of four light chain framework sequences, wherein FR-L1 (frame work light chain No. 1) is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.

The frameworks are the non-CDR sequences of the chain variable regions. FR-H1 is the sequence before CDR1 in the heavy variable chain, FR-H2 is the sequence between CDR1 and CDR2, FR-H3 is the sequence between CDR2 and CDR3, and FR-H4 is the sequence after CDR3. FR-L1 is the sequence before CDR1 in the light variable chain, FR-L2 is the sequence between CDR1 and CDR2, FL-H3 is the sequence between CDR2 and CDR3, and FR-L4 is the sequence after CDR3.

According to an additional aspect, the present invention provides a humanized antibody or antigen binding fragment thereof comprising a heavy chain variable region and a light chain variable region, the heavy chain variable region comprising:

i. a set of three CDR sequences, the CDRs comprising the sequences SYW, SEQ ID NO: 8, and SEQ ID NO: 3; and

ii. a set of four heavy chain framework sequences, wherein: FR-H1 is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22;

FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; FR-H4 is SEQ ID NO: 24;

and the light chain variable region comprising:

i. a set of three CDR sequences, the CDRs comprising the sequences set forth in SEQ ID NO: 10, SAS, and SEQ ID NO: 6; and

ii. a set of four light chain framework sequences, wherein: FR-L1 is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.

According to some embodiments, the humanized antibody or fragment thereof comprises a heavy chain variable region comprising a set of three CDR sequences, the CDRs comprising the sequences SEQ ID NO: 7, SEQ ID NO: 8, and SEQ ID NO: 9; and a light chain variable region comprising a set of three CDR sequences, the CDRs comprising the sequences SEQ ID NO: 10, SAS, and SEQ ID NO: 6.

Among the provided antibodies are monoclonal antibodies, polyclonal antibodies, multispecific antibodies (for example, bispecific antibodies and polyreactive antibodies), and antibody fragments. The antibodies include antibody-conjugates and molecules comprising the antibodies, such as chimeric molecules. Thus, an antibody includes, but is not limited to, full-length, as well as fragments and portion thereof retaining the binding specificities thereof, such as any specific binding portion thereof including those having any number of, immunoglobulin classes and/or isotypes (e.g., IgGl, IgG2, IgG3, IgG4, IgM, IgA, IgD, IgE and IgM); and biologically relevant (antigen-binding) fragments or specific binding portions thereof, including but not limited to Fab, F(ab')2, Fv, and scFv (single chain or related entity). A monoclonal antibody is generally one within a composition of substantially homogeneous antibodies; thus, any individual antibodies comprised within the monoclonal antibody composition are identical except for possible naturally occurring mutations that may be present in minor amounts. A polyclonal antibody is a preparation that includes different antibodies of varying sequences that generally are directed against two or more different determinants (epitopes). The monoclonal antibody can comprise a human IgG1 constant region. The monoclonal antibody can comprise a human IgG4 constant region.

The term “antibody” herein is used in the broadest sense and includes polyclonal and monoclonal antibodies, including intact antibodies and functional (antigen-binding) antibody

fragments thereof, including fragment antigen binding (Fab) fragments, F(ab')2 fragments, Fab' fragments, Fv fragments, recombinant IgG (rIgG) fragments, single chain antibody fragments, including single chain variable fragments (sFv or scFv), and single domain antibodies (e.g., sdAb, sdFv, nanobody) fragments. The term encompasses genetically engineered and/or otherwise modified forms of immunoglobulins, such as intrabodies, peptibodies, fully human antibodies, humanized antibodies, and heteroconjugate antibodies, multispecific, e.g., bispecific, antibodies, diabodies, triabodies, and tetrabodies, tandem di-scFv, tandem tri-scFv. Unless otherwise stated, the term "antibody" should be understood to encompass functional antibody fragments thereof. The term also encompasses intact or full- length antibodies, including antibodies of any class or sub-class, including IgG and sub-classes thereof, IgM, IgE, IgA, and IgD. The antibody can comprise a human IgG1 constant region. The antibody can comprise a human IgG4 constant region.

CDR identification or determination from a given heavy or light chain variable sequence, is typically made using one of few methods known in the art. For example, such determination is made according to the Kabat (Wu T.T and Kabat E.A., *J Exp Med*, 1970; 132:211–50) and IMGT (Lefranc M-P, et al., *Dev Comp Immunol*, 2003, 27:55-77).

When the term "CDR having a sequence", or a similar term is used, it includes options wherein the CDR comprises the specified sequences and also options wherein the CDR consists of the specified sequence.

The antigen specificity of an antibody is based on the hyper variable region (HVR), namely the unique CDR sequences of both light and heavy chains that together form the antigen-binding site.

Among the provided antibodies are antibody fragments. An "antibody fragment" refers to a molecule other than an intact antibody that comprises a portion of an intact antibody that binds the antigen to which the intact antibody binds. Examples of antibody fragments include, but are not limited to, Fv, Fab, Fab', Fab'-SH, F(ab')2; diabodies; linear antibodies; single-chain antibody molecules (e.g., scFv or sFv); and multispecific antibodies formed from antibody fragments. In particular embodiments, the antibodies are single-chain antibody fragments comprising a variable heavy chain region and/or a variable light chain region, such as scFvs.

A “humanized” antibody is an antibody in which all or substantially all CDR amino acid residues are derived from non-human CDRs and all or substantially all framework region (FR) amino acid residues are derived from human FRs. A humanized antibody optionally may include at least a portion of an antibody constant region derived from a human antibody. A “humanized form” of a non-human antibody refers to a variant of the non-human antibody that has undergone humanization, typically to reduce immunogenicity to humans, while retaining the specificity and affinity of the parental non-human antibody. According to some embodiments, some FR residues in a humanized antibody are substituted with corresponding residues from a non-human antibody (e.g., the antibody from which the CDR residues are derived), e.g., to restore or improve antibody specificity or affinity.

The amino acid residues in the Fc domain can be substituted to be null, meaning the Fc domain does not bind Fc receptors or can bind with such low affinity and/or avidity as to not cause any Fc receptor signaling as a result of binding. The Fc domain can be null for binding to Fcγ receptors. Some example Fcγ receptors for which the Fc domain can be null for binding can be, but not limited to, FcγRI (CD64), FcγRIIA (CD32a), FcγRIIB (CD32b), FcγRIIIA (CD16a), FcγRIIIA (CD16a) F158 variant, FcγRIIIA (CD16a) V158 variant, or FcγRIIIB (CD16b). The Fc domain may have one or more, two or more, three or more, or four or more amino acid substitutions that decrease binding of the Fc domain to an Fc receptor.

According to some embodiments, the humanized antibody has a mutated Fc domain that prevents FcγR-mediated internalization.

According to some embodiments, the humanized antibody comprises a Fc null domain. According to certain embodiments, the Fc domain is null for binding to a Fcγ receptors.

As used herein, an "Fc null" refers to a domain that exhibits weak to no binding to one or more of the Fcγ receptors.

Antibody-drug conjugates

According to an aspect, the present invention provides a conjugate comprising the humanized antibody as described herein fused to a toxin.

According to some embodiments, the conjugate comprises an antibody or fragment thereof comprising a heavy chain and a light chain, wherein the heavy chain comprises a

variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and wherein the light chain comprises a variable region having an amino acid sequence at least about 90% identical to a sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20.

According to some embodiments, the toxin is selected from the group consisting of microtubule inhibitor, DNA synthesis inhibitor, topoisomerase inhibitor, and RNA polymerase inhibitor. Each possibility represents a separate embodiment of the invention.

According to certain embodiments, the toxin is a microtubule-destroying drug. According to certain exemplary embodiments, the toxin is auristatin or a derivative thereof. According to certain embodiments, the auristatin derivative is monomethyl auristatin E (MMAE) or monomethyl auristatin F (MMAF).

According to some embodiments, the toxin is saponin.

According to some embodiments, the toxin is a maytansine derivative. According to certain embodiments, the maytansine derivative is DM4 or DM1.

According to some embodiments, the toxin is quinoline alkaloid. According to certain embodiments, the quinoline alkaloid is SN-38.

According to additional embodiments, the toxin is selected from the group consisting of MMAE, MMAF, Saporin, DM4, DM1, SN-38, Calicheamicin, DXd, PBD, Duocarmycin, Sandramycin, alpha-Amanitin, Chaetocin, Daunorubicin, 17-AAG, Agrochelin A, Doxorubicin, Methotrexate, Colchicine, Cordycepin, Hygrolidin, Herboxidiene, Ferulenol, Curvulin, Englerin A, Taltobulin, Triptolide, Cryptophycin, and Nemorubicin. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the toxin is a DNA topoisomerase I (TOP1) inhibitor. According to certain embodiments, the DNA topoisomerase I (TOP1) inhibitor is DXd.

The toxins names are used herein as known in the art. Non limiting examples of suitable payloads include:

- DM1 - a $N^{2'}$-deacetyl-$N^{2'}$-(3-mercapto-1-oxopropyl)-maytansine- a tubulin inhibitor.

- DM4 - a $N^{2'}$-deacetyl-$N^{2'}$-(4-mercapto-4-methyl-1-oxopentyl)- Ravtansine - a tubulin inhibitor.

- SN-38 - a potent DNA topoisomerase I inhibitor, a member of the class of pyranoindolizinoquinolines that is (4S)-pyrano[3',4':6,7]indolizino[1,2-b]quinoline-3,14-dione bearing two additional ethyl substituents at positions 4 and 11 as well as two additional hydroxy substituents at positions 4 and 9.

- DXd – an exatecan derivative, a potent DNA topoisomerase I inhibitor (For example Cat. No.: HY-13631D of MCE®).

- MMAF – a monomethyl auristatin F – a tubulin inhibitor, having the formula C39H65N5O8.

- MMEA - a monomethyl auristatin E- a tubulin inhibitor, having the formula C39H67N5O7.

According to some embodiments, the antibody is directly linked to the toxin. According to other embodiments, the antibody and the toxin are linked through a linker. According to some embodiments, the humanized described herein is covalently linked to the toxin.

According to some embodiments, the linker is cleavable. According to additional embodiments, the linker is not cleavable.

According to some embodiments, the linker is cleaved in response to changes in pH or redox potential. According to some embodiments, the linker is cleaved when contacted with lysosomal enzymes.

The present invention provides, according to another aspect, a pharmaceutical composition comprising the humanized antibody or antigen binding fragment described herein or a conjugate comprising the antibody and a pharmaceutically acceptable excipient, carrier, or diluent.

According to other embodiments, the pharmaceutical composition according to the invention is for use in treating cancer characterized by overexpression of Nectin-2. Nectin-2 overexpression related cancer types can be identified using known data bases such as The

Cancer Genome Atlas (TCGA). According to certain embodiments, the cancer treatable with a composition according to the present invention is selected from the group consisting of adrenocortical carcinoma (ACC), chromophobe renal cell carcinoma (KICH), liver hepatocellular carcinoma (LIHC), colon and rectal adenocarcinoma (COAD, READ), pancreatic ductal adenocarcinoma (PAAD), pheochromocytoma & paraganglioma (PCPG), papillary kidney carcinoma (KIRP), lung adenocarcinoma (LUAD), head and neck squamous cell carcinoma (HNSC), prostate adenocarcinoma (PRAD), uterine corpus endometrial carcinoma (UCEC), cervical cancer (CESC), cutaneous melanoma (SKCM), mesothelioma (MESO), urothelial bladder cancer (BLCA), clear cell kidney carcinoma (KIRC), lung squamous cell carcinoma (LUSC), uterine carcinosarcoma (UCS), sarcoma (SARC), ovarian serous cystadenocarcinoma (OV), papillary thyroid carcinoma (THCA), glioblastoma multiforme (GBM), breast cancer (BRCA), lower grade glioma (LGG), and diffuse large B-cell lymphoma (DLBC). Each possibility represents a separate embodiment of the invention.

As used herein the term "individual," "patient," or "subject" refers to individuals diagnosed with, suspected of being afflicted with, or at-risk of developing at least one disease for which the described compositions and method are useful for treating. According to some embodiments the individual is a mammal. According to some embodiments, the mammal is a mouse, rat, rabbit, dog, cat, horse, cow, sheep, pig, goat, llama, alpaca, or yak. According to some embodiments, the individual is a human.

As used herein the term an "effective amount" refers to the amount of a therapeutic that causes a biological effect when administered to a mammal. Biological effects include, but are not limited to, inhibition or blockade of a receptor ligand interaction (e.g., PVR-TIGIT, PD-1-PD-L1/PD-L-2), inhibition of a signaling pathway, reduced tumor growth, reduced tumor metastasis, or prolonged survival of an animal bearing a tumor. A "therapeutic amount" is the concertation of a drug calculated to exert a therapeutic effect. A therapeutic amount encompasses the range of dosages capable of inducing a therapeutic response in a population of individuals. The mammal can be a human individual. The human individual can be afflicted with or suspected or being afflicted with a tumor.

As used herein the term "combination" or "combination treatment" can refer either to concurrent administration of the articles to be combined or sequential administration of the articles to be combined. As described herein, when the combination refers to sequential administration of the articles, the articles can be administered in any temporal order.

As used herein “checkpoint inhibitor” refers a drug that inhibits a biological molecule (“checkpoint molecule”) produced by an organism that negatively regulates the anti-tumor/cancer activity of T cells in the organism. Checkpoint molecules include without limitation PD-1, PD-L-1, PD-L-2, CTLA4, TIM-3, LAG-3, VISTA, SIGLEC7, PVR, TIGIT, IDO, KIR, A2AR, B7-H3, B7H4, CEACAM1, and CD112R.

