(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
7 April 2011 (07.04.2011)

PCT

(10) International Publication Number
WO 2011/041336 A2

(51) International Patent Classification:
C07K 16/28 (2006.01)

(21) International Application Number:
PCT/US2010/050610

(22) International Filing Date:
29 September 2010 (29.09.2010)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
61/247,298 30 September 2009 (30.09.2009) US

(71) Applicant *(for all designated States except AL, AT, BE, BG, CH, CN, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IN, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR, US)*: **GENENTECH, INC.** [US/US]; 1 DNA Way, South San Francisco, California 94080-4990 (US).

(71) Applicant *(for AL, AT, BE, BG, CH, CN, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IN, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR only)*: **F. HOFFMANN-LA ROCHE AG** [CH/CH]; Grenzacherstrasse 124, CH-4070 Basel (CH).

(72) Inventor; and

(75) Inventor/Applicant *(for US only)*: **SIEBEL, Christian W.** [US/US]; c/o Genentech, Inc., 1 DNA Way, MS 49, South San Francisco, California 94080 (US).

(74) Agents: **PASQUALONE, Danielle, M.** et al.; GENENTECH, INC., 1 DNA Way, MS-49, South San Francisco, California 94080-4990 (US).

(81) Designated States *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IS, JP, KE, KG, KM, KN, KP, KR, KZ, LA, LC, LK, LR, LS, LT, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PE, PG, PH, PL, PT, RO, RS, RU, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) Designated States *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report (Rule 48.2(g))*

— *with sequence listing part of description (Rule 5.2(a))*

(54) **Title**: METHODS OF TREATING CANCER USING NOTCH ANTAGONISTS

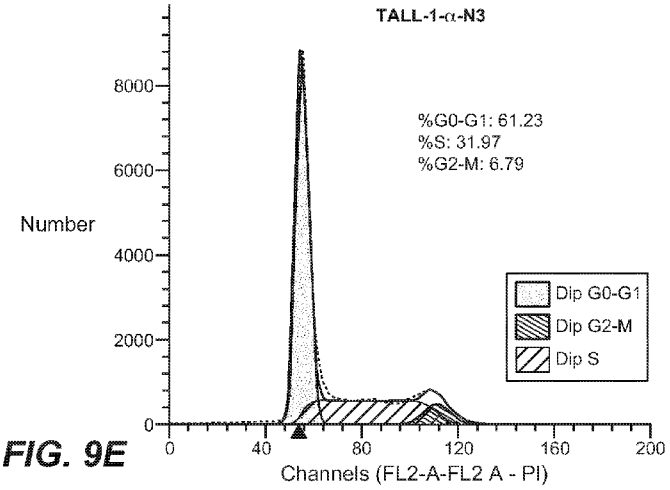


FIG. 9E

(57) **Abstract**: The present invention relates to methods of treating cancer in general, and leukemia in particular, using Notch1 and Notch3 antagonists singly or in combination. Compositions and methods for the treatment and diagnosis of Notch-associated cancers are also provided.

WO 2011/041336 A2

METHODS OF TREATING CANCER USING NOTCH ANTAGONISTS

RELATED APPLICATIONS

This application claims the benefit under 35 USC 119(e) of provisional application number 61/247298 filed September 30, 2009, the contents of which are incorporated herein by reference.

FIELD OF THE INVENTION

The present invention relates to methods of treating cancer in general, and leukemia in particular, using Notch1 and Notch3 antagonists singly or in combination. Compositions and methods for the treatment and diagnosis of Notch-associated cancers are also provided.

SEQUENCE LISTING

The present application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on September 3, 2010, is named P4371.txt and is 65,600 bytes in size.

BACKGROUND

The Notch receptor family is a class of evolutionarily conserved transmembrane receptors that transmit signals affecting development in organisms as diverse as sea urchins and humans. Notch receptors and their ligands Delta and Serrate (known as Jagged in mammals) are transmembrane proteins with large extracellular domains that contain epidermal growth factor (EGF)-like repeats. The number of Notch paralogues differs between species. For example, there are four Notch receptors in mammals (Notch1-Notch4), two in *Caenorhabditis elegans* (LIN-12 and GLP-1) and one in *Drosophila melanogaster* (Notch). Notch receptors are proteolytically processed during transport to the cell surface by a furin-like protease at a site S1, which is N-terminal to the transmembrane domain, producing an extracellular Notch (ECN) subunit and a Notch transmembrane subunit (NTM). These two subunits remain non-covalently associated and constitute the mature heterodimeric cell-surface receptor.

Notch1 ECN subunits contain 36 N-terminal EGF-like repeats followed by three tandemly repeated Lin 12/Notch Repeat (LNR) modules that precede the S1 site. Notch3 ECN has a similar structure, but with 34 EGF-like repeats. Each LNR module contains three disulfide bonds and a group of conserved acidic and polar residues predicted to coordinate a calcium ion. Within the EGF repeat region lie binding sites for the activating ligands. The Notch1 and Notch3 NTMs comprises an extracellular region (which harbors the S2 cleavage site), a transmembrane segment (which harbors the S3 cleavage site), and a large intracellular region (ICN or ICD) that includes a RAM domain, ankyrin repeats, a transactivation domain and a carboxy-teminal PEST domain. Stable association of the ECN and NTM subunits depends upon a heterodimerization domain (HD) comprising the carboxy-terminal end of the ECN (termed HD-N) and the extracellular amino-terminal end of NTM (termed HD-C). Before ligand-induced activation, Notch is maintained in a resting conformation by a negative regulatory region (NRR), which comprises the three LNRs and the HD domain.

Binding of a Notch ligand to the ECN subunit initiates two successive proteolytic cleavages that occur through regulated intramembrane proteolysis. The first cleavage by a metalloprotease (ADAM17) at site S2 renders the Notch transmembrane subunit susceptible to the second cleavage at site S3 close to the inner leaflet of the plasma membrane. Site S3 cleavage, which is catalyzed by a multiprotein complex containing presenilin and nicastrin and promoting γ-secretase activity, liberates the intracellular portion of the Notch transmembrane subunit, allowing it to translocate to the nucleus and activate transcription of target genes. (For review of the proteolytic cleavage of Notch, see, e.g., Sisodia et al., *Nat. Rev. Neurosci.* 3:281-290, 2002.)

Five Notch ligands of the Jagged and Delta-like classes have been identified in humans (Jagged1 (also termed Serrate1), Jagged2 (also termed Serrate2), Delta-like1 (also termed DLL1), Delta-like3 (also termed DLL3), and Delta-like4 (also termed DLL4)). Each of the ligands is a single-pass transmembrane protein with a conserved N-terminal Delta, Serrate, LAG-2 (DSL) motif essential for binding Notch. A series of EGF-like modules C-terminal to the DSL motif precede the membrane-spanning segment. Unlike the Notch receptors, the ligands have short cytoplasmic tails of 70-215 amino acids at the C-terminus. In addition, other types of ligands have been reported (e.g., DNER, NB3, and F3/Contactin). (For review of Notch ligands and ligand-mediated Notch activation, see, e.g., D'Souza et al., *Oncogene* 27:5148-5167, 2008.)

The Notch pathway functions during diverse developmental and physiological processes including those affecting neurogenesis in flies and vertebrates. In general, Notch signaling is involved in lateral inhibition, lineage decisions, and the establishment of boundaries between groups of cells. (See, e.g., Bray, *Mol. Cell Biol.* 7:678-679, 2006.) A variety of human diseases, including cancers and neurodegenerative disorders have been shown to result from mutations in genes encoding Notch receptors or their ligands. (See, e.g., Nam et al., *Curr. Opin. Chem. Biol.* 6:501-509, 2002.)

The role of Notch1 as an oncoprotein was demonstrated in leukemia involving T-cell progenitors. This role was first recognized in human acute lymphoblastic leukemia (T-ALL). (See, e.g., Aster et al., *Annu. Rev. Pathol. Mech. Dis.* 3:587-613, 2008.) T-ALL is an aggressive leukemia that preferentially afflicts children and adolescents. A recurrent t(7;9)(q34;q34.3) chromosomal translocation, which creates a truncated, constitutively active variant of human Notch1, was identified in a subset of T-ALLs. In addition to the (7;9) translocation, frequent gain-of-function mutations in human Notch1 were later discovered in more than 50% of all human T-ALLs. (See Weng et al., *Science*, 306:269-271, 2004.) Those mutations occur in the extracellular HD domain and the intracellular PEST domain. Other studies showed that retroviral-based expression of Notch1 ICN in bone marrow cells caused T-ALL in mouse models that received the transplanted bone marrow cells. (See Aster et al., *Mol. Cell Biol.* 20:7505-7515, 2000.)

Consistent with this role for Notch1 in leukemia involving T cell progenitors, Notch1 signaling has been shown to be essential for T cell development in mouse models, and Notch1-mediated signals promote T cell development at the expense of B cell development. (See, e.g., Wilson et al., *J. Exp. Med.* 194:1003-1012, 2001.) Further roles for Notch1 in leukemia have been described. Activating mutations in the Notch1 PEST domain have been reported at low frequency in human acute myeloid leukemia (AML) and in lineage switch leukemias, suggesting that activating mutations in Notch1 may occur in a leukemic stem cell that precedes myeloid and T-lineage commitment. (See Palomero et al., *Leukemia* 20:1963-1966, 2006.)

Prior to the discovery of the frequent Notch1 gain-of-function mutations in T-ALL, it was observed that enforced expression of Notch3 ICN in the thymus caused T-cell leukemia/lymphoma in transgenic mice. (See Bellavia et al., *EMBO J.* 19:3337-3348, 2000.) Notch3 mRNA was also reported as being expressed in all of thirty T-ALL patient samples

analyzed, whereas it was not detected in normal peripheral blood T lymphocytes and non-T cell leukemias. (See Bellavia et al., *Proc. Nat'l Acad. Sci. USA* 99:3788-3793, 2002.)

