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(54) Title: ANTI-huLRRC15 ANTIBODY DRUG CONJUGATES AND METHODS FOR THEIR USE

(57) Abstract: The present disclosure provides antibodies, antibody binding fragments, and antibody drug conjugates that bind human LRRC15, their methods of making, and their uses to treat patients having cancer.



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## ANTI-huLRRC15 ANTIBODY DRUG CONJUGATES AND METHODS FOR THEIR USE

**1. CROSS REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims the benefit under 35 U.S.C. § 119(e) of U. S. provisional application no. 62/261,114, filed November 30, 2015, and U. S. provisional application no. 62/417,489, filed November 4, 2016, the contents of both of which are incorporated herein in their entireties by reference thereto.

**2. SEQUENCE LISTING**

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on November 11, 2016, is named 381493-260WO(144358)\_SL.txt and is 106,484 bytes in size.

**3. FIELD**

[0003] The present application pertains to, among other things, anti-huLRRC15 antibodies, antibody drug conjugates (“ADCs”), compositions including the ADCs, methods of making the ADCs, and methods of using the ADCs to treat cancers.

**4. BACKGROUND**

[0004] Cancer therapies comprise a wide range of therapeutic approaches, including surgery, radiation, and chemotherapy. While the often complementary approaches allow a broad selection to be available to the medical practitioner to treat the cancer, existing therapeutics suffer from a number of disadvantages, such as a lack of selectivity of targeting cancer cells over normal, healthy cells, and the development of resistance by the cancer to the treatment.

[0005] Recent approaches based on targeted therapeutics, which interfere with cellular processes of cancer cells preferentially over normal cells, have led to chemotherapeutic regimens with fewer side effects as compared to non-targeted therapies such as radiation treatment. Nevertheless, cancers treated with targeted therapeutics may still develop resistance. For example, resistance to bevacizumab, a monoclonal antibody therapeutic that targets VEGF-positive cancer cells, has been reported in some colorectal cancers (Mesange *et al.* Oncotarget 2014; 5(13): 4709-4721).

[0006] A mechanism for treatment resistance is believed to be the formation by activated fibroblasts (*e.g.*, cancer associated fibroblasts (CAFs), mesenchymal stem cells (MSCs)) in the tumor microenvironment which prevents cancer drugs from physically reaching the cancer cells (Kalluri R., Nature Reviews Cancer 2016; 16: 582-598). In addition, the fibroblast-mediated stromal barrier is

understood to give rise to an immunosuppressive environment that can prevent immune effector cells from penetrating deep into the tumor and targeting cancer cells (Turley, S.J. *Nature Reviews Immunology* 2015; 15:669-682). Hence, a cancer drug that targets these stromal fibroblast populations within the tumor microenvironment would complement existing therapeutic strategies and may overcome chemoresistance and increase sensitivity to immune mediated therapies.

[0007] Another source of treatment resistance is thought to be the plasticity of cancer cells. For example, the plasticity of cancer cells between epithelial and mesenchymal states has been implicated as a mechanism for the generation of cancer stem cells, which can initiate tumors, as well as serve as a starting point for metastasis. See Ye, X.; Weinberg, R. A. *Trends in Cell Biology* 2015; 25 (11): 675-686. Further, mesenchymal cancer cells have been reported to be resistant to standard cancer therapies, such as docetaxel. See Singh and Settleman. *Oncogene* 2010; 29(34): 4741-4751; Ippolito, L. et al. *Oncotarget* 2016; 7 (38): 61890-61904. A cancer therapy that is effective against these resistant cancer cells would complement existing therapeutic approaches.

[0008] Thus, cancer therapeutics that spare normal cells and are less prone to developing clinical resistance would provide additional options for treating cancer, such as by augmenting existing standard of care regimens.

## 5. SUMMARY

[0009] Human LRRC15 (leucine-rich repeat-containing protein 15) is a cell surface protein that has been reported to exist in two isoforms: one containing 587 amino acids (SEQ ID NO:1; NP\_001128529.2) and another containing 581 amino acids (SEQ ID NO:3; NP\_570843.2) that is truncated at its N-terminus as compared to the longer isoform of SEQ ID NO:1. The amino acid sequences of both isoforms are illustrated in FIGS. 1A-1D. For ease of discussion, human LRRC15 is abbreviated herein as “huLRRC15.” This abbreviation is intended to refer to either isoform. In instances where a specific isoform is intended, the abbreviations “huLRRC15l” and “huLRRC15s” for the longer isoform of SEQ ID NO:1 and shorter isoform of SEQ ID NO:3, respectively, are used.

[0010] Referring to FIGS. 1C-1D (SEQ ID NO:3), huLRRC15 comprises an extracellular domain (“ECD”) spanning residues 22 to 538, a transmembrane domain (“TMD”) spanning residues 539 to 559, and an intracellular domain (“ICD”) spanning residues 560 to 581. The leader sequence of huLRRC15, illustrated in FIGS. 1A-1B (SEQ ID NO:1), is shown in bold text and the transmembrane domain underlined, thereby indicating the ECD, TMD and ICD of their isoforms. Referring again to FIGS. 1C-1D (SEQ ID NO:3), the ECD contains a proteolytic cleavage site approximately between residues Arg<sup>527</sup> and Ser<sup>528</sup>, the cleavage of which results in shedding of the portion of the ECD spanning approximately

residues 24-527 (“shed ECD” or “sECD”) from the cell surface and into the blood stream. huLRRC15 is highly expressed in the stromal microenvironment (and specifically on cancer-associated fibroblasts) of several solid tumors (*see, e.g.*, Example 4 and FIG. 7), and exhibits limited expression in normal tissue types (*see, e.g.*, Example 5 and FIG. 8). It is also expressed on certain cancer cells *per se* (*e.g.*, sarcomas, melanomas and brain cancers, *e.g.*, gliomas, such as glioblastoma). Data presented herein demonstrate, for the first time, that antibody drug conjugates (“ADCs”) that specifically target huLRRC15 exhibit potent antitumor effects against solid tumors in which huLRRC15 is expressed in the tumor stromal microenvironment, as well as on the cancer cells *per se* ((referred to herein as “huLRRC15 stromal(+)/cancer(+) tumors”). Data demonstrating *in vivo* anti-tumor efficacy of anti-huLRRC15 ADCs administered as monotherapy are provided in Example 12 and FIGS. 14A-14E. While not intending to be bound by any theory of operation, it is believed that this potent antitumor effect is mediated, at least in part, via a tumor localized concentration effect that combines direct cancer cell killing by anti-huLRRC15 ADCs as well as a targeted bystander killing effect. In addition to the localized uptake of the ADCs and subsequent release of the cytotoxic and/or cytostatic agent within the cancer cells in order to halt the growth of and/or kill the cancer cells, an indirect killing of stromal cells expressing huLRRC15 may also play a role. This potent antitumor activity is surprisingly observed with anti-LRRC15 ADCs that specifically bind the portion of the huLRRC15 ECD domain that is shed from the cell surface, and demonstrates for the first time that such anti-LRRC15 ADCs may be used therapeutically for the treatment of huLRRC15 stromal(+)/cancer(+) tumors.

[0011] Accordingly, in one aspect, the present disclosure provides ADCs that specifically bind huLRRC15 (“anti-huLRRC15 ADCs”). The anti-huLRRC15 ADCs comprise cytotoxic and/or cytostatic agents linked by way of linkers to an antigen binding moiety that specifically binds huLRRC15 at a portion of the ECD that is shed from the cell surface. The antigen binding moiety may be any moiety capable of specifically binding huLRRC15. In some embodiments, the antigen binding moiety is an antibody and/or an antibody antigen binding fragment.

[0012] Antibodies and/or binding fragments composing the anti-huLRRC15 ADCs generally comprise a heavy chain comprising a variable region ( $V_H$ ) having three complementarity determining regions (“CDRs”) referred to herein (in N→C order) as  $V_H$  CDR#1,  $V_H$  CDR#2, and  $V_H$  CDR#3, and a light chain comprising a variable region ( $V_L$ ) having three complementarity determining regions referred to herein (in N→C order) as  $V_L$  CDR#1,  $V_L$  CDR#2, and  $V_L$  CDR#3. The amino acid sequences of exemplary CDRs, as well as the amino acid sequence of the  $V_H$  and  $V_L$  regions of the heavy and light chains of exemplary anti-huLRRC15 antibodies and/or binding fragments that can be included in antigen binding moieties composing the anti-huLRRC15 ADCs are provided herein. Specific embodiments of anti-



huLRRC15 ADCs include, but are not limited to, those that comprise antibodies and/or binding fragments that include these exemplary CDRs and/or V<sub>H</sub> and/or V<sub>L</sub> sequences, as well as antibodies and/or binding fragments that compete for binding huLRRC15 with such antibodies and/or binding fragments.

**[0013]** Antibodies may be in the form of full-length antibodies, bispecific antibodies, dual variable domain antibodies, multiple chain or single chain antibodies, surrobodyes (including surrogate light chain construct), single domain antibodies, camelized antibodies, scFv-Fc antibodies, and the like. They may be of, or derived from, any isotype, including, for example, IgA (*e.g.*, IgA<sub>1</sub> or IgA<sub>2</sub>), IgD, IgE, IgG (*e.g.*, IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub> or IgG<sub>4</sub>), IgM, or IgY. In some embodiments, the anti-huLRRC15 antibody is an IgG (*e.g.*, IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub> or IgG<sub>4</sub>). Antibodies may be of human or non-human origin. Examples of non-human origin include, but are not limited to, mammalian origin (*e.g.*, simians, rodents, goats, and rabbits) or avian origin (*e.g.*, chickens). In specific embodiments, antibodies composing the anti-huLRRC15 ADCs are suitable for administration to humans, such as, for example, humanized antibodies and/or fully human antibodies.

**[0014]** Antibody antigen binding fragments composing the anti-huLRRC15 ADCs may include any fragment of an antibody capable of specifically binding huLRRC15. Specific examples of antibody antigen binding fragments that may be included in the anti-huLRRC15 ADCs include, but are not limited to, Fab, Fab', (Fab')<sub>2</sub>, Fv and scFv.

**[0015]** Antibodies and/or binding fragments composing the anti-huLRRC15 ADCs may include modifications and/or mutations that alter the properties of the antibodies and/or fragments, such as those that increase half-life, increase or decrease ADCC, *etc.*, as is known in the art.

**[0016]** For therapeutic uses, it may be desirable to utilize anti-huLRRC15 ADCs that bind huLRRC15 with an affinity of at least 100 nM. Accordingly, in some embodiments, the anti-huLRRC15 ADCs comprise an anti-huLRRC15 antibody and/or anti-huLRRC15 binding fragment that binds huLRRC15 with an affinity of at least about 100 nM, or even higher, for example, at least about 90 nM, 80 nM, 70 nM, 60 nM, 50 nM, 40 nM, 30 nM, 25 nM, 20 nM, 15 nM, 10 nM, 7 nM, 6 nM, 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.1 nM, 0.01 nM, or greater. Affinity of anti-huLRRC15 antibodies and/or binding fragments can be determined using techniques well known in the art or described herein, such as for example, ELISA, isothermal titration calorimetry (ITC), surface plasmon resonance, flow cytometry, or fluorescent polarization assay.

**[0017]** The cytotoxic and/or cytostatic agents composing the anti-huLRRC15 ADCs may be any agents known to inhibit the growth and/or replication of, and/or kill cells. Numerous agents having cytotoxic and/or cytostatic properties are known in the literature. Non-limiting examples of classes of cytotoxic

and/or cytostatic agents include, by way of example and not limitation, cell cycle modulators, apoptosis regulators, kinase inhibitors, protein synthesis inhibitors, alkylating agents, DNA cross-linking agents, intercalating agents, mitochondria inhibitors, nuclear export inhibitors, topoisomerase I inhibitors, topoisomerase II inhibitors, RNA/DNA antimetabolites and antimitotic agents.

[0018] As will be discussed in more detail in the Detailed Description, and while not intending to be bound by any particular theory of operation, data included herein demonstrate that anti-huLRRC15 ADCs exert potent anti-tumor activities mediated, at least in part, by a concentration effect that localizes the anti-huLRRC15 ADCs to the desired site of action. For example, it is demonstrated herein that anti-huLRRC15 ADCs possess significantly greater *in vitro* LRRC15-expressing cell killing activity as compared with a non-targeted isotype control ADC (*see, e.g.*, Examples 10 and 11, and FIGS. 13A-13F). Specifically, the *in vitro* cell killing of huLRRC15 expressing cancer cell lines is demonstrated for huLRRC15-ADCs containing the microtubule inhibitor monomethyl auristatin E (“MMAE”) and DNA minor groove-binding agent pyrrolobenzodiazepine (“PBD”) (*see, e.g.*, Example 10, Example 11 and FIGS. 13A-13F). Additionally, an anti-huLRRC15 ADC comprising the microtubule inhibitor monomethyl auristatin E (“MMAE”) linked to an anti-huLRRC15 antibody by way of linkers cleavable by lysosomal enzymes potentially inhibits and/or kills huLRRC15 stromal(+)/cancer(+) tumors (FIGS. 14A-14E), yet does not significantly inhibit or kill more weakly huLRRC15-expressing osteosarcomas in a manner greater than isotype control ADC (*see, e.g.*, Example 12 and FIG. 14F). Together, these data indicate that anti-huLRRC15 ADCs may be used to localize a cytostatic and/or cytotoxic agent to the LRRC15(+) stromal and cancer cells in order to potentially inhibit huLRRC15 stromal(+)/cancer(+) tumors via two different mechanisms of action, or a combination of both mechanisms: a first mechanism in which the cytotoxic and/or cytostatic agents composing the anti-huLRRC15 ADCs are cytotoxic and/or cytostatic to the huLRRC15-expressing stromal cells and cancer cells *per se*, thereby disrupting and/or destroying the stromal microenvironment crucial to support and/or growth of the huLRRC15 stromal(+)/cancer(+) tumor as well as direct killing of the cancer cells; and a second mechanism in which the cytotoxic and/or cytostatic agents composing the anti-huLRRC15 ADCs are not necessarily cytotoxic and/or cytostatic to the huLRRC15-expressing stromal cells, but are cytostatic and/or cytotoxic to the rapidly dividing huLRRC15-expressing cancer cells. Skilled artisans will appreciate that for this latter mechanism of action, the cytotoxic and/or cytostatic agents composing the anti-huLRRC15 ADCs, once cleaved from the anti-huLRRC15 ADCs, should be capable of traversing cell membranes. For the former mechanism of action, the cytotoxic and/or cytostatic agents, once cleaved from the anti-huLRRC15 ADC, need not be capable of traversing cell membranes. Cytotoxic and/or cytostatic agents having hydrophobicities sufficient to traverse cell membranes such that they are useful for inhibiting and/or

killing tumors via a targeted bystander effect may be identified using routine methods known to those of skill in the art. Cytotoxic and/or cytostatic agents having hydrophobicities such that they are capable of traversing cell membranes and permeating into cells are referred to herein as “cell-permeating cytotoxic and/or cytostatic agents.”

**[0019]** Skilled artisans will also appreciate that the above two mechanisms of action are not mutually exclusive, and that in some embodiments it may be desirable to utilize anti-huLRRC15 ADCs capable of exerting antitumor activity against huLRRC15 stromal(+)/cancer(+) tumors via both mechanisms of action. As a specific example, such an anti-huLRRC15 ADC may include a cell-permeating cytotoxic and/or cytostatic agent that is cytotoxic and/or cytostatic to both huLRRC15-expressing stromal cells and huLRRC15-expressing cancer tumor cells linked to an anti-huLRRC15 antibody by way of a cleavable linker. As another specific embodiment, such an anti-huLRRC15 ADC may include two different cytotoxic and/or cytostatic agents: a first that is cytotoxic and/or cytostatic to the huLRRC15-expressing stromal cells (and optionally, but not necessarily, also cytotoxic and/or cytostatic to the huLRRC15 cancer(+) tumor cells); and a second that is cytotoxic and/or cytostatic to the huLRRC15-expressing cancer cells. The first agent could be, but need not be, a cell-permeating cytotoxic and/or cytostatic agent, and could be, but need not be, linked to the antigen binding moiety of the anti-huLRRC15 ADC by way of a cleavable linker. The second agent is a cell-permeating cytotoxic and/or cytostatic agent and is linked to the antigen binding moiety of the anti-huLRRC15 ADC by way of a cleavable linker.

**[0020]** In a specific embodiment, a cytotoxic and/or cytostatic agent composing an anti-huLRRC15 ADC is a cell-permeating antimitotic agent, such as, for example, an auristatin. Specific examples of cell-permeating auristatins include, but are not limited to, dolastatin-10 and monomethyl auristatin E (“MMAE”). In another specific embodiment, a cytotoxic and/or cytostatic agent composing an anti-huLRRC15 ADC is a cell-permeating DNA cross-linking agent, such as a cell-permeating minor groove-binding DNA cross-linking agent. Specific examples of cell-permeating DNA minor groove-binding agents include, but are not limited to, pyrrolobenzodiazepines (“PBD”) and PBD dimers.

**[0021]** The linkers linking the cytotoxic and/or cytostatic agents to the antigen binding moiety of an anti-huLRRC15 ADC may be long, short, flexible, rigid, hydrophilic or hydrophobic in nature, or may comprise segments that have different characteristics, such as segments of flexibility, segments of rigidity, *etc.* The linker may be chemically stable to extracellular environments, for example, chemically stable in the blood stream, or may include linkages that are not stable and release the cytotoxic and/or cytostatic agents in the extracellular milieu. In some embodiments, the linkers include linkages that are designed to release the cytotoxic and/or cytostatic agents upon internalization of the anti-huLRRC15

ADC within the cell. In some specific embodiments, the linkers includes linkages designed to cleave and/or immolate or otherwise breakdown specifically or non-specifically inside cells. A wide variety of linkers useful for linking drugs to antigen binding moieties such as antibodies in the context of ADCs are known in the art. Any of these linkers, as well as other linkers, may be used to link the cytotoxic and/or cytostatic agents to the antigen binding moiety of the anti-huLRRC15 ADCs described herein.

[0022] The number of cytotoxic and/or cytostatic agents linked to the antigen binding moiety of an anti-huLRRC15 ADC can vary (called the “drug-to-antibody ratio,” or “DAR”), and will be limited only by the number of available attachments sites on the antigen binding moiety and the number of agents linked to a single linker. Typically, a linker will link a single cytotoxic and/or cytostatic agent to the antigen binding moiety of an anti-huLRRC15 ADC. In embodiments of anti-huLRRC15 ADCs which include more than a single cytotoxic and/or cytostatic agent, each agent may be the same or different. As long as the anti-huLRRC15 ADC does not exhibit unacceptable levels of aggregation under the conditions of use and/or storage, anti-huLRRC15 ADCs with DARs of twenty, or even higher, are contemplated. In some embodiments, the anti-huLRRC15 ADCs described herein may have a DAR in the range of about 1-10, 1-8, 1-6, or 1-4. In certain specific embodiments, the anti-huLRRC15 ADCs may have a DAR of 2, 3 or 4.

[0023] In some embodiments, the anti-huLRRC15 ADCs are compounds according to structural formula (I):



or salts thereof, where each “D” represents, independently of the others, a cytotoxic and/or cytostatic agent; each “L” represents, independently of the others, a linker; “Ab” represents an anti-huLRRC15 antigen binding moiety, such as an anti-huLRRC15 antibody or binding fragment; each “XY” represents a linkage formed between a functional group  $R^x$  on the linker and a “complementary” functional group  $R^y$  on the antigen binding moiety; and  $n$  represents the DAR of the anti-huLRRC15 ADC. In a specific exemplary embodiment, the anti-huLRRC15 ADCs are compounds according to structural formula (I) in which each “D” is the same and is either a cell-permeating auristatin (for example, dolastatin-10 or MMAE) or a cell-permeating minor groove-binding DNA cross-linking agent (for example, a PBD or a PBD dimer); each “L” is the same and is a linker cleavable by a lysosomal enzyme; each “XY” is a linkage formed between a maleimide and a sulfhydryl group; “Ab” is an antibody comprising six CDRs corresponding to the six CDRs of antibody huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD210.40.9 or muAD209.9.1, or an antibody that competes for binding huLRRC15 with such an antibody; and  $n$  is 2, 3 or 4. In a specific embodiment of this exemplary embodiment or the anti-

huLRRC15 ADCs of structural formula (I), “Ab” is a humanized antibody, for example, a humanized antibody comprising V<sub>H</sub> and V<sub>L</sub> chains corresponding to the V<sub>H</sub> and V<sub>L</sub> chains of antibody huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, or hu139.10. In another specific embodiment of this exemplary embodiment or the anti-huLRRC15 ADCs of structural formula (I), Ab is a humanized antibody selected from huM25, huM25-S239C, huAD208.4.1, huAD208.4.1-S239C, huAD208.12.1, huAD208.14.1 and hu139.10.

[0024] In another aspect, the present disclosure provides compositions including the anti-huLRRC15 ADCs. The compositions generally comprise one or more anti-huLRRC15 ADCs as described herein, and/or salts thereof, and one or more excipients, carriers or diluents. The compositions may be formulated for pharmaceutical use, or other uses. In one specific embodiment, the composition is formulated for pharmaceutical use and comprises an anti-huLRRC15 ADC according to structural formula (I) or any of the specific exemplary embodiments thereof, and one or more pharmaceutically acceptable excipients, carriers or diluents.

[0025] Compositions formulated for pharmaceutical use may be packaged in bulk form suitable for multiple administrations, or may be packaged in the form of unit doses suitable for a single administration. Whether packaged in bulk or in the form of unit doses, the composition may be presented in dry form, such as a lyophilate, or in liquid form. Unit dosage liquid compositions may be conveniently packaged in the form of syringes pre-filled with a quantity of anti-huLRRC15 ADC suitable for a single administration.

[0026] Also provided are unconjugated anti-huLRRC15 antibodies and/or binding fragments. Such antibodies may be used in a variety of contexts *in vitro* and *in vivo*, including, by way of example and not limitation, as cellular stains for biological assays and as diagnostic agents to monitor treatment of huLRRC15 stromal(+)/cancer(+) tumors, whether the treatment is with anti-huLRRC15 ADCs or other agents, or a combination of agents. The anti-huLRRC15 antibodies and/or binding fragments may be labeled with moieties to aid detection in diagnostic or other assays, or may be unlabeled. Suitable labels include, by way of example and not limitation, isotopic labels, fluorescent labels, chemiluminescent labels, substrates for enzymes or other binding molecules, *etc.* Exemplary embodiments of anti-huLRRC15 antibodies and/or binding fragments include the various exemplary anti-huLRRC15 antibodies and/or binding fragments described herein in connection with the anti-huLRRC15 antibodies and/or binding fragments described herein in connection with the anti-huLRRC15 ADCs.

[0027] Also provided are polynucleotides encoding antigen binding moieties (for example antibodies and/or binding fragments) that compose the anti-huLRRC15 ADCs described herein, host cells

transformed or transfected with the polynucleotides, and compositions and methods useful for making the various anti-huLRRC15 ADCs described herein.

[0028] As noted above, anti-huLRRC15 ADCs including cell-permeating cytotoxic and/or cytostatic agents exhibit potent antitumor activity against huLRRC15 stromal(+)/cancer(+) tumors that is believed to be mediated, at least in part, by a targeted bystander killing effect, and that this potent antitumor activity is observed with anti-huLRRC15 ADCs that specifically bind the portion of the huLRRC15 ECD that can be shed from the cell surface. This is surprising, as the shed ECD is available as a “sink” or “decoy” for the anti-huLRRC15 ADCs, thereby interfering with their ability to bind and become internalized into huLRRC15-expressing cells. Data provided herein demonstrate, for the first time, that ADCs targeting huLRRC15 may be used therapeutically for the treatment of huLRRC15 stromal(+)/cancer(+) tumors.

[0029] Accordingly, in another aspect, the present disclosure provides methods of using anti-huLRRC15 ADCs therapeutically for the treatment of huLRRC15 stromal(+)/cancer(+) tumors. The methods generally involve administering to a human patient having a huLRRC15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit. Human LRRC15 stromal(+)/cancer(+) tumors that can be beneficially treated with anti-huLRRC15 ADCs include, but are not limited to brain cancers (*e.g.*, gliomas, *e.g.*, glioblastoma), sarcomas (*e.g.*, osteosarcoma, soft tissue sarcoma, liposarcoma, leiomyosarcoma, synovial sarcoma, rhabdomyosarcoma, fibrosarcoma, malignant fibrous histiocytoma, epithelioid sarcoma, Ewing’s sarcoma, gastrointestinal stromal tumor (GIST), undifferentiated pleiomorphic sarcoma, undifferentiated spindle cell sarcoma, chondrosarcoma, mesenchymoma, malignant peripheral nerve sheath tumor, vascular sarcoma, Kaposi’s sarcoma, uterine sarcoma), and melanomas. The cancer may be newly diagnosed and naïve to treatment, or may be relapsed, refractory, or relapsed and refractory, or a metastatic form of a huLRRC15 stromal(+)/cancer(+) tumor.

[0030] The anti-huLRRC15 ADCs may be administered as single therapeutic agents (monotherapy) or adjunctively with or to other anti-cancer treatments and/or therapeutic agents, typically but not necessarily those used to treat the type of huLRRC15 stromal(+)/cancer(+) tumors being treated. Indeed, data presented herein demonstrate that tumors that exhibit resistance to other targeted or non-targeted chemotherapies, retain sensitivity to anti-huLRRC15 ADCs (*see, e.g.*, Example 15 and FIGS. 18A-18D). While not wishing to be bound by theory, one possible mechanism of action of the anti-huLRRC15 ADCs of the disclosure may be the killing of cancer cells that exhibit mesenchymal-like properties which lend them resistance to standard therapies. Accordingly, the anti-huLRRC15 ADCs described herein provide significant benefits over current targeted and non-targeted approaches toward the treatment of huLRRC15

stromal(+)/cancer(+) tumors. Adjunctive therapies and/or therapeutic agents typically will be used at their approved dose, route of administration, and frequency of administration, but may be used at lower dosages and/or less frequently. When administered as monotherapy, the anti-huLRRC15 ADC will typically be administered on a schedule that balances patient convenience and therapeutic benefit. It is contemplated that anti-huLRRC15 ADCs administered once a week, once every two weeks, once every three weeks, once every four weeks, once every five weeks, once every six weeks, once every seven weeks or once every eight weeks will provide therapeutic benefit, although more or less frequent administration may be beneficial. When administered adjunctive to or with another therapy and/or agent, the anti-huLRRC15 ADC may be administered before, after or concurrently with the other therapy or agent.

[0031] The anti-huLRRC15 ADCs may be administered via a variety of routes or modes of administration, including but not limited to, intravenous infusion and/or injection and subcutaneous injection. The amount administered will depend upon the route of administration, the dosing schedule, the type of cancer being treated, the stage of the cancer being treated, and other parameters such as the age and weight of the patient, as is well known in the art. Specific exemplary dosing schedules expected to provide therapeutic benefit are provided in the Detailed Description. Generally, an amount of anti-huLRRC15 ADC in the range of about 0.01 to 10 mg/kg when administered intravenously on a weekly basis from once weekly to and including once every eight weeks is expected to provide therapeutic benefit.

## 6. BRIEF DESCRIPTION OF THE FIGURES

[0032] FIGS. 1A-1D provide the amino acid sequences of the two reported isoforms of human LRRC15, and the corresponding DNA sequences encoding each. FIGS. 1A-1B show the encoding DNA sequence (SEQ ID NO:2) and amino acid sequence (SEQ ID NO:1) for longer huLRRC15 isoform 1: FIG. 1A corresponds to coding DNA residues 1-1020; FIG. 1B corresponds to coding DNA residues 1021-1761. FIGS. 1C-1D show the encoding DNA sequence (SEQ ID NO:4) and amino acid sequence (SEQ ID NO:3) for shorter huLRRC15 isoform 2: FIG. 1C corresponds to coding DNA residues 1-1020; FIG. 1D corresponds to coding DNA residues 1021-1743. The predicted signal peptide is indicated in bold italics; the predicted protease cleavage site is boxed; and the predicted transmembrane domain is underlined.

[0033] FIG. 2A provides the amino acid sequences of the V<sub>H</sub> chains of antibodies huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD210.40.9 and muAD209.9.1. The CDRs are underlined.

[0034] FIG. 2B provides the amino acid sequences of the V<sub>L</sub> chains of antibodies huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD210.40.9 and muAD209.9.1. The CDRs are underlined.

[0035] FIG. 3A provides the amino acid sequence of the heavy chain of antibody huM25 (SEQ ID NO:18). The CDRs are underlined, and the constant region (Fc gamma) is italicized. Linear amino acid sequence numbering is shown.

[0036] FIG. 3B provides the amino acid sequence of the light chain of antibody huM25 (SEQ ID NO:19). The CDRs are underlined, and the constant region (kappa) is italicized. Linear amino acid sequence numbering is shown.

[0037] FIG. 4 provides a graph illustrating the ability of various exemplary anti-huLRRC15 antibodies having CDRs that may be included in anti-huLRRC15 ADCs to bind to cells expressing huLRRC15.

[0038] FIG. 5 provides a graph illustrating the ability of various exemplary anti-huLRRC15 antibodies having CDRs that may be included in anti-huLRRC15 to bind the extracellular domain (ECD) of huLRRC15.

[0039] FIGS. 6A and 6B together provide results of antibody competition assays illustrating that exemplary anti-huLRRC15 antibodies having CDRs that may be included in anti-huLRRC15 ADCs bind different epitopes on huLRRC15. FIG. 6A shows binding competition of muM25, huM25, hu139.10 or isotype antibodies against muM25-AF488; FIG. 6B shows binding competition of muM25, muAD208.4.1, muAD208.12.1, muAD208.14.1, muAD209.9.1 or isotype antibodies against muM25-AF488.

[0040] FIG. 7 provides pictures of immunohistochemistry (IHC) and immunofluorescence (IF) stained tissues illustrating that huLRRC15 is highly expressed in various solid tumors.

[0041] FIG. 8 provides pictures of IHC stained tissues illustrating that huLRRC15 is either not expressed, or only minimally expressed, on various normal tissue types.

[0042] FIG. 9A depicts huLRRC15 expression levels as measured by Western blot analysis in a patient-derived breast cancer-associated fibroblast (CAF) lysate, or in commercially available patient-derived mesenchymal stem cell (MSC) lysates from bone marrow, in the absence (-) or presence (+) of 10 ng/mL TGFβ. Anti-huLRRC15 antibody used for detection was muAD210.40.9.

[0043] FIGS. 9B-9C depict huLRRC15 expression in commercial mesenchymal stem cell (MSC) lines, with and without 10 ng/mL TGFβ, as measured by flow cytometry: FIG. 9B depicts huLRRC15 expression as compared with isotype in human BM-MSC cells (Lonza); FIG. 9C depicts huLRRC15 expression as compared with isotype in murine Balb/c BM-MSC cells (Cyagen). Anti-huLRRC15 antibody used for detection was AF647-labeled huM25.



[0044] FIG. 10 depicts expression levels of huLRRC15, Snail, TCF8/ZEB1, N-Cadherin, E-Cadherin, and GAPDH as determined by Western blot analysis of A549 lung cancer or PANC1 pancreatic cancer cells with 5 day treatment of 10 ng/mL TGF $\beta$ , StemXVivo™ EMT Inducing Media Supplement (R&D Systems, “EMT Kit”), or control. Anti-LRRC15 antibody used for detection was muAD210.40.9; all other antibodies were obtained from the EMT Antibody Panel (Cell Signaling Technology).

[0045] FIG. 11A depicts protein expression as determined by fluorescence in A549 lung cancer or PANC1 pancreatic cancer cells after 5 day treatment of 10 ng/mL TGF $\beta$ , StemXVivo™ EMT Inducing Media Supplement (R&D Systems, “EMT Kit”), or control. Fluorescence using AF647-labeled isotype (“Isotype-AF647”), AF647-labeled huM25 (“huM25-AF647”), PE-labeled isotype (“Isotype-PE”), and PE-labeled anti-EpCAM (“anti-EPCAM-PE”) antibodies is shown.

[0046] FIG. 11B depicts microscopy images of A549 cells after continued treatment of 10 ng/mL TGF $\beta$  over 9 days (upper left, “continued treatment”), or treatment with 10 ng/mL TGF $\beta$  for 5 days followed by washout and culturing in the absence of TGF $\beta$  for an additional 4 days (lower left, “discontinued treatment”). Flow cytometry (middle and right graphs) depicts huLRRC15 (upper and lower middle) and EpCAM (upper and lower right) levels after continued treatment, discontinued treatment, or control. Anti-huLRRC15 antibody huM25-AF647 was used in the analysis.

[0047] FIG. 11C depicts protein expression as determined by fluorescence in A549 lung cancer (left graphs) or PANC1 pancreatic cancer cells (right graphs) after 9 day continued treatment of 10 ng/mL TGF $\beta$  or StemXVivo™ EMT Inducing Media Supplement (R&D Systems, “EMT Kit”), or treatment with TGF $\beta$  or EMT Kit for 5 days followed by washout and culturing for an additional 4 days. Top panels depict huLRRC15 levels; bottom panels depict EpCAM levels.

[0048] FIG. 12 provides chromatograms of ADC preparations. The top panel illustrates a chromatographic resolution of a conjugation carried out according to Example 8. Several peaks are present, corresponding to antibodies having zero (“DAR0”), two (“DAR2”), four (“DAR4”), six (“DAR6”) and eight (“DAR8”) linked cytostatic and/or cytotoxic agents. The preparation has an average DAR of 4. This crude average DAR4 preparation was subjected to hydrophobic interaction chromatography to isolate the peak corresponding to DAR2. The chromatogram of the resultant preparation enriched in DAR2 (referred to herein as an “E2” preparation) is shown in the bottom panel. The enriched E2 ADC preparation is approximately 98% pure in ADCs having a DAR of 2.

[0049] FIGS. 13A-13J provide graphs showing potent *in vitro* cell killing abilities of exemplary anti-huLRRC15 ADCs against a variety of LRRC15-expressing cells. FIG. 13A depicts the effects of anti-huLRRC15 huM25 antibody and MMAE ADCs on the viability of U118MG glioblastoma cells. FIG.

13B depicts the effects of anti-huLRRC15 huM25 antibody and MMAE ADCs on the viability of RPMI-7951 melanoma cells. FIG. 13C depicts the effects of anti-huLRRC15 huM25 antibody and MMAE ADCs on the viability of G292 clone A141B1 osteosarcoma cells. FIG. 13D depicts the effects of anti-huLRRC15 huM25 antibody and MMAE ADCs on the viability of EBC-1 squamous cell non small cell lung cancer (NSCLC) cells. FIG. 13E depicts the effects of anti-huLRRC15 PBD ADCs and isotype PBD ADCs on the viability of U118MG glioblastoma cells. FIG. 13F depicts the effects of anti-huLRRC15 PBD ADCs and isotype PBD ADCs on the viability of RPMI-7951 melanoma cells. FIG. 13G shows *in vitro* cell killing in LRRC15 transfected 3T12 cells by isotype-S239C-PBD-E2 (solid line) or huM25-S239C-PBD-E2 (dashed line). FIG. 13H shows *in vitro* cell killing in human BM-MS (Lonza) mesenchymal stem cells in the presence of 10 ng/mL TGF $\beta$  by isotype-PBD-DAR2 or huAD208.4.1-PBD-DAR2. FIG. 13I shows *in vitro* cell killing in murine Balb/c BM-MS (Cyagen) mesenchymal stem cells in the presence of 10 ng/mL TGF $\beta$  by isotype-PBD-DAR2 or huAD208.4.1-PBD-DAR2. FIG. 13J shows *in vitro* cell killing in A549 lung cancer cells (top graph) or A549 cells that have undergone epithelial to mesenchymal transition (EMT) in the presence of 10 ng/mL TGF $\beta$  (bottom graph) by isotype-S239C-PBD-E2, huM25-S239C-PBD-E2, or huM25-S239C antibody. Y-axis shows percent cell viability; x-axis shows antibody or ADC concentration in nM.

[0050] FIGS. 14A-14E provide graphs demonstrating the potent *in vivo* efficacy of exemplary anti-huLRRC15 ADCs against a variety of stromal(+)/cancer(+) tumors. In the graphs, arrows indicate dosing days. Also shown are pictures illustrating LRRC15 expression on cancer cells as assessed by IHC in an untreated xenograft tumor of 100-800 mm<sup>3</sup> in volume, representative for each xenograft model. FIG. 14A demonstrates *in vivo* activity of huM25-vcMMAE-E2 in U118MG xenografts; FIG. 14B demonstrates *in vivo* activity of huM25-vcMMAE-E2 in patient-derived CTG-0241 xenografts; FIG. 14C demonstrates *in vivo* activity of huM25-vcMMAE-E2 in patient-derived CTG-1095 xenografts; FIG. 14D demonstrates *in vivo* activity of huM25-vcMMAE-DAR4 and hu139.10-vcMMAE-DAR4 in U118MG xenografts; FIG. 14E demonstrates *in vivo* activity of huM25-vcMMAE-DAR4, huAD208.4.1-vcMMAE-DAR4 and huAD208.14.1-vcMMAE-DAR4 in U118MG xenografts.

[0051] FIG. 14F provides a graph illustrating that huM25-vcMMAE-DAR4 is not statistically more active *in vivo* compared to isotype control against xenografts generated with Saos-2 osteosarcoma cells. Arrows indicate dosing days. Also shown is a representative IHC picture illustrating LRRC15 expression on cancer cells for this xenograft model.

[0052] FIG. 15 provides a graph demonstrating that U118MG tumors that regrow following treatment with exemplary anti-huLRRC15 ADC huM25-vcMMAE-DAR4 retain expression of huLRRC15, and

therefore retain sensitivity to anti-huLRRC15 ADCs. Arrows represent dosing days. Also shown are pictures illustrating LRRC15 expression on cancer cells, as assessed by IHC, in a representative untreated U118MG xenograft tumor.

[0053] FIGS. 16A and 16B provide data demonstrating that, on an equivalent drug basis, E2 enriched preparations of anti-huLRRC15 ADCs are better tolerated than higher loaded E4 preparations when assessed by survival (FIG. 16A) or weight loss (FIG. 16B). Arrows represent dosing days.

[0054] FIG. 17 provides data demonstrating that, on an equivalent drug basis, E2 enriched preparations of anti-huLRRC15 ADCs have higher efficacy against U118MG xenografts than higher drug loaded ADC preparations (*e.g.*, E4 or DAR4). Arrows represent dosing days. Also shown is a representative IHC picture illustrating LRRC15 expression on cancer cells for this xenograft model.

[0055] FIGS. 18A-18D provides data demonstrating the *in vivo* efficacy of exemplary anti-huLRRC15 ADCs are statistically significantly higher than comparison chemotherapeutics across multiple stromal(+)/cancer(+) tumors. In the graphs, arrows represent dosing days. Also shown are pictures illustrating LRRC15 expression on cancer cells as assessed by IHC in an untreated tumor of 100-800 mm<sup>3</sup> in volume, representative for each xenograft model. FIG. 18A shows the effect of huM25-vcMMAE-E2 in comparison to isotype antibody or temozolomide in U118MG xenografts; FIG. 18B shows the effect of huM25-vcMMAE-E2 in comparison with isotype antibody, isotype ADC, cisplatin, doxorubicin, gemcitabine, or ifosfamide in CTG-0241 osteosarcoma patient-derived xenografts; FIG. 18C shows the effect of huM25-vcMMAE-E2 in comparison with isotype antibody, isotype ADC or cisplatin in CTG-1095 osteosarcoma patient-derived xenografts; FIG. 18D shows the effect of huM25-vcMMAE-E2 or gemcitabine, alone or in combination, in comparison with isotype antibody or isotype-vcMMAE-E2 ADC in CTG-1095 osteosarcoma patient-derived xenografts.

## 7. DETAILED DESCRIPTION

[0056] The present disclosure concerns antibody drug conjugates that specifically bind human LRRC15, compositions comprising the ADCs, anti-huLRRC15 antibodies and/or binding fragments that can compose the ADCs, polynucleotides encoding anti-huLRRC15 antibodies and/or binding fragments that compose the ADCs, host cells capable of producing the antibodies and/or binding fragments, methods and compositions useful for making the antibodies, binding fragments and ADCs, and various methods of using the ADCs.

[0057] As will be appreciated by skilled artisans, antibodies and/or binding fragments are “modular” in nature. Throughout the disclosure, various specific embodiments of the various “modules” composing

the antibodies and/or binding fragments are described. As specific non-limiting examples, various specific embodiments of V<sub>H</sub> CDRs, V<sub>H</sub> chains, V<sub>L</sub> CDRs and V<sub>L</sub> chains are described. It is intended that all of the specific embodiments may be combined with each other as though each specific combination were explicitly described individually.

[0058] The ADCs disclosed herein are also “modular” in nature. Throughout the disclosure, various specific embodiments of the various “modules” composing the ADCs are described. As specific non-limiting examples, specific embodiments of antibodies, linkers, and cytotoxic and/or cytostatic agents that may compose the ADCs are described. It is intended that all of the specific embodiments described may be combined with each other as though each specific combination were explicitly described individually.

[0059] It will also be appreciated by skilled artisans that the various ADCs described herein may be in the form of salts, and in some specific embodiments, pharmaceutically acceptable salts. The ADCs of the disclosure that possess a sufficiently acidic, a sufficiently basic, or both functional groups, can react with any of a number of inorganic bases, and inorganic and organic acids, to form a salt. Alternatively, compounds that are inherently charged, such as those with a quaternary nitrogen, can form a salt with an appropriate counter ion, *e.g.*, a halide such as a bromide, chloride, or fluoride.

[0060] Acids commonly employed to form acid addition salts are inorganic acids such as hydrochloric acid, hydrobromic acid, hydroiodic acid, sulfuric acid, phosphoric acid, and the like, and organic acids such as *p*-toluenesulfonic acid, methanesulfonic acid, oxalic acid, *p*-bromophenyl-sulfonic acid, carbonic acid, succinic acid, citric acid, *etc.* Base addition salts include those derived from inorganic bases, such as ammonium and alkali or alkaline earth metal hydroxides, carbonates, bicarbonates, and the like.

### 7.1. Abbreviations

[0061] The antibodies, binding fragments, ADCs and polynucleotides described herein are, in many embodiments, described by way of their respective polypeptide or polynucleotide sequences. Unless indicated otherwise, polypeptide sequences are provided in N→C orientation; polynucleotide sequences in 5'→3' orientation. For polypeptide sequences, the conventional three or one-letter abbreviations for the genetically encoded amino acids may be used, as noted in TABLE 1, below.

TABLE 1		
Encoded Amino Acid Abbreviations		
Amino Acid	Three Letter Abbreviation	One-Letter Abbreviation
Alanine	Ala	A

TABLE 1		
Encoded Amino Acid Abbreviations		
Amino Acid	Three Letter Abbreviation	One-Letter Abbreviation
Arginine	Arg	R
Asparagine	Asn	N
Aspartic acid	Asp	D
Cysteine	Cys	C
Glutamic acid	Glu	E
Glutamine	Gln	Q
Glycine	Gly	G
Histidine	His	H
Isoleucine	Ile	I
Leucine	Leu	L
Lysine	Lys	K
Methionine	Met	M
Phenylalanine	Phe	F
Proline	Pro	P
Serine	Ser	S
Threonine	Thr	T
Tryptophan	Trp	W
Tyrosine	Tyr	Y
Valine	Val	V

[0062] Certain sequences are defined by structural formulae specifying amino acid residues belonging to certain classes (*e.g.*, aliphatic, hydrophobic, *etc.*). The various classes to which the genetically encoded amino acids belong as used herein are noted in TABLE 2, below. Some amino acids may belong to more than one class. Cysteine, which contains a sulfhydryl group, and proline, which is conformationally constrained, are not assigned classes.

TABLE 2	
Encoded Amino Acid Classes	
Class	Amino Acids
Aliphatic	A, I, L, V
Aromatic	F, Y, W
Non-Polar	M, A, I, L, V
Polar	N, Q, S, T
Basic	H, K, R
Acidic	D, E
Small	A, G

## 7.2. Definitions

[0063] Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art.

## 7.3. Anti-huLRRC15 Antibody Drug Conjugates

[0064] In one aspect, the disclosure concerns antibody drug conjugates (“ADCs”) that specifically bind human LRRC15 isoform 1 (SEQ ID NO:1) or isoform 2 (SEQ ID NO:3). The anti-huLRRC15 ADCs generally comprise an anti-huLRRC15 antigen binding moiety, for example an anti-huLRRC15 antibody or binding fragment, having one or more cytotoxic and/or cytostatic agents linked thereto by way of one or more linkers.

### 7.3.1. Anti-huLRRC15 Antibodies And Binding Fragments

[0065] In specific exemplary embodiments, the antigen binding moiety is an antibody or an antibody antigen binding fragment. Antibodies and/or binding fragments composing the anti-huLRRC15 ADCs specifically bind huLRRC15 at a region of the extracellular domain (residues 22 to 527 of SEQ ID NO:3) that is shed from the cell surface and into the blood stream (“shed ECD” or “sECD”) following cleavage at a proteolytic cleavage site between Arg<sup>527</sup> and Ser<sup>528</sup> of SEQ ID NO:3.

[0066] As used herein, the term “antibody” (Ab) refers to an immunoglobulin molecule that specifically binds to, or is immunologically reactive with, a particular antigen- here, the sECD of huLRRC15. Antibodies comprise complementarity determining regions (CDRs), also known as hypervariable regions,

in both the light chain and heavy chain variable domains. The more highly conserved portions of the variable domains are called the framework (FR). As is known in the art, the amino acid position/boundary delineating a hypervariable region of an antibody can vary, depending on the context and the various definitions known in the art. Some positions within a variable domain may be viewed as hybrid hypervariable positions in that these positions can be deemed to be within a hypervariable region under one set of criteria, while being deemed to be outside a hypervariable region under a different set of criteria. One or more of these positions can also be found in extended hypervariable regions. The variable domains of native heavy and light chains each comprise four FR regions, largely by adopting a  $\beta$ -sheet configuration, connected by three CDRs, which form loops connecting, and in some cases forming part of, the  $\beta$ -sheet structure. The CDRs in each chain are held together in close proximity by the FR regions and, with the CDRs from the other chain, contribute to the formation of the antigen binding site of antibodies. *See Kabat et al.*, Sequences of Proteins of Immunological Interest (National Institute of Health, Bethesda, Md. 1987). As used herein, numbering of immunoglobulin amino acid residues is done according to the immunoglobulin amino acid residue numbering system of Kabat *et al.* unless otherwise indicated.

[0067] Antibodies composing anti-huLRRC15 ADCs may be polyclonal, monoclonal, genetically engineered, and/or otherwise modified in nature, including but not limited to, chimeric antibodies, humanized antibodies, human antibodies, primatized antibodies, single chain antibodies, bispecific antibodies, dual-variable domain antibodies, *etc.* In various embodiments, the antibodies comprise all or a portion of a constant region of an antibody. In some embodiments, the constant region is an isotype selected from: IgA (*e.g.*, IgA<sub>1</sub> or IgA<sub>2</sub>), IgD, IgE, IgG (*e.g.*, IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub> or IgG<sub>4</sub>), IgM, and IgY. In specific embodiments, antibodies composing an anti-huLRRC15 ADC comprise an IgG<sub>1</sub> constant region isotype.

[0068] The term “monoclonal antibody” as used herein is not limited to antibodies produced through hybridoma technology. A monoclonal antibody is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, by any means available or known in the art. Monoclonal antibodies useful with the present disclosure can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. In many uses of the present disclosure, including *in vivo* use of ADCs including anti-huLRRC15 antibodies in humans, chimeric, primatized, humanized, or human antibodies can suitably be used.

[0069] The term “chimeric” antibody as used herein refers to an antibody having variable sequences derived from a non-human immunoglobulin, such as a rat or a mouse antibody, and human

immunoglobulin constant regions, typically chosen from a human immunoglobulin template. Methods for producing chimeric antibodies are known in the art. *See, e.g.*, Morrison, 1985, *Science* 229(4719):1202-7; Oi *et al.*, 1986, *BioTechniques* 4:214-221; Gillies *et al.*, 1985, *J. Immunol. Methods* 125:191-202; U.S. Pat. Nos. 5,807,715; 4,816,567; and 4,816,397, which are incorporated herein by reference in their entireties.

**[0070]** “Humanized” forms of non-human (*e.g.*, murine) antibodies are chimeric immunoglobulins that contain minimal sequences derived from non-human immunoglobulin. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin sequence. The humanized antibody can also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin consensus sequence. Methods of antibody humanization are known in the art. *See, e.g.*, Riechmann *et al.*, 1988, *Nature* 332:323-7; U.S. Patent Nos. 5,530,101; 5,585,089; 5,693,761; 5,693,762; and 6,180,370 to Queen *et al.*; EP239400; PCT publication WO 91/09967; U.S. Patent No. 5,225,539; EP592106; EP519596; Padlan, 1991, *Mol. Immunol.*, 28:489-498; Studnicka *et al.*, 1994, *Prot. Eng.* 7:805-814; Roguska *et al.*, 1994, *Proc. Natl. Acad. Sci.* 91:969-973; and U.S. Patent No. 5,565,332, all of which are hereby incorporated by reference in their entireties.

**[0071]** “Human antibodies” are antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins. Human antibodies can be made by a variety of methods known in the art including phage display methods using antibody libraries derived from human immunoglobulin sequences. *See* U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645; WO 98/50433; WO 98/24893; WO 98/16654; WO 96/34096; WO 96/33735; and WO 91/10741, each of which is incorporated herein by reference in its entirety. Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins but which can express human immunoglobulin genes. *See, e.g.*, PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825; 5,661,016; 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entireties. In addition, companies such as Medarex (Princeton, NJ), Astellas Pharma (Deerfield, IL), Amgen (Thousand Oaks, CA) and Regeneron (Tarrytown, NY) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above. Fully human antibodies that recognize a selected epitope can be generated using a technique referred to as “guided selection.” In this approach,



a selected non-human monoclonal antibody, *e.g.*, a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope (*see*, Jespers *et al.*, 1988, Biotechnology 12:899-903).

[0072] “Primatized antibodies” comprise monkey variable regions and human constant regions. Methods for producing primatized antibodies are known in the art. *See, e.g.*, U.S. Patent Nos. 5,658,570; 5,681,722; and 5,693,780, which are incorporated herein by reference in their entireties.

[0073] Anti-huLRRC15 ADCs may comprise full-length (intact) antibody molecules, as well as antigen binding fragments that are capable of specifically binding huLRRC15. Examples of antibody binding fragments include by way of example and not limitation, Fab, Fab', F(ab')<sub>2</sub>, Fv fragments, single chain Fv fragments and single domain fragments.

[0074] A Fab fragment contains the constant domain of the light chain and the first constant domain (CH<sub>2</sub>) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxyl terminus of the heavy chain CH<sub>2</sub> domain including one or more cysteines from the antibody hinge region. F(ab') fragments are produced by cleavage of the disulfide bond at the hinge cysteines of the F(ab')<sub>2</sub> pepsin digestion product. Additional chemical couplings of antibody fragments are known to those of ordinary skill in the art. Fab and F(ab')<sub>2</sub> fragments lack the Fc fragment of intact antibody, clear more rapidly from the circulation of animals, and may have less non-specific tissue binding than an intact antibody (*see, e.g.*, Wahl *et al.*, 1983, J. Nucl. Med. 24:316).

[0075] An “Fv” fragment is the minimum fragment of an antibody that contains a complete target recognition and binding site. This region consists of a dimer of one heavy and one light chain variable domain in a tight, non-covalent association (V<sub>H</sub>-V<sub>L</sub> dimer). It is in this configuration that the three CDRs of each variable domain interact to define an antigen binding site on the surface of the V<sub>H</sub>-V<sub>L</sub> dimer. Often, the six CDRs confer antigen binding specificity upon the antibody. However, in some instances even a single variable domain (or half of an Fv comprising only three CDRs specific for a target) may have the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

[0076] “Single-chain Fv” or “scFv” antibody binding fragments comprise the V<sub>H</sub> and V<sub>L</sub> domains of an antibody, where these domains are present in a single polypeptide chain. Generally, the Fv polypeptide further comprises a polypeptide linker between the V<sub>H</sub> and V<sub>L</sub> domains which enables the scFv to form the desired structure for antigen binding.

[0077] “Single domain antibodies” are composed of a single V<sub>H</sub> or V<sub>L</sub> domains which exhibit sufficient affinity to huLRRC15. In a specific embodiment, the single domain antibody is a camelized antibody (*See, e.g.*, Riechmann, 1999, Journal of Immunological Methods 231:25–38).

**[0078]** Antibodies composing the anti-huLRRC15 ADCs may also be bispecific antibodies. Bispecific antibodies are monoclonal, often human or humanized, antibodies that have binding specificities for two different epitopes on the same or different antigens. In the present disclosure, one of the binding specificities can be directed towards huLRRC15, the other can be for any other antigen, *e.g.*, for a cell-surface protein, receptor, receptor subunit, tissue-specific antigen, virally derived protein, virally encoded envelope protein, bacterially derived protein, or bacterial surface protein, *etc.*

**[0079]** Antibodies composing anti-huLRRC15 ADCs may be derivatized. Derivatized antibodies are typically modified by glycosylation, acetylation, pegylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to a cellular ligand or other protein. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to, specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, *etc.* Additionally, the derivative may contain one or more non-natural amino acids, *e.g.*, using ambrx technology. *See, e.g.*, Wolfson, 2006, Chem. Biol. 13(10):1011-2.

**[0080]** Antibodies or binding fragments composing anti-huLRRC15 ADCs may be antibodies or fragments whose sequences have been modified to alter at least one constant region-mediated biological effector function. For example, in some embodiments, an anti-huLRRC15 antibody may be modified to reduce at least one constant region-mediated biological effector function relative to the unmodified antibody, *e.g.*, reduced binding to the Fc receptor (FcγR). FcγR binding may be reduced by mutating the immunoglobulin constant region segment of the antibody at particular regions necessary for FcγR interactions (*See, e.g.*, Canfield and Morrison, 1991, J. Exp. Med. 173:1483-1491; and Lund *et al.*, 1991, J. Immunol. 147:2657-2662). Reducing FcγR binding may also reduce other effector functions which rely on FcγR interactions, such as opsonization, phagocytosis and antigen-dependent cellular cytotoxicity ("ADCC").

**[0081]** Antibodies or binding fragments composing anti-huLRRC15 ADCs may include modifications that increase or decrease their binding affinities to the neonatal Fc receptor, FcRn, for example, by mutating the immunoglobulin constant region segment at particular regions involved in FcRn interactions (*see, e.g.*, WO 2005/123780). In particular embodiments, an anti-huLRRC15 antibody of the IgG class is mutated such that at least one of amino acid residues 250, 314, and 428 of the heavy chain constant region is substituted alone, or in any combinations thereof, such as at positions 250 and 428, or at positions 250 and 314, or at positions 314 and 428, or at positions 250, 314, and 428, with substitution at positions 250 and 428 being a specific combination. For position 250, the substituting amino acid residue may be any amino acid residue other than threonine, including, but not limited to, alanine, cysteine, aspartic acid,

glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, asparagine, proline, glutamine, arginine, serine, valine, tryptophan, or tyrosine. For position 314, the substituting amino acid residue may be any amino acid residue other than leucine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, methionine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. For position 428, the substituting amino acid residues may be any amino acid residue other than methionine, including, but not limited to, alanine, cysteine, aspartic acid, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, asparagine, proline, glutamine, arginine, serine, threonine, valine, tryptophan, or tyrosine. Specific combinations of suitable amino acid substitutions are identified in Table 1 of U.S. Patent No. 7,217,797, which is incorporated herein by reference. In yet further embodiments, the variant Fc domains have at least one or more modifications that enhance the affinity to FcRn, *e.g.*, a modification of one or more amino acid residues 251-256, 285-290, 308-314, 385-389, and 428-436 (*e.g.*, M428L), or a modification at positions 250 and 428 (*e.g.*, T250Q/M428L). See, *e.g.*, Hinton et al., 2004, J. Biol. Chem. 279 (8): 6213-6216; PCT Publication Nos. WO 97/34631 and WO 02/060919. Such mutations increase binding to FcRn, which protects the antibody from degradation and increases its half-life.

**[0082]** An anti-huLRRC15 antibody and/or binding fragment may have one or more amino acids inserted into one or more of its hypervariable regions, for example as described in Jung & Plückthun, 1997, Protein Engineering 10:9, 959-966; Yazaki *et al.*, 2004, Protein Eng. Des Sel. 17(5):481-9; and U.S. Pat. App. No. 2007/0280931.

**[0083]** Post-translational modifications of an antibody included in an anti-huLRRC15 ADC may include glycosylation. Common biantennary complexes can comprise a core structure having two N-acetylglucosamine (GlcNAc), three mannose, and two GlcNAc residues that are  $\beta$ -1,2 linked to  $\alpha$ -6 mannose and  $\alpha$ -3 mannose to form two antennae. One or more fucose (Fuc), galactose (Gal), high mannose glycans Man-5 or Man-9, bisecting GlcNAc, and sialic acid including N-acetylneuraminic acid (NANA) or N-glycolylneuraminic acid (NGNA) residues may be attached to the core. N-linked glycoforms may include G0 (protein having a core biantennary glycosylation structure), G0F (fucosylated G0), G0F GlcNAc, G1 (protein having a core glycosylation structure with one galactose residue), G1F (fucosylated G1), G2 (protein having a core glycosylation structure with two galactose residues), and/or G2F (fucosylated G2).

**[0084]** Antibodies included in anti-huLRRC15 ADCs may have low levels of, or lack, fucose. Antibodies lacking fucose have been correlated with enhanced ADCC activity, especially at low doses of

antibody. See Shields *et al.*, 2002, J. Biol. Chem. 277:26733-26740; Shinkawa *et al.*, 2003, J. Biol. Chem. 278:3466-73. Methods of preparing fucose-less antibodies include growth in rat myeloma YB2/0 cells (ATCC CRL 1662). YB2/0 cells express low levels of FUT8 mRNA, which encodes  $\alpha$ -1,6-fucosyltransferase, an enzyme necessary for fucosylation of polypeptides.

**[0085]** Anti-huLRRC15 antibodies and/or binding fragments with high affinity for huLRRC15 may be desirable for therapeutic uses. Accordingly, the present disclosure contemplates ADCs comprising anti-huLRRC15 antibodies and/or binding fragments having a high binding affinity to huLRRC15. In specific embodiments, the antibodies and/or binding fragments bind huLRRC15 with an affinity of at least about 100 nM, but may exhibit higher affinity, for example, at least about 90 nM, 80 nM, 70 nM, 60 nM, 50 nM, 40 nM, 30 nM, 25 nM, 20 nM, 15 nM, 10 nM, 7 nM, 6 nM, 5 nM, 4 nM, 3 nM, 2 nM, 1 nM, 0.1 nM, 0.01 nM, or even higher. In some embodiments, the antibodies bind huLRRC15 with an affinity in the range of about 1 pM to about 100 nM, or an affinity ranging between any of the foregoing values, such as but not limited to from about 0.01 to 100, 0.01 to 10, 0.01 to 2, 0.1 to 100, 0.1 to 10, or 0.1 to 2 nM.

**[0086]** Affinity of antibodies and/or binding fragments for huLRRC15 can be determined using techniques well known in the art or described herein, such as for example, but not by way of limitation, ELISA, isothermal titration calorimetry (ITC), surface plasmon resonance, flow cytometry or fluorescent polarization assays.