The molecules of the present invention as active ingredients are dissolved, dispersed or admixed in an excipient that is pharmaceutically acceptable and compatible with the active ingredient as is well known. Suitable excipients are, for example, water, saline, phosphate buffered saline (PBS), dextrose, glycerol, ethanol, or the like and combinations thereof. Other suitable carriers are well known to those skilled in the art. In addition, if desired, the composition can contain minor amounts of auxiliary substances such as wetting or emulsifying agents, pH buffering agents.

The term "treatment" as used herein refers to both therapeutic treatment and prophylactic or preventative measures. Those in need of treatment include those already with the disorder as well as those in which the disorder is to be prevented.

The terms “cancer” and “tumor” relate to the physiological condition in mammals characterized by deregulated cell growth. Cancer is a class of diseases in which a group of cells display uncontrolled growth or unwanted growth. Cancer cells can also spread to other locations, which can lead to the formation of metastases. Spreading of cancer cells in the body can, for example, occur via lymph or blood. Uncontrolled growth, intrusion, and metastasis formation are also termed malignant properties of cancers. These malignant properties differentiate cancers from benign tumors, which typically do not invade or metastasize.

According to some embodiments, the method of treating cancer comprises administering the pharmaceutical composition as part of a treatment regimen comprising administration of at least one additional anti-cancer agent.

According to some embodiments, the anti-cancer agent is selected from the group consisting of an antimetabolite, a mitotic inhibitor, a taxane, a topoisomerase inhibitor, a topoisomerase II inhibitor, an asparaginase, an alkylating agent, an antitumor antibiotic, and combinations thereof. Each possibility represents a separate embodiment of the invention.

According to some embodiments, the antimetabolite is selected from the group consisting of cytarabine, fludarabine, fluorouracil, mercaptopurine, methotrexate, thioguanine, gemcitabine, and hydroxyurea. According to some embodiments, the mitotic inhibitor is selected from the group consisting of vincristine, vinblastine, and vinorelbine. According to some embodiments, the topoisomerase inhibitor is selected from the group consisting of topotecan and irinotecan. According to some embodiments, the alkylating agent is selected from the group consisting of busulfan, carmustine, lomustine, chlorambucil, cyclophosphamide, cisplatin, carboplatin, ifosfamide, mechlorethamine, melphalan, thiotepa, dacarbazine, and procarbazine. According to some embodiments, the antitumor antibiotic is selected from the group consisting of bleomycin, dactinomycin, daunorubicin, doxorubicin, idarubicin, mitomycin, mitoxantrone, and plicamycin. According to some embodiments, the topoisomerase II is selected from the group consisting of etoposide and teniposide. Each possibility represents a separate embodiment of the present invention.

The present invention provides, according to another aspect, a method of treating a cancer in an individual afflicted with a cancer comprising administering to the individual a therapeutically effective amount of the humanized antibody or antigen binding fragment thereof or the pharmaceutical composition, and an inhibitor of PD-1, PD-L1, CTLA-4 or CD112R signaling. In certain embodiments, the cancer comprises a solid tumor. In certain embodiments, the cancer is selected from the group consisting of lung cancer, colon cancer, glioblastoma, pancreatic cancer, breast cancer, bladder cancer, kidney cancer, head and neck cancer, ovarian cancer, cervical cancer, or prostate cancer. In certain embodiments, the inhibitor of PD-1 signaling is an antibody or fragment thereof that binds to PD-1. In certain embodiments, the antibody or fragment thereof that binds to PD-1 is Pembrolizumab, Nivolumab, AMP-514, Tislelizumab, Spartalizumab, or a PD-1 binding fragment thereof. In certain embodiments, the inhibitor of PD-1 signaling is an antibody that specifically binds PD-L-1 or PD-L-2. In certain embodiments, the antibody that specifically binds PD-L1 or PD-L2 comprises Durvalumab, Atezolizumab, Avelumab, BMS-936559, or FAZ053, or a PD-L1 or PD-L2 binding fragment thereof. In certain embodiments, the inhibitor of PD-1 signaling comprises an Fc-fusion protein that binds PD-1, PD-L1, or PD-L2. In certain embodiments, the Fc-fusion protein comprises AMP-224 or a PD-1 binding fragment thereof. In certain embodiments, the inhibitor of PD-1 signaling comprises a small molecule inhibitor of PD-1, PD-L1, or PD-L2. In certain embodiments, the small molecule inhibitor of PD-1, PD-L1, or PD-L2 signaling comprises on or more of: N-{2-[({2-methoxy-6-[(2-methyl[1,1'-biphenyl]-3-

yl)methoxy]pyridin-3-yl}methyl)amino]ethyl}acetamide (BMS 202); (2-((3-cyanobenzyl)oxy)-4-((3-(2,3-dihydrobenzo[b][1,4]dioxin-6-yl)-2-methylbenzyl)oxy)-5-methylbenzyl)-D-serine hydrochloride; (2R,4R)-1-(5-chloro-2-((3-cyanobenzyl)oxy)-4-((3-(2,3-dihydrobenzo[b][1,4]dioxin-6-yl)-2-methylbenzyl)oxy)benzyl)-4-hydroxypyrrolidine-2-carboxylic acid; 3-(4,6-dichloro-1,3,5-triazin-2-yl)-1-phenylindole; 3-(4,6-dichloro-1,3,5-triazin-2-yl)-1-phenyl-1h-indole; L-α-Glutamine, N2,N6-bis(L-seryl-L-asparaginyl-L-threonyl-L-seryl-L-α-glutamyl-L-seryl-L-phenylalanyl)-L-lysyl-L-phenylalanyl-L-arginyl-L-valyl-L-threonyl-L-glutaminyl-L-leucyl-L-alanyl-L-prolyl-L-lysyl-L-alanyl-L-glutaminyl-L-isoleucyl-L-lysyl; (2S)-1-[[2,6-dimethoxy-4-[(2-methyl[1,1'-biphenyl]-3-yl)methoxy]phenyl]methyl]-2-piperidinecarboxylic acid; Glycinamide, N-(2-mercaptoacetyl)-L-phenylalanyl-N-methyl-L-alanyl-L-asparaginyl-L-prolyl-L-histidyl-L-leucyl-N-methylglycyl-L-tryptophyl-L-seryl-L-tryptophyl-N-methyl-L-norleucyl-N-methyl-L-norleucyl-L-arginyl-L-cysteinyl-, cyclic (1→14)-thioether; or a derivative or analog thereof.

Also described herein is a method of making composition for treating a cancer in an individual afflicted with cancer comprising admixing the humanized antibody or antigen binding fragment thereof and a pharmaceutically acceptable excipient, carrier, or diluent. In certain embodiments, the cancer comprises a solid tumor. In certain embodiments, the cancer is selected from the group consisting of colon cancer, pancreatic cancer, breast cancer, bladder cancer, kidney cancer, head and neck cancer, ovarian cancer, glioblastoma, cervical cancer, prostate cancer, and lung cancer.

Also described herein is a method of producing the humanized antibody or antigen binding fragment thereof comprising incubating the cell line described herein in a cell culture medium under conditions sufficient to allow expression and secretion of the humanized antibody or antigen binding fragment thereof.

According to some particular embodiments, the additional anti-cancer agent is selected from the group consisting of bevacizumab, carboplatin, cyclophosphamide, doxorubicin hydrochloride, gemcitabine hydrochloride, topotecan hydrochloride, thiotepa, and combinations thereof. Each possibility represents a separate embodiment of the present invention.

EXAMPLES

Reference is now made to the following examples, which together with the above descriptions, illustrate the invention in a non-limiting fashion.

Generally, the nomenclature used herein, and the laboratory procedures utilized in the present invention include molecular, biochemical, microbiological, immunological, and recombinant DNA techniques. Such techniques are well known in the art. Other general references referring to well-known procedures are provided throughout this document for the convenience of the reader.

Example 1. High expression of Nectin-2 mRNA correlates with poor survival probability of various cancer patients.

The correlation between Nectin-2 mRNA expression levels and survival probability was examined on data from TCGA site, and analyzed using the oncolnc.org site, (https://doi.org/10.7717/peerj-cs.67). Nectin-2 mRNA expression levels were the basis for dividing patients for two subgroups of low and high expressors, as indicated by the arrows in Figure 1 for Low grade glioma (Figure 1A; p=5.22E-5), Kidney Renal Clear Cell Carcinoma (Figure 1B; p=0.00037) and lung adenocarcinoma (Figure 1C; p=0.0319) patients.

Example 2. Nectin-2 binds and affects immune cells through specific receptors.

The schematic illustration of Figure 2 demonstrates receptors expressed on immune cells and their respective affinities to Nectin-2 expressed by tumors or on antigen presenting cells (APCs). TIGIT relates to a co-inhibitory receptor on immune cells such as T and NK cells; DNAM-1 (also termed CD226) relates to an activating receptor on immune cells (e.g., T cells), and CD112R (also termed PVRIG) relates to a co-inhibitory receptor on lymphoid immune cells (e.g., T and NK cells); Nectin-2 (CD112) servs as an inhibitory ligand for immune cells, mainly via its binding to CD112R. According to the present invention, humanized anti-Nectin-2 mAbs block Nectin-2 interactions with its high affinity receptor CD112R and may target cancer cells for specific toxin delivery and killing.

Example 3. Nectin-2 is expressed on the majority of solid tumors

The database Proteinatlas.com was searched for all the aliases of Nectin-2 (NECTIN2, CD112, HVEB, PRR2, PVRL2, PVRR2). Under the pathology rubric, data using three different mAbs was found. HPA0127569 mAb has the highest validation score (Enhanced) as

it was validated by orthogonal method. Thus, the expression data across different tumors was selected for this clone only, and is depicted in Figure 3. The graph is showing percent of tumors positive for Nectin-2 expression. In 17/20 indications membranous expression of Nectin-2 is seen at Moderate-High levels.

Example 4. Improved properties of humanized anti-Nectin-2 mAbs

Murine anti-human Nectin-2 clone 2.11, disclosed in Patent application publication No. WO2020144697, was selected as the lead mAb for humanization. Based on structural analysis, a large preliminary set of sequence segments were identified that were used to create the humanized variants. These segments were selected and analyzed using iTope™ technology for in silico analysis of peptide binding to human MHC class II alleles (Perry et al., 2008) and using the TCED™ of known antibody sequence-related T cell epitopes (Bryson et al., 2010). Sequence segments that were identified as significant non-human germline binders to human MHC class II, or that scored significant hits against the TCED™, were discarded. This resulted in a reduced set of segments, and combinations of these were further analyzed, as described above, to ensure that the junctions between segments did not contain potential T cell epitopes. Selected sequence segments were assembled into complete V region sequences that were devoid of significant T cell epitopes. Five heavy chain (VH1 to VH5) and 5 light chain (VK1 to VK5) sequences were then chosen. The data at Table 1 present the readout of the iTope™ algorithm. To reduce the potential for anti-drug antibody (ADA) generation, the sequence of the mAbs was analyzed for potential binding of MHCII. The main risk is linked to the high affinity binding peptides, which are separated from the moderated affinity binding peptides.

Table 1. Improved characteristics of the humanized anti-Nectin-2 mAbs. Illustration of predicted MHCII epitopes (iTope score) of the parental (V0) and humanized heavy (VH1-5) and light (Vk1-5) variable chains used to generate humanized variants for lead drug selection.

Heavy Chain

Predicted affinity MHCII	VH0	VH1	VH2	VH3	VH4	VH5
Moderate	5	6	4	4	4	3
High	8	4	3	3	1	1

Light Chain

Predicted affinity MHCII	Vk0	Vk1	Vk2	Vk3	Vk4	Vk5
Moderate	8	4	3	3	3	1
High	4	3	3	2	2	2

The parental heavy chain (VH0) has 8 predicted high affinity motifs and the parental light chain (Vk0) has 4 such motifs. Following the humanization process, the number of predicted high affinity MHCII epitopes for the heavy chain was reduced to 3 (VH2, VH3) or even to 1 (VH4, VH5) and for the light chain the predicted high affinity MHCII motifs were reduced to 2 (VK3-5).

Thus, the humanization process eliminated the majority of the predicted high affinity MHCII motifs that may trigger immunogenicity against the mAb.

Stability of the humanized variants was assessed by thermal ramp stability experiments that are well established methods for ranking proteins and formulations for stability. A protein's denaturation profile provides information about its thermal stability and represents a structural 'fingerprint' for assessing structural and formulation buffer modifications. A widely used measure of the thermal structural stability of a protein is the temperature at which it unfolds from the native state to a denatured state.

For many proteins, this unfolding process occurs over a narrow temperature range and the mid-point of this transition is termed 'melting temperature' or 'Tm'. To determine the melting temperature of a protein, UNcle measures the fluorescence of Sypro Orange (which binds to exposed hydrophobic regions of proteins) as the protein undergoes conformational changes. Increased Tm is a desired characteristic in Ab lead selection as it predicts a more stable Ab.

Purified lead humanized antibody variants, in duplicates, were diluted to a final test concentration of 0.5 mg/ml in PBS into which Sypro Orange (at 160x Stock solution) was added to a final concentration of 20x solution. 9 µL of each sample mixture was loaded in duplicate into UNi microcuvettes. Samples were subjected to a thermal ramp from 15 - 95 °C, with a ramp rate of 0.3 °C/minute and excitation at 473 nm. Full emission spectra were collected from 250-720 nm, and the area under the curve between 510 - 680 nm was used to calculate the inflection points of the transition curves (Tonset and Tm). As seen in Table 2, for all of the antibodies tested, Tm1 and Tonset are higher for the humanized variants compared with the chimeric antibody (VH0/Vκ0).