Notch1 and Notch3 are also associated with a variety of other cancers. For instance, in solid tumors, increased Notch1 expression has been observed in human cancers of the cervix, colon, lung, pancreas, skin, and brain (see, e.g., Leong et al., *Blood* 107:2223-2233, 2006), and elevated expression of Notch1 is correlated with poor outcome in breast cancer (see, e.g., Parr et al., *Int. J. Mol. Med.* 14:779-786, 2004; Reedijk et al., *Cancer Res.* 65:8530-8537, 2005). A chromosomal translocation (15;19) has been identified in a subset of non-small cell lung tumors, and the translocation is thought to elevate Notch3 transcription. In ovarian cancer, Notch3 gene amplification was found to occur in ~19% of tumors, and overexpression of Notch3 was found in more than half of ovarian serous carcinomas. Overexpression of activated Notch1 and Notch3 in transgenic mice induces mouse breast tumors, and overexpression of Notch3 is sufficient to induce choroid plexus tumor formation in a mouse model, suggesting a role for Notch3 in the development of certain brain tumors. (For review of Notch3 in cancer, see Shih et al. *Cancer Res.* 67:1879-1882, 2007.)

Certain anti-Notch1 antagonist antibodies having therapeutic efficacy have been described. (See U.S. Patent Application Publication No. US 2009/0081238 A1, expressly incorporated by reference in its entirety herein.) For example, such antibodies bind to the negative regulatory region (NRR) of Notch1, block Notch1 signaling, disrupt angiogenesis and vascularization, and inhibit tumor growth in mouse xenograft models of non small cell lung carcinoma and colon adenocarcinoma. Certain antibodies described therein bind to LNR-A and LNR-B (the first and second of the three LIN12/Notch Repeats) and HD-C of Notch1 NRR. Other anti-Notch1 antibodies that bind to the EGF repeat region of Notch1 and block Notch1 activity, perhaps by blocking ligand binding, have also been described. (See International Publication No. WO 2008/091641.)

Certain anti-Notch3 antagonist antibodies have also been described. (See U.S. Patent Application Publication No. US 2008/0226621 A1, expressly incorporated by reference in its entirety herein.) Such antibodies bind to the negative regulatory region (NRR) of Notch3 and block Notch3 signaling. Certain antibodies described therein bind to LNR-A (the first of the three LIN12/Notch Repeats) and HD-C (referred to alternatively as the second dimerization domain in US 2008/0226621 A1) of Notch3 NRR. Other anti-Notch3 antibodies that bind to the EGF-like repeat region of Notch3 and block Notch3 activity, perhaps by blocking ligand binding, have also been described. (See Li et al., *J. Biol. Chem.* 283:8046-8054, 2008.)

Gamma-secretase inhibitors (GSIs), which are pan-Notch inhibitors that inhibit multiple Notch receptors, have been proposed for treatment of Notch-related diseases, and in fact have been used in clinical trials for the treatment of T-ALL . (See Roy et al., *Curr. Opin. Genet. Dev.* 17:52-59, 2007; Deangelo et al., *J. Clin. Oncol. 2006 ASCO Annual Meeting Proceedings Part I* 24:6586, 2006.) However, GSIs cause weight loss and intestinal goblet cell metaplasia, reflecting the role that Notch plays in determining cell fate by maintaining proliferation of intestinal crypt progenitor cells and prohibiting differentiation to a secretory cell fate. (See van Es *et al., Nature* 435:959-963, 2005). Although these side effects of pan-Notch inhibition may be manageable in a clinical setting, inhibitors that target individual Notch receptors, and therefore minimize or reduce these side effects, may be advantageous.

There is a need in the art for further therapeutic methods of treating cancer by targeting Notch receptors. The invention described herein meets the above-described needs and provides other benefits.

SUMMARY

The present invention relates to the treatment of cancer using Notch antagonists singly or in combination. The present invention specifically relates, in part, to the characterization of different classes of T-ALL. One class of T-ALL is sensitive to treatment with GSI and is also sensitive to treatment with a Notch1-specific antagonist. In contrast, another class of T-ALL is sensitive to treatment with GSI, but insensitive (i.e., resistant) to treatment with a Notch1-specific antagonist. As shown herein, the latter class of T-ALL is partially sensitive to treatment with a Notch3-specific antagonist, and even more sensitive to a combination of a Notch1-specific antagonist and a Notch3-specific antagonist. These results suggest a role for both Notch1 and Notch3 in leukemias, particularly T cell progenitor leukemias such as T-ALL.

In one aspect, a method of treating a GSI-responsive cancer that does not respond to a Notch1-specific antagonist is provided, the method comprising administering to a patient having such cancer an effective amount of a Notch3-specific antagonist. In certain embodiments, the cancer is T-cell leukemia. In certain embodiments, the T-cell leukemia is a lymphoblastic leukemia. In certain embodiments, the T-cell leukemia is T-ALL. In certain embodiments, the Notch3-specific antagonist is an anti-Notch3 antagonist antibody. In certain embodiments, the anti-Notch3 antagonist antibody is an anti-Notch3 NRR antibody. In certain embodiments, the anti-Notch3 NRR antibody binds to the LNR-A and HD-C

domains of Notch3 NRR. In certain embodiments, the anti-Notch3 NRR antibody comprises the heavy and light chain variable region CDRs of antibody 256A-4 or 256A-8. In certain embodiments, the anti-Notch3 NRR antibody is a humanized form of antibody 256A-4 or 256A-8. In certain embodiments, the anti-Notch3 antagonist antibody is an anti-Notch3 antibody that binds to one or more EGF-like repeats of Notch3.

In a further embodiment, the method further comprises administering an effective amount of a Notch1-specific antagonist. In certain embodiments, the Notch1-specific antagonist that is administered is an anti-Notch1 antagonist antibody. In certain embodiments, the anti-Notch1 antagonist antibody is an anti-Notch1 NRR antibody. In certain embodiments, the anti-Notch1 NRR antibody binds to the LNR-A, LNR-B, and HD-C domains of Notch1 NRR. In certain embodiments, the anti-Notch1 NRR antibody is selected from Antibody A, A-1, A-2, and A-3. In certain embodiments, the anti-Notch1 NRR antibody comprises the heavy and light chain variable region CDRs of an antibody selected from Antibody A, A-1, A-2, and A-3. In certain embodiments, the anti-Notch1 antagonist antibody is an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1.

In a further aspect of the invention, an antibody that binds to activated Notch3 ICD is provided. In certain embodiments, the antibody binds to the peptide of SEQ ID NO:4. In certain embodiments, the antibody is polyclonal. In certain embodiments, the antibody is monoclonal.

In a further aspect of the invention, a method of identifying a cancer that is suitable for treatment with an antagonist of Notch3 is provided, the method comprising contacting a sample of the cancer with the antibody of claim 15, and determining whether significantly increased levels of activated Notch3 are present in the sample, wherein the presence of significantly increased levels of activated Notch3 indicates that the cancer is suitable for treatment with an antagonist of Notch3. In certain embodiments, the cancer is GSI-responsive.

The above and further aspects and embodiments of the invention are provided herein.

BRIEF DESCRIPTION OF THE FIGURES

Figure 1A-1D shows an alignment of human Notch1 (SEQ ID NO:1) and mouse Notch1 (SEQ ID NO:2), with motifs and other features indicated.

Figure 2 shows the sequence of human Notch3 (SEQ ID NO:3). The EGF repeat region extends from amino acid residue 43 to 1383; the LNR modules extend from amino

acid residue 1384 to 1503, with LNR-A extending from amino acid residues 1384-1422; and the dimerization domain extends from amino acid residue 1504 to 1640, with HD-C extending from amino acid residues 1572-1640.

Figure 3A-3D shows that the T-ALL cell line, P-12 Ichikawa, is resistant to both GSI (DAPT) and anti-NRR1 (α-N1).

Figure 4A-4D shows that the T-ALL cell line, HPB-ALL, is sensitive to both GSI (DAPT) and anti-NRR1 (α-N1), as evidenced by the accumulation of cells in G0/G1 and the reduction of cells in S/G2/M, relative to control cells.

Figure 5A-5D shows that the T-ALL cell line, TALL-1, is sensitive to GSI but resistant to anti-NRR1 (α-N1).

Figure 6 shows that cell size measurements reflect the three classes of T-ALL identified in Figures 3-5.

Figure 7 shows that staining with Annexin V (marker for apoptosis) and 7-AAD (marker for cell death) reflects the three classes of T-ALL identified in Figures 3-5.

Figure 8, left panel, shows that Ki-67 staining (marker for cell proliferation) reflects the three classes of T-ALL identified in Figures 3-5. Left-shifted peaks indicate lower staining for Ki-67 and decreased proliferation relative to right-shifted peaks. Figure 8, right panel, shows that decreased staining for Ki-67 (i.e., decreased proliferation) correlates inversely with the number of Annexin V/7-AAD double negative (i.e., non-apoptotic) cells.

Figure 9A-9F shows that the TALL-1 cell line is partially sensitive to anti-NRR3 (α-N3) and sensitive to treatment with anti-NRR1 (α-N1) and anti-NRR3.

Figure 10A-10F shows that the T-ALL cell line, CCRF-CEM, is resistant to both GSI, anti-NRR1 (α-N1) and anti-NRR3 (α-N3).

Figure 11A-11F shows that the HPB-ALL cell line is sensitive to anti-NRR1 (α-N1) but not anti-NRR3 (α-N3).

Figure 12 shows an immunoblot using an antibody that recognizes activated Notch3 ICD (α-Notch3 ICD), which detects activated Notch3 ICD in the nuclear fraction of Jag 1-stimulated MDA-MB-468 cells.

Figure 13 shows that the TALL-1 cell line expresses high levels of cleaved, activated Notch3 (lower panel), which can be blocked by DAPT but not anti-NRR1 (α-N1), whereas the HPB-ALL cell line expresses high levels of cleaved, activated Notch1, which can be blocked by DAPT and anti-NRR1 (α-N1).

Figure 14 shows a graph of the results of the experiments depicted in Figure 9A-9F.

DETAILED DESCRIPTION OF EMBODIMENTS

I. DEFINITIONS

For purposes of interpreting this specification, the following definitions will apply and whenever appropriate, terms used in the singular will also include the plural and vice versa. In the event that any definition set forth below conflicts with any document incorporated herein by reference, the definition set forth below shall control.

The term "Notch," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) Notch polypeptide (Notch1-4). The term "native sequence" specifically encompasses naturally occurring truncated forms (e.g., an extracellular domain sequence or a transmembrane subunit sequence), naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants. The term "wild-type Notch" generally refers to a polypeptide comprising an amino acid sequence of a naturally occurring, non-mutated Notch protein. The term "wild-type Notch sequence" generally refers to an amino acid sequence found in a naturally occurring, non-mutated Notch.