**[0087]** In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1, V<sub>H</sub> CDR#2 and V<sub>H</sub> CDR#3 have sequences selected from their respective V<sub>H</sub> CDR sequences in the table below:

CDR	Sequence (N→C)	Identifier
huM25 V <sub>H</sub> CDR#1	SYWIE	SEQ ID NO:10
huAD208.4.1 V <sub>H</sub> CDR#1	DYYIH	SEQ ID NO:20
huAD208.12.1 V <sub>H</sub> CDR#1	NYWMH	SEQ ID NO:30
huAD208.14.1 V <sub>H</sub> CDR#1	DYYIH	SEQ ID NO:40
hu139.10 V <sub>H</sub> CDR#1	SYGVH	SEQ ID NO:50
muAD210.40.9 V <sub>H</sub> CDR#1	NYWLG	SEQ ID NO:60
muAD209.9.1 V <sub>H</sub> CDR#1	NFGMN	SEQ ID NO:70
huM25 V <sub>H</sub> CDR#2	EILPGSDTTNYNEKFKD	SEQ ID NO:11
huAD208.4.1 V <sub>H</sub> CDR#2	LVYPYIGGTNYNQKFKG	SEQ ID NO:21
huAD208.12.1 V <sub>H</sub> CDR#2	MIHPNSGSTKHNEKFRG	SEQ ID NO:31

CDR	Sequence (N→C)	Identifier
huAD208.14.1 V <sub>H</sub> CDR#2	LVYPYIGGSSYNQQFKG	SEQ ID NO:41
hu139.10 V <sub>H</sub> CDR#2	VIWAGGSTNYNSALMS	SEQ ID NO:51
muAD210.40.9 V <sub>H</sub> CDR#2	DIYPGGGNTYYNEKLKG	SEQ ID NO:61
muAD209.9.1 V <sub>H</sub> CDR#2	WINLYTGEPTFADDFKG	SEQ ID NO:71
huM25 V <sub>H</sub> CDR#3	DRGNYRAWFGY	SEQ ID NO:12
huAD208.4.1 V <sub>H</sub> CDR#3	GDNKYDAMDY	SEQ ID NO:22
huAD208.12.1 V <sub>H</sub> CDR#3	SDFGNYRWYFDV	SEQ ID NO:32
huAD208.14.1 V <sub>H</sub> CDR#3	GDNNYDAMDY	SEQ ID NO:42
hu139.10 V <sub>H</sub> CDR#3	HMITEDYYGMDY	SEQ ID NO:52
muAD210.40.9 V <sub>H</sub> CDR#3	WGDKKGNFYAY	SEQ ID NO:62
muAD209.9.1 V <sub>H</sub> CDR#3	KGETYYRYDGFAY	SEQ ID NO:72

[0088] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1, V<sub>L</sub> CDR#2 and V<sub>L</sub> CDR#3 have sequences selected from their respective V<sub>L</sub> CDR sequences in the table below:

CDR	Sequence (N→C)	Identifier
huM25 V <sub>L</sub> CDR#1	RASQDISNYLN	SEQ ID NO:13
huAD208.4.1 V <sub>L</sub> CDR#1	RASQSVSTSSYSYMH	SEQ ID NO:23
huAD208.12.1 V <sub>L</sub> CDR#1	RASQSSSNLH	SEQ ID NO:33
huAD208.14.1 V <sub>L</sub> CDR#1	RASQSVSTSTYNYMH	SEQ ID NO:43
hu139.10 V <sub>L</sub> CDR#1	KSSQSLLNSRTRKNYLA	SEQ ID NO:53
muAD210.40.9 V <sub>L</sub> CDR#1	TASSSVYSSYLH	SEQ ID NO:63
muAD209.9.1 V <sub>L</sub> CDR#1	RSSKSLHNSNGNTHLY	SEQ ID NO:73
huM25 V <sub>L</sub> CDR#2	YTSRLHS	SEQ ID NO:14
huAD208.4.1 V <sub>L</sub> CDR#2	YASSLES	SEQ ID NO:24
huAD208.12.1 V <sub>L</sub> CDR#2	YVSQSI	SEQ ID NO:34
huAD208.14.1 V <sub>L</sub> CDR#2	YASNLES	SEQ ID NO:44
hu139.10 V <sub>L</sub> CDR#2	WASTRES	SEQ ID NO:54
muAD210.40.9 V <sub>L</sub> CDR#2	STSNLAS	SEQ ID NO:64

CDR	Sequence (N→C)	Identifier
muAD209.9.1 V <sub>L</sub> CDR#2	RMSNLAS	SEQ ID NO:74
huM25 V <sub>L</sub> CDR#3	QQGEALPWT	SEQ ID NO:15
huAD208.4.1 V <sub>L</sub> CDR#3	EQSWEIRT	SEQ ID NO:25
huAD208.12.1 V <sub>L</sub> CDR#3	QQSNSWPFT	SEQ ID NO:35
huAD208.14.1 V <sub>L</sub> CDR#3	HHTWEIRT	SEQ ID NO:45
hu139.10 V <sub>L</sub> CDR#3	KQSYNLPT	SEQ ID NO:55
muAD210.40.9 V <sub>L</sub> CDR#3	HQYHRSPT	SEQ ID NO:65
muAD209.9.1 V <sub>L</sub> CDR#3	MLLEYPYT	SEQ ID NO:75

[0089] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1, V<sub>H</sub> CDR#2 and V<sub>H</sub> CDR#3 have sequences selected from their respective V<sub>H</sub> CDR sequences in the table below, and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1, V<sub>L</sub> CDR#2 and V<sub>L</sub> CDR#3 have sequences selected from their respective V<sub>L</sub> CDR sequences in the table below:

CDR	Sequence (N→C)	Identifier
huM25 V <sub>H</sub> CDR#1	SYWIE	SEQ ID NO:10
huAD208.4.1 V <sub>H</sub> CDR#1	DYYIH	SEQ ID NO:20
huAD208.12.1 V <sub>H</sub> CDR#1	NYWMH	SEQ ID NO:30
huAD208.14.1 V <sub>H</sub> CDR#1	DYYIH	SEQ ID NO:40
hu139.10 V <sub>H</sub> CDR#1	SYGVH	SEQ ID NO:50
muAD210.40.9 V <sub>H</sub> CDR#1	NYWLG	SEQ ID NO:60
muAD209.9.1 V <sub>H</sub> CDR#1	NFGMN	SEQ ID NO:70
huM25 V <sub>H</sub> CDR#2	EILPGSDTTNYNEKFKD	SEQ ID NO:11
huAD208.4.1 V <sub>H</sub> CDR#2	LVYPYIGGTNYNQKFKG	SEQ ID NO:21
huAD208.12.1 V <sub>H</sub> CDR#2	MIHPNSGSTKHNEKFRG	SEQ ID NO:31
huAD208.14.1 V <sub>H</sub> CDR#2	LVYPYIGGSSYNQQFKG	SEQ ID NO:41
hu139.10 V <sub>H</sub> CDR#2	VIWAGGSTNYNSALMS	SEQ ID NO:51
muAD210.40.9 V <sub>H</sub> CDR#2	DIYPGGGNTYYNEKLKG	SEQ ID NO:61
muAD209.9.1 V <sub>H</sub> CDR#2	WINLYTGEPTFADDFKG	SEQ ID NO:71
huM25 V <sub>H</sub> CDR#3	DRGNYRAWFGY	SEQ ID NO:12

CDR	Sequence (N→C)	Identifier
huAD208.4.1 V <sub>H</sub> CDR#3	GDNKYDAMDY	SEQ ID NO:22
huAD208.12.1 V <sub>H</sub> CDR#3	SDFGNYRWYFDV	SEQ ID NO:32
huAD208.14.1 V <sub>H</sub> CDR#3	GDNNYDAMDY	SEQ ID NO:42
hu139.10 V <sub>H</sub> CDR#3	HMITEDYYGMDY	SEQ ID NO:52
muAD210.40.9 V <sub>H</sub> CDR#3	WGDKKGNFYAY	SEQ ID NO:62
muAD209.9.1 V <sub>H</sub> CDR#3	KGETYYRYDGFAY	SEQ ID NO:72
huM25 V <sub>L</sub> CDR#1	RASQDISNYLN	SEQ ID NO:13
huAD208.4.1 V <sub>L</sub> CDR#1	RASQSVSTSSYSYMH	SEQ ID NO:23
huAD208.12.1 V <sub>L</sub> CDR#1	RASQSSSNLH	SEQ ID NO:33
huAD208.14.1 V <sub>L</sub> CDR#1	RASQSVSTSTYNYMH	SEQ ID NO:43
hu139.10 V <sub>L</sub> CDR#1	KSSQSLLNSRTRKNYLA	SEQ ID NO:53
muAD210.40.9 V <sub>L</sub> CDR#1	TASSSVYSSYLH	SEQ ID NO:63
muAD209.9.1 V <sub>L</sub> CDR#1	RSSKSLLHSNGNTHLY	SEQ ID NO:73
huM25 V <sub>L</sub> CDR#2	YTSRLHS	SEQ ID NO:14
huAD208.4.1 V <sub>L</sub> CDR#2	YASSLES	SEQ ID NO:24
huAD208.12.1 V <sub>L</sub> CDR#2	YVSQSI	SEQ ID NO:34
huAD208.14.1 V <sub>L</sub> CDR#2	YASNLES	SEQ ID NO:44
hu139.10 V <sub>L</sub> CDR#2	WASTRES	SEQ ID NO:54
muAD210.40.9 V <sub>L</sub> CDR#2	STSNLAS	SEQ ID NO:64
muAD209.9.1 V <sub>L</sub> CDR#2	RMSNLAS	SEQ ID NO:74
huM25 V <sub>L</sub> CDR#3	QQGEALPWT	SEQ ID NO:15
huAD208.4.1 V <sub>L</sub> CDR#3	EQSWEIRT	SEQ ID NO:25
huAD208.12.1 V <sub>L</sub> CDR#3	QQSNSWPFT	SEQ ID NO:35
huAD208.14.1 V <sub>L</sub> CDR#3	HHTWEIRT	SEQ ID NO:45
hu139.10 V <sub>L</sub> CDR#3	KQSYNLPT	SEQ ID NO:55
muAD210.40.9 V <sub>L</sub> CDR#3	HQYHRSPT	SEQ ID NO:65
muAD209.9.1 V <sub>L</sub> CDR#3	MLLEYPYT	SEQ ID NO:75

[0090] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>H</sub> chain having three CDRs in which:

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:10, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:11 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:12; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:20, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:21 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:22; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:30, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:31 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:32; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:40, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:41 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:42; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:50, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:51 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:52; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:60, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:61 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:62; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:70, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:71 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:72.

[0091] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>L</sub> chain having three CDRs in which:

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:13, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:14 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:15; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:23, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:24 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:25; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:33, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:34 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:35; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:43, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:44 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:45; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:53, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:54 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:55; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:63, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:64 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:65; or



V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:73, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:74 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:75.

[0092] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises:

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:10, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:11 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:12 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:13, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:14 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:15; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:20, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:21 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:22 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:23, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:24 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:25; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:30, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:31 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:32 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:33, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:34 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:35; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:40, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:41 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:42 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:43, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:44 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:45; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:50, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:51 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:52 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:53, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:54 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:55; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:60, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:61 and V<sub>H</sub> CDR#3 corresponds in sequence to

SEQ ID NO:62 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:63, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:64 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:65; or

a V<sub>H</sub> chain having three CDRs in which V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:70, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:71 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:72 and a V<sub>L</sub> chain having three CDRs in which V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:73, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:74 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:75.

[0093] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>H</sub> chain having a sequence corresponding to a sequence selected from one of the sequences in the table below:

Chain	Sequence (N→C)	Identifier
huM25 V <sub>H</sub>	EVQLVQSGAEVKKPGASVKVSCKASGYKFSYWIEWVKQAP GQGLEWIGEILPGSDTTNYNEKFKDRATFTSDTSINTAYMELS RLRSDDTAVYYCARGDRGNRAWFGYWGQGTLVTVSS	SEQ ID NO:16
huAD208.4.1 V <sub>H</sub>	EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAP GQGLEWIGLVYPYIGGTNYNQKFKGKATLTVDTSTTTAYME MSSLRSEDVAVYYCARGDNKYDAMDYWGQGTTVTVSS	SEQ ID NO:26
huAD208.12.1 V <sub>H</sub>	EVQLVQSGAEVKKPGSSVKVSCKASGYTFTNYWMHWVKQA PGQGLEWIGMIHPNSGSTKHNEKFRGKATLTVDESTTTAYME LSSLRSEDVAVYYCARSDFGNYRWYFDVWGQGTTVTVSS	SEQ ID NO:36
huAD208.14.1 V <sub>H</sub>	EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAP GQGLEWIGLVYPYIGGSSYNQQFKGKATLTVDTSTSTAYMEL SSLRSEDVAVYYCARGDNNYDAMDYWGQGTTVTVSS	SEQ ID NO:46
hu139.10 V <sub>H</sub>	EVQLVESGGGLVQPGGSLRLSCAVSGFSLTSYGVHWVRQAT GKGLEWLGVIWAGGSTNYNSALMSRLTISKENAKSSVYLQM NSLRAGDTAMYYCATHMITEDYYGMDYWGQGTTVTVSS	SEQ ID NO:56
muAD210.40.9 V <sub>H</sub>	QVQLQQSGAELVRPGTSVKISCKASGYDFTNYWLGWVKQRP GHGLEWIGDIYPGGGNTYYNEKLKKGKATLTADKSSSTAYIHL ISLTSEDSSVYFCARWGDKKGNFYAYWGQGTLVTVSA	SEQ ID NO:66
muAD209.9.1 V <sub>H</sub>	QIQLVQSGPELKKPGETVKISCKASGFAITNFGMNWVKQAPG KGLKWMGWINLYTGEPTFADDFKGRFAFSLETSASTAYLQIN NLKNEDTVIYFCARKGETYYRYDGFAYWGQGTLVTVSA	SEQ ID NO:76

[0094] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises a V<sub>L</sub> chain having a sequence corresponding to a sequence selected from one of the sequences in the table below:

Chain	Sequence (N→C)	Identifier
huM25 V <sub>L</sub>	DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPG GAVKFLIYYTSRLHSGVPSRFSGSGSGTDYTLTISSLQPEDF ATYFCQQGEALPWTFGGGTKVEIK	SEQ ID NO:17
huAD208.4.1 V <sub>L</sub>	DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQ QKPGQPPKLLIKYASSLESGVPDRFSGSGSGTDFTLTISSLQ AEDVAVYYCEQSWEIRTFGGGTKVEIK	SEQ ID NO:27
huAD208.12.1 V <sub>L</sub>	EIVLTQSPATLSLSPGERATLSCRASQSSNNLHWYQQKPG QAPRVLIKYSQSISGIPARFSGSGSGTDFTLTISSLEPEDFA VYFCQQSNSWPFTFGQGTKLEIK	SEQ ID NO:37
huAD208.14.1 V <sub>L</sub>	DIVLTQSPDSLAVSLGERATISCRASQSVSTSTYNYMHWYQ QKPGQPPKLLVKYASNLESGVPDRFSGSGSGTDFTLTISSL QAEDVAVYYCHHTWEIRTFGGGTKVEIK	SEQ ID NO:47
hu139.10 V <sub>L</sub>	DIVMTQSPDSLAVSLGERATINCKSSQSLNSRTRKNYLAW YQQKPGQSPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISS LQAEDVAVYYCKQSYNLPFTFGGGTKVEIK	SEQ ID NO:57
muAD210.40.9 V <sub>L</sub>	QIVLTQSPAISASLGERVTMTCTASSSVYSSYLHWYQQK PGSSPKLWIYSTSNLASGVPGRFSGSGSGTSYSLTISSMEAE DAATYYCHQYHRSPTFGGGTKLEIK	SEQ ID NO:67
muAD209.9.1 V <sub>L</sub>	DIVMTQAAPSPVPTPGESVSISCRSSKSLLSNGNTHLYWF LQRPQGSPQLLIYRMSNLASGVPDRFSGSGSGTAFTLRISRV EAEDVGVYYCMQLLEYPYTFGGGTKLEIE	SEQ ID NO:77

[0095] In some embodiments, an antibody and/or binding fragment composing an anti-huLRRC15 ADC comprises:

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:16 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:17; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:26 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:36 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:37; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:46 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:47; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:56 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:57; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:66 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:67; or

a V<sub>H</sub> chain having a sequence corresponding to SEQ ID NO:76 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:77.

**[0096]** The anti-huLRRC15 ADCs have myriad uses, and in particular are useful therapeutically for the treatment of huLRRC15 stromal(+)/cancer(+) tumors in humans. Accordingly, in some embodiments, an anti-huLRRC15 antibody and/or binding fragment composing an anti-huLRRC15 ADC is suitable for administration to humans. In a specific embodiment, the anti-huLRRC15 antibody is humanized. In some embodiments, the humanized anti-huLRRC15 antibody and/or binding fragment composing an anti-huLRRC15 ADC is an antibody and/or binding fragment comprising a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:16, SEQ ID NO:26, SEQ ID NO:36, SEQ ID NO:46 or SEQ ID NO:56 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:17, SEQ ID NO:27, SEQ ID NO:37, SEQ ID NO:47 or SEQ ID NO:57. In some embodiments, the humanized anti-huLRRC15 antibody and/or binding fragment is a full length antibody selected from huM25, huM25-S239C, huAD208.4.1, huAD208.4.1-S239C, huAD208.12.1, huAD208.14.1 and hu139.10.

**[0097]** In some embodiments, an anti-huLRRC15 antibody and/or binding fragment composing an anti-huLRRC15 ADC is an IgG<sub>1</sub>.

**[0098]** In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC comprises a heavy chain having a constant region corresponding in sequence to residues 121-450 of SEQ ID NO:18 by linear amino acid sequence numbering.

**[0099]** In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC comprises a light chain having a constant region corresponding in sequence to residues 108-214 of SEQ ID NO:19 by linear amino acid sequence numbering.

**[0100]** In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC comprises a heavy chain having a constant region corresponding in sequence to residues 121-450 of

SEQ ID NO:18 and a light chain having a constant region corresponding in sequence to residues 108-214 of SEQ ID NO:19 by linear amino acid sequence numbering.

[0101] In some embodiments, anti-huLRR15 antibodies and/or binding fragments composing an anti-huLRR15 ADC compete for binding huLRR15 on cells expressing huLRR15, or the sECD of huLRR15, in *in vitro* assays with a reference antibody. The reference antibody may be any antibody that specifically binds huLRR15 within a region of the sECD. In one specific embodiment, the reference antibody is huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD210.40.9 or muAD209.9.1.

[0102] In some embodiments, an anti-huLRR15 antibody composing an anti-huLRR15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGASVKVSCKASGYKFSYWIEWVKQAPGQGLEWIGEILPGSDTTNYNEKF  
KDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTLVTVSSASTKGPSV  
*FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ*  
*TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPCVFLFPPKPKDTLMISRTPEVTCV*  
*VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP*  
*IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDS*  
*DGSFFLYSKLTVDKSRWQQGNV**FSCSV**MHEALHNHYTQKSLSLSPGK* (SEQ ID NO: 100),

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 19, wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0103] In some embodiments, an anti-huLRR15 antibody composing an anti-huLRR15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGASVKVSCKASGYKFSYWIEWVKQAPGQGLEWIGEILPGSDTTNYNEKF  
KDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTLVTVSSASTKGPSV  
*FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ*  
*TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVD*  
*VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE*  
*KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDS*  
*DSGSFFLYSKLTVDKSRWQQGNV**FSCSV**MHEALHNHYTQKSLSLSPG* (SEQ ID NO: 102),

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 19, wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0104] In some embodiments, an anti-huLRR15 antibody composing an anti-huLRR15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGASVKVSCKASGYKFSYWIEWVKQAPGQGLEWIGEILPGSDTTNYNEKF  
KDRATFTSDTSINTAYMELSRLRSDDTAVYYCARDRGNYRAWFGYWGQGTLVTVSSASTKGPSV  
*FPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGTQ*  
*TYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPCVFLFPPKPKDTLMISRTPEVTCV*  
*VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP*  
*IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD*  
*DGSFFLYSKLTVDKSRWQQGNV**FSCSV**MHEALHNHYTQKSLSLSPG* (SEQ ID NO: 103),

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 19, wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0105] In some embodiments, an anti-huLRR15 antibody composing an anti-huLRR15 ADC has a heavy chain amino acid sequence (N→C) according to SEQ ID NO: 18 or 102;

and a light chain amino acid sequence (N→C) according to:

DIQMTQSPSSLSASVGDRVTITCRASQDISNYLNWYQQKPGGAVKFLIYYTSRLHSGVPSRFSGSG  
 SGTDTYLTISLQPEDFATYFCQQGEALPWTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVC  
 LLNMFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSS  
 PVTKSFNRGEA (SEQ ID NO: 110),

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0106] In some embodiments, an anti-huLRR15 antibody composing an anti-huLRR15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHVVKQAPGQGLEWIGLVYPYIGGTNYNQK  
EKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTTVTVSSASTKGPS  
*VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT*  
*QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV*  
*VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP*  
*IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD*  
*DGSFFLYSKLTVDKSRWQQGNV**FSCSV**MHEALHNHYTQKSLSLSPGK* (SEQ ID NO: 28);

and a light chain amino acid sequence (N→C) according to:

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLESGVPDFR  
SGSGSGTDFTLTISLQAEDVAVYYCEQSWEIRTFGGGTKVEIKRTVAAPS*VFIFPPSDEQLKSGTAS*  
*VVCLLNNFY*PREAKVQWKVDNALQSGNSQESVTEQDSKDSYSLSSLTLSKADYEKHKVYACEVTHQ  
GLSSPVTKSFNRGEC (SEQ ID NO: 29),

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0107] In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHVWKQAPGQGLEWIGLVYPYIGGTNYNQK  
FKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTTVTVSSASTKGPS  
VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT  
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPCVFLFPPKPKDTLMISRTPEVTCVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA  
PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD  
SDGSFFLYSKLTVDKSRWQQGNVFSFSVMHEALHNHYTQKSLSLSPGK (SEQ ID NO: 101);

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 29,

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0108] In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHVWKQAPGQGLEWIGLVYPYIGGTNYNQK  
FKGKATLTVDTSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTTVTVSSASTKGPS  
VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT  
QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVV  
VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP  
IEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLD  
DGSFFLYSKLTVDKSRWQQGNVFSFSVMHEALHNHYTQKSLSLSPG (SEQ ID NO: 104);

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 29,

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0109] In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC has a heavy chain amino acid sequence (N→C) according to:

EVQLVQSGAEVKKPGSSVKVSCKASGFTFTDYYIHWVKQAPGQGLEWIGLVYPYIGGTNYNQK  
FKGKATLTVDTSSTTTAYMEMSSLRSEDTAVYYCARGDNKYDAMDYWGQGTTVTVSSASTKGPS  
*VFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVTVPSSSLGT*  
*QTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPCVFLFPPKPKDTLMISRTPEVTCVV*  
*VDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA*  
*PIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD*  
*SDGSFFLYSKLTVDKSRWQQGNVFC**SMHEALHNHYTQKSLSLSPG* (SEQ ID NO: 105);

and a light chain amino acid sequence (N→C) according to SEQ ID NO: 29,

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0110] In some embodiments, an anti-huLRRC15 antibody composing an anti-huLRRC15 ADC has a heavy chain amino acid sequence (N→C) according to SEQ ID NO: 28 or 104;

and a light chain amino acid sequence (N→C) according to:

DIVLTQSPDSLAVSLGERATINCRASQSVSTSSYSYMHWYQQKPGQPPKLLIKYASSLESQVDRF  
 SGSGSGTDFLTITSSSLQAEDVAVYYCEQSWEIRTFGGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGTAS  
*VVCLLN**NFYPREAKVQWKVDNALQSGNSQESVTEQDSK**STYLSSTLTLSKADYEKHKVYACEVTHQ*  
*GLSSPVTKSFNRGEA* (SEQ ID NO: 111),

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

[0111] Assays for competition include, but are not limited to, a radioactive material labeled immunoassay (RIA), an enzyme-linked immunosorbent assay (ELISA), a sandwich ELISA, flow cytometry assays and surface plasmon resonance assays.

[0112] In one exemplary embodiment of conducting an antibody competition assay between a reference antibody and a test antibody (irrespective of species or isotype), one may first label the reference with a detectable label, such as a fluorophore, biotin or an enzymatic (or even radioactive label) to enable subsequent detection. In this case, cells expressing huLRRC15, or the sECD of huLRRC15, are incubated with unlabeled test antibody, labeled reference antibody is added, and the intensity of the bound label is measured. If the test antibody competes with the labeled reference antibody by binding to the



same, proximal or overlapping epitope, the intensity of the detection signal will be decreased relative to a control reaction carried out without test antibody.

[0113] In a specific embodiment of this assay, the concentration of labeled reference antibody that yields 80% of maximal binding (“ $\text{conc}_{80\%}$ ”) under the assay conditions (*e.g.*, a specified density of cells or a specified concentration of sECD) is first determined, and a competition assay is carried out with 10X  $\text{conc}_{80\%}$  of unlabeled test antibody and  $\text{conc}_{80\%}$  of labeled reference antibody.

[0114] In another exemplary embodiment of conducting a flow cytometry competition assay, cells expressing huLRRC15 are incubated with a titration series of antibodies comprising increasing ratios of unlabeled test antibody versus fluorescently labeled anti-huLRRC15 reference antibody. The labeled reference anti-huLRRC15 antibody is used at a fixed concentration X (for example,  $X = 1 \mu\text{g/ml}$ ) and the unlabeled test antibody is used in a range of concentrations (for example, from  $10^{-4}X$  to 100X). Cells or sECD is incubated with both unlabeled test antibody and labeled reference antibody concurrently. Flow cytometry data is normalized relative to fluorescently labeled reference antibody alone, where the fluorescence intensity of a sample carried out without unlabeled test antibody is assigned 100% binding. If a test antibody competes for binding huLRRC15 with the labeled reference antibody, an assay carried out with equal concentration of each (for example,  $1 \mu\text{g/mL}$  of unlabeled test antibody and  $1 \mu\text{g/mL}$  of labeled reference antibody) will yield an approx. 50% reduction in fluorescence intensity as compared to the 100% control, indicating approx. 50% binding.

[0115] The inhibition can be expressed as an inhibition constant, or  $K_i$ , which is calculated according to the following formula:

$$K_i = \text{IC}_{50} / (1 + [\text{reference Ab concentration}] / K_d),$$

where  $\text{IC}_{50}$  is the concentration of test antibody that yields a 50% reduction in binding of the reference antibody and  $K_d$  is the dissociation constant of the reference antibody, a measure of its affinity for huLRRC15. Antibodies that compete with reference anti-huLRRC15 antibodies can have a  $K_i$  from 10 pM to 10 nM under assay conditions described herein.

[0116] In various embodiments, a test antibody is considered to compete with a reference antibody if it decreases binding of the reference antibody to cells expressing huLRRC15 or the sECD by at least about 20% or more, for example, by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or even more, or by a percentage ranging between any of the foregoing values, at a reference antibody concentration that is 80% of maximal binding under the specific assay conditions used, and a test antibody concentration that is 10-fold higher than the reference antibody concentration.

[0117] In various embodiments of a flow cytometry competition assay, a test antibody is considered to compete with a reference antibody if it decreases binding of the reference antibody to cells expressing huLRRC15 by at least about 20% or more, for example, by at least about 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or even more, or by a percentage ranging between any of the foregoing values, at a concentration of test antibody that is 10X greater than that of the reference antibody.

[0118] A specific assay and assay conditions useful for assessing whether an antibody competes for binding huLRRC15 with a reference antibody as described herein is provided in Example 3.

[0119] The anti-huLRRC15 antibodies described herein may be used in the non-ADC context for a variety of purposes, such as to assist purification of huLRRC15 and/or huLRRC15 sECD, *in vitro*, *in vivo* and *ex vivo* diagnostics, cell and/or tissue stains, *etc.* As a specific example, the antibodies have use in immunoassays for qualitatively and/or quantitatively measuring levels of huLRRC15 in biological samples. *See, e.g.*, Harlow *et al.*, *Antibodies: A Laboratory Manual*, Second Edition (Cold Spring Harbor Laboratory Press, 1988).

[0120] For such uses, detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance can be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. Examples of enzymatic labels include luciferases (*e.g.*, firefly luciferase and bacterial luciferase; U.S. Patent No. 4,737,456), luciferin, 2,3-dihydrophthalazinediones, malate dehydrogenase, urease, peroxidase such as horseradish peroxidase (HRPO), alkaline phosphatase,  $\beta$ -galactosidase, acetylcholinesterase, glucoamylase, lysozyme, saccharide oxidases (*e.g.*, glucose oxidase, galactose oxidase, and glucose-6-phosphate dehydrogenase), heterocyclic oxidases (such as uricase and xanthine oxidase), lactoperoxidase, microperoxidase, and the like. Examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{111}\text{In}$  or  $^{99\text{m}}\text{Tc}$ .

[0121] Detection of expression of huLRRC15 generally involves contacting a biological sample (cells, tissue, or body fluid of an individual) with one or more anti-huLRRC15 antibodies described herein

(optionally conjugated to detectable moiety), and detecting whether or not the sample is positive for huLRRC15 expression, or whether the sample has altered (*e.g.*, reduced or increased) expression as compared to a control sample.

### **7.3.2. Polynucleotides Encoding Anti-huLRRC15 Antibodies, Expression Systems and Methods of Making the Antibodies**

[0122] Anti-huLRRC15 antibodies can be prepared by recombinant expression of immunoglobulin light and heavy chain genes in a host cell. To express an antibody recombinantly, a host cell is transfected with one or more recombinant expression vectors carrying DNA fragments encoding the immunoglobulin light and heavy chains of the antibody such that the light and heavy chains are expressed in the host cell and, optionally, secreted into the medium in which the host cells are cultured, from which medium the antibodies can be recovered. Standard recombinant DNA methodologies are used to obtain antibody heavy and light chain genes, incorporate these genes into recombinant expression vectors and introduce the vectors into host cells, such as those described in *Molecular Cloning; A Laboratory Manual*, Second Edition (Sambrook, Fritsch and Maniatis (eds), Cold Spring Harbor, N. Y., 1989), *Current Protocols in Molecular Biology* (Ausubel, F.M. *et al.*, eds., Greene Publishing Associates, 1989) and in U.S. Patent No. 4,816,397.

[0123] To generate nucleic acids encoding such anti-huLRRC15 antibodies, DNA fragments encoding the light and heavy chain variable regions are first obtained. These DNAs can be obtained by amplification and modification of germline DNA or cDNA encoding light and heavy chain variable sequences, for example using the polymerase chain reaction (PCR). Germline DNA sequences for human heavy and light chain variable region genes are known in the art (*See, e.g.*, the “VBASE” human germline sequence database; see also Kabat *et al.*, 1991, *Sequences of Proteins of Immunological Interest*, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242; Tomlinson *et al.*, 1992, *J. Mol. Biol.* 22T:116-198; and Cox *et al.*, 1994, *Eur. J. Immunol.* 24:827-836; the contents of each of which are incorporated herein by reference).

[0124] Once DNA fragments encoding anti-huLRRC15 antibody-related V<sub>H</sub> and V<sub>L</sub> segments are obtained, these DNA fragments can be further manipulated by standard recombinant DNA techniques, for example to convert the variable region genes to full-length antibody chain genes, to Fab fragment genes or to a scFv gene. In these manipulations, a V<sub>L</sub>- or V<sub>H</sub>-encoding DNA fragment is operatively linked to another DNA fragment encoding another protein, such as an antibody constant region or a flexible linker. The term “operatively linked,” as used in this context, is intended to mean that the two DNA fragments are joined such that the amino acid sequences encoded by the two DNA fragments remain in-frame.

[0125] The isolated DNA encoding the V<sub>H</sub> region can be converted to a full-length heavy chain gene by operatively linking the V<sub>H</sub>-encoding DNA to another DNA molecule encoding heavy chain constant regions (CH<sub>1</sub>, CH<sub>2</sub>, CH<sub>3</sub> and, optionally, CH<sub>4</sub>). The sequences of human heavy chain constant region genes are known in the art (*See, e.g.*, Kabat *et al.*, 1991, Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The heavy chain constant region can be an IgG<sub>1</sub>, IgG<sub>2</sub>, IgG<sub>3</sub>, IgG<sub>4</sub>, IgA, IgE, IgM or IgD constant region, but in certain embodiments is an IgG<sub>1</sub> or IgG<sub>4</sub> constant region. For a Fab fragment heavy chain gene, the V<sub>H</sub>-encoding DNA can be operatively linked to another DNA molecule encoding only the heavy chain CH<sub>1</sub> constant region.

[0126] The isolated DNA encoding the V<sub>L</sub> region can be converted to a full-length light chain gene (as well as a Fab light chain gene) by operatively linking the V<sub>L</sub>-encoding DNA to another DNA molecule encoding the light chain constant region, CL. The sequences of human light chain constant region genes are known in the art (*See, e.g.*, Kabat *et al.*, 1991, Sequences of Proteins of Immunological Interest, Fifth Edition, U.S. Department of Health and Human Services, NIH Publication No. 91-3242) and DNA fragments encompassing these regions can be obtained by standard PCR amplification. The light chain constant region can be a kappa or lambda constant region, but in certain embodiments is a kappa constant region. To create a scFv gene, the V<sub>H</sub>- and V<sub>L</sub>-encoding DNA fragments are operatively linked to another fragment encoding a flexible linker, *e.g.*, encoding the amino acid sequence (Gly<sub>4</sub>~Ser)<sub>3</sub> (SEQ ID NO:82), such that the V<sub>H</sub> and V<sub>L</sub> sequences can be expressed as a contiguous single-chain protein, with the V<sub>L</sub> and V<sub>H</sub> regions joined by the flexible linker (*See, e.g.*, Bird *et al.*, 1988, Science 242:423-426; Huston *et al.*, 1988, Proc. Natl. Acad. Sci. USA 85:5879-5883; McCafferty *et al.*, 1990, Nature 348:552-554).

[0127] To express the anti-huLRRC15 antibodies, DNAs encoding partial or full-length light and heavy chains, obtained as described above, are inserted into expression vectors such that the genes are operatively linked to transcriptional and translational control sequences. In this context, the term “operatively linked” is intended to mean that an antibody gene is ligated into a vector such that transcriptional and translational control sequences within the vector serve their intended function of regulating the transcription and translation of the antibody gene. The expression vector and expression control sequences are chosen to be compatible with the expression host cell used. The antibody light chain gene and the antibody heavy chain gene can be inserted into separate vectors or, more typically, both genes are inserted into the same expression vector.

[0128] The antibody genes are inserted into the expression vector by standard methods (*e.g.*, ligation of complementary restriction sites on the antibody gene fragment and vector, or blunt end ligation if no restriction sites are present). Prior to insertion of the anti-huLRRC15 antibody-related light or heavy chain sequences, the expression vector can already carry antibody constant region sequences. For example, one approach to converting the anti-hPG monoclonal antibody-related V<sub>H</sub> and V<sub>L</sub> sequences to full-length antibody genes is to insert them into expression vectors already encoding heavy chain constant and light chain constant regions, respectively, such that the V<sub>H</sub> segment is operatively linked to the CH segment(s) within the vector and the V<sub>L</sub> segment is operatively linked to the CL segment within the vector. Additionally or alternatively, the recombinant expression vector can encode a signal peptide that facilitates secretion of the antibody chain from a host cell. The antibody chain gene can be cloned into the vector such that the signal peptide is linked in-frame to the amino terminus of the antibody chain gene. The signal peptide can be an immunoglobulin signal peptide or a heterologous signal peptide (*i.e.*, a signal peptide from a non-immunoglobulin protein).

[0129] In addition to the antibody chain genes, the recombinant expression vectors carry regulatory sequences that control the expression of the antibody chain genes in a host cell. The term “regulatory sequence” is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals) that control the transcription or translation of the antibody chain genes. Such regulatory sequences are described, for example, in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA, 1990. It will be appreciated by those skilled in the art that the design of the expression vector, including the selection of regulatory sequences may depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, *etc.* Suitable regulatory sequences for mammalian host cell expression include viral elements that direct high levels of protein expression in mammalian cells, such as promoters and/or enhancers derived from cytomegalovirus (CMV) (such as the CMV promoter/enhancer), Simian Virus 40 (SV40) (such as the SV40 promoter/enhancer), adenovirus, (*e.g.*, the adenovirus major late promoter (AdMLP)) and polyoma. For further description of viral regulatory elements, and sequences thereof, *see, e.g.*, U.S. Patent No. 5,168,062 by Stinski, U.S. Patent No. 4,510,245 by Bell *et al.*, and U.S. Patent No. 4,968,615 by Schaffner *et al.*

[0130] Recombinant expression vectors of the disclosure can carry sequences in addition to the antibody chain genes and regulatory sequences, such as sequences that regulate replication of the vector in host cells (*e.g.*, origins of replication) and selectable marker genes. Selectable marker genes facilitate selection of host cells into which the vector has been introduced (*See, e.g.*, U.S. Patents Nos. 4,399,216, 4,634,665 and 5,179,017, all by Axel *et al.*). For example, typically a selectable marker gene confers

resistance to drugs, such as G418, hygromycin or methotrexate, on a host cell into which the vector has been introduced. Suitable selectable marker genes include the dihydrofolate reductase (DHFR) gene (for use in DHFR<sup>-</sup> host cells with methotrexate selection/amplification) and the neo gene (for G418 selection). For expression of the light and heavy chains, the expression vector(s) encoding the heavy and light chains is transfected into a host cell by standard techniques. The various forms of the term “transfection” are intended to encompass a wide variety of techniques commonly used for the introduction of exogenous DNA into a prokaryotic or eukaryotic host cell, *e.g.*, electroporation, lipofection, calcium-phosphate precipitation, DEAE- dextran transfection and the like.

[0131] It is possible to express anti-huLRRC15 antibodies composing anti-huLRRC15 ADCs in either prokaryotic or eukaryotic host cells. In certain embodiments, expression of antibodies is performed in eukaryotic cells, *e.g.*, mammalian host cells, of optimal secretion of a properly folded and immunologically active antibody. Exemplary mammalian host cells for expressing the recombinant antibodies of the disclosure include Chinese Hamster Ovary (CHO cells) (including DHFR<sup>-</sup> CHO cells, described in Urlaub and Chasin, 1980, Proc. Natl. Acad. Sci. USA 77:4216-4220, used with a DHFR selectable marker, *e.g.*, as described in Kaufman and Sharp, 1982, Mol. Biol. 159:601-621), NS0 myeloma cells, COS cells and SP2 cells. When recombinant expression vectors encoding antibody genes are introduced into mammalian host cells, the antibodies are produced by culturing the host cells for a period of time sufficient to allow for expression of the antibody in the host cells or secretion of the antibody into the culture medium in which the host cells are grown. Antibodies can be recovered from the culture medium using standard protein purification methods. Host cells can also be used to produce portions of intact antibodies, such as Fab fragments or scFv molecules. It is understood that variations on the above procedure are within the scope of the present disclosure. For example, it can be desirable to transfect a host cell with DNA encoding either the light chain or the heavy chain (but not both) of an anti-huLRRC15 antibody.

[0132] Recombinant DNA technology can also be used to remove some or all of the DNA encoding either or both of the light and heavy chains that is not necessary for binding to huLRRC15. The molecules expressed from such truncated DNA molecules are also encompassed by the antibodies of the disclosure.

[0133] For recombinant expression of an anti-huLRRC15 antibody, the host cell can be co-transfected with two expression vectors, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors can contain identical selectable

markers, or they can each contain a separate selectable marker. Alternatively, a single vector can be used which encodes both heavy and light chain polypeptides.

[0134] Once a nucleic acid encoding one or more portions of an anti-huLRRC15 antibody is obtained, further alterations or mutations can be introduced into the coding sequence, for example to generate nucleic acids encoding antibodies with different CDR sequences, antibodies with reduced affinity to the Fc receptor, or antibodies of different subclasses.

[0135] Antibodies and/or binding fragments composing anti-huLRRC15 ADCs can also be produced by chemical synthesis (*e.g.*, by the methods described in Solid Phase Peptide Synthesis, 2<sup>nd</sup> ed., 1984 The Pierce Chemical Co., Rockford, Ill.). Variant antibodies can also be generated using a cell-free platform, *See, e.g.*, Chu *et al.*, Biochemia No. 2, 2001 (Roche Molecular Biologicals) and Murray *et al.*, 2013, Current Opinion in Chemical Biology, 17:420–426.

[0136] Once an anti-huLRRC15 antibody and/or binding fragment has been produced by recombinant expression, it can be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (*e.g.*, ion exchange, affinity, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. Further, the anti-huLRRC15 antibodies and/or binding fragments can be fused to heterologous polypeptide sequences described herein or otherwise known in the art to facilitate purification.

[0137] Once isolated, the anti-huLRRC15 antibody and/or binding fragment can, if desired, be further purified, *e.g.*, by high performance liquid chromatography. (*see, e.g.*, Fisher, Laboratory Techniques In Biochemistry And Molecular Biology, Work and Burdon, eds., Elsevier, 1980), or by gel filtration chromatography on a Superdex™ 75 column (Pharmacia Biotech AB, Uppsala, Sweden).

#### 7.4. Specific Anti-huLRRC15 Antibody Drug Conjugates

[0138] As mentioned, anti-huLRRC15 ADCs generally comprise an anti-huLRRC15 antigen binding moiety, such as an anti-huLRRC15 antibody and/or binding fragment, having one or more cytotoxic and/or cytostatic agents, which may be the same or different, linked thereto by way of one or more linkers, which may also be the same or different. In specific embodiments, the anti-huLRRC15 ADCs are compounds according to structural formula (I):



or salts thereof, where each “D” represents, independently of the others, a cytotoxic and/or cytostatic agent (“drug”); each “L” represents, independently of the others, a linker; “Ab” represents an

anti-huLRRC15 antigen binding moiety, such as an anti-huLRRC15 antibody or binding fragment; each “XY” represents a linkage formed between a functional group  $R^x$  on the linker and a “complementary” functional group  $R^y$  on the antigen binding moiety; and  $n$  represents the number of drugs linked to Ab, or the drug-to-antibody ratio (DAR), of the ADC.

[0139] Specific embodiments of various antibodies or binding fragments (Ab) that may compose ADCs according to structural formula (I) include the various embodiments of anti-huLRRC15 antibodies and/or binding fragments described above.

[0140] In some specific embodiments of the ADCs or salts of structural formula (I), each D is the same and/or each L is the same.

[0141] Specific embodiments of cytotoxic and/or cytostatic agents (D) and linkers (L) that may compose the anti-huLRRC15 ADCs, as well as the number of cytotoxic and/or cytostatic agents linked to the anti-huLRRC15 ADCs, are described in more detail below.

#### 7.4.1. Cytotoxic and/or Cytostatic Agents

[0142] The cytotoxic and/or cytostatic agents may be any agents known to inhibit the growth and/or replication of and/or kill cells, and in particular cancer and/or tumor cells. Numerous agents having cytotoxic and/or cytostatic properties are known in the literature. Non-limiting examples of classes of cytotoxic and/or cytostatic agents include, by way of example and not limitation, radionuclides, alkylating agents, DNA cross-linking agents, DNA intercalating agents (*e.g.*, groove binding agents such as minor groove binders), cell cycle modulators, apoptosis regulators, kinase inhibitors, protein synthesis inhibitors, mitochondria inhibitors, nuclear export inhibitors, topoisomerase I inhibitors, topoisomerase II inhibitors, RNA/DNA antimetabolites and antimetabolic agents.

[0143] Specific non-limiting examples of agents within certain of these various classes are provided below.

[0144] **Alkylating Agents:** asaley (L-Leucine, N-[N-acetyl-4-[bis-(2-chloroethyl)amino]-DL-phenylalanyl]-, ethylester); AZQ (1,4-cyclohexadiene-1,4-dicarbamic acid, 2, 5-bis(1-aziridinyl)-3,6-dioxo-, diethyl ester); BCNU (N,N'-Bis(2-chloroethyl)-N-nitrosourea); busulfan (1,4-butanediol dimethanesulfonate); (carboxyphthalato)platinum; CBDCA (cis-(1,1-cyclobutanedicarboxylato)diammineplatinum(II)); CCNU (N-(2-chloroethyl)-N'-cyclohexyl-N-nitrosourea); CHIP (ipropatin; NSC 256927); chlorambucil; chlorozotocin (2-[[[(2-chloroethyl)nitrosoamino]carbonyl]amino]-2-deoxy-D-glucopyranose); *cis*-platinum (cisplatin); clomesone; cyanomorpholinodoxorubicin; cyclodisone; dianhydrogalactitol (5,6-diepoxydulcitol); fluorodopan ((5-



[(2-chloroethyl)-(2-fluoroethyl)amino]-6-methyl-uracil); hepsulfam; hycanthone; indolinobenzodiazepine dimer DGN462; melphalan; methyl CCNU ((1-(2-chloroethyl)-3-(trans-4-methylcyclohexane)-1-nitrosourea); mitomycin C; mitozolamide; nitrogen mustard ((bis(2-chloroethyl) methylamine hydrochloride); PCNU ((1-(2-chloroethyl)-3-(2,6-dioxo-3-piperidyl)-1-nitrosourea)); piperazine alkylator ((1-(2-chloroethyl)-4-(3-chloropropyl)-piperazine dihydrochloride)); piperazinedione; pipobroman (N,N'-bis(3-bromopropionyl) piperazine); porfiromycin (N-methylmitomycin C); spirohydantoin mustard; teroxirone (triglycidylisocyanurate); tetraplatin; thio-tepa (N,N',N''-tri-1,2-ethanediylthio phosphoramidate); triethylenemelamine; uracil nitrogen mustard (desmethylodopan); Yoshi-864 ((bis(3-mesyloxy propyl)amine hydrochloride).

**[0145] DNA Alkylating-like Agents:** Cisplatin; Carboplatin; Nedaplatin; Oxaliplatin; Satraplatin; Triplatin tetranitrate; Procarbazine; altretamine; dacarbazine; mitozolomide; temozolomide.

**[0146] Alkylating Antineoplastic Agents:** Carboquone; Carmustine; Chlornaphazine; Chlorozotocin; Duocarmycin; Evofosfamide; Fotemustine; Glufosfamide; Lomustine; Mannosulfan; Nimustine; Phenanthriplatin; Pipobroman; Ranimustine; Semustine; Streptozotocin; ThioTEPA; Treosulfan; Triaziquone; Triethylenemelamine; Triplatin tetranitrate.

**[0147] DNA replication and repair inhibitors:** Altretamine; Bleomycin; Dacarbazine; Dactinomycin; Mitobronitol; Mitomycin; Pingyangmycin; Plicamycin; Procarbazine; Temozolomide; ABT-888 (veliparib); olaparib; KU-59436; AZD-2281; AG-014699; BSI-201; BGP-15; INO-1001; ONO-2231.

**[0148] Cell Cycle Modulators:** Paclitaxel; Nab-Paclitaxel; Docetaxel; Vincristine; Vinblastine; ABT-348; AZD-1152; MLN-8054; VX-680; Aurora A-specific kinase inhibitors; Aurora B-specific kinase inhibitors and pan-Aurora kinase inhibitors; AZD-5438; BMI-1040; BMS-032; BMS-387; CVT-2584; flavopyridol; GPC-286199; MCS-5A; PD0332991; PHA-690509; seliciclib (CYC-202, R-roscovitine); ZK-304709; AZD4877, ARRY-520; GSK923295A.

**[0149] Apoptosis Regulators:** AT-101 ((-)-gossypol); G3139 or oblimersen (Bcl-2-targeting antisense oligonucleotide); IPI-194; IPI-565; N-(4-(4-((4'-chloro(1,1'-biphenyl)-2-yl)methyl)piperazin-1-yl)benzoyl)-4-(((1R)-3-(dimethylamino)-1-((phenylsulfanyl)methyl)propyl)amino)-3-nitrobenzenesulfonamide); N-(4-(4-((2-(4-chlorophenyl)-5,5-dimethyl-1-cyclohex-1-en-1-yl)methyl)piperazin-1-yl)benzoyl)-4-(((1R)-3-(morpholin-4-yl)-1-((phenylsulfanyl)methyl)propyl)amino)-3-((trifluoromethyl)sulfonyl)benzenesulfonamide; GX-070 (Obatoclox®; 1H-Indole, 2-(2-((3,5-dimethyl-1H-pyrrol-2-yl)methylene)-3-methoxy-2H-pyrrol-5-yl)-)); HGS1029; GDC-0145; GDC-0152; LCL-161; LBW-242; venetoclax; agents that target TRAIL or death receptors (*e.g.*, DR4 and DR5) such as ETR2-ST01, GDC0145, HGS-1029, LBY-135, PRO-1762; drugs

that target caspases, caspase-regulators, BCL-2 family members, death domain proteins, TNF family members, Toll family members, and/or NF-kappa-B proteins.

**[0150] Angiogenesis Inhibitors:** ABT-869; AEE-788; axitinib (AG-13736); AZD-2171; CP-547,632; IM-862; pegaptamib; sorafenib; BAY43-9006; pazopanib (GW-786034); vatalanib (PTK-787, ZK-222584); sunitinib; SU-11248; VEGF trap; vandetanib; ABT-165; ZD-6474; DLL4 inhibitors.

**[0151] Proteasome Inhibitors:** Bortezomib; Carfilzomib; Epoxomicin; Ixazomib; Salinosporamide A.

**[0152] Kinase Inhibitors:** Afatinib; Axitinib; Bosutinib; Crizotinib; Dasatinib; Erlotinib; Fostamatinib; Gefitinib; Ibrutinib; Imatinib; Lapatinib; Lenvatinib; Mubritinib; Nilotinib; Pazopanib; Pegaptanib; Sorafenib; Sunitinib; SU6656; Vandetanib; Vemurafenib; CEP-701 (lesaurtinib); XL019; INCB018424 (ruxolitinib); ARRY-142886 (selemetinib); ARRY-438162 (binimetinib); PD-325901; PD-98059; AP-23573; CCI-779; everolimus; RAD-001; rapamycin; temsirolimus; ATP-competitive TORC1/TORC2 inhibitors including PI-103, PP242, PP30, Torin 1; LY294002; XL-147; CAL-120; ONC-21; AEZS-127; ETP-45658; PX-866; GDC-0941; BGT226; BEZ235; XL765.

**[0153] Protein Synthesis Inhibitors:** Streptomycin; Dihydrostreptomycin; Neomycin; Framycetin; Paromomycin; Ribostamycin; Kanamycin; Amikacin; Arbekacin; Bekanamycin; Dibekacin; Tobramycin; Spectinomycin; Hygromycin B; Paromomycin; Gentamicin; Netilmicin; Sisomicin; Isepamicin; Verdamycin; Astromicin; Tetracycline; Doxycycline; Chlortetracycline; Clomocycline; Demeclocycline; Lymecycline; Meclocycline; Metacycline; Minocycline; Oxytetracycline; Penimepicycline; Rolitetracycline; Tetracycline; Glycylcyclines; Tigecycline; Oxazolidinone; Eperezolid; Linezolid; Posizolid; Radezolid; Ranbezolid; Sutezolid; Tedizolid; Peptidyl transferase inhibitors; Chloramphenicol; Azidamfenicol; Thiamphenicol; Florfenicol; Pleuromutilins; Retapamulin; Tiamulin; Valnemulin; Azithromycin; Clarithromycin; Dirithromycin; Erythromycin; Flurithromycin; Josamycin; Midecamycin; Miocamycin; Oleandomycin; Rokitamycin; Roxithromycin; Spiramycin; Troleandomycin; Tylosin; Ketolides; Telithromycin; Cethromycin; Solithromycin; Clindamycin; Lincomycin; Pirlimycin; Streptogramins; Pristinamycin; Quinupristin/dalfopristin; Virginiamycin.

**[0154] Histone deacetylase inhibitors:** Vorinostat; Romidepsin; Chidamide; Panobinostat; Valproic acid; Belinostat; Mocetinostat; Abexinostat; Entinostat; SB939 (pracinostat); Resminostat; Givinostat; Quisinostat; thioureaobutyronitrile (Kevetrin<sup>TM</sup>); CUDC-10; CHR-2845 (tefinostat); CHR-3996; 4SC-202; CG200745; ACY-1215 (rocilinostat); ME-344; sulforaphane.

**[0155] Topoisomerase I Inhibitors:** camptothecin; various camptothecin derivatives and analogs (for example, NSC 100880, NSC 603071, NSC 107124, NSC 643833, NSC 629971, NSC 295500, NSC 249910, NSC 606985, NSC 74028, NSC 176323, NSC 295501, NSC 606172, NSC 606173, NSC

610458, NSC 618939, NSC 610457, NSC 610459, NSC 606499, NSC 610456, NSC 364830, and NSC 606497); morpholinisoxorubicin; SN-38.

**[0156] Topoisomerase II Inhibitors:** doxorubicin; amonafide (benzisoquinolinedione); m-AMSA (4'-(9-acridinylamino)-3'-methoxymethanesulfonanilide); anthrapyrazole derivative ((NSC 355644); etoposide (VP-16); pyrazoloacridine ((pyrazolo[3,4,5-kl]acridine-2(6H)-propanamine, 9-methoxy-N, N-dimethyl-5-nitro-, monomethanesulfonate); bisantrene hydrochloride; daunorubicin; deoxydoxorubicin; mitoxantrone; menogaril; N,N-dibenzyl daunomycin; oxanthrazole; rubidazone; teniposide.

**[0157] DNA Intercalating Agents:** anthramycin; chicamycin A; tomaymycin; DC-81; sibiromycin; pyrrolobenzodiazepine derivative; SGD-1882 ((S)-2-(4-aminophenyl)-7-methoxy-8-(3-(((S)-7-methoxy-2-(4-methoxyphenyl)-5-oxo-5,11a-dihydro-1H-benzo[e]pyrrolo[1,2-a][1,4]diazepin-8-yl)oxy)propoxy)-1H-benzo[e]pyrrolo[1,2-a][1,4]diazepin-5(11aH)-one); SG2000 (SJG-136; (11aS,11a'S)-8,8'-(propane-1,3-diylbis(oxy))bis(7-methoxy-2-methylene-2,3-dihydro-1H-benzo[e]pyrrolo[1,2-a][1,4]diazepin-5(11aH)-one)).

**[0158] RNA/DNA Antimetabolites:** L-alanosine; 5-azacytidine; 5-fluorouracil; acivicin; aminopterin derivative N-[2-chloro-5-[[[(2, 4-diamino-5-methyl-6-quinazoliny)l)methyl]amino]benzoyl] L-aspartic acid (NSC 132483); aminopterin derivative N-[4-[[[(2, 4-diamino-5-ethyl-6-quinazoliny)l)methyl]amino]benzoyl] L-aspartic acid; aminopterin derivative N-[2-chloro-4-[[[(2, 4-diamino-6-pteridiny)l)methyl] amino]benzoyl] L-aspartic acid monohydrate; antifolate PT523 ((N<sup>α</sup>-(4-amino-4-deoxypteroyl)-N<sup>γ</sup>-hemiphthaloyl-L-ornithine)); Baker's soluble antifol (NSC 139105); dichlorallyl lawsone ((2-(3, 3-dichloroallyl)-3-hydroxy-1,4-naphthoquinone); brequinar; ftorafur ((pro-drug; 5-fluoro-1-(tetrahydro-2-furyl)-uracil); 5,6-dihydro-5-azacytidine; methotrexate; methotrexate derivative (N-[[4-[[[(2, 4-diamino-6-pteridiny)l)methyl]methylamino]-1-naphthalenyl]carbonyl ] L-glutamic acid); PALA ((N-(phosphonoacetyl)-L-aspartate); pyrazofurin; trimetrexate.

**[0159] DNA Antimetabolites:** 3-HP; 2'-deoxy-5-fluorouridine; 5-HP; α-TGDR (α-2'-deoxy-6-thioguanosine); aphidicolin glycinate; ara C (cytosine arabinoside); 5-aza-2'-deoxycytidine; β-TGDR (β-2'-deoxy-6-thioguanosine); cyclocytidine; guanazole; hydroxyurea; inosine glycodialdehyde; macbecin II; pyrazoloimidazole; thioguanine; thiopurine.

**[0160] Mitochondria Inhibitors:** pancratistatin; phenpanstatin; rhodamine-123; edelfosine; d-alpha-tocopherol succinate; compound 11β; aspirin; ellipticine; berberine; cerulenin; GX015-070 (Obatoclax®; 1H-Indole, 2-(2-((3,5-dimethyl-1H-pyrrol-2-yl)methylene)-3-methoxy-2H-pyrrol-5-yl)-); celastrol (tripterine); metformin; Brilliant green; ME-344.

[0161] **Antimitotic Agents:** allocolchicine; auristatins, such as MMAE (monomethyl auristatin E) and MMAF (monomethyl auristatin F); halichondrin B; cemadotin; colchicine; colchicine derivative (N-benzoyl-deacetyl benzamide); dolastatin-10; dolastatin-15; maytansine; maytansinoids, such as DM1 (*N*<sub>2</sub>'-deacetyl-*N*<sub>2</sub>'-(3-mercapto-1-oxopropyl)-maytansine); rhoxoxin; paclitaxel; paclitaxel derivative ((2'-N-[3-(dimethylamino)propyl]glutaramate paclitaxel); docetaxel; thiocolchicine; trityl cysteine; vinblastine sulfate; vincristine sulfate.

[0162] **Nuclear Export Inhibitors:** callystatin A; delactonmycin; KPT-185 (propan-2-yl (Z)-3-[3-[3-methoxy-5-(trifluoromethyl)phenyl]-1,2,4-triazol-1-yl]prop-2-enoate); kazusamycin A; leptolstatin; leptofuranin A; leptomycin B; ratjadone; Verdinexor ((Z)-3-[3-[3,5-bis(trifluoromethyl)phenyl]-1,2,4-triazol-1-yl]-N'-pyridin-2-ylprop-2-enehydrazide).

[0163] **Hormonal Therapies:** anastrozole; exemestane; arzoxifene; bicalutamide; cetrorelix; degarelix; deslorelin; trilostane; dexamethasone; flutamide; raloxifene; fadrozole; toremifene; fulvestrant; letrozole; formestane; glucocorticoids; doxercalciferol; sevelamer carbonate; lasofoxifene; leuprolide acetate; megestrol; mifepristone; nilutamide; tamoxifen citrate; abarelix; prednisone; finasteride; rilostane; buserelin; luteinizing hormone releasing hormone (LHRH); Histrelin; trilostane or modrastane; fosrelin; goserelin.

[0164] Any of these agents that include, or that may be modified to include, a site of attachment to an antibody and/or binding fragment may be included in an anti-huLRRC15 ADC.

[0165] Data presented herein demonstrate that anti-huLRRC15 ADCs exert potent anti-tumor activity against huLRRC15 stromal(+)/cancer(+) tumors that is mediated, at least in part, by a concentration effect that localizes anti-huLRRC15 ADCs to the desired target cancer cells. Hence, anti-huLRRC15 ADCs can be directly taken up by huLRRC15-expressing cancer cells, release the cytotoxic and/or cytostatic agent within the cell and cause direct cell killing. In addition, the direct cancer cell killing may also be supplemented by a targeted-bystander activity upon uptake in huLRRC15-expressing stromal cells, and subsequent release of the cytotoxic and/or cytostatic agent. For example, as demonstrated in FIGS. 13A-13D, cancer cells expressing huLRRC15 are sensitive *in vitro* to anti-huLRRC15 ADCs containing monomethyl auristatin E ("MMAE") as the drug. *In vivo*, huLRRC15 stromal(+)/cancer(+) U118MG glioblastoma xenografts are more sensitive to the anti-huLRRC15 ADC containing MMAE as compared with the corresponding isotype ADC, as demonstrated in FIGS. 14A, 14D, and 14E, and more sensitive than would be predicted based solely on the relative *in vitro* cytotoxic activities. This is also observed with huLRRC15 stromal(+)/cancer(+) patient-derived osteosarcoma xenografts, as demonstrated in FIGS. 14B and 14C. Together, these data demonstrate that anti-huLRRC15 ADCs containing cell-permeating

cytostatic and/or cytotoxic agents exert anti-tumor activity against huLRRC15 stromal(+)/cancer(+) tumors via a concentration effect localizing the anti-huLRRC15 ADCs within the huLRRC15(+) cancer cells to exert a cell killing activity, supplemented by a targeted-bystander anti-tumor effect in a number of cancer cell models. Hence, the anti-huLRRC15 ADCs described herein are useful therapeutically for the treatment of huLRRC15 stromal(+)/cancer(+) tumors.

[0166] Accordingly, in some embodiments, the cytotoxic and/or cytostatic agents included in an anti-huLRRC15 ADC will, upon cleavage of the ADC, be able to traverse cell membranes (“cell permeable cytostatic and/or cytotoxic agents”). Specific cytotoxic and/or cytostatic agents of interest, and/or cleavage products of ADCs including such agents, may be tested for the ability to traverse cell membranes using routine methods known to those of skill in the art. Permeability (P) of molecules across a membrane can be expressed as  $P = KD/\Delta x$  where K is the partition coefficient, D is the diffusion coefficient, and  $\Delta x$  is the thickness of the cell membrane. The diffusion coefficient (D) is a measure of the rate of entry into the cytoplasm depending on the molecular weight or size of a molecule. K is a measure of the solubility of the substance in lipids. A low value of K describes a molecule like water that is not soluble in lipid. Graphically, it is expected that permeability (P) as a function of the partition coefficient (K) will increase linearly when D and  $\Delta x$  are constants. (Walter & Gutknecht, 1986, “Permeability of small nonelectrolytes through lipid bilayer membranes,” *Journal of Membrane Biology* 90:207-217; Diamond & Katz, 1974, “Interpretation of nonelectrolyte partition coefficients between dimyristoyl lecithin and water,” *Journal of Membrane Biology* 17:121-154).

[0167] In a specific embodiment, the cytotoxic and/or cytostatic agent is a cell-permeable antimetabolic agent.

[0168] In another specific embodiment, the cytotoxic and/or cytostatic agent is a cell-permeable auristatin, such as, for example, dolastatin-10 or MMAE.

[0169] In another specific embodiment, the cytotoxic and/or cytostatic agent is a cell-permeable minor groove-binding DNA cross-linking agent, such as, for example, a pyrrolobenzodiazepine (“PBD”) dimer.

#### 7.4.2. Linkers

[0170] In the anti-huLRRC15 ADCs described herein, the cytotoxic and/or cytostatic agents are linked to the antigen binding moiety by way of linkers. The linkers may be short, long, hydrophobic, hydrophilic, flexible or rigid, or may be composed of segments that each independently have one or more of the above-mentioned properties such that the linker may include segments having different properties.

The linkers may be polyvalent such that they covalently link more than one agent to a single site on the antibody, or monovalent such that covalently they link a single agent to a single site on the antibody.

[0171] As will be appreciated by skilled artisans, the linkers link the cytotoxic and/or cytostatic agents to the antigen binding moiety by forming a covalent linkage to the cytotoxic and/or cytostatic agent at one location and a covalent linkage to the antigen binding moiety at another. The covalent linkages are formed by reaction between functional groups on the linker and functional groups on the agents and the antigen binding moiety. As used herein, the expression “linker” is intended to include (i) unconjugated forms of the linker that include a functional group capable of covalently linking the linker to a cytotoxic and/or cytostatic agent and a functional group capable of covalently linking the linker to the antigen binding moiety such as an antibody; (ii) partially conjugated forms of the linker that includes a functional group capable of covalently linking the linker to an antigen binding moiety such as an antibody and that is covalently linked to a cytotoxic and/or cytostatic agent, or *vice versa*; and (iii) fully conjugated forms of the linker that is covalently linked to both a cytotoxic and/or cytostatic agent and an antigen binding moiety such as an antibody. In some specific embodiments of linkers and ADCs described herein, as well as synthons used to conjugate linker-agents to antibodies, moieties comprising the functional groups on the linker and covalent linkages formed between the linker and antibody are specifically illustrated as R<sup>x</sup> and XY, respectively.

[0172] The linkers are preferably, but need not be, chemically stable to conditions outside the cell, and may be designed to cleave, immolate and/or otherwise specifically degrade inside the cell. Alternatively, linkers that are not designed to specifically cleave or degrade inside the cell may be used. Particular linkers may also be processed extracellularly in the tumor microenvironment by enzymes present at high levels in tumor stroma. Choice of stable versus unstable linker may depend upon the toxicity of the cytotoxic and/or cytostatic agent. A wide variety of linkers useful for linking drugs to antibodies in the context of ADCs are known in the art. Any of these linkers, as well as other linkers, may be used to link the cytotoxic and/or cytostatic agents to the antibody of the ADCs described herein.

[0173] Exemplary polyvalent linkers that may be used to link many cytotoxic and/or cytostatic agents to a single antibody molecule are described, for example, in WO 2009/073445; WO 2010/068795; WO 2010/138719; WO 2011/120053; WO 2011/171020; WO 2013/096901; WO 2014/008375; WO 2014/093379; WO 2014/093394; WO 2014/093640, the contents of which are incorporated herein by reference in their entireties. For example, the Fleximer linker technology developed by Mersana *et al.* has the potential to enable high-DAR ADCs with good physicochemical properties. As shown below, the Mersana technology is based on incorporating drug molecules into a solubilizing poly-acetal backbone

via a sequence of ester bonds. The methodology renders highly-loaded ADCs (DAR up to 20) while maintaining good physicochemical properties.