Table 2. A summary of thermal stability values for the parental/chimeric (VH0/Vk0) antibody and for six purified lead humanized variants as determined using the UNcle biostability platform. Improved stability of both Tonset and TM1 (measuring of unfolding) above 5 degrees Celsius, was considered significant and is marked in bold fonts.

Variant	Average Tonset (°C)	Average Tm1 (°C)
VH0/Vκ0	58.1	67.3
VH3/Vκ3	**65.6**	**74.3**
VH4/Vκ2	60.7	71.9
VH4/Vκ3	60.6	70.8
VH5/Vκ3	58.8	72.7
VH5/Vκ4	59.9	68.3
VH5/Vκ5	61.3	69.4

Example 5. Improved binding to Nectin-2, and blocking of CD112R binding by the humanized anti-Nectin-2 mAbs

The humanized anti-Nectin-2 mAbs binding to human Nectin-2 expressed by 293T cells, (protein id: Q92692) and Chlorocebus (African green monkey, AFG) Vero cells were assessed and EC50 values were established. AFG expresses Nectin-2 protein (XP_007995342.1) with 97% similarity to human Nectin-2. Figures 4A and 4B depict fold change of EC50 values to human and AFG cells expressed Nectin-2, respectively. Both cell lines were plated at $0.5x10^5$ cells per well. The chimeric (H0K0) and humanized mAbs were added at concentration range of 20-0.001 nM. For detection, anti-human-APC Ab was used at 1:200 dilution (Jackson Immunoresearch AB_2340526). Cells were analyzed by FACS and EC50 was calculated and compared to that of the chimeric Ab (fold improve). This analysis revealed improved binding of the humanized variants, and similar degree of cross-reactivity to monkey Nectin-2, comparing to the chimeric mAb (Figures 4A vs. 4B). To evaluate the blocking capacity of the humanized Abs, human Nectin-2 was overexpressed in Chinese hamster ovary (CHO) cells. Figure 4C shows data generated when 10^5 of CHO-hNectin-2/well were incubated with 30nM of human CD112R-mIgG2a in presence of the indicated humanized Abs, in concentrations ranging from 66-0.81nM. Bound CD112R was detected by using αmIgG2a-647 (Jackson Immunoresearch Cat 115-607-186) at 1:200 dilution followed by FACS analysis. As can be seen, all humanized variants maintained full blocking capacity.

Example 6. Anti-hNectin-2 humanized variant H3K3 can serve as an ADC driver in an Fc independent manner

To assess the capacity of the mAbs to serve as ADCs, the streptavidin-saporin (ZAP), IT-27-250 (ATS), was used. The mAbs indicated in Figure 5 were biotinylated using the biotinylation kit Ab207195 (Abcam) at 1:1 ratio. Figure 5A depicts the results of the initial screen which included top humanized clones and A549 (lung adenocarcinoma) cells as targets. $2x10^3$ cells per well were plated and allowed to adhere over 4-6 hours period. The ADCs were added, and the cells were incubated with the ADCs. After 72 hours, the assay was harvested and tumor cell killing was evaluated using CellTiter-Glo® 2.0 Cell Viability Assay – (Promega G9242) following standard protocol. Only clone H3K3 showed robust killing. Next, clone H3K3 was directly compared to clone H4K2 (Figure 5B). Both clones exhibited robust killing, and H3K3 was selected for future analysis due to superior developability properties. The chimeric parental clone and the $FcgR^{null}$ variant (IgG2-P238H)(In $FcgR^{null}$, the g is for gamma

or γ) of clone H3K3 (IgG1) were tested under the above conditions and results are shown in Figure 5C. Significant killing ($p<0.001$) by both the chimeric and humanized H3K3 variants was seen at all concentrations of these ADCs, and the $FcgR^{null}$ variant led to identical level of target cell killing compared to the hIgG1 clone.

Example 7. Anti-hNectin-2 H3K3-$FcgR^{null}$ ADCs lead to robust killing of solid tumor cell lines in-vitro

Additional H3K3-$FcgR^{null}$ mAbs were generated by mutating key residues in the hinge region of human IgG1 as indicated in Table 3.

Table 3. A summary of the Fc-substitution for the humanized IgG1 $FcgR^{null}$ linker-payload combinations, release mechanisms, and the relevant drug-to-antibody ratios (DARs) for the H3K3-based ADCs.

Fc-Mutation ($FcgR^{null}$)	**Linker**	**Payload**	**Release mechanism**	**Average DAR (LC-MS)**
hIgG1 G237I	MC-VC-PAB	MMAE	Proteolytic cleavage	4.3
hIgG1 G237I	MC	MMAF	Degradation	4.2
hIgG1 L235S	SMCC	DM1	Degradation	4.0
hIgG1 L235S	SPDB	DM4	Redox	4.2
hIgG1 L235S/G237I	Lys-PAB-CO	SN38	pH	8

The presented linker payload combinations were chosen according to the desired release mechanism and were generated according to the standard protocol by Abzena LTD. Briefly, the mAbs were reduced and incubated with an excess of the linker-payload to obtain the desired drug antibody ratio (DAR) of 4 for all the linker-payloads except for SN-38, which had a target DAR of 8. The final products were then purified, and the DARs were established by LC/MS method. Selected tumor cell lines, representing various solid tumors, were used to assess potency of the various linker-payload combinations in-vitro. The indicated target cells were plated at $2x10^3$ cells per well and allowed to adhere over 4-6 hours period. The ADCs were

added at concentrations of 4-0.16μg/ml using 5-fold dilutions, and the cells were incubated with the ADCs. After 72 hours, the assay was harvested and tumor cell killing was evaluated using CellTiter-Glo® 2.0 Cell Viability Assay – (Promega G9242) following standard protocol. Robust killing of RKO cells (colorectal adenocarcinoma), MDA-MB-231 cells (triple negative breast cancer) and of A549 cells (lung adenocarcinoma) is depicted in Figures 6A-6C, respectively. Killing of target cells was significant ($p<0.001$) by two-tailed student t-test, unless indicated by NS (not significant, $p>0.05$).

Example 8. Selected FcgR^{null} mutations prevent ADC killing via FcgR

To evaluate the degree of non-target specific killing by the humanized anti-Nectin-2 ADCs, which is due to the Ab Fc binding to its FcγR, and which may contribute to non-specific effect of the ADC, CHO cells overexpressing the high affinity Fc receptor hCD64 (CHO-hCD64) were generated. These cells do not express human Nectin-2 and thus no target-specific killing is expected. Parental CHO cells and CHO-hCD64 were plated at $2x10^3$ cells per well and allowed to adhere over 4-6 hours. The different Fc variant ADCs were added at 12μg/ml. After incubation of 72 hours, the assay was harvested and tumor cell killing was evaluated using CellTiter-Glo® 2.0 Cell Viability Assay – (Promega G9242).

As seen in Figure 7, both the IgG4-S228P and the hIgG1-positive controls, led, as expected, to significantly higher degree of the killing of the CHO-hCD64 cells compared to parental CHO cells. On the other hand, the IgG1 G237I substitution resulted in similar low-level of killing of both parental and hCD64 overexpressing cells (non-specific killing). These results confirm that the FcgR^{null} variant is not bound and internalized by the high affinity FcgR CD64.

Example 9. Anti-hNectin-2 humanized H3K3-FcgR^{null} ADCs lead to robust killing of the hematological tumor cell line HL-60 in-vitro

HL-60 cells (AML model) were plated at $2x10^3$ cells per well and the ADCs were added at concentrations of 9-1μg/ml, using 3-fold dilutions. The cells were incubated with the ADCs for 72 hours. Then, the assay was harvested and tumor cell killing was evaluated using CellTiter-Glo® 2.0 Cell Viability Assay – (Promega G9242) as described above. As seen in Figure 8, except for the DM1 payload (indicated in the graph), all other compounds led to significant killing of the targets in all concentrations tested and all exceeded 90% killing at the

highest concentration (>60nM). Based on these results the SMCC-DM1 linker payload was excluded from future experiments.

Example 10. Anti-hNectin-2 H3K3-FcgR^{null}-MC-VC-PAB-MMAE ADC leads to tumor regression in an aggressive AML model

Nude female mice (n=25) were injected s.c. with 10x10^6 HL-60 cells in 1:1 Matrigel. Once tumors reached an average volume of 205 mm^3, mice were randomized into five groups (n=5 per group) and treated in a blinded manner, by i.v. injection of either PBS (vehicle), H3K3-FcgR^{null}-MMAE, H3K3-FcgR^{null}-MMAF, H3K3-FcgR^{null}-DM4 or H3K3-FcgR^{null}-SN-38. All treatments were at 5 mg/kg, given every 4 days, for 4 consecutive doses. As can be seen in Figure 9A, on day 23 after randomization, H3K3-FcgR^{null}-MMAF and the SN-38 variants did not attenuate tumor growth. H3K3-FcgR^{null}-DM4 led to significant tumor growth inhibition (TGI) of 49%, while H3K3-FcgR^{null}-MMAE led to significant tumor regression. Figure 9B shows the mean effect of H3K3-FcgR^{null}-MMAE.

Example 11. Anti-hNectin-2 H3K3-FcgR^{null}-MC-VC-PAB-MMAE ADC leads to tumor regression in an aggressive colon adenocarcinoma model

Nude female mice (n=5 per group) were injected SC with 5x10^6 RKO cells in 1:1 Matrigel. Once tumors reached an average volume of 160 mm^3, mice were randomized into two groups and treated every 4 days, in a blinded manner, by i.v. injection of either PBS (Vehicle) or H3K3-FcgR^{null}-MMAE (1107-MC-VC-MMAE) at 5 mg/kg for 4 consecutive doses. On day 13 after randomization, H3K3-FcgR^{null}-MMAE, led to significant tumor regression, as can be seen in Figure 10, representing >80% TGI compared to vehicle treated group.

Example 12. Anti-hNectin-2 H3K3-FcgR^{null} mAb has similar in vitro killing activity compared to Trodelvy

For the in vitro killing assay (Figure 11) MDA-MB-231 target cells were plated at 2x10^3 cells per well and allowed to adhere over 4-6 hours. Next, H3K3-FcgR^{null} anti-Nectin-2 mAb (NTX1107) linked to Dxd, and Trodelvy (Sacituzumab govitecan), an approved ADC drug for TNBC, were added at concentrations of 12µg/ml (dark grey bars) and 3µg/ml (light grey bars). Of note, both ADCs use the same class of cytotoxic payload (i.e., topoisomerase I (TOP1) inhibitors). The cells were incubated with the ADCs for 120 hours, after which tumor cell

killing was evaluated using CellTiter-Glo® 2.0 Cell Viability Assay – (Promega G9242), following a standard protocol. Robust killing of MDA-MB-231 cells was induced by both ADCs with significant superiority of Trodelvy at both concentrations (***$p < 0.0005$).

Example 13. Anti-hNectin-2 H3K3-FcgR^{null} conjugated to Topoisomerase 1 inhibitor, but not Trodelvy, inhibits in vivo growth of aggressive MDA-MB-231 tumors

Nude female mice (n=7 per group) were injected s.c. with $5x10^6$ MDA-MB-231 cells in 1:1 Matrigel. Once tumors reached an average volume of 230 mm^3 mice were randomized into treatment groups and treated every 4 days, for 3 consecutive doses, in a blinded manner, by i.v. injection of either PBS (vehicle), NTX1107-Dxd, or Trodelvy at 5 mg/kg. There was no effect for Trodelvy treatment on the tumor growth.

As seen in Figure 12, NTX1107-Dxd was able to significantly inhibit tumor growth (*$p<0.02$, **< 0.005.***$p < 0.0005$). These findings were unexpected since the in-vitro killing potency of Trodelvy was higher than that of NTX1107-Dxd Figure 11), and Trodelvy is an approved ADC for TNBC. These observations suggest that anti-Nectin-2 (NTX1107) is a uniquely potent ADC for the treatment of solid tumors.

Example 14. Anti-hNectin-2 H3K3-FcgR^{null} can regress aggressive MDA-MB-231 tumors in vivo when conjugated to tubulin or TOP1 targeting agents

Nude female mice (n=7 per group) were injected s.c. with $5x10^6$ MDA-MB-231 cells in 1:1 Matrigel. Once tumors reached an average volume of 210 mm^3 mice were randomized into treatment groups and treated every 4 days, for 5 consecutive doses, in a blinded manner, by i.v. injection of either PBS (vehicle), H3K3-FcgR^{null} (NTX1107)-MMAE, or NTX1107-Dxd. As can be seen in Figure 13, all animals treated with NTX1107-MMAE had no detectable tumors at the end of the study. For the animals treated with NTX1107-Dxd, four had no tumors, while for the remaining three the average tumor volume was 210mm^3, indicating tumor stasis. These findings suggest that the humanized antibodies targeting Nectin-2 described herein (NTX1107) may form uniquely potent ADCs for treatment of solid tumors, when using payloads of various classes.