The term "Notch1," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) Notch1 polypeptide. The term "native sequence" specifically encompasses naturally occurring truncated forms (e.g., an extracellular domain sequence or a transmembrane subunit sequence), naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants. The term "wild-type Notch1" generally refers to a polypeptide comprising an amino acid sequence of a naturally occurring, non-mutated Notch1 protein. The term "wild type Notch1 sequence" generally refers to an amino acid sequence found in a naturally occurring, non-mutated Notch1.

The term "Notch1 ligand," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) Notch1 ligand (for example, Jagged1, Jagged2, Delta-like1, Delta-like3, and/or Delta-like4) polypeptide. The term "native sequence" specifically encompasses naturally occurring truncated forms (e.g., an extracellular domain sequence or a transmembrane subunit sequence), naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants. The term "wild-type Notch1 ligand" generally refers to a polypeptide comprising an amino acid sequence of a naturally occurring, non-mutated Notch1 ligand. The term "wild type Notch1

ligand sequence" generally refers to an amino acid sequence found in a naturally occurring, non-mutated Notch1 ligand.

The term "Notch1 NRR," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) polypeptide region of Notch1 consisting of the 3 LNR modules and the amino acid sequences extending from the carboxy-terminus of the LNR modules to the transmembrane domain, such sequences including the HD domain (HD-N and HD-C). Exemplary Notch1 NRRs consist of the region from about amino acid 1446 to about amino acid 1735 of the human Notch1 amino acid sequence (SEQ ID NO:1, Figure 1), and the region from about amino acid 1446 to about amino acid 1725 of the mouse Notch1 amino acid sequence (SEQ ID NO:2, Figure 1). The term "native sequence Notch1 NRR" specifically encompasses naturally occurring truncated forms, naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of a Notch1 NRR. The term "wild-type Notch1 NRR" generally refers to a naturally occurring, non-mutated Notch1 NRR. In some embodiments, a Notch1 NRR is contained in a Notch1, such as, for example, a Notch1 processed at the S1, S2 and/or S3 site(s), or an unprocessed Notch1. In some embodiments, a Notch1 NRR contains two or more non-covalently linked fragments of a Notch1 NRR amino acid sequence, e.g., a fragment containing amino acids 1446 to 1664 of SEQ ID NO:1 non-covalently linked to a fragment containing amino acids 1665 to 1735 of SEQ ID NO:1. In another embodiment, a fragment containing amino acids 1446 to 1654 of SEQ ID NO:2 is non-covalently linked to a fragment containing amino acids 1655 to 1725 of SEQ ID NO:2.

The term "increased Notch1 signaling," as used herein, refers to an increase in Notch1 signaling that is significantly above the level of Notch1 signaling observed in a control under substantially identical conditions. In certain embodiments, the increase in Notch1 signaling is at least two fold, three fold, four fold, five fold, or ten fold above the level observed in the control.

The term "decreased Notch1 signaling," as used herein, refers to a decrease in Notch1 signaling that is significantly below the level of Notch1 signaling observed in a control under substantially identical conditions. In certain embodiments, the decrease in Notch1 signaling is at least two fold, three fold, four fold, five fold, or ten fold below the level observed in the control.

In certain embodiments, Notch1 signaling (i.e., increased or decreased Notch1 signaling) is assessed using a suitable reporter assay, e.g, as described in Example 5 of U.S.

Patent Application Publication No. US 2009/0081238 A1. In certain embodiments, Notch1 signaling is assessed using an in vitro activity assay, such as the C2C12 myoblast differentiation assay or the HUVEC cell sprouting assay, as described in Examples 5 and 7, respectively, of US 2009/0081238 A1. In certain embodiments, Notch1 signaling is assessed using an in vivo xenograft model, such as the Calu6 and HM7 models described in Example 8 of US 2009/0081238 A1.

The terms "Notch1 activating mutation" and "mutation that activates Notch1 signaling" refer to an insertion of one or more amino acids, a deletion of one or more amino acids, or a substitution of one or more amino acids relative to a Notch1 wild-type amino acid sequence that results in increased Notch1 signaling as compared with Notch1 signaling from the corresponding Notch1 wild-type amino acid sequence, or to an insertion of one or more nucleotides, a deletion of one or more nucleotides, a translocation of one or more nucleotides, or a substitution of one or more nucleotides relative to a Notch1 wild-type nucleic acid sequence that results in increased Notch1 signaling in a cell containing the mutant nucleic acid sequence as compared with Notch1 signaling in a cell containing the corresponding Notch1 wild-type nucleic acid sequence. Notch1 signaling from a Notch1 receptor containing an activating mutation may be ligand dependent or ligand independent.

The term "anti-Notch1 antibody" or "an antibody that binds to Notch1" refers to an antibody that is capable of binding Notch1 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting Notch1. Preferably, the extent of binding of an anti-Notch1 antibody to an unrelated, non-Notch protein is less than about 10% of the binding of the antibody to Notch1 as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to Notch1 has a dissociation constant (Kd) of $\leq$ 1μM, $\leq$ 0.5 μM, $\leq$ 100 nM, $\leq$ 50 nM, $\leq$ 10 nM, $\leq$ 5 nM, $\leq$ 1 nM, $\leq$ 0.5 nM, or $\leq$ 0.1 nM. In certain embodiments, an anti-Notch1 antibody binds to an epitope of Notch1 that is conserved among Notch1 from different species, e.g., rodents (mice, rats) and primates.

The term "anti-Notch1 NRR antibody" or "an antibody that binds to Notch1 NRR" refers to an antibody that is capable of binding Notch1 NRR with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting Notch1. Preferably, the extent of binding of an anti-Notch1 NRR antibody antibody to an unrelated, non-Notch protein is less than about 10% of the binding of the antibody to Notch1 NRR as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to Notch1 NRR has a dissociation constant (Kd) of $\leq$ 1μM, $\leq$ 0.5 μM, $\leq$ 100 nM, $\leq$ 50

nM, ≤ 10 nM, ≤ 5 nM, ≤ 1 nM, ≤ 0.5 nM, or ≤ 0.1 nM. In certain embodiments, an anti-Notch1 NRR antibody binds to an epitope of Notch that is conserved among Notch from different species, e.g., rodents (mice, rats) and primates.

The term "Notch1-specific antagonist" refers to an agent that effects decreased Notch1 signaling, as defined above, and does not significantly affect signaling by another Notch receptor (Notch2, 3, or 4 in mammals).

An "anti-Notch1 antagonist antibody" is an anti-Notch1 antibody (including an anti-Notch1 NRR antibody) that effects decreased Notch1 signaling, as defined above.

Reference to "Antibody A, A-1, A-2, and A-3," singly or in any combination, means the heavy and light chain variable regions of the phage and reformatted antibodies designated Antibody A, A-1, A-2, and A-3 in U.S. Patent Application Publication No. US 2009/0081238 A1, unless otherwise indicated.

The term "Notch3," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) Notch3 polypeptide. The term "native sequence" specifically encompasses naturally occurring truncated forms (e.g., an extracellular domain sequence or a transmembrane subunit sequence), naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants. The term "wild-type Notch3" generally refers to a polypeptide comprising an amino acid sequence of a naturally occurring, non-mutated Notch3 protein. The term "wild type Notch3 sequence" generally refers to an amino acid sequence found in a naturally occurring, non-mutated Notch3.

The term "Notch3 ligand," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) Notch3 ligand (for example, Jagged1, Jagged2, Delta-like1, Delta-like3, and/or Delta-like4) polypeptide. The term "native sequence" specifically encompasses naturally occurring truncated forms (e.g., an extracellular domain sequence or a transmembrane subunit sequence), naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants. The term "wild-type Notch3 ligand" generally refers to a polypeptide comprising an amino acid sequence of a naturally occurring, non-mutated Notch3 ligand. The term "wild type Notch3 ligand sequence" generally refers to an amino acid sequence found in a naturally occurring, non-mutated Notch3 ligand.

The term "activated Notch3 ICD" refers to the Notch3 cleavage product that results from cleavage at site S3 and that is capable of translocating to the nucleus. In certain

embodiments, activated Notch3 ICD consists of amino acids 1662-2321 of human Notch3 (SEQ ID NO:3).

The term "Notch3 NRR," as used herein, refers, unless specifically or contextually indicated otherwise, to any native or variant (whether native or synthetic) polypeptide region of Notch3 consisting of the 3 LNR modules and the amino acid sequences extending from the carboxy-terminus of the LNR modules to the transmembrane domain, such sequences including the HD domain (HD-N and HD-C). Exemplary Notch3 NRRs consist of the region from about amino acid 1384 to about amino acid 1640 of the human Notch3 amino acid sequence (SEQ ID NO:3, Figure 2). The term "native sequence Notch3 NRR" specifically encompasses naturally occurring truncated forms, naturally occurring variant forms (e.g., alternatively spliced forms) and naturally-occurring allelic variants of a Notch3 NRR. The term "wild-type Notch3 NRR" generally refers to a naturally occurring, non-mutated Notch3 NRR. In some embodiments, a Notch3 NRR is contained in a Notch3, such as, for example, a Notch3 processed at the S1, S2 and/or S3 site(s), or an unprocessed Notch3. In some embodiments, a Notch3 NRR contains two or more non-covalently linked fragments of a Notch3 NRR amino acid sequence, e.g., a fragment containing amino acids 1384 to 1571 of human Notch3 (SEQ ID NO:3) non-covalently linked to a fragment containing amino acids 1572 to 1640 of human Notch3 (SEQ ID NO:3).

The term "increased Notch3 signaling," as used herein refers to an increase in Notch3 signaling that is significantly above the level of Notch3 signaling observed in a control under substantially identical conditions. In certain embodiments, the increase in Notch3 signaling is at least two fold, three fold, four fold, five fold, or ten fold above the level observed in the control.

The term "decreased Notch3 signaling," as used herein refers to a decrease in Notch3 signaling that is significantly below the level of Notch3 signaling observed in a control under substantially identical conditions. In certain embodiments, the decrease in Notch3 signaling is at least two fold, three fold, four fold, five fold, or ten fold below the level observed in the control.