[0174] Additional examples of dendritic type linkers can be found in US 2006/116422; US 2005/271615; de Groot et al (2003) *Angew. Chem. Int. Ed.* 42:4490-4494; Amir et al (2003) *Angew. Chem. Int. Ed.* 42:4494-4499; Shamis et al (2004) *J. Am. Chem. Soc.* 126:1726-1731; Sun et al (2002) *Bioorganic & Medicinal Chemistry Letters* 12:2213-2215; Sun et al (2003) *Bioorganic & Medicinal Chemistry* 11:1761-1768; King et al (2002) *Tetrahedron Letters* 43:1987-1990, each of which is incorporated herein by reference.

[0175] Exemplary monovalent linkers that may be used are described, for example, in Nolting, 2013, *Antibody-Drug Conjugates, Methods in Molecular Biology* 1045:71-100; Kitson et al., 2013, *CROs/CMOs - Chemica Oggi – Chemistry Today* 31(4):30-38; Ducry et al., 2010, *Bioconjugate Chem.* 21:5-13; Zhao et al., 2011, *J. Med. Chem.* 54:3606-3623; U.S. Patent No. 7,223,837; U.S. Patent No. 8,568,728; U.S. Patent No. 8,535,678; and WO2004/010957, each of which is incorporated herein by reference.

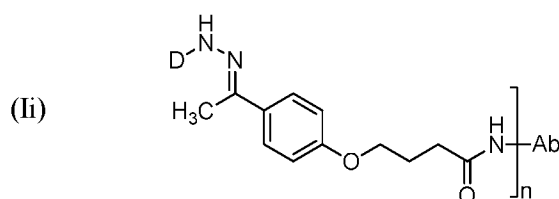
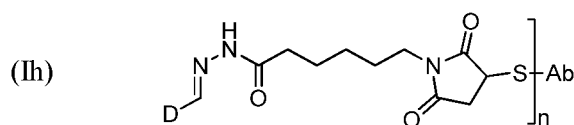
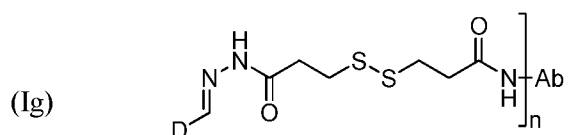
[0176] By way of example and not limitation, some cleavable and noncleavable linkers that may be included in the anti-huLRRC15 ADCs described herein are described below.

#### 7.4.2.1. Cleavable Linkers

[0177] In certain embodiments, the linker selected is cleavable *in vivo*. Cleavable linkers may include chemically or enzymatically unstable or degradable linkages. Cleavable linkers generally rely on processes inside the cell to liberate the drug, such as reduction in the cytoplasm, exposure to acidic conditions in the lysosome, or cleavage by specific proteases or other enzymes within the cell. Cleavable linkers generally incorporate one or more chemical bonds that are either chemically or enzymatically cleavable while the remainder of the linker is noncleavable. In certain embodiments, a linker comprises a chemically labile group such as hydrazone and/or disulfide groups. Linkers comprising chemically labile groups exploit differential properties between the plasma and some cytoplasmic compartments. The intracellular conditions to facilitate drug release for hydrazone containing linkers are the acidic environment of endosomes and lysosomes, while the disulfide containing linkers are reduced in the cytosol, which contains high thiol concentrations, *e.g.*, glutathione. In certain embodiments, the plasma stability of a linker comprising a chemically labile group may be increased by introducing steric hindrance using substituents near the chemically labile group.

[0178] Acid-labile groups, such as hydrazone, remain intact during systemic circulation in the blood's neutral pH environment (pH 7.3-7.5) and undergo hydrolysis and release the drug once the ADC is internalized into mildly acidic endosomal (pH 5.0-6.5) and lysosomal (pH 4.5-5.0) compartments of the cell. This pH dependent release mechanism has been associated with nonspecific release of the drug. To increase the stability of the hydrazone group of the linker, the linker may be varied by chemical modification, *e.g.*, substitution, allowing tuning to achieve more efficient release in the lysosome with a minimized loss in circulation.

[0179] Hydrazone-containing linkers may contain additional cleavage sites, such as additional acid-labile cleavage sites and/or enzymatically labile cleavage sites. ADCs including exemplary hydrazone-containing linkers include the following structures:



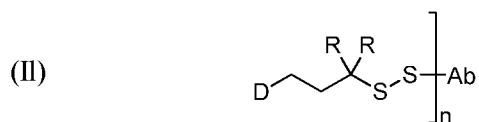
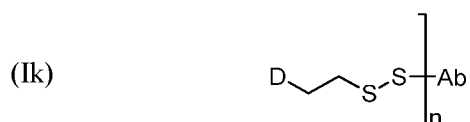
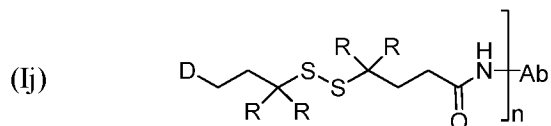
wherein D and Ab represent the cytotoxic and/or cytostatic agent (drug) and antibody, respectively, and n represents the number of drug-linkers linked to the antibody. In certain linkers such as linker (Ig), the linker comprises two cleavable groups – a disulfide and a hydrazone moiety. For such linkers, effective release of the unmodified free drug requires acidic pH or disulfide reduction and acidic pH. Linkers such as (Ih) and (Ii) have been shown to be effective with a single hydrazone cleavage site.

[0180] Other acid-labile groups that may be included in linkers include cis-aconityl-containing linkers. cis-Aconityl chemistry uses a carboxylic acid juxtaposed to an amide bond to accelerate amide hydrolysis under acidic conditions.



[0181] Cleavable linkers may also include a disulfide group. Disulfides are thermodynamically stable at physiological pH and are designed to release the drug upon internalization inside cells, wherein the cytosol provides a significantly more reducing environment compared to the extracellular environment. Scission of disulfide bonds generally requires the presence of a cytoplasmic thiol cofactor, such as (reduced) glutathione (GSH), such that disulfide-containing linkers are reasonably stable in circulation, selectively releasing the drug in the cytosol. The intracellular enzyme protein disulfide isomerase, or similar enzymes capable of cleaving disulfide bonds, may also contribute to the preferential cleavage of disulfide bonds inside cells. GSH is reported to be present in cells in the concentration range of 0.5-10 mM compared with a significantly lower concentration of GSH or cysteine, the most abundant low-molecular weight thiol, in circulation at approximately 5  $\mu$ M. Tumor cells, where irregular blood flow leads to a hypoxic state, result in enhanced activity of reductive enzymes and therefore even higher glutathione concentrations. In certain embodiments, the *in vivo* stability of a disulfide-containing linker may be enhanced by chemical modification of the linker, *e.g.*, use of steric hinderance adjacent to the disulfide bond.

[0182] ADCs including exemplary disulfide-containing linkers include the following structures:



wherein D and Ab represent the drug and antibody, respectively, n represents the number of drug-linkers linked to the antibody, and R is independently selected at each occurrence from hydrogen or alkyl, for example. In certain embodiments, increasing steric hinderance adjacent to the disulfide bond increases the stability of the linker. Structures such as (Ij) and (II) show increased *in vivo* stability when one or more R group is selected from a lower alkyl such as methyl.

[0183] Another type of cleavable linker that may be used is a linker that is specifically cleaved by an enzyme. Such linkers are typically peptide-based or include peptidic regions that act as substrates for enzymes. Peptide based linkers tend to be more stable in plasma and extracellular milieu than chemically labile linkers. Peptide bonds generally have good serum stability, as lysosomal proteolytic enzymes have very low activity in blood due to endogenous inhibitors and the unfavorably high pH value of blood compared to lysosomes. Release of a drug from an antibody occurs specifically due to the action of lysosomal proteases, *e.g.*, cathepsin and plasmin. These proteases may be present at elevated levels in certain tumor cells.

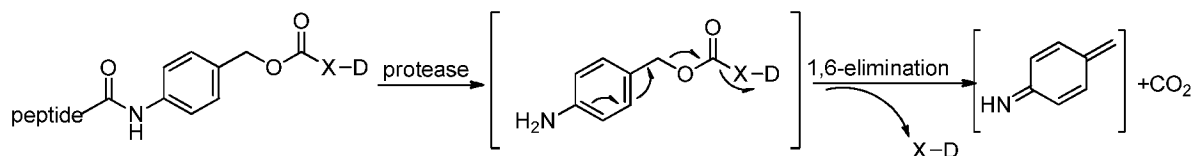
[0184] In exemplary embodiments, the cleavable peptide is selected from tetrapeptides such as Gly-Phe-Leu-Gly (SEQ ID NO:80), Ala-Leu-Ala-Leu (SEQ ID NO:81) or dipeptides such as Val-Cit, Val-Ala, Met-(D)Lys, Asn-(D)Lys, Val-(D)Asp, Phe-Lys, Ile-Val, Asp-Val, His-Val, NorVal-(D)Asp, Ala-(D)Asp, Met-Lys, Asn-Lys, Ile-Pro, Me3Lys-Pro, PhenylGly-(D)Lys, Met-(D)Lys, Asn-(D)Lys, Pro-(D)Lys, Met-(D)Lys, Asn-(D)Lys, Met-(D)Lys, Asn-(D)Lys. In certain embodiments, dipeptides are preferred over longer polypeptides due to hydrophobicity of the longer peptides.

[0185] A variety of dipeptide-based cleavable linkers useful for linking drugs such as doxorubicin, mitomycin, camptothecin, tallysomycin and auristatin/auristatin family members to antibodies have been described (*see*, Dubowchik *et al.*, 1998, *J. Org. Chem.* 67:1866-1872; Dubowchik *et al.*, 1998, *Bioorg. Med. Chem. Lett.* 8(21):3341-3346; Walker *et al.*, 2002, *Bioorg. Med. Chem. Lett.* 12:217-219; Walker *et al.*, 2004, *Bioorg. Med. Chem. Lett.* 14:4323-4327; and Francisco *et al.*, 2003, *Blood* 102:1458-1465, Dornina *et al.*, 2008, *Bioconjugate Chemistry* 19:1960-1963, of each of which is incorporated herein by reference). All of these dipeptide linkers, or modified versions of these dipeptide linkers, may be used in the ADCs described herein. Other dipeptide linkers that may be used include those found in ADCs such as Seattle Genetics' Brentuximab Vedotin SGN-35 (Adcetris™), Seattle Genetics SGN-75 (anti-CD-70, Val-Cit-MMAF), Celldex Therapeutics glembatumumab (CDX-011) (anti-GPNMB, Val-Cit-MMAE), and Cytogen PSMA-ADC (PSMA-ADC-1301) (anti-PSMA, Val-Cit-MMAE).

[0186] Enzymatically cleavable linkers may include a self-immolative spacer to spatially separate the drug from the site of enzymatic cleavage. The direct attachment of a drug to a peptide linker can result in proteolytic release of an amino acid adduct of the drug, thereby impairing its activity. The use of a self-immolative spacer allows for the elimination of the fully active, chemically unmodified drug upon amide bond hydrolysis.

[0187] One self-immolative spacer is the bifunctional *para*-aminobenzyl alcohol group, which is linked to the peptide through the amino group, forming an amide bond, while amine containing drugs may be

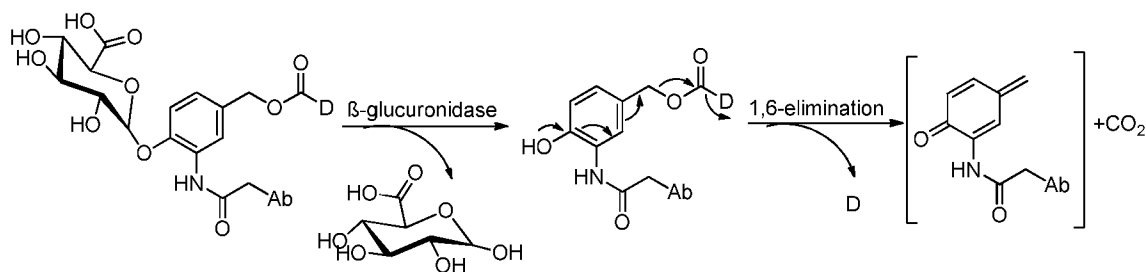
attached through carbamate functionalities to the benzylic hydroxyl group of the linker (PABC). The resulting prodrugs are activated upon protease-mediated cleavage, leading to a 1,6-elimination reaction releasing the unmodified drug, carbon dioxide, and remnants of the linker group. The following scheme depicts the fragmentation of *p*-amidobenzyl ether and release of the drug:



wherein X-D represents the unmodified drug.

[0188] Heterocyclic variants of this self-immolative group have also been described. *See* for example, US 7,989,434, incorporated herein by reference.

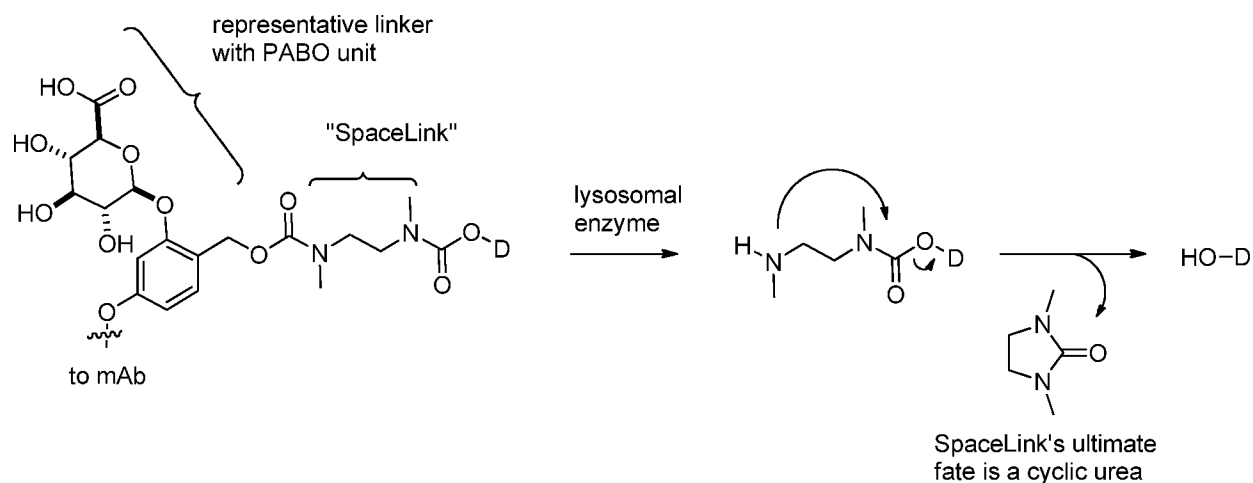
[0189] In some embodiments, the enzymatically cleavable linker is a  $\beta$ -glucuronic acid-based linker. Facile release of the drug may be realized through cleavage of the  $\beta$ -glucuronide glycosidic bond by the lysosomal enzyme  $\beta$ -glucuronidase. This enzyme is present abundantly within lysosomes and is overexpressed in some tumor types, while the enzyme activity outside cells is low.  $\beta$ -Glucuronic acid-based linkers may be used to circumvent the tendency of an ADC to undergo aggregation due to the hydrophilic nature of  $\beta$ -glucuronides. In some embodiments,  $\beta$ -glucuronic acid-based linkers are preferred as linkers for ADCs linked to hydrophobic drugs. The following scheme depicts the release of the drug from an ADC containing a  $\beta$ -glucuronic acid-based linker:



[0190] A variety of cleavable  $\beta$ -glucuronic acid-based linkers useful for linking drugs such as auristatins, camptothecin and doxorubicin analogues, CBI minor-groove binders, and psymberin to antibodies have been described (*see, see* Nolting, Chapter 5 “Linker Technology in Antibody-Drug Conjugates,” *In: Antibody-Drug Conjugates: Methods in Molecular Biology*, vol. 1045, pp. 71-100, Laurent Ducry (Ed.), Springer Science & Business Media, LLC, 2013; Jeffrey *et al.*, 2006, *Bioconjug. Chem.* 17:831-840; Jeffrey *et al.*, 2007, *Bioorg. Med. Chem. Lett.* 17:2278-2280; and Jiang *et al.*, 2005, *J. Am. Chem. Soc.*

127:11254-11255, each of which is incorporated herein by reference). All of these  $\beta$ -glucuronic acid-based linkers may be used in the anti-huLRRC15 ADCs described herein.

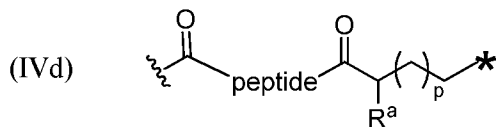
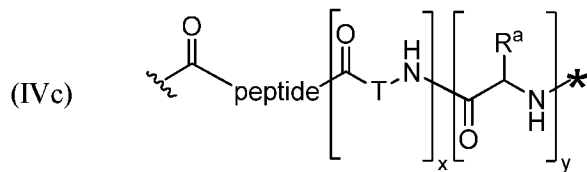
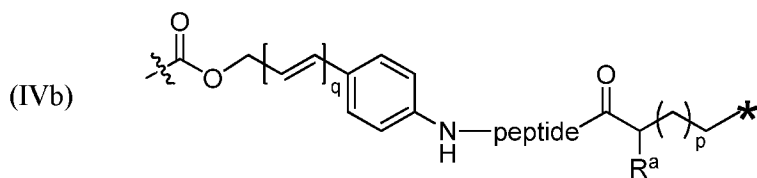
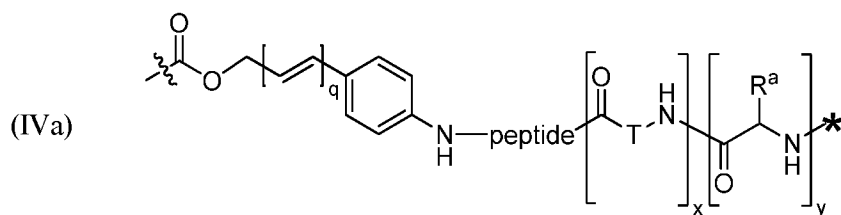
[0191] Additionally, cytotoxic and/or cytostatic agents containing a phenol group can be covalently bonded to a linker through the phenolic oxygen. One such linker, described in WO 2007/089149, relies on a methodology in which a diamino-ethane "SpaceLink" is used in conjunction with traditional "PABO"-based self-immolative groups to deliver phenols. The cleavage of the linker is depicted schematically below, where D represents a cytotoxic and/or cytostatic agent having a phenolic hydroxyl group.



[0192] Cleavable linkers may include noncleavable portions or segments, and/or cleavable segments or portions may be included in an otherwise non-cleavable linker to render it cleavable. By way of example only, polyethylene glycol (PEG) and related polymers may include cleavable groups in the polymer backbone. For example, a polyethylene glycol or polymer linker may include one or more cleavable groups such as a disulfide, a hydrazone or a dipeptide.

[0193] Other degradable linkages that may be employed in linkers include, but are not limited to, ester linkages formed by the reaction of PEG carboxylic acids or activated PEG carboxylic acids with alcohol groups on a biologically active agent, wherein such ester groups generally hydrolyze under physiological conditions to release the biologically active agent. Hydrolytically degradable linkages include, but are not limited to, carbonate linkages; imine linkages resulting from reaction of an amine and an aldehyde; phosphate ester linkages formed by reacting an alcohol with a phosphate group; acetal linkages that are the reaction product of an aldehyde and an alcohol; orthoester linkages that are the reaction product of a formate and an alcohol; and oligonucleotide linkages formed by a phosphoramidite group, including but not limited to, at the end of a polymer, and a 5'-hydroxyl group of an oligonucleotide.

[0194] In certain embodiments, the linker comprises an enzymatically cleavable peptide moiety, for example, a linker comprising structural formula (IVa), (IVb), (IVc), or (IVd):



or a salt thereof, wherein:

peptide represents a peptide (illustrated C $\rightarrow$ N and not showing the carboxy and amino “termini”) cleavable by a lysosomal enzyme;

T represents a polymer comprising one or more ethylene glycol units or an alkylene chain, or combinations thereof;


$R^a$  is selected from hydrogen, alkyl, sulfonate and methyl sulfonate;

$p$  is an integer ranging from 0 to 5;

$q$  is 0 or 1;

$x$  is 0 or 1;

y is 0 or 1;

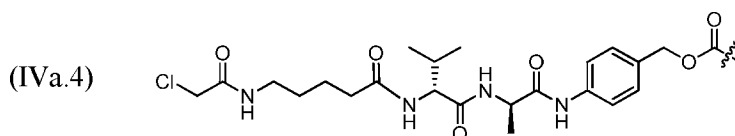
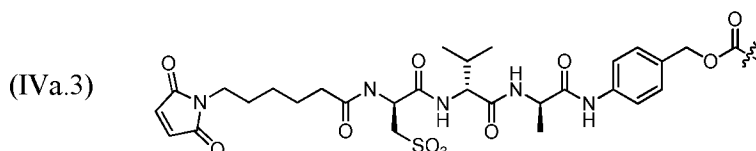
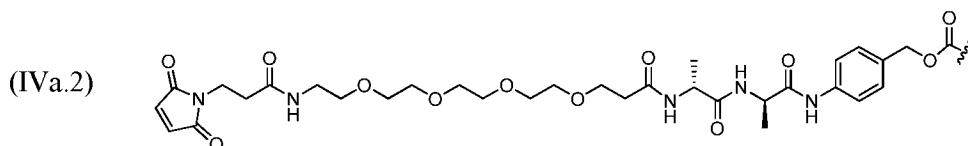
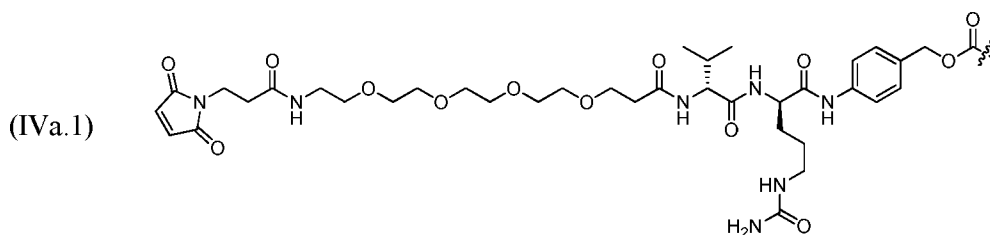
 represents the point of attachment of the linker to a cytotoxic and/or cytostatic agent;

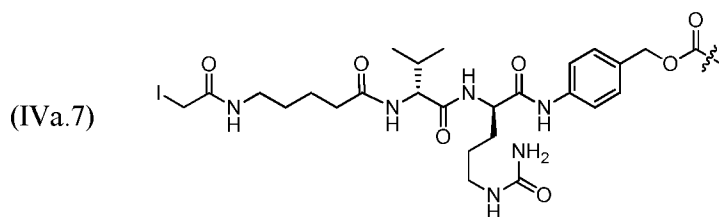
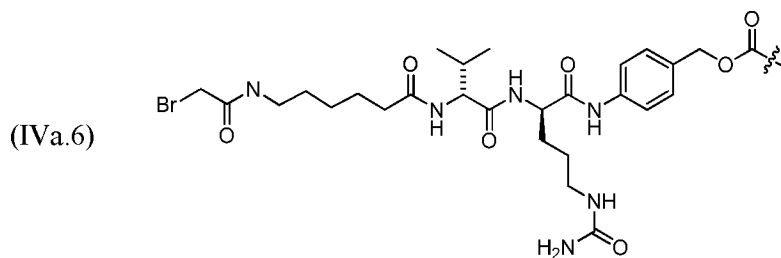
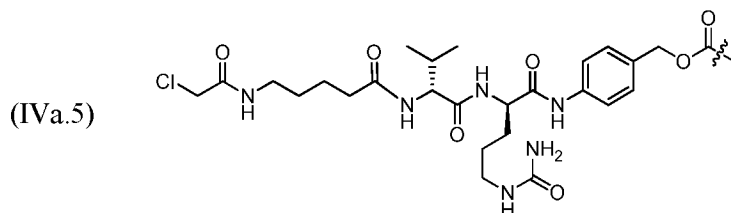
and

\* represents the point of attachment to the remainder of the linker.

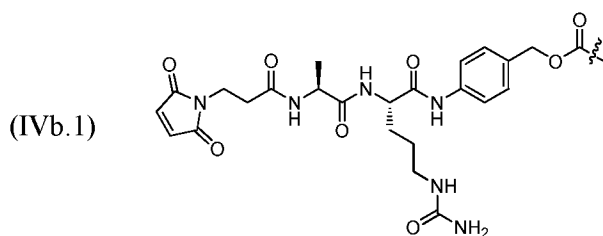
[0195] In certain embodiments, the peptide is selected from a tripeptide or a dipeptide. In particular embodiments, the dipeptide is selected from: Val-Cit; Cit-Val; Ala-Ala; Ala-Cit; Cit-Ala; Asn-Cit; Cit-Asn; Cit-Cit; Val-Glu; Glu-Val; Ser-Cit; Cit-Ser; Lys-Cit; Cit-Lys; Asp-Cit; Cit-Asp; Ala-Val; Val-Ala; Phe-Lys; Val-Lys; Ala-Lys; Phe-Cit; Leu-Cit; Ile-Cit; Phe-Arg; and Trp-Cit.

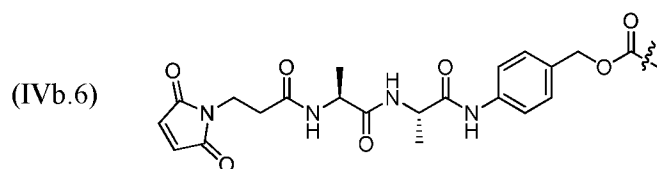
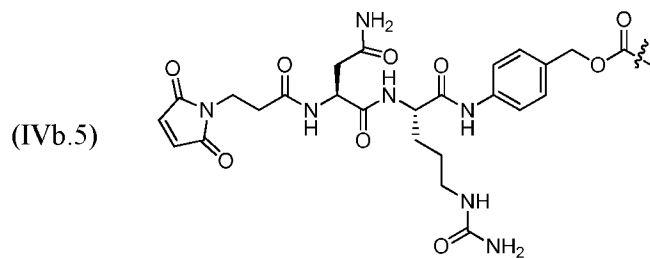
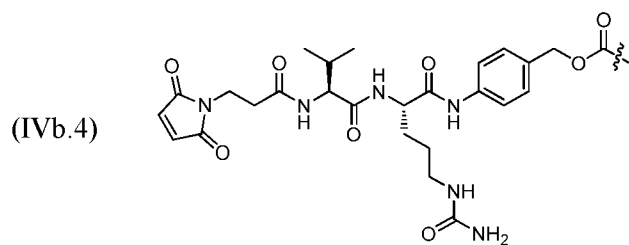
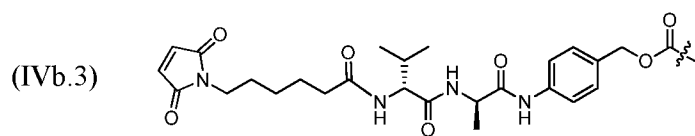
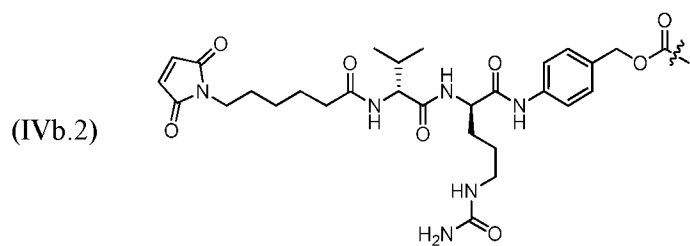
[0196] Specific exemplary embodiments of linkers according to structural formula (IVa) that may be included in the ADCs described herein include the linkers illustrated below (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody):



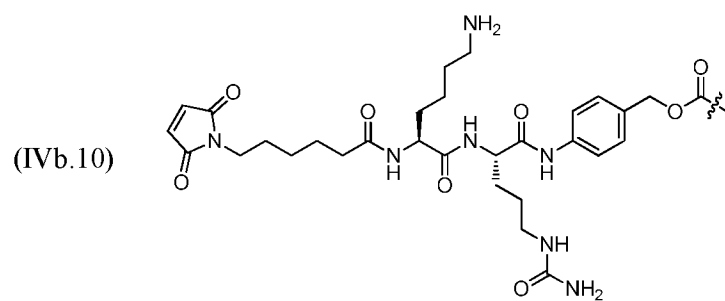
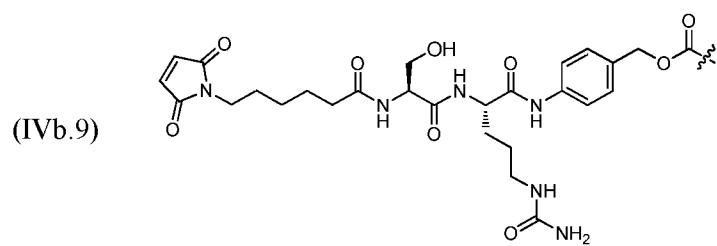
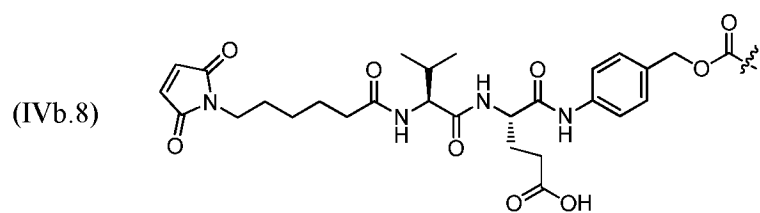
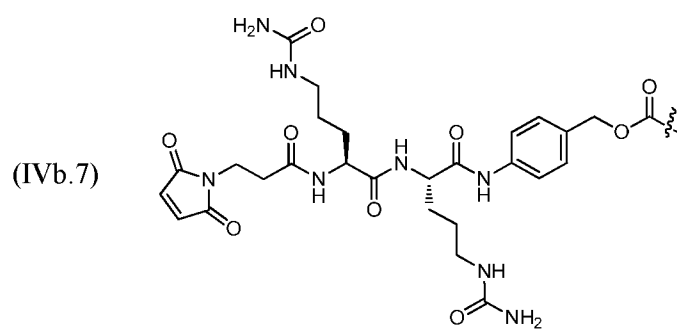


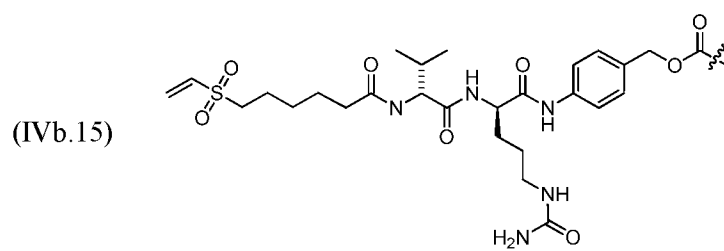
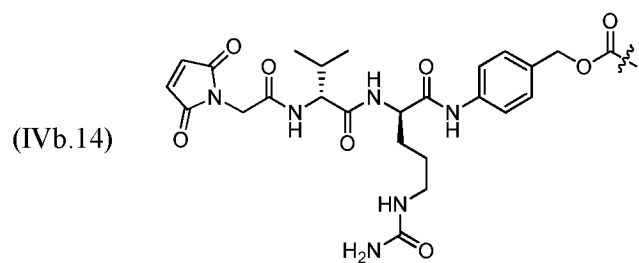
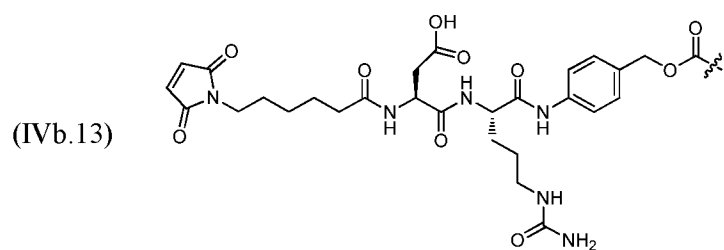
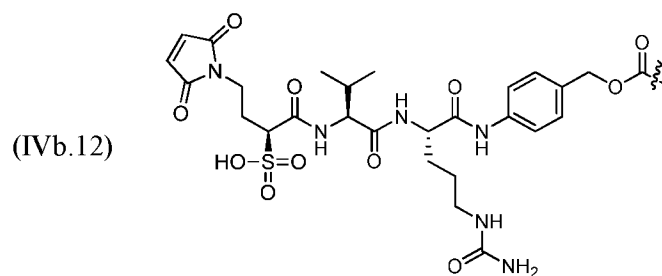
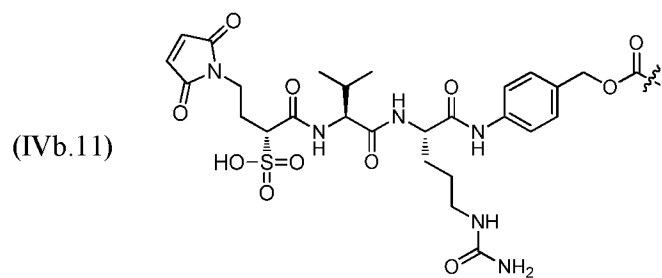
**[0197]** Specific exemplary embodiments of linkers according to structural formula (IVb) that may be included in the ADCs described herein include the linkers illustrated below (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody):

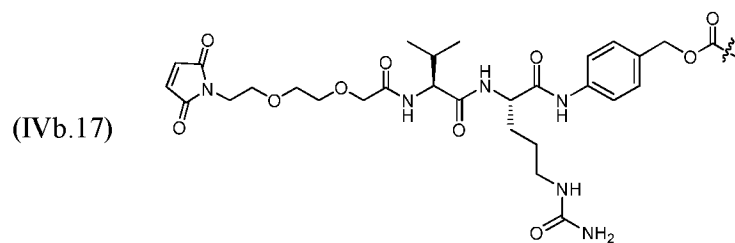
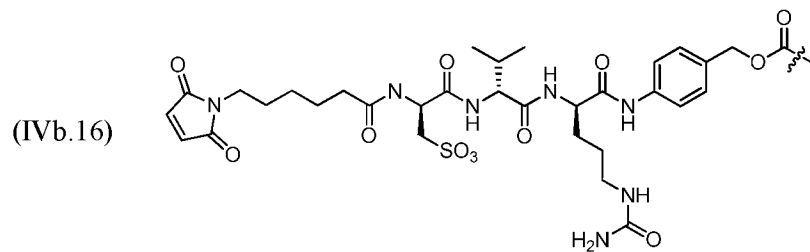




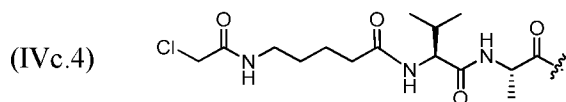
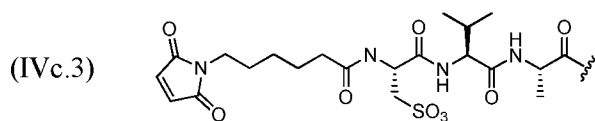
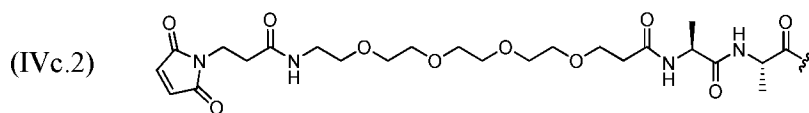
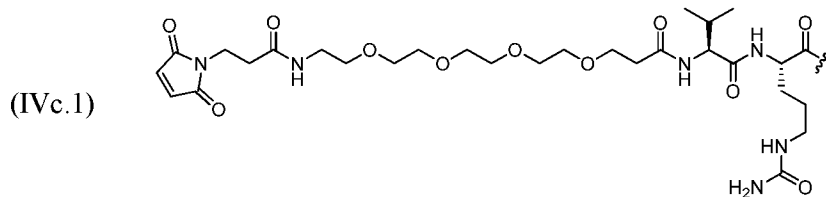


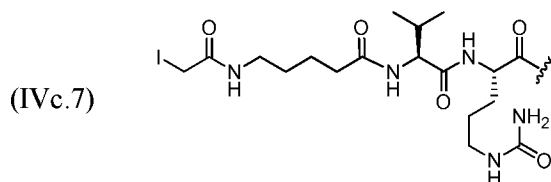
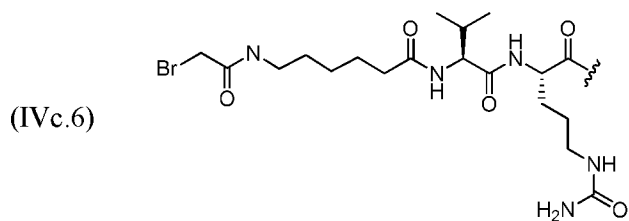
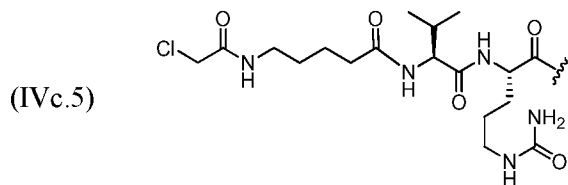




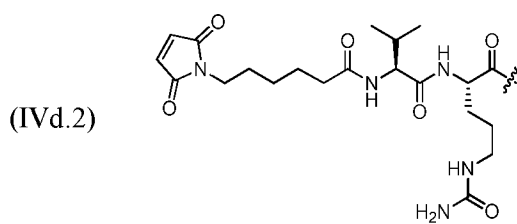
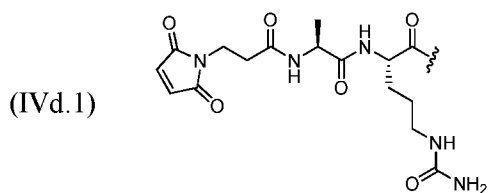


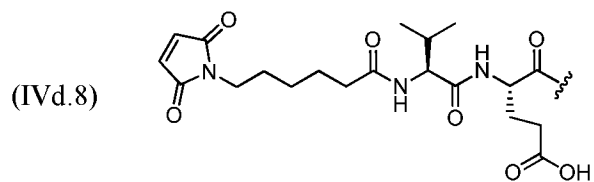
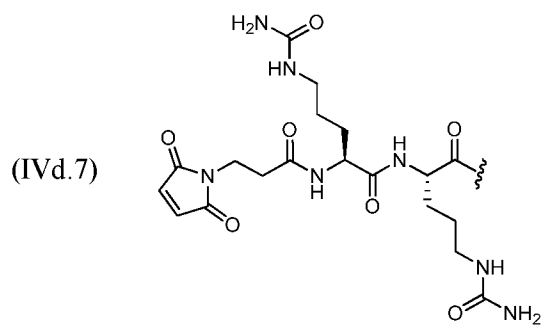
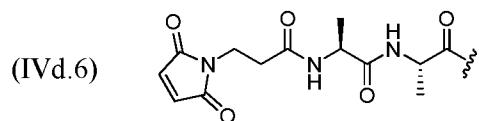
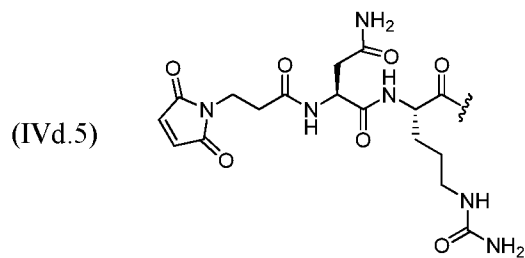
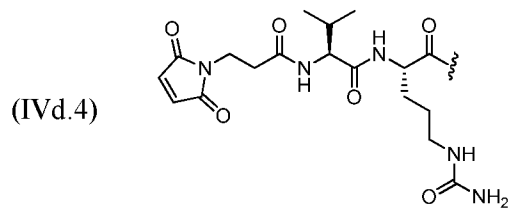
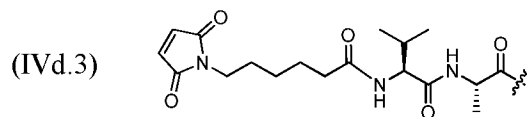
[0198] Specific exemplary embodiments of linkers according to structural formula (IVc) that may be included in the ADCs described herein include the linkers illustrated below (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody):

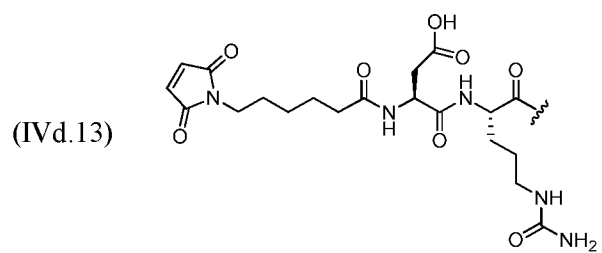
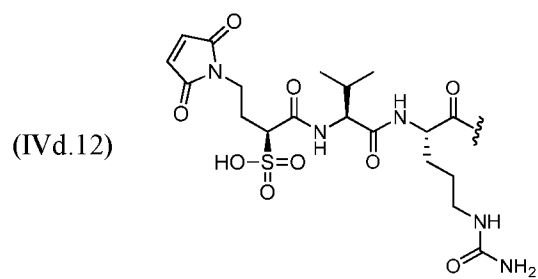
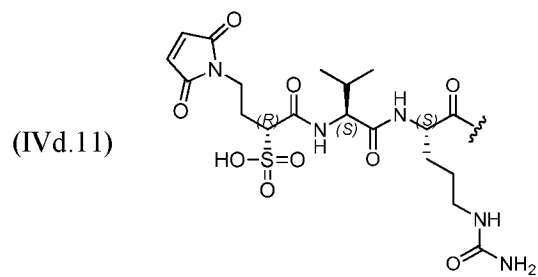
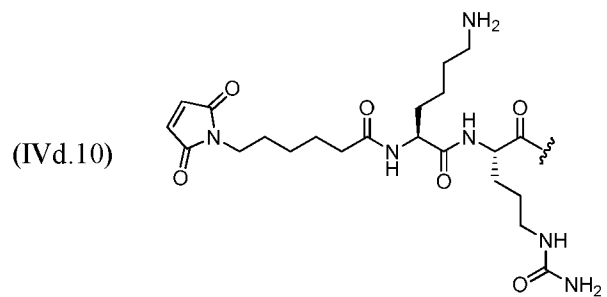
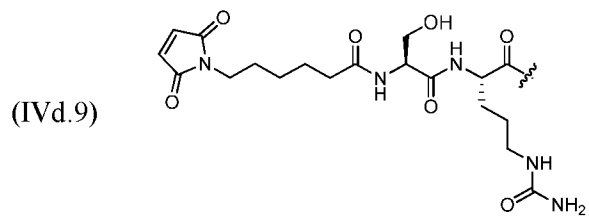


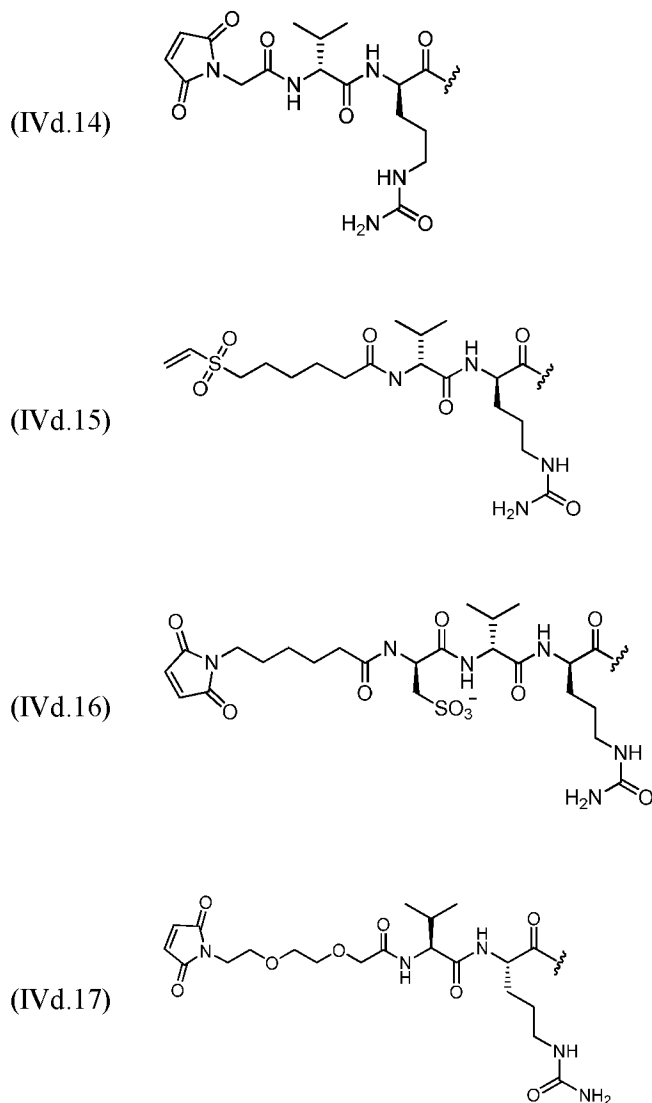


[0199] Specific exemplary embodiments of linkers according to structural formula (IVd) that may be included in the ADCs described herein include the linkers illustrated below (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody):









[0200] In certain embodiments, the linker comprising structural formula (IVa), (IVb), (IVc), or (IVd) further comprises a carbonate moiety cleavable by exposure to an acidic medium. In particular embodiments, the linker is attached through an oxygen to a cytotoxic and/or cytostatic agent.

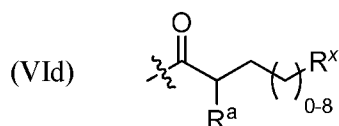
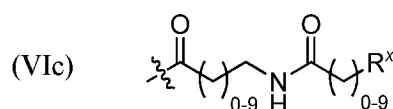
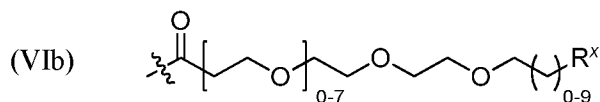
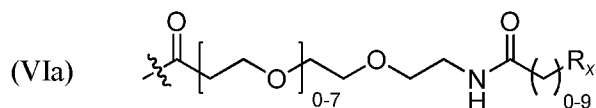
#### 7.4.2.2. Non-Cleavable Linkers

[0201] Although cleavable linkers may provide certain advantages, the linkers composing the ADC described herein need not be cleavable. For non-cleavable linkers, the release of drug does not depend on the differential properties between the plasma and some cytoplasmic compartments. The release of the drug is postulated to occur after internalization of the ADC via antigen-mediated endocytosis and delivery to lysosomal compartment, where the antibody is degraded to the level of amino acids through

intracellular proteolytic degradation. This process releases a drug derivative, which is formed by the drug, the linker, and the amino acid residue to which the linker was covalently attached. The amino acid drug metabolites from conjugates with non-cleavable linkers are more hydrophilic and generally less membrane permeable, which leads to less bystander effects and less nonspecific toxicities compared to conjugates with a cleavable linker. In general, ADCs with non-cleavable linkers have greater stability in circulation than ADCs with cleavable linkers. Non-cleavable linkers may be alkylene chains, or may be polymeric in nature, such as, for example, those based upon polyalkylene glycol polymers, amide polymers, or may include segments of alkylene chains, polyalkylene glycols and/or amide polymers.

**[0202]** A variety of non-cleavable linkers used to link drugs to antibodies have been described. *See*, Jeffrey *et al.*, 2006, *Bioconjug. Chem.* 17:831-840; Jeffrey *et al.*, 2007, *Bioorg. Med. Chem. Lett.* 17:2278-2280; and Jiang *et al.*, 2005, *J. Am. Chem. Soc.* 127:11254-11255, each of which is incorporated herein by reference. All of these linkers may be included in the ADCs described herein.

**[0203]** In certain embodiments, the linker is non-cleavable *in vivo*, for example a linker according to structural formula (VIa), (VIb), (VIc) or (VIId) (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody:





or salts thereof, wherein:

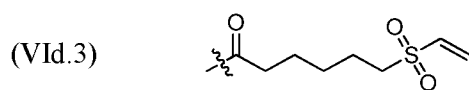
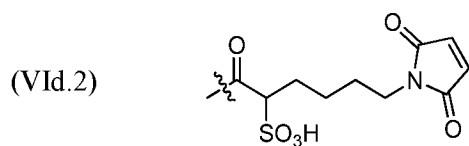
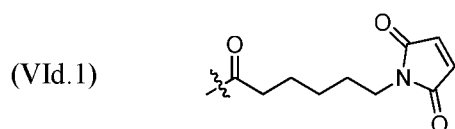
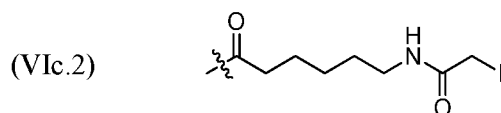
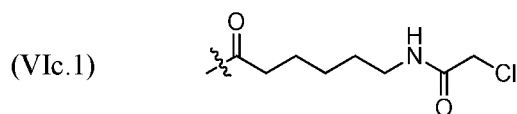
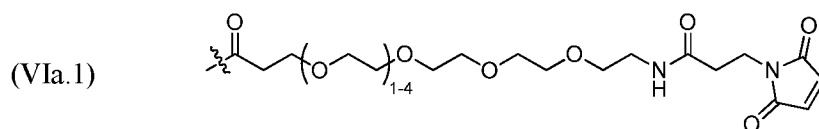


$R^a$  is selected from hydrogen, alkyl, sulfonate and methyl sulfonate;

$R^x$  is a moiety including a functional group capable of covalently linking the linker to an antibody; and

 represents the point of attachment of the linker to a cytotoxic and/or cytostatic agent.

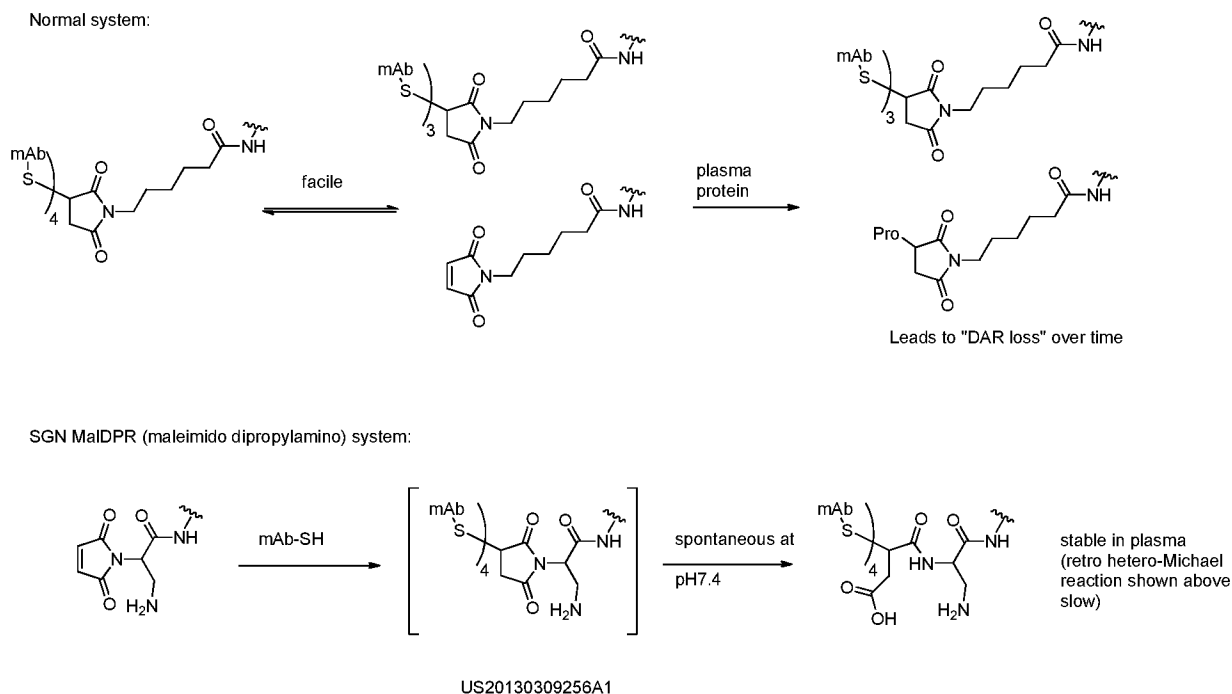
[0204] Specific exemplary embodiments of linkers according to structural formula (VIa)-(VId) that may be included in the ADCs described herein include the linkers illustrated below (as illustrated, the linkers include a group suitable for covalently linking the linker to an antibody, and “” represents the point of attachment to a cytotoxic and/or cytostatic agent):



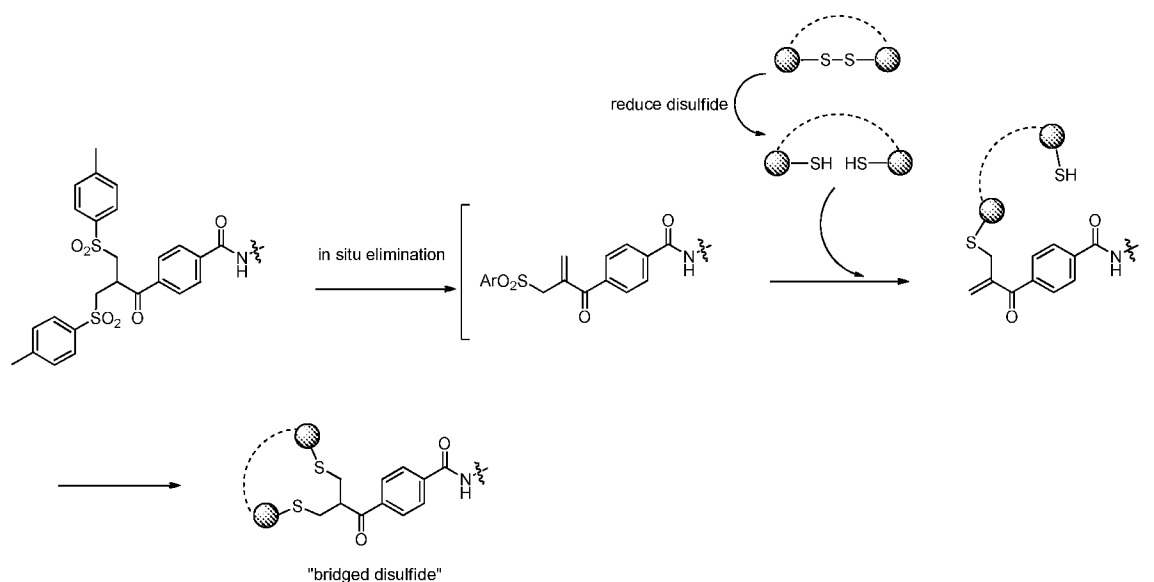
### 7.4.2.3. Groups Used to Attach Linkers to Antibodies

[0205] A variety of groups may be used to attach linker-drug synthons to antibodies to yield ADCs. Attachment groups can be electrophilic in nature and include: maleimide groups, activated disulfides, active esters such as NHS esters and HOBt esters, haloformates, acid halides, alkyl and benzyl halides such as haloacetamides. As discussed below, there are also emerging technologies related to “self-stabilizing” maleimides and “bridging disulfides” that can be used in accordance with the disclosure. The specific group used will depend, in part, on the site of attachment to the antibody.

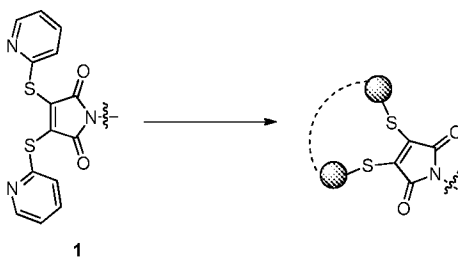
[0206] One example of a “self-stabilizing” maleimide group that hydrolyzes spontaneously under antibody conjugation conditions to give an ADC species with improved stability is depicted in the schematic below. See US20130309256 A1; also Lyon et al., Nature Biotech published online, doi:10.1038/nbt.2968).



[0207] Polytherics has disclosed a method for bridging a pair of sulfhydryl groups derived from reduction of a native hinge disulfide bond. See, Badescu et al., 2014, Bioconjugate Chem. 25:1124-1136. The reaction is depicted in the schematic below. An advantage of this methodology is the ability to synthesize homogeneous DAR4 ADCs by full reduction of IgGs (to give 4 pairs of sulfhydryls) followed by reaction with 4 equivalents of the alkylating agent. ADCs containing “bridged disulfides” are also claimed to have increased stability.



[0208] Similarly, as depicted below, a maleimide derivative (1, below) that is capable of bridging a pair of sulfhydryl groups has been developed. See WO2013/085925.



#### 7.4.2.4. Linker Selection Considerations

[0209] As is known by skilled artisans, the linker selected for a particular ADC may be influenced by a variety of factors, including but not limited to, the site of attachment to the antibody (*e.g.*, Lys, Cys or other amino acid residues), structural constraints of the drug pharmacophore and the lipophilicity of the drug. The specific linker selected for an ADC should seek to balance these different factors for the specific antibody/drug combination. For a review of the factors that are influenced by choice of linkers in ADCs, see Nolting, Chapter 5 "Linker Technology in Antibody-Drug Conjugates," *In: Antibody-Drug Conjugates: Methods in Molecular Biology*, vol. 1045, pp. 71-100, Laurent Ducry (Ed.), Springer Science & Business Media, LLC, 2013.

[0210] For example, as discussed above, anti-huLRRC15 ADCs have been observed to induce bystander killing of cancer cells present in the vicinity of huLRRC15-expressing stromal cells for huLRRC15 stromal(+)/cancer (-) tumors. The mechanism of bystander cell killing by ADCs has indicated that

metabolic products formed during intracellular processing of the ADCs may play a role. Cell-permeable cytotoxic and/or cytostatic metabolites generated by metabolism of the ADCs in huLRRC15-expressing cells appear to play a role in bystander cell killing, while non-cell-permeable metabolites, which are incapable of traversing the cell membrane and diffusing into the medium cannot effect bystander killing. In certain embodiments, the linker is selected to effect, enhance or increase the bystander killing effect of the anti-huLRRC15 ADCs.

[0211] The properties of the linker may also impact aggregation of the ADC under conditions of use and/or storage. Typically, ADCs reported in the literature contain no more than 3-4 drug molecules per antigen-binding moiety, for example, per antibody molecule (*see, e.g.*, Chari, 2008, *Acc Chem Res* 41:98-107). Attempts to obtain higher drug-to-antibody ratios ("DAR") often failed, particularly if both the drug and the linker were hydrophobic, due to aggregation of the ADC (King *et al.*, 2002, *J Med Chem* 45:4336-4343; Hollander *et al.*, 2008, *Bioconjugate Chem* 19:358-361; Burke *et al.*, 2009 *Bioconjugate Chem* 20:1242-1250). In many instances, DARs higher than 3-4 could be beneficial as a means of increasing potency. In instances where the cytotoxic and/or cytostatic agent is hydrophobic in nature, it may be desirable to select linkers that are relatively hydrophilic as a means of reducing ADC aggregation, especially in instances where DARs greater than 3-4 are desired. Thus, in certain embodiments, the linker incorporates chemical moieties that reduce aggregation of the ADCs during storage and/or use. A linker may incorporate polar or hydrophilic groups such as charged groups or groups that become charged under physiological pH to reduce the aggregation of the ADCs. For example, a linker may incorporate charged groups such as salts or groups that deprotonate, *e.g.*, carboxylates, or protonate, *e.g.*, amines, at physiological pH.

[0212] Exemplary polyvalent linkers that have been reported to yield DARs as high as 20 that may be used to link numerous cytotoxic and/or cytostatic agents to an antibody are described in WO 2009/073445; WO 2010/068795; WO 2010/138719; WO 2011/120053; WO 2011/171020; WO 2013/096901; WO 2014/008375; WO 2014/093379; WO 2014/093394; WO 2014/093640, the contents of which are incorporated herein by reference in their entireties.

[0213] In particular embodiments, the aggregation of the ADCs during storage or use is less than about 10% as determined by size-exclusion chromatography (SEC). In particular embodiments, the aggregation of the ADCs during storage or use is less than 10%, such as less than about 5%, less than about 4%, less than about 3%, less than about 2%, less than about 1%, less than about 0.5%, less than about 0.1%, or even lower, as determined by size-exclusion chromatography (SEC). In particular embodiments, the

aggregation of the ADCs during storage or use is in a range of any two of the foregoing values, such as but not limited to from about 0.1% to 10%, 0.1% to 5%, 0.5% to 10%, 0.5% to 5%, or 1% to 10%.

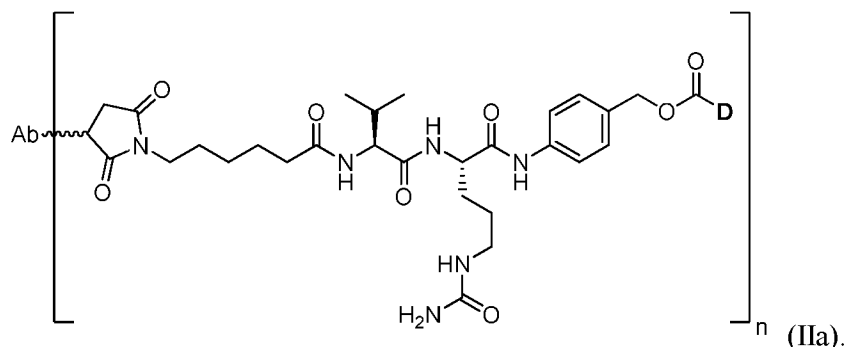
#### 7.4.3. Embodiments of Anti-huLRRC15 Antibody Drug Conjugates

[0214] As described above, embodiments of an anti-huLRRC15 ADC include compounds having a structure according to formula (I):  $[D-L-XY]_n$ -Ab (I), or a salt thereof, wherein **D** is the cytotoxic and/or cytostatic agent; **L** is the linker; **Ab** is the antibody; **XY** represents a covalent linkage linking linker **L** to antibody **Ab**; and **n** is an integer ranging from 2 to 8.

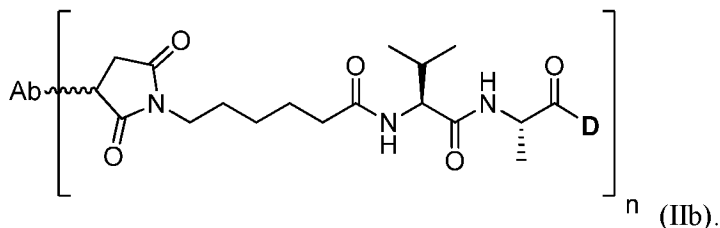
[0215] In some embodiments, **XY** is a linkage formed with an amino group on antibody **Ab**, such as an amide or a thiourea, or a linkage formed with a sulfhydryl group on antibody **Ab**, such as a thioether. In certain such embodiments, **XY** is a thioether.

[0216] In some embodiments, **L** comprises Val-Cit or Val-Ala.