Sequences

Table 4: CDR sequences:

Description	KABAT	IMGT	Overlapping sequence
Heavy Chain CDR1	SYWIH (SEQ ID NO: 1)	GYIFTSYW (SEQ ID NO: 7)	SYW
Heavy Chain CDR2	AVYPGNSDSNYNQKF(KA/QG) (SEQ ID NO: 2)	VYPGNSDS (SEQ ID NO: 8)	SEQ ID NO: 8
Heavy Chain CDR3	LVGTFDY (SEQ ID NO: 3)	TKLVGTFDY (SEQ ID NO: 9)	SEQ ID NO: 3
Light Chain CDR1	(K/R)ASQNVGINV(V/A) (SEQ ID NO: 4)	QNVGIN (SEQ ID NO: 10)	SEQ ID NO: 10
Light Chain CDR2	SASYRYS (SEQ ID NO: 5)	SAS	SAS
Light Chain CDR3	QQYNTNPFT (SEQ ID NO: 6)	SEQ ID NO: 6	SEQ ID NO: 6

SEQ ID NO: 11 - heavy chain variable region NT20-11_VH3
QVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFKARVTITAVTSTSTAYMELSSLRSEDTAVYYCTKLVGTFDYWGQGTTV
TVSS

SEQ ID NO: 12 light chain variable region NT20-11_Vk3
DIQMTQSPSTLSASVGDRVSVTCKASQNVGINVVWYQQKPGQPPKTLIYSASYRYSG
VPDRFSGSGSGTDFTLTISSLQAEDLAEYFCQQYNTNPFTFGQGTKLEIK

SEQ ID NO: 13 - heavy chain variable region NT20-11_VH1
EVQLVQSGTELKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFKARATITAVTSTSTAYMELSSLTSEDSAVYYCTKLVGTFDYWGQGTTV
TVSS

SEQ ID NO: 14 - heavy chain variable region NT20-11_VH2

EVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFKARATITAVTSTSTAYMELSSLRSEDTAVYYCTKLVGTFDYWGQGTTV
TVSS

SEQ ID NO: 15 - heavy chain variable region NT20-11_VH4
QVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFQGRVTITAVTSTSTAYMELSSLRSEDTAVYYCTKLVGTFDYWGQGTTV
TVSS

SEQ ID NO: 16 - heavy chain variable region NT20-11_VH5
QVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFQGRVTITADESTSTAYMELSSLRSEDTAVYYCTKLVGTFDYWGQGTTV
TVSS

SEQ ID NO: 17 - light chain variable region NT20-11_Vk1
DIVMTQSPSFLSASVGDRVSVTCKASQNVGINVVWYQQRAGQPPKTLIYSASYRYSG
VPDRFTGSGSGTDFTLTISSLQSEDLAEYFCQQYNTNPFTFGQGTKLEIK

SEQ ID NO: 18 - light chain variable region NT20-11_Vk2
DIVMTQSPSTLSASVGDRVSVTCKASQNVGINVVWYQQKPGQPPKTLIYSASYRYSG
VPDRFTGSGSGTDFTLTISSLQAEDLAEYFCQQYNTNPFTFGQGTKLEIK

SEQ ID NO: 19 - light chain variable region NT20-11_Vk4
DIQMTQSPSTLSASVGDRVTITCRASQNVGINVVWYQQKPGQPPKTLIYSASYRYSG
VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYNTNPFTFGQGTKLEIK

SEQ ID NO: 20 - light chain variable region NT20-11_Vk5
DIQMTQSPSTLSASVGDRVTITCRASQNVGINVAWYQQKPGQPPKTLIYSASYRYSG
VPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYNTNPFTFGQGTKLEIK

Table 5: Framework (Non-CDR) sequences of the humanized heavy chain variable regions.

Chain	FR-H1	FR-H2	FR-H3	FR-H4

VH3	QVQLVQSGAEVKKPGSSVKVSCKASGYIFT (SEQ ID NO: 21)	WVRQPPGKGLEWIG (SEQ ID NO: 22)	RVTITAVTSTSTAYMELSSLRSEDTAVYYCTK (SEQ ID NO: 23)	WGQGTTVTVSS (SEQ ID NO: 24)
VH1	EVQLVQSGTELKKPGSSVKVSCKASGYIFT (SEQ ID NO: 25)	WVRQPPGKGLEWIG (SEQ ID NO: 22)	RATITAVTSTSTAYMELSSLTSEDSAVYYCTK (SEQ ID NO: 26)	WGQGTTVTVSS (SEQ ID NO: 24)
VH2	EVQLVQSGAEVKKPGSSVKVSCKASGYIFT (SEQ ID NO: 27)	WVRQPPGKGLEWIG (SEQ ID NO: 22)	RATITAVTSTSTAYMELSSLRSEDTAVYYCTK (SEQ ID NO: 28)	WGQGTTVTVSS (SEQ ID NO: 24)
VH4	QVQLVQSGAEVKKPGSSVKVSCKASGYIFT (SEQ ID NO: 21)	WVRQPPGKGLEWIG (SEQ ID NO: 22)	RVTITAVTSTSTAYMELSSLRSEDTAVYYCTK (SEQ ID NO: 23)	WGQGTTVTVSS (SEQ ID NO: 24)
VH5	QVQLVQSGAEVKKPGSSVKVSCKASGYIFT (SEQ ID NO: 21)	WVRQPPGKGLEWIG (SEQ ID NO: 22)	RVTITADESTSTAYMELSSLRSEDTAVYYCTK (SEQ ID NO: 29)	WGQGTTVTVSS (SEQ ID NO: 24)

Table 6: Framework (Non-CDR) sequences of the humanized light variable regions.

Chain	FR-L1	FR-L2	FR-L3	FR-L4
LK3	DIQMTQSPSTLSASVGDRVSVTC (SEQ ID NO: 30)	WYQQKPGQPPKTLIY (SEQ ID NO: 31)	GVPDRFSGSGSGTDFTLTISSLQAEDLAEYFC (SEQ ID NO: 32)	FGQGTKLEIK (SEQ ID NO: 33)
LK1	DIVMTQSPSFLSASVGDRVSVTC (SEQ ID NO: 34)	WYQQRAGQPPKTLIY (SEQ ID NO: 35)	GVPDRFTGSGSGTDFTLTISSLQSEDLAEYFC (SEQ ID NO: 36)	FGQGTKLEIK (SEQ ID NO: 33)
LK2	DIVMTQSPSTLSASVGDRVSVTC (SEQ ID NO: 37)	WYQQKPGQPPKTLIY (SEQ ID NO: 31)	GVPDRFTGSGSGTDFTLTISSLQAEDLAEYFC (SEQ ID NO: 38)	FGQGTKLEIK (SEQ ID NO: 33)
LK4	DIQMTQSPSTLSASVGDRVTITC (SEQ ID NO: 39)	WYQQKPGQPPKTLIY (SEQ ID NO: 31)	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC (SEQ ID NO: 40)	FGQGTKLEIK (SEQ ID NO: 33)
LK5	DIQMTQSPSTLSASVGDRVTITC (SEQ ID NO: 39)	WYQQKPGQPPKTLIY (SEQ ID NO: 31)	GVPDRFSGSGSGTDFTLTISSLQAEDVAVYYC (SEQ ID NO: 40)	FGQGTKLEIK (SEQ ID NO: 33)

SEQ ID NO: 41 - HC CDR2 AVYPGNSDSNYNQKFKA

SEQ ID NO: 42 - HC CDR2 AVYPGNSDSNYNQKFQG

SEQ ID NO: 43 – LC CDR1 KASQNVGINVV

SEQ ID NO: 44 – LC CDR1 KASQNVGINVA

SEQ ID NO: 45 – LC CDR1 RASQNVGINVV

SEQ ID NO: 46 – LC CDR1 RASQNVGINVA

SEQ ID NO: 47 - amino acid sequence of VH3 Full length hIgG1 heavy chain

QVQLVQSGAEVKKPGSSVKVSCKASGYIFTSYWIHWVRQPPGKGLEWIGAVYPGNS
DSNYNQKFKARVTITAVTSTSTAYMELSSLRSEDTAVYYCTKLVGTFDYWGQGTTV
TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP

AVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPC
PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN
AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD
SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

SEQ ID NO: 48 - DNA Sequence VH3 Full length hIgG1

caggtgcagctggtgcagagcggcgcggaagtgaaaaaaccgggcagcagcgtgaaagtg
agctgcaaagcgagcggctatatttttaccagctattggattcattgggtgcgccagccg
ccgggcaaaggcctggaatggattggcgcggtgtatccgggcaacagcgatagcaactat
aaccagaaatttaaagcgcgcgtgaccattaccgcggtgaccagcaccagcaccgcgtat
atggaactgagcagcctgcgcagcgaagataccgcggtgtattattgcaccaaactggtg
ggcacctttgattattggggccagggcaccaccgtgaccgtgagcagcgcgagcaccaaa
ggcccgagcgtgtttccgctggcgccgagcagcaaaagcaccagcggcggcaccgcggcg
ctgggctgcctggtgaaagattattttccggaaccggtgaccgtgagctggaacagcggc
gcgctgaccagcggcgtgcataccttccggcggtgctgcagagcagcggcctgtatagc
ctgagcagcgtggtgaccgtgccgagcagcagcctgggcacccagacctatatttgcaac
gtgaaccataaaccgagcaacaccaaagtggataaacgcgtggaaccgaaaagctgcgat
aaaacccatacctgcccgccgtgcccggcgccggaactgctgggcggcccgagcgtgttt
ctgtttccgccgaaaccgaaagataccctgatgattagccgcaccccggaagtgacctgc
gtggtggtggatgtgagccatgaagatccggaagtgaaatttaactggtatgtggatggc
gtggaagtgcataacgcgaaaaccaaaccgcgcgaagaacagtataacagcacctatcgc
gtggtgagcgtgctgaccgtgctgcatcaggattggctgaacggcaaagaatataaatgc
aaagtgagcaacaaagcgctgccggcgccgattgaaaaaaccattagcaaagcgaaaggc
cagccgcgcgaaccgcaggtgtataccctgccgccgagccgcgaagaaatgaccaaaaac
caggtgagcctgacctgcctggtgaaaggcttttatccgagcgatattgcggtggaatgg
gaaagcaacggccagccggaaaacaactataaaaccaccccgccggtgctggatagcgat
ggcagctttttctgtatagcaaactgaccgtggataaaagccgctggcagcagggcaac
gtgtttagctgcagcgtgatgcatgaagcgctgcataaccattatacccagaaaagcctg
agcctgagcccgggcaaa

SEQ ID NO: 49 – amino acid sequence of Vk3 Full length Kappa light chain

DIQMTQSPSTLSASVGDRVSVTCKASQNVGINVVWYQQKPGQPPKTLIYSASYRYSG
VPDRFSGSGSGTDFTLTISSLQAEDLAEYFCQQYNTNPFTFGQGTKLEIKRTVAAPSV
FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDST
YSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC

SEQ ID NO: 50 - DNA Sequence Vk3 Full length Kappa

gatattcagatgacccagagcccgagcaccctgagcgcgagcgtgggcgatcgcgtgagc
gtgacctgcaaagcgagccagaacgtgggcattaacgtggtgtggtatcagcagaaaccg
ggccagccgccgaaaaccctgatttatagcgcgagctatcgctatagcggcgtgccggat
cgctttagcggcagcggcagcggcaccgattttaccctgaccattagcagcctgcaggcg
gaagatctggcggaatatttttgccagcagtataacaccaacccgtttacctttggccag

ggcaccaaactggaaattaaacgcaccgtggcggcgccgagcgtgtttatttttccgccg
agcgatgaacagctgaaaagcggcaccgcgagcgtggtgtgcctgctgaacaacttttat
ccgcgcgaagcgaaagtgcagtggaaagtggataacgcgctgcagagcggcaacagccag
gaaagcgtgaccgaacaggatagcaaagatagcacctatagcctgagcagcaccctgacc
ctgagcaaagcggattatgaaaaacataaagtgtatgcgtgcgaagtgacccatcagggc
ctgagcagcccggtgaccaaaagctttaaccgcggcgaatgc

SEQ ID NO: 51 – VH3 nucleic acids

SEQ ID NO: 52 – VH1 nucleic acids

SEQ ID NO: 53 – VH2 nucleic acids

SEQ ID NO: 54 – VH4 nucleic acids

SEQ ID NO: 55 – VH5 nucleic acids

SEQ ID NO: 56 – Vk3 nucleic acids

SEQ ID NO: 57 – Vk1 nucleic acids

SEQ ID NO: 58 – Vk2 nucleic acids

SEQ ID NO: 59 – Vk4 nucleic acids

SEQ ID NO: 60 – Vk5 nucleic acids

SEQ ID NO: 61 - Human IgG1 (L235S) (including VH3)

SEQ ID NO: 62 – Human IgG1 (L235S / E272K) (including VH3)

SEQ ID NO: 63 – Human IgG1 (G237I) (including VH3)

SEQ ID NO: 64 – Human IgG1 (G237I / E272I) (including VH3)

SEQ ID NO: 65 – Human IgG1 (G237I / V264R) (including VH3)

SEQ ID NO: 66 – Human IgG1 (V215A / E269R / K322A) (including VH3)

SEQ ID NO: 67 – Human IgG1 (L234A/ L235A / P329G) (including VH3)

SEQ ID NO: 68 – Human IgG4 (S228P / L235P / V264R) (including VH3)

SEQ ID NO: 69 – Human IgG2 (P238H) (including VH3)

SEQ ID NO: 70 – Human IgG2 (P238H / V264R) (including VH3)

SEQ ID NO: 71 - Leader peptide sequence.