In certain embodiments, Notch3 signaling (i.e., increased or decreased Notch3 signaling) is assessed using a suitable reporter assay, e.g, as described in Example 5 of U.S. Patent Application Publication No. US 2008/0226621 A1. In certain embodiments, Notch3 signaling is assessed using an in vitro activity assay, such as the apoptosis, cell migration, invasion, and morphology assays described in Example 7 of U.S. Patent Application

Publication No. US 2008/0226621 A1. In certain embodiments, Notch3 signaling is assessed using an in vivo xenograft model, such as those described in Example 11 of US 2008/0226621 A1.

The term "anti-Notch3 antibody" or "an antibody that binds to Notch3" refers to an antibody that is capable of binding Notch3 with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting Notch3. Preferably, the extent of binding of an anti-Notch3 antibody to an unrelated, non-Notch protein is less than about 10% of the binding of the antibody to Notch3 as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to Notch3 NRR has a dissociation constant (Kd) of $\leq$ 1μM, $\leq$ 0.5 μM, $\leq$ 100 nM, $\leq$ 50 nM, $\leq$ 10 nM, $\leq$ 5 nM, $\leq$ 1 nM, $\leq$ 0.5 nM, or $\leq$ 0.1 nM. In certain embodiments, an anti-Notch3 antibody binds to an epitope of Notch3 that is conserved among Notch3 from different species, e.g., rodents (mice, rats) and primates.

The term "anti-Notch3 NRR antibody" or "an antibody that binds to Notch3 NRR" refers to an antibody that is capable of binding Notch3 NRR with sufficient affinity such that the antibody is useful as a diagnostic and/or therapeutic agent in targeting Notch3. Preferably, the extent of binding of an anti-Notch3 NRR antibody to an unrelated, non-Notch protein is less than about 10% of the binding of the antibody to Notch3 NRR as measured, e.g., by a radioimmunoassay (RIA). In certain embodiments, an antibody that binds to Notch3 NRR has a dissociation constant (Kd) of $\leq$ 1μM, $\leq$ 0.5 μM, $\leq$ 100 nM, $\leq$ 50 nM, $\leq$ 10 nM, $\leq$ 5 nM, $\leq$ 1 nM, $\leq$ 0.5 nM, or $\leq$ 0.1 nM. In certain embodiments, an anti-Notch3 NRR antibody binds to an epitope of Notch3 that is conserved among Notch3 from different species, e.g., rodents (mice, rats) and primates.

The term "Notch3-specific antagonist" refers to an agent that effects decreased Notch3 signaling, as defined above, and does not significantly affect signaling by another Notch receptor (Notch1, 2, or 4 in mammals).

An "anti-Notch3 antagonist antibody" is an anti-Notch3 antibody (including an anti-Notch3 NRR antibody) that effects decreased Notch3 signaling, as defined above.

Reference to "antibody 256A-4 and 256A-8," singly or in combination, means the mouse monoclonal antibodies designated 256A-4 and 256A-8 in U.S. Patent Application Publication No. 2008/0226621 A1.

The term "antagonist" refers to an agent that significantly inhibits (either partially or completely) the biological activity of a target molecule.

An "antibody that binds activated Notch3 ICD" refers to an antibody that binds activated Notch3 ICD such that the antibody is useful in distinguishing activated Notch3 ICD from Notch3 comprising an intact NTM.

The term "antibody" herein is used in the broadest sense and specifically covers monoclonal antibodies, polyclonal antibodies, multispecific antibodies (*e.g.* bispecific antibodies) formed from at least two intact antibodies, and antibody fragments so long as they exhibit the desired biological activity.

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with research, diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In some embodiments, an antibody is purified (1) to greater than 95% by weight of antibody as determined by, for example, the Lowry method, and in some embodiments, to greater than 99% by weight; (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of, for example, a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using, for example, Coomassie blue or silver stain. Isolated antibody includes the antibody *in situ* within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

"Native antibodies" are usually heterotetrameric glycoproteins of about 150,000 daltons, composed of two identical light (L) chains and two identical heavy (H) chains. Each light chain is linked to a heavy chain by one covalent disulfide bond, while the number of disulfide linkages varies among the heavy chains of different immunoglobulin isotypes. Each heavy and light chain also has regularly spaced intrachain disulfide bridges. Each heavy chain has at one end a variable domain (V_H) followed by a number of constant domains. Each light chain has a variable domain at one end (V_L) and a constant domain at its other end; the constant domain of the light chain is aligned with the first constant domain of the heavy chain, and the light chain variable domain is aligned with the variable domain of the heavy chain. Particular amino acid residues are believed to form an interface between the light chain and heavy chain variable domains.

The "variable region" or "variable domain" of an antibody refers to the amino-terminal domains of the heavy or light chain of the antibody. The variable domain of the

heavy chain may be referred to as "VH." The variable domain of the light chain may be referred to as "VL." These domains are generally the most variable parts of an antibody and contain the antigen-binding sites.

The term "variable" refers to the fact that certain portions of the variable domains differ extensively in sequence among antibodies and are used in the binding and specificity of each particular antibody for its particular antigen. However, the variability is not evenly distributed throughout the variable domains of antibodies. It is concentrated in three segments called hypervariable regions (HVRs) both in the light-chain and the heavy-chain variable domains. The more highly conserved portions of variable domains are called the framework regions (FR). The variable domains of native heavy and light chains each comprise four FR regions, largely adopting a beta-sheet configuration, connected by three HVRs, which form loops connecting, and in some cases forming part of, the beta-sheet structure. The HVRs in each chain are held together in close proximity by the FR regions and, with the HVRs 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*, Fifth Edition, National Institute of Health, Bethesda, MD (1991)). The constant domains are not involved directly in the binding of an antibody to an antigen, but exhibit various effector functions, such as participation of the antibody in antibody-dependent cellular toxicity.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa (κ) and lambda (λ), based on the amino acid sequences of their constant domains.

Depending on the amino acid sequences of the constant domains of their heavy chains, antibodies (immunoglobulins) can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG_1, IgG_2, IgG_3, IgG_4, IgA_1, and IgA_2 . The heavy chain constant domains that correspond to the different classes of immunoglobulins are called α, δ, ε, γ, and μ, respectively. The subunit structures and three-dimensional configurations of different classes of immunoglobulins are well known and described generally in, for example, Abbas et al. *Cellular and Mol. Immunology*, 4th ed. (W.B. Saunders, Co., 2000). An antibody may be part of a larger fusion molecule, formed by covalent or non-covalent association of the antibody with one or more other proteins or peptides.

The terms "full length antibody," "intact antibody" and "whole antibody" are used herein interchangeably to refer to an antibody in its substantially intact form, not antibody

fragments as defined below. The terms particularly refer to an antibody with heavy chains that contain an Fc region.

A "naked antibody" for the purposes herein is an antibody that is not conjugated to a cytotoxic moiety or radiolabel.

"Antibody fragments" comprise a portion of an intact antibody, preferably comprising the antigen binding region thereof. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies; single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, whose name reflects its ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-binding site. In one embodiment, a two-chain Fv species consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. In a single-chain Fv (scFv) species, one heavy- and one light-chain variable domain can be covalently linked by a flexible peptide linker such that the light and heavy chains can associate in a "dimeric" structure analogous to that in a two-chain Fv species. It is in this configuration that the three HVRs of each variable domain interact to define an antigen-binding site on the surface of the VH-VL dimer. Collectively, the six HVRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three HVRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment contains the heavy- and light-chain variable domains and also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab' fragments differ from Fab fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

"Single-chain Fv" or "scFv" antibody fragments comprise the VH and VL domains of antibody, wherein these domains are present in a single polypeptide chain. Generally, the

scFv polypeptide further comprises a polypeptide linker between the VH and VL domains which enables the scFv to form the desired structure for antigen binding. For a review of scFv, see, *e.g.*, Pluckthün, in *The Pharmacology of Monoclonal Antibodies*, vol. 113, Rosenburg and Moore eds., (Springer-Verlag, New York, 1994), pp. 269-315.

The term "diabodies" refers to antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain (VH) connected to a light-chain variable domain (VL) in the same polypeptide chain (VH-VL). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies may be bivalent or bispecific. Diabodies are described more fully in, for example, EP 404,097; WO 1993/01161; Hudson et al., *Nat. Med.* 9:129-134 (2003); and Hollinger et al., *Proc. Natl. Acad. Sci. USA* 90: 6444-6448 (1993). Triabodies and tetrabodies are also described in Hudson et al., *Nat. Med.* 9:129-134 (2003).

The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible mutations, e.g., naturally occurring mutations, that may be present in minor amounts. Thus, the modifier "monoclonal" indicates the character of the antibody as not being a mixture of discrete antibodies. In certain embodiments, such a monoclonal antibody typically includes an antibody comprising a polypeptide sequence that binds a target, wherein the target-binding polypeptide sequence was obtained by a process that includes the selection of a single target binding polypeptide sequence from a plurality of polypeptide sequences. For example, the selection process can be the selection of a unique clone from a plurality of clones, such as a pool of hybridoma clones, phage clones, or recombinant DNA clones. It should be understood that a selected target binding sequence can be further altered, for example, to improve affinity for the target, to humanize the target binding sequence, to improve its production in cell culture, to reduce its immunogenicity *in vivo*, to create a multispecific antibody, etc., and that an antibody comprising the altered target binding sequence is also a monoclonal antibody of this invention. In contrast to polyclonal antibody preparations, which typically include different antibodies directed against different determinants (epitopes), each monoclonal antibody of a monoclonal antibody preparation is directed against a single determinant on an antigen. In addition to their specificity, monoclonal antibody preparations are advantageous in that they are typically uncontaminated by other immunoglobulins.