[0217] In some embodiments, the compound according to structural formula (I) has a structure of formula (IIa):



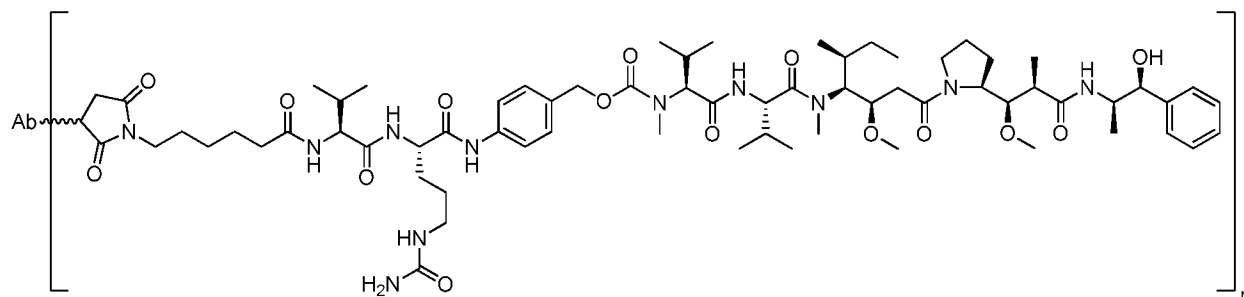
[0218] In some embodiments, the compound according to structural formula (I) has a structure of formula (IIb):



[0219] In some embodiments of the compound of formula (I), (IIa), or (IIb), **D** is an antimitotic agent or a DNA-intercalating agent. In some such embodiments, **D** is an antimitotic agent which is a cell-permeable antimitotic agent. In certain such embodiments, the cell-permeable antimitotic agent is

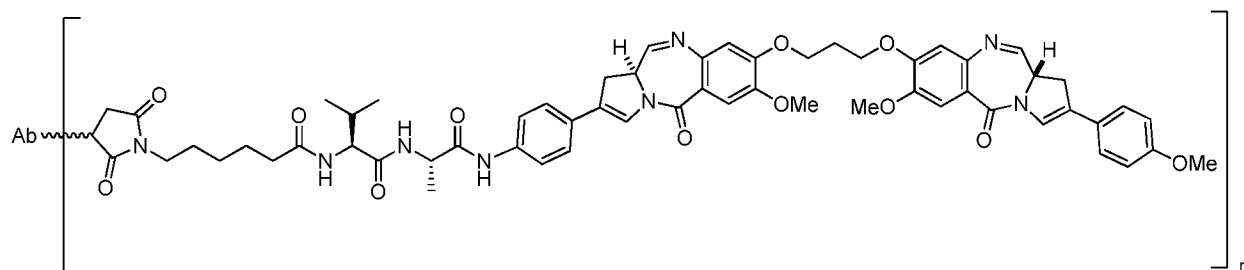
MMAE. In other such embodiments, D is a DNA-intercalating agent which is a pyrrolobenzodiazepine (PBD) dimer.

[0220] In some embodiments, the compound according to structural formula (I) has a structure of formula (IIIa):



(IIIa).

[0221] In some embodiments, the compound according to structural formula (I) has a structure of formula (IIIb):



(IIIb).

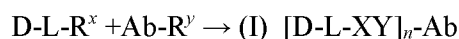
[0222] In some embodiments of the compound of formula (I), (IIa), (IIb), (IIIa), or (IIIb), Ab is an antibody comprising three V<sub>H</sub> CDRs corresponding in sequence, respectively, to SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12 and three V<sub>L</sub> CDRs corresponding in sequence, respectively, to SEQ ID NO:13, SEQ ID NO:14 and SEQ ID NO:15. In some such embodiments, Ab is an antibody with a V<sub>H</sub> having an amino acid sequence of SEQ ID NO:16, and a V<sub>L</sub> having an amino acid sequence of SEQ ID NO:17. In other embodiments, Ab is an antibody comprising three V<sub>H</sub> CDRs corresponding in sequence, respectively, to SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22 and three V<sub>L</sub> CDRs corresponding in sequence, respectively, to SEQ ID NO:23, SEQ ID NO:24 and SEQ ID NO:25. In some such embodiments, Ab is an antibody with a V<sub>H</sub> having an amino acid sequence of SEQ ID NO:26, and a V<sub>L</sub> having an amino acid sequence of SEQ ID NO:27. In some embodiments, Ab is a human IgG<sub>1</sub>. In some such embodiments, Ab is an antibody with a heavy chain having an amino acid sequence of SEQ ID

NO:18 or 102, and a light chain having an amino acid sequence of SEQ ID NO:19. In other such embodiments, Ab is an antibody with a heavy chain having an amino acid sequence of SEQ ID NO:100 or 103, and a light chain having an amino acid sequence of SEQ ID NO:19. In other such embodiments, Ab is an antibody with a heavy chain having an amino acid sequence of SEQ ID NO:28 or 101, and a light chain having an amino acid sequence of SEQ ID NO:29. In other such embodiments, Ab is an antibody with a heavy chain having an amino acid sequence of SEQ ID NO:104 or 105, and a light chain having an amino acid sequence of SEQ ID NO:29. In some embodiments, Ab is an antibody selected from huM25, huM25-S239C, huAD208.4.1, and huAD208.4.1-S239C. In certain such embodiments, Ab is huM25. In other such embodiments, Ab is huM25-S239C. In yet other such embodiments, Ab is huAD208.4.1. In yet other such embodiments, Ab is huAD208.4.1-S239C.

[0223] In some embodiments of the compound of formula (I), (IIa), (IIb), (IIIa), or (IIIb),  $n$  is 2, 3, or 4. In certain such embodiments,  $n$  is 2 or 4.

### 7.5. Methods of Making Anti-huLRRC15 Antibody Drug Conjugates

[0224] The ADCs described herein may be synthesized using chemistries that are well-known. The chemistries selected will depend upon, among other things, the identity of the cytotoxic and/or cytostatic agent(s), the linker and the groups used to attach linker to the antibody. Generally, ADCs according to formula (I) may be prepared according to the following scheme:



where D, L, Ab, XY and  $n$  are as previously defined, and  $R^x$  and  $R^y$  represent complementary groups capable of forming covalent linkages with one another, as discussed above.

[0225] The identities of groups  $R^x$  and  $R^y$  will depend upon the chemistry used to link synthon D-L- $R^x$  to the antibody. Generally, the chemistry used should not alter the integrity of the antibody, for example its ability to bind its target. Preferably, the binding properties of the conjugated antibody will closely resemble those of the unconjugated antibody. A variety of chemistries and techniques for conjugating molecules to biological molecules such as antibodies are known in the art and in particular to antibodies, are well-known. See, e.g., Amon *et al.*, "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy," in: *Monoclonal Antibodies And Cancer Therapy*, Reisfeld *et al.* Eds., Alan R. Liss, Inc., 1985; Hellstrom *et al.*, "Antibodies For Drug Delivery," in: *Controlled Drug Delivery*, Robinson *et al.* Eds., Marcel Dekker, Inc., 2nd Ed. 1987; Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review," in: *Monoclonal Antibodies '84: Biological And Clinical Applications*, Pinchera *et al.* Eds., 1985; "Analysis, Results, and Future Prospective of the Therapeutic Use of Radiolabeled

Antibody In Cancer Therapy,” in: *Monoclonal Antibodies For Cancer Detection And Therapy*, Baldwin *et al.*, Eds., Academic Press, 1985; Thorpe *et al.*, 1982, *Immunol. Rev.* 62:119-58; PCT publication WO 89/12624. Any of these chemistries may be used to link the synthons to an antibody.

[0226] A number of functional groups  $R^x$  and chemistries useful for linking synthons to accessible lysine residues are known, and include by way of example and not limitation NHS-esters and isothiocyanates.

[0227] A number of functional groups  $R^x$  and chemistries useful for linking synthons to accessible free sulfhydryl groups of cysteine residues are known, and include by way of example and not limitation haloacetyls and maleimides.

[0228] However, conjugation chemistries are not limited to available side chain groups. Side chains such as amines may be converted to other useful groups, such as hydroxyls, by linking an appropriate small molecule to the amine. This strategy can be used to increase the number of available linking sites on the antibody by conjugating multifunctional small molecules to side chains of accessible amino acid residues of the antibody. Functional groups  $R^x$  suitable for covalently linking the synthons to these “converted” functional groups are then included in the synthons.

[0229] An antibody may also be engineered to include amino acid residues for conjugation. An approach for engineering antibodies to include non-genetically encoded amino acid residues useful for conjugating drugs in the context of ADCs is described by Axup *et al.*, 2012, *Proc Natl Acad Sci U S A.* 109(40):16101-16106, as are chemistries and functional groups useful for linking synthons to the non-encoded amino acids.

[0230] Typically, the synthons are linked to the side chains of amino acid residues of the antibody, including, for example, the primary amino group of accessible lysine residues or the sulfhydryl group of accessible cysteine residues. Free sulfhydryl groups may be obtained by reducing interchain disulfide bonds.

[0231] For linkages where  $R^y$  is a sulfhydryl group (for example, when  $R^x$  is a maleimide), the antibody is generally first fully or partially reduced to disrupt interchain disulfide bridges between cysteine residues. Specific cysteine residues and interchain disulfide bridges that may be reduced for attachment of drug-linker synthons including a group suitable for conjugation to a sulfhydryl group for exemplary antibodies huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD208.9.1, muAD210.40.9, include by way of example and not limitation, residues C233, C239, and C242 (Kabat numbering system; corresponding to residues C220, C226, and C229 Eu numbering) on the human IgG<sub>1</sub> heavy chain, and residue C214 (Kabat numbering system) on the human Ig kappa light chain.



[0232] Cysteine residues for synthon attachment that do not participate in disulfide bridges may be engineered into an antibody by mutation of one or more codons. Reducing these unpaired cysteines yields a sulfhydryl group suitable for conjugation. Preferred positions for incorporating engineered cysteines include, by way of example and not limitation, positions S112C, S113C, A114C, S115C, A176C, S180C, S239C, S252C, V286C, V292C, S357C, A359C, S398C, S428C (Kabat numbering) on the human IgG<sub>1</sub> heavy chain and positions V110C, S114C, S121C, S127C, S168C, V205C (Kabat numbering) on the human Ig kappa light chain (*see, e.g.*, U.S. Patent No. 7,521,541, U.S. Patent No. 7,855,275 and U.S. Patent No. 8,455,622).

[0233] Mutation of a cysteine residue known to participate in an existing disulfide bridge may also be engineered such that the resulting unpaired cysteine partner is available to form a sulfide linker to a drug. Examples of engineered cysteine mutations include, but are not limited to, light chain constant C214 mutations, for example C214A.

[0234] As will be appreciated by skilled artisans, the number of cytotoxic and/or cytostatic agents linked to an antibody molecule may vary, such that an ADC preparation may be heterogeneous in nature, where some antibodies in the preparation contain one linked agent, some two, some three, *etc.* (and some none). The degree of heterogeneity will depend upon, among other things, the chemistries used for linking the cytotoxic and/or cytostatic agents. For example, where the antibodies are reduced to yield sulfhydryl groups for attachment, heterogeneous mixtures of antibodies having zero, 2, 4, 6 or 8 linked agents per molecule are often produced. Furthermore, by limiting the molar ratio of attachment compound, antibodies having zero, 1, 2, 3, 4, 5, 6, 7 or 8 linked agents per molecule are often produced. Thus, it will be understood that depending upon context, stated drug antibody ratios (DARs) may be averages for a collection of antibodies. For example, "DAR4" refers to an ADC preparation that has not been subjected to purification to isolate specific DAR peaks and comprises a heterogeneous mixture of ADC molecules having different numbers of cytostatic and/or cytotoxic agents attached per antibody (*e.g.*, 0, 2, 4, 6, 8 agents per antibody), but has an average drug-to-antibody ratio of 4. Similarly, "DAR8" refers to a heterogeneous ADC preparation in which the average drug-to-antibody ratio is 8.

[0235] Heterogeneous ADC preparations may be processed, for example, by hydrophobic interaction chromatography ("HIC") to yield preparations enriched in an ADC having a specified DAR of interest (or a mixture of two or more specified DARs). Such enriched preparations are designed herein as "EX," where "E" indicates the ADC preparation has been processed and is enriched in an ADC having a specific DAR and "X" represents the number of cytostatic and/or cytotoxic agents linked per ADC molecule. Preparations enriched in a mixture of ADCs having two specific DARs are designated "EX/EY," three

specific DARs “EX/EY/EZ” *etc.*, where “E” indicates the ADC preparation has been processed to enrich the specified DARs and “X,” “Y” and “Z” represent the DARs enriched. As specific examples, “E2” refers to an ADC preparation that has been enriched to contain primarily ADCs having two cytostatic and/or cytotoxic agents linked per ADC molecule. “E4” refers to an ADC preparation that has been enriched to contain primarily ADCs having four cytostatic and/or cytotoxic agents linked per ADC molecule. “E2/E4” refers to an ADC preparation that has been enriched to contain primarily two ADC populations, one having two cytostatic and/or cytotoxic agents linked per ADC molecule and another having four cytostatic and/or cytotoxic agents linked per ADC molecule.

[0236] An enriched “E” preparation can also refer to an ADC that has been prepared from an antibody that has been engineered, *e.g.*, by insertion or deletion of a cysteine residue, to form a linkage to a drug at a specific site. For example, an antibody with a S239C mutation in each heavy chain can primarily have a drug attached via a linker at that site, and, hence, can afford an E2 ADC preparation having mostly DAR2 without additional processing, such as chromatographic processing.

[0237] As used herein, enriched “E” preparations will generally be at least about 80% pure in the stated DAR ADCs, although higher levels of purity, such as purities of at least about 85%, 90%, 95%, 98%, 99% or even higher, may be obtainable and desirable. In some embodiments, the enriched “E” preparations have a range of purity within any two of the foregoing values, such as but not limited to from about 80-99%, 80-98%, 85-95%, 90-98%, 95-98%, or 80-90%. For example, an “EX” preparation will generally be at least about 80% pure in ADCs having X cytostatic and/or cytotoxic agents linked per ADC molecule. For “higher order” enriched preparations, such as, for example, “EX/EY” preparations, the sum total of ADCs having X and Y cytostatic and/or cytotoxic agents linked per ADC molecule will generally comprise at least about 80% of the total ADCs in the preparation. Similarly, in an enriched “EX/EY/EZ” preparation, the sum total of ADCs having X, Y and Z cytostatic and/or cytotoxic agents linked per ADC molecule will comprise at least about 80% of the total ADCs in the preparation.

[0238] Purity may be assessed by a variety of methods, as is known in the art. As a specific example, an ADC preparation may be analyzed via HPLC or other chromatography and the purity assessed by analyzing areas under the curves of the resultant peaks. Specific chromatography methods that may be employed to assess purity of ADC preparations are provided in Example 8.

[0239] FIG. 12 is illustrative. The top panel shows a chromatogram of a crude preparation of an ADC prepared according to Example 8. The preparation contains antibodies having no cytostatic and/or cytotoxic agents attached (DAR0), two agents attached (DAR2), four agents (DAR4), six agents attached (DAR6) and eight agents attached (DAR8). This crude preparation has an average DAR of 4. HIC

chromatography yields an E2 preparation in which approximately 95% of the ADCs in the preparation have two cytostatic and/or cytotoxic agents linked per ADC molecule (stated another way, approximately 95% of the ADCs are DAR2).

[0240] Specific methods for obtaining heterogenous mixtures of ADCs comprising humanized antibody huM25 having an average DAR of 4, as well as highly purified preparations containing 2 and 4 linked agents are provided in the Examples section. These specific methods may be modified using routine skill to obtain heterogeneous and/or homogeneous ADCs comprising other anti-huLRRC15 antibodies, linkers and/or cytotoxic and/or cytostatic agents.

### 7.6. Compositions

[0241] The ADCs described herein may be in the form of compositions comprising the ADC and one or more carriers, excipients and/or diluents. The compositions may be formulated for specific uses, such as for veterinary uses or pharmaceutical uses in humans. The form of the composition (*e.g.*, dry powder, liquid formulation, *etc.*) and the excipients, diluents and/or carriers used will depend upon the intended uses of the antibody and/or ADC and, for therapeutic uses, the mode of administration.

[0242] For therapeutic uses, the compositions may be supplied as part of a sterile, pharmaceutical composition that includes a pharmaceutically acceptable carrier. This composition can be in any suitable form (depending upon the desired method of administering it to a patient). The pharmaceutical composition can be administered to a patient by a variety of routes such as orally, transdermally, subcutaneously, intranasally, intravenously, intramuscularly, intratumorally, intrathecally, topically or locally. The most suitable route for administration in any given case will depend on the particular antibody and/or ADC, the subject, and the nature and severity of the disease and the physical condition of the subject. Typically, the pharmaceutical composition will be administered intravenously or subcutaneously.

[0243] Pharmaceutical compositions can be conveniently presented in unit dosage forms containing a predetermined amount of an antibody and/or ADC described herein per dose. The quantity of antibody and/or ADC included in a unit dose will depend on the disease being treated, as well as other factors as are well known in the art. Such unit dosages may be in the form of a lyophilized dry powder containing an amount of antibody and/or ADC suitable for a single administration, or in the form of a liquid. Dry powder unit dosage forms may be packaged in a kit with a syringe, a suitable quantity of diluent and/or other components useful for administration. Unit dosages in liquid form may be conveniently supplied in the form of a syringe pre-filled with a quantity of antibody and/or ADC suitable for a single administration.

[0244] The pharmaceutical compositions may also be supplied in bulk form containing quantities of ADC suitable for multiple administrations.

[0245] Pharmaceutical compositions may be prepared for storage as lyophilized formulations or aqueous solutions by mixing an antibody and/or ADC having the desired degree of purity with optional pharmaceutically-acceptable carriers, excipients or stabilizers typically employed in the art (all of which are referred to herein as “carriers”), *i.e.*, buffering agents, stabilizing agents, preservatives, isotonicifiers, non-ionic detergents, antioxidants, and other miscellaneous additives. *See*, Remington’s Pharmaceutical Sciences, 16th edition (Osol, ed. 1980). Such additives should be nontoxic to the recipients at the dosages and concentrations employed.

[0246] Buffering agents help to maintain the pH in the range which approximates physiological conditions. They may be present at a wide variety of concentrations, but will typically be present in concentrations ranging from about 2 mM to about 50 mM. Suitable buffering agents for use with the present disclosure include both organic and inorganic acids and salts thereof such as citrate buffers (*e.g.*, monosodium citrate-disodium citrate mixture, citric acid-trisodium citrate mixture, citric acid-monosodium citrate mixture, *etc.*), succinate buffers (*e.g.*, succinic acid-monosodium succinate mixture, succinic acid-sodium hydroxide mixture, succinic acid-disodium succinate mixture, *etc.*), tartrate buffers (*e.g.*, tartaric acid-sodium tartrate mixture, tartaric acid-potassium tartrate mixture, tartaric acid-sodium hydroxide mixture, *etc.*), fumarate buffers (*e.g.*, fumaric acid-monosodium fumarate mixture, fumaric acid-disodium fumarate mixture, monosodium fumarate-disodium fumarate mixture, *etc.*), gluconate buffers (*e.g.*, gluconic acid-sodium gluconate mixture, gluconic acid-sodium hydroxide mixture, gluconic acid-potassium gluconate mixture, *etc.*), oxalate buffer (*e.g.*, oxalic acid-sodium oxalate mixture, oxalic acid-sodium hydroxide mixture, oxalic acid-potassium oxalate mixture, *etc.*), lactate buffers (*e.g.*, lactic acid-sodium lactate mixture, lactic acid-sodium hydroxide mixture, lactic acid-potassium lactate mixture, *etc.*) and acetate buffers (*e.g.*, acetic acid-sodium acetate mixture, acetic acid-sodium hydroxide mixture, *etc.*). Additionally, phosphate buffers, histidine buffers and trimethylamine salts such as Tris can be used.

[0247] Preservatives may be added to retard microbial growth, and can be added in amounts ranging from about 0.2%-1% (w/v). Suitable preservatives for use with the present disclosure include phenol, benzyl alcohol, meta-cresol, methyl paraben, propyl paraben, octadecyldimethylbenzyl ammonium chloride, benzalconium halides (*e.g.*, chloride, bromide, and iodide), hexamethonium chloride, and alkyl parabens such as methyl or propyl paraben, catechol, resorcinol, cyclohexanol, and 3-pentanol. Isotonicifiers sometimes known as “stabilizers” can be added to ensure isotonicity of liquid compositions of the present disclosure and include polyhydric sugar alcohols, for example trihydric or higher sugar

alcohols, such as glycerin, erythritol, arabitol, xylitol, sorbitol and mannitol. Stabilizers refer to a broad category of excipients which can range in function from a bulking agent to an additive which solubilizes the therapeutic agent or helps to prevent denaturation or adherence to the container wall. Typical stabilizers can be polyhydric sugar alcohols (enumerated above); amino acids such as arginine, lysine, glycine, glutamine, asparagine, histidine, alanine, ornithine, L-leucine, 2-phenylalanine, glutamic acid, threonine, *etc.*, organic sugars or sugar alcohols, such as lactose, trehalose, stachyose, mannitol, sorbitol, xylitol, ribitol, myoinositol, galactitol, glycerol and the like, including cyclitols such as inositol; polyethylene glycol; amino acid polymers; sulfur containing reducing agents, such as urea, glutathione, thioctic acid, sodium thioglycolate, thioglycerol,  $\alpha$ -monothioglycerol and sodium thiosulfate; low molecular weight polypeptides (*e.g.*, peptides of 10 residues or fewer); proteins such as human serum albumin, bovine serum albumin, gelatin or immunoglobulins; hydrophilic polymers, such as polyvinylpyrrolidone monosaccharides, such as xylose, mannose, fructose, glucose; disaccharides such as lactose, maltose, sucrose and trehalose; and trisaccharides such as raffinose; and polysaccharides such as dextran. Stabilizers may be present in amounts ranging from 0.5 to 10 weight% per weight of ADC.

[0248] Non-ionic surfactants or detergents (also known as “wetting agents”) may be added to help solubilize the glycoprotein as well as to protect the glycoprotein against agitation-induced aggregation, which also permits the formulation to be exposed to shear surface stressed without causing denaturation of the protein. Suitable non-ionic surfactants include polysorbates (20, 80, *etc.*), poloxamers (184, 188 *etc.*), and pluronic polyols. Non-ionic surfactants may be present in a range of about 0.05 mg/mL to about 1.0 mg/mL, for example about 0.07 mg/mL to about 0.2 mg/mL.

[0249] Additional miscellaneous excipients include bulking agents (*e.g.*, starch), chelating agents (*e.g.*, EDTA), antioxidants (*e.g.*, ascorbic acid, methionine, vitamin E), and cosolvents.

[0250] A specific exemplary embodiment of an aqueous composition suitable for administration via intravenous infusion comprises 20 mg/mL anti-huLRRC15 ADC, 10 mM histidine buffer, pH 6.0, 7% (w/v) sucrose, 0.03% (w/v) polysorbate 80. The composition may be in the form of a lyophilized powder that, upon reconstitution with 5.2 mL sterile water or other solution suitable for injection or infusion (for example, 0.9% saline, Ringer’s solution, lactated Ringer’s solution, *etc.*) provides the above aqueous composition. This embodiment, or other embodiments of compositions, may also be in the form of a syringe or other device suitable for injection and/or infusion pre-filled with a quantity of composition suitable for a single administration of anti-huLRRC15 ADC.

### 7.7. Methods of Use

[0251] As discussed previously, for a variety of solid tumors, huLRRC15 is expressed in the tumor stromal microenvironment, as well as on the cancer cells *per se*. Data provided herein demonstrate that anti-huLRRC15 ADCs exert potent anti-tumor activity against these stromal(+)/cancer(+) tumors *in vivo*. Accordingly, the ADCs and/or pharmaceutical compositions comprising the ADCs may be used therapeutically to treat stromal(+)/cancer(+) tumors.

[0252] Generally, the methods involve administering to a human patient having a stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC effective to provide therapeutic benefit. Stromal(+)/cancer(+) tumors that may be treated with the ADCs include, but are not limited to, brain cancers (*e.g.*, gliomas, *e.g.*, glioblastoma), sarcomas (*e.g.*, osteosarcoma, soft tissue sarcoma, liposarcoma, leiomyosarcoma, synovial sarcoma, rhabdomyosarcoma, fibrosarcoma, malignant fibrous histiocytoma, epithelioid sarcoma, Ewing's sarcoma, gastrointestinal stromal tumor (GIST), undifferentiated pleiomorphic sarcoma, undifferentiated spindle cell sarcoma, chondrosarcoma, mesenchymoma, malignant peripheral nerve sheath tumor, vascular sarcoma, Kaposi's sarcoma, uterine sarcoma), melanoma, and mesenchymal tumors. Mesenchymal tumors can be either benign or malignant (*i.e.*, sarcomas) and can arise in a number of body organs (*e.g.*, mesenchymal tumors of the breast, lung, pancreas, brain, or stomach). The cancer may be newly diagnosed and naïve to treatment, or may be relapsed, refractory, or relapsed and refractory, or a metastatic form of a huLRRC15 stromal(+)/cancer(+) tumor. Indeed, as demonstrated in FIGS. 18A-18C, anti-huLRRC15 ADCs are more effective than standard of care anti-cancer agents against a variety of stromal(+)/cancer(+) tumors.

[0253] While not wishing to be bound by theory, the anti-huLRRC15 ADCs may exhibit an anti-tumor effect in part by killing cancer cells that have undergone epithelial-mesenchymal transition (EMT) and have acquired stem cell-like properties such as a mesenchymal phenotype. Data provided herein indicated that cancer cells that acquired mesenchymal-like properties exhibited higher huLRRC15 expression than cells with epithelial characteristics (FIGS. 10 and 11A-11C). Cancer cells that have undergone EMT transition were more sensitive to an anti-huLRRC15 ADC than epithelial cancer cells (FIG. 13J). The higher killing effect may result in part due to the localization of the ADC to LRRC15-expressing cells, followed by release of the cytotoxic agent.

[0254] FIGS. 9A-9C demonstrate that bone marrow derived mesenchymal stem cells, hypothesized to localize to the tumor microenvironment and form part of the tumor stroma, exhibit significant huLRRC15 expression (Karnoub, AE et al., *Nature* (2007), 449, 557-563; Droujinine, IA et al., *Oncotarget* (2013), 4(5), 651-664). Additionally, significant huLRRC15 expression can be induced by TGFβ in these

mesenchymal stem cells. Bone marrow mesenchymal stem cells (BM-MSCs) stimulated with TGF $\beta$  to express significant levels of LRRC15 (FIG. 13H and 13I), were sensitive to killing by an anti-huLRRC15 ADC. The killing effect may be a result in part of the localization to LRRC15-expressing cells by the ADC, followed by release of the cytotoxic agent. FIGS. 13H and 13I demonstrated that mesenchymal stem cells are able to take up and process anti-huLRRC15 ADCs, which may direct kill the mesenchymal stem cell as well as kill the cancer cells in proximity to the mesenchymal stem cells via a bystander effect through the release of the cytotoxic and/or cytostatic agent.

[0255] Anti-huLRRC15 ADCs may be administered alone (monotherapy) or adjunctive to, or with, other anti-cancer therapies and/or targeted or non-targeted anti-cancer agents. When administered as anti-huLRRC15 ADC monotherapy, one or more anti-huLRRC15 ADCs may be used. Whether administered as monotherapy or adjunctive to, or with, other therapies or agents, an amount of anti-huLRRC15 ADC is administered such that the overall treatment regimen provides therapeutic benefit.

[0256] By therapeutic benefit is meant that the use of anti-huLRRC15 ADCs to treat cancer in a patient results in a demonstrated improvement in survival compared with no therapy (when appropriate) or to a known standard of care. In some cases, therapeutic benefit may constitute an improvement in time to disease progression together with an improvement in symptoms or quality of life. In other cases, therapeutic benefit may not translate to an increased period of disease control, but rather a markedly reduced symptom burden resulting in improved quality of life. As will be apparent to those of skill in the art, a therapeutic benefit may be observed using the anti-huLRRC15 ADCs alone (monotherapy) or adjunctive to, or with, other anti-cancer therapies and/or targeted or non-targeted anti-cancer agents.

[0257] Typically, therapeutic benefit is assessed using standard clinical tests designed to measure the response to a new treatment for cancer. To assess the therapeutic benefits of the anti-huLRRC15 ADCs described herein one or a combination of the following tests can be used: (1) the Response Evaluation Criteria In Solid Tumors (RECIST) version 1.1, (2) immune-related RECIST (irRECIST), (3) Eastern Cooperative Oncology Group (ECOG) Performance Status, (4) immune-related response criteria (irRC), (5) disease evaluable by assessment of tumor antigens, (6) validated patient reported outcome scales, and/or (7) Kaplan-Meier estimates for overall survival and progression free survival.

[0258] Assessment of the change in tumor burden is an important feature of the clinical evaluation of cancer therapeutics. Both tumor shrinkage (objective response) and time to the development of disease progression are important endpoints in cancer clinical trials. Standardized response criteria, known as RECIST (Response Evaluation Criteria in Solid Tumors), were published in 2000. An update (RECIST 1.1) was released in 2009. RECIST criteria are typically used in clinical trials where objective response is

the primary study endpoint, as well as in trials where assessment of stable disease, tumor progression or time to progression analyses are undertaken because these outcome measures are based on an assessment of anatomical tumor burden and its change over the course of the trial. TABLE 3 provides the definitions of the response criteria used to determine objective tumor response to a study drug, such as the anti-huLRRC15 ADCs described herein.

<b>TABLE 3</b>	
<b>Response</b>	<b>Criteria</b>
Complete Response (CR)	Disappearance of all target lesions. Any pathological lymph nodes (whether target or non-target) must have reduction in short axis to <10 mm.
Partial Response (PR)	At least a 30% decrease in the sum of diameters of target lesions, taking as reference the baseline sum diameters.
Progressive Disease (PD)	At least a 20% increase in the sum of diameters of target lesions, taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). In addition to the relative increase of 20%, the sum must also demonstrate an absolute increase of at least 5 mm. (Note: the appearance of one or more new lesions is also considered progression).
Stable Disease (SD)	Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.

**[0259]** Secondary outcome measures that can be used to determine the therapeutic benefit of the anti-huLRRC15 ADCs described herein include, Objective Response Rate (ORR), Progression Free Survival (PFS), Overall Survival (OS), Duration of Overall Response (DOR), and Depth of Response (DpR). ORR is defined as the proportion of the participants who achieve a complete response (CR) or partial response (PR). PFS is defined as the time from the first dose date of an anti-huLRRC15 ADC to either disease progression or death, whichever occurs first. OS is defined as the length of time from either the date of diagnosis or the start of treatment for a disease, that patients diagnosed with the disease are still alive. DOR is defined as the time from the participant's initial CR or PR to the time of disease progression. DpR is defined as the percentage of tumor shrinkage observed at the maximal response point compared to baseline tumor load. Clinical endpoints for both ORR and PFS can be determined based on RECIST 1.1 criteria described above.



[0260] Additional criteria that may be used for clinical evaluation specific to cancer patients undergoing immune therapy treatment include the standardized immune-related RECIST (irRECIST) criteria. See, e.g., Nishino, M. et al. *Eur. J. Radiol.*, 84(7), pages 1259-1268 (2015 July). These guidelines modified the RECIST 1.1 criteria above with consideration of potential immunomodulatory effects. TABLE 5 provides the definitions of the response criteria used to determine objective tumor response to an immunomodulatory drug, such as the anti-huLRRC15 ADCs described herein.

TABLE 4	
Response	Criteria
Complete Response (irCR)	Complete disappearance of all measurable and non-measurable lesions. Lymph nodes must decrease to < 10 mm in short axis.
Partial Response (irPR)	Decrease of $\geq 30\%$ in total measured tumor burden relative to baseline, non-target lesions are irNN, and no unequivocal progression of new non-measurable lesions
Progressive Disease (irPD)	At least a 20% increase and at least 5 mm absolute increase in TMTB compared to nadir, or irPD for non-target or new non-measurable lesions. Confirmation of progression is recommended at least 4 weeks after the first irPD assessment.
Non-irCR or non-irPD (irNN)	No target disease was identified at baseline and at follow-up the patient fails to meet criteria for irCR or irPD
Stable Disease (irSD)	Neither sufficient shrinkage to qualify for irPR nor sufficient increase to qualify for irPD, taking as reference the smallest sum diameters while on study.
irNE	Used in exceptional cases where insufficient data exists.

[0261] The ECOG Scale of Performance Status shown in TABLE 5 is used to describe a patient's level of functioning in terms of their ability to care for themselves, daily activity, and physical ability. The scale was developed by the Eastern Cooperative Oncology Group (ECOG), now part of the ECOG-ACRIN Cancer Research Group, and published in 1982.

TABLE 5	
Grade	ECOG Performance Status
0	Fully active, able to carry on all pre-disease performance without restriction

TABLE 5	
Grade	ECOG Performance Status
1	Restricted in physically strenuous activity but ambulatory and able to carry out work of a light or sedentary nature, <i>e.g.</i> , light house work, office work
2	Ambulatory and capable of all selfcare but unable to carry out any work activities; up and about more than 50% of waking hours
3	Capable of only limited selfcare; confined to bed or chair more than 50% of waking hours
4	Completely disabled; cannot carry on any selfcare; totally confined to bed or chair
5	Dead

[0262] Another set of criteria that can be used to characterize fully and to determine response to immunotherapeutic agents, such as antibody-based cancer therapies, is the immune-related response criteria (irRC), which was developed for measurement of solid tumors in 2009, and updated in 2013 (Wolchok, et al. Clin. Cancer Res. 2009; 15(23): 7412-7420 and Nishino, et al. Clin. Cancer Res. 2013; 19(14): 3936-3943, each of which is incorporated by reference in its entirety). The updated irRC criteria are typically used to assess the effect of an immunotherapeutic agent, such as an anti-huLRRC15 ADC described herein, on tumor burden, and defines response according to TABLE 6.

TABLE 6	
Response	Criteria
Complete Response (CR)	Disappearance of all target lesions in two consecutive observations not less than 4 weeks apart
Partial Response (PR)	At least a 30% decrease in the sum of the longest diameters of target lesions, taking as reference the baseline sum diameters.
Progressive Disease (PD)	At least a 20% increase in the sum of diameters of target lesions, taking as reference the smallest sum on study (this includes the baseline sum if that is the smallest on study). (Note: the appearance of one or more new lesions is not considered progression. The measurement of new lesions is included in the sum of the measurements).
Stable Disease (SD)	Neither sufficient shrinkage to qualify for PR nor sufficient increase to qualify for PD, taking as reference the smallest sum diameters while on study.

**[0263]** Tumor antigens that can be used to evaluate the therapeutic benefit of the anti-huLRRC15 ADCs described herein include ApoE, CD11c, CD40, CD45 (PTPRC), CD49D (ITGA4), CD80, CSF1R, CTSD, GZMB, Ly86, MS4A7, PIK3AP1, PIK3CD, CD74, CCL5, CCR5, CXCL10, IFNG, IL10RA1, IL-6, ACTA2, COL7A1, LOX, LRRC15, MCPT8, MMP10, NOG, SERPINE1, STAT1, TGFBR1, CTSS, PGF, VEGFA, C1QA, C1QB, ANGPTL4, EGLN, ANGPTL4, EGLN3, BNIP3, AIF1, CCL5, CXCL10, CXCL11, IFI6, PLOD2, KISS1R, STC2, DDIT4, PFKFB3, PGK1, PDK1, AKR1C1, AKR1C2, CADM1, CDH11, COL6A3, CTGF, HMOX1, KRT33A, LUM, WNT5A, IGFBP3, MMP14, CDCP1, PDGFRA, TCF4, TGF, TGFB1, TGFB2, CD11b, ADGRE1 (EMR1, F4/80), CD86, CD68, MHC-Class II, CD3, HLA-DR, CD4, CD3, CD5, CD19, CD7, CD8, CD16, TCR $\alpha\beta$ , TCR $\gamma\delta$ , PD-1, PDL-1, CTLA-4, acid phosphatase, ACTH, alkaline phosphatase, alpha-fetoprotein CA-125, CA15-3, CA19-9, CA-195, C-212, CA-549, calcitonin, catecholamines, cathepsin-D, CEA, ERBB2 (HER2/neu), chromagranin-A, c-Myc, EGFR, ERA (estrogen receptor assay), ferritin, gastrin, 5-HIAA, hCG, alpha-HCG, beta-HCG, HVA, LDH1-5, NSE (neuron specific enolase), pancreatic polypeptide, PLAP, PLP, PRA (progesterone receptor A), proinsulin C-peptide, PSA, SMA, SCC, thyroglobulin, TDT, TPA, and alpha-TSH. These antigens can be assessed at the DNA, RNA or protein level using DNA sequencing techniques, RNA sequencing techniques, gene chip microarray, PCR based methods, flow cytometry or immunohistochemistry methods as known to experts in the art.

**[0264]** One exemplary therapeutic benefit resulting from the use of anti-huLRRC15 ADCs described herein to treat stromal(+)/cancer(+) tumors, whether administered as monotherapy or adjunctive to, or with, other therapies or agents, is a complete response. Another exemplary therapeutic benefit resulting from the use of anti-huLRRC15 ADCs described herein to treat stromal(+)/cancer(+) tumors, whether administered as monotherapy or adjunctive to, or with, other therapies or agents, is a partial response.

**[0265]** Validated patient reported outcome scales can also be used to denote response provided by each patient through a specific reporting system. Rather than being disease focused, such outcome scales are concerned with retained function while managing a chronic condition. One non-limiting example of a validated patient reported outcome scale is PROMIS® (Patient Reported Outcomes Measurement Information System) from the United States National Institutes of Health. For example, PROMIS® Physical Function Instrument for adult cancer patients can evaluate self-reported capabilities for the functioning of upper extremities (*e.g.*, dexterity), lower extremities (*e.g.*, walking or mobility), and central regions (*e.g.*, neck, back mobility), and also includes routine daily activities, such as running errands.

[0266] Kaplan-Meier curves (Kaplan and Meier, J. Am. Stat. Assoc. 1958; 53(282): 457-481) can also be used to estimate overall survival and progression free survival for cancer patients undergoing anti-huLRRC15 antibody or ADC therapy in comparison to standard of care.

#### 7.7.1. Adjunctive Therapies

[0267] Anti-huLRRC15 ADCs may be used adjunctive to, or with, other agents or treatments having anti-cancer properties. When used adjunctively, the anti-huLRRC15 and other agent(s) may be formulated together in a single, combination pharmaceutical formulation, or may be formulated and administered separately, either on a single coordinated dosing regimen or on different dosing regimens. Agents administered adjunctively with anti-huLRRC15 ADCs will typically have complementary activities to the anti-huLRRC15 ADCs such that the ADCs and other agents do not adversely affect each other.

[0268] Agents that may be used adjunctively with anti-huLRRC15 ADCs include, but are not limited to, alkylating agents, angiogenesis inhibitors, antibodies, antimetabolites, antimitotics, antiproliferatives, antivirals, aurora kinase inhibitors, apoptosis promoters (for example, Bcl-2 family inhibitors), activators of death receptor pathway, Bcr-Abl kinase inhibitors, BiTE (Bi-Specific T cell Engager) antibodies, antibody drug conjugates, biologic response modifiers, cyclin-dependent kinase inhibitors, cell cycle inhibitors, cyclooxygenase-2 inhibitors, DVDs, leukemia viral oncogene homolog (ErbB2) receptor inhibitors, growth factor inhibitors, heat shock protein (HSP)-90 inhibitors, histone deacetylase (HDAC) inhibitors, hormonal therapies, immunologicals, inhibitors of inhibitors of apoptosis proteins (IAPs), intercalating antibiotics, kinase inhibitors, kinesin inhibitors, Jak2 inhibitors, mammalian target of rapamycin inhibitors, microRNAs, mitogen-activated extracellular signal-regulated kinase inhibitors, multivalent binding proteins, non-steroidal anti-inflammatory drugs (NSAIDs), poly ADP (adenosine diphosphate)-ribose polymerase (PARP) inhibitors, platinum chemotherapeutics, polo-like kinase (Plk) inhibitors, phosphoinositide-3 kinase (PI3K) inhibitors, proteasome inhibitors, purine analogs, pyrimidine analogs, receptor tyrosine kinase inhibitors, retinoids/deltoids plant alkaloids, small inhibitory ribonucleic acids (siRNAs), topoisomerase inhibitors, ubiquitin ligase inhibitors, and the like, as well as combinations of one or more of these agents.

[0269] BiTE antibodies are bispecific antibodies that direct T-cells to attack cancer cells by simultaneously binding the two cells. The T-cell then attacks the target cancer cell. Examples of BiTE antibodies include adecatumumab (Micromet MT201), blinatumomab (Micromet MT103) and the like. Without being limited by theory, one of the mechanisms by which T-cells elicit apoptosis of the target cancer cell is by exocytosis of cytolytic granule components, which include perforin and granzyme B.

[0270] siRNAs are molecules having endogenous RNA bases or chemically modified nucleotides. The modifications do not abolish cellular activity, but rather impart increased stability and/or increased cellular potency. Examples of chemical modifications include phosphorothioate groups, 2'-deoxynucleotide, 2'-OCH<sub>3</sub>-containing ribonucleotides, 2'-F-ribonucleotides, 2'-methoxyethyl ribonucleotides, combinations thereof and the like. The siRNA can have varying lengths (*e.g.*, 10-200 bps) and structures (*e.g.*, hairpins, single/double strands, bulges, nicks/gaps, mismatches) and are processed in cells to provide active gene silencing. A double-stranded siRNA (dsRNA) can have the same number of nucleotides on each strand (blunt ends) or asymmetric ends (overhangs). The overhang of 1-2 nucleotides can be present on the sense and/or the antisense strand, as well as present on the 5'- and/or the 3'-ends of a given strand.

[0271] Multivalent binding proteins are binding proteins comprising two or more antigen binding sites. Multivalent binding proteins are engineered to have the three or more antigen binding sites and are generally not naturally occurring antibodies. The term "multispecific binding protein" means a binding protein capable of binding two or more related or unrelated targets. Dual variable domain (DVD) binding proteins are tetravalent or multivalent binding proteins comprising two or more antigen binding sites. Such DVDs may be monospecific (*i.e.*, capable of binding one antigen) or multispecific (*i.e.*, capable of binding two or more antigens). DVD binding proteins comprising two heavy chain DVD polypeptides and two light chain DVD polypeptides are referred to as DVD Ig's. Each half of a DVD Ig comprises a heavy chain DVD polypeptide, a light chain DVD polypeptide, and two antigen binding sites. Each binding site comprises a heavy chain variable domain and a light chain variable domain with a total of 6 CDRs involved in antigen binding per antigen binding site.

[0272] Alkylating agents include, but are not limited to, altretamine, AMD-473, AP-5280, apaziquone, bendamustine, brostallicin, busulfan, carboquone, carmustine (BCNU), chlorambucil, CLORETAZINE<sup>®</sup> (laromustine, VNP 40101M), cyclophosphamide, dacarbazine, estramustine, fotemustine, glufosfamide, ifosfamide, KW-2170, lomustine (CCNU), mafosfamide, melphalan, mitobronitol, mitolactol, nimustine, nitrogen mustard N-oxide, ranimustine, temozolomide, thiotepa, TREANDA<sup>®</sup> (bendamustine), treosulfan, and trofosfamide.

[0273] Angiogenesis inhibitors include, but are not limited to, endothelial-specific receptor tyrosine kinase (Tie-2) inhibitors, epidermal growth factor receptor (EGFR) inhibitors, insulin growth factor-2 receptor (IGFR-2) inhibitors, matrix metalloproteinase-2 (MMP-2) inhibitors, matrix metalloproteinase-9 (MMP-9) inhibitors, platelet-derived growth factor receptor (PDGFR) inhibitors, thrombospondin analogs, and vascular endothelial growth factor receptor tyrosine kinase (VEGFR) inhibitors.

[0274] Antimetabolites include, but are not limited to, ALIMTA® (pemetrexed disodium, LY231514, MTA), 5-azacitidine, XELODA® (capecitabine), capecitabine, LEUSTAT® (cladribine), clofarabine, cytarabine, cytarabine ocfosfate, cytosine arabinoside, decitabine, deferoxamine, doxifluridine, eflornithine, EICAR (5-ethynyl-1-β-D-ribofuranosylimidazole-4-carboxamide), enocitabine, ethnylecytidine, fludarabine, 5-fluorouracil alone or in combination with leucovorin, GEMZAR® (gemcitabine), hydroxyurea, ALKERAN® (melphalan), mercaptopurine, 6-mercaptopurine riboside, methotrexate, mycophenolic acid, nelarabine, nolatrexed, ocfosfate, pelitrexol, pentostatin, raltitrexed, Ribavirin, triapine, trimetrexate, S-1, tiazofurin, tegafur, TS-1, vidarabine, and UFT.

[0275] Antivirals include, but are not limited to, ritonavir, acyclovir, cidofovir, ganciclovir, foscarnet, zidovudine, ribavirin, and hydroxychloroquine.

[0276] Aurora kinase inhibitors include, but are not limited to, ABT-348, AZD-1152, MLN-8054, VX-680, Aurora A-specific kinase inhibitors, Aurora B-specific kinase inhibitors and pan-Aurora kinase inhibitors.

[0277] Bcl-2 protein inhibitors include, but are not limited to, AT-101 ((-)-gossypol), GENASENSE® (G3139 or oblimersen (Bcl-2-targeting antisense oligonucleotide)), IPI-194, IPI-565, N-(4-(4-((4'-chloro(1,1'-biphenyl)-2-yl)methyl)piperazin-1-yl)benzoyl)-4-(((1R)-3-(dimethylamino)-1-((phenylsulfanyl)methyl)propyl)amino)-3-nitrobenzenesulfonamide), N-(4-(4-((2-(4-chlorophenyl)-5,5-dimethyl-1-cyclohex-1-en-1-yl)methyl)piperazin-1-yl)benzoyl)-4-(((1R)-3-(morpholin-4-yl)-1-((phenylsulfanyl)methyl)propyl)amino)-3-((trifluoromethyl)sulfonyl)benzenesulfonamide, venetoclax and GX-070 (obatoclax).

[0278] Bcr-Abl kinase inhibitors include, but are not limited to, DASATINIB® (BMS-354825) and GLEEVEC® (imatinib).

[0279] BRAF kinase inhibitors include, but are not limited to, TAFINLAR® (dabrafenib) and ZELBORAF® (vemurafenib).

[0280] CDK inhibitors include, but are not limited to, AZD-5438, BMI-1040, BMS-032, BMS-387, CVT-2584, flavopyridol, GPC-286199, MCS-5A, PD0332991, PHA-690509, seliciclib (CYC-202, R-roscovitine), and ZK-304709.

[0281] COX-2 inhibitors include, but are not limited to, ABT-963, ARCOXIA® (etoricoxib), BEXTRA® (valdecoxib), BMS347070, CELEBREX® (celecoxib), COX-189 (lumiracoxib), CT-3, DERAMAXX® (deracoxib), JTE-522, 4-methyl-2-(3,4-dimethylphenyl)-1-(4-sulfamoylphenyl)-1H-

pyrrole), MK-663 (etoricoxib), NS-398, parecoxib, RS-57067, SC-58125, SD-8381, SVT-2016, S-2474, T-614, and VIOXX® (rofecoxib).

[0282] EGFR inhibitors include, but are not limited to, ABX-EGF, anti-EGFR immunoliposomes, EGF-vaccine, EMD-7200, ERBITUX® (cetuximab), HR3, IgA antibodies, IRESSA® (gefitinib), TARCEVA® (erlotinib or OSI-774), TP-38, EGFR fusion protein, and TYKERB® (lapatinib).

[0283] ErbB2 receptor inhibitors include, but are not limited to, CP-724-714, CI-1033 (canertinib), HERCEPTIN® (trastuzumab), TYKERB® (lapatinib), OMNITARG® (2C4, pertuzumab), TAK-165, GW-572016 (ionafamib), GW-282974, EKB-569, PI-166, dHER2 (HER2 vaccine), APC-8024 (HER-2 vaccine), KADCYLA® (T-DM1), anti-HER/2neu bispecific antibody, B7.her2IgG3, AS HER2 trifunctional bispecific antibodies, mAB AR-209, and mAB 2B-1.

[0284] Histone deacetylase inhibitors include, but are not limited to, depsipeptide, LAQ-824, MS-275, trapoxin, suberoylanilide hydroxamic acid (SAHA), TSA, and valproic acid.

[0285] HSP-90 inhibitors include, but are not limited to, 17-AAG-nab, 17-AAG, CNF-101, CNF-1010, CNF-2024, 17-DMAG, geldanamycin, IPI-504, KOS-953, MYCOGRAB® (human recombinant antibody to HSP-90), NCS-683664, PU24FCI, PU-3, radicicol, SNX-2112, STA-9090, and VER49009.

[0286] Inhibitors of apoptosis proteins include, but are not limited to, HGS1029, GDC-0145, GDC-0152, LCL-161, and LBW-242.

[0287] Activators of death receptor pathway include, but are not limited to, TRAIL, antibodies or other agents that target TRAIL or death receptors (*e.g.*, DR4 and DR5) such as Apomab, conatumumab, ETR2-ST01, GDC0145 (lexatumumab), HGS-1029, LBY-135, PRO-1762 and trastuzumab.

[0288] Kinesin inhibitors include, but are not limited to, Eg5 inhibitors such as AZD4877, ARRY-520; and CENPE inhibitors such as GSK923295A.

[0289] JAK-2 inhibitors include, but are not limited to, CEP-701 (lesaurtinib), XL019 and INCB018424.

[0290] MEK inhibitors include, but are not limited to, ARRY-142886, ARRY-438162, PD-325901, and PD-98059.

[0291] mTOR inhibitors include, but are not limited to, AP-23573, CCI-779, everolimus, RAD-001, rapamycin, temsirolimus, ATP-competitive TORC1/TORC2 inhibitors, including PI-103, PP242, PP30, and Torin 1.

[0292] Non-steroidal anti-inflammatory drugs include, but are not limited to, AMIGESIC® (salsalate), DOLOBID® (diflunisal), MOTRIN® (ibuprofen), ORUDIS® (ketoprofen), RELAFEN® (nabumetone),

FELDENE® (piroxicam), ibuprofen cream, ALEVE® (naproxen) and NAPROSYN® (naproxen), VOLTAREN® (diclofenac), INDOCIN® (indomethacin), CLINORIL® (sulindac), TOLECTIN® (tolmetin), LODINE® (etodolac), TORADOL® (ketorolac), and DAYPRO® (oxaprozin).

[0293] PDGFR inhibitors include, but are not limited to, C-451, CP-673 and CP-868596.

[0294] Platinum chemotherapeutics include, but are not limited to, cisplatin, ELOXATIN® (oxaliplatin) eptaplatin, lobaplatin, nedaplatin, PARAPLATIN® (carboplatin), satraplatin, and picoplatin.

[0295] Polo-like kinase inhibitors include, but are not limited to, BI-2536.

[0296] Phosphoinositide-3 kinase (PI3K) inhibitors include, but are not limited to, wortmannin, LY294002, XL-147, CAL-120, ONC-21, AEZS-127, ETP-45658, PX-866, GDC-0941, BGT226, BEZ235, and XL765.

[0297] Thrombospondin analogs include, but are not limited to, ABT-510, ABT-567, ABT-898, and TSP-1.

[0298] VEGFR inhibitors include, but are not limited to, AVASTIN® (bevacizumab), ABT-869, AEE-788, ANGIOZYME™ (a ribozyme that inhibits angiogenesis (Ribozyme Pharmaceuticals (Boulder, CO) and Chiron (Emeryville, CA)), axitinib (AG-13736), AZD-2171, CP-547,632, IM-862, MACUGEN® (pegaptamib), NEXAVAR® (sorafenib, BAY43-9006), pazopanib (GW-786034), vatalanib (PTK-787, ZK-222584), SUTENT® (sunitinib, SU-11248), VEGF trap, and ZACTIMA™ (vandetanib, ZD-6474).

[0299] Antibiotics include, but are not limited to, intercalating antibiotics aclarubicin, actinomycin D, amrubicin, annamycin, adriamycin, BLENOXANE® (bleomycin), daunorubicin, CAELYX® or MYOCET® (liposomal doxorubicin), elsamitrucin, epirubicin, glarbuicin, ZAVEDOS® (idarubicin), mitomycin C, nemorubicin, neocarzinostatin, peplomycin, pirarubicin, rebeccamycin, stimalamer, streptozocin, VALSTAR® (valrubicin), and zinostatin.

[0300] Topoisomerase inhibitors include, but are not limited to, aclarubicin, 9-aminocamptothecin, amonafide, amsacrine, becatecarin, belotecan, BN-80915, CAMPTOSAR® (irinotecan hydrochloride), camptothecin, CARDIOXANE® (dexrazoxine), diflomotecan, edotecarin, ELLENCE® or PHARMORUBICIN® (epirubicin), etoposide, exatecan, 10-hydroxycamptothecin, gimatecan, lurtotecan, mitoxantrone, Onivyde™ (liposomal irinotecan), orathecin, pirarubicin, pixantrone, rubitecan, sobuzoxane, SN-38, tafluposide, and topotecan.

[0301] Antibodies include, but are not limited to, AVASTIN® (bevacizumab), CD40-specific antibodies, chTNT-1/B, denosumab, ERBITUX® (cetuximab), HUMAX-CD4® (zanolimumab), IGF1R-specific antibodies, lintuzumab, PANOREX® (edrecolomab), RENCAREX® (WX G250), RITUXAN®



(rituximab), ticilimumab, trastuzumab, pertuzumab, VECTIBIX® (panitumumab) and CD20 antibodies types I and II.

[0302] Hormonal therapies include, but are not limited to, ARIMIDEX® (anastrozole), AROMASIN® (exemestane), arzoxifene, CASODEX® (bicalutamide), CETROTIDE® (cetorelix), degarelix, deslorelin, DESOPAN® (trilostane), dexamethasone, DROGENIL® (flutamide), EVISTA® (raloxifene), AFEMA™ (fadrozole), FARESTON® (toremifene), FASLODEX® (fulvestrant), FEMARA® (letrozole), formestane, glucocorticoids, HECTOROL® (doxercalciferol), RENAGEL® (sevelamer carbonate), lasofoxifene, leuprolide acetate, MEGACE® (megesterol), MIFEPREX® (mifepristone), NILANDRON™ (nilutamide), NOLVADEX® (tamoxifen citrate), PLENAXIS™ (abarelix), prednisone, PROPECIA® (finasteride), rilostane, SUPREFACT® (buserelin), TRELSTAR® (luteinizing hormone releasing hormone (LHRH)), VANTAS® (Histrelin implant), VETORYL® (trilostane or modrastane), and ZOLADEX® (fosreltin, goserelin).

[0303] Deltoids and retinoids include, but are not limited to, seocalcitol (EB1089, CB1093), lexacalcitrol (KH1060), fenretinide, PANRETIN® (aliretinoin), ATRAGEN® (liposomal tretinoin), TARGRETIN® (bexarotene), and LGD-1550.

[0304] PARP inhibitors include, but are not limited to, ABT-888 (veliparib), olaparib, KU-59436, AZD-2281, AG-014699, BSI-201, BGP-15, INO-1001, and ONO-2231.

[0305] Plant alkaloids include, but are not limited to, vincristine, vinblastine, vindesine, and vinorelbine.

[0306] Proteasome inhibitors include, but are not limited to, VELCADE® (bortezomib), KYPROLIS® (carfilzomib), MG132, NPI-0052, and PR-171.

[0307] Examples of immunologicals include, but are not limited to, interferons, immune checkpoint inhibitors, co-stimulatory agents, and other immune-enhancing agents. Interferons include interferon alpha, interferon alpha-2a, interferon alpha-2b, interferon beta, interferon gamma-1a, ACTIMMUNE® (interferon gamma-1b) or interferon gamma-n1, combinations thereof and the like. Immune check point inhibitors include antibodies that target PD-1 (*e.g.*, pembrolizumab and nivolumab), PD-L1 (*e.g.*, durvalumab, atezolizumab, avelumab, MEDI4736, MSB0010718C and MPDL3280A), and CTLA4 (cytotoxic lymphocyte antigen 4; *e.g.*, ipilimumab, tremelimumab). Additional exemplary anti-PD-1 antibodies include those described in US provisional application no. 62/394,314, such as an anti-PD-1 antibody having a heavy chain amino acid sequence according to:

EIQLVQSGAEVKKPGSSVKVSCKASGYTFTHYGMNWVRQAPGQGLEWVGWVNTYTGEPTYAD  
DFKGRLTFTLDTSTSTAYMELSSLRSEDTAVYYCTREGEGLGFGDWGQGTTVTVSSASTKGPSVF

*PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT  
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVD  
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG  
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK* (SEQ ID NO:91) or

EIQLVQSGAEVKKPGSSVKVSCKASGYTFTHYGMNWVRQAPGQGLEWVGWVNTYTGEPTYAD  
DFKGRLTFTLDTSTSTAYMELSSLRSEDTAVYYCTREGEGLGFGDWGQGTITVTVSSASTKGPSVF  
*PLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQT  
YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPEAAGGPSVFLFPPKPKDTLMISRTPEVTCVVD  
VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE  
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDG  
SFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG* (SEQ ID NO:92); and

a light chain amino acid sequence according to:

DVVMQTQSPLSLPVTGPGEPAISCRSSQSIVHSHGDTYLEWYLQKPGQSPQLLIYKVSNRFSGVPDR  
FSGSGSGTDFTLKISRVEAEDVGVYYCFQGSHIPVTFGGGTKLEIKRTVAAPSVFIFPPSDEQLKSGT  
ASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSSTLSSTLTLSKADYEKHKVYACEVTH  
QGLSSPVTKSFNRGEC (SEQ ID NO:93),

wherein the underlined amino acids represent the CDRs and the italicized amino acids represent the constant regions.

**[0308]** Co-stimulatory agents include, but are not limited to, antibodies against CD3, CD40, CD40L, CD27, CD28, CSF1R, CD137 (*e.g.*, urelumab), B7H1, GITR, ICOS, CD80, CD86, OX40, OX40L, CD70, HLA-DR, LIGHT, LIGHT-R, TIM3, A2AR, NKG2A, KIR (*e.g.*, lirilumab), TGF- $\beta$  (*e.g.*, fresolimumab) and combinations thereof.

**[0309]** Other agents include, but are not limited to, ALFAFERONE® (IFN- $\alpha$ ), BAM-002 (oxidized glutathione), BEROMUN® (tasonermin), BEXXAR® (tositumomab), CAMPATH® (alemtuzumab), dacarbazine, denileukin, epratuzumab, GRANOCYTE® (lenograstim), lentinan, leukocyte alpha interferon, imiquimod, melanoma vaccine, mitumomab, molgramostim, MYLOTARG™ (gemtuzumab ozogamicin), NEUPOGEN® (filgrastim), OncoVAC-CL, OVAREX® (oregovomab), pentumomab (Y-muHMFG1), PROVENGE® (sipuleucel-T), sargaramostim, sizofilan, teceleukin, THERACYS® (Bacillus Calmette-Guerin), ubenimex, VIRULIZIN® (immunotherapeutic, Lorus Pharmaceuticals), Z-100 (Specific Substance of Maruyama (SSM)), WF-10 (Tetrachlorodecaoxide (TCDO)), PROLEUKIN®

(aldesleukin), ZADAXIN® (thymalfasin), ZINBRYTA® (daclizumab high-yield process), and ZEVALIN® (<sup>90</sup>Y-Ibritumomab tiuxetan).

[0310] Biological response modifiers are agents that modify defense mechanisms of living organisms or biological responses, such as survival, growth or differentiation of tissue cells to direct them to have anti-tumor activity and include, but are not limited to, krestin, lentinan, sizofiran, picibanil PF-3512676 (CpG-8954), and ubenimex.

[0311] Pyrimidine analogs include, but are not limited to, cytarabine (ara C or Arabinoside C), cytosine arabinoside, doxifluridine, FLUDARA® (fludarabine), 5-FU (5-fluorouracil), floxuridine, GEMZAR® (gemcitabine), TOMUDEX® (ratitrexed), and TROXATYL™ (triacetyluridine troxacitabine).

[0312] Purine analogs include, but are not limited to, LANVIS® (thioguanine) and PURI-NETHOL® (mercaptapurine).

[0313] Antimitotic agents include, but are not limited to, batabulin, epothilone D (KOS-862), N-(2-((4-hydroxyphenyl)amino)pyridin-3-yl)-4-methoxybenzenesulfonamide, ixabepilone (BMS 247550), TAXOL® (paclitaxel), TAXOTERE® (docetaxel), PNU100940 (109881), patupilone, XRP-9881 (larotaxel), vinflunine, and ZK-EPO (synthetic epothilone).

[0314] Ubiquitin ligase inhibitors include, but are not limited to, MDM2 inhibitors, such as nutlins, and NEDD8 inhibitors such as MLN4924.

[0315] Anti-huLRRC15 ADCs may also be used to enhance the efficacy of radiation therapy. Examples of radiation therapy include external beam radiation therapy, internal radiation therapy (*i.e.*, brachytherapy) and systemic radiation therapy.