CLAIMS

1. A humanized antibody that specifically binds human Nectin-2, or a fragment thereof comprising at least the antigen binding site, wherein the antibody, or a fragment thereof, comprises a heavy chain variable region and a light chain variable region, the heavy chain variable region comprising:
   (i) a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 1-3; and
   (ii) a set of four heavy chain (HC) framework (FR) sequences, wherein: FR-H1 is selected from the group consisting of SEQ ID NOs: 21, 25, and 27; FR-H2 is SEQ ID NO: 22; FR-H3 is selected from the group consisting of SEQ ID NOs: 23, 26, 28, and 29; FR-H4 is SEQ ID NO: 24;
   and the light chain variable region comprising:
   (i) a set of three CDR sequences comprising the sequences set forth in SEQ ID NOs: 4-6; and
   (ii) a set of four light chain (LC) framework (FR) sequences, wherein: FR-L1 is selected from the group consisting of SEQ ID NOs: 30, 34, 37, and 39; FR-L2 is selected from the group consisting of SEQ ID NOs: 31 and 35; FR-L3 is selected from the group consisting of SEQ ID NOs: 32, 36, 38, and 40; and FR-L4 is SEQ ID NO: 33.
2. The humanized antibody of claim 1, wherein the heavy chain comprises a variable region sequence selected from the group consisting of SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15 and SEQ ID NO: 16; and wherein the light chain comprises a variable region sequence selected from the group consisting of SEQ ID NO: 12, SEQ ID NO: 17, SEQ ID NO: 18, SEQ ID NO: 19 and SEQ ID NO: 20.
3. The humanized antibody of any one of claims 1 or 2, wherein the humanized antibody, or fragment thereof, comprising a heavy chain and a light chain selected from the group consisting of:
   (i) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 11, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 12;
   (ii) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 15, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 18;

(iii) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 13, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 17;

(iv) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 14, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 18;

(v) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 15, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 19; and

(vi) a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 16, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 20.

4. The humanized antibody of any one of the preceding claims, wherein the humanized antibody, or a fragment thereof, comprises a heavy chain and a light chain, wherein a heavy chain comprises a variable region having an amino acid sequence at least about 95% identical to SEQ ID NO: 11, and a light chain comprises a variable region having an amino acid sequence at least about 95% identical to SEQ ID NO: 12.

5. The humanized antibody of claim 4, wherein the humanized antibody, or a fragment thereof, comprises a heavy chain and a light chain, wherein a heavy chain comprises a variable region having an amino acid sequence SEQ ID NO: 11, and a light chain comprises a variable region having an amino acid sequence SEQ ID NO: 12.

6. The humanized antibody of any one of the preceding claims, wherein the humanized monoclonal antibody has a heavy chain constant region selected from IgG1, IgG4, and IgG2.

7. The humanized antibody of any one of the preceding claims, wherein the humanized antibody has a mutated Fc domain that prevents FcγR-mediated internalization.

8. The humanized antibody of claim 7, wherein the Fc domain is null for binding to Fcγ receptors.

9. A conjugate comprising the antibody, or fragment thereof, according to any one of the preceding claims.

10. The conjugate of claim 9, wherein the humanized antibody, or fragment thereof, is attached to a cytotoxic moiety, a radioactive moiety, an affinity moiety, or labeling moiety.

11. The conjugate of claim 9, wherein the humanized antibody, or fragment thereof, is attached to toxin (payload).
12. The conjugate of claim 11, wherein the toxin is selected from the group consisting of microtubule inhibitor, DNA synthesis inhibitor, topisomerase inhibitor and RNA polymerase inhibitor.
13. The conjugate of claim 12, wherein the microtubule inhibitor is auristatin or a derivative thereof.
14. The conjugate of claim 13, wherein the auristatin derivative is monomethyl auristatin E (MMAE) or monomethyl auristatin F (MMAF).
15. The conjugate of claim 12, wherein the toxin is a maytansine derivative.
16. The conjugate of claim 15, wherein the maytansine derivative is DM4 or DM1.
17. The conjugate of claim 12, wherein the toxin is a DNA topoisomerase I (TOP1) inhibitor.
18. The conjugate of claim 17, wherein the DNA topoisomerase I (TOP1) inhibitor is DXd.
19. The conjugate of claim 17, wherein the DNA topoisomerase I (TOP1) inhibitor is SN-38.
20. The conjugate of claim 11, wherein the antibody and the toxin are connected through a linker.
21. The conjugate of claim 20, wherein the linker is cleavable.
22. A polynucleotide sequence encoding the amino acid sequences of the heavy chain variable region and the light chain variable region of the humanized antibody or fragment thereof according to any one of claims 1-8.
23. A pharmaceutical composition comprising the humanized antibody or antigen binding fragment according to any one of claims 1-8, and/or the conjugate of any one of claims 9-20, and a pharmaceutically acceptable excipient, carrier, or diluent.
24. The pharmaceutical composition of claim 23, for use in treating cancer.
25. A method of treating cancer comprising administering to a subject in need thereof, a therapeutically effective amount of at least one humanized antibody or fragment thereof according to any one of claims 1-8 or conjugate according to any one of claims 9-21.
26. The method of claim 25, wherein the cancer is a solid cancer.
27. The method of claim 25, wherein the cancer is selected from the group consisting of prostate cancer, colorectal cancer, liver cancer, ovarian cancer, endometrial cancer, stomach cancer, thyroid cancer, carcinoid tumor, head and neck cancer, breast cancer,

pancreatic cancer, testis cancer, urothelial cancer, cervical cancer, melanoma, lymphoma and lung cancer.

28. The method of claim 25, wherein the cancer is colorectal adenocarcinoma or lung adenocarcinoma.
29. The method of claim 25, wherein the cancer is hematological cancer.
30. The method of any one of claims 25-29, wherein the method further comprising administering or performing at least one additional anti-cancer therapy.
31. A method of diagnosing or prognosing cancer in a subject, the method comprises determining the expression level of Nectin-2 in a biological sample of said subject using at least one humanized antibody or fragment according to any one of claims 1-8.

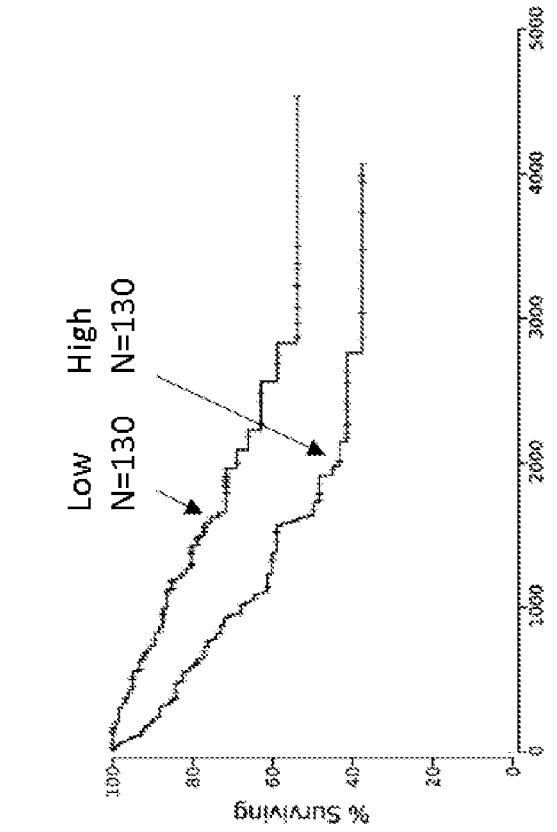

FIGURE 1B

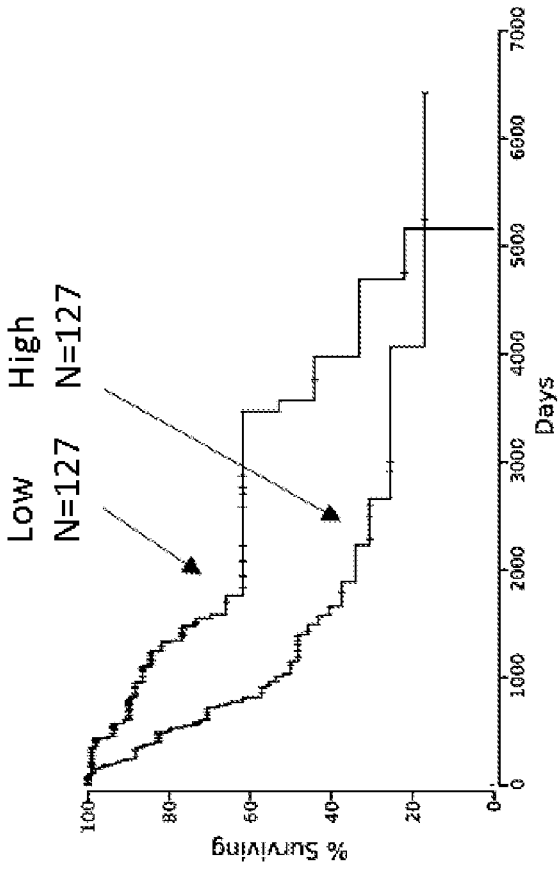

FIGURE 1A

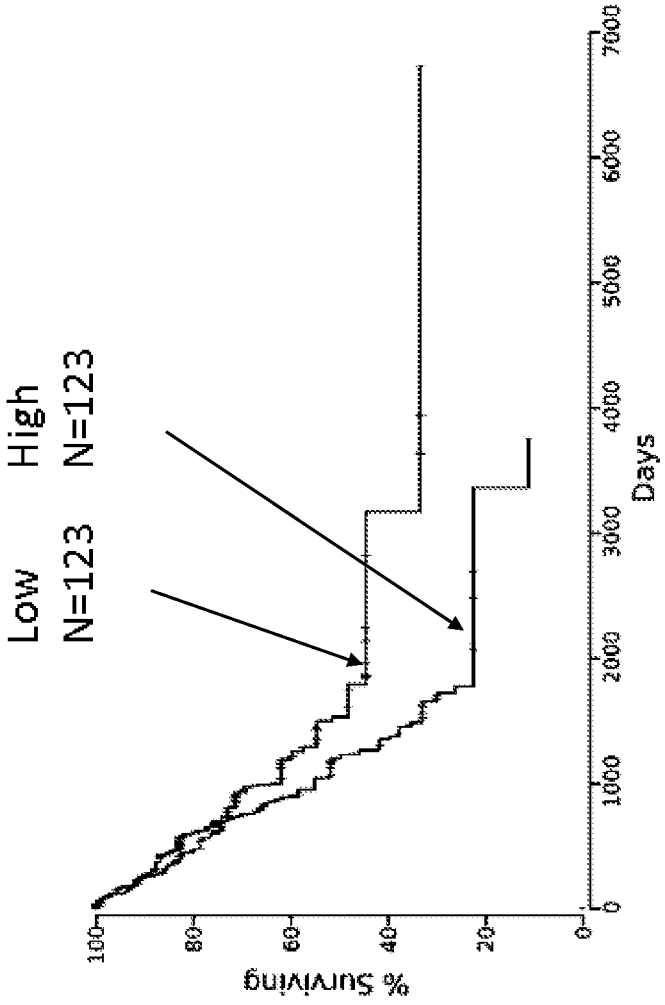
Low N=123
High N=123
% Surviving
Days
100
80
60
40
20
0
0
1000
2000
3000
4000
5000
6000
7000

FIGURE 1C

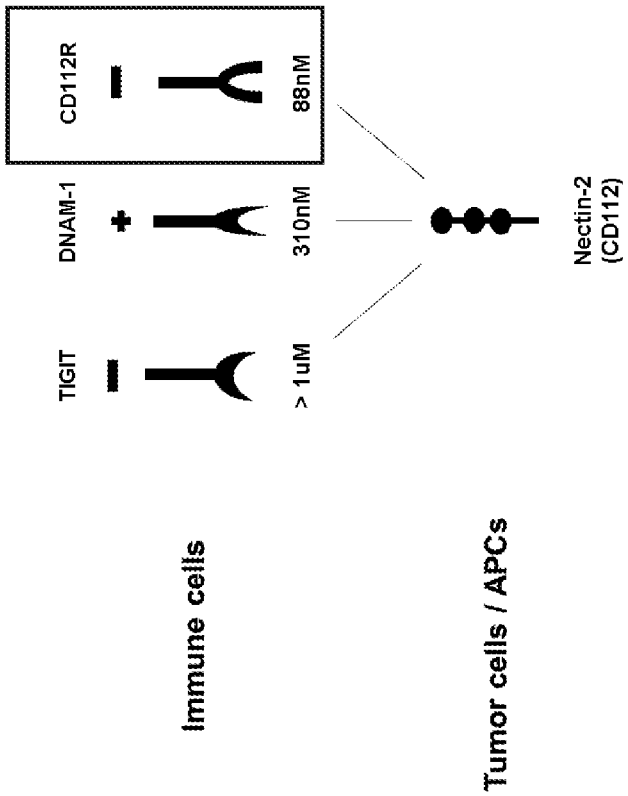
CD112R
88nM
DNAM-1
+
310nM
TIGIT
> 1uM
Immune cells
Nectin-2
(CD112)
Tumor cells / APCs