The modifier "monoclonal" indicates the character of the antibody as being obtained from a substantially homogeneous population of antibodies, and is not to be construed as requiring production of the antibody by any particular method. For example, the monoclonal antibodies to be used in accordance with the present invention may be made by a variety of techniques, including, for example, the hybridoma method (e.g., Kohler and Milstein, *Nature*, 256:495-97 (1975); Hongo *et al.*, *Hybridoma*, 14 (3): 253-260 (1995), Harlow *et al.*, *Antibodies: A Laboratory Manual*, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling *et al.*, in: *Monoclonal Antibodies and T-Cell Hybridomas* 563-681 (Elsevier, N.Y., 1981)), recombinant DNA methods (see, e.g., U.S. Patent No. 4,816,567), phage-display technologies (see, e.g., Clackson *et al.*, *Nature*, 352: 624-628 (1991); Marks *et al.*, *J. Mol. Biol.* 222: 581-597 (1992); Sidhu *et al.*, *J. Mol. Biol.* 338(2): 299-310 (2004); Lee *et al.*, *J. Mol. Biol.* 340(5): 1073-1093 (2004); Fellouse, *Proc. Natl. Acad. Sci. USA* 101(34): 12467-12472 (2004); and Lee *et al.*, *J. Immunol. Methods* 284(1-2): 119-132(2004), and technologies for producing human or human-like antibodies in animals that have parts or all of the human immunoglobulin loci or genes encoding human immunoglobulin sequences (see, e.g., WO 1998/24893; WO 1996/34096; WO 1996/33735; WO 1991/10741; Jakobovits *et al.*, *Proc. Natl. Acad. Sci. USA* 90: 2551 (1993); Jakobovits *et al.*, *Nature* 362: 255-258 (1993); Bruggemann *et al.*, *Year in Immunol.* 7:33 (1993); U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; and 5,661,016; Marks *et al.*, *Bio/Technology* 10: 779-783 (1992); Lonberg et al., *Nature* 368: 856-859 (1994); Morrison, *Nature* 368: 812-813 (1994); Fishwild *et al.*, *Nature Biotechnol.* 14: 845-851 (1996); Neuberger, *Nature Biotechnol.* 14: 826 (1996); and Lonberg and Huszar, *Intern. Rev. Immunol.* 13: 65-93 (1995).

The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired biological activity (see, *e.g.*,U.S. Patent No. 4,816,567; and Morrison *et al., Proc. Natl. Acad. Sci. USA* 81:6851-6855 (1984)). Chimeric antibodies include PRIMATIZED® antibodies wherein the antigen-binding region of the antibody is derived from an antibody produced by, e.g., immunizing macaque monkeys with the antigen of interest.

"Humanized" forms of non-human (*e.g.,* murine) antibodies are chimeric antibodies that contain minimal sequence derived from non-human immunoglobulin. In one embodiment, a humanized antibody is a human immunoglobulin (recipient antibody) in which residues from a HVR of the recipient are replaced by residues from a HVR of a non-human species (donor antibody) such as mouse, rat, rabbit, or nonhuman primate having the desired specificity, affinity, and/or capacity. In some instances, FR residues of the human immunoglobulin are replaced by corresponding non-human residues. Furthermore, humanized antibodies may comprise residues that are not found in the recipient antibody or in the donor antibody. These modifications may be made to further refine antibody performance. 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 hypervariable loops correspond to those of a non-human immunoglobulin, and all or substantially all of the FRs are those of a human immunoglobulin sequence. The humanized antibody optionally will also comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin. For further details, see, *e.g.*, Jones *et al., Nature* 321:522-525 (1986); Riechmann *et al., Nature* 332:323-329 (1988); and Presta, *Curr. Op. Struct. Biol.* 2:593-596 (1992). See also, *e.g.*, Vaswani and Hamilton, *Ann. Allergy, Asthma & Immunol.* 1:105-115 (1998); Harris, *Biochem. Soc. Transactions* 23:1035-1038 (1995); Hurle and Gross, *Curr. Op. Biotech.* 5:428-433 (1994); and U.S. Pat. Nos. 6,982,321 and 7,087,409.

A "human antibody" is one which possesses an amino acid sequence which corresponds to that of an antibody produced by a human and/or has been made using any of the techniques for making human antibodies as disclosed herein. This definition of a human antibody specifically excludes a humanized antibody comprising non-human antigen-binding residues. Human antibodies can be produced using various techniques known in the art, including phage-display libraries. Hoogenboom and Winter, *J. Mol. Biol.*, 227:381 (1991); Marks *et al.*, *J. Mol. Biol.*, 222:581 (1991). Also available for the preparation of human monoclonal antibodies are methods described in Cole *et al.*, *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, p. 77 (1985); Boerner *et al.*, *J. Immunol.*, 147(1):86-95 (1991). See also van Dijk and van de Winkel, *Curr. Opin. Pharmacol.,* 5: 368-74 (2001). Human antibodies can be prepared by administering the antigen to a transgenic animal that has been modified to produce such antibodies in response to antigenic challenge, but whose endogenous loci have been disabled, *e.g.*, immunized xenomice (see, *e.g.*, U.S. Pat. Nos. 6,075,181 and 6,150,584 regarding XENOMOUSE™ technology). See also, for example, Li

et al., Proc. Natl. Acad. Sci. USA, 103:3557-3562 (2006) regarding human antibodies generated via a human B-cell hybridoma technology.

The term "hypervariable region," "HVR," or "HV," when used herein refers to the regions of an antibody variable domain which are hypervariable in sequence and/or form structurally defined loops. Generally, antibodies comprise six HVRs; three in the VH (H1, H2, H3), and three in the VL (L1, L2, L3). In native antibodies, H3 and L3 display the most diversity of the six HVRs, and H3 in particular is believed to play a unique role in conferring fine specificity to antibodies. See, *e.g.*, Xu et al., *Immunity* 13:37-45 (2000); Johnson and Wu, in *Methods in Molecular Biology* 248:1-25 (Lo, ed., Human Press, Totowa, NJ, 2003). Indeed, naturally occurring camelid antibodies consisting of a heavy chain only are functional and stable in the absence of light chain. See, *e.g.*, Hamers-Casterman et al., *Nature* 363:446-448 (1993); Sheriff et al., *Nature Struct. Biol.* 3:733-736 (1996).

A number of HVR delineations are in use and are encompassed herein. The Kabat Complementarity Determining Regions (CDRs) are based on sequence variability and are the most commonly used (Kabat *et al., Sequences of Proteins of Immunological Interest*, 5th Ed. Public Health Service, National Institutes of Health, Bethesda, MD. (1991)). Chothia refers instead to the location of the structural loops (Chothia and Lesk *J. Mol. Biol.* 196:901-917 (1987)). The AbM HVRs represent a compromise between the Kabat HVRs and Chothia structural loops, and are used by Oxford Molecular's AbM antibody modeling software. The "contact" HVRs are based on an analysis of the available complex crystal structures. The residues from each of these HVRs are noted below.

Loop	Kabat	AbM	Chothia	Contact
L1	L24-L34	L24-L34	L26-L32	L30-L36
L2	L50-L56	L50-L56	L50-L52	L46-L55
L3	L89-L97	L89-L97	L91-L96	L89-L96
H1	H31-H35B	H26-H35B	H26-H32	H30-H35B
	(Kabat Numbering)			
H1	H31-H35	H26-H35	H26-H32	H30-H35
	(Chothia Numbering)			
H2	H50-H65	H50-H58	H53-H55	H47-H58
H3	H95-H102	H95-H102	H96-H101	H93-H101

HVRs may comprise "extended HVRs" as follows: 24-36 or 24-34 (L1), 46-56 or 50-56 (L2) and 89-97 or 89-96 (L3) in the VL and 26-35 (H1), 50-65 or 49-65 (H2) and 93-102, 94-102, or 95-102 (H3) in the VH. The variable domain residues are numbered according to Kabat et al., supra, for each of these definitions.

"Framework" or "FR" residues are those variable domain residues other than the HVR residues as herein defined.

The term "variable domain residue numbering as in Kabat" or "amino acid position numbering as in Kabat," and variations thereof, refers to the numbering system used for heavy chain variable domains or light chain variable domains of the compilation of antibodies in Kabat et al., *supra*. Using this numbering system, the actual linear amino acid sequence may contain fewer or additional amino acids corresponding to a shortening of, or insertion into, a FR or HVR of the variable domain. For example, a heavy chain variable domain may include a single amino acid insert (residue 52a according to Kabat) after residue 52 of H2 and inserted residues (e.g. residues 82a, 82b, and 82c, etc. according to Kabat) after heavy chain FR residue 82. The Kabat numbering of residues may be determined for a given antibody by alignment at regions of homology of the sequence of the antibody with a "standard" Kabat numbered sequence.

The Kabat numbering system is generally used when referring to a residue in the variable domain (approximately residues 1-107 of the light chain and residues 1-113 of the heavy chain) (e.g, Kabat *et al.*, *supra*). The "EU numbering system" or "EU index" is generally used when referring to a residue in an immunoglobulin heavy chain constant region (e.g., the EU index reported in Kabat *et al., supra*). The "EU index as in Kabat" refers to the residue numbering of the human IgG1 EU antibody. Unless stated otherwise herein, references to residue numbers in the variable domain of antibodies means residue numbering by the Kabat numbering system. Unless stated otherwise herein, references to residue numbers in the constant domain of antibodies means residue numbering by the EU numbering system (e.g., see United States Patent Application Publication US 2008/0181888 A1, Figures for EU numbering).

An "affinity matured" antibody is one with one or more alterations in one or more HVRs thereof which result in an improvement in the affinity of the antibody for antigen, compared to a parent antibody which does not possess those alteration(s). In one embodiment, an affinity matured antibody has nanomolar or even picomolar affinities for the target antigen. Affinity matured antibodies may be produced using certain procedures known

in the art. For example, Marks *et al. Bio/Technology* 10:779-783 (1992) describe affinity maturation by VH and VL domain shuffling. Random mutagenesis of HVR and/or framework residues is described by, for example, in Barbas *et al. Proc Nat. Acad. Sci. USA* 91:3809-3813 (1994); Schier *et al. Gene* 169:147-155 (1995); Yelton *et al. J. Immunol.* 155:1994-2004 (1995); Jackson *et al., J. Immunol.* 154(7):3310-9 (1995); and Hawkins *et al, J. Mol. Biol.* 226:889-896 (1992).

Antibody "effector functions" refer to those biological activities attributable to the Fc region (a native sequence Fc region or amino acid sequence variant Fc region) of an antibody, and vary with the antibody isotype. Examples of antibody effector functions include: C1q binding and complement dependent cytotoxicity (CDC); Fc receptor binding; antibody-dependent cell-mediated cytotoxicity (ADCC); phagocytosis; down regulation of cell surface receptors (*e.g.* B cell receptor); and B cell activation.