[0316] Anti-huLRRC15 ADCs may be administered adjunctive to or with other chemotherapeutic agents such as ABRAXANE™ (ABI-007), ABT-100 (farnesyl transferase inhibitor), ADVEXIN® (Ad5CMV-p53 vaccine), ALTOCOR® or MEVACOR® (lovastatin), AMPLIGEN® (poly I:poly C12U, a synthetic RNA), APTOSYN® (exisulind), AREDIA® (pamidronic acid), arglabin, L-asparaginase, atamestane (1-methyl-3,17-dione-androsta-1,4-diene), AVAGE® (tazarotene), AVE-8062 (combreastatin derivative) BEC2 (mitumomab), cachectin or cachexin (tumor necrosis factor), canvaxin (vaccine), CEAVAC® (cancer vaccine), CELEUK® (celmoleukin), CEPLENE® (histamine dihydrochloride), CERVARIX® (human papillomavirus vaccine), CHOP® (C: CYTOXAN® (cyclophosphamide); H: ADRIAMYCIN® (hydroxydoxorubicin); O: Vincristine (ONCOVIN®); P: prednisone), CYPAT™ (cyproterone acetate), combrestatin A4P, DAB(389)EGF (catalytic and translocation domains of diphtheria toxin fused via a His-Ala linker to human epidermal growth factor) or TransMID-107R™ (diphtheria toxins), dacarbazine,

dactinomycin, 5,6-dimethylxanthenone-4-acetic acid (DMXAA), eniluracil, EVIZON™ (squalamine lactate), DIMERICINE® (T4N5 liposome lotion), discodermolide, DX-8951f (exatecan mesylate), enzastaurin, EPO906 (epithilone B), GARDASIL® (quadrivalent human papillomavirus (Types 6, 11, 16, 18) recombinant vaccine), GASTRIMMUNE®, GENASENSE®, GMK (ganglioside conjugate vaccine), GVAX® (prostate cancer vaccine), halofuginone, histrelin, hydroxycarbamide, ibandronic acid, IGN-101, IL-13-PE38, IL-13-PE38QQR (cintredekin besudotox), IL-13-pseudomonas exotoxin, interferon- $\alpha$ , interferon- $\gamma$ , JUNOVAN™ or MEPACT™ (mifamurtide), lonafarnib, 5,10-methylenetetrahydrofolate, miltefosine (hexadecylphosphocholine), NEOVASTAT® (AE-941), NEUTREXIN® (trimetrexate glucuronate), NIPENT® (pentostatin), ONCONASE® (a ribonuclease enzyme), ONCOPHAGE® (melanoma vaccine treatment), ONCOVAX® (IL-2 Vaccine), ORATHECIN™ (rubitecan), OSIDEM® (antibody-based cell drug), OVAREX® MAb (murine monoclonal antibody), paclitaxel, PANDIMEX™ (aglycone saponins from ginseng comprising 20(S)protopanaxadiol (aPPD) and 20(S)protopanaxatriol (aPPT)), panitumumab, PANVAC®-VF (investigational cancer vaccine), pegaspargase, PEG Interferon A, phenoxodiol, procarbazine, rebimastat, REMOVAB® (catumaxomab), REVLIMID® (lenalidomide), RSR13 (efaproxiral), SOMATULINE® LA (lanreotide), SORIATANE® (acitretin), staurosporine (Streptomyces staurospores), talabostat (PT100), TARGRETIN® (bexarotene), TAXOPREXIN® (DHA-paclitaxel), TELCYTA® (canfosfamide, TLK286), temilifene, TEMODAR® (temozolomide), tesmilifene, thalidomide, THERATOPE® (STn-KLH), thymitaq (2-amino-3,4-dihydro-6-methyl-4-oxo-5-(4-pyridylthio)quinazoline dihydrochloride), TNFERADE™ (adenovector: DNA carrier containing the gene for tumor necrosis factor- $\alpha$ ), TRACLEER® or ZAVESCA® (bosentan), tretinoin (Retin-A), tetrandrine, TRISENOX® (arsenic trioxide), VIRULIZIN®, ukrain (derivative of alkaloids from the greater celandine plant), vitaxin (anti- $\alpha$ 5 $\beta$ 3 antibody), XCYTRIN® (motexafin gadolinium), XINLAY™ (atrasentan), XYOTAX™ (paclitaxel poliglumex), YONDELIS® (trabectedin), ZD-6126, ZINECARD® (dexrazoxane), ZOMETA® (zoledronic acid), and zorubicin, as well as combinations of any of these agents.

### 7.8. Dosages and Administration Regimens

[0317] The amount of anti-huLRRC15 ADC administered will depend upon a variety of factors, including but not limited to, the particular type of stromal(+)/cancer(+) tumor treated, the stage of the stromal(+)/cancer(+) tumor being treated, the mode of administration, the frequency of administration, the desired therapeutic benefit, and other parameters such as the age, weight and other characteristics of the patient, *etc.* Determination of dosages effective to provide therapeutic benefit for specific modes and frequency of administration is within the capabilities of those skilled in the art.

[0318] Dosages effective to provide therapeutic benefit may be estimated initially from *in vivo* animal models or clinical. Suitable animal models for a wide variety of diseases are known in the art.

[0319] The anti-huLRRC15 ADCs may be administered by any route appropriate to the condition to be treated. An anti-huLRRC15 ADC will typically be administered parenterally, *i.e.*, infusion, subcutaneous, intramuscular, intravenous (IV), intradermal, intrathecal, bolus, intratumor injection or epidural ((Shire *et al.*, 2004, *J. Pharm. Sciences* 93(6):1390-1402)). In one embodiment, an anti-huLRRC15 ADC is provided as a lyophilized powder in a vial. The vials may contain 50 mg, 100 mg, or 200 mg of anti-huLRRC15 ADC. Prior to administration, the lyophilized powder is reconstituted with sterile water for injection (SWFI) or other suitable medium to provide a solution containing 20 mg/mL anti-huLRRC15 ADC. The resulting reconstituted solution is further diluted with saline or other suitable medium and administered via an IV infusion once every 7 days, once every 14 days, once every 21 days, or once every 28 days. In some embodiments, for the first cycle, the infusion occurs over 180 minutes, subsequent infusions are over 90 minutes. In other embodiments, the infusion occurs over 60 minutes.

[0320] In one exemplary embodiment, an anti-huLRRC15 ADC is administered once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 6.0 mg/kg, 6.3 mg/kg, 6.6 mg/kg, 6.9 mg/kg, or 7.2 mg/kg.

[0321] In another exemplary embodiment, an anti-huLRRC15 ADC is administered once every 7 days at 0.15 mg/kg, 0.3 mg/kg, 0.45 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, or 4.2 mg/kg..

[0322] In another exemplary embodiment, an anti-huLRRC15 ADC is administered once every 28 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg, 6.0 mg/kg, 6.3 mg/kg, 6.6 mg/kg, 6.9 mg/kg, 7.2 mg/kg, 7.5 mg/kg, 7.8 mg/kg, 8.1 mg/kg, or 8.4 mg/kg.

[0323] In another exemplary embodiment, an anti-huLRRC15 ADC is administered once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg, 6.0 mg/kg, 6.3 mg/kg, 6.6 mg/kg, 6.9 mg/kg, or 7.2 mg/kg.

[0324] When administered adjunctive to, or with, other agents, such as other chemotherapeutic agents, the ADCs may be administered on the same schedule as the other agent(s), or on a different schedule.

When administered on the same schedule, the ADC may be administered before, after, or concurrently

with the other agent. In some embodiments where an ADC is administered adjunctive to, or with, standards of care, the ADC may be initiated prior to commencement of the standard therapy, for example a day, several days, a week, several weeks, a month, or even several months before commencement of standard of care therapy.

**[0325]** In one exemplary embodiment, an anti-huLRRC15 ADC is used adjunctively to radiation to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Typically, fractionated localized radiotherapy (60 Gy of 30-33 distinct 1.8-2 Gy doses/fractionations) is applied over a 5-7 week period via external beam radiation. Shorter hypo-fractionated regimens (*e.g.*, 50 Gy in 28 fractions of 1.8 Gy, or 40 Gy in 15 fractions of 2 Gy) may also be used in patients with low performance status. The number of radiation fractionations and radiation dose level may vary depending on the health status and age of the patient as well as the type of external beam radiation being administered. The adjunctive anti-huLRRC15 ADC/radiation therapy is continued until disease progression or no longer tolerated by the patient.

**[0326]** In another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to temozolomide and radiation to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Typically, fractionated localized radiotherapy (60 Gy of 30-33 distinct 1.8-2 Gy doses/fractionations) is applied over a 5-7 week period via external beam radiation., but this will vary depending on the type of external beam radiation therapy that is used, as well as the age and health status of the patient. Temozolomide is administered by intravenous infusion at a dose of 75 mg/m<sup>2</sup> over 90 minutes or by oral capsule (75 mg/m<sup>2</sup>) once daily for up to 6 weeks concomitant with radiation. Subsequent cycles should consist of temozolomide infusions of 150 mg/m<sup>2</sup> once daily for 5 days every 4 weeks without radiation. The adjunctive anti-huLRRC15 ADC/temozolomide/radiation therapy is continued until disease progression or no longer tolerated by the patient.

**[0327]** In another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to carmustine for injection (BiCNU<sup>®</sup>) to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. The recommended dose and schedule for carmustine is 150

to 200 mg/m<sup>2</sup> administered as an intravenous infusion every six weeks. The dose may be given in a single dose or divided into daily injections such as 75 to 100 mg/m<sup>2</sup> on two successive days. The adjunctive anti-huLRRC15 ADC/BiCNU<sup>®</sup> therapy is continued until disease progression or no longer tolerated by the patient.

[0328] In another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to lomustine (CeeNU<sup>®</sup>) to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. The recommended dose and schedule for lomustine is 130 mg/m<sup>2</sup> administered as a single oral dose every six weeks. The adjunctive anti-huLRRC15 ADC/CeeNU<sup>®</sup> therapy is continued until disease progression or no longer tolerated by the patient.

[0329] In another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to bevacizumab (AVASTIN<sup>®</sup>) to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. The recommended dose and schedule for bevacizumab is 10 mg/kg administered as an intravenous infusion over 30, 60 or 90 minutes every two weeks. The adjunctive anti-huLRRC15 ADC/AVASTIN<sup>®</sup> therapy is continued until disease progression or no longer tolerated by the patient.

[0330] In another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to ABT-414 to treat glioblastoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. The recommended dose and schedule for ABT-414 is 1.25 mg/kg via IV infusion every 2 weeks. The adjunctive anti-huLRRC15 ADC/ABT-414 therapy is continued until disease progression or no longer tolerated by the patient.

[0331] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to radiation to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Typically, fractionated localized radiotherapy (60 Gy of 30-33 distinct 1.8-2 Gy doses/fractionations) is applied over a 5-7 week period via external beam radiation, but this will vary

depending on the type of external beam radiation therapy that is used, as well as the health status and age of the patient. The adjunctive anti-huLRRC15 ADC/radiation therapy is continued until disease progression or no longer tolerated by the patient.

**[0332]** In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to cisplatin to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Cisplatin is administered intravenously at 20-100 mg/m<sup>2</sup>, once every 2 to 4 weeks. The adjunctive anti-huLRRC15 ADC/cisplatin therapy is continued until disease progression or no longer tolerated by the patient.

**[0333]** In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to carboplatin to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Carboplatin is administered intravenously at 300-400 mg/m<sup>2</sup>, once every 4 weeks. The adjunctive anti-huLRRC15 ADC/carboplatin therapy is continued until disease progression or no longer tolerated by the patient.

**[0334]** In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to gemcitabine to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Gemcitabine is administered by intravenous infusion at a dose of 1000 mg/m<sup>2</sup> over 30 minutes once weekly for up to 7 weeks, followed by a week of rest from treatment. If myelosuppression is observed, dose modifications as provided in the prescribing information for gemcitabine may be used. Subsequent cycles should consist of infusions once weekly for 3 consecutive weeks out of every 4 weeks. The adjunctive anti-huLRRC15 ADC/gemcitabine therapy is continued until disease progression or no longer tolerated by the patient.

**[0335]** In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to pazopanib to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Pazopanib is administered orally at 800 mg once a day, or at 200 mg orally once a



day in patients with impaired baseline hepatic function. The adjunctive anti-huLRRC15 ADC/pazopanib therapy is continued until disease progression or no longer tolerated by the patient.

[0336] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to ifosfamide to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Ifosfamide is administered intravenously at a dose of 2000-2400 mg/m<sup>2</sup> per day for 5 consecutive days. Treatment is repeated every 3 weeks or after recovery from hematologic toxicity (Platelets  $\geq$ 100,000/ $\mu$ L, WBC  $\geq$ 4,000/ $\mu$ L). The adjunctive anti-huLRRC15 ADC/ifosfamide therapy is continued until disease progression or no longer tolerated by the patient.

[0337] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to carboplatin to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Carboplatin is administered intravenously at 300-500 mg/m<sup>2</sup>, once every 4 weeks. The adjunctive anti-huLRRC15 ADC/carboplatin therapy is continued until disease progression or no longer tolerated by the patient.

[0338] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to doxorubicin to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. When used in combination with other drugs, the most commonly used dosage of doxorubicin is 20 to 60 mg/m<sup>2</sup> given as a single intravenous injection every 21 to 28 days. The adjunctive anti-huLRRC15 ADC/doxorubicin therapy is continued until disease progression or no longer tolerated by the patient.

[0339] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctively to imatinib (GLEEVEC<sup>®</sup>) to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Dosages for imatinib vary between 100 mg/day to 800 mg/day. Commonly used dosages include 100 mg/day, 300 mg/day, 400 mg/day, 340 mg/m<sup>2</sup>/day, 600 mg/day or

800 mg/day. The adjunctive anti-huLRRC15 ADC/imatinib therapy is continued until disease progression or no longer tolerated by the patient.

[0340] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to nivolumab (OPDIVO®) to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Nivolumab is administered by an intravenous infusion at 1-3 mg/kg over 60 minutes every 2-3 weeks. The adjunctive anti-huLRRC15 ADC/nivolumab therapy is continued until disease progression or no longer tolerated by the patient.

[0341] In still another exemplary embodiment, an anti-huLRRC15 ADC can be used adjunctive to pembrolizumab (KEYTRUDA®) to treat sarcoma. The anti-huLRRC15 ADC is administered via IV infusion once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Pembrolizumab is administered as an intravenous infusion at 2 mg/kg over 30 minutes every 3 weeks. The adjunctive anti-huLRRC15 ADC/pembrolizumab therapy is continued until disease progression or no longer tolerated by the patient.

[0342] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to radiation to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Typically, localized fractionated radiation therapy (8 Gy or 2.5 Gy fractions) is applied via external beam radiation, but this will vary depending on the type of external beam radiation therapy that is used, as well as the health status and age of the patient. The adjunctive anti-huLRRC15 ADC/radiation therapy is continued until disease progression or no longer tolerated by the patient.

[0343] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to nivolumab (OPDIVO®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Nivolumab is administered by an intravenous infusion at 1-3 mg/kg over 60 minutes every 2-3 weeks. The adjunctive anti-huLRRC15 ADC/nivolumab therapy is continued until disease progression or no longer tolerated by the patient.

[0344] In still another exemplary embodiment, an anti-huLRRC15 ADC can be used adjunctive to pembrolizumab (KEYTRUDA®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Pembrolizumab is administered as an intravenous infusion at 2 mg/kg over 30 minutes every 3 weeks. The adjunctive anti-huLRRC15 ADC/pembrolizumab therapy is continued until disease progression or no longer tolerated by the patient.

[0345] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to ipilimumab (YERVOY®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 21 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.4 mg/kg, 3.0 mg/kg, 3.6 mg/kg, 4.2 mg/kg, 4.8 mg/kg, 5.4 mg/kg, or 6.0 mg/kg. Ipilimumab is administered at 3 mg/kg intravenously over 90 minutes every 3 weeks for 3 months, or at 10 mg/kg intravenously over 90 minutes every 3 weeks for 4 doses, followed by 10 mg/kg every 12 weeks for up to 3 years or until documented disease recurrence or unacceptable toxicity in the adjuvant melanoma setting. The anti-huLRRC15 ADC therapy is continued until disease progression or no longer tolerated by the patient.

[0346] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to vemurafenib (ZELBORAF®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.4 mg/kg, 3.0 mg/kg, 3.6 mg/kg, 4.2 mg/kg, 4.8 mg/kg, 5.4 mg/kg, or 6.0 mg/kg. Vemurafenib is administered at 960 mg orally twice daily approximately 12 hours apart with or without a meal. The anti-huLRRC15 ADC/vemurafenib therapy is continued until disease progression or no longer tolerated by the patient.

[0347] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to vemurafenib (ZELBORAF®) and cobimetinib (COTELLIC®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.4 mg/kg, 3.0 mg/kg, 3.6 mg/kg, 4.2 mg/kg, 4.8 mg/kg, 5.4 mg/kg, or 6.0 mg/kg. Vemurafenib is administered at 960 mg orally twice daily approximately 12 hours apart with or without a meal. Cobimetinib is administered at 60 mg orally once daily for the first 21 days of each 28-day cycle. The anti-huLRRC15 ADC/vemurafenib/cobimetinib therapy is continued until disease progression or no longer tolerated by the patient.

[0348] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to dabrafenib (TAFINLAR®) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every

14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.4 mg/kg, 3.0 mg/kg, 3.6 mg/kg, 4.2 mg/kg, 4.8 mg/kg, 5.4 mg/kg, or 6.0 mg/kg. Dabrafenib is administered at 150 mg orally twice daily. The anti-huLRRC15 ADC/dabrafenib therapy is continued until disease progression or no longer tolerated by the patient.

[0349] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to dabrafenib (TAFINLAR<sup>®</sup>) and trametinib (MEKINIST<sup>®</sup>) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.4 mg/kg, 3.0 mg/kg, 3.6 mg/kg, 4.2 mg/kg, 4.8 mg/kg, 5.4 mg/kg, or 6.0 mg/kg. Dabrafenib is administered at 150 mg orally twice daily in combination with trametinib 2 mg orally once daily. The anti-huLRRC15 ADC/dabrafenib/trametinib therapy is continued until disease progression or no longer tolerated by the patient.

[0350] In still another exemplary embodiment, an anti-huLRRC15 ADC is used adjunctive to nivolumab (OPDIVO<sup>®</sup>) and ipilimumab (YERVOY<sup>®</sup>) to treat melanoma. The anti-huLRRC15 ADC is administered via IV infusion once every 14 days at 0.3 mg/kg, 0.6 mg/kg, 0.9 mg/kg, 1.2 mg/kg, 1.5 mg/kg, 1.8 mg/kg, 2.1 mg/kg, 2.4 mg/kg, 2.7 mg/kg, 3.0 mg/kg, 3.3 mg/kg, 3.6 mg/kg, 3.9 mg/kg, 4.2 mg/kg, 4.5 mg/kg, 4.8 mg/kg, 5.1 mg/kg, 5.4 mg/kg, 5.7 mg/kg or 6.0 mg/kg. Nivolumab is administered by an intravenous infusion at 1 mg/kg and ipilimumab is administered by intravenous infusion at 3 mg/kg every 3 weeks for 4 doses. The adjunctive anti-huLRRC15 ADC/nivolumab/ipilimumab therapy is continued until disease progression or no longer tolerated by the patient.

[0351] As will be appreciated by those of skill in the art, the recommended dosages for the various agents described above may need to be adjusted to optimize patient response and maximize therapeutic benefit.

## 8. EXAMPLES

[0352] The following Examples, which highlight certain features and properties of exemplary embodiments of anti-huLRRC15 ADCs are provided for purposes of illustration, and not limitation.

### Example 1. Preparation of Exemplary Anti-huLRRC15 Antibodies

[0353] Antibodies against huLRRC15 were prepared against a cell line expressing huLRRC15 (U118MG glioblastoma cells) using standard techniques. Exemplary antibodies having specified affinities and other desirable characteristics, for example, cross-reactive with cynomolgus LRRC15 (“cynoLRRC15”), were isolated and certain of these antibodies humanized. Exemplary humanized antibodies include huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.1 and exemplary murine

antibodies include muAD209.9.1 and muAD210.40.9. Sequences of the V<sub>H</sub> and V<sub>L</sub> chains of these exemplary antibodies are provided in FIGS. 2A and 2B, respectively. Sequences of the heavy and light chains of exemplary antibody huM25 are provided in FIGS. 3A and 3B, respectively.

[0354] Binding of these exemplary antibodies to endogenous huLRRC15, as well as their respective EC<sub>50</sub>s, was demonstrated with U118MG glioblastoma cells via a conventional flow cytometry assay using test antibody concentrations of 0.0001 µg/mL, 0.001 µg/mL, 0.01 µg/mL, 0.1 µg/mL, 1 µg/mL, 10 µg/mL and 100 µg/mL. Isotype control antibodies (mouse or human) were used as appropriate. Flow cytometry binding data for various representative anti-huLRRC15 antibodies are shown in FIG. 4. TABLE 7 provides EC<sub>50</sub> values for various anti-huLRRC15 antibodies as determined by flow cytometry.

<b>TABLE 7</b>			
<b>Binding of Antibodies to Cells Expressing huLRRC15 (Flow Cytometry)</b>			
<b>Antibody</b>	<b>U118MG EC<sub>50</sub> (nM)</b>	<b>Antibody</b>	<b>U118MG EC<sub>50</sub> (nM)</b>
muIgG <sub>2a</sub> Isotype mAb		huIgG <sub>1</sub> Isotype mAb	NA
muM25	0.496	huM25	0.498
mu139.10	0.207	hu139.10	0.28
muAD208.4.1	0.934	huAD208.4.1	0.29
muAD208.14.1	2.05	huAD208.14.1	5.25
muAD209.9.1	0.787		
muAD210.40.9	0.08		

#### **Example 2. The Anti-huLRRC15 Antibodies Bind the Extracellular Domain of huLRRC15 Shed From the Cell Surface**

[0355] Binding of the exemplary anti-huLRRC15 to the portion of the extracellular domain of huLRRC15 shed from the cell surface was demonstrated in an ELISA assay. huLRRC15-Fc fusion protein was generated using amino acid residues 22 to 526 of SEQ ID NO:3, which corresponds to a portion of the huLRRC15 extracellular protein domain to the cleavage site. 96-well Immulon 4HBX plates (Thermo, cat. #3855) were coated with 100 µL/well of this huLRRC15 fusion ECD protein at 2 µg/mL in carbonate-bicarbonate buffer (Thermo, cat.# 28382) pH 9.4 and allowed to bind overnight at 4°C. Plates were washed three times with PBST and then incubated with various concentrations of antibodies in PBST + 0.3% BSA at room temperature for one hour. Plates were washed three times with PBST and then incubated with 100 µL of goat anti-human kappa light chain HRP (Bethyl, cat.# A80-

115P) at 1:5000 dilution for 30 min at RT. Plates were washed three times in PBST and 100  $\mu$ L of TMB (Surmodics BioF<sub>x</sub> cat.# TMBW-1000-01) was added to each well and incubated at RT until color developed (approximately 10 minutes). Reactions were stopped by the addition of 650nm Stop Reagent for TMB (Surmodics BioF<sub>x</sub>, cat.# BSTP-0100-01), and optical density (OD) was read at 650 nm (Molecular Devices Versamax PLUS). ELISA binding data for certain exemplary anti-huLRRC15 antibodies are shown in FIG. 5. EC<sub>50</sub> (nM) values for various anti-huLRRC15 antibodies are provided in TABLE 8, below.

TABLE 8			
Binding of Antibodies to huLRRC15 ECD (ELISA)			
Antibody	huLRRC15-ECD-Fc EC <sub>50</sub> (nM)	Antibody	huLRRC15-ECD-Fc EC <sub>50</sub> (nM)
muIgG <sub>2a</sub> Isotype mAb	NA	huIgG <sub>1</sub> Isotype mAb	NA
muM25	0.22	huM25	0.26
mu139.10	0.15	hu139.10	0.11
muAD208.4.1	0.15	huAD208.4.1	0.25
muAD208.14.1	0.22	huAD208.14.1	0.8
muAD209.9.1	0.14		

[0356] All antibodies tested bound the huLRRC15 fusion with EC<sub>50</sub>s in the sub-nanomolar range, indicating that the antibodies bind the portion of the huLRRC15 extracellular domain shed from the cell surface following cleavage.

### Example 3. Exemplary Anti-huLRRC15 Antibodies Bind to Different Epitopes

[0357] The ability of various exemplary anti-huLRRC15 antibodies to compete with muM25 for binding cells expressing huLRRC15, and hence whether the antibodies bind the same or different epitopes, was assessed in a flow cytometry competition assay using fluorescently labeled muM25 (“muM25-AF488”) as a “reference antibody” and unlabeled anti-huLRRC15 antibody as a “test antibody.” For the assay, aliquots of U118MG cells (200,000 cells per well) were incubated simultaneously with 1  $\mu$ g/mL labeled muM25 and either 0.0001, 0.001, 0.01, 0.1, 1, 10 or 100  $\mu$ g/mL unlabeled test antibody and the amount of bound antibody (normalized to a control aliquot incubated with 1  $\mu$ g/mL labeled muM25 alone) determined via flow cytometry. Isotype control antibodies (human or mouse) were used as negative controls, and unlabeled muM25 was used as a positive control.

[0358] In this assay, competition due to a test antibody binding to the same or a proximal epitope as the labeled reference antibody reduce binding of the reference labeled antibody. A positive result in this assay occurs when a test antibody inhibits  $\geq 20\%$  of the binding of the fluorescently labeled reference antibody at a concentration of test antibody that is 10 times greater than the concentration of the reference antibody.

[0359] Unlabeled huM25 competes fully with labeled muM25 as expected (FIG. 6A). Murine antibodies muAD208.4.1 and muAD208.14.1 partially compete with huM25 (FIG. 6B). Both of these antibodies inhibit  $>20\%$  of the binding of labeled muM25. This indicates that they bind a similar or proximal huLRRC15 epitope as muM25. In contrast, mu139.10, muAD208.12.1 and muAD209.9.1 do not inhibit the binding of labeled muM25, demonstrating that they bind distinct epitopes of huLRRC15 (FIG. 6B).

#### **Example 4. huLRRC15 Is Highly Expressed In Stroma and Cells of Major Solid Tumor Types**

[0360] Expression of huLRRC15 in the stroma and cells of various solid tumor types was assessed using immunohistochemistry (IHC) staining on formalin fixed paraffin embedded (FFPE) tissues. Biopsies from different tumor types were used to generate tissue microarrays (TMA) which were assessed for huLRRC15 expression. Tissue sections (4  $\mu\text{m}$ ) were cut, deparaffinized and antigen retrieval was performed using BORG Decloaker antigen retrieval buffer at  $125^\circ\text{C}$  for 1 min. Leica autostainer was used to block slides and incubate with anti-huLRRC15 antibody (muAD210.40.9 at 1  $\mu\text{g/mL}$  for 60 minutes) and HRP anti-mouse secondary (Dako) together with DAB reagent (Dako) for detection. Results of the experiment are shown in TABLE 9 and FIG. 7.

**TABLE 9**  
**huLRRC15 Stromal and Cell Positive Expression in Cancer**  
**(detected by immunohistochemistry)**

Tumor Type	IHC Score	
	<i>(TMA+ individual tissues)</i>	
	> 2+	% Positive
Sarcoma	22/32	69%
Melanoma	28/48	58%
Glioblastoma	7/31	23%

[0361] The TMA samples were scored on a scale of 0 to 4. A score of  $\geq 2$  was chosen to identify tumors that express huLRRC15 at high levels. The huLRRC15 staining and expression data in TABLE 9 represents that seen in huLRRC15 stromal positive, cancer positive tumors (FIG. 7).

**Example 5. huLRRC15 Exhibits Limited Expression In Normal Tissues**

[0362] The expression of huLRRC15 on normal, healthy tissues was assessed using protein immunohistochemical staining of normal tissues. The results are shown in FIG. 8. huLRRC15 has limited expression in most normal tissues, with expression being localized to certain tissues including cardia/pylorus in the stomach, spleen peritrabeculae, osteoblasts, and hair follicles (“ECM” refers to extracellular matrix). Limited expression was also observed in tonsil and placenta (data not shown). No expression of huLRRC15 was observed in major organs (*e.g.*, heart, liver, pancreas, lung).

**Example 6. huLRRC15 Is Expressed by Mesenchymal Stem Cells**

[0363] Expression of huLRRC15 was measured by Western blot protein analysis of cancer-associated fibroblast (CAF) lysates from a breast cancer patient, or commercial mesenchymal stem cell (MSC) lysates using biotinylated anti-huLRRC15 antibody muAD210.40.9 as shown in FIG. 9A. huLRRC15 was observed to be upregulated in a breast CAF lysate sample upon treatment with TGF $\beta$  with low or negligible detectable expression in the absence of TGF $\beta$ . By contrast, huLRRC15 expression was higher in the absence of TGF $\beta$  in all three MSC lysate samples, and this expression was significantly upregulated upon TGF $\beta$  treatment. As previously discussed, MSCs are believed to make up a significant component of the cancer associated fibroblast population in the tumor stroma (Cirri, P and Chiarugi P. American Journal of Cancer Research 2011; 1 (4): 482-497).

[0364] Similar upregulation of huLRRC15 expression was observed by flow cytometry of two commercial mesenchymal stem cell populations upon treatment with TGF $\beta$  (FIGS. 9B, 9C). In human BM-MSC (Lonza), using CD29, CD44, CD105, CD166 as positive MSC markers and CD14, CD34, and CD45 as negative MSC markers, a significant positive shift in the MSC population expressing huLRRC15 was observed upon treatment with TGF $\beta$  as compared with isotype (FIG. 9B). Correspondingly, in murine Balb/c BM-MSC (Cyagen), using CD29, CD44, CD34, and Sca-1 as positive MSC markers and CD117 as a negative MSC marker, a significant increase in the MSC population expressing muLRRC15 was observed upon treatment with TGF $\beta$  as compared with isotype (FIG. 9C).

**Example 7. huLRRC15 Is Associated with Cells Undergoing Epithelial-Mesenchymal Transition**



[0365] The epithelial-mesenchymal transition (EMT) is a cellular mechanism which is believed to confer cellular plasticity on cancer cells. This transition to a more mesenchymal phenotype is thought to increase the motility and invasiveness of a primary cancer cell, potentially leading to cancer metastasis, drug resistance, or evasion of the immune system. *See, e.g.,* Ye, X. and Weinberg, R. A. Trends in Cell Biology, 2015, 25 (11), pages 675-686. Data provided in this Example demonstrate that cancer cells that had undergone EMT had an increased expression of huLRRC15 relative to their parental epithelial cancer cells.

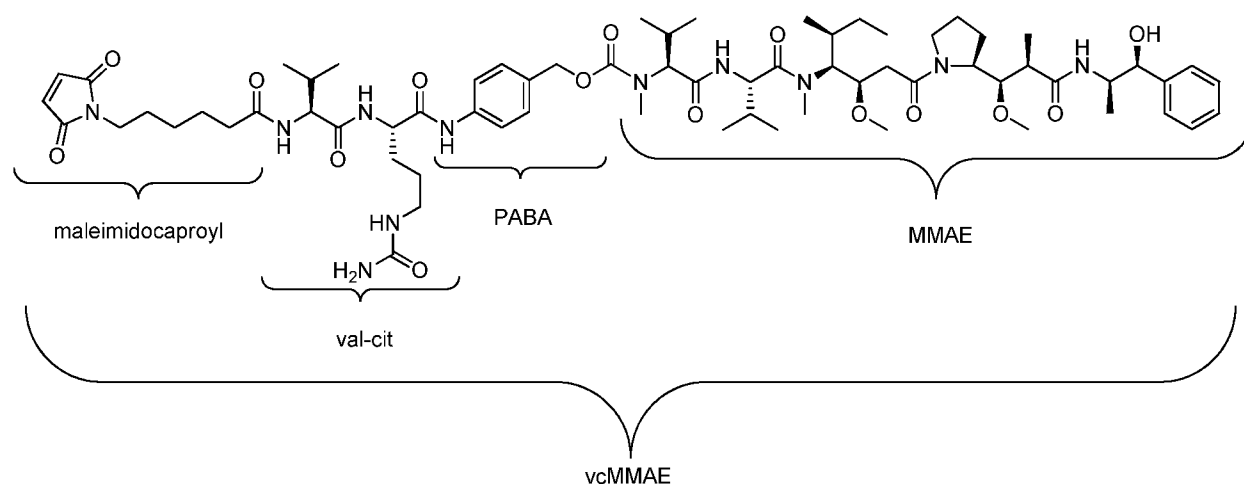
[0366] FIG. 10 depicts the effect as determined by Western blot analysis of treating baseline negative A549 (lung cancer) or PANC1 (pancreatic cancer) cells with TGF $\beta$  or StemXVivo™ EMT Inducing Media Supplement (“EMT Kit,” Catalog #CCM017, R&D Systems) to induce EMT. Proteins recognized as hallmarks of EMT, including N-cadherin, Snail, TCF8/ZEB1, increased expression, and proteins indicative of epithelial cell characteristics such as E-cadherin decreased expression. Expression of the housekeeping protein and protein loading control GAPDH did not change significantly. huLRRC15 expression (measured using anti-LRRC15 antibody muAD210.40.9) was observed to have increased in both A549 and PANC1 cells treated with either TGF $\beta$  or EMT Kit, and that have subsequently undergone EMT.

[0367] FIGS. 11A-11C show that huLRRC15 expression increased in cells that have undergone EMT, with the reverse mesenchymal-epithelial transition (MET) process occurring with the removal of EMT inducers. FIG. 11A shows A549 or PANC1 cells untreated, or treated with TGF $\beta$  or EMT Kit for 5 days. In A549 or PANC1 cells, EpCAM expression, indicating epithelial-like character, was highest in untreated cells. After treatment with TGF $\beta$  or EMT Kit, huLRRC15 (as measured with AF647-labeled huM25) in both cell types was induced, while the epithelial marker EpCAM was reduced, suggesting a transition to a more mesenchymal phenotype (huLRRC15 positive). FIG. 11B depicts the morphology of A549 cells treated with TGF $\beta$  (10 ng/mL continuously for 9 days) (top left), showing elongated cells with fibrotic-like processes which appear mesenchymal-like, while A549 cells treated with TGF $\beta$  (10 ng/mL continuously for 5 days) and then washed to remove the TGF $\beta$  no longer exhibited the mesenchymal cell morphology after an additional 4 days (corresponding 9 days total) (bottom left). Hence, the EMT induced by TGF $\beta$  was reversible upon its removal. The induction of EMT by TGF $\beta$  and reversal of mesenchymal-like properties was also observed by flow cytometry (FIG. 11B). An increase in huLRRC15 expression (indicating more mesenchymal-like characteristics) (upper middle), and a decrease in EpCAM expression (indicating less epithelial-like characteristics) (upper right) was observed after treatment with TGF $\beta$  or EMT Kit. Upon discontinuation of TGF $\beta$  or EMT Kit treatment, levels of huLRRC15 reverted to that observed at baseline (lower graphs).

[0368] FIG. 11C depicts the increase in mesenchymal character, and corresponding decrease in epithelial character, of cells treated with TGF $\beta$ , as indicated by huLRRC15 (top graphs) and EpCAM levels (bottom graphs) in A549 (left graphs) or PANC1 (right graphs) cells *in vitro*. In both A549 and PANC1 cells, huLRRC15 expression increased upon treatment of cells with TGF $\beta$  or EMT Kit over 9 days, while EpCAM expression, an indicator of epithelial character, decreased. Consistent with the cell morphology data in FIG. 11B, the protein expression of huLRRC15 and EpCAM indicated the LRRC15 positive mesenchymal cells reverted to an epithelial-like state after removal of TGF $\beta$  or EMT Kit, and additional cell culturing over 4 days.

#### Example 8. Preparation of Heterogeneous DAR huM25-vcMMAE ADCs

[0369] A huM25-val-cit-MMAE ADC composition heterogeneous in DAR was prepared by a two-step chemical process: disulfide reduction of huM25 followed by alkylation (conjugation) with maleimidocaproyl valine-citrulline (“val-cit”) para-aminobenzyl alcohol (“PABA”) monomethyl auristatin E (referred to herein as “vcMMAE”), illustrated below:



[0370] In the first step, a limited number of interchain disulfide bonds of huM25 are reduced with tris(2-carboxyethyl) phosphine (“TCEP”) ( $\geq 0.8$  equiv). Partially-reduced huM25 is then conjugated to vcMMAE ( $\geq 1.8$  equiv) in DMSO. Residual unreacted vcMMAE is quenched with N-acetyl-L-cysteine.

[0371] The top panel of FIG. 12 shows a chromatographic resolution of the resultant ADC preparation. As can be seen, the resultant ADC preparation is a heterogeneous mixture containing antibodies having zero MMAE molecules attached (“DAR0” peak), two MMAE molecules attached (“DAR2” peak), four MMAE molecules attached (“DAR4” peak), six MMAE molecules attached (“DAR6” peak) and eight MMAE molecules attached (“DAR8” peak) and has an average DAR of 4. Using huM25 as an example,

specific ADC preparations that comprise heterogeneous mixtures having an average DAR of 4 are designated herein with “DAR4,” *e.g.*, huM25-vcMMAE-DAR4.

**Example 9. Preparation of huM25-vcMMAE ADCs Enriched in DAR2**

[0372] Preparations of huM25-vcMMAE ADCs enriched DAR2 (referred to herein as “huM25-vcMMAE-E2”) were obtained via hydrophobic interaction chromatographic (“HIC”) resolution of the heterogeneous DAR ADC composition of Example 8. General methods for separating heterogeneous ADC mixtures and isolating specific homogeneous species such as the DAR2 and DAR4 peaks via HIC are described by Hamblett *et al.*, 2004, Clin Cancer Res 10:7063-7070.

[0373] A chromatogram of the enriched huM25-vcMMAE E2 ADC preparation is shown in the bottom panel of FIG. 12. The preparation is approximately 98% pure in the DAR2 ADC. Using huM25 as an example, specific ADC preparations enriched in DAR2 are designated herein with “E2,” *e.g.*, huM25-vcMMAE-E2.

[0374] For the preparation of huM25-vcMMAE-E2, the heterogeneous DAR ADC material as described in Example 8 was adjusted to column-binding salt conditions by the addition of 1/3 volume of 4.5M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> to give 110 mS conductivity. This load material was pumped onto a 2.6 x 150-cm column packed with 70 mL GE Butyl Sepharose-HP resin and equilibrated with Buffer A [1.5M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>, 20 mM sodium phosphate, pH 7], using a GE ÄKTAprius plus liquid chromatography system. After loading and washing to baseline, unconjugated antibody huM25 (“DAR0”) was eluted with a 90 mS step-gradient blend of Buffers A and B (Buffer B = 20 mM sodium phosphate, pH 7 + 25% isopropanol) (retention time = 3 min). Next, huM25-vcMMAE-E2 was prepared by elution with a 60 mS step-gradient blend of Buffers A and B (retention time = 4 min). The eluted pool of material enriched in huM25-vcMMAE-DAR2 was buffer exchanged and concentrated on a Pellicon® tangential-flow filtration system (membrane XL- 30kD) using 15 mM MES buffer pH 6.0 to afford the E2 preparation. Preparations of “E4” (enriched preparation of huM25-vcMMAE containing 4 MMAE molecules) and “E6” (enriched preparation of huM25-vcMMAE containing 6 MMAE molecules) and “E8” (enriched preparation of huM25-vcMMAE containing 8 MMAE molecules) can also be isolated with this gradient. Final material was quantified via absorbance at 280 nm, assessed for purity via HIC, and assessed for aggregation via size-exclusion chromatography (“SEC”).

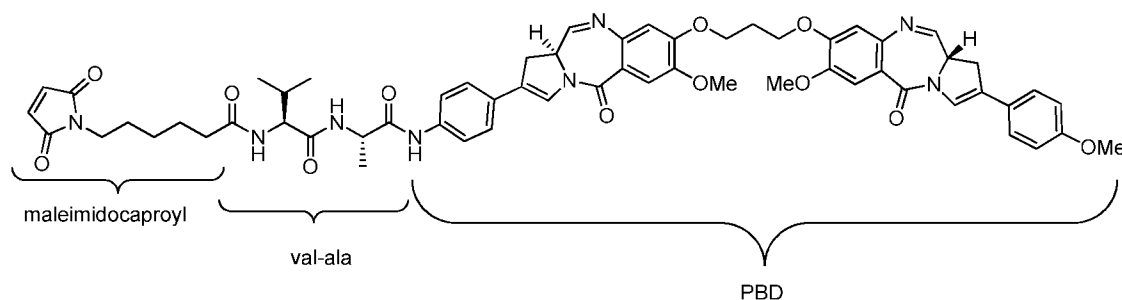
**Example 10. huM25-vcMMAE ADC Has Potent *In vitro* Efficacy Against LRRC15-Expressing Cells**

[0375] The potent *in vitro* cell killing abilities of anti-huLRRC15 ADCs huM25-vcMMAE-E2 and huM25-vcMMAE-DAR4 against huLRRC15-expressing cells U118MG (glioblastoma), RPMI-7951 (melanoma), and G292 clone A141B1 (osteosarcoma), as contrasted with huLRRC15-negative cell line EBC-1 (squamous NSCLC), are demonstrated in FIGS. 13A-13D. In the *in vitro* cell killing assays, cells are seeded at 500-3000 cells per well into 96-well plates with varying concentrations (1  $\mu$ M to 3 pM) of antibodies and ADCs. The cells are incubated for 4 days in culture and then the percent cell viability relative to untreated cells is determined using Cell TiterGlo™ which measures ATP content within the treated cells. On-target specific cell killing with anti-huLRRC15 ADCs (*e.g.*, huM25-vcMMAE-E2, huM25-vcMMAE-DAR4) is observed in cancer cell lines endogenously expressing huLRRC15, which is superior to that seen with non-targeting isotype-vcMMAE ADCs. In a huLRRC15-negative cancer cell line (EBC-1), minimal cancer cell killing was seen with huLRRC15 targeting ADCs, and the non-specific cell killing observed was similar to that seen with isotype-vcMMAE ADCs (FIG. 13D).

**Example 11. Anti-huLRRC15 PBD ADCs Have Potent *In vitro* Efficacy Against LRRC15-Expressing Cells**

[0376] As described above in Example 7, cancer cells that have undergone EMT had an increased expression of huLRRC15 as compared to cells that had not undergone EMT. Data provided in the present Example show that this increased level of huLRRC15 expression correlated with an increased sensitivity to ADCs that targeted huLRRC15. Accordingly, anti-huLRRC15 ADCs may be efficacious in patients with mesenchymal tumors, such as mesenchymal cancer of the breast, sarcoma, melanoma or glioblastoma.

[0377] For the experiments, anti-huLRRC15 ADCs comprising a pyrrolobenzodiazepine dimer (“PBD”) cytostatic and/or cytotoxic agent were prepared by conjugating the PBD synthon illustrated below with anti-huLRRC15 antibody huM25 or an isotype control antibody to yield a DAR of 2. Preparation of the huM25-PBD-DAR2 ADC was accomplished according to the procedure described in Example 8.



[0378] FIG. 13E depicts the potent *in vitro* 4-day cell killing ability of anti-huLRRC15 ADC huM25-PBD-DAR2 as compared with the isotype control PBD DAR2 ADC in U118MG (glioblastoma) cells. As with the MMAE ADCs, in the huLRRC15-expressing cell line, significantly higher cell killing ability for the anti-huLRRC15 ADC is observed on an equivalent drug basis.

[0379] Similarly, PBD-containing ADCs were prepared with huM25 comprising an engineered S239C mutation in the constant region ("huM25-S239C") to allow for preferential generation of a DAR2 ADC with PBD linking moiety shown above. As used herein, huM25-S239C refers to an anti-huLRRC15 antibody or ADC having a heavy chain amino acid sequence according to SEQ ID NO:100 or 103, and a light chain amino acid sequence according to SEQ ID NO:19. Accordingly, ADCs comprising the S239C mutation did not require chromatographic separation in order to exhibit enrichment in ADCs having DAR2. Hence, the ADCs prepared comprising a huLRRC15 antibody and S239C mutation, including those comprising huM25-S239C, are referred to herein as "E2" (e.g., huM25-S239C-PBD-E2).

[0380] FIG. 13F shows *in vitro* cell killing ability of anti-huLRRC15 ADC huM25-S239C-PBD-E2 in the RPMI-7951 melanoma cell line as compared with an isotype ADC exhibiting equivalent drug loading of the PBD.

[0381] FIG. 13G shows that *in vitro* cell killing of 3T12-huLRRC15 transfected cells by huLRRC15-targeting ADC huM25-S239C-PBD-E2 is significantly higher than that of isotype ADC isotype-S239C-PBD-E2 having the same Fc region and PBD drug displayed in the same manner. Such a result is presumably owing to the localization of the ADC huM25-S239C-PBD-E2 to the huLRRC15-expressing cell surface before release of the cytotoxic PBD agent.

[0382] As shown in FIGS. 13H and 13I, anti-LRRC15 ADC huAD208.4.1-PBD-DAR2, which was cross-reactive to human and mouse LRRC15, demonstrated cell killing effects *in vitro* against mesenchymal stem cells expressing LRRC15. In human BM-MSC (Lonza) treated with 10 ng/mL TGF $\beta$ , huAD208.4.1-PBD-DAR2 exhibited a higher cell killing effect than isotype-PBD-DAR2 at the same doses (FIG. 13H). A similar *in vitro* cell killing effect profile was also observed in murine Balb/c BM-MSC (Cyagen) treated with TGF $\beta$  (10 ng/mL) and each of the ADCs (FIG. 13I).

[0383] Additionally, FIG. 13J depicts experiments in which anti-huLRRC ADCs killed A549 lung cancer cells that have undergone epithelial-mesenchymal transition (EMT). Standard A549 cells did not show a viability difference after treatment with isotype-S239C-PBD-E2 or huM25-S239C-PBD-E2 (top graph). However, in A549 treated with TGF $\beta$  to effect EMT, the huLRRC15-specific ADC huM25-S239C-PBD-E2 exhibited a significantly higher cell killing effect than isotype ADC ( $EC_{50}$  = 0.01 nM vs. 2.3 nM for isotype ADC) (bottom graph).

**Example 12. huM25-vcMMAE-E2 ADC Has Potent Efficacy Against LRRC15 Stromal(+)/Cancer(+) Tumors**

[0384] The potent anti-tumor activity of an exemplary anti-huLRRC15 ADC, huM25-vcMMAE-E2, against huLRRC15 stromal(+)/cancer(+) tumors was demonstrated in a xenograft model with U118MG (glioblastoma) cells. For the experiments, ten million cells (U118MG) that were grown *in vitro* were inoculated subcutaneously per mouse into the right flank of female SCID mice. Tumors were size matched at  $\sim 100 \text{ mm}^3$ , and dosed intraperitoneally (IP) Q6Dx2 (1 dose given every 6 days for a total of 2 doses) as shown in FIG. 14A. Measurements of the length (L) and width (W) of the tumors were taken via electronic caliper and the volume was calculated according to the following equation:  $V = L \times W^2/2$ . In mice treated at 8 mg/kg, maximum tumor growth inhibition ( $\text{TGI}_{\text{max}}$ ) of 97% was noted for huM25-vcMMAE-E2 treatment, which was significantly improved ( $p < 0.001$ ) compared to treatment with isotype control antibody or corresponding isotype control ADC administered at the same regimen (FIG. 14A).

[0385] The potent anti-tumor activity of huM25-vcMMAE-E2 was also demonstrated in a patient-derived xenograft (PDX) model with patient-derived CTG-0241 (human osteosarcoma) cells. Female nu/nu mice were implanted unilaterally on the left flank region with CTG-0241 tumor fragments harvested from host animals, each implanted from a specific passage lot. When tumors reached approximately  $250\text{-}350 \text{ mm}^3$ , animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing was performed intraperitoneally (IP) Q4Dx6 (1 dose given every 4 days for a total of 6 doses) as shown in FIG. 14B. In mice treated at 6 mg/kg, a  $\text{TGI}_{\text{max}}$  of 91% was noted, which was significantly improved ( $p < 0.001$ ) compared to treatment with isotype control antibody or corresponding isotype control ADC administered at the same regimen (FIG. 14B).

[0386] The potent anti-tumor activity of huM25-vcMMAE-E2 was also demonstrated in a PDX model with patient-derived CTG-1095 (human osteosarcoma) cells. Female NSG mice were implanted unilaterally on the left flank region with CTG-1095 tumor fragments harvested from host animals, each implanted from a specific passage lot. When tumors reached approximately  $250\text{-}350 \text{ mm}^3$ , animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing was performed intraperitoneally (IP) Q4Dx6 (1 dose given every 4 days for a total of 6 doses) as shown in FIG. 14C. In mice treated at 12 mg/kg, a  $\text{TGI}_{\text{max}}$  of 87% was noted, which was significantly improved ( $p < 0.001$ ) compared to treatment with isotype control antibody or corresponding isotype control ADC administered at the same regimen (FIG. 14C).

[0387] The anti-huLRRC15 ADC huM25-vcMMAE-E2 displays potent anti-tumor activity in differing tumor models (FIG. 14A, 14B, 14C). Anti-tumor efficacy was observed for several anti-huLRRC15

ADCs (FIG. 14D, 14E) in the glioblastoma xenograft model. The efficacies of huAD208.4.1-vcMMAE-DAR4, huAD208.14.1-vcMMAE-DAR4 and huM25-vcMMAE-DAR4 were similar in magnitude ( $TGI_{max}$ ) and duration (TGD) when dosed at 4 mg/kg in U118MG tumors (FIG. 14E), and hu139.10-vcMMAE-DAR4 was comparable to huM25-vcMMAE-DAR4 when dosed at 6 mg/kg (FIG. 14D). The efficacies were significantly improved ( $p < 0.001$ ) compared to treatment with an isotype control antibody or a corresponding isotype control conjugate administered at the same regimen.

[0388] No statistically significant difference in anti-tumor activity was observed with huM25-vcMMAE-DAR4 in the xenograft model Saos-2 (osteosarcoma) as compared with isotype control, which may be due to the modest huLRRC15 expression observed by IHC (1+ score). In this experiment, 5 million cells (Saos-2) that were grown *in vitro* were inoculated subcutaneously per mouse into the right flank of female SCID-Beige mice. When tumors reached approximately 250-350 mm<sup>3</sup>, animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing was performed intraperitoneally (IP) Q4Dx6 (1 dose given every 4 days for a total of 6 doses) as shown in FIG. 14F. In mice treated at 6 mg/kg, no enhancement in anti-tumor activity was observed as compared with the isotype ADC with the same drug loading (FIG. 14F).

### **Example 13. Anti-huLRRC15 ADCs Are Active Against Large Tumors that Regrow Following Earlier Rounds of Treatment**

[0389] To demonstrate that tumors that regrow post treatment with anti-huLRRC15 ADCs are sensitive to anti-huLRRC15 ADCs, tumors were treated with an anti-huLRRC15 ADC, permitted to regrow and retreated. For the experiment, U118MG human glioblastoma cells were grown *in vitro*, and were inoculated subcutaneously (10 million cells per mouse) into the right flank of female SCID mice. Tumors were size matched at ~150 mm<sup>3</sup>, antibodies and immunoconjugates were administered IP Q4Dx6 (one dose given every 4 days for a total of 6 doses) at 10 or 6 mg/kg, respectively. At Day 165 post sizematch when tumors had regrown to ~450 mm<sup>3</sup>, animals were retreated with huM25-vcMMAE-DAR4 IP Q4Dx3 (one dose given every 4 days for a total of 3 doses) at 6 mg/kg.

[0390] Results are shown in FIG. 15. Maximum tumor growth inhibition ( $TGI_{max}$ ) of 98% was observed for initial treatment with huM25-vcMMAE-DAR4, which was significantly ( $p < 0.001$ ) better than the isotype control antibody or corresponding isotype control conjugate administered at the same regimen.

[0391] Following retreatment after growth, tumor regression was again observed, indicating tumors remained sensitive to huM25-vcMMAE (DAR4), with an overall  $TGI_{max}$  of 70% ( $p < 0.01$ ) relative to the

tumor volume at time of redosing. Expression of huLRRC15 was retained in these previously treated tumors.

**Example 14. E2 ADCs Have Equal or Better Therapeutic Index**

[0392] The safety profiles of E2, E4 and E2/E4 preparations of huM25-vcMMAE ADCs were assessed in a rat tolerability experiment (FIGS. 16A, 16B). For the assay, Sprague Dawley wild type rats were dosed with a single IV dose at MMAE equivalent levels of each antibody drug conjugate. Death occurred earlier (day 3/4) and at a higher percentage (50%) with huM25-vcMMAE-E4 than was seen for huM25-vcMMAE-E2 (day 8, 25%) (FIG. 16A). Double the protein antibody dose was delivered with equal amounts of MMAE, and improved survival for E2 was seen over E4. Fewer deaths occurred in the animals dosed with E2 than E4 ADCs, and the deaths that did occur happened later on Day 8. Broad drug distribution DAR4 has an MTD of 20 mg/kg. Weight loss was not significant for huM25-vcMMAE-E2 when dosed at 60 mg/kg, but there was increased weight loss for rats dosed at the MMAE equivalent dose level of 30 mg/kg with huM25-vcMMAE-E4 (FIG. 16B). This observation demonstrates that higher drug loaded anti-huLRRC15 ADCs are not as well tolerated as when a higher protein dose is delivered with a lower MMAE drug antibody ratio such as 2 cytostatic and/or cytotoxic agents per antibody (E2).

[0393] Four preparations of huM25-vcMMAE that differed in their relative DAR profile (E2, E2/E4, E4 or DAR4) were tested for efficacy in U118MG tumors. Ten million cells were implanted subcutaneously into SCID mice, and mice were randomized when tumor group mean volumes reached  $\sim 100 \text{ mm}^3$ . HuM25-vcMMAE was administered intraperitoneally at MMAE-equivalent doses every seven days for a total of three doses. Maximum tumor growth inhibition ( $\text{TGI}_{\text{max}}$ ) of  $\geq 84\%$  was noted for the group treated with huM25-vcMMAE-E2, which was significantly ( $p < 0.001$ ) better than the isotype control antibody or corresponding isotype control conjugate administered at the same regimen (FIG. 17). All doses were well tolerated and no significant body weight reductions were observed (data not shown). Efficacy in the U118MG tumor model for huM25-vcMMAE-E2 was comparable to huM25-vcMMAE-E2E4 (*i.e.*, the E2/E4 preparation of huM25-vcMMAE) ( $\text{TGI}_{\text{max}}$  of 82%), and superior to that seen for huM25-vcMMAE-E4 ( $\text{TGI}_{\text{max}}$  of 76%) and huM25-vcMMAE-DAR4 ( $\text{TGI}_{\text{max}}$  of 67%), suggesting that higher order DAR is not required for optimal anti-tumor potency and that higher antibody dosing with huM25-vcMMAE-E2 allows for comparable or superior efficacy to that seen with higher drug loaded ADCs.

[0394] The ability to administer more MMAE by dosing a higher total antibody dose with a lower drug antibody ratio (DAR) of E2 resulted in less toxicity than when dosing with a lower antibody dose with a higher drug antibody ratio (*e.g.*, E4) was shown in rat tolerability studies (FIG. 16A, 16B). Also FIG. 17 shows that using a lower drug-antibody ratio of E2 provides equivalent or improved anti-tumor efficacy



as ADC preparations containing a higher drug load (*e.g.*, E2/E4, DAR4, E4) when dosed at MMAE equivalent levels. Taken together these data demonstrate that an improved therapeutic index can be achieved by using anti-huLRRC15 ADCs containing 2 drug/linkers per antibody compared to an ADC preparation containing a higher DAR (*e.g.*, DAR4, E4). These data suggest that anti-huLRRC15 ADCs containing a lower DAR will be able to be dosed clinically at higher levels than ADCs containing a higher DAR (*e.g.*, DAR4 or E4) and will have an improved therapeutic index.

**Example 15. Anti-huLRRC15 ADCs Are Superior to Current Standards of Care**

[0395] The potency of anti-huLRRC15 ADCs as compared to current standards of care was assessed in xenograft model U118MG (glioblastoma), and patient-derived xenograft models CTG-0241 (osteosarcoma) and CTG-1095 (osteosarcoma). Anti-huLRRC15 ADC huM25-vcMMAE-E2 was compared to temozolomide, cisplatin, doxorubicin, gemcitabine, or ifosfamide. Standard of care agents were dosed at maximally efficacious or maximally tolerated dose levels. For FIG. 18A (U118MG), 10 million cells were implanted subcutaneously into female SCID mice and tumors were randomized when they reached  $\sim 100 \text{ mm}^3$  and dosed with biologics at 8 mg/kg intraperitoneally on a Q7Dx2 (one dose given every 7 days for a total of 2 doses), while temozolomide was dosed orally daily for the first 5 days of a 7-day cycle at 20 mg/kg for two cycles. The anti-tumor efficacy for huM25-vcMMAE-E2 ( $\text{TGI}_{\text{max}}$  of 88%) was superior to that seen for temozolomide ( $\text{TGI}_{\text{max}}$  of 67%).

[0396] In FIG. 18B, female nu/nu mice were implanted unilaterally on the left flank region with CTG-0241 tumor fragments harvested from host animals, each implanted from a specific passage lot. When tumors reached approximately  $250\text{-}350 \text{ mm}^3$ , animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing with isotype mAb or ADCs was performed IP at 6 mg/kg on a Q4Dx6 (one dose given every 4 days for a total of 6 doses), while cisplatin was dosed IP Q7Dx3 (once every 7 days for a total of 3 doses) at 7.5 mg/kg, doxorubicin was dosed intravenously (IV) once daily at 1 mg/kg for 5 days, gemcitabine was dosed IP Q3Dx4 (every 3 days for a total of 4 doses) at 80 mg/kg, and ifosfamide was dosed IP QDx3 (one dose given every day for a total of 3 doses) at 120 mg/kg. The anti-tumor efficacy for huM25-vcMMAE-E2 ( $\text{TGI}_{\text{max}}$  of 91%) was superior to that seen for cisplatin ( $\text{TGI}_{\text{max}}$  of 44%), doxorubicin ( $\text{TGI}_{\text{max}}$  of 27%), gemcitabine ( $\text{TGI}_{\text{max}}$  of 64%), or ifosfamide ( $\text{TGI}_{\text{max}}$  of 10%).

[0397] In FIG. 18C, female NSG mice were implanted unilaterally on the left flank region with CTG-1095 tumor fragments harvested from host animals, each implanted from a specific passage lot. When tumors reached approximately  $150\text{-}300 \text{ mm}^3$ , animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing with isotype mAb or ADCs was performed IP at 12

mg/kg Q4Dx6 (one dose given every 4 days for a total of 6 doses), while cisplatin was dosed intraperitoneally Q7Dx2 (once every 7 days for a total of 2 doses) at 7.5 mg/kg. The anti-tumor efficacy for huM25-vcMMAE-E2 (TGI<sub>max</sub> of 87%) was superior to that seen for cisplatin (TGI<sub>max</sub> of 70%).

[0398] In FIG. 18D, female NSG mice were implanted unilaterally on the left flank region with CTG-1095 tumor fragments harvested from host animals, each implanted from a specific passage lot. When tumors reached approximately 200 mm<sup>3</sup>, animals were matched by tumor volume into treatment and control groups and dosing initiated (Day 0). Dosing with isotype mAb or ADCs was performed IP at 6 mg/kg on a Q4Dx6 (one dose given every 4 days for a total of 6 doses), while gemcitabine was dosed IP Q3Dx4 (every 3 days for a total of 4 doses) at 80 mg/kg. The anti-tumor efficacy for the combination of huM25-vcMMAE-E2 and gemcitabine (TGI<sub>max</sub> of 88%; TGD > 319%) was superior to that seen for either gemcitabine alone (TGI<sub>max</sub> of 84%; TGD 241%) or huM25-vcMMAE-E2 alone (TGI<sub>max</sub> of 75%; TGD 193%).

[0399] The *in vivo* efficacy data shown in FIG. 18A-18C provides examples of where anti-huLRRC15 ADCs such as huM25-vcMMAE-E2 outperformed standard of care agents (*e.g.*, temozolomide, cisplatin, doxorubicin, gemcitabine, or ifosfamide) commonly used in cancer therapy. This data suggests that anti-huLRRC15 ADCs (*e.g.*, huM25-vcMMAE-E2) may be more clinically efficacious than certain commonly used anti-cancer therapies.

[0400] Additionally, the data provided in FIG. 18D supports the combination of anti-huLRRC15 ADCs such as huM25-vcMMAE-E2 with standard of care agents (*e.g.*, gemcitabine) to afford a greater anti-tumor effect than observed with dosing of either agent alone.

## 9. EMBODIMENTS

1. An antibody or binding fragment thereof that specifically binds huLRRC15 extracellular domain, wherein said extracellular domain comprises the proteolytic cleavage site defined by Arg<sup>527</sup> and Ser<sup>528</sup> of SEQ ID NO:3.

2. The antibody or binding fragment of **Embodiment 1** that competes for binding cells expressing human LRRC15 with a control antibody selected from huM25, huAD208.4.1, huAD208.12.1, huAD208.14.1, hu139.10, muAD210.40.9, and muAD209.9.1.

3. The antibody or binding fragment of **Embodiment 1** in which the control antibody is huM25.

4. The antibody or binding fragment of **Embodiment 1** in which the control antibody is huAD208.4.1.

5. The antibody or binding fragment of **Embodiment 1**, which comprises a V<sub>H</sub> chain having three CDRs in which:

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:10, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:11 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:12;

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:20, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:21 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:22;

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:30, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:31 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:32;

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:40, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:41 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:42;

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:50, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:51 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:52;

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:60, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:61 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:62; or

V<sub>H</sub> CDR#1 corresponds in sequence to SEQ ID NO:70, V<sub>H</sub> CDR#2 corresponds in sequence to SEQ ID NO:71 and V<sub>H</sub> CDR#3 corresponds in sequence to SEQ ID NO:72.

6. The antibody or binding fragment of **Embodiment 1**, which comprises a V<sub>L</sub> chain having three CDRs in which:

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:13, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:14 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:15;

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:23, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:24 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:25;

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:33, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:34 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:35;

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:43, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:44 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:45;

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:53, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:54 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:55;

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:63, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:64 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:65; or

V<sub>L</sub> CDR#1 corresponds in sequence to SEQ ID NO:73, V<sub>L</sub> CDR#2 corresponds in sequence to SEQ ID NO:74 and V<sub>L</sub> CDR#3 corresponds in sequence to SEQ ID NO:75.

7. The antibody or binding fragment of **Embodiment 1** which comprises a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:16 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:17.

8. The antibody or binding fragment of **Embodiment 1** which comprises a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:26 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27.

9. The antibody or binding fragment of any one of **Embodiments 1-7** which comprises a heavy chain corresponding in sequence to SEQ ID NO:18 and a light chain corresponding in sequence to SEQ ID NO:19.