FIGURE 2

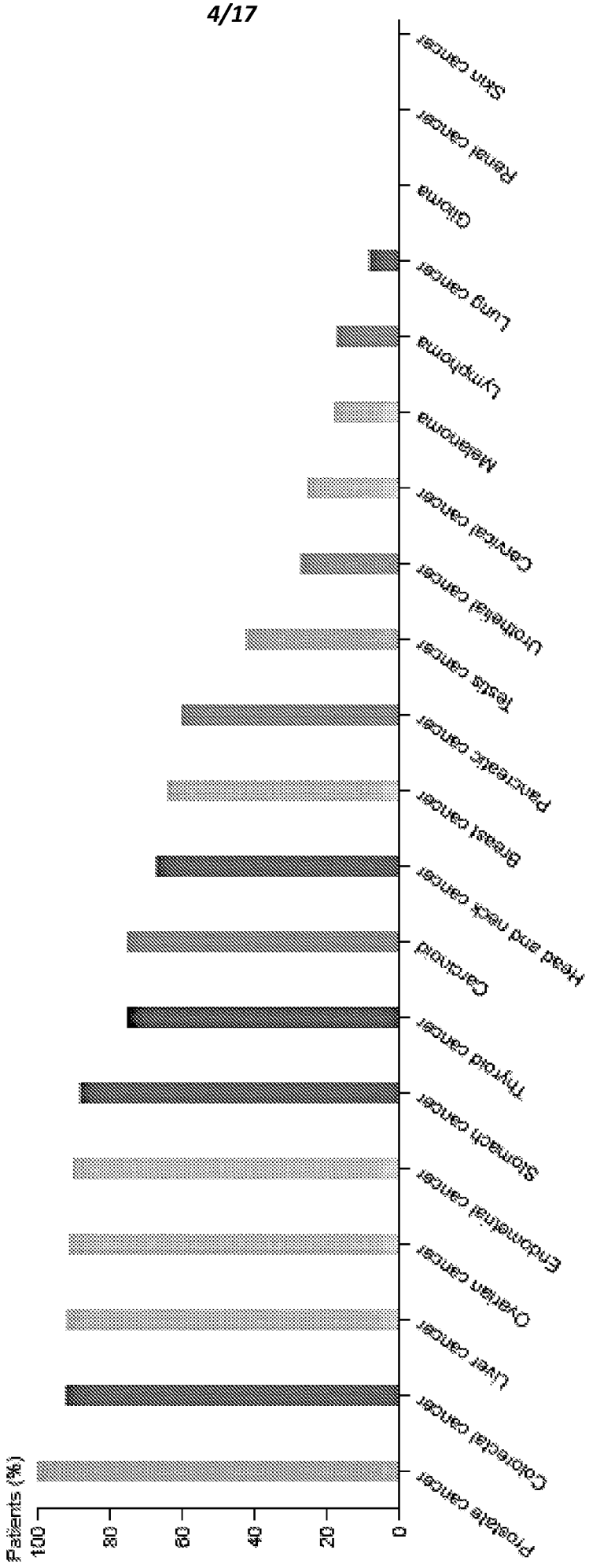
Patients (%)
100
80
60
40
20
0
Prostate cancer
Colorectal cancer
Liver cancer
Ovarian cancer
Endometrial cancer
Stomach cancer
Thyroid cancer
Carcinoid
Head and neck cancer
Breast cancer
Pancreatic cancer
Testis cancer
Urothelial cancer
Cervical cancer
Melanoma
Lymphoma
Lung cancer
Glioma
Renal cancer
Skin cancer

FIGURE 3

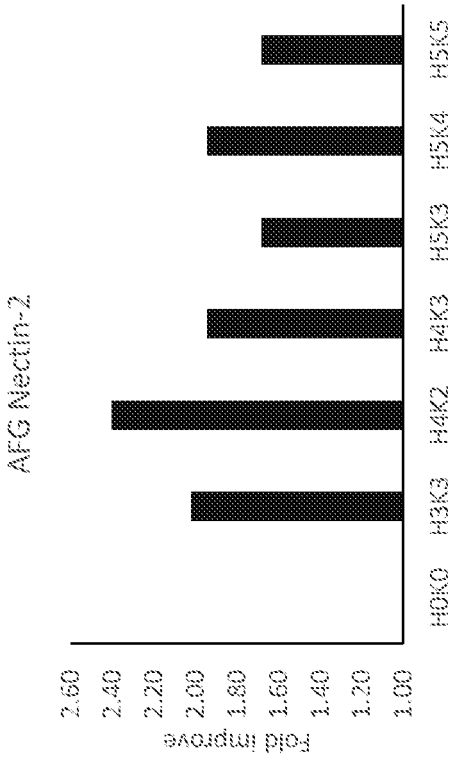

FIGURE 4B

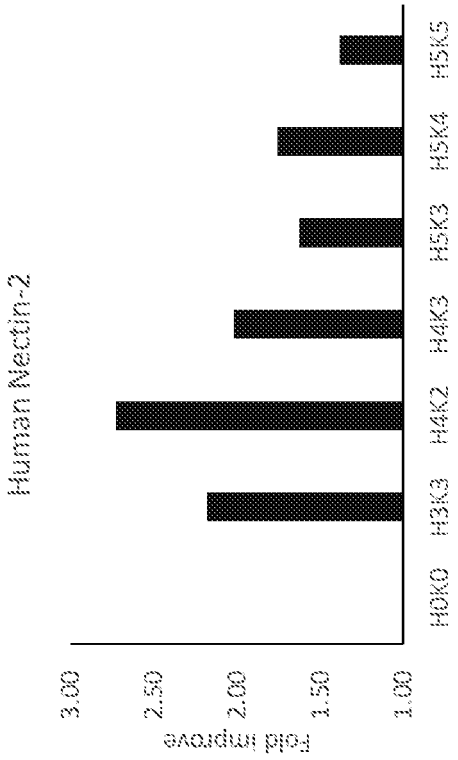

FIGURE 4A

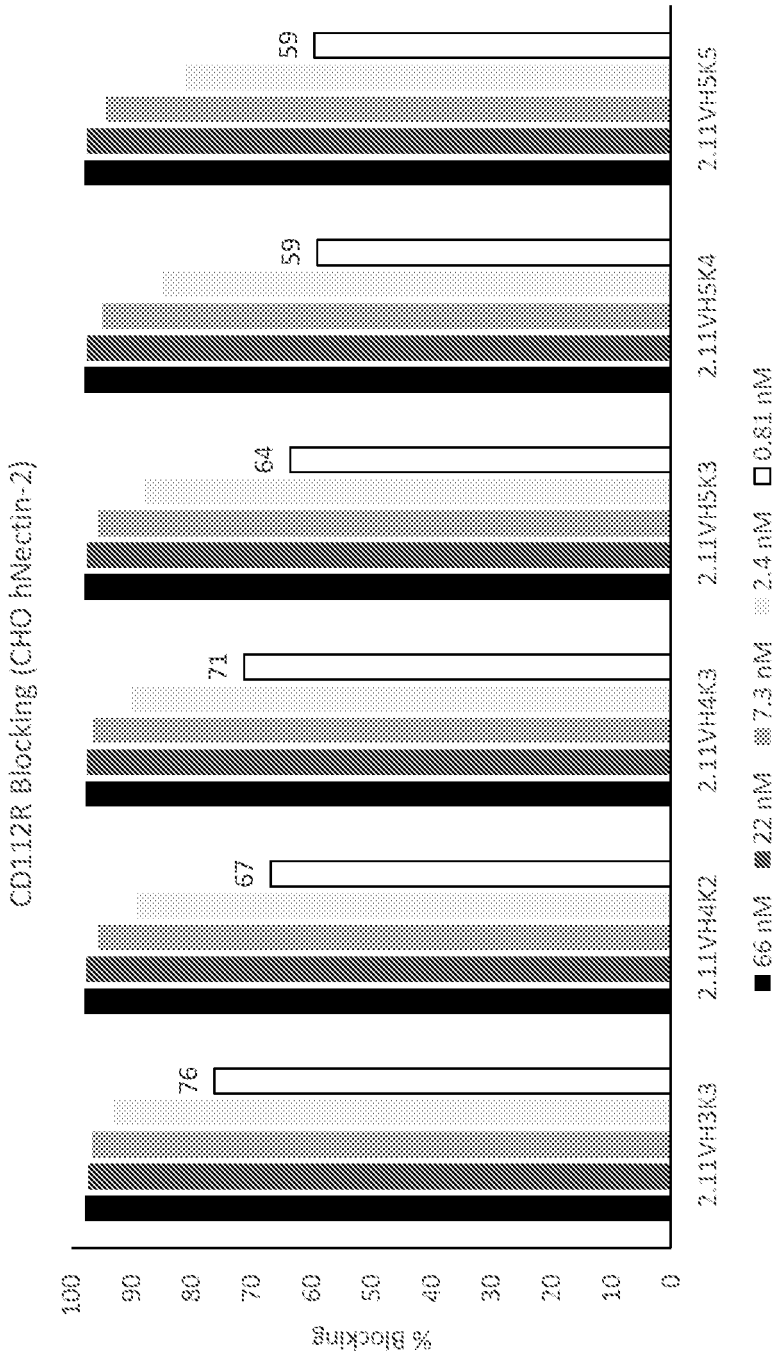
CD112R Blocking (CHO hNectin-2)
% Blocking
100
90
80
70
60
50
40
30
20
10
0
76
67
71
64
59
59
2.11VH3K3
2.11VH4K2
2.11VH4K3
2.11VH5K3
2.11VH5K4
2.11VH5K5
66 nM
22 nM
7.3 nM
2.4 nM
0.81 nM

FIGURE 4C

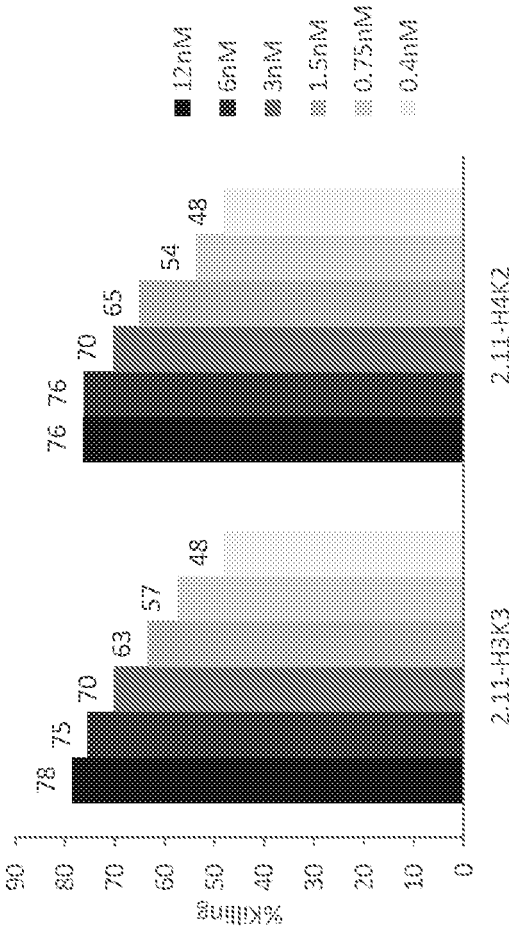

FIGURE 5B

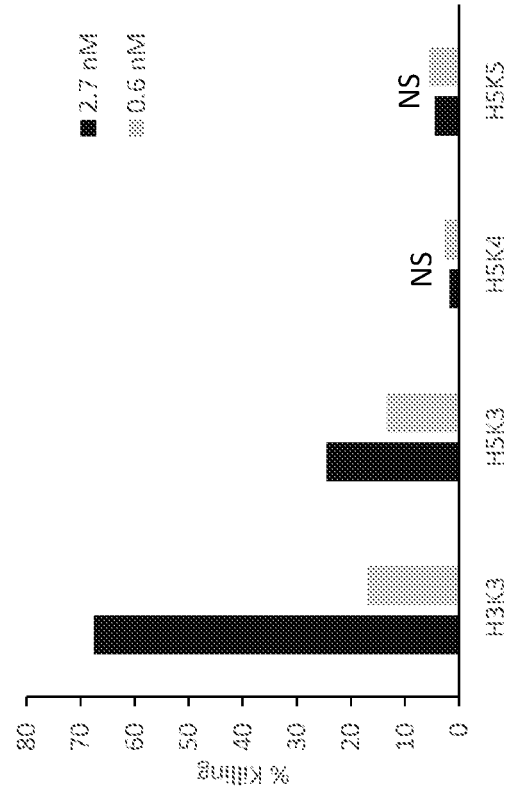

FIGURE 5A

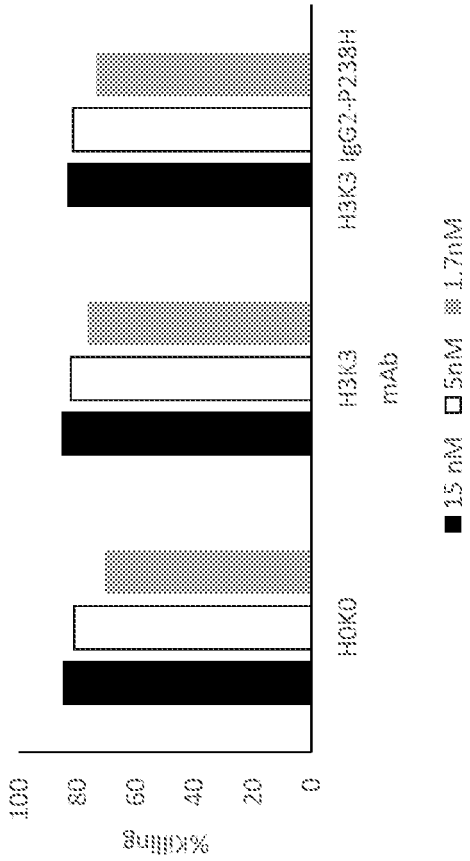
%killing
100
80
60
40
20
0
H0KO
H3K3
H3K3 IgG2-P238H
mAb
1.5 nM
5nM
1.7nM