"Binding affinity" generally refers to the strength of the sum total of noncovalent interactions between a single binding site of a molecule (*e.g.*, an antibody) and its binding partner (*e.g.*, an antigen). Unless indicated otherwise, as used herein, "binding affinity" refers to intrinsic binding affinity which reflects a 1:1 interaction between members of a binding pair (*e.g.*, antibody and antigen). The affinity of a molecule X for its partner Y can generally be represented by the dissociation constant (Kd). Affinity can be measured by common methods known in the art, including those described herein. Low-affinity antibodies generally bind antigen slowly and tend to dissociate readily, whereas high-affinity antibodies generally bind antigen faster and tend to remain bound longer. A variety of methods of measuring binding affinity are known in the art, any of which can be used for purposes of the present invention. Specific illustrative and exemplary embodiments for measuring binding affinity are described in the following.

In one embodiment, the "Kd" or "Kd value" according to this invention is measured by a radiolabeled antigen binding assay (RIA) performed with the Fab version of an antibody of interest and its antigen as described by the following assay. Solution binding affinity of Fabs for antigen is measured by equilibrating Fab with a minimal concentration of (^{125}I)-labeled antigen in the presence of a titration series of unlabeled antigen, then capturing bound antigen with an anti-Fab antibody-coated plate (see, *e.g.*, Chen, et al., *J. Mol. Biol.* 293:865-881(1999)). To establish conditions for the assay, MICROTITER® multi-well plates (Thermo Scientific) are coated overnight with 5 μg/ml of a capturing anti-Fab antibody (Cappel Labs) in 50 mM sodium carbonate (pH 9.6), and subsequently blocked with 2% (w/v) bovine serum

albumin in PBS for two to five hours at room temperature (approximately 23°C). In a non-adsorbent plate (Nunc #269620), 100 pM or 26 pM [^{125}I]-antigen are mixed with serial dilutions of a Fab of interest (*e.g.*, consistent with assessment of the anti-VEGF antibody, Fab-12, in Presta *et al.*, *Cancer Res.* 57:4593-4599 (1997)). The Fab of interest is then incubated overnight; however, the incubation may continue for a longer period (e.g., about 65 hours) to ensure that equilibrium is reached. Thereafter, the mixtures are transferred to the capture plate for incubation at room temperature (e.g., for one hour). The solution is then removed and the plate washed eight times with 0.1% TWEEN-20™ in PBS. When the plates have dried, 150 µl/well of scintillant (MICROSCINT-20 ™; Packard) is added, and the plates are counted on a TOPCOUNT ™ gamma counter (Packard) for ten minutes. Concentrations of each Fab that give less than or equal to 20% of maximal binding are chosen for use in competitive binding assays.

According to another embodiment, the Kd or Kd value is measured by using surface plasmon resonance assays using a BIACORE®-2000 or a BIACORE ®-3000 (BIAcore, Inc., Piscataway, NJ) at 25°C with immobilized antigen CM5 chips at ~10 response units (RU). Briefly, carboxymethylated dextran biosensor chips (CM5, BIACORE, Inc.) are activated with *N*-ethyl-*N'*- (3-dimethylaminopropyl)-carbodiimide hydrochloride (EDC) and *N*-hydroxysuccinimide (NHS) according to the supplier's instructions. Antigen is diluted with 10 mM sodium acetate, pH 4.8, to 5 µg/ml (~0.2 µM) before injection at a flow rate of 5 µl/minute to achieve approximately 10 response units (RU) of coupled protein. Following the injection of antigen, 1 M ethanolamine is injected to block unreacted groups. For kinetics measurements, two-fold serial dilutions of Fab (0.78 nM to 500 nM) are injected in PBS with 0.05% TWEEN-20™ surfactant (PBST) at 25°C at a flow rate of approximately 25 µl/min. Association rates (k_{on}) and dissociation rates (k_{off}) are calculated using a simple one-to-one Langmuir binding model (BIACORE ® Evaluation Software version 3.2) by simultaneously fitting the association and dissociation sensorgrams. The equilibrium dissociation constant (Kd) is calculated as the ratio k_{off}/k_{on}. See, *e.g.*, Chen et al., *J. Mol. Biol.* 293:865-881 (1999). If the on-rate exceeds 10^6 M^{-1} s^{-1} by the surface plasmon resonance assay above, then the on-rate can be determined by using a fluorescent quenching technique that measures the increase or decrease in fluorescence emission intensity (excitation = 295 nm; emission = 340 nm, 16 nm band-pass) at 25°C of a 20 nM anti-antigen antibody (Fab form) in PBS, pH 7.2, in the presence of increasing concentrations of antigen as measured in a spectrometer,

such as a stop-flow equipped spectrophometer (Aviv Instruments) or a 8000-series SLM-AMINCO ™ spectrophotometer (ThermoSpectronic) with a stirred cuvette.

An "on-rate," "rate of association," "association rate," or "k_{on}" according to this invention can also be determined as described above using a BIACORE ®-2000 or a BIACORE ®-3000 system (BIAcore, Inc., Piscataway, NJ).

A "disorder" is any condition or disease that would benefit from treatment with a composition or method of the invention. This includes chronic and acute disorders including those pathological conditions which predispose the mammal to the disorder in question. Non-limiting examples of disorders to be treated herein include conditions such as cancer.

The terms "cell proliferative disorder" and "proliferative disorder" refer to disorders that are associated with some degree of abnormal cell proliferation. In one embodiment, the cell proliferative disorder is cancer.

"Tumor," as used herein, refers to all neoplastic cell growth and proliferation, whether malignant or benign, and all pre-cancerous and cancerous cells and tissues. The terms "cancer," "cancerous," "cell proliferative disorder," "proliferative disorder," and "tumor" are not mutually exclusive as referred to herein.

The terms "cancer" and "cancerous" refer to or describe the physiological condition in mammals that is typically characterized by unregulated cell growth/proliferation. Examples of cancer include but are not limited to, carcinoma, lymphoma, blastoma, sarcoma, and leukemia. More particular examples of such cancers include squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, adenocarcinoma of the lung, squamous carcinoma of the lung, cancer of the peritoneum, hepatocellular cancer, gastrointestinal cancer, pancreatic cancer, glioblastoma, cervical cancer, ovarian cancer, liver cancer, bladder cancer, hepatoma, breast cancer, colon cancer, colorectal cancer, endometrial or uterine carcinoma, salivary gland carcinoma, kidney cancer, liver cancer, prostate cancer, vulval cancer, thyroid cancer, hepatic carcinoma, gastric cancer, melanoma, and various types of head and neck cancer. Dysregulation of angiogenesis can lead to many disorders that can be treated by compositions and methods of the invention. These disorders include both non-neoplastic and neoplastic conditions. Neoplastics include but are not limited those described above. Non-neoplastic disorders include but are not limited to undesired or aberrant hypertrophy, arthritis, rheumatoid arthritis (RA), psoriasis, psoriatic plaques, sarcoidosis, atherosclerosis, atherosclerotic plaques, diabetic and other proliferative retinopathies including retinopathy of prematurity, retrolental fibroplasia, neovascular glaucoma, age-related macular degeneration,

diabetic macular edema, corneal neovascularization, corneal graft neovascularization, corneal graft rejection, retinal/choroidal neovascularization, neovascularization of the angle (rubeosis), ocular neovascular disease, vascular restenosis, arteriovenous malformations (AVM), meningioma, hemangioma, angiofibroma, thyroid hyperplasias (including Grave's disease), corneal and other tissue transplantation, chronic inflammation, lung inflammation, acute lung injury/ARDS, sepsis, primary pulmonary hypertension, malignant pulmonary effusions, cerebral edema (e.g., associated with acute stroke/ closed head injury/ trauma), synovial inflammation, pannus formation in RA, myositis ossificans, hypertropic bone formation, osteoarthritis (OA), refractory ascites, polycystic ovarian disease, endometriosis, 3rd spacing of fluid diseases (pancreatitis, compartment syndrome, burns, bowel disease), uterine fibroids, premature labor, chronic inflammation such as IBD (Crohn's disease and ulcerative colitis), renal allograft rejection, inflammatory bowel disease, nephrotic syndrome, undesired or aberrant tissue mass growth (non-cancer), hemophilic joints, hypertrophic scars, inhibition of hair growth, Osler-Weber syndrome, pyogenic granuloma retrolental fibroplasias, scleroderma, trachoma, vascular adhesions, synovitis, dermatitis, preeclampsia, ascites, pericardial effusion (such as that associated with pericarditis), and pleural effusion.

The term "leukemia" refers to an acute or chronic disease characterized by an abnormal increase in the number of white blood cells (leukocytes) in hemopoietic tissues, other organs, and often in the blood. Leukemias include, but are not limited to, acute lymphoblastic leukemia (ALL), including T-lineage acute lymphoblastic leukemia (T-ALL) as well as other lymphocytic leukemias; adult T-cell leukemia/lymphoma; chronic myeloid (myelogenous) leukemia (CML), acute myeloid (myelogenous) leukemia (AML), and other granulocytic leukemias; and lineage switch leukemias.

The term "T-cell leukemia" refers to a leukemia characterized by an abnormal increase in the number of T-lineage lymphoblasts or T-lymphocytes.

The term "T-cell progenitor leukemia" refers to a leukemia characterized by an abnormal increase in the number of T-lineage lymphoblasts.

A "GSI-responsive cancer" is a cancer (such as a leukemia) that responds to a gamma secretase inhibitor or that would respond to a gamma secretase inhibitor if treated with such.

A cancer that "responds" to a therapeutic agent is one that shows a significant decrease in cancer or tumor progression, including but not limited to, (1) inhibition, to some extent, of tumor growth, including slowing down and complete growth arrest; (2) reduction in the number of cancer or tumor cells; (3) reduction in tumor size; (4) inhibition (i.e., reduction,

slowing down or complete stopping) of cancer cell infiltration into adjacent peripheral organs and/or tissues; and/or (5) inhibition (i.e. reduction, slowing down or complete stopping) of metastasis.

A cancer that "does not respond to a Notch1-specific antagonist" is a cancer that does not respond to treatment with a Notch1-specific antagonist (in the absence of any other Notch antagonist, i.e., a Notch2, Notch3 or Notch4 antagonist), or that would not respond to such treatment if given.