10. The antibody of **Embodiment 1** which is an IgG<sub>1</sub>.

11. The antibody of **Embodiment 1** having one or more reduced cysteine residues bearing a free sulfhydryl group.

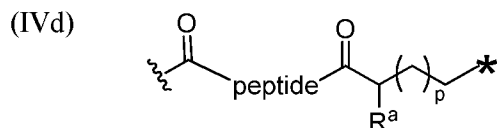
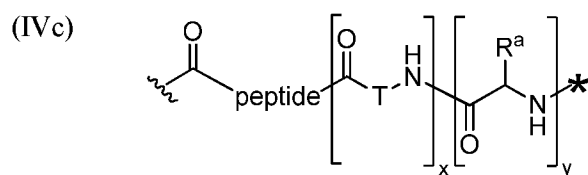
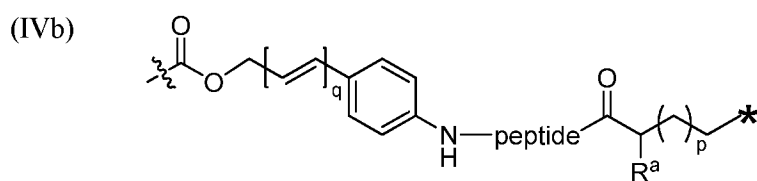
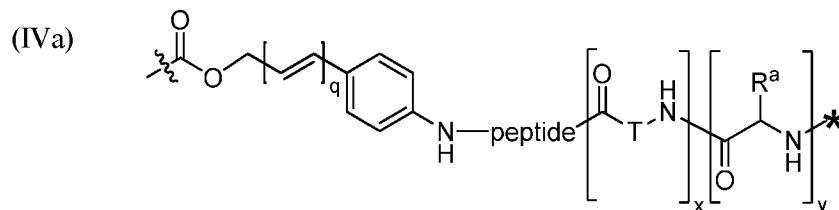
12. An antibody drug conjugate ("ADC") comprising a cytotoxic and/or cytostatic agent linked to an antibody by way of a linker, wherein the antibody is an antibody according to **any one of Embodiments 1-11**, the cytotoxic and/or cytostatic agent is capable of traversing a cell membrane, and the linker is cleavable by a lysosomal enzyme.

13. The ADC of **Embodiment 12** which has an average drug-to-antibody ratio in the range of 1-10.

14. The ADC of **Embodiment 12** which has an average drug-to-antibody ratio in the range of 2-4.

15. The ADC of **Embodiment 12** in which the lysosomal enzyme is Cathepsin B.

16. The ADC of **Embodiment 15** in which the linker comprises a segment according to structural formula (IVa), (IVb), (IVc), or (IVd):



or a salt thereof, wherein:

**peptide** represents a peptide (illustrated C→N and not showing the carboxy and amino “termini”) cleavable by a lysosomal enzyme;

**T** represents a polymer comprising one or more ethylene glycol units or an alkylene chain, or combinations thereof;


**R<sup>a</sup>** is selected from hydrogen, alkyl, sulfonate and methyl sulfonate;

**p** is an integer ranging from 0 to 5;

**q** is 0 or 1;

$x$  is 0 or 1;

$y$  is 0 or 1;

 represents the point of attachment of the linker to a cytotoxic and/or cytostatic agent;

and

\* represents the point of attachment to the remainder of the linker.

17. The ADC of **Embodiment 16** in which **peptide** is selected from the group consisting of Val-Cit; Cit-Val; Ala-Ala; Ala-Cit; Cit-Ala; Asn-Cit; Cit-Asn; Cit-Cit; Val-Glu; Glu-Val; Ser-Cit; Cit-Ser; Lys-Cit; Cit-Lys; Asp-Cit; Cit-Asp; Ala-Val; and Val-Ala and salts thereof.

18. The ADC of **Embodiment 12** in which the lysosomal enzyme is  $\beta$ -glucuronidase.

19. The ADC of **Embodiment 12** in which the cytotoxic and/or cytostatic agent is MMAE.

20. The ADC of **Embodiment 12** in which the cytotoxic and/or cytostatic agent is a PBD dimer.

21. The ADC of **Embodiment 12** in which the antibody comprises three  $V_H$  CDRs corresponding in sequence, respectively, to SEQ ID NO:10, SEQ ID NO:11 and SEQ ID NO:12 and three  $V_L$  CDRs corresponding in sequence, respectively, to SEQ ID NO:13, SEQ ID NO:14 and SEQ ID NO:15.

22. The ADC of **Embodiment 21** in which the antibody comprises a  $V_H$  corresponding in sequence to SEQ ID NO:16.

23. The ADC of **Embodiment 21** in which the antibody comprises a  $V_L$  corresponding in sequence to SEQ ID NO:17.

24. The ADC of **Embodiment 21** in which the antibody comprises a  $V_H$  corresponding in sequence to SEQ ID NO:16 and a  $V_L$  corresponding to SEQ ID NO:17.

25. The ADC of **Embodiment 24** which is an IgG<sub>1</sub>.

26. The ADC of **Embodiment 21** in which the antibody comprises three  $V_H$  CDRs corresponding in sequence, respectively, to SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:22 and three

V<sub>L</sub> CDRs corresponding in sequence, respectively, to SEQ ID NO:23, SEQ ID NO:24 and SEQ ID NO:25.

27. The ADC of **Embodiment 26** in which the antibody comprises a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:26.

28. The ADC of **Embodiment 26** in which the antibody comprises a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27.

29. The ADC of **Embodiment 26** in which the antibody comprises a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:26 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27.

30. The ADC of **Embodiment 29** which is an IgG<sub>1</sub>.

31. The ADC of **Embodiment 12** in which the antibody is huM25.

32. The ADC of **Embodiment 12** in which the antibody is huAD208.4.1.

33. The ADC of **Embodiment 12** in which the antibody competes for binding huLRRC15 with huM25 in an *in vitro* assay.

34. The ADC of **Embodiment 12** in which the antibody competes for binding huLRRC15 with huAD208.4.1 in an *in vitro* assay.

35. The ADC of **Embodiment 12** which is a compound according to structural formula (I):



or a salt thereof, wherein:

**D** is the cytotoxic and/or cytostatic agent;

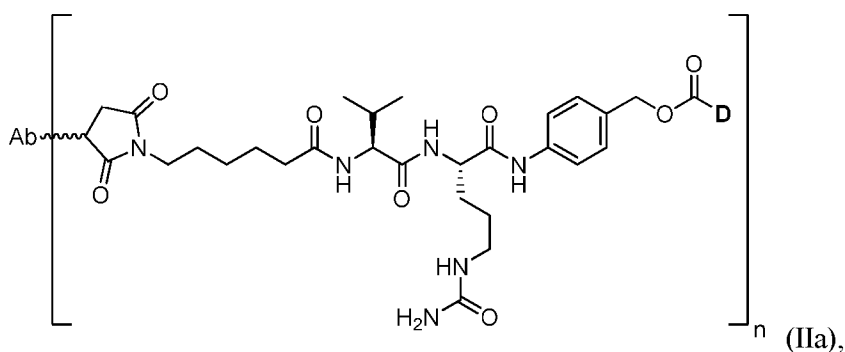
**L** is the linker;

**Ab** is the antibody;

**XY** represents a covalent linkage linking linker **L** to antibody **Ab**; and

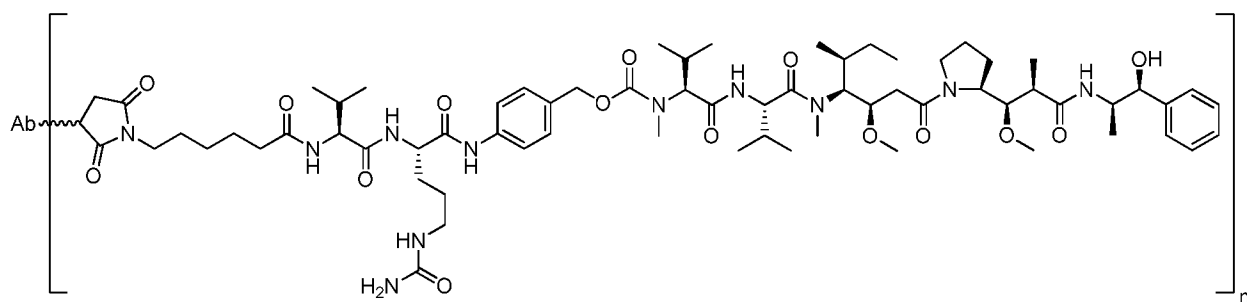
**n** is an integer ranging from 2 to 8.

36. The ADC of **Embodiment 35** in which **n** is 2, 3 or 4.
37. The ADC of **Embodiment 35** in which **XY** is a linkage formed with an amino group on antibody **Ab**.
38. The ADC of **Embodiment 37** in which **XY** is an amide or a thiourea.
39. The ADC of **Embodiment 35** in which **XY** is a linkage formed with a sulfydryl group on antibody **Ab**.
40. The ADC of **Embodiment 39** in which **XY** is a thioether.
41. The ADC of **Embodiment 35** in which the compound according to structural formula (I) has the structure of formula (IIa):



where Ab is antibody huM25.

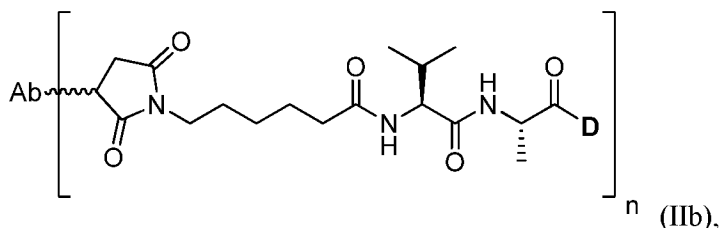
42. The ADC of **Embodiment 35** which has the structure:



where Ab is antibody huM25 and n is 2 or 4.

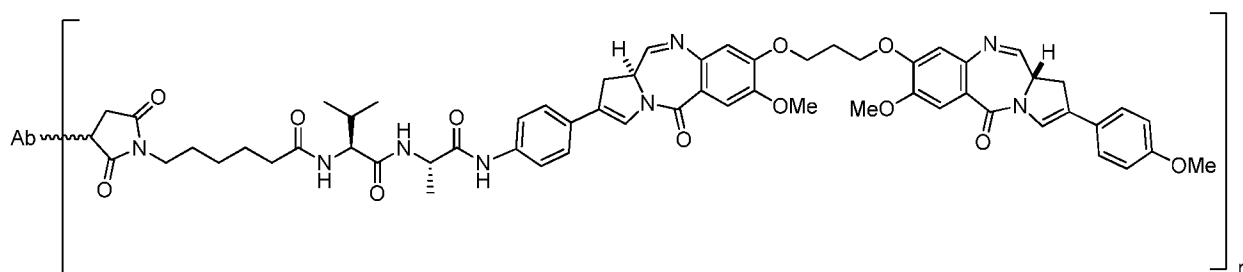


43. The ADC of **Embodiment 35** in which the compound according to structural formula (I) has the structure of formula (IIb):



where Ab is antibody huM25.

44. The ADC of **Embodiment 35** which has the structure:



where Ab is huM25 and n is 2 or 4.

45. A composition comprising an ADC according to **any one of Embodiments 12-44** and a carrier, excipient and/or diluent.

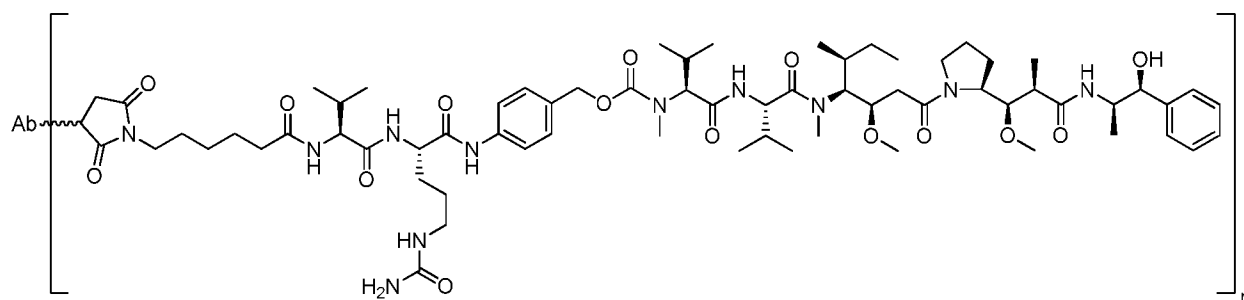
46. The composition of **Embodiment 45** which is formulated for pharmaceutical use in humans.

47. The composition of **Embodiment 45** which is in unit dosage form.

48. An ADC formed by contacting an antibody that specifically binds huLRRC15 extracellular domain, wherein said extracellular domain comprises the proteolytic cleavage site defined by Arg<sup>527</sup> and Ser<sup>528</sup> of SEQ ID NO:3, with a synthon according to structural formula (III) D-L-R<sup>x</sup>, where D is a cytotoxic and/or cytostatic agent capable of crossing a cell membrane, L is a linker cleavable by a lysosomal enzyme and R<sup>x</sup> comprises a functional group capable of covalently linking the synthon to the antibody, under conditions in which the synthon covalently links the synthon to the antibody.

49. The ADC of **Embodiment 48** in which the antibody is huM25 and the cytotoxic and/or cytostatic agent is MMAE.

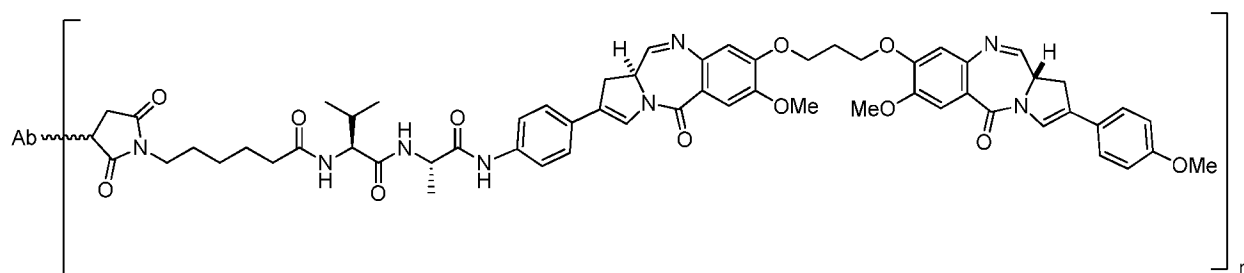
50. The ADC of **Embodiment 49** which has the structure



where Ab is the antibody, and n is 2 or 4.

51. The ADC of **Embodiment 48** in which the antibody is huM25 and the cytotoxic and/or cytostatic agent is a PBD dimer.

52. The ADC of **Embodiment 51** which has the structure



where Ab is the antibody, and n is 2 or 4.

53. The ADC according to **any one of Embodiments 48-52** in which the contacting step is carried out under conditions such that the ADC has a DAR of 2, 3 or 4.

54. A composition comprising an ADC according to **Embodiment 48** and an excipient, carrier and/or diluent.

55. The composition of **Embodiment 54** which is formulated for pharmaceutical use in humans.

56. The composition of **Embodiment 55** which is in unit dosage form.
57. A method of making an ADC, comprising contacting an antibody that specifically binds huLRRC15 extracellular domain, wherein said extracellular domain comprises the proteolytic cleavage site defined by Arg<sup>527</sup> and Ser<sup>528</sup> of SEQ ID NO:3, with a synthon according to structural formula (III) D-L-R<sup>x</sup>, where D is cytotoxic and/or cytostatic agent capable of crossing a cell membrane, L is a linker capable of being cleaved by a lysosomal enzyme, and R<sup>x</sup> comprises a functional group capable of covalently linking the synthon to the antibody, under conditions in which the synthon covalently links the synthon to the antibody.
58. The method of **Embodiment 57** in which the antibody is huM25 and the cytotoxic and/or cytostatic agent is MMAE.
59. The method of **Embodiment 57** in which the antibody is huM25 and the cytotoxic and/or cytostatic agent is a PBD dimer.
60. A method of treating a huLRRC15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC15 stromal(+)/cancer(+) tumor an amount of an ADC according to any one of **Embodiments 12-44** sufficient to provide therapeutic benefit.
61. The method of **Embodiment 60** in which the huLRRC15 stromal(+)/cancer(+) tumor is relapsed, refractory, or relapsed and refractory.
62. The method of **Embodiment 60** in which the huLRRC15 stromal(+)/cancer(+) tumor is glioblastoma, sarcoma, or melanoma.
63. The method of **Embodiment 60** in which the huLRRC15 stromal(+)/cancer(+) tumor is a metastatic cancer.
64. The method of **Embodiment 60** in which the ADC is administered as monotherapy.
65. The method of **Embodiment 64** in which the ADC is administered intravenously at a dose ranging from about 0.3 mg/kg to about 6.0 mg/kg.
66. The method of **Embodiment 60** in which the ADC is administered adjunctive to or with another anti-cancer therapy or agent.

67. The method of **Embodiment 66** in which the anti-cancer therapy or agent is a non-targeted anti-cancer therapy.

68. The method of **Embodiment 67** in which the non-targeted anti-cancer therapy is cisplatin, gemcitabine, docetaxel, carboplatin, doxorubicin, ifosfamide, temozolomide, or radiation.

69. The method of **Embodiment 66** in which anti-cancer therapy or agent is a targeted anti-cancer agent.

70. The method of **Embodiment 69** in which the huLRRC15 stromal(+)/cancer(+) tumor is glioblastoma and the targeted anti-cancer agent is bevacizumab, cetuximab, gefitinib, erlotinib, cediranib, imatinib, sorafenib, sunitinib, tipifarnib, lonafarnib, tamoxifen, enzastaurin, sirolimus, temsirolimus, everolimus, ABT-414, vironistat, or cilengitide.

71. The method of **Embodiment 69** in which the huLRRC15 stromal(+)/cancer(+) tumor is sarcoma and the targeted anti-cancer agent is imatinib, dasatinib, sorafenib, sunitinib, regorafenib, pazopanib, trastuzumab, rituximab, pembrolizumab, or nivolumab.

72. The method of **Embodiment 69** in which the huLRRC15 stromal(+)/cancer(+) tumor is melanoma and the targeted anti-cancer agent is vemurafenib, dabrafenib, trametinib, cobimetinib, ipilimumab, pembrolizumab, or nivolumab.

73. The method of **Embodiment 60** in which the ADC is administered adjunctively with or to a non-targeted anti-cancer therapy and a targeted anti-cancer agent.

**[0401]** All publications, patents, patent applications and other documents cited in this application are hereby incorporated by reference in their entireties for all purposes to the same extent as if each individual publication, patent, patent application or other document were individually indicated to be incorporated by reference for all purposes.

**[0402]** While various specific embodiments have been illustrated and described, it will be appreciated that various changes can be made without departing from the spirit and scope of the invention(s).

**10. CLAIMS****WHAT IS CLAIMED IS:**

1. A method of treating a huLRRC15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises a DNA intercalating agent linked to an anti-huLRRC15 antibody by way of a linker according to a structure of formula (I):



or a salt thereof, wherein:

**D** is the DNA intercalating agent;

**L** is the linker;

**Ab** is the anti-huLRRC15 antibody;

**XY** represents a covalent linkage linking linker L to antibody Ab; and

**n** is an integer ranging from 2 to 8;

wherein

**Ab** comprises

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:16 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:17,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:26 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:36 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:37,

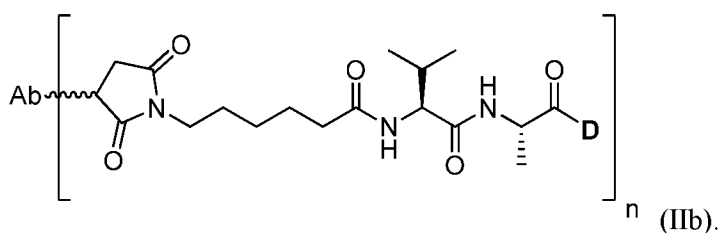
a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:46 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:47,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:56 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:57,

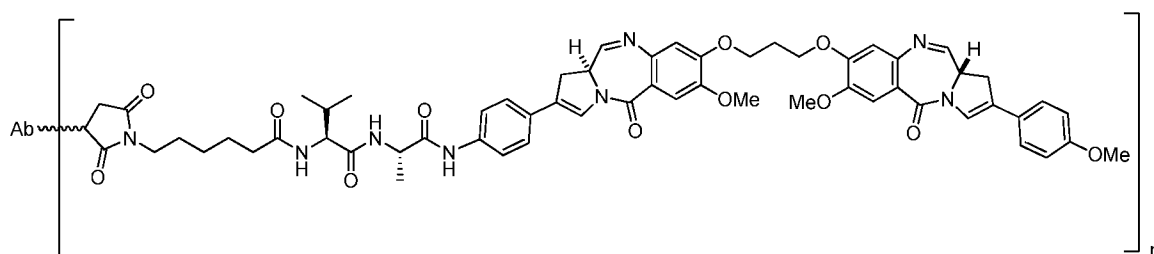
a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:66 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:67, or

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:76 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:77.

2. The method of **claim 1** in which **n** is 2, 3 or 4.
3. The method of **claim 1** in which **XY** is a thioether linkage formed with a sulfydryl group on antibody **Ab**.
4. The method of **claim 1** in which **L** comprises Val-Cit or Val-Ala.
5. The method of **claim 1** in which **D** is a pyrrolobenzodiazepine.
6. The method of **claim 1** in which **Ab** is an IgG<sub>1</sub>.
7. The method of **claim 1** in which the ADC has a structure of formula (IIb):



8. The method of **claim 7** in which **n** is 2, 3 or 4.
9. The method of **claim 7** in which **Ab** comprises:
  - (a) a heavy chain having an amino acid sequence of SEQ ID NO: 18, 100, 102, or 103; and a light chain of SEQ ID NO:19;
  - (b) a heavy chain having an amino acid sequence of SEQ ID NO: 28, 101, 104, or 105; and a light chain of SEQ ID NO:29.
10. The method of **claim 7** in which the ADC has a structure of formula (IIIb)



(IIIb).

11. The method of **claim 10** in which  $n$  is 2 or 4.
12. The method of **claim 10** in which **Ab** comprises:
  - (a) a heavy chain having an amino acid sequence of SEQ ID NOS: 18, 100, 102, or 103; and a light chain of SEQ ID NO:19;
  - (b) a heavy chain having an amino acid sequence of SEQ ID NOS: 28, 101, 104, or 105; and a light chain of SEQ ID NO:29.
13. A method of treating a huLRRC15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent linked to an anti-huLRRC15 antibody by way of a linker according to a structure of formula (I):



or a salt thereof, wherein:

**D** is the antimitotic agent;

**L** is the linker;

**Ab** is the anti-huLRRC15 antibody;

**XY** represents a covalent linkage linking linker **L** to antibody **Ab**; and

**n** is an integer ranging from 2 to 8;

wherein

**Ab** comprises

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:16 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:17,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:26 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:27,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:36 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:37,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:46 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:47,

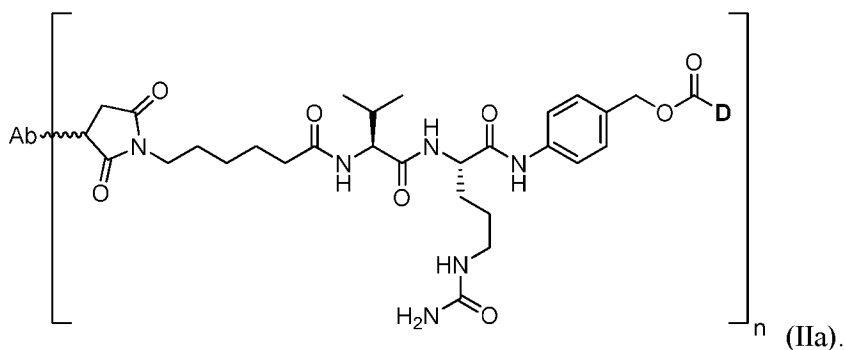
a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:56 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:57,

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:66 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:67, or

a V<sub>H</sub> chain corresponding in sequence to SEQ ID NO:76 and a V<sub>L</sub> chain corresponding in sequence to SEQ ID NO:77.

14. The method of **claim 13** in which **n** is 2, 3 or 4.
15. The method of **claim 13** in which **XY** is a thioether linkage formed with a sulfydryl group on antibody **Ab**.
16. The method of **claim 13** in which **L** comprises Val-Cit or Val-Ala.
17. The method of **claim 13** in which **D** is an auristatin.
18. The method of **claim 13** in which **Ab** is an IgG<sub>1</sub>.
19. The method of **claim 13** in which the ADC has a structure of formula (IIa):





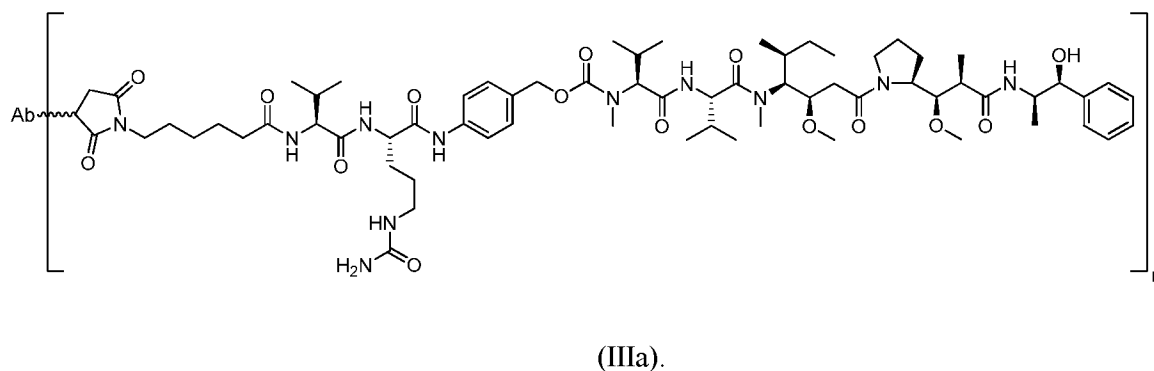
20. The method of **claim 19** in which **n** is 2, 3 or 4.

21. The method of **claim 19** in which **Ab** comprises:

(a) a heavy chain having an amino acid sequence of SEQ ID NOS: 18, 100, 102, or 103; and a light chain of SEQ ID NO:19; or

(b) a heavy chain having an amino acid sequence of SEQ ID NOS: 28, 101, 104, or 105; and a light chain of SEQ ID NO:29.

22. The method of **claim 19** in which the ADC has a structure of formula (IIIa):



23. The method of **claim 22** in which **n** is 2 or 4.

24. The method of **claim 22** in which **Ab** comprises:

(a) a heavy chain having an amino acid sequence of SEQ ID NOS: 18, 100, 102, or 103; and a light chain of SEQ ID NO:19; or

(b) a heavy chain having an amino acid sequence of SEQ ID NOS: 28, 101, 104, or 105; and a light chain of SEQ ID NO:29.

25. The method of **claim 1** in which the huLRRC15 stromal(+)/cancer(+) tumor is relapsed, refractory, or relapsed and refractory.

26. The method of **claim 1** in which the huLRRC15 stromal(+)/cancer(+) tumor is glioblastoma, sarcoma, or melanoma.

27. The method of **claim 1** in which the ADC is administered as monotherapy.

28. The method of **claim 1** in which the ADC is administered intravenously at a dose ranging from about 0.3 mg/kg to about 6.0 mg/kg.

29. The method of **claim 13** in which the huLRRC15 stromal(+)/cancer(+) tumor is relapsed, refractory, or relapsed and refractory.

30. The method of **claim 13** in which the huLRRC15 stromal(+)/cancer(+) tumor is glioblastoma, sarcoma, or melanoma.

31. The method of **claim 13** in which the ADC is administered as monotherapy.

32. The method of **claim 13** in which the ADC is administered intravenously at a dose ranging from about 0.3 mg/kg to about 6.0 mg/kg.

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huLRRC15 isoform 1 (NCBI accession: NP\_001128529, REFSEQ: NM\_001135057.2)

1	<b>M</b>	<b>P</b>	<b>L</b>	<b>D</b>	<b>K</b>	<b>A</b>	<b>M</b>	<b>P</b>	<b>L</b>	<b>K</b>	<b>H</b>	<b>Y</b>	<b>L</b>	<b>L</b>	<b>L</b>	<b>V</b>	<b>G</b>	<b>C</b>	<b>Q</b>	
	ATG	CCT	TTG	GAC	AAG	GCT	ATG	CCA	CTG	AAG	CAT	TAT	CTC	CTT	TTG	CTG	GTG	GGC	TGC	CAA
61	<b>A</b>	<b>W</b>	<b>G</b>	<b>A</b>	<b>G</b>	<b>L</b>	<b>A</b>	<b>Y</b>	<b>H</b>	<b>G</b>	<b>C</b>	<b>P</b>	<b>S</b>	<b>E</b>	<b>C</b>	<b>T</b>	<b>C</b>	<b>S</b>	<b>R</b>	<b>A</b>
	GCC	TGG	GGT	GCA	GGG	TTG	GCC	TAC	CAT	GGC	TGC	CCT	AGC	GAG	TGT	ACC	TGC	TCC	AGG	GCC
121	<b>S</b>	<b>Q</b>	<b>V</b>	<b>E</b>	<b>C</b>	<b>T</b>	<b>G</b>	<b>A</b>	<b>R</b>	<b>I</b>	<b>V</b>	<b>A</b>	<b>V</b>	<b>P</b>	<b>T</b>	<b>P</b>	<b>L</b>	<b>P</b>	<b>W</b>	<b>N</b>
	TCC	CAG	GTG	GAG	TGC	ACC	GGG	GCA	CGC	ATT	GTG	GCA	GTG	CCC	ACC	CCT	CTG	CCC	TGG	AAC
181	<b>A</b>	<b>M</b>	<b>S</b>	<b>L</b>	<b>Q</b>	<b>I</b>	<b>L</b>	<b>N</b>	<b>T</b>	<b>H</b>	<b>I</b>	<b>T</b>	<b>E</b>	<b>L</b>	<b>N</b>	<b>E</b>	<b>S</b>	<b>P</b>	<b>F</b>	<b>L</b>
	GCC	ATG	AGC	CTG	CAG	ATC	CTC	AAC	ACG	CAC	ATC	ACT	GAA	CTC	AAT	GAG	TCC	CCG	TTC	CTC
241	<b>N</b>	<b>I</b>	<b>S</b>	<b>A</b>	<b>L</b>	<b>I</b>	<b>A</b>	<b>L</b>	<b>R</b>	<b>I</b>	<b>E</b>	<b>K</b>	<b>N</b>	<b>E</b>	<b>L</b>	<b>S</b>	<b>R</b>	<b>I</b>	<b>T</b>	<b>P</b>
	AAT	ATC	TCA	GCC	CTC	ATC	GCC	CTG	AGG	ATT	GAG	AAG	AAT	GAG	CTG	TGC	CGC	ATC	ACG	CCT
301	<b>G</b>	<b>A</b>	<b>F</b>	<b>R</b>	<b>N</b>	<b>L</b>	<b>G</b>	<b>S</b>	<b>L</b>	<b>R</b>	<b>Y</b>	<b>L</b>	<b>S</b>	<b>L</b>	<b>A</b>	<b>N</b>	<b>N</b>	<b>K</b>	<b>L</b>	<b>Q</b>
	GGG	GCC	TTC	CGA	AAC	CTG	GGC	TGC	CTG	CGC	TAT	CTC	AGC	CTC	GCC	AAC	AAC	AAG	CTG	CAG
361	<b>V</b>	<b>L</b>	<b>P</b>	<b>I</b>	<b>G</b>	<b>L</b>	<b>F</b>	<b>Q</b>	<b>G</b>	<b>L</b>	<b>D</b>	<b>S</b>	<b>L</b>	<b>E</b>	<b>S</b>	<b>L</b>	<b>L</b>	<b>L</b>	<b>S</b>	<b>S</b>
	GTT	CTG	CCC	ATC	GGC	CTC	TTC	CAG	GGC	CTG	GAC	AGC	CTC	GAG	TCT	CTC	CTT	CTG	TCC	AGT
421	<b>N</b>	<b>Q</b>	<b>L</b>	<b>L</b>	<b>Q</b>	<b>I</b>	<b>Q</b>	<b>P</b>	<b>A</b>	<b>H</b>	<b>F</b>	<b>S</b>	<b>Q</b>	<b>C</b>	<b>S</b>	<b>N</b>	<b>L</b>	<b>K</b>	<b>E</b>	<b>L</b>
	AAC	CAG	CTG	TTG	CAG	ATC	CAG	CCG	GCC	CAC	TTC	TCC	CAG	TGC	AGC	AAC	CTC	AAG	GAG	CTG
481	<b>Q</b>	<b>L</b>	<b>H</b>	<b>G</b>	<b>N</b>	<b>H</b>	<b>L</b>	<b>E</b>	<b>Y</b>	<b>I</b>	<b>P</b>	<b>D</b>	<b>G</b>	<b>A</b>	<b>F</b>	<b>D</b>	<b>H</b>	<b>L</b>	<b>V</b>	<b>G</b>
	CAG	TTG	CAC	GGC	AAC	CAC	CTG	GAA	TAC	ATC	CCT	GAC	GGC	TTC	GAC	TTC	GAC	CAC	CTG	GGA
541	<b>L</b>	<b>T</b>	<b>K</b>	<b>L</b>	<b>N</b>	<b>L</b>	<b>G</b>	<b>K</b>	<b>N</b>	<b>S</b>	<b>L</b>	<b>T</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>P</b>	<b>R</b>	<b>V</b>	<b>F</b>	<b>Q</b>
	CTC	ACG	AAG	CTC	AAT	CTG	GGC	AAG	AAT	AGC	CTC	ACC	CAC	ATC	TCA	CCC	AGG	GTC	TTC	CAG
601	<b>H</b>	<b>L</b>	<b>G</b>	<b>N</b>	<b>L</b>	<b>Q</b>	<b>V</b>	<b>L</b>	<b>R</b>	<b>L</b>	<b>Y</b>	<b>E</b>	<b>N</b>	<b>R</b>	<b>L</b>	<b>T</b>	<b>D</b>	<b>I</b>	<b>P</b>	<b>M</b>
	CAC	CTG	GGC	AAC	CTC	CAG	GTC	CTC	CGG	CTG	TAT	GAG	AAC	AGG	CTC	ACG	GAT	ATC	CCC	ATG
661	<b>G</b>	<b>T</b>	<b>F</b>	<b>D</b>	<b>G</b>	<b>L</b>	<b>V</b>	<b>N</b>	<b>L</b>	<b>Q</b>	<b>E</b>	<b>L</b>	<b>A</b>	<b>L</b>	<b>Q</b>	<b>Q</b>	<b>N</b>	<b>Q</b>	<b>I</b>	<b>G</b>
	GGC	ACT	TTT	GAT	GGG	CTT	GTT	AAC	CTG	CAG	GAA	CTG	GCT	CTG	CAG	CAG	AAC	CAG	ATT	GGA
721	<b>L</b>	<b>L</b>	<b>S</b>	<b>P</b>	<b>G</b>	<b>L</b>	<b>F</b>	<b>H</b>	<b>N</b>	<b>N</b>	<b>H</b>	<b>N</b>	<b>L</b>	<b>L</b>	<b>Q</b>	<b>R</b>	<b>L</b>	<b>Y</b>	<b>L</b>	<b>S</b>
	CTG	CTC	TCC	CCT	GGT	CTC	TTT	CAC	AAC	AAC	CAC	AAC	CTC	CAG	AGA	CTC	TAC	CTG	TCC	AAC
781	<b>N</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>Q</b>	<b>L</b>	<b>P</b>	<b>P</b>	<b>S</b>	<b>V</b>	<b>F</b>	<b>M</b>	<b>Q</b>	<b>L</b>	<b>P</b>	<b>Q</b>	<b>L</b>	<b>N</b>	<b>R</b>	<b>L</b>
	AAC	CAC	ATC	TCC	CAG	CTG	CCA	CCC	AGC	GTC	TTC	ATG	CAG	CTG	CCC	CAG	CTC	AAC	CGT	CTT
841	<b>T</b>	<b>L</b>	<b>F</b>	<b>G</b>	<b>N</b>	<b>S</b>	<b>L</b>	<b>K</b>	<b>E</b>	<b>L</b>	<b>S</b>	<b>P</b>	<b>G</b>	<b>I</b>	<b>F</b>	<b>G</b>	<b>P</b>	<b>M</b>	<b>P</b>	<b>N</b>
	ACT	CTC	TTT	GGG	AAT	TCC	CTG	AAG	GAG	CTC	TCT	CCG	GGG	ATC	TTC	GGG	CCC	ATG	CCC	AAC
901	<b>L</b>	<b>R</b>	<b>E</b>	<b>L</b>	<b>W</b>	<b>L</b>	<b>Y</b>	<b>D</b>	<b>N</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>L</b>	<b>P</b>	<b>D</b>	<b>N</b>	<b>V</b>	<b>F</b>	<b>S</b>	<b>S</b>
	CTG	CGG	GAG	CTT	TGG	CTC	TAT	GAC	AAC	CAC	ATC	TCT	TCT	CTA	CCC	GAC	AAT	GTC	TTC	AGC
961	<b>N</b>	<b>L</b>	<b>R</b>	<b>Q</b>	<b>L</b>	<b>Q</b>	<b>V</b>	<b>L</b>	<b>I</b>	<b>L</b>	<b>S</b>	<b>R</b>	<b>N</b>	<b>Q</b>	<b>I</b>	<b>S</b>	<b>F</b>	<b>I</b>	<b>S</b>	<b>P</b>
	AAC	CTC	CGC	CAG	TTG	CAG	GTC	CTG	ATT	CTT	AGC	CGC	AAT	CAG	ATC	AGC	TTC	ATC	TCC	CCG

FIG. 1A

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G   A   F   N   G   L   T   E   L   R   E   L   S   L   H   T   N   A   L   Q
1021 GGT GCC TTC AAC GGG CTA ACG GAG CTT CGG GAG CTG TCC CTC CAC ACC AAC GCA CTG CAG
D   L   D   G   N   V   F   R   A   N   L   Q   N   I   S   L   Q   N
1081 GAC CTG GAC GGG AAC GTC TTC CGC ATG TTG GCC AAC CTG CAG AAC ATC TCC CTG CAG AAC
N   R   L   R   Q   L   P   G   N   I   F   A   N   V   N   G   L   M   A   I
1141 AAC CGC CTC AGA CAG CTC CCA GGG AAT ATC TTC GCC AAC GTC AAT GGC CTC ATG GCC ATC
Q   L   Q   N   N   Q   L   E   N   L   P   L   G   I   F   D   H   L   G   K
1201 CAG CTG CAG AAC AAC CAG CTG GAG AAC TTG CCC CTC GGC ATC TTC GAT CAC CTG GGG AAA
L   C   E   L   R   L   Y   D   N   P   W   R   C   D   S   D   I   L   P   L
1261 CTG TGT GAG CTG CGG CTG TAT GAC AAT CCC TGG AGG TGT GAC TCA GAC ATC CTT CCG CTC
R   N   W   L   L   L   N   Q   P   R   L   G   T   D   T   V   P   V   C   F
1321 CGC AAC TGG CTC CTG CTC AAC CAG CCT AGG TTA GGG ACG GAC ACT GTA CCT GTG TGT TTC
S   P   A   N   V   R   G   Q   S   L   I   I   N   V   N   V   A   V   P
1381 AGC CCA GCC AAT GTC CGA GGC CAG TCC CTC ATT ATC AAT GTC AAC GTT GCT GTT CCA
S   V   H   V   P   E   V   P   S   Y   P   E   T   P   W   Y   P   D   T   P
1441 AGC GTC CAT GTC CCC GAG GTG CCT AGT TAC CCA GAA ACA CCA TGG TAC CCA GAC ACA CCC
S   Y   P   D   T   T   S   V   T   TCT TCT ACC ACT GAG CTA ACC AGC CCT GTG GAA GAC
1501 AGT TAC CCT GAC ACC ACA TCC GTC TCT TCT ACC ACT GAG CTA ACC AGC CCT GTG GAA GAC
Y   T   D   L   T   T   I   Q   V   T   D   D   D   RS V   W   G   M   T   Q
1561 TAC ACT GAT CTG ACT ACC ATT CAG GTC ACT GAT GAC CGC AGC GTT TGG GGC ATG ACC CAG
A   Q   S   G   L   A   I   A   I   V   I   G   I   V   A   L   A   C   S
1621 GCC CAG AGC GGG CTG GCC ATT GCC GGC ATT GTA ATT GGC ATT GTC GCC CTG GCC TGC TCC
L   A   A   C   V   G   C   C   C   C   K   R   S   Q   A   V   L   M   Q
1681 CTG GCT GCC TGC GTC GGC TGT TGC TGC TGC AAG AAG AGG AGC CAA GCT GTC CTG ATG CAG
M   K   A   A   P   N   E   C   (SEQ ID NO:1)
1741 ATG AAG GCA CCC AAT GAG TGT (SEQ ID NO:2)

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Legend:  
 predicted signal peptide is **bold italicized**  
 predicted transmembrane domain is underlined  
 predicted protease cleavage site is boxed

FIG. 1B

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huLRRRC15 isoform 2 (NCBI accession: NP\_570843, REFSEQ: NM\_130830.4)

1	<b>M</b>	<b>P</b>	<b>L</b>	<b>K</b>	<b>H</b>	<b>Y</b>	<b>L</b>	<b>L</b>	<b>L</b>	<b>L</b>	<b>V</b>	<b>G</b>	<b>C</b>	<b>Q</b>	<b>A</b>	<b>W</b>	<b>G</b>	<b>A</b>	<b>G</b>	<b>L</b>
	ATG	CCA	CTG	AAG	CAT	TAT	CTC	CTT	TTG	CTG	GTG	GGC	TGC	CAA	GCC	TGG	GGT	GCA	GGG	TTG
61	<b>A</b>	<b>Y</b>	<b>H</b>	<b>G</b>	<b>C</b>	<b>P</b>	<b>S</b>	<b>E</b>	<b>C</b>	<b>T</b>	<b>C</b>	<b>S</b>	<b>R</b>	<b>A</b>	<b>S</b>	<b>Q</b>	<b>V</b>	<b>E</b>	<b>C</b>	<b>T</b>
	GCC	TAC	CAT	GGC	TGC	CCT	AGC	GAG	TGT	ACC	TGC	TCC	AGG	GCC	TCC	CAG	GTG	GAG	TGC	ACC
121	<b>G</b>	<b>A</b>	<b>R</b>	<b>I</b>	<b>V</b>	<b>A</b>	<b>V</b>	<b>P</b>	<b>T</b>	<b>P</b>	<b>L</b>	<b>P</b>	<b>W</b>	<b>N</b>	<b>A</b>	<b>M</b>	<b>S</b>	<b>L</b>	<b>Q</b>	<b>I</b>
	GGG	GCA	CGC	ATT	GTG	GCA	GTG	CCC	ACC	CCT	CTG	CCC	TGG	AAC	GCC	ATG	AGC	CTG	CAG	ATC
181	<b>L</b>	<b>N</b>	<b>T</b>	<b>H</b>	<b>I</b>	<b>T</b>	<b>E</b>	<b>L</b>	<b>N</b>	<b>E</b>	<b>S</b>	<b>P</b>	<b>F</b>	<b>L</b>	<b>N</b>	<b>I</b>	<b>S</b>	<b>A</b>	<b>L</b>	<b>I</b>
	CTC	AAC	ACG	CAC	ATC	ACT	GAA	CTC	AAT	GAG	TCC	CCG	TTC	CTC	AAT	ATC	TCA	GCC	CTC	ATC
241	<b>A</b>	<b>L</b>	<b>R</b>	<b>I</b>	<b>E</b>	<b>K</b>	<b>N</b>	<b>E</b>	<b>L</b>	<b>S</b>	<b>R</b>	<b>I</b>	<b>T</b>	<b>P</b>	<b>G</b>	<b>A</b>	<b>F</b>	<b>R</b>	<b>N</b>	<b>L</b>
	GCC	CTG	AGG	ATT	GAG	AAG	AAT	GAG	CTG	TCG	CGC	ATC	ACG	CCT	GGG	GCC	TTC	CGA	AAC	CTG
301	<b>G</b>	<b>S</b>	<b>L</b>	<b>R</b>	<b>Y</b>	<b>L</b>	<b>S</b>	<b>L</b>	<b>A</b>	<b>N</b>	<b>N</b>	<b>K</b>	<b>L</b>	<b>Q</b>	<b>V</b>	<b>L</b>	<b>P</b>	<b>I</b>	<b>G</b>	<b>L</b>
	GGC	TCG	CTG	CGC	TAT	CTC	AGC	CTC	GCC	AAC	AAC	AAG	CTG	CAG	GTT	CTG	CCC	ATC	GGC	CTC
361	<b>F</b>	<b>Q</b>	<b>G</b>	<b>L</b>	<b>D</b>	<b>S</b>	<b>L</b>	<b>E</b>	<b>S</b>	<b>L</b>	<b>L</b>	<b>S</b>	<b>S</b>	<b>S</b>	<b>N</b>	<b>Q</b>	<b>L</b>	<b>L</b>	<b>Q</b>	<b>I</b>
	TTC	CAG	GGC	CTG	GAC	AGC	CTC	GAG	TCT	CTC	CTT	CTG	TCC	AGT	AAC	CAG	CTG	TTG	CAG	ATC
421	<b>Q</b>	<b>P</b>	<b>A</b>	<b>H</b>	<b>F</b>	<b>S</b>	<b>Q</b>	<b>C</b>	<b>S</b>	<b>N</b>	<b>L</b>	<b>K</b>	<b>E</b>	<b>L</b>	<b>Q</b>	<b>L</b>	<b>H</b>	<b>G</b>	<b>N</b>	<b>H</b>
	CAG	CCG	GCC	CAC	TTC	TCC	CAG	TGC	AGC	AAC	CTC	AAG	GAG	CTG	CAG	TTG	CAC	GGC	AAC	CAC
481	<b>L</b>	<b>E</b>	<b>Y</b>	<b>I</b>	<b>P</b>	<b>D</b>	<b>G</b>	<b>A</b>	<b>F</b>	<b>D</b>	<b>H</b>	<b>L</b>	<b>V</b>	<b>G</b>	<b>L</b>	<b>T</b>	<b>K</b>	<b>L</b>	<b>N</b>	<b>L</b>
	CTG	GAA	TAC	ATC	CCT	GAC	GGA	GCC	TTC	GAC	CAC	CTG	GTA	GGA	CTC	ACG	AAG	CTC	AAT	CTG
541	<b>G</b>	<b>K</b>	<b>N</b>	<b>S</b>	<b>L</b>	<b>T</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>P</b>	<b>R</b>	<b>V</b>	<b>F</b>	<b>Q</b>	<b>H</b>	<b>L</b>	<b>G</b>	<b>N</b>	<b>L</b>	<b>Q</b>
	GGC	AAG	AAT	AGC	CTC	ACC	CAC	ATC	TCA	CCC	AGG	GTC	TTC	CAG	CAC	CTG	GGC	AAC	CTC	CAG
601	<b>V</b>	<b>L</b>	<b>R</b>	<b>L</b>	<b>Y</b>	<b>E</b>	<b>N</b>	<b>R</b>	<b>L</b>	<b>T</b>	<b>D</b>	<b>I</b>	<b>P</b>	<b>M</b>	<b>G</b>	<b>T</b>	<b>F</b>	<b>D</b>	<b>G</b>	<b>L</b>
	GTC	CTC	CGG	CTG	TAT	GAG	AAC	AGG	CTC	ACG	GAT	ATC	CCC	ATG	GGC	ACT	TTT	GAT	GGG	CTT
661	<b>V</b>	<b>N</b>	<b>L</b>	<b>Q</b>	<b>E</b>	<b>L</b>	<b>A</b>	<b>L</b>	<b>Q</b>	<b>Q</b>	<b>N</b>	<b>Q</b>	<b>I</b>	<b>G</b>	<b>L</b>	<b>L</b>	<b>S</b>	<b>P</b>	<b>G</b>	<b>L</b>
	GTT	AAC	CTG	CAG	GAA	CTG	GCT	CTG	CAG	CAG	AAC	CAG	ATT	GGA	CTG	CTC	TCC	CCT	GGT	CTC
721	<b>F</b>	<b>H</b>	<b>N</b>	<b>N</b>	<b>H</b>	<b>N</b>	<b>L</b>	<b>Q</b>	<b>R</b>	<b>L</b>	<b>Y</b>	<b>L</b>	<b>S</b>	<b>N</b>	<b>N</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>Q</b>	<b>L</b>
	TTC	CAC	AAC	AAC	CAC	AAC	CTC	CAG	AGA	CTC	TAC	CTG	TCC	AAC	AAC	CAC	ATC	TCC	CAG	CTG
781	<b>P</b>	<b>P</b>	<b>S</b>	<b>V</b>	<b>F</b>	<b>M</b>	<b>Q</b>	<b>L</b>	<b>P</b>	<b>Q</b>	<b>L</b>	<b>N</b>	<b>R</b>	<b>L</b>	<b>T</b>	<b>L</b>	<b>F</b>	<b>G</b>	<b>N</b>	<b>S</b>
	CCA	CCC	AGC	GTC	TTC	ATG	CAG	CTG	CCC	CAG	CTC	AAC	CGT	CTT	ACT	CTC	TTT	GGG	AAT	TCC
841	<b>L</b>	<b>K</b>	<b>E</b>	<b>L</b>	<b>S</b>	<b>P</b>	<b>G</b>	<b>I</b>	<b>F</b>	<b>G</b>	<b>P</b>	<b>M</b>	<b>P</b>	<b>N</b>	<b>L</b>	<b>R</b>	<b>E</b>	<b>L</b>	<b>W</b>	<b>L</b>
	CTG	AAG	GAG	CTC	TCT	CCG	GGG	ATC	TTC	GGG	CCC	ATG	CCC	AAC	CTG	CGG	GAG	CTT	TGG	CTC
901	<b>Y</b>	<b>D</b>	<b>N</b>	<b>H</b>	<b>I</b>	<b>S</b>	<b>S</b>	<b>L</b>	<b>P</b>	<b>D</b>	<b>N</b>	<b>V</b>	<b>F</b>	<b>S</b>	<b>N</b>	<b>L</b>	<b>R</b>	<b>Q</b>	<b>L</b>	<b>Q</b>
	TAT	GAC	AAC	CAC	ATC	TCT	TCT	CTA	CCC	GAC	AAT	GTC	TTC	AGC	AAC	CTC	CGC	CAG	TTG	CAG
961	<b>V</b>	<b>L</b>	<b>I</b>	<b>L</b>	<b>S</b>	<b>R</b>	<b>N</b>	<b>Q</b>	<b>I</b>	<b>S</b>	<b>F</b>	<b>I</b>	<b>S</b>	<b>P</b>	<b>G</b>	<b>A</b>	<b>F</b>	<b>N</b>	<b>G</b>	<b>L</b>
	GTC	CTG	ATT	CTT	AGC	CGC	AAT	CAG	ATC	AGC	TTC	ATC	TCC	CCG	GGT	GCC	TTC	AAC	GGG	CTA

FIG. 1C

```

T   E   L   R   E   L   S   L   H   T   N   A   L   Q   D   L   D   G   N   V
1021 ACG GAG CTT CGG GAG CTG TCC CTC CAC ACC AAC GCA CTG CAG GAC CTG GAC GGG AAC GTC
F   R   M   L   A   N   L   Q   N   I   S   L   Q   N   N   R   L   R   Q   L
1081 TTC CGC ATG TTG GCC AAC CTG CAG AAC ATC TCC CTG CAG AAC AAC CGC CTC AGA CAG CTC
P   G   N   I   F   A   N   V   N   G   L   L   M   A   I   Q   L   Q   N   N   Q
1141 CCA GGG AAT ATC TTC GCC AAC GTC AAT GGC CTC CTC ATG GCC ATC CAG CTG CAG AAC AAC CAG
L   E   N   L   P   L   G   I   F   D   H   L   G   K   L   C   E   L   R   L
1201 CTG GAG AAC TTG CCC CTC GGC ATC TTC GAT CAC CTG GGG AAA CTG TGT GAG CTG CGG CTG
Y   D   N   P   W   R   C   D   S   D   I   L   P   L   R   N   W   L   L   L
1261 TAT GAC AAT CCC TGG AGG TGT GAC TCA GAC ATC CTT CCG CTC CGC AAC TGG CTC CTG CTC
N   Q   P   R   L   G   T   D   T   V   P   P   F   S   P   A   N   V   R
1321 AAC CAG CCT AGG TTA GGG ACG GAC ACT GTA CCT GTG TGT TTC AGC CCA GCC AAT GTC CGA
G   Q   S   L   I   I   I   N   V   N   V   A   V   P   S   V   H   V   P   E
1381 GGC CAG TCC CTC ATT ATC ATC AAT GTC AAC GTT GCT GTT CCA AGC GTC CAT GTC CCC GAG
V   P   S   Y   P   E   T   P   W   Y   P   P   D   T   P   S   Y   P   D   T   T
1441 GTG CCT AGT TAC CCA GAA ACA CCA TGG TAC CCA GAC ACA CCC AGT TAC CCT GAC ACC ACA
S   V   S   S   T   T   E   L   T   S   P   P   V   E   D   Y   T   D   L   T   T
1501 TCC GTC TCT TCT ACC ACT GAG CTA ACC AGC CCT GTG GAA GAC TAC ACT GAT CTG ACT ACC
I   Q   V   T   D   D   R S V W G M T Q A Q S G L A
1561 ATT CAG GTC ACT GAT GAC CGC AGC GTT TGG GGC ATG ACC CAG GCC CAG AGC GGG CTG GCC
I   A   A   I   V   I   G   I   V   A   L   A   C   S   L   A   A   C   V   G
1621 ATT GCC GCC ATT GTA ATT GGC ATT GTC GCC CTG TCC TCC CTG GCT TGC GTC GTC GGC
C   C   C   C   K   K   R   S   Q   A   V   L   M   Q   M   K   A   P   N   E
1681 TGT TGC TGC TGC AAG AAG AGG AGC CAA GCT GTC CTG ATG CAG ATG AAG GCA CCC AAT GAG
C                                     (SEQ ID NO:3)
1741 TGT                                     (SEQ ID NO:4)

```

Legend:  
 predicted signal peptide is ***bold italicized***  
 predicted transmembrane domain is underlined  
 predicted protease cleavage site is boxed

**FIG. 1D**

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Exemplary Anti-huLRRRC15 Antibody V<sub>H</sub> Chains

	1	2	3	4	5	6	7	8
huM25	1234567890	1234567890	1234567890	1234567890	12a34567890	1234567890	1234567890	1234567890
huAD208.4.1	EVQLVQSGAE	VKKPGASVKV	SCKASGYKFS	<u>SYWIEWVKQA</u>	PGQLEWIGE	<u>ILPGSDTTNYN</u>	<u>EKFKDRATFT</u>	<u>SDTSINTAYM</u>
huAD208.12.1	EVQLVQSGAE	VKKPGSSVKV	SCKASGFTFT	<u>DYIHHWVKQA</u>	PGQLEWIGL	<u>VYPYIGGTNYN</u>	<u>QKFKGKATLT</u>	<u>VDTSTTTAYM</u>
huAD208.14.1	EVQLVQSGAE	VKKPGSSVKV	SCKASGYTFT	<u>NYNMHWVKQA</u>	PGQLEWIGM	<u>IHPNSGSTKHN</u>	<u>EKFRGKATLT</u>	<u>VDESTTTAYM</u>
hu139.10	EVQLVESGGG	LVQPGGSLRL	SCAVSGFSLT	<u>DYIHHWVKQA</u>	PGQLEWIGL	<u>VYPYIGGSSYN</u>	<u>QKFKGKATLT</u>	<u>VDTSTSTAYM</u>
muAD210.40.9	QVQLQQSGAE	LVRPGTSVKI	SCKASGYDFT	<u>SYGVHWVRQA</u>	TGKGLEWLG	<u>IW-AGGSTNYN</u>	<u>SALMSRLTIS</u>	<u>KENAKSSVYL</u>
muAD209.9.1	QIQLVQSGPE	LKKPGETVKI	SCKASGFAIT	<u>NYWLGVWVKQR</u>	PGHGLEWIGD	<u>IYPGGGNTYYN</u>	<u>EKLKGKATLT</u>	<u>ADKSSSTAYI</u>
				<u>NFGMNWVKQA</u>	PGKGLKNMGW	<u>INLYTGEPTFA</u>	<u>DDFKGRFAFS</u>	<u>LETSASTAYL</u>

	1	9	1	1
huM25	12abc34567890	1234567890	<u>abcde1234567890</u>	123
huAD208.4.1	ELSLRSDDTAVY	YCARDRGNYR	<u>ANF--GYWGQGTTLVT</u>	VSS (SEQ ID NO:16)
huAD208.12.1	EMSSLRSEDVAVY	YCARGDNKYD	<u>AM---DYWGQGTTLVT</u>	VSS (SEQ ID NO:26)
huAD208.14.1	ELSSLRSEDVAVY	YCARSDFGNY	<u>RWYF-DVWGQGTTLVT</u>	VSS (SEQ ID NO:36)
hu139.10	ELSSLRSEDVAVY	YCARGDNNYD	<u>AM---DYWGQGTTLVT</u>	VSS (SEQ ID NO:46)
muAD210.40.9	QMNSLRAGDTAMY	YCATHMITED	<u>YYGM-DYWGGQGTTLVT</u>	VSS (SEQ ID NO:56)
muAD209.9.1	HLISLTSEDSSVY	FCARWGDKKG	<u>NYF--AYWGQGTTLVT</u>	VSA (SEQ ID NO:66)
	QINNLKNETVIY	FCARKGETIY	<u>RYDGFAYWGQGTTLVT</u>	VSA (SEQ ID NO:76)

FIG. 2A

Legend:

Complementarity determining regions (CDR's) are underlined

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Exemplary Anti-huLRRRC15 Antibody V<sub>L</sub> Chains

	1	2	3	4	5	6	7
huM25	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890	1234567890
huAD208.4.1	DIQMTQSPSS	LSASVGDRTV	ITCRASQ-----DIS	NYLNWYQQKP	GGAVKFLIYY	<u>TSRLHSGVPS</u>	<u>RFSGSGSGTD</u>
huAD208.12.1	DIVLTQSPDS	LAVSLGERAT	INCRASQSVST--SSY	SYMHWYQQKP	GQPPKLLIKY	<u>ASSLES</u>	<u>GVPD RFSGSGSGTD</u>
huAD208.14.1	EIVLTQSPAT	LSLSPGERAT	LSCRASQ-----SSS	NNLHWYQQKP	GQAPRVLIKY	<u>VSQSIGGIPA</u>	<u>RFSGSGSGTD</u>
hu139.10	DIVLTQSPDS	LAVSLGERAT	ISCRASQSVST--STY	NYMHWYQQKP	GQPPKLLIKY	<u>ASNLES</u>	<u>GVPD RFSGSGSGTD</u>
muAD210.40.9	QIVLTQSPAI	MSASLGERVT	MTCTASSS-----VYS	SYLHWYQQKP	GSSPKLWIYS	<u>TSNLAS</u>	<u>GVPD RFSGSGSGTS</u>
muAD209.9.1	DIVMTQAAPS	VPVTPGESVS	ISCRSSKSLIHS--NGN	THLYWFLORP	GQSPQLLIYR	<u>MSNLAS</u>	<u>GVPD RFSGSGSGTA</u>

	8	9	1	0
huM25	1234567890	1234567890	1234567890	1234567890
huAD208.4.1	YTLTISSLQP	EDFATYFCQQ	<u>GEALPWT</u>	<u>FGG GTKVEIK</u> (SEQ ID NO:17)
huAD208.12.1	FTLTISSLQA	EDVAVYYCEQ	<u>SWEI-RT</u>	<u>FGG GTKVEIK</u> (SEQ ID NO:27)
huAD208.14.1	FTLTISSLEP	EDFAVYFCQQ	<u>SNSWFT</u>	<u>FGG GTKLEIK</u> (SEQ ID NO:37)
hu139.10	FTLTISSLQA	EDVAVYYCHH	<u>TWEI-RT</u>	<u>FGG GTKVEIK</u> (SEQ ID NO:47)
muAD210.40.9	FTLTISSLQA	EDVAVYYCKQ	<u>SYNL-PT</u>	<u>FGG GTKVEIK</u> (SEQ ID NO:57)
muAD209.9.1	FTLRISRVEA	EDVGVYYCMQ	<u>LLEYPT</u>	<u>FGG GTKLEIE</u> (SEQ ID NO:77)

FIG. 2B

Legend:  
Complementarity determining regions (CDR's) are underlined



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Antibody huM25 Heavy Chain (SEQ ID NO: 18)

```

EVQLVQSGAE VKKPGASVKV SCKASGYKFS SYWIEWVKQA PGQGLEWIGE ILPGSDTTNY 60
NEKFKDRATF TSDTSINTAY MELSRLRSDD TAVYYCARDR GNYRAWFGYW GQGTLLTVSS 120
ASTKGPSVFP LAPSSKSTSG GTAALGCLVK DYFPEPVTVS WNSGALTSGV HTFPAVLQSS 180
GLYSLSSVVT VPSSSLGTQT YICNVNHKPS NTKVDKKVEP KSCDKTHTCP PCPAPELLGG 240
PSVFLFPPKP KDTLMISRTP EVTCVVVDVS HEDPEVKFNW YVDGVEVHNA KTKPREEQYN 300
STYRVVSVLT VLHQDWLNGK EYKCKVSNKA LPAPIEKTIS KAKGQPREPQ VYTLPPSREE 360
MTKNQVSLTC LVKGFYPSDI AVEWESNGQP ENNYKTPPV LDSDGSFFLY SKLTVDKSRW 420
QQGNVFSCSV MHEALHNHYT QKSLSLSPGK 450

```

Legend:

Complementarity determining regions (CDR's) are underlinedHeavy chain F<sub>c</sub> gamma (γ) is *italicized***FIG. 3A**