FIGURE 5C

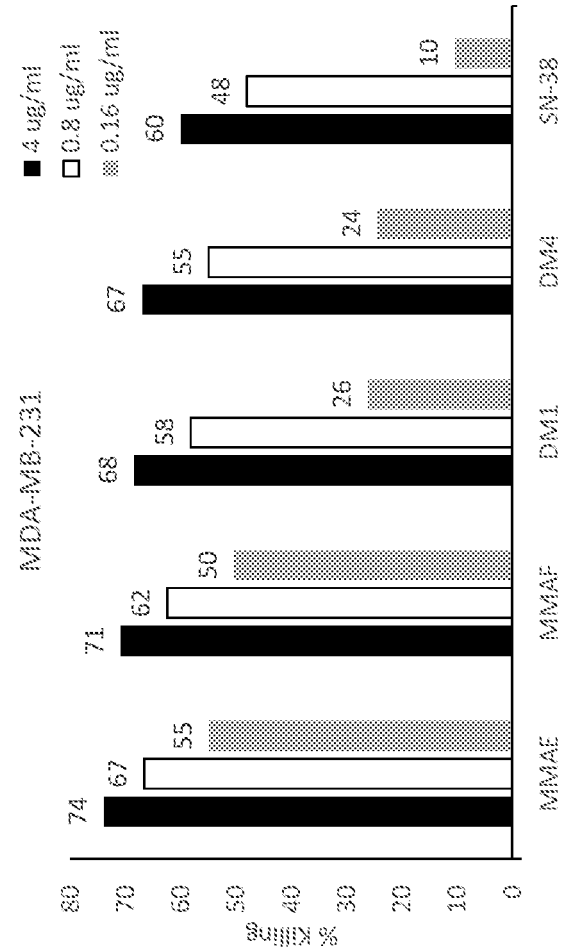

FIGURE 6B

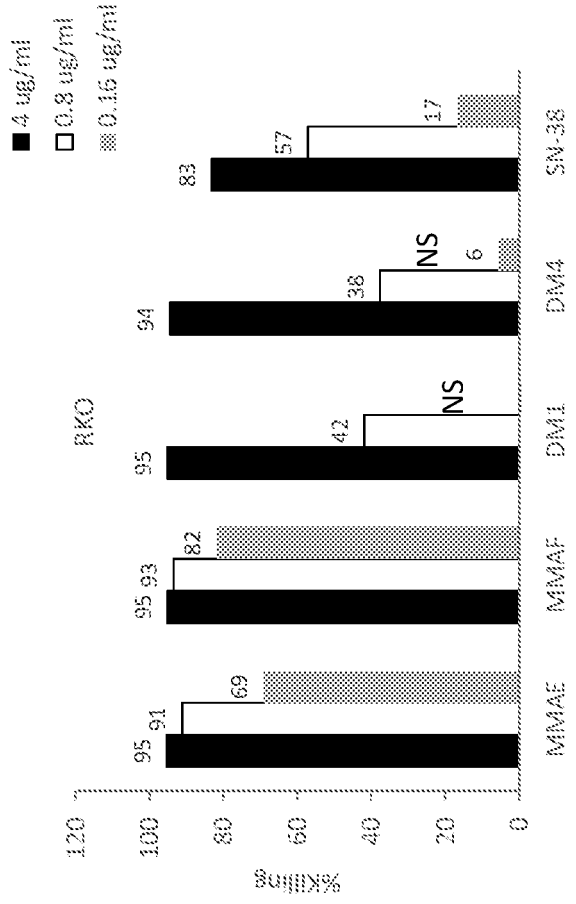

FIGURE 6A

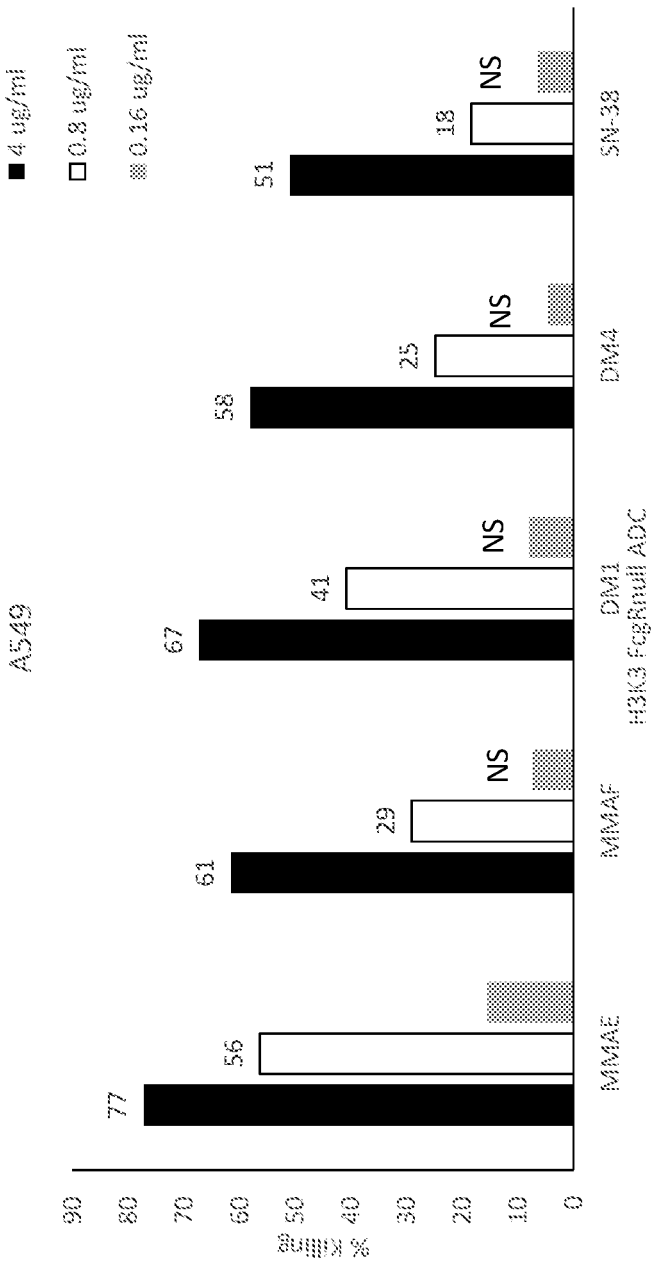
A549
4 ug/ml
0.8 ug/ml
0.16 ug/ml
% Killing
0
10
20
30
40
50
60
70
80
90
77
56
61
29
67
41
58
25
51
18
NS
NS
NS
NS
MMAE
MMAF
DM1
H3K3 FcgRnull ADC
DM4
SN-38

FIGURE 6C

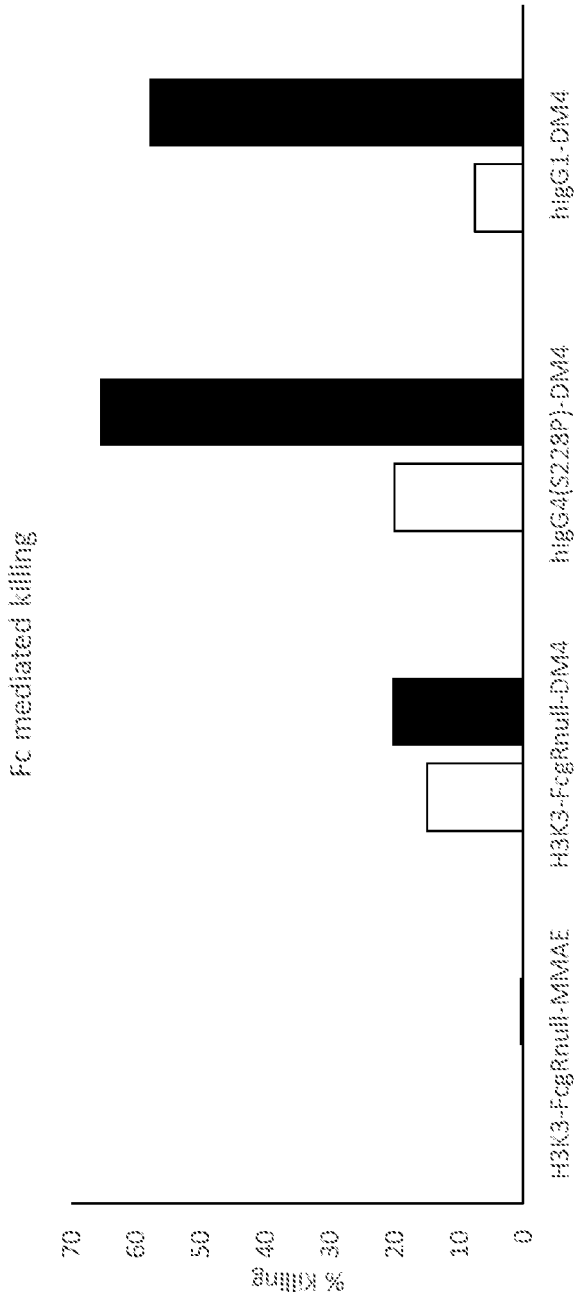
Fc mediated killing
% killing
70
60
50
40
30
20
10
0
H3K3-FcgRnull-MMAE
H3K3-FcgRnull-DM4
hIgG4(S228P)-DM4
hIgG1-DM4
CHO
CHO hCD64

FIGURE 7

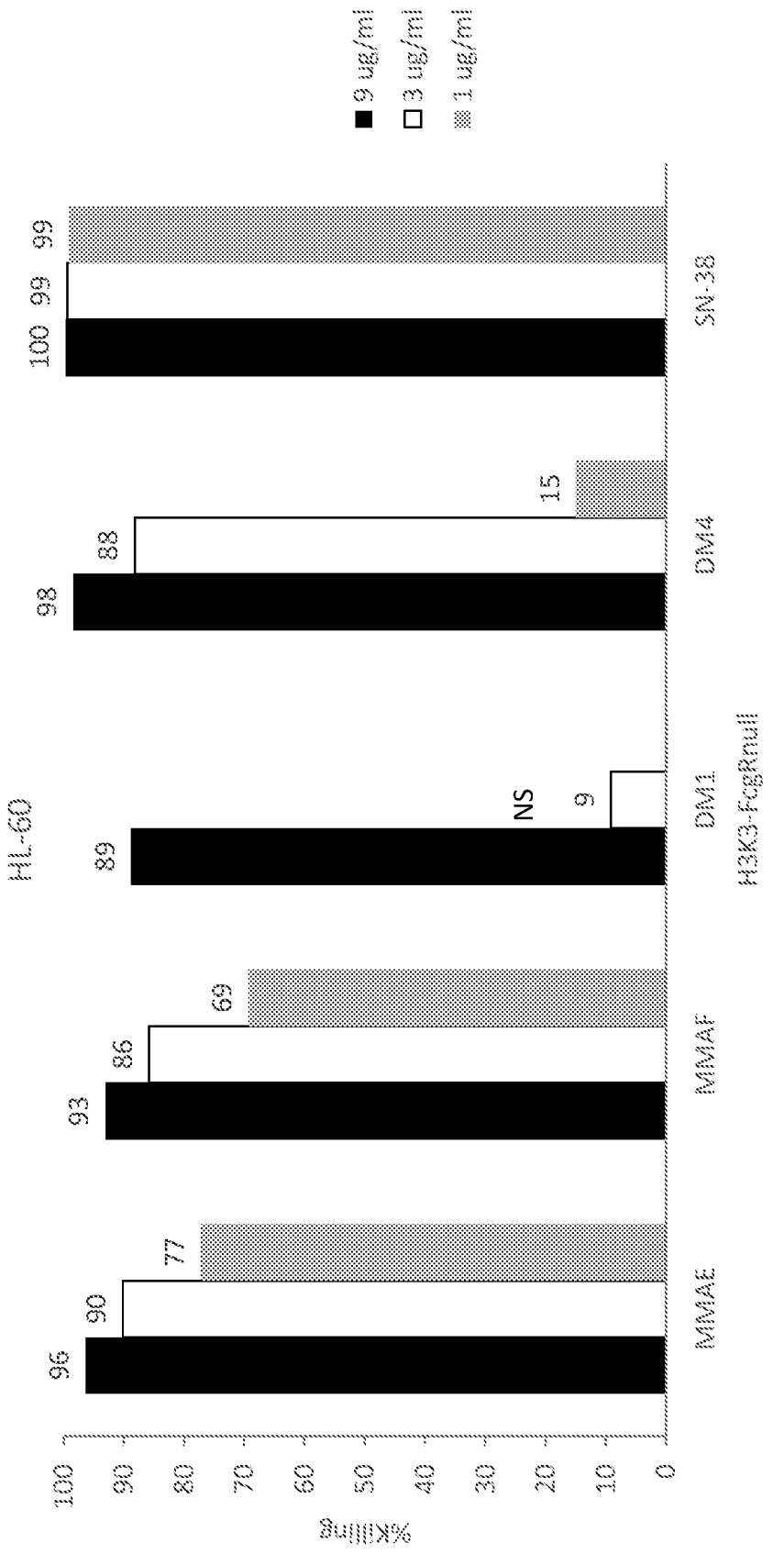
9 ug/ml
3 ug/ml
1 ug/ml
%Killing
0
10
20
30
40
50
60
70
80
90
100
HL-60
96
90
77
MMAE
93
86
69
MMAF
89
NS
9
DM1
98
88
15
DM4
100
99
99
SN-38
H3K3-FcgRnull