As used herein, "treatment" (and variations such as "treat" or "treating") refers to clinical intervention in an attempt to alter the natural course of the individual or cell being treated, and can be performed either for prophylaxis or during the course of clinical pathology. Desirable effects of treatment include preventing occurrence or recurrence of disease, alleviation of symptoms, diminishment of any direct or indirect pathological consequences of the disease, preventing metastasis, decreasing the rate of disease progression, amelioration or palliation of the disease state, and remission or improved prognosis. In some embodiments, antibodies of the invention are used to delay development of a disease or disorder or to slow the progression of a disease or disorder.

An "individual," "subject," or "patient" is a vertebrate. In certain embodiments, the vertebrate is a mammal. Mammals include, but are not limited to, farm animals (such as cows), sport animals, pets (such as cats, dogs, and horses), primates, mice and rats. In certain embodiments, a mammal is a human.

The term "pharmaceutical formulation" refers to a preparation which is in such form as to permit the biological activity of the active ingredient to be effective, and which contains no additional components which are unacceptably toxic to a subject to which the formulation would be administered. Such formulations may be sterile.

An "effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic or prophylactic result.

II. EMBODIMENTS OF THE INVENTION

The present invention relates, in part, to the characterization of different classes of T-ALL. One class of T-ALL is sensitive to treatment with GSI, which is a pan-Notch inhibitor, and is also sensitive to treatment with a Notch1-specific antagonist, indicating that Notch1 specifically drives this class of T-ALL. Another class of T-ALL is sensitive to treatment with GSI, but insensitive (i.e., resistant) to treatment with a Notch1-specific antagonist, indicating that an alternative or additional Notch receptor may drive this class of T-ALL. As shown

herein, the inventors have discovered that this latter class of T-ALL is partially sensitive to treatment with a Notch3-specific antagonist, and even more sensitive to a combination of a Notch1-specific antagonist and a Notch3-specific antagonist. These results suggest a role for both Notch1 and Notch3 in leukemias, particularly T-cell and T-cell progenitor leukemias such as T-ALL.

A. Methods of Treatment

1. Treatment of cancer with a Notch3-specific antagonist, singly or in combination with a Notch1-specific antagonist

In various aspects of the invention, methods of treating a GSI-responsive cancer are provided, the method comprising administering to a patient having such cancer an effective amount of a Notch3-specific antagonist. In certain embodiments, the GSI-responsive cancer is leukemia. In certain embodiments, the GSI-responsive cancer does not respond to a Notch1-specific antagonist, e.g., the cancer has significantly increased levels of activated Notch3 and/or the cancer has absent or reduced levels of activated Notch1. In a further embodiment, the method further comprises administering an effective amount of a Notch1-specific antagonist. These and further aspects of the invention are described below.

In a particular aspect of the invention, a method of treating a GSI-responsive leukemia that does not respond to a Notch1-specific antagonist is provided, the method comprising administering to a patient having such leukemia an effective amount of a Notch3-specific antagonist.

A GSI-responsive leukemia may be identified by various ways. For example, a patient having leukemia may be treated with a GSI to determine whether or not the leukemia is GSI-responsive. Such a GSI may include any GSI that significantly inhibits Notch receptors. Such a GSI includes, but is not limited to, N-[N-(3,5-difluorophenacetyl)-L-alanyl]-S-phenylglycine t-butyl ester (DAPT); dibenzazepine; MK-0752 (Merck); the tripeptide z-Leu-Leu-Nle-CHO (Curry et al., *Oncogene* 24:6333-6344); and cbz-IL-CHO (Weijzen et al., *Nat. Med.* 8:979-986, 2002). It is noted, however, that a patient having leukemia need not have been treated with a GSI in order to determine whether the leukemia is GSI-responsive. Other methods may be employed. For example, leukemic cells removed from the patient may be assessed for cell proliferation or survival in the presence of a GSI, such as any of those listed above. In a further example, leukemic cells removed from the patient may be examined for increased Notch signaling by one or more Notch receptors,

which would predict that the cells are GSI-responsive. For example, the cells may be assessed for the presence of a mutated, overexpresssed, or activated Notch receptor. Methods similar to those described above may be used to determine whether any cancer is GSI-responsive.

A leukemia (e.g., a GSI-responsive leukemia) may be identified as one that does not respond to a Notch1-specific antagonist by various ways. For example, a patient having a leukemia may be treated with a Notch1-specific antagonist to determine whether or not the leukemia responds to the Notch1-specific antagonist. In certain embodiments, the Notch1-specific antagonist to which a leukemia does not respond is an anti-Notch1 antagonist antibody. In one such embodiment, the anti-Notch1 antagonist antibody is an antibody that binds to the extracellular domain of Notch1 and effects decreased Notch1 signaling. In one such embodiment, the anti-Notch1 antagonist antibody is an anti-Notch1 NRR antibody. Anti-Notch1 NRR antibodies include, but are not limited to, any of the anti-Notch1 NRR antibodies disclosed in U.S. Application Publication No. US 2009/0081238 A1, which is expressly incorporated by reference herein in its entirety. Such antibodies include, but are not limited to, anti-Notch1 NRR antibodies that bind to Notch1 NRR with an affinity of ≤ 0.1 μM; anti-Notch1 NRR antibodies that bind to LNR-A, LNR-B and HD-C of the Notch1 NRR; or a combination of the foregoing. Exemplary anti-Notch1 NRR antibodies include but are not limited to Antibodies A, A-1, A-2, and A-3 as described in US 2009/0081238 A1, or antibodies comprising the heavy and light chain variable region CDRs of an antibody selected from Antibody A, A-1, A-2, and A-3. In another such embodiment, an anti-Notch1 antagonist antibody is an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1. Examples of such antibodies are described in International Publication No. WO 2008/091641. In certain embodiments, an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1 effects decreased Notch1 signaling by significantly blocking binding of ligand to Notch1.

It is noted, however, that a patient having leukemia need not have been treated with a Notch1-specific antagonist in order to determine whether the leukemia is one that does not respond to a Notch1-specific antagonist. Other methods may be employed. For example, leukemic cells removed from the patient may be assessed for absent or reduced Notch1 activation, or in certain embodiments, the presence of wild-type Notch1, which would predict that the leukemia is one that does not respond to a Notch1-specific antagonist. For example, the cells may be assessed for absent or reduced Notch1 signaling by assessing absent or

reduced transcription of Notch1 target genes, such as Hey1 and Hey2. In a further example, the cells may be assessed for absent or reduced Notch1 signaling by detecting absent or reduced levels of an activated form of Notch1, e.g., by using an antibody specific for activated Notch1 such as anti-active Notch1 Val1744 (commercially available from Cell Signaling Technologies). In certain embodiments, a suitable comparator cell (positive control) may be a leukemic cell that responds to a Notch1-specific antagonist, e.g., a leukemic cell in which the Notch1 pathway is activated. Such a comparator cell may include, e.g., a T-ALL cell in which Notch1 is known to be overexpressed, mutated (e.g., having a Notch1 activating mutation) or activated (e.g., constitutively activated), such as an HPB-ALL cell. If leukemic cells removed from a patient have absent or significantly reduced levels of activated Notch1 compared to the comparator cell, then the patient's leukemia is presumptively one that does not respond to a Notch1-specific antagonist.

Leukemic cells may also be assessed for activation of Notch3, indicating that the Notch3 pathway is activated and that the leukemia is therefore predicted to be one that does not respond to a Notch1-specific antagonist. In one embodiment, leukemic cells may be examined for the presence of overexpressed, mutated or activated Notch3. In certain embodiments, a suitable comparator cell (negative control) for purposes of assessing Notch3 activation status may be a leukemic cell that responds to a Notch1-specific antagonist, e.g., a leukemic cell in which the Notch1 pathway is activated. Such a comparator cell may include, e.g., a T-ALL cell in which Notch1 is known to be overexpressed, mutated or activated such as an HPB-ALL cell. In such a cell, Notch3 is not expected to be significantly activated. Therefore, if leukemic cells removed from a patient have significantly increased levels of activated Notch3 compared to the comparator cell, then the patient's leukemia is presumptively one that does not respond to a Notch1-specific antagonist. In certain other embodiments, a suitable comparator cell (positive control) may be a leukemic cell in which Notch3 is known to be overexpressed, mutated or activated, such as a TALL-1 cell. In such a cell, Notch3 is expected to have significantly increased levels of activated Notch3. Therefore, if leukemic cells removed from a patient have comparable levels of activated Notch3 compared to the comparator cell, then the patient's leukemia is presumptively one that does not respond to a Notch1-specific antagonist. Methods similar to those described above can be used to determine whether any cancer is one that does not respond to a Notch1-specific antagonist.

A useful tool for assessing Notch3 activation status is the new anti-Notch3 ICD antibody described in the Examples, which binds to activated Notch3 ICD.

In certain embodiments, the Notch3-specific antagonist that is administered is an anti-Notch3 antagonist antibody. In one such embodiment, the anti-Notch3 antagonist antibody is an antibody that binds to the extracellular domain of Notch3 and effects decreased Notch3 signaling. In one such embodiment, the anti-Notch3 antagonist antibody is an anti-Notch3 NRR antibody. Anti-Notch3 NRR antibodies include, but are not limited to, any of the anti-Notch3 NRR antibodies disclosed in U.S. Patent Application Publication No. US 2008/0226621 A1, which is expressly incorporated by reference herein in its entirety. Such antibodies include, but are not limited to anti-Notch3 NRR antibodies that bind to the LNR-A and HD-C domains of Notch3 NRR. Exemplary anti-Notch3 NRR antibodies are monoclonal antibodies 256A-4 and 256A-8, as described in US 2008/0226621 A1, and humanized forms thereof, as well as anti-Notch3 NRR antibodies comprising the heavy and light chain variable region CDRs of antibody 256A-4 or 256A-8. In another such embodiment, an anti-Notch3 antagonist antibody is an anti-Notch3 antibody that binds to one or more EGF-like repeats of Notch3. Examples of such antibodies are described in Li et al., *J. Biol. Chem.* 283:8046-8054, 2008. In certain embodiments, an anti-Notch3 antibody that binds to one or more EGF-like repeats of Notch3 effects decreased Notch3 signaling by significantly blocking binding of ligand to Notch3.