Antibody huM25 Light Chain (SEQ ID NO: 19)

```

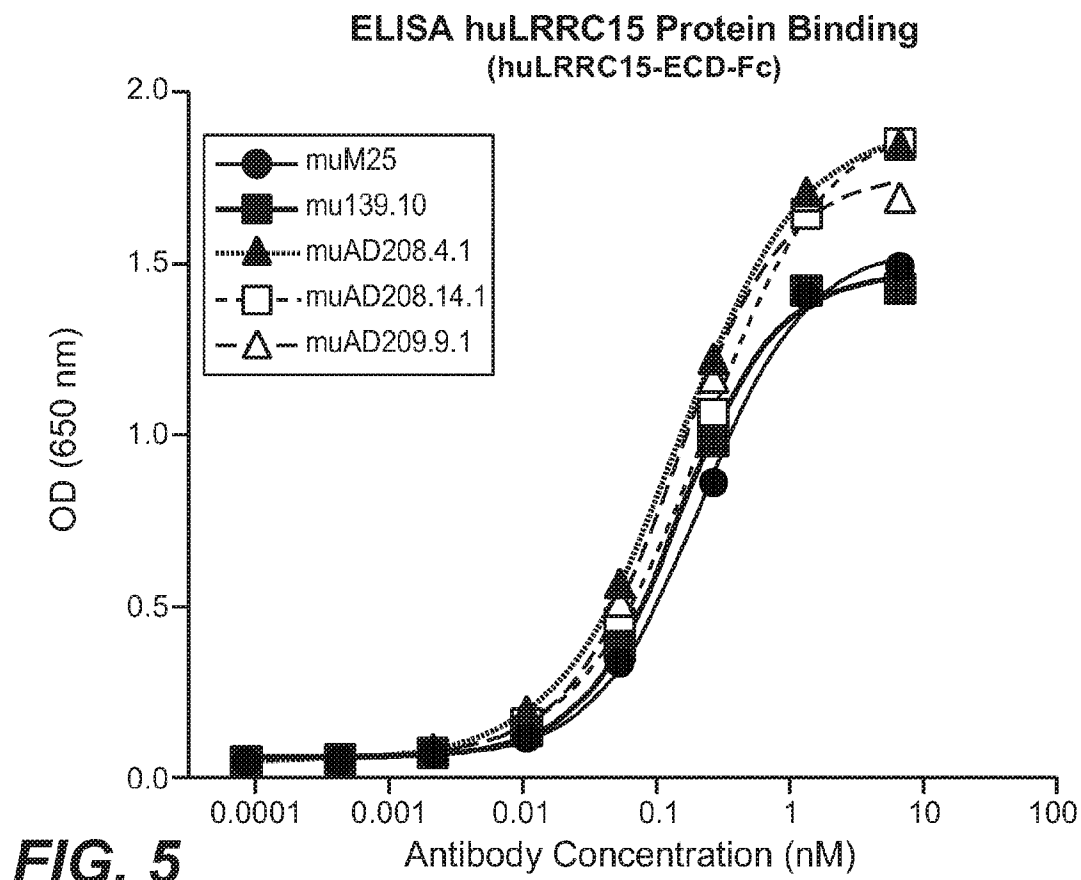
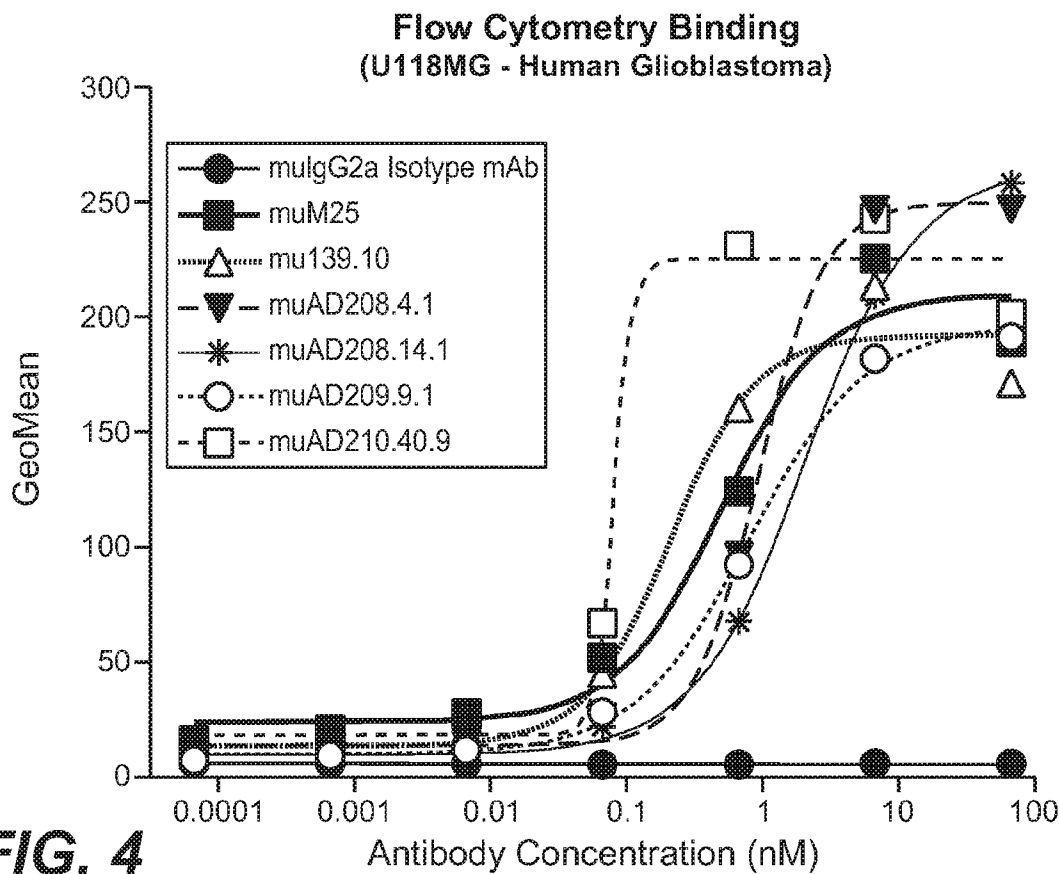
DIQMTQSPSS LSASVGDRVIT ITCRASQDIS NYLNWYQQKP GGAVKFLIYY TSRLHSGVPS 60
RFSGSGSGTD YTLTISSLQP EDFATYFCQQ GEALPWTFGG GTKVEIKRTV AAPSVFIFPP 120
SDEQLKSGTA SVVCLLNNFY PREAKVQWKV DNALQSGNSQ ESVTEQDSKD STYSLSTLT 180
LSKADYEKHK VYACEVTHQG LSSPVTKSFN RGEC

```

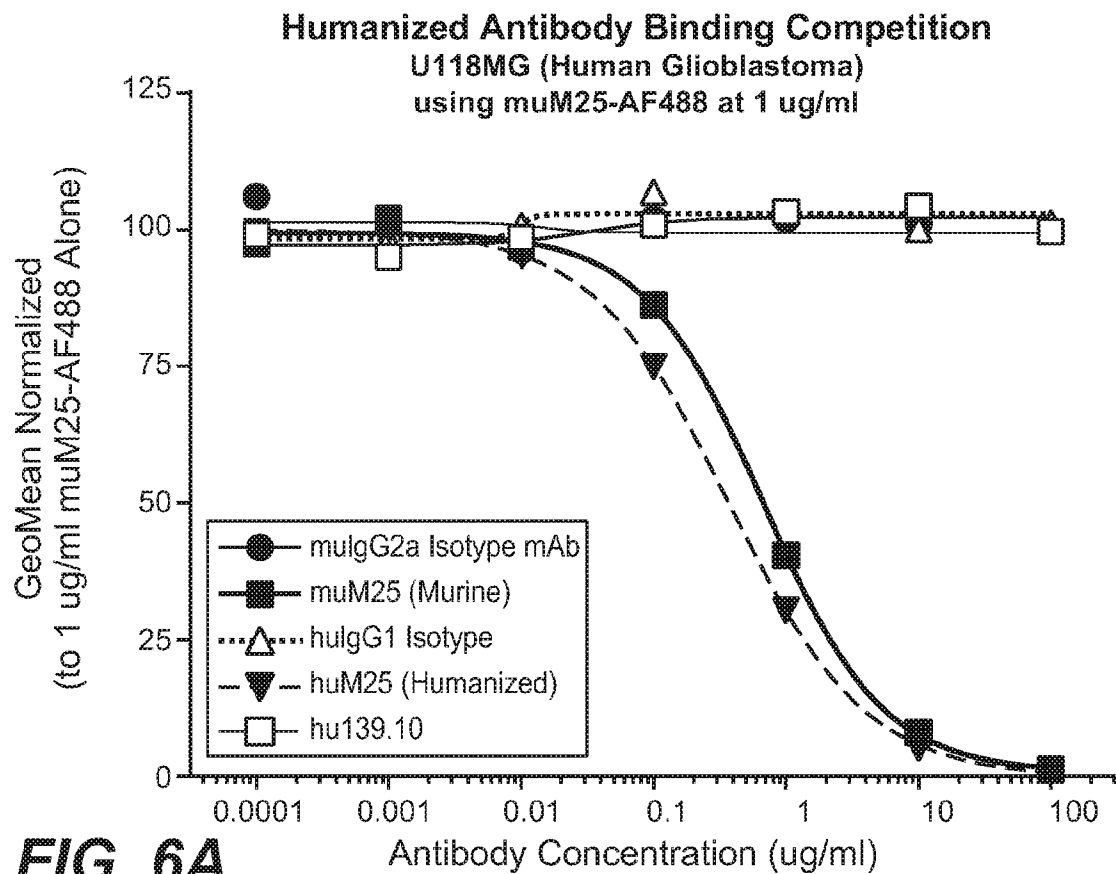
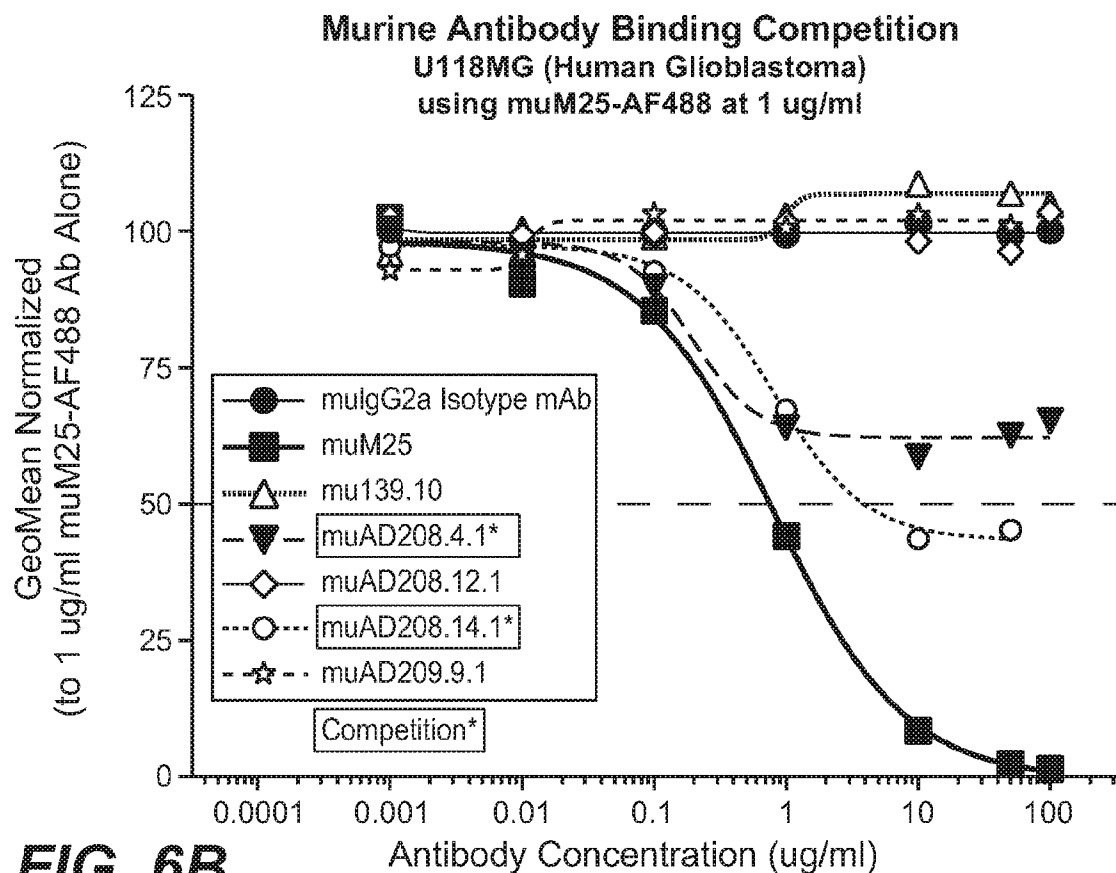
Legend:

Complementarity determining regions (CDR's) are underlinedLight chain kappa (κ) is *italicized***FIG. 3B**

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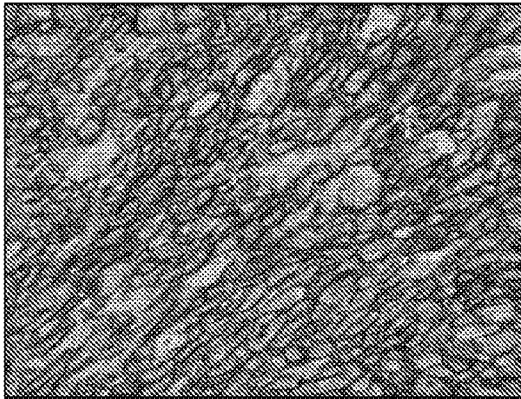


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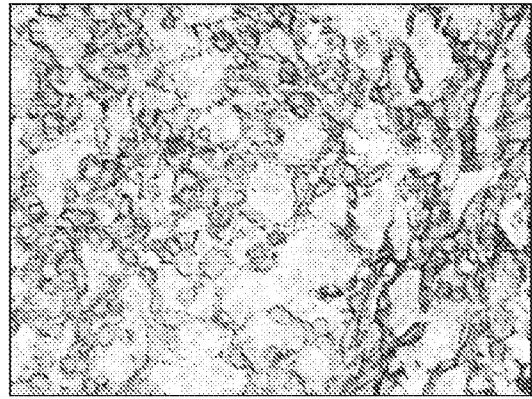
**FIG. 6A****FIG. 6B**

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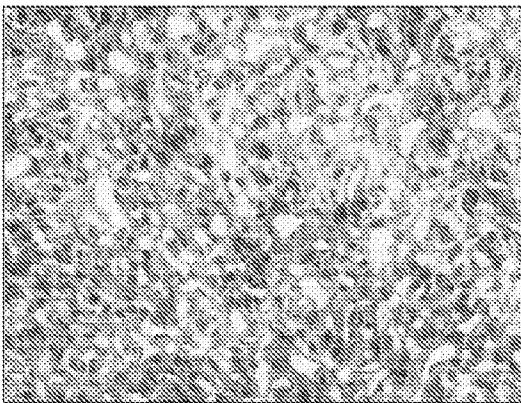
**Osteosarcoma**



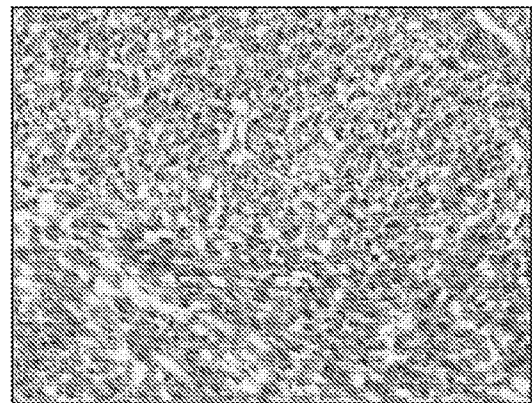
**Undifferentiated Pleiomorphic Sarcoma (UPS)**



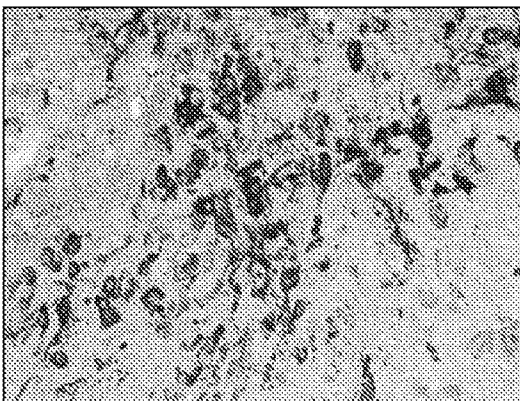
**Liposarcoma\***



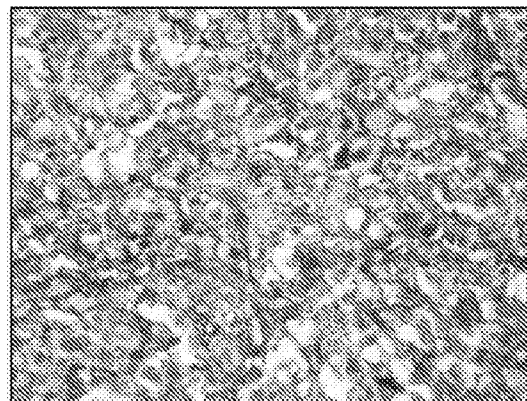
**Leiomyosarcoma\***



**Glioblastoma**

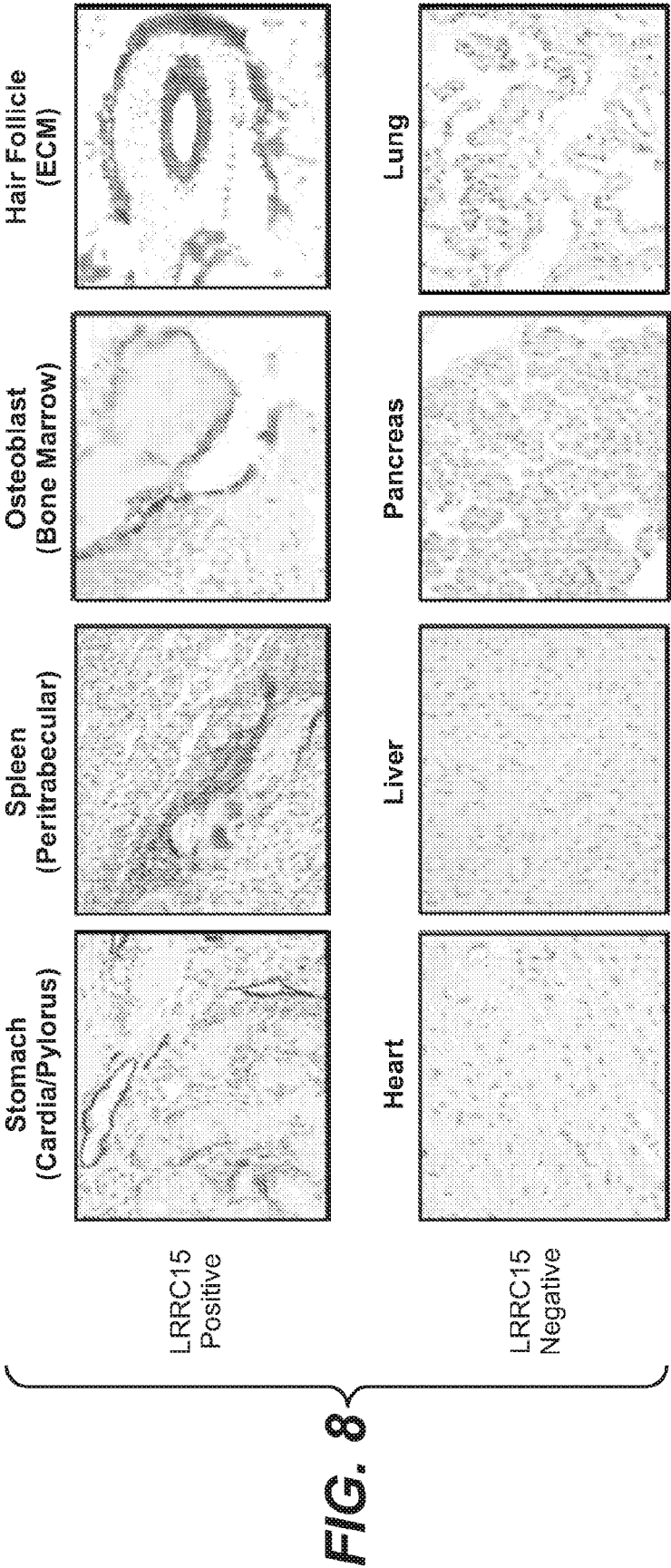


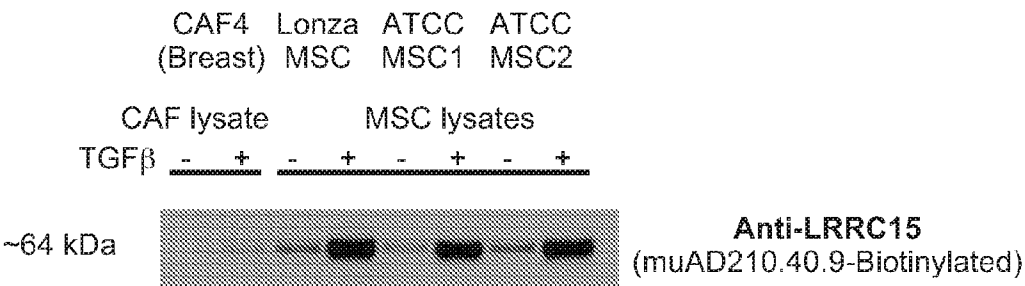
**Melanoma (Bone Metastasis)**



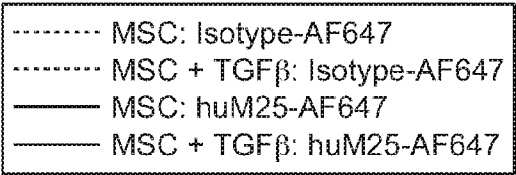
\* Patient derived xenograft (PDX)

**FIG. 7**

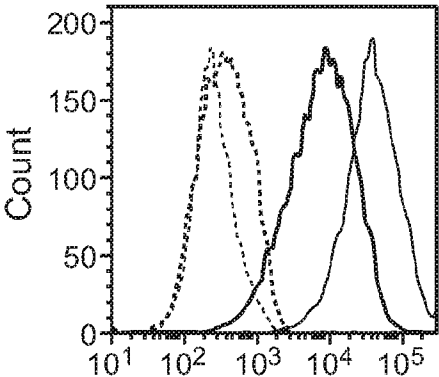




**FIG. 9A**



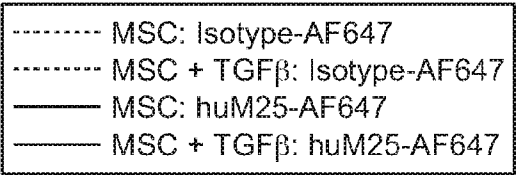
Human BM-MSc  
(Lonza)



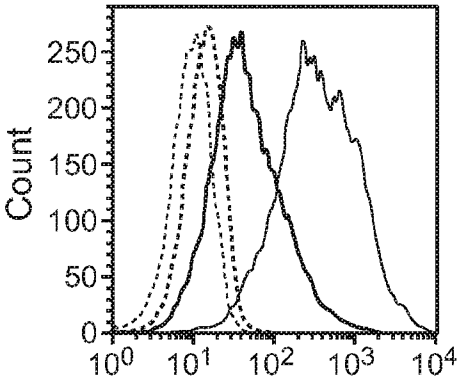
FL4-H::FL4-Height

Human MSC markers:  
CD29, CD44, CD105, CD166 Pos.  
CD14, CD34, CD45 Neg.

**FIG. 9B**



Balb/c BM-MSc ( Cyagen)



FL4-H::FL4-Height

Cyagen Balb/c MSC markers:  
CD29, CD44, CD34 and Sca-1 Pos.  
CD117 Neg.

**FIG. 9C**

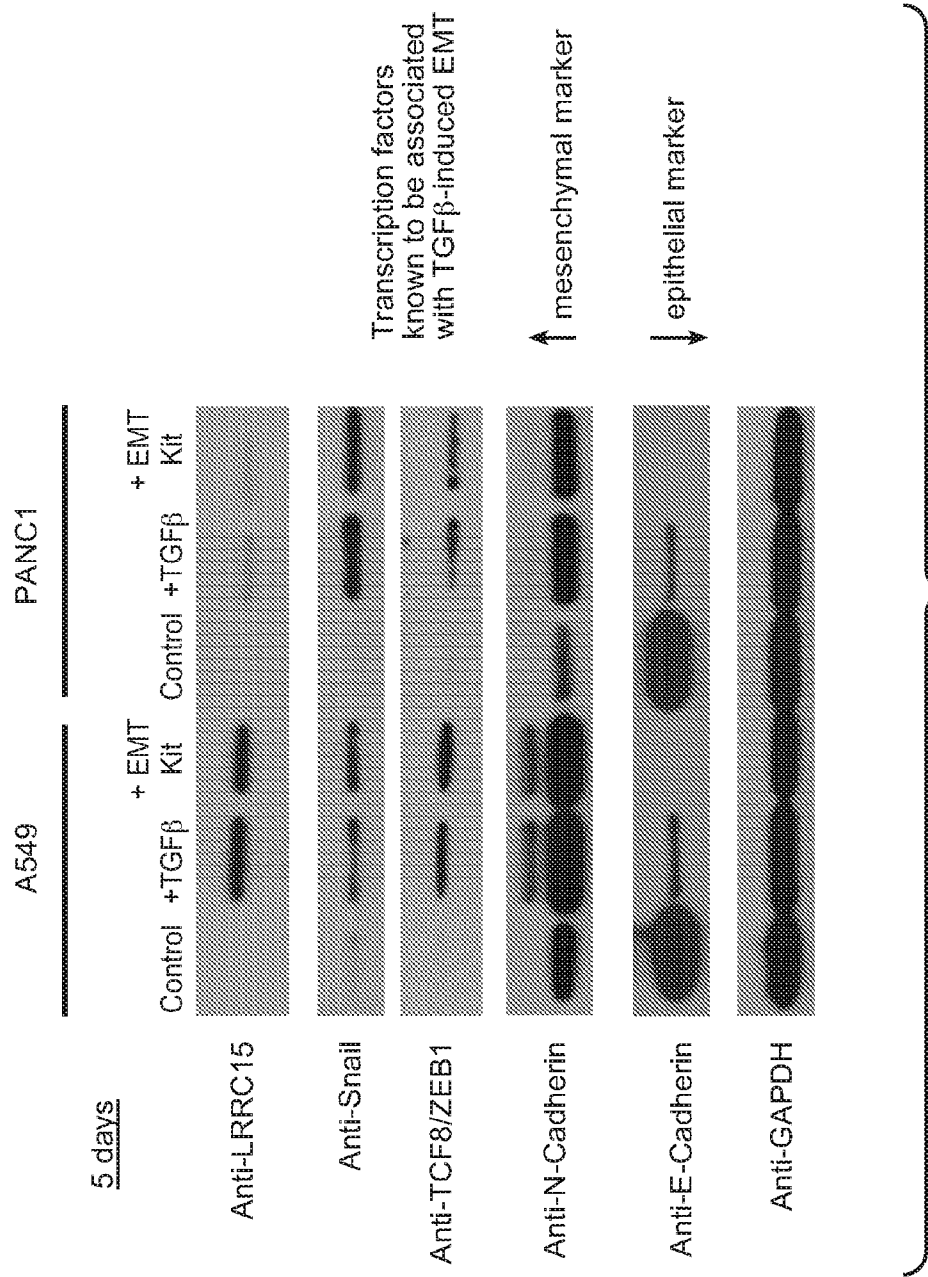
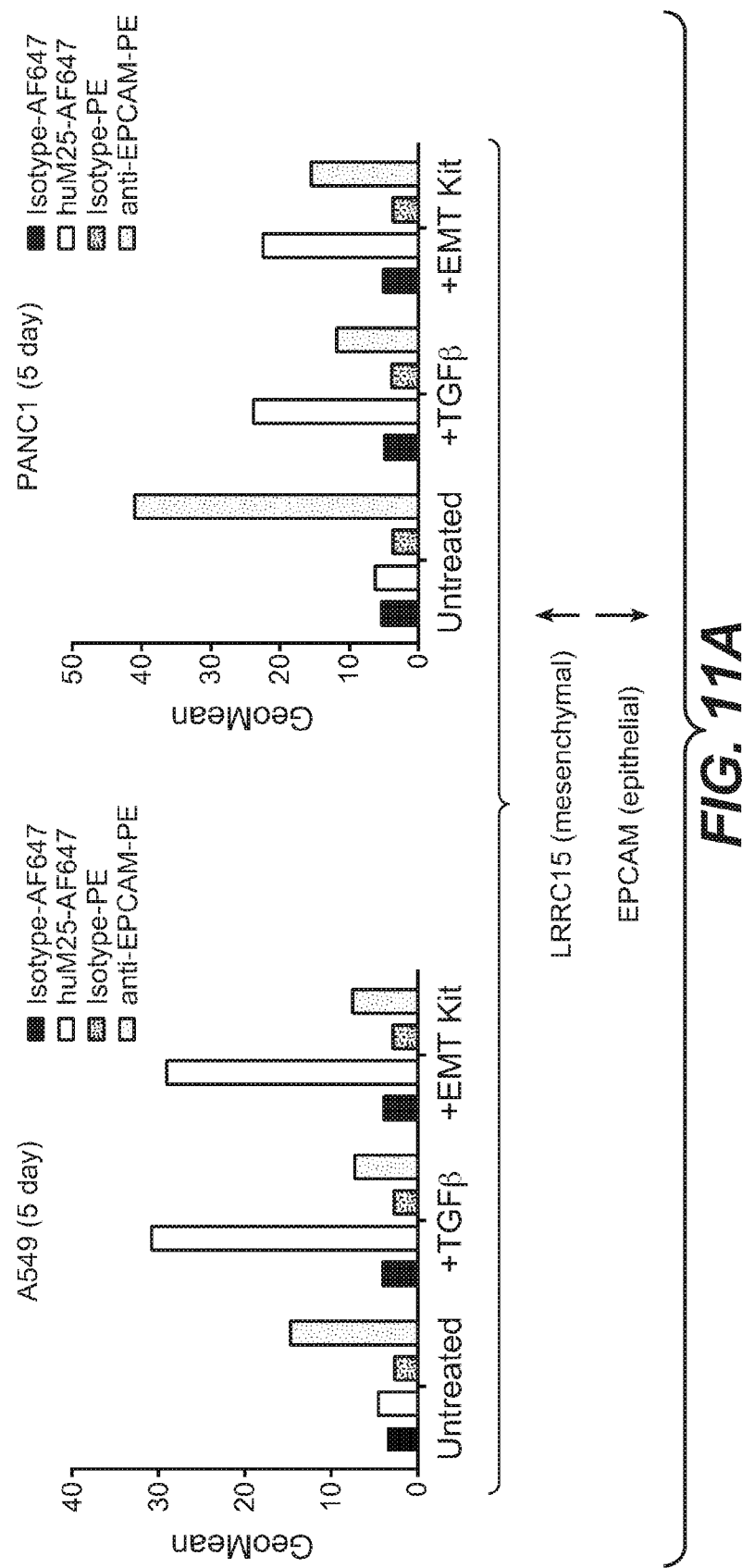
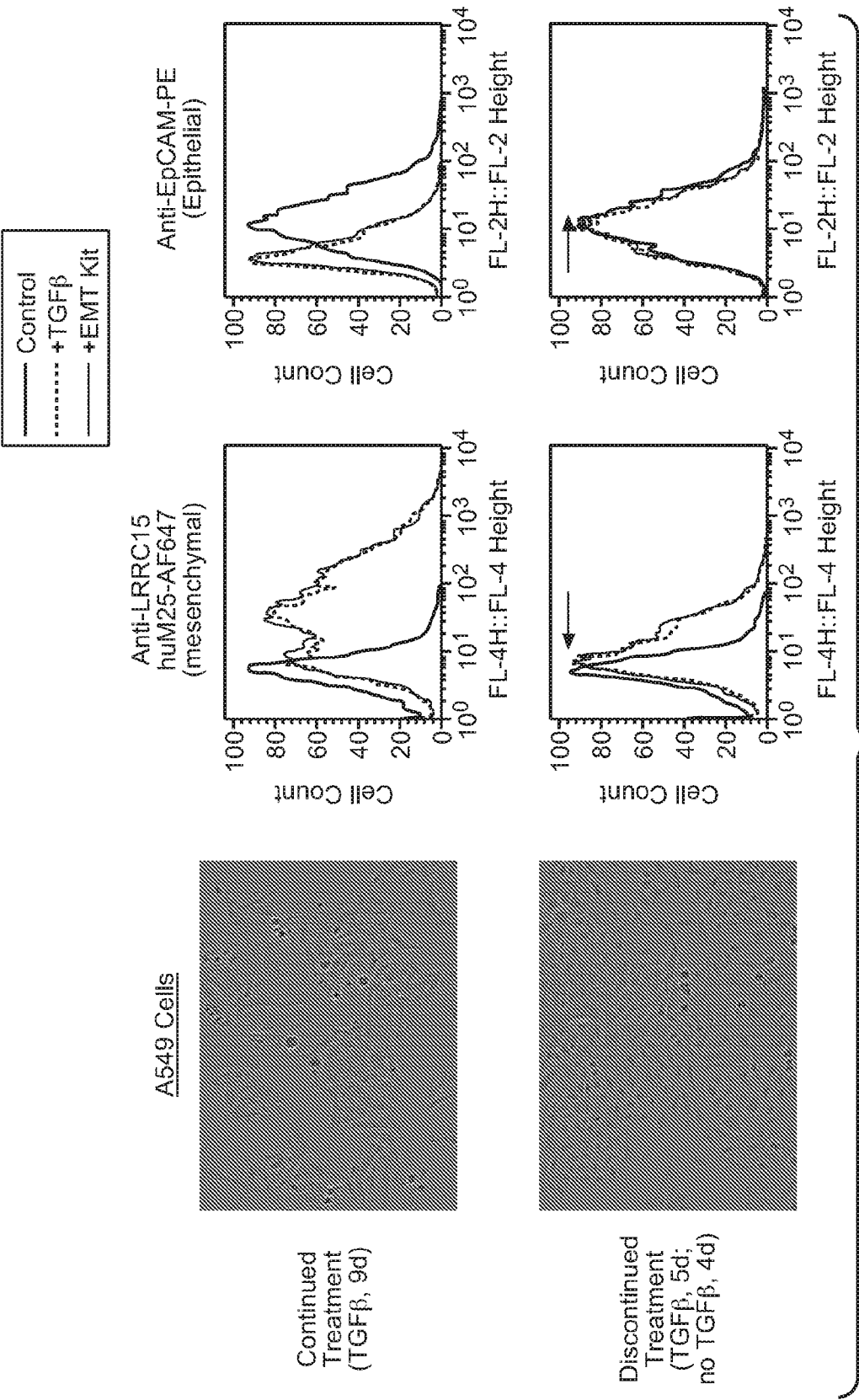
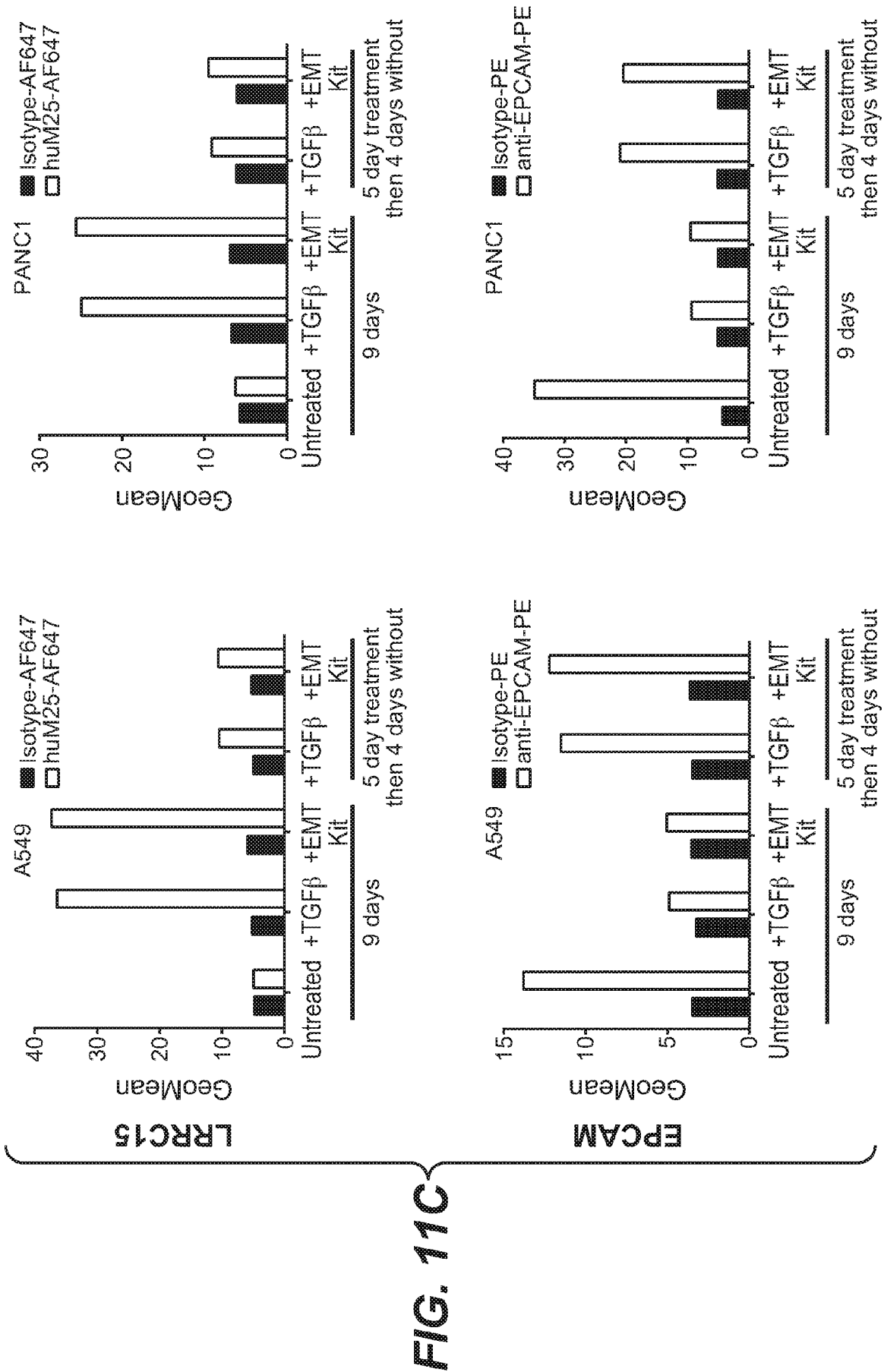


FIG. 10









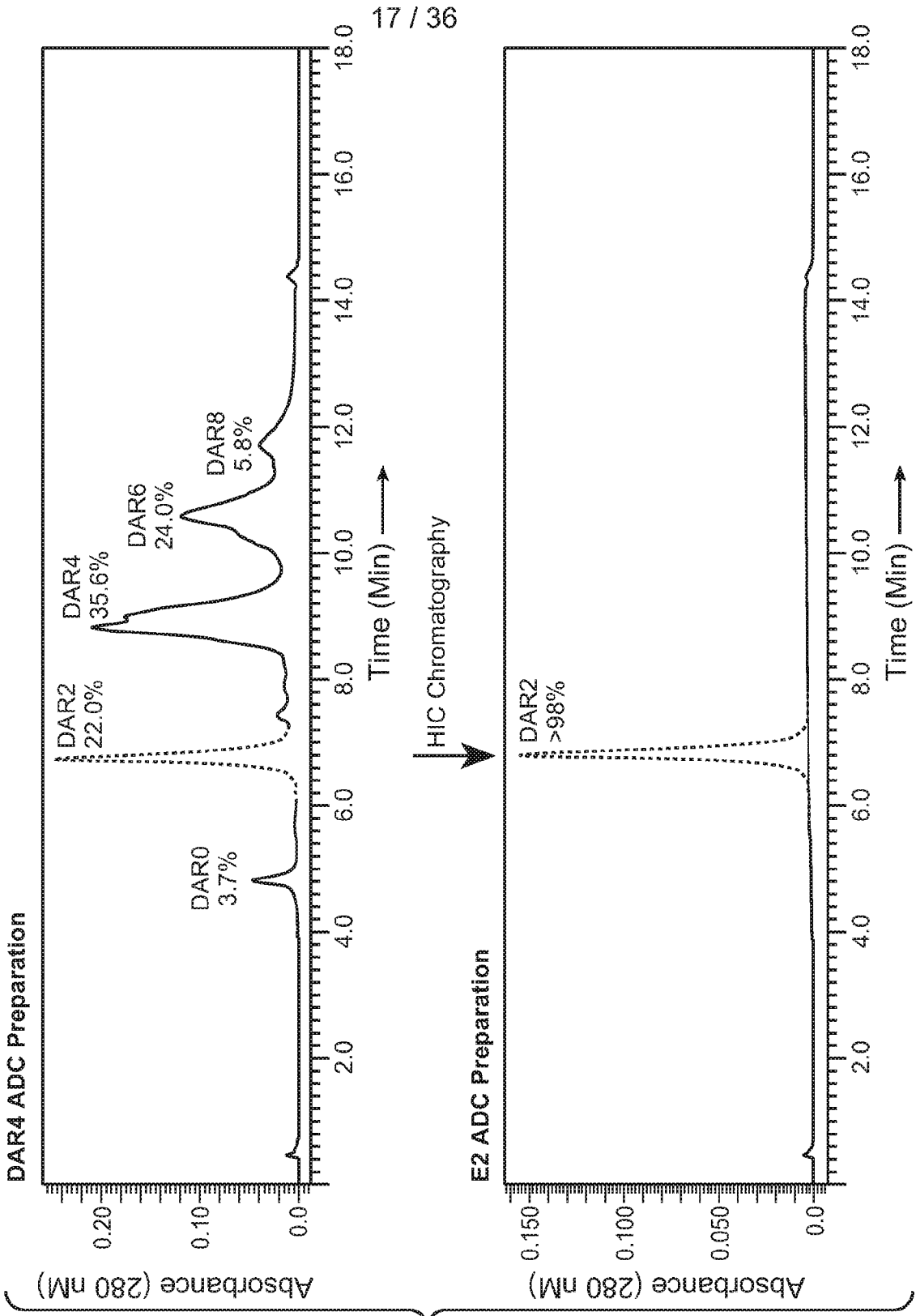
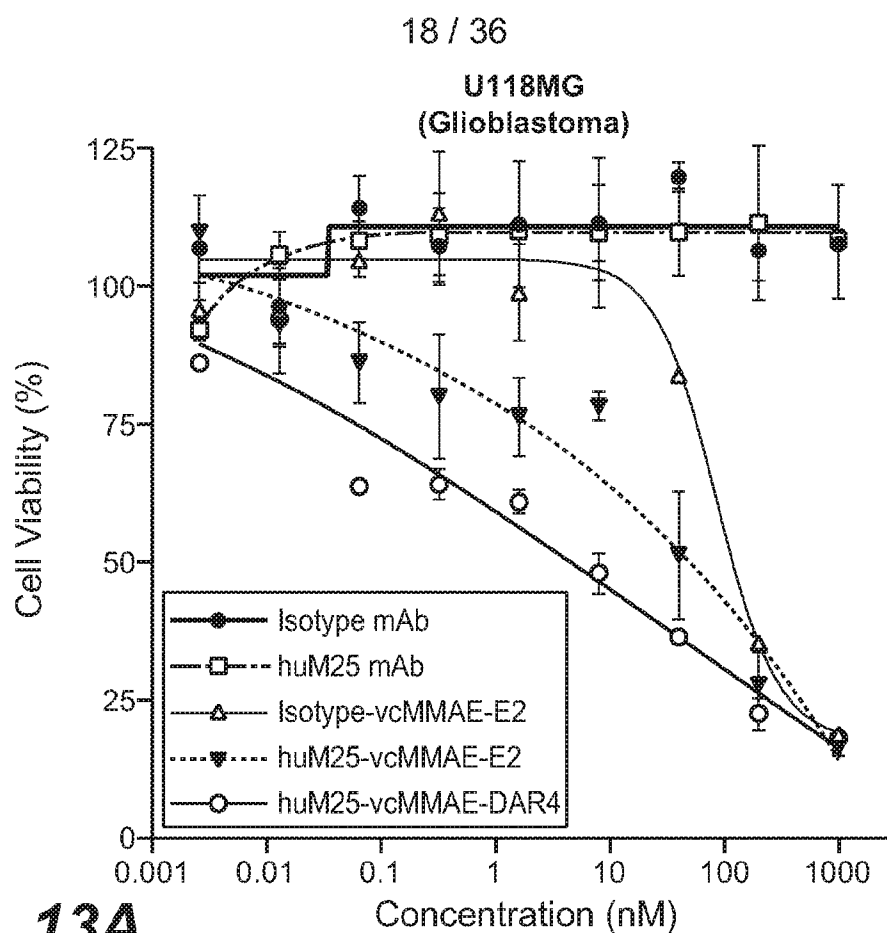
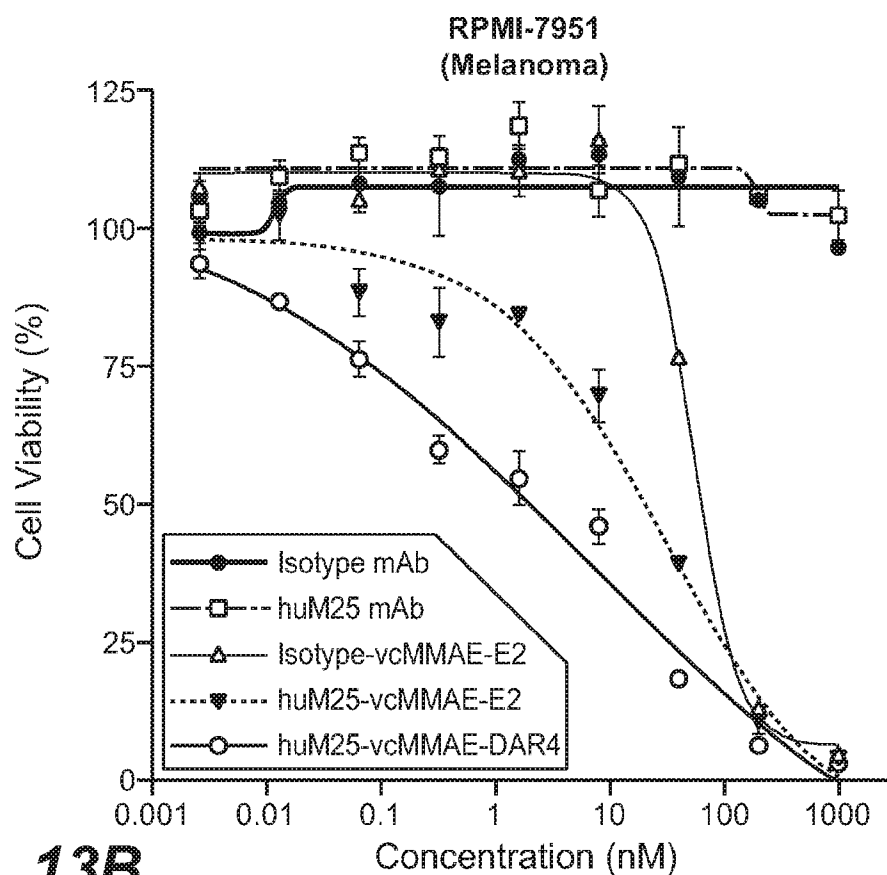
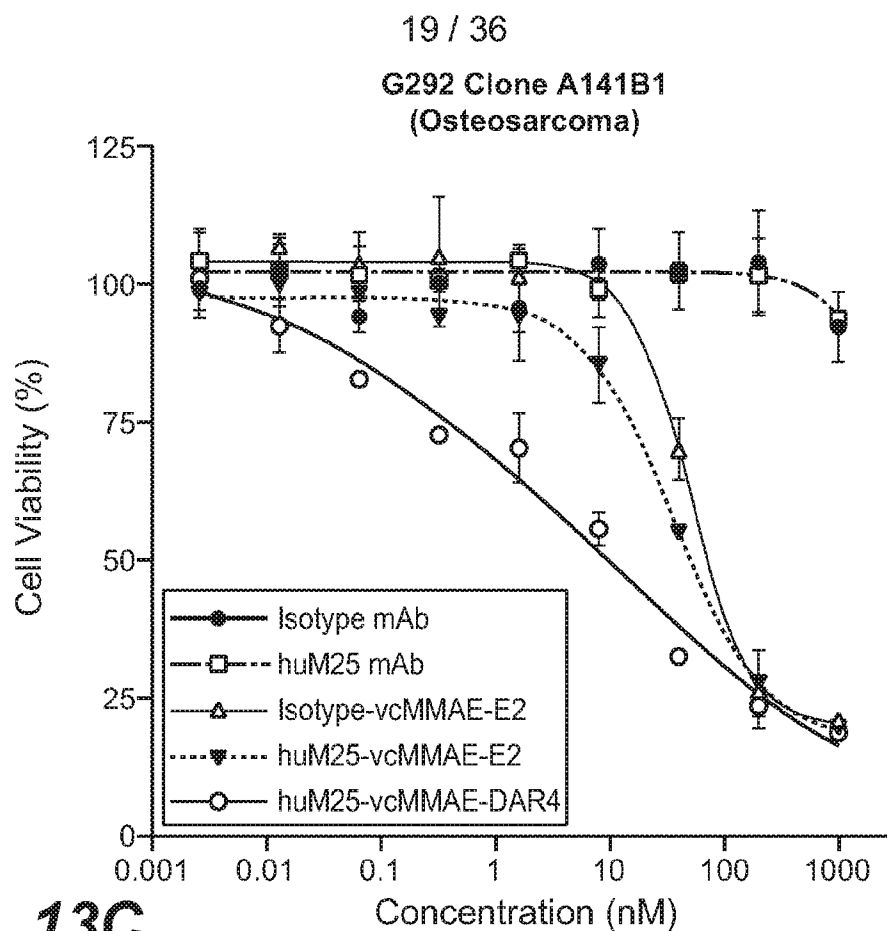
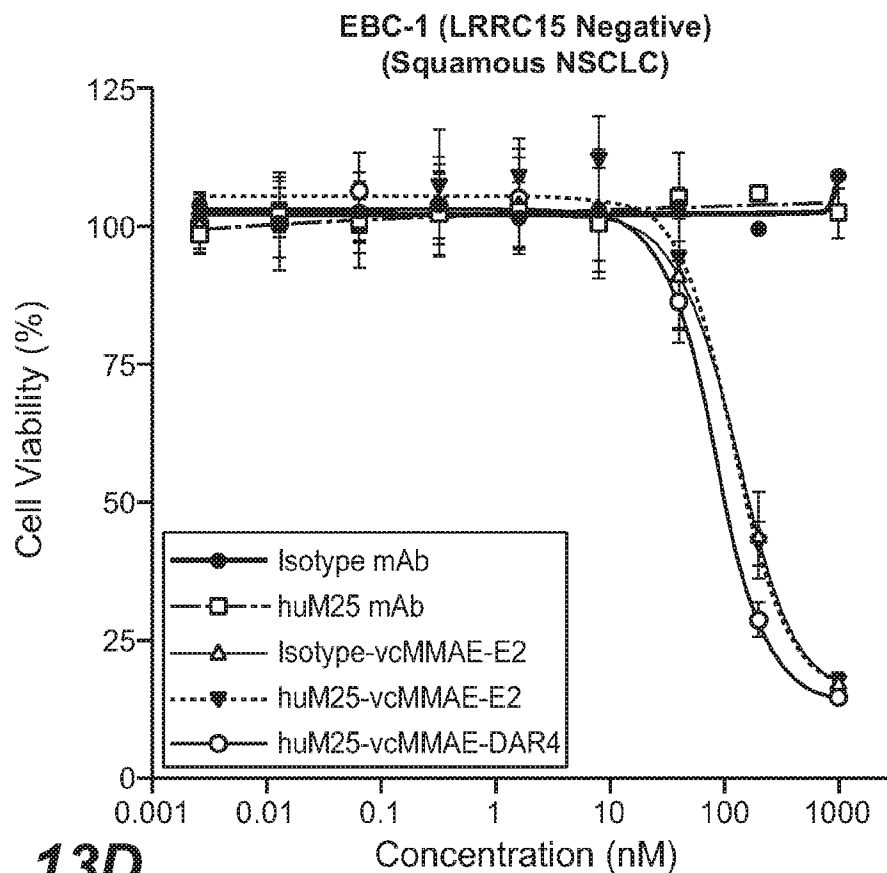
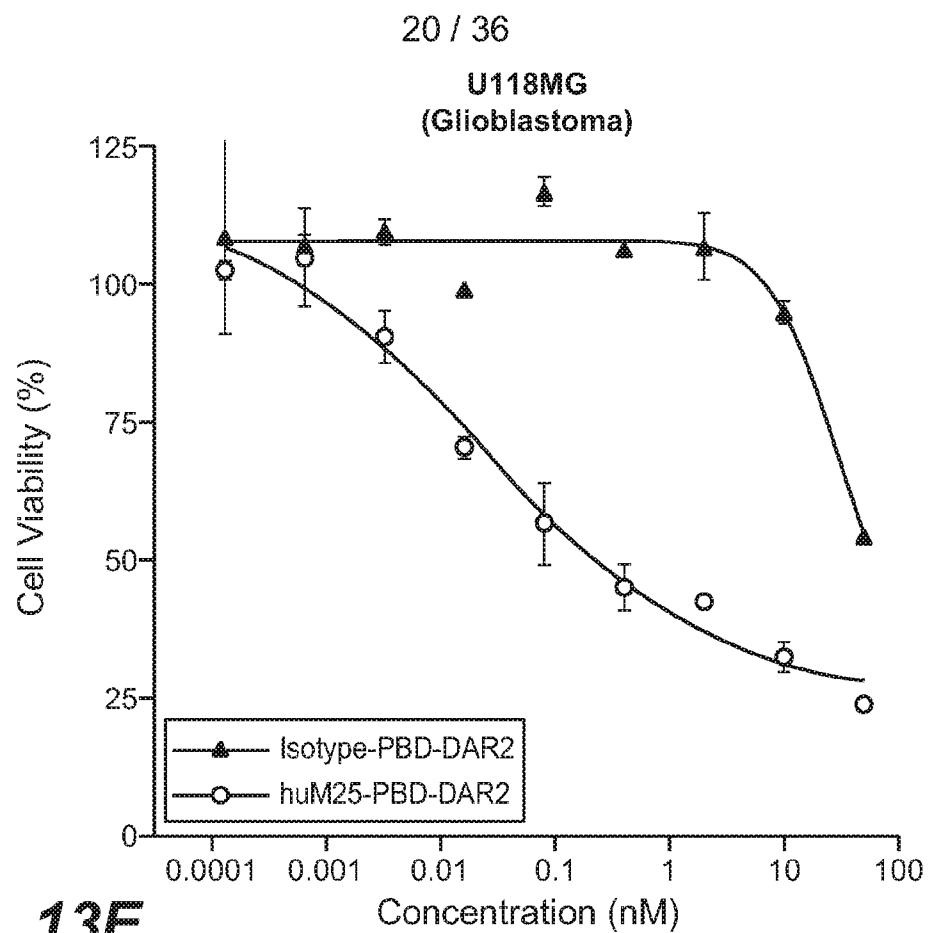
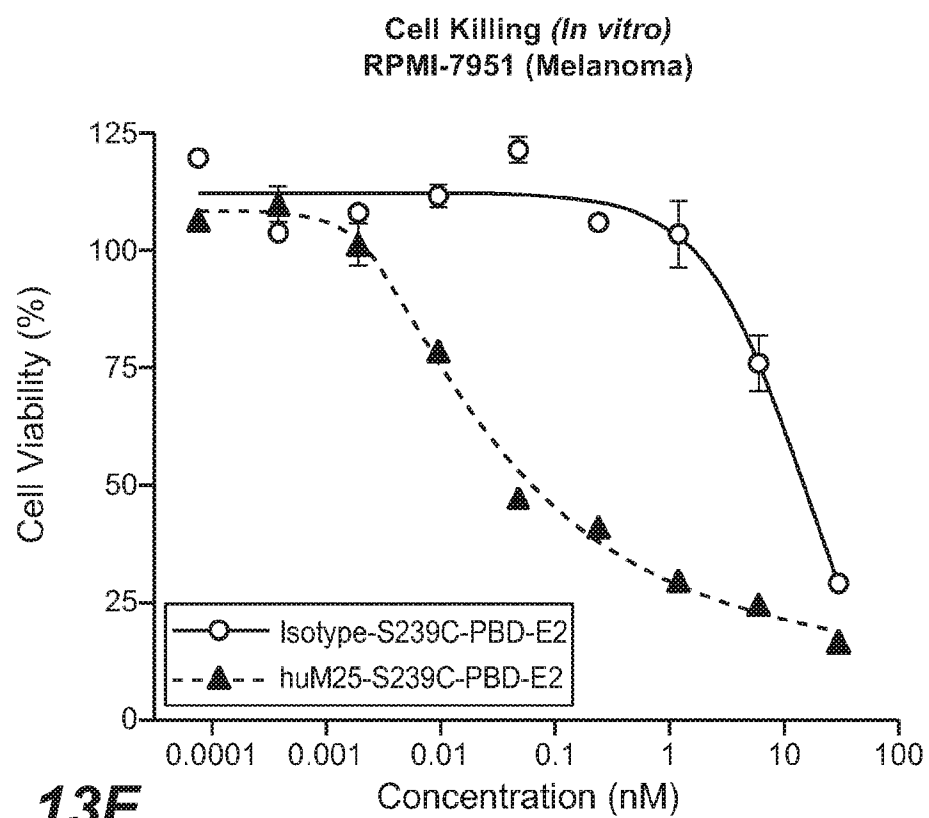


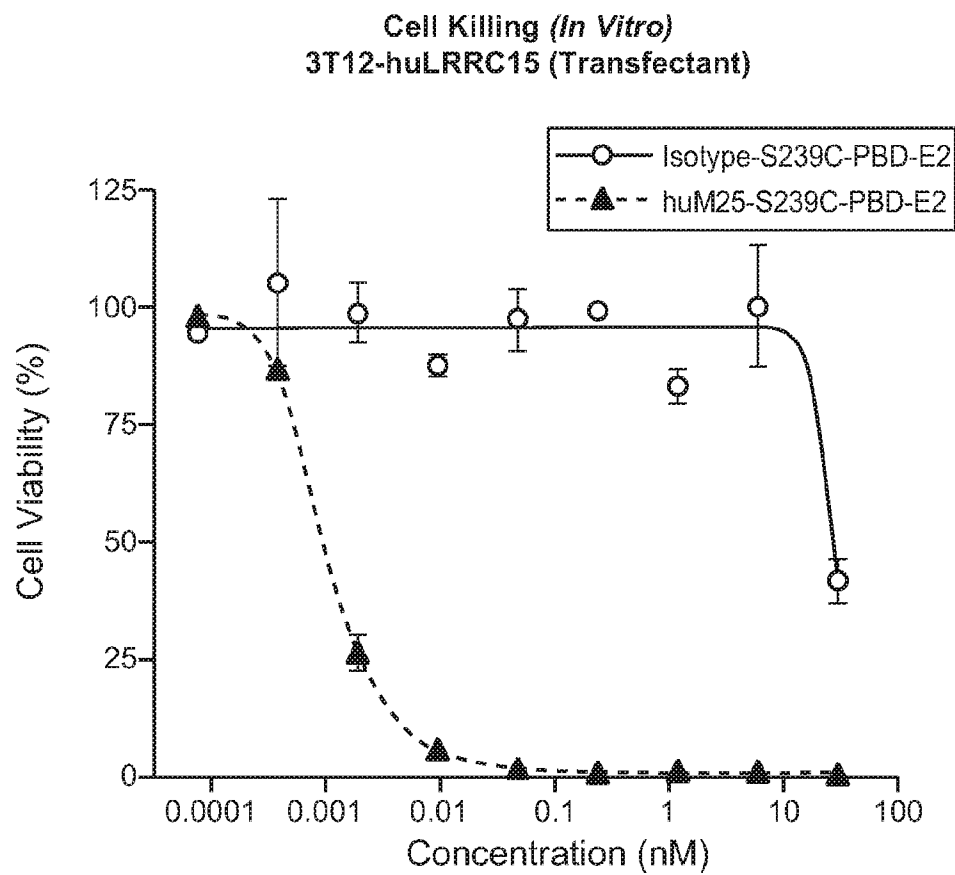
FIG. 12

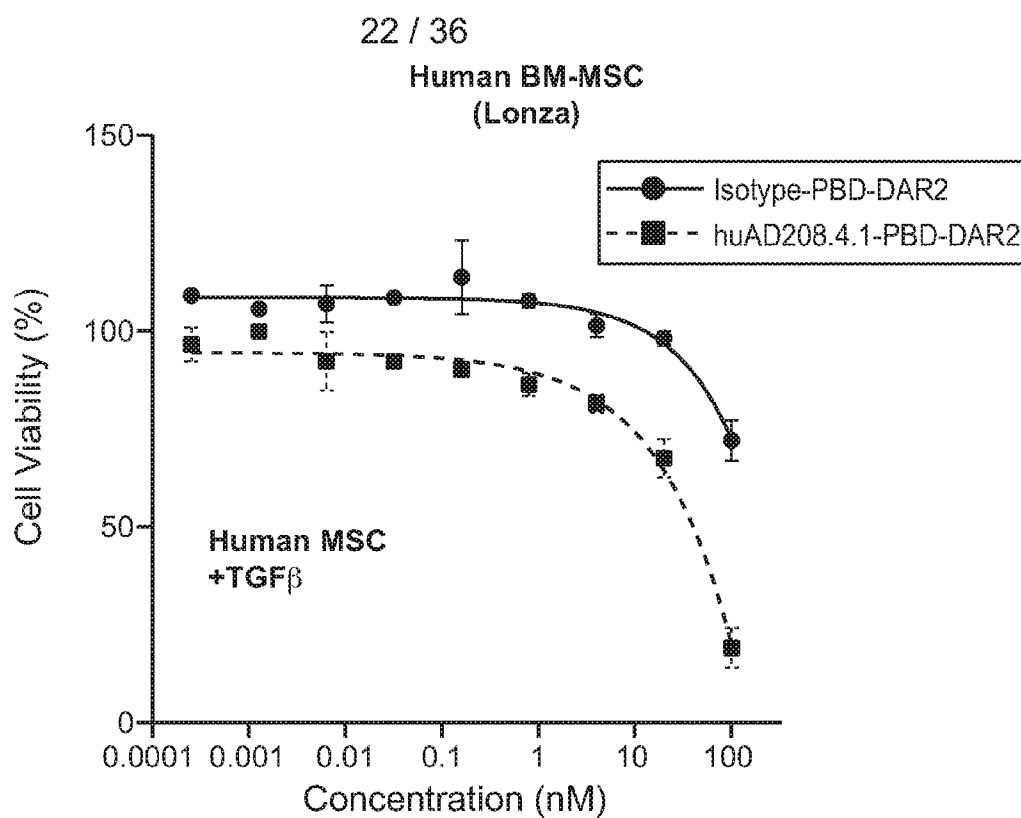
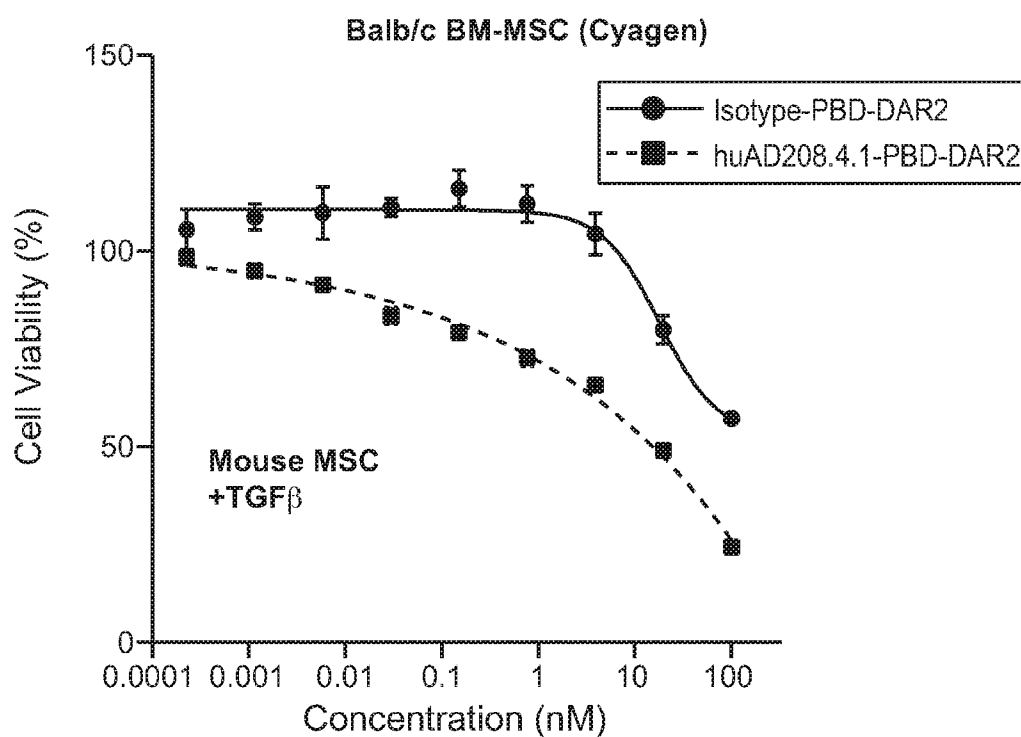
**FIG. 13A****FIG. 13B**