FIGURE 8

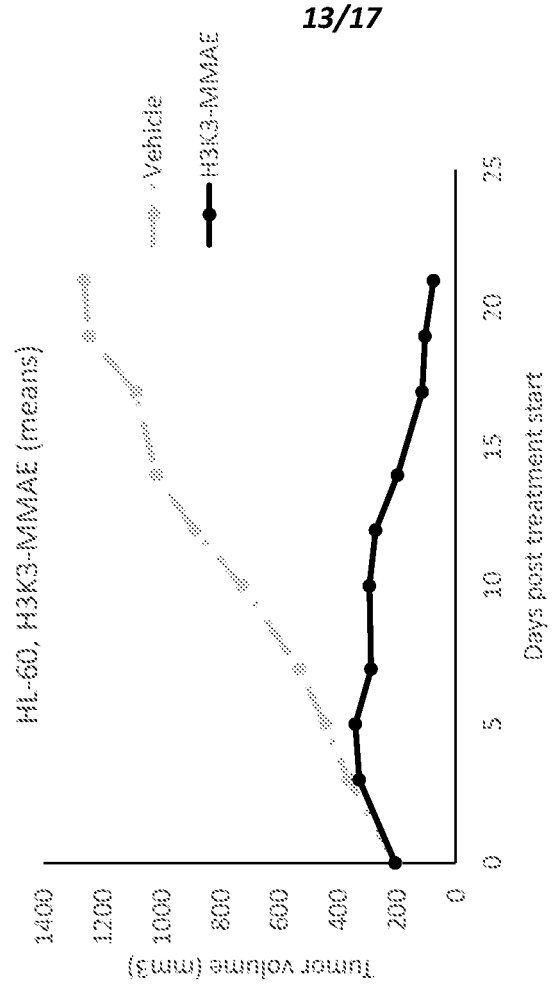

FIGURE 9B

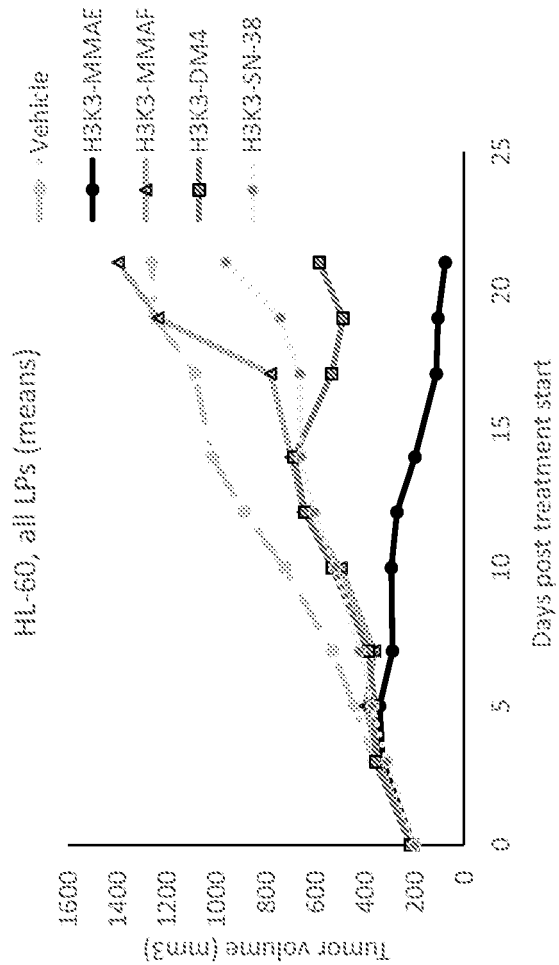

FIGURE 9A

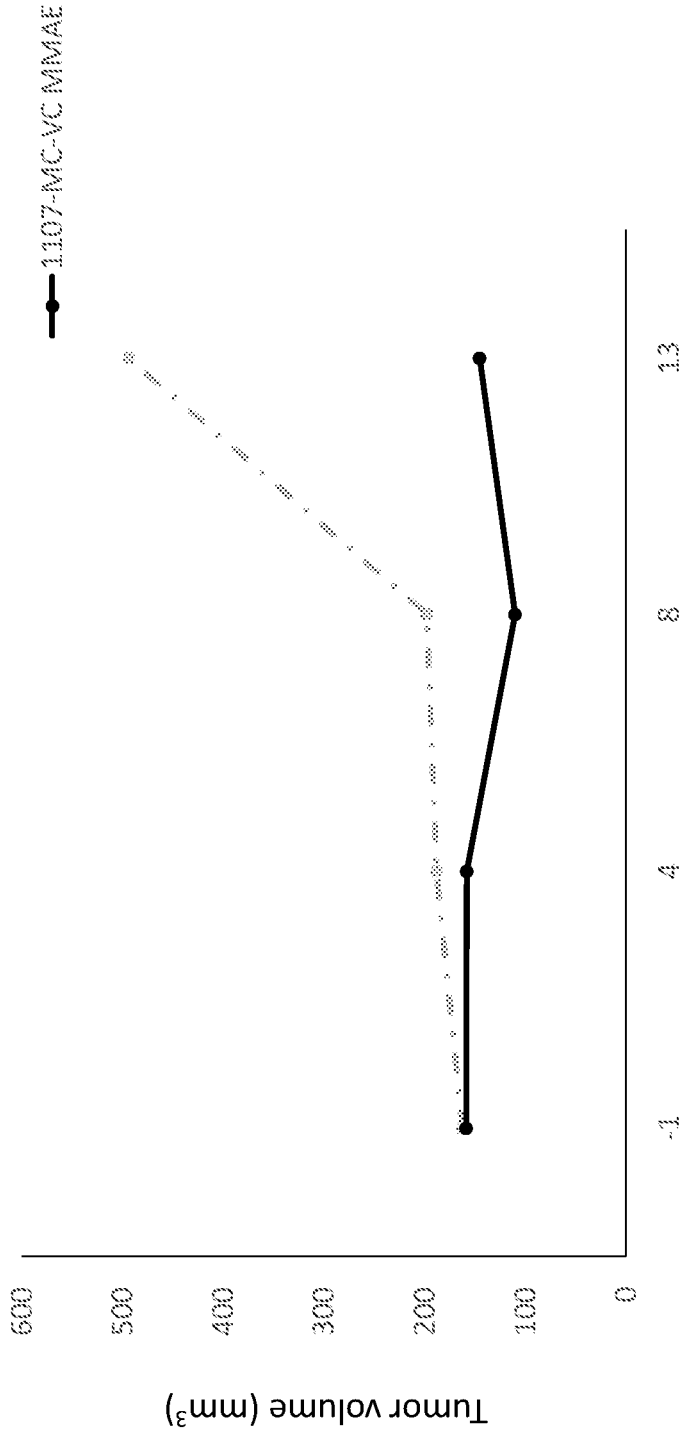
RKO (means)
Vehicle
1107-MC-VC MMAE
Tumor volume (mm³)
600
500
400
300
200
100
0
-1
4
8
13
Days post treatment start

FIGURE 10

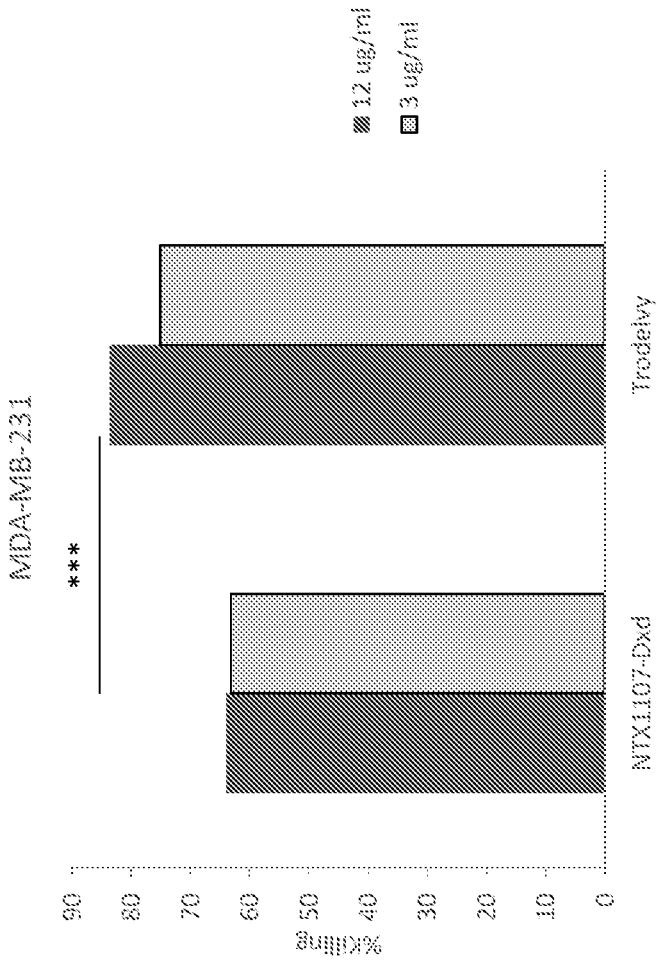
12 ug/ml
3 ug/ml
MDA-MB-231
***
%Killing
0
10
20
30
40
50
60
70
80
90
NTX1107-Dxd
Trodelvy
ADC

FIGURE 11

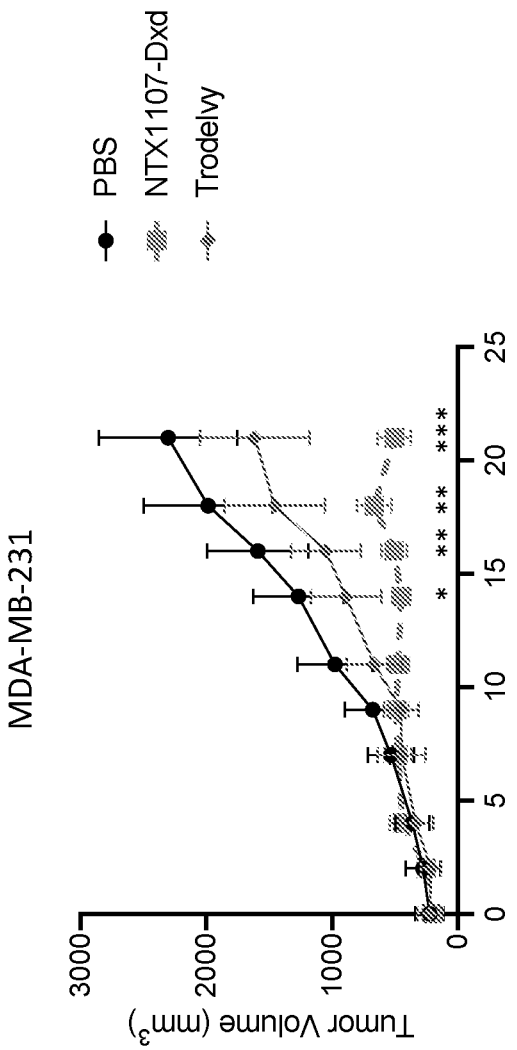
MDA-MB-231
PBS
NTX1107-Dxd
Trodelvy
Tumor Volume (mm3)
3000
2000
1000
0
0
5
10
15
20
25
Days Post Treatment Start
* ** ** ***

FIGURE 12

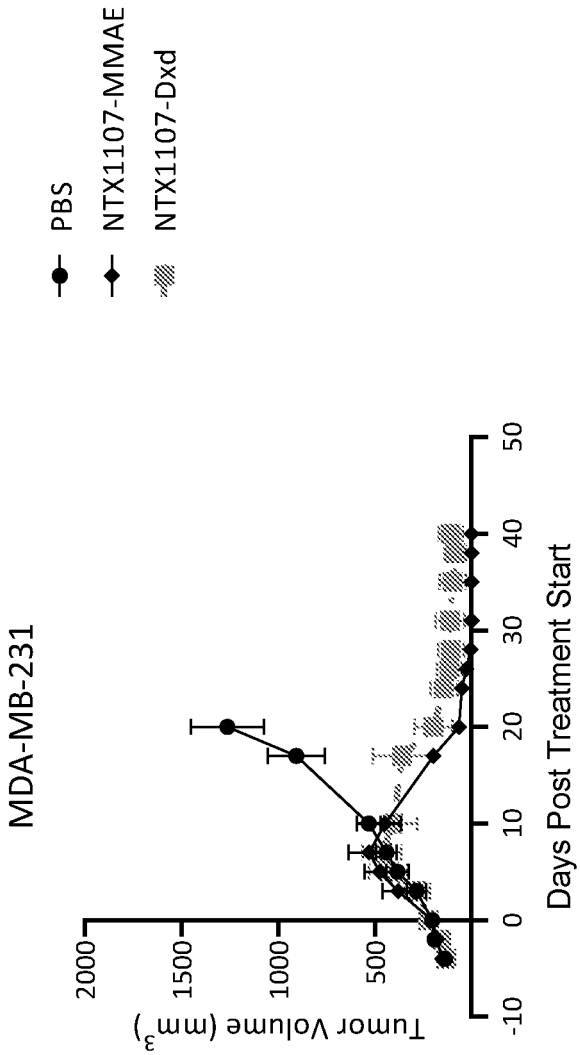
PBS
NTX1107-MMAE
NTX1107-Dxd
MDA-MB-231
Tumor Volume (mm3)
2000
1500
1000
500
-10
0
10
20
30
40
50
Days Post Treatment Start

FIGURE 13