**FIG. 13C****FIG. 13D**

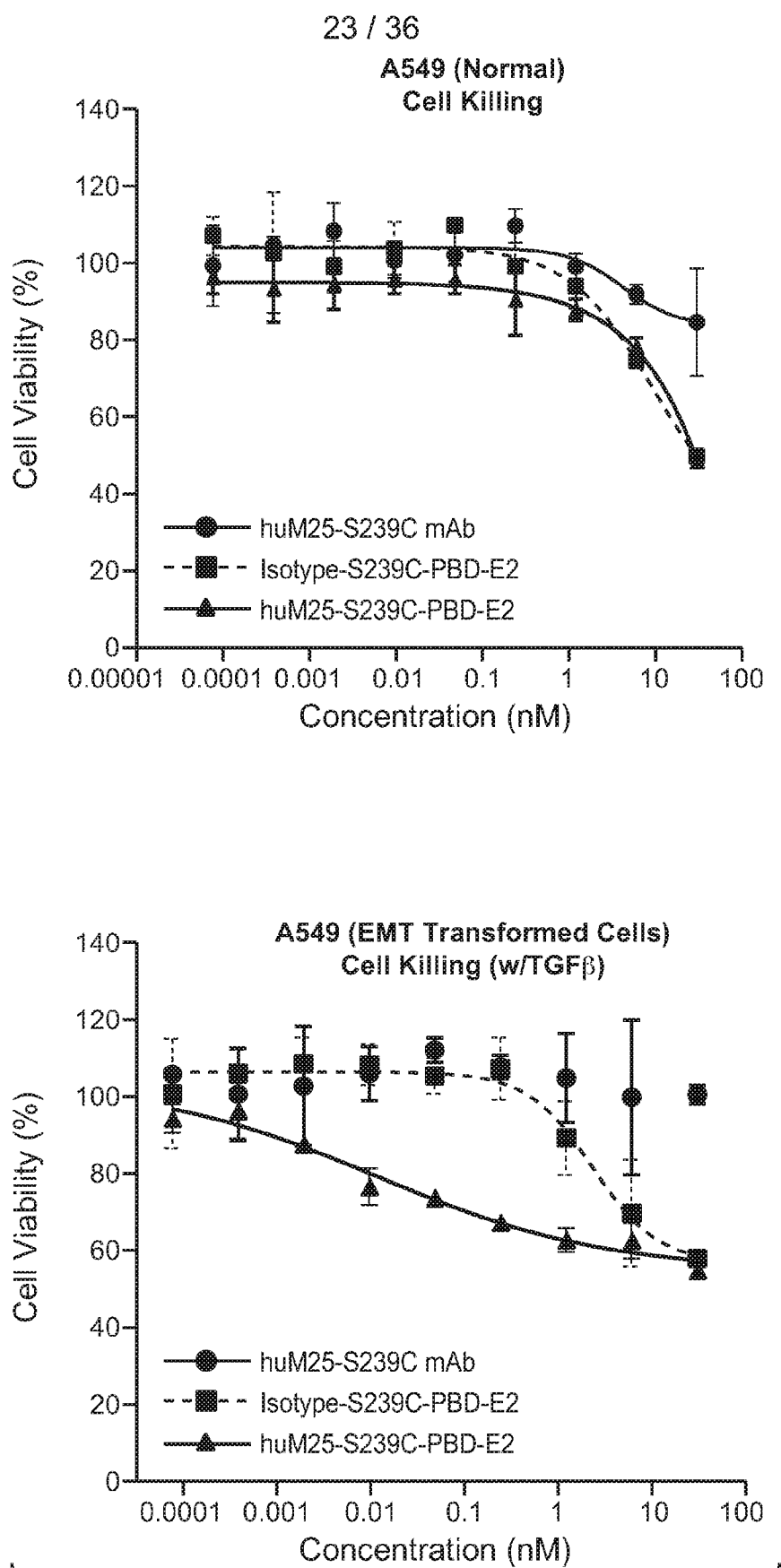
**FIG. 13E****FIG. 13F**

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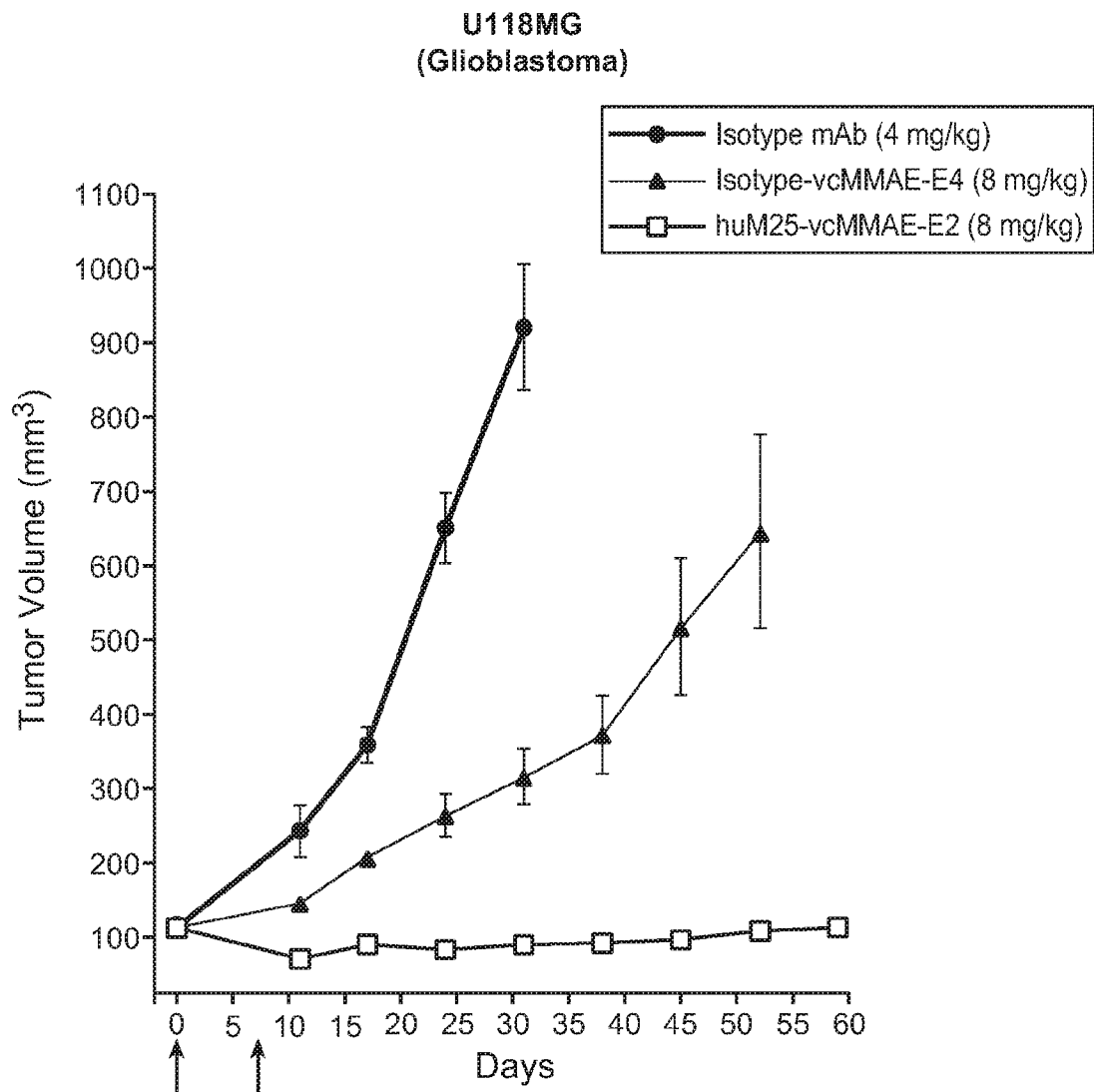
**FIG. 13G**

**FIG. 13H****FIG. 13I**

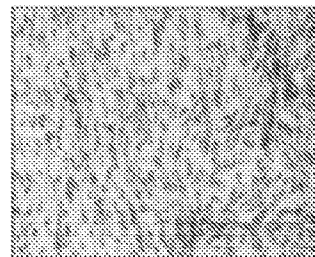


**FIG. 13J**

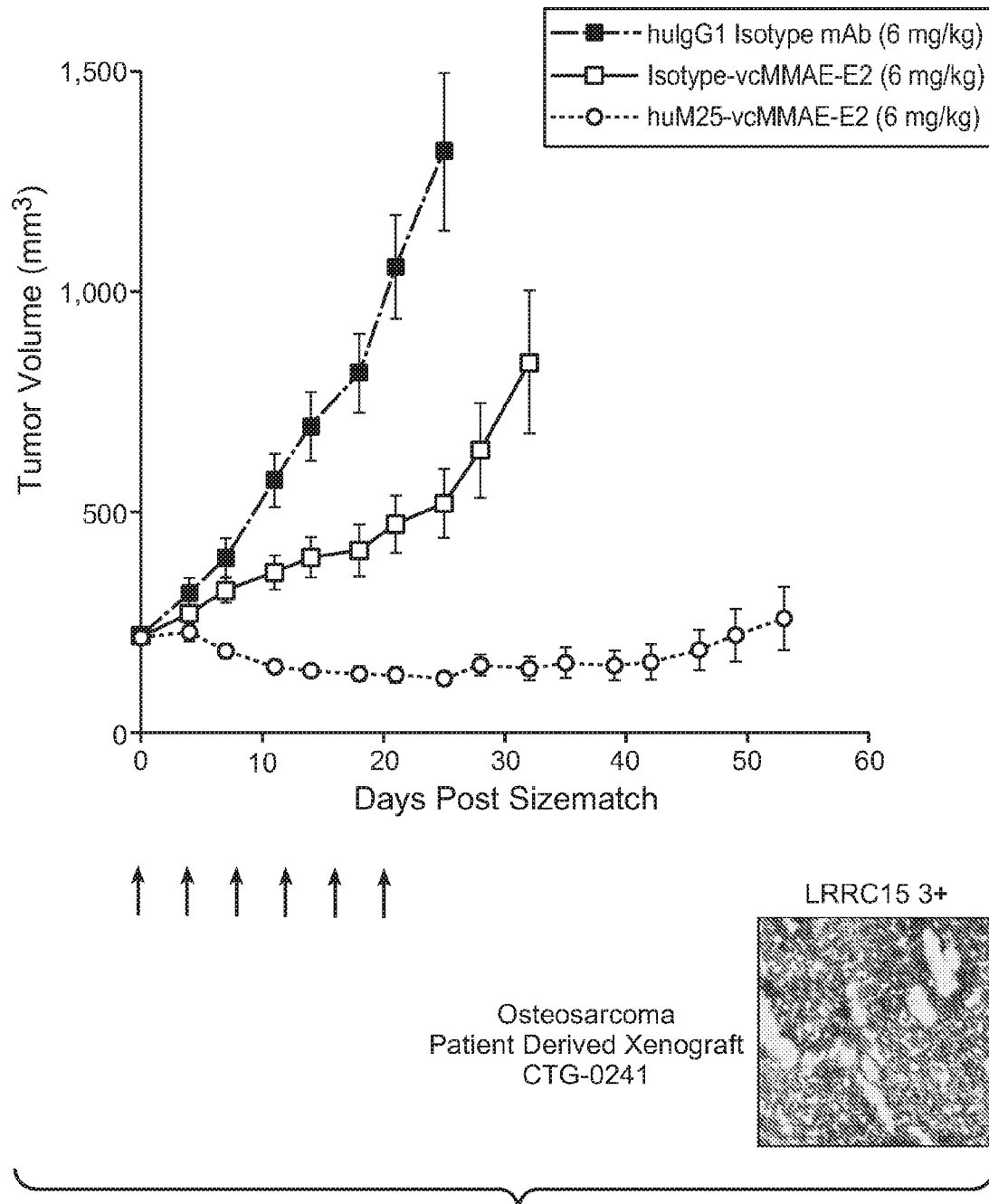
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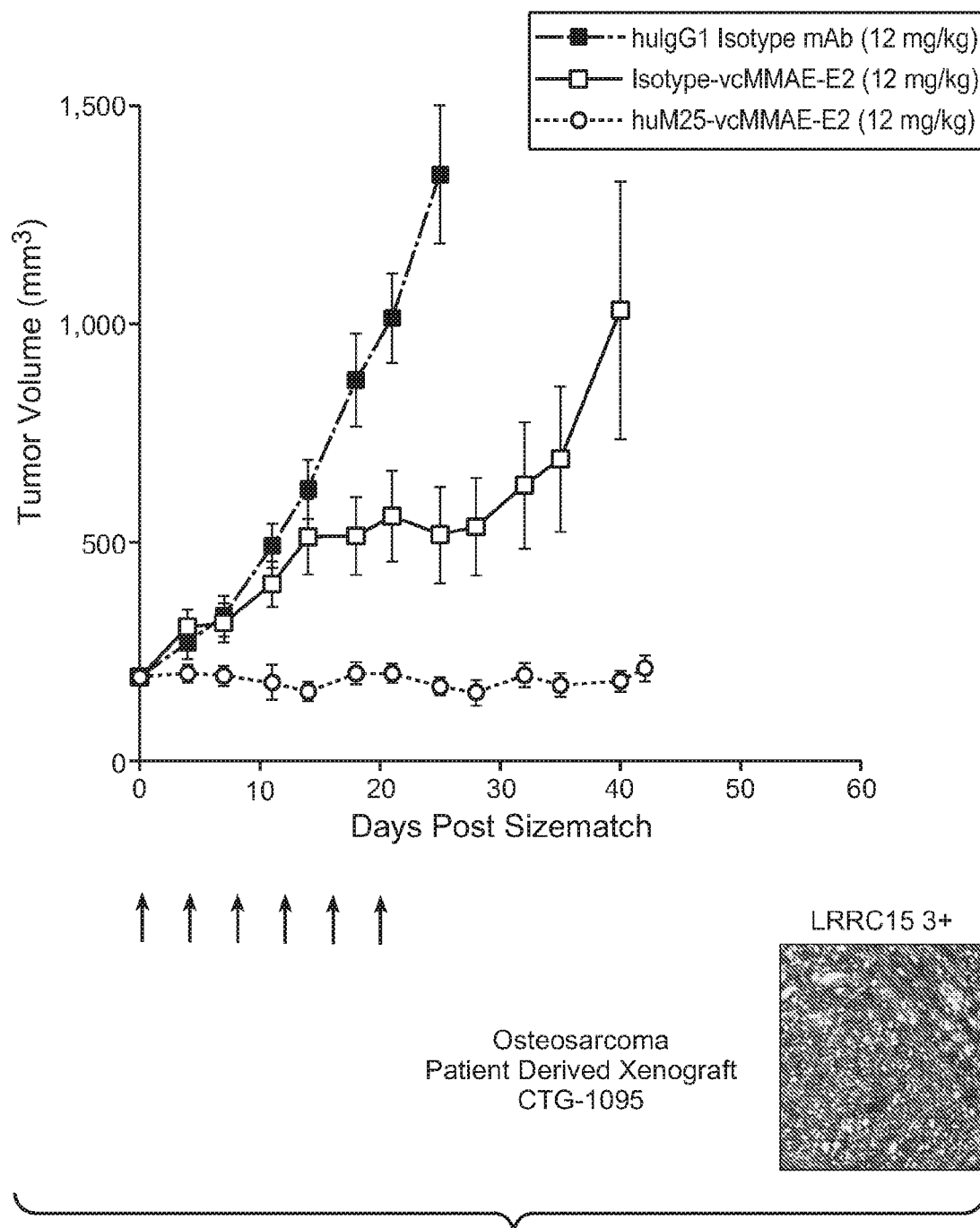
LRRC15 Cancer 2+

U118MG  
(Glioblastoma)**FIG. 14A**

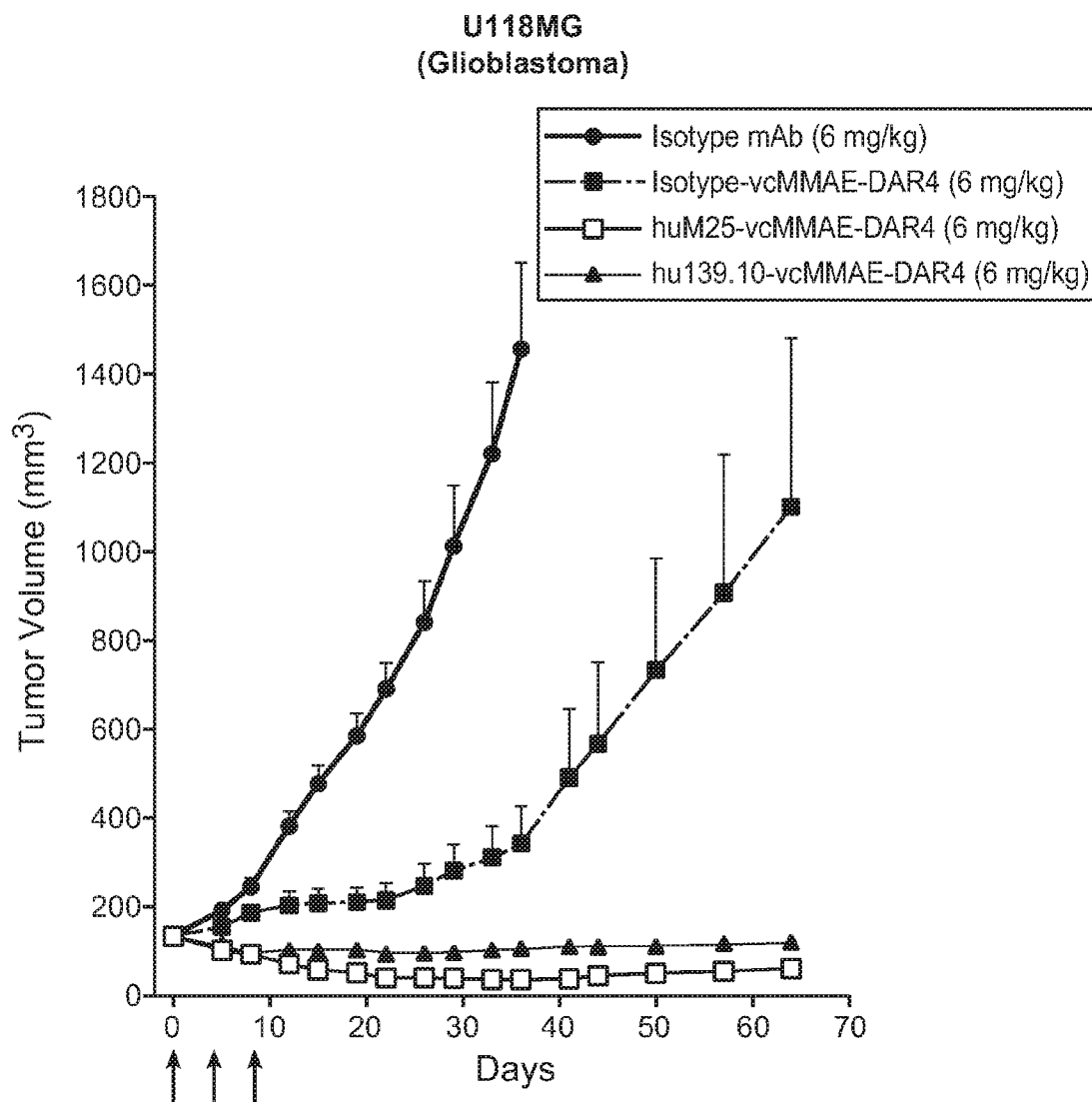
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**FIG. 14B**

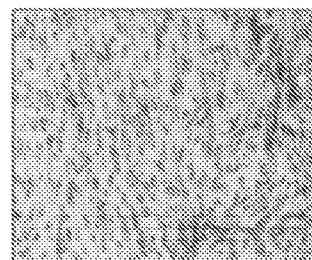
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**FIG. 14C**

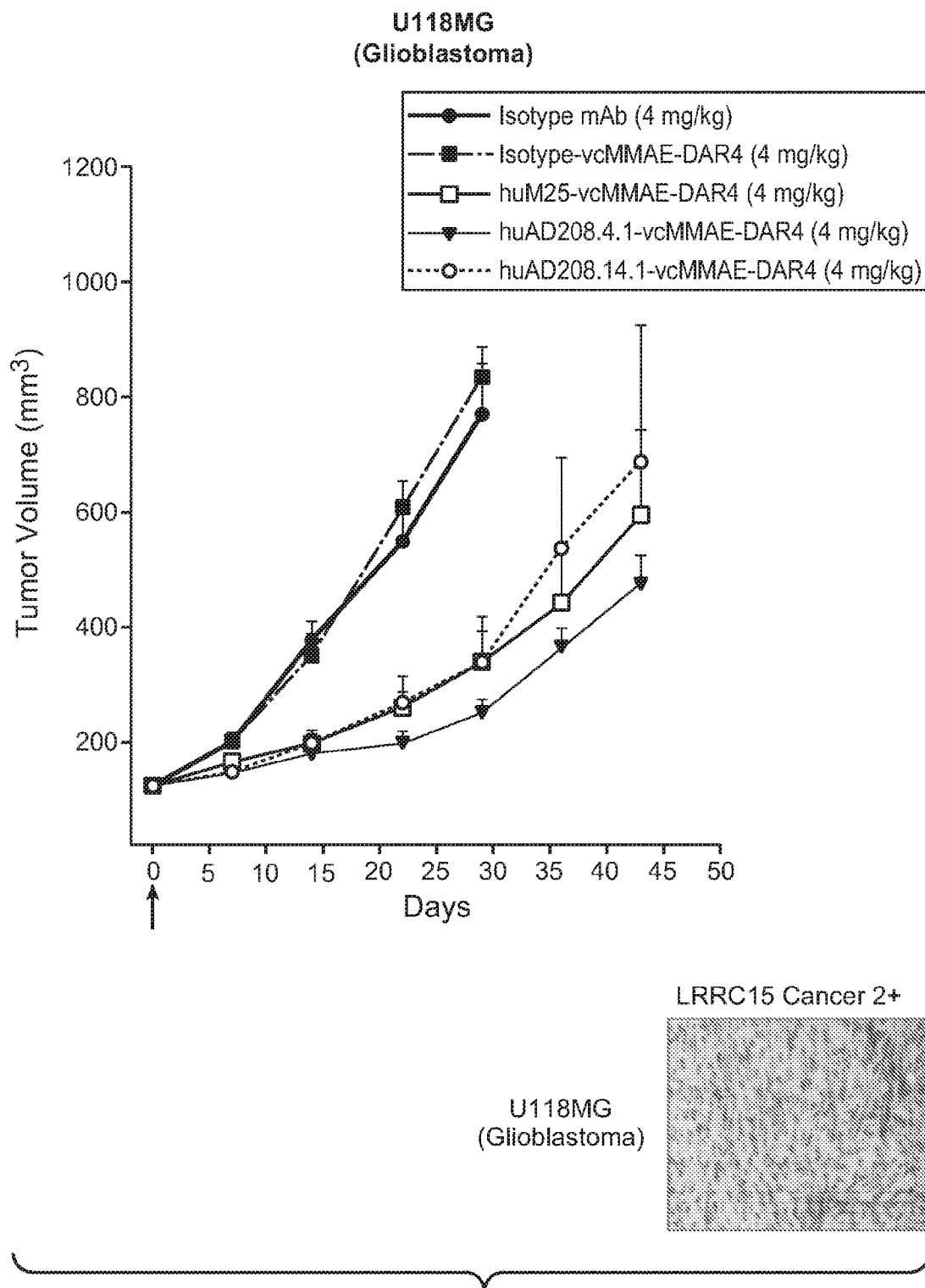
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LRRC15 Cancer 2+

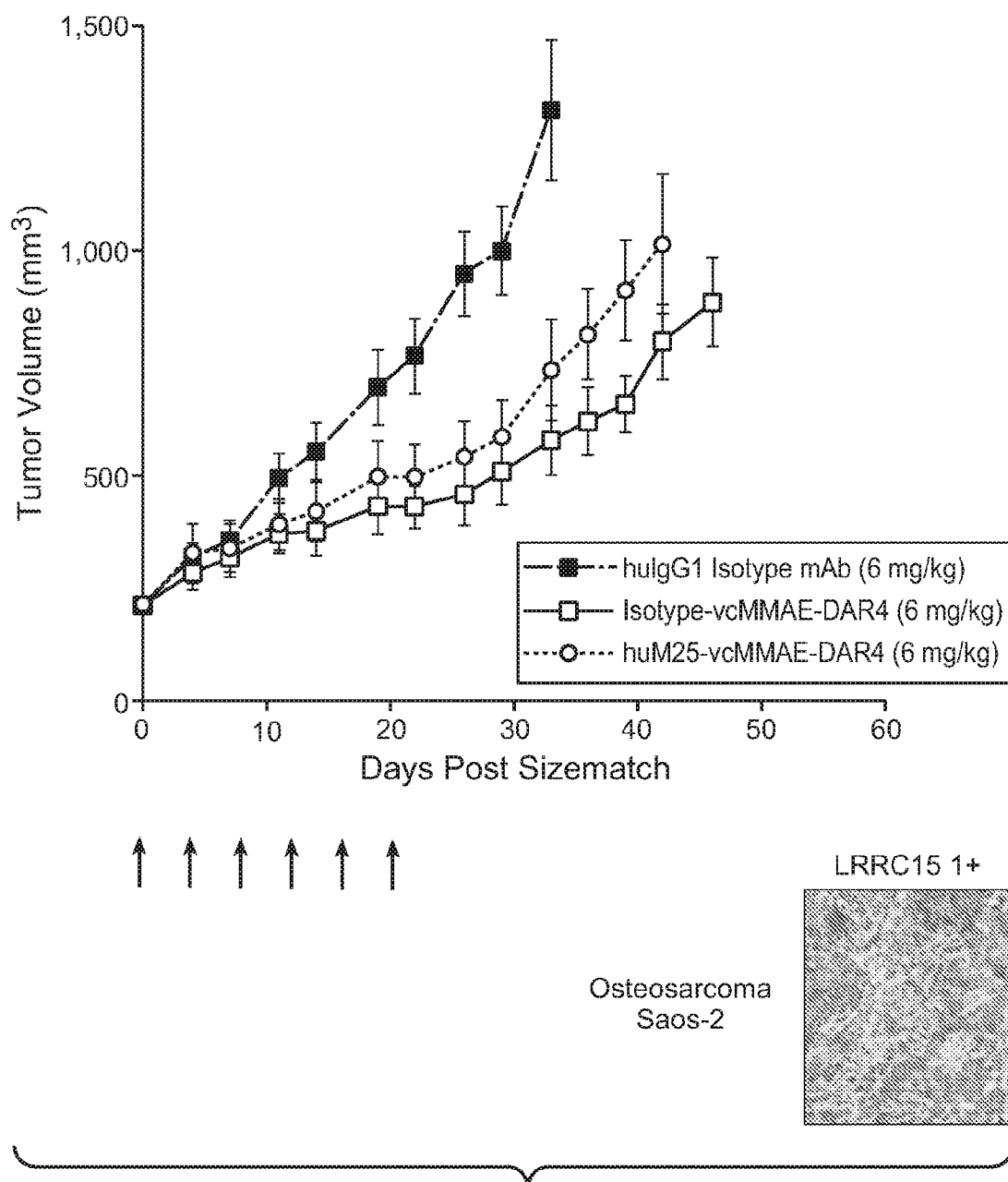
U118MG  
(Glioblastoma)**FIG. 14D**

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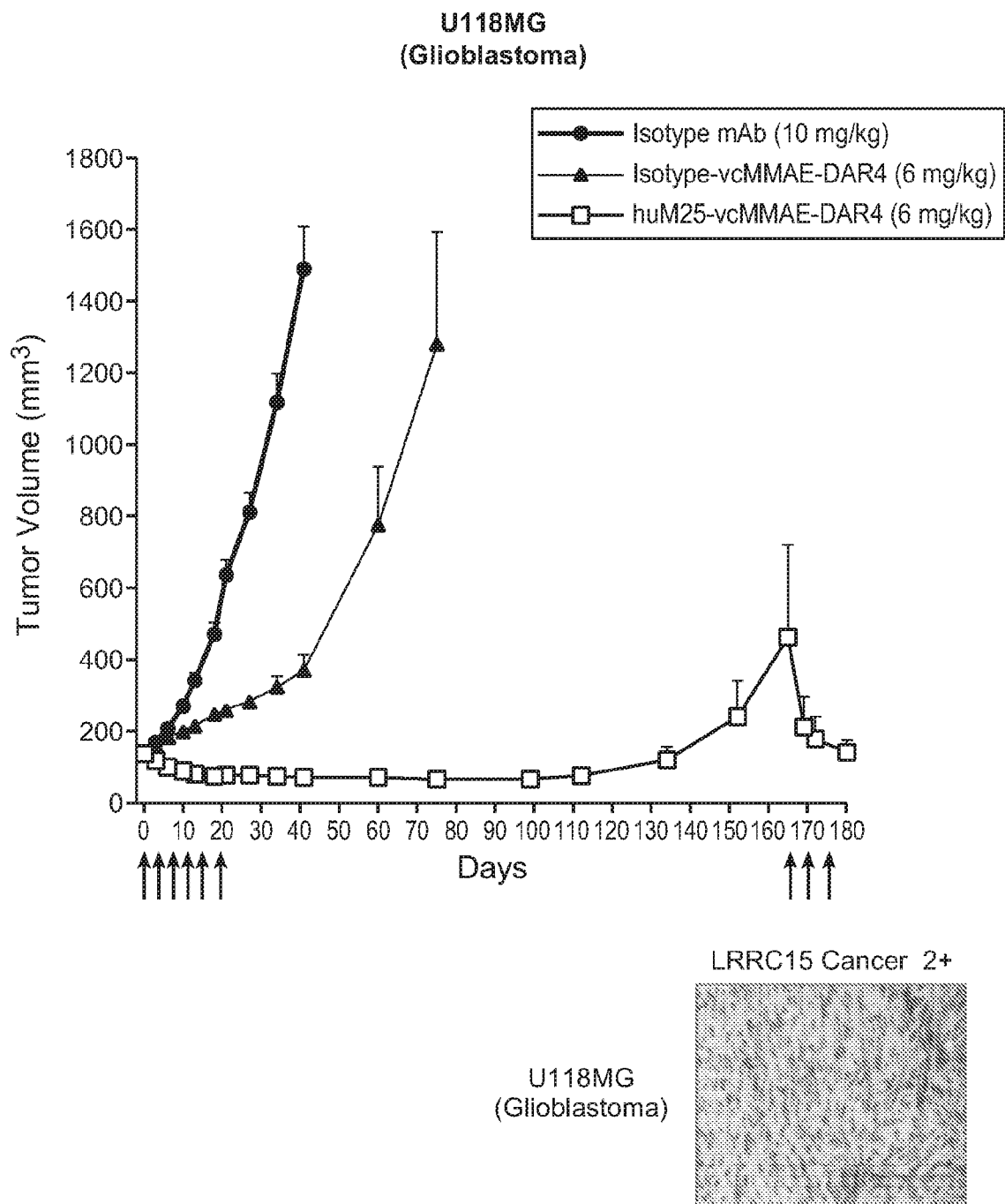


**FIG. 14E**

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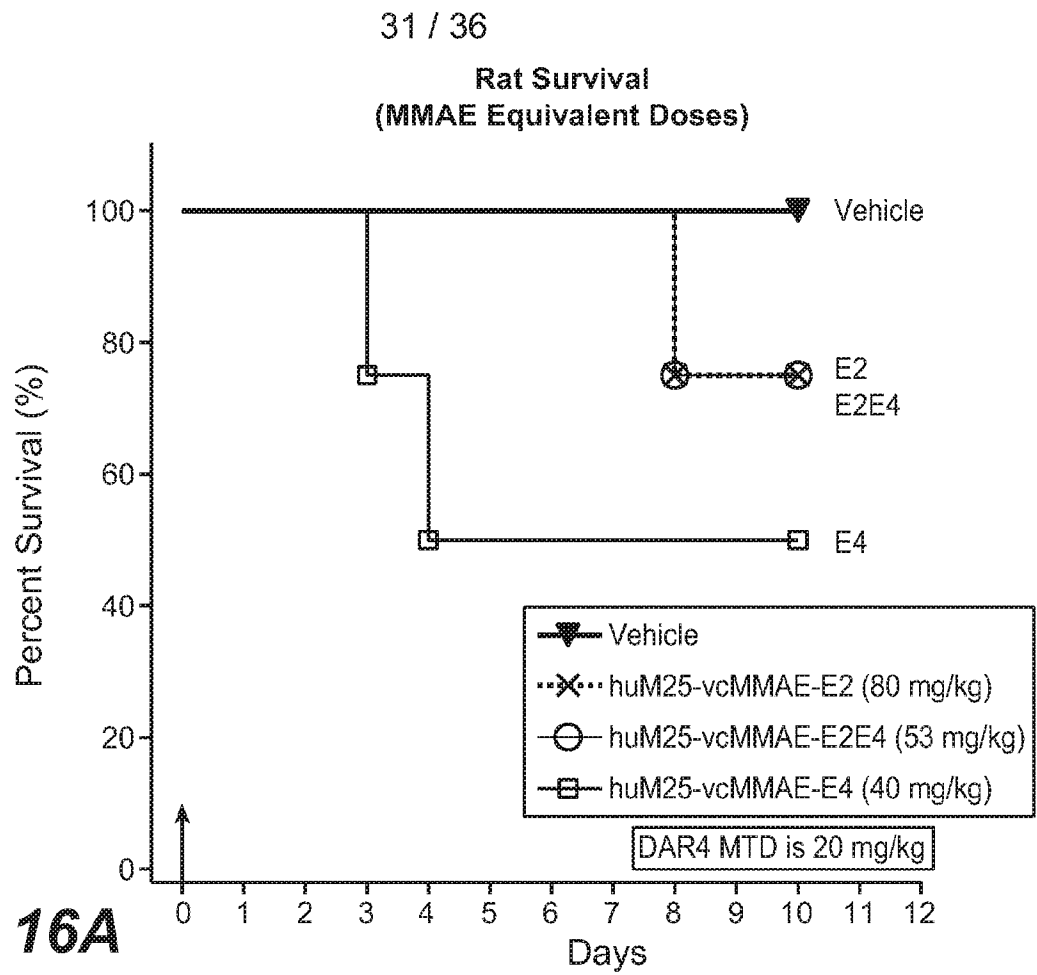


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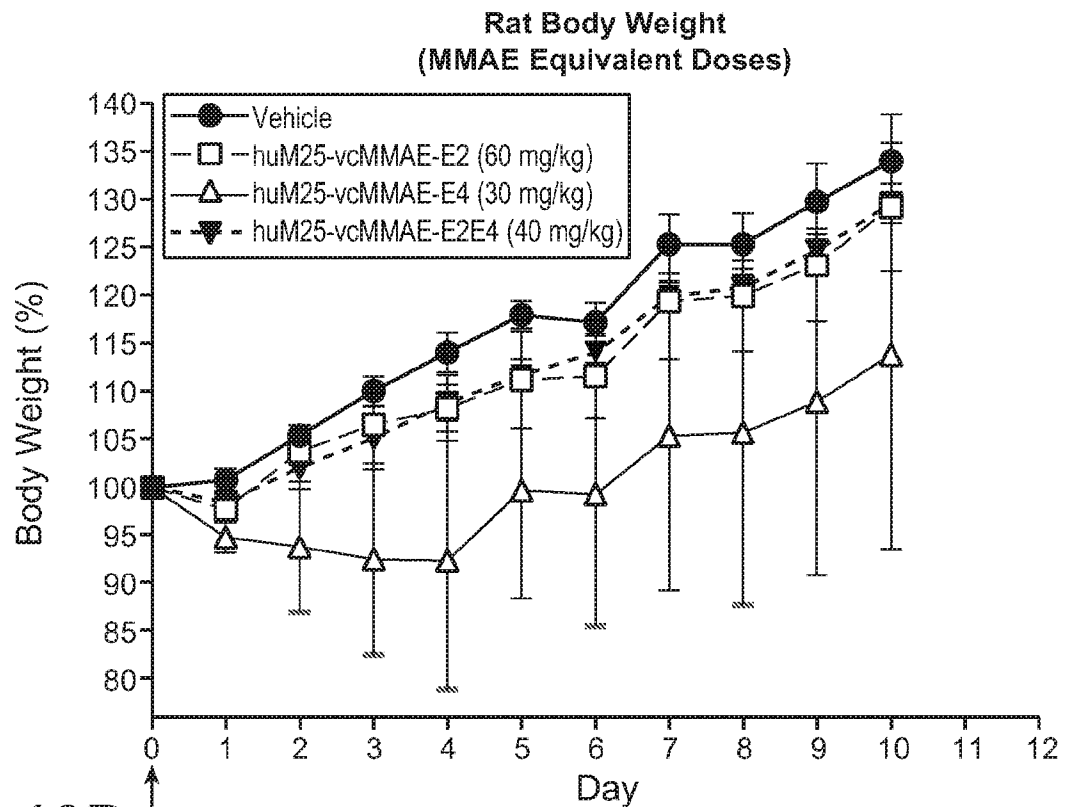


**FIG. 15**

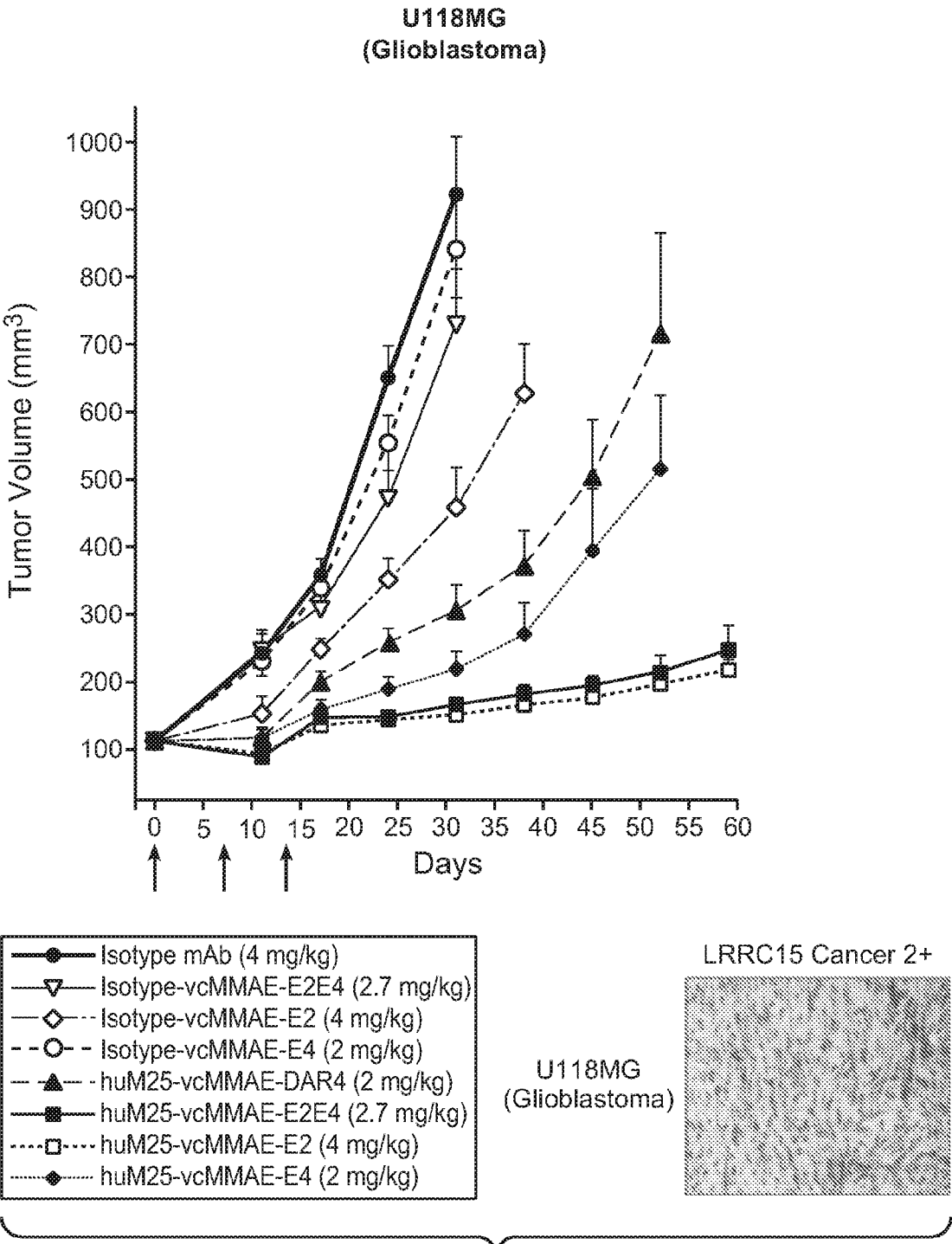




**FIG. 16A**

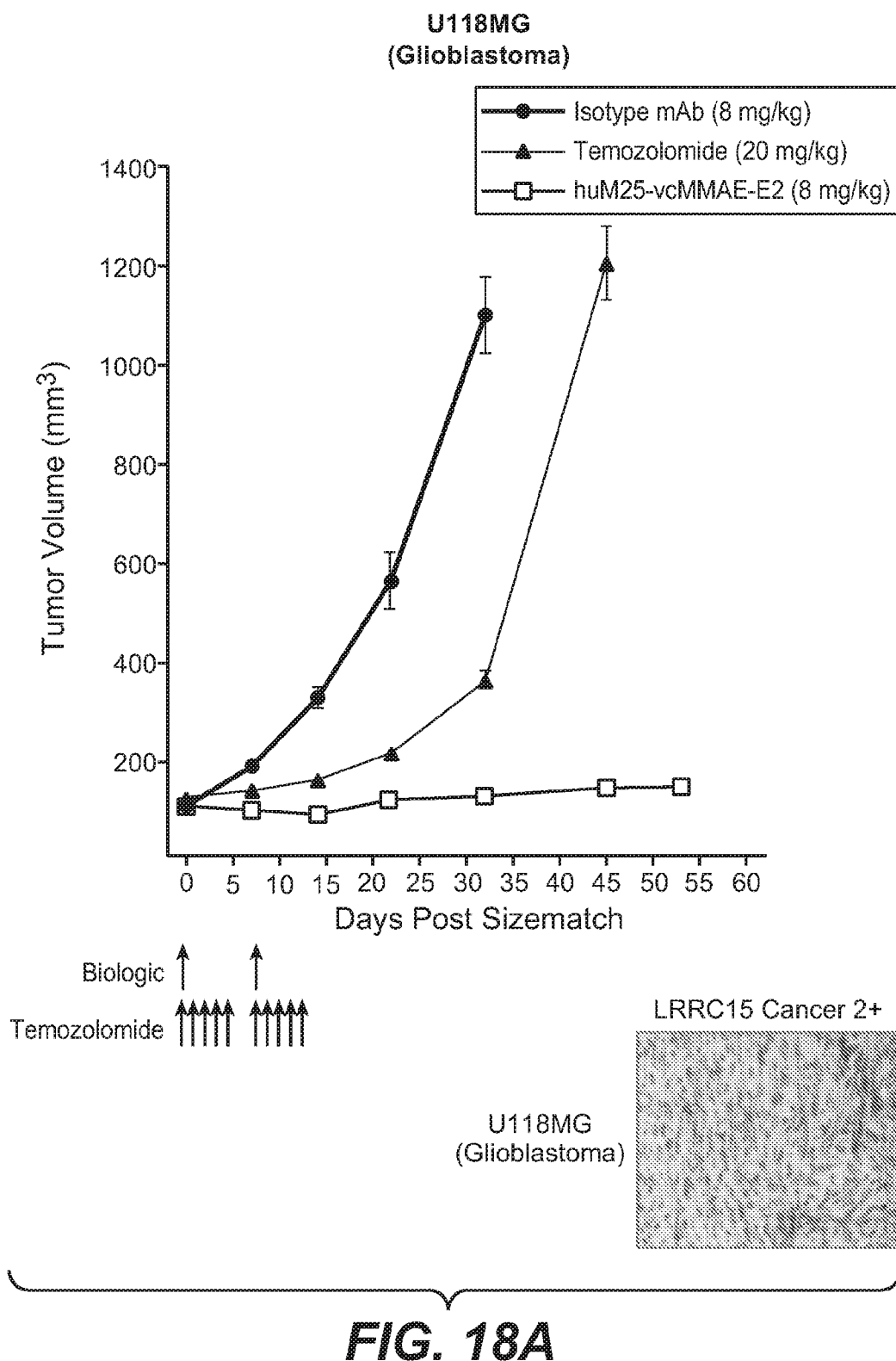


**FIG. 16B**

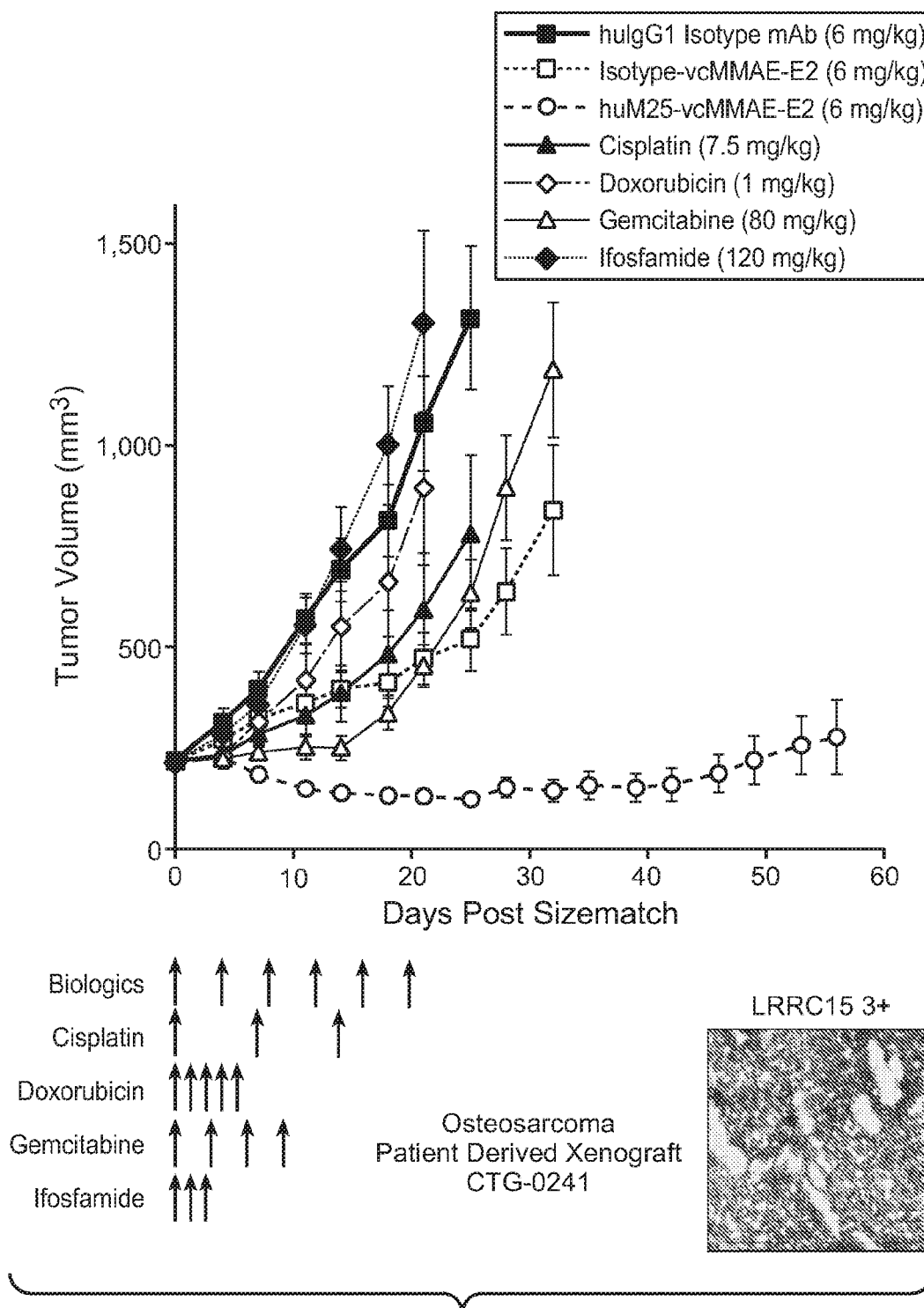


**FIG. 17**

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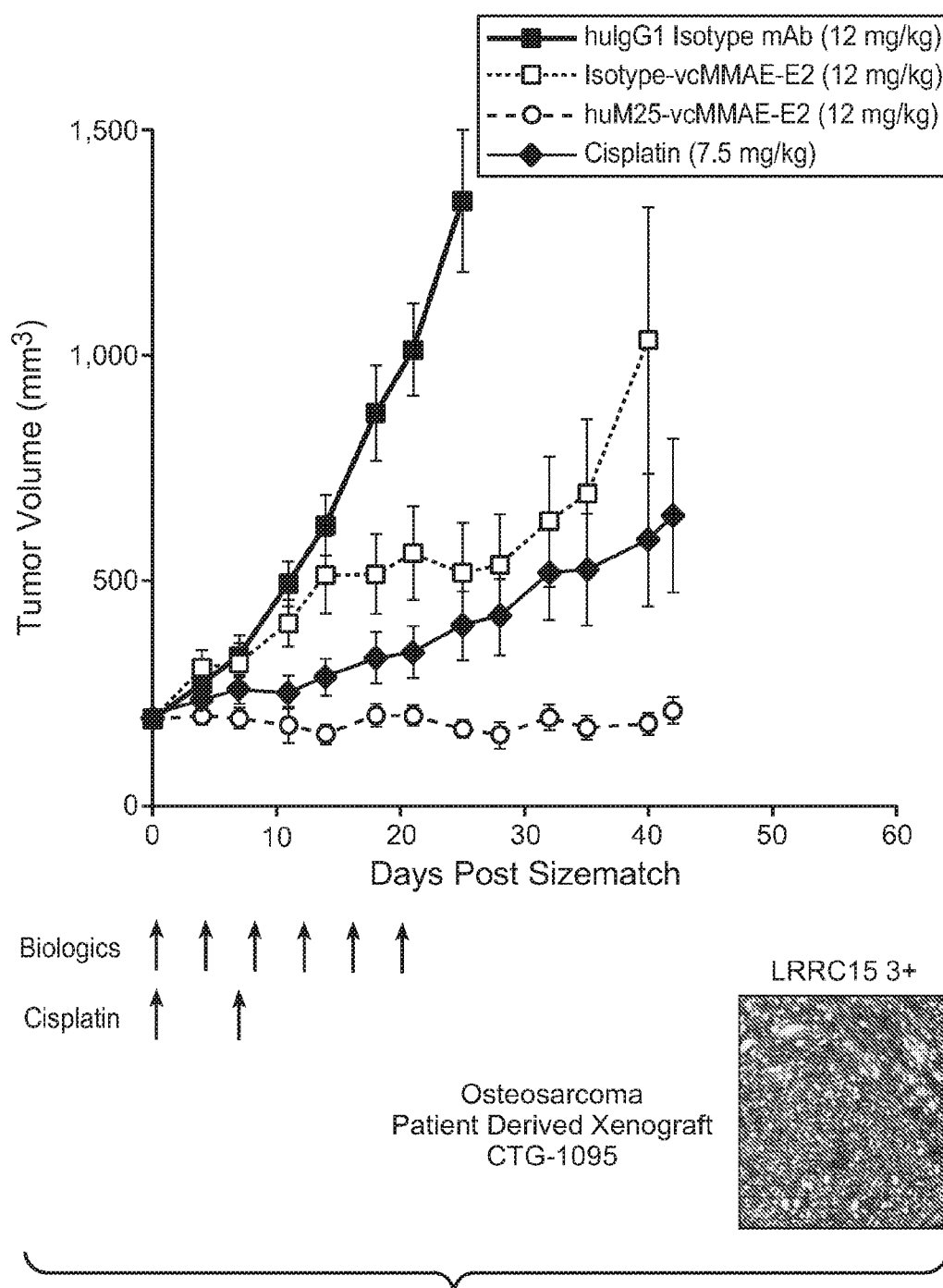


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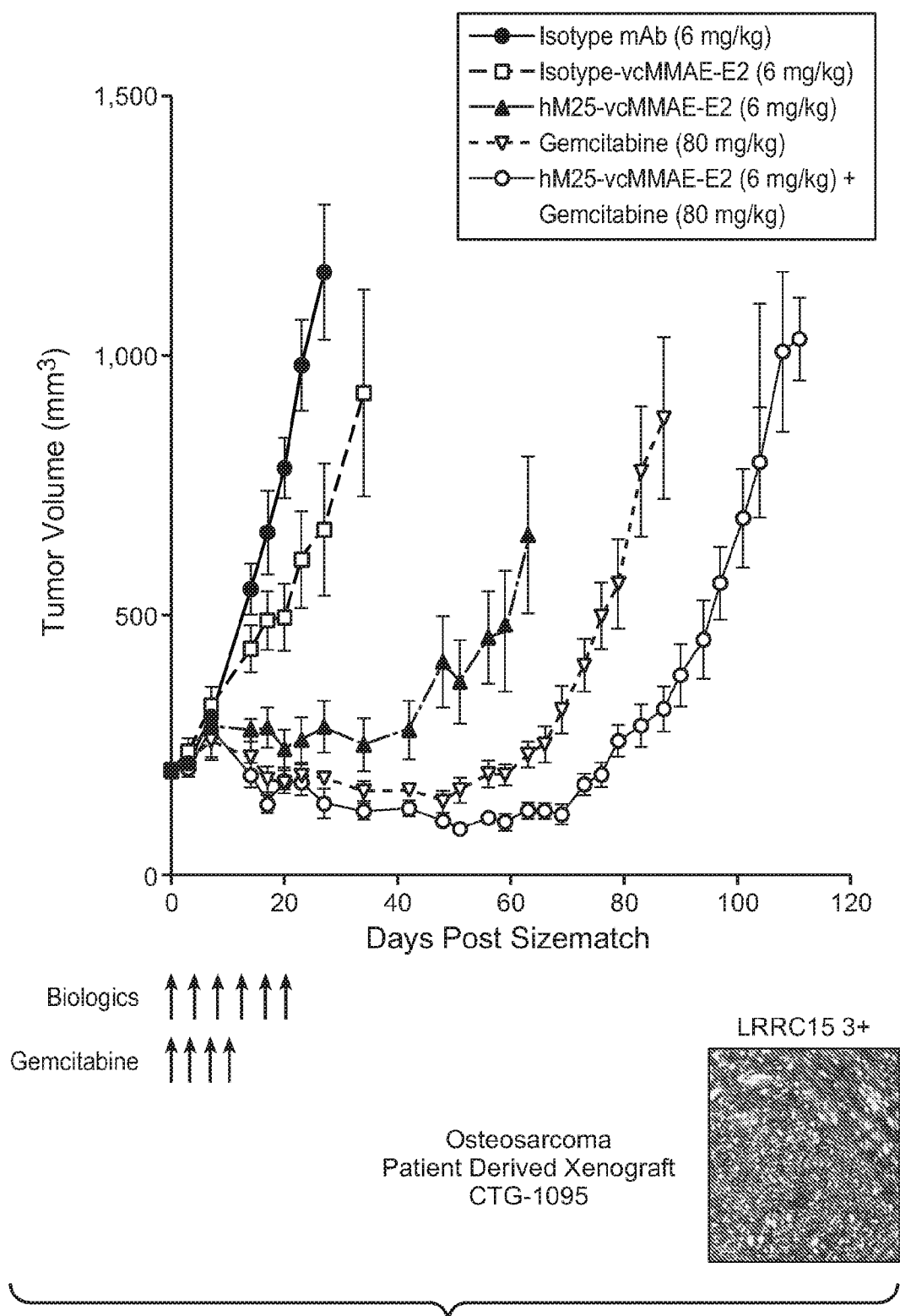


**FIG. 18B**

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**FIG. 18C**

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# INTERNATIONAL SEARCH REPORT

International application No  
PCT/US2016/063998

A. CLASSIFICATION OF SUBJECT MATTER  
INV. C07K16/28 C07K16/30 A61K47/68  
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EP0-Internal, WPI Data

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 2005/094348 A2 (PROTEIN DESIGN LABS INC [US]; ZHANG YONGKE [US]; RAMAKRISHNAN VANITHA) 13 October 2005 (2005-10-13) claims 1-25; examples 2,6; table 1 -----	1-12, 25-28
Y	WO 2015/052532 A1 (SPIROGEN SARL [CH]; ADC THERAPEUTICS S RL [CH]) 16 April 2015 (2015-04-16) claims 1-17 -----	1-12, 25-28
A	WO 2005/037999 A2 (BIOGEN IDEC INC [US]; KLOETZER BILL [US]; MCLACHLAN KAREN [US]; LABARR) 28 April 2005 (2005-04-28) claims 1-61 ----- -/--	1-12, 25-28

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

\* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

11 April 2017

Date of mailing of the international search report

24/04/2017

Name and mailing address of the ISA/

European Patent Office, P.B. 5818 Patentlaan 2  
NL - 2280 HV Rijswijk  
Tel. (+31-70) 340-2040,  
Fax: (+31-70) 340-3016

Authorized officer

Le Flao, Katell

# INTERNATIONAL SEARCH REPORT

International application No  
PCT/US2016/063998

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 2014/174111 A1 (PF MEDICAMENT [FR]; SPIROGEN SARL [CH]) 30 October 2014 (2014-10-30) claims 1-27	1-12, 25-28
A	----- CHRISTINA S SCHUETZ ET AL: "Progression-Specific Genes Identified by Expression Profiling of Matched Ductal Carcinomas In situ and Invasive Breast Tumors, Combining Laser Capture Microdissection and Oligonucleotide Microarray Analysis", CANCER RESEARCH, AMERICAN ASSOCIATION FOR CANCER RESEARCH, US, vol. 66, no. 10, 15 May 2006 (2006-05-15), pages 5278-5286, 1, XP002632523, ISSN: 0008-5472, DOI: 10.1158/0008-5472.CAN-05-4610 abstract	1-12, 25-28
A	----- R. L. EVANS ET AL: "Classifying Patients for Breast Cancer by Detection of Autoantibodies against a Panel of Conformation-Carrying Antigens", CANCER PREVENTION RESEARCH, vol. 7, no. 5, 18 March 2014 (2014-03-18), pages 545-555, XP055191113, ISSN: 1940-6207, DOI: 10.1158/1940-6207.CAPR-13-0416 abstract -----	1-12, 25-28



## INTERNATIONAL SEARCH REPORT

International application No.  
PCT/US2016/063998

### Box No. II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This international search report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:  
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:  
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claims Nos.:  
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

### Box No. III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fees, this Authority did not invite payment of additional fees.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-12, 25-28

#### Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest and, where applicable, the payment of a protest fee.
- ☐ The additional search fees were accompanied by the applicant's protest but the applicable protest fee was not paid within the time limit specified in the invitation.
- ☐ No protest accompanied the payment of additional search fees.

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-12, 25-28

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises a DNA intercalating agent, further defined as in claim 1.

---

2. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 16 and a VL chain corresponding in sequence to SEQ ID NO: 17.

---

3. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 26 and a VL chain corresponding in sequence to SEQ ID NO: 27.

---

4. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 36 and a VL chain corresponding in sequence to SEQ ID NO: 37.

---

5. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC

**FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210**

comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 46 and a VL chain corresponding in sequence to SEQ ID NO: 47.

---

6. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 56 and a VL chain corresponding in sequence to SEQ ID NO: 57.

---

7. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 66 and a VL chain corresponding in sequence to SEQ ID NO: 67.

---

8. claims: 13-24, 29-32(all partially)

A method of treating a huLRRC 15 stromal(+)/cancer(+) tumor, comprising administering to a human having a huLRRC 15 stromal(+)/cancer(+) tumor an amount of an anti-huLRRC15 ADC sufficient to provide therapeutic benefit, wherein the ADC comprises an antimitotic agent, further defined as in claim 13 and wherein the antibody comprises a VH chain corresponding in sequence to SEQ ID NO: 76 and a VL chain corresponding in sequence to SEQ ID NO: 77.

---

# INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2016/063998

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2005094348 A2	13-10-2005	EP 1742654 A2	17-01-2007
		US 2005260212 A1	24-11-2005
		US 2008260740 A1	23-10-2008
		WO 2005094348 A2	13-10-2005
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WO 2015052532 A1	16-04-2015	EP 3054983 A1	17-08-2016
		US 2016263239 A1	15-09-2016
		WO 2015052532 A1	16-04-2015
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WO 2005037999 A2	28-04-2005	US 2005239700 A1	27-10-2005
		WO 2005037999 A2	28-04-2005
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WO 2014174111 A1	30-10-2014	JP 2016518382 A	23-06-2016
		US 2016106861 A1	21-04-2016
		WO 2014174111 A1	30-10-2014
-----			