In certain embodiments, a leukemia is a T-cell leukemia. In certain such embodiments, a T-cell leukemia is a T-cell progenitor leukemia. In certain such embodiments, a T-cell progenitor leukemia is T-ALL.

In further embodiments, a method of treating a GSI-responsive cancer that does not respond to a Notch1-specific antagonist is provided, the method comprising administering to a patient having such cancer an effective amount of a Notch3-specific antagonist, and further comprising administering to such patient an effective amount of a Notch-1 specific antagonist. In certain embodiments, the GSI-responsive cancer is a GSI-responsive leukemia. In certain embodiments, the Notch1-specific antagonist to be administered is an anti-Notch1 antagonist antibody. In one such embodiment, the anti-Notch1 antagonist antibody is an antibody that binds to the extracellular domain of Notch1 and effects decreased Notch1 signaling. In one such embodiment, the anti-Notch1 antagonist antibody is an anti-Notch1 NRR antibody. Anti-Notch1 NRR antibodies include, but are not limited to, any of the anti-Notch1 NRR antibodies disclosed in U.S. Application Publication No. US 2009/0081238 A1,

which is expressly incorporated by reference herein. Such antibodies include, but are not limited to, anti-Notch1 NRR antibodies that bind to Notch1 NRR with an affinity of ≤ 0.1 μM; anti-Notch1 NRR antibodies that bind to LNR-A, LNR-B and HD-C of the Notch1 NRR; or a combination of the foregoing. Exemplary anti-Notch1 NRR antibodies include but are not limited to Antibodies A, A-1, A-2, and A-3 as described in US 2009/0081238 A1, or antibodies comprising the heavy and light chain variable region CDRs of an antibody selected from Antibody A, A-1, A-2, and A-3. In another such embodiment, the anti-Notch1 antagonist antibody is an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1. Examples of such antibodies are described in International Publication No. WO 2008/091641. In certain embodiments, an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1 effects decreased Notch1 signaling by significantly blocking binding of ligand to Notch1.

2. Treatment of leukemia with a Notch1-specific antagonist

Further aspects of the invention are based, in part, on the identification of a class of T-ALL that is responsive to GSI and is also responsive to a Notch1-specific antagonist, but is not responsive to a Notch3-specific antagonist, indicating that Notch1 drives the T-ALL. In various aspects of the invention, methods of treating a GSI-responsive cancer are provided, the method comprising administering to a patient having such cancer an effective amount of a Notch1-specific antagonist. In certain embodiments, the GSI-responsive cancer is leukemia. In certain embodiments, the GSI-responsive cancer does not respond to a Notch3-specific antagonist, e.g., the cancer has absent or reduced levels of activated Notch3 (e.g., as compared to a comparator cell that responds to a Notch3-specific antagonist) and/or has significantly increased levels of activated Notch1 (e.g., as compared to a comparator cell that does not respond to a Notch1-specific antagonist).

In certain embodiments, the leukemia belongs to a class of leukemias characterized by sensitivity to GSI and sensitivity to a Notch1-specific antagonist. In one embodiment, the leukemia is a T-cell leukemia. In one such embodiment, the T-cell leukemia is a T-cell progenitor leukemia. In one such embodiment, the T-cell leukemia is T-ALL. In another embodiment, the leukemia is characterized by a Notch1 activating mutation.

In certain embodiments, a Notch1-specific antagonist is any of those provided above. In further embodiments, a Notch3-specific antagonist is any of those provided above.

B. Compositions and Diagnostic Methods

The invention further provides an antibody that binds activated human Notch3 ICD. In one embodiment, the antibody binds to the peptide sequence VMVARRKREHSTLW (SEQ ID NO:4). In one embodiment, the antibody is monoclonal. In one embodiment, the antibody is polyclonal. The above embodiments may be present alone or in combination.

Such an antibody is useful in diagnostic methods, e.g., to identify patient populations suitable for treatment with a Notch3-specific antagonist, as described above. Accordingly, in certain embodiments, a method of identifying a cancer suitable for treatment with an antagonist of Notch3 is provided, the method comprising determining whether Notch3 is activated in the cancer. In one embodiment, the cancer is a GSI-responsive cancer. In another embodiment, the cancer is a leukemia. In another embodiment, the leukemia is a T-cell leukemia. In one such embodiment, the T-cell leukemia is a T-cell progenitor leukemia. In one such embodiment, the T-cell leukemia is T-ALL.

In further embodiments, determining whether Notch3 is activated in the cancer comprises contacting a sample of the cancer with an antibody that binds activated Notch3 ICD, and determining whether significantly increased levels of activated Notch3 (as reflected by levels of activated Notch3 ICD) are present, wherein the presence of significantly increased levels of activated Notch3 indicates that the cancer is suitable for treatment with an antagonist of Notch3. To determine whether significantly increased levels of activated Notch3 are present in the sample, an appropriate comparator (positive control) may be, e.g., a sample from a cancer known to respond to an antagonist of Notch3. If the "test" sample and the "control" sample contain comparable levels of activated Notch3, then the cancer from which the "test" sample was obtained is suitable for treatment with an antagonist of Notch3. Another appropriate comparator (negative control) may be, e.g., a sample from a cancer that does not to respond to an antagonist of Notch3. If the "test" sample contains significantly increased levels of activated Notch3 compared to the control sample, then the cancer from which the "test" sample was obtained is suitable for treatment with an antagonist of Notch3.

In certain embodiments of the above methods, an antagonist of Notch3 is a Notch3-specific antagonist. In certain embodiments, a Notch3-specific antagonist is any of those discussed above.

III. EXAMPLES

A. T-ALL Falls Into Three Classes

Previous studies have shown that T-ALL cell lines may be sensitive or insensitive to treatment with GSI. For example, certain T-ALL cell lines are resistant to GSI despite expression of activating Notch1 mutations, possibly due to activation of a non-Notch pathway, e.g., a pathway that circumvents the need for Notch. (See, e.g., Palomero et al., *Nat. Med.* 13:1203-1210, 2007.) However, in one study, five of thirty T-ALL cell lines were GSI-sensitive, showing cell cycle arrest in response to GSI. (See Weng et al., *Science*, 306:269-271, 2004.) The studies reported below further explored the response of T-ALL cell lines not only to GSI, but also to Notch1- and Notch3-specific antagonists.

Three classes of T-ALL were characterized based on their sensitivity to GSI and to a Notch1-specific antagonist. The Notch1-specific antagonist used in the following studies was the anti-Notch1 NRR antibody, "Antibody A-2," the isolation and characterization of which are discussed in U.S. Patent Application Publication No. US 2009/0081238 A1. For convenience, "Antibody A-2" is referred to herein as "anti-NRR1," and is also referred to as "α-Notch1," "aNotch1," or "α-N1" in the figures.

Figures 3-5 presents the classification of three representative human T-ALL cell lines. Those cell lines include the P-12 Ichikawa cell line, the HPB-ALL cell line, and the TALL-1 cell line. The cells were grown for eight days in control conditions (DMSO alone (the vehicle for DAPT) or anti-gD (an isotype control antibody)); in the presence of the gamma-secretase inhibitor, DAPT (5 μM); or in the presence of anti-NRR1 (5 μg/ml). The cells were fixed, stained with propidium iodide and prepared for FACS to analyze the cell cycle status, according to standard procedures. Growth sensitivity was assessed by examining whether a given treatment caused an increase in the percentage of cells in G0/G1 with a corresponding decrease in the percentage of cells in S/G2/M. The results show that P-12 Ichikawa cells are resistant to both DAPT and anti-NRR1 (Figure 3A-3D), with no significant difference in cell cycle status among DAPT-treated, anti-NRR1-treated, and control (DMSO- and anti-gD-treated) cells. HPB-ALL cells are sensitive to both DAPT and anti-NRR1 (Figure 4A-4D), with DAPT- and anti-NRR1-treated cells showing about 78% and 76% of cells in G0/G1, respectively, compared to about 33-34% of the control cells. TALL-1 cells are sensitive to DAPT but resistant to anti-NRR1 (Figure 5A-5D), with about 87% of DAPT-treated cells in G0/G1, compared to about 55% of anti-NRR1-treated cells and about 53-54% of control

cells. It is noted that Notch1 is not mutated in TALL-1 cells. Further studies revealed that a fourth cell line, CCRF-CEM, fell into the same class as P-12 Ichikawa cells (i.e., resistant to both GSI and anti-NRR1). (Data not shown and Figure 10.)

As shown in Figure 6, cell size measurements reflect these three classes of T-ALL. The P-12 Ichikawa cell line, the HPB-ALL cell line, and the TALL-1 cell line were grown for approximately one week in control conditions (DMSO alone (the vehicle for DAPT) or anti-gD (an isotype control antibody)); in the presence of the gamma-secretase inhibitor, DAPT (5 μM); or in the presence of anti-NRR1 (5 μg/ml). Cell diameter was measured using a cell counter (Vi-Cell, Beckman Coulter). Consistent with the growth inhibition studies, the P-12 Ichikawa line is resistant to both DAPT and anti-NRR1, as indicated by relatively consistent cell diameter among treated and control cells. HPB-ALL is sensitive to both DAPT and anti-NRR1, as indicated by the significantly smaller size of cells treated with those agents, respectively. TALL-1 is sensitive to DAPT but resistant to anti-NRR1, as indicated by the significantly smaller size of cells treated with DAPT but not with anti-NRR1 or control agents. These results are consistent with the growth studies described above.

As shown in Figure 7, apoptosis measurements also reflect these three classes of T-ALL. The P-12 Ichikawa cell line, the HPB-ALL cell line, and the TALL-1 cell line were treated as described above for Figure 6. The cells were analyzed by FACS, with staining for 7-AAD (cell death marker) on the x-axis of Figure 7, and staining for Annexin V (marker for apoptosis) on the y-axis of Figure 7. Based on the percentage of cells in the double positive population, treatment with either DAPT or anti-NRR1 increases apoptotic cell death in HPB-ALL cells. In contrast, P-12 Ichikawa cells are resistant to both treatments, whereas TALL-1 cells are sensitive to DAPT but not to anti-NRR1. These results are consistent with the growth studies and cell diameter measurements described above.

As shown in Figure 8, the results of a cell proliferation assay also reflect these three classes of T-ALL. The P-12 Ichikawa cell line, the HPB-ALL cell line, and the TALL-1 cell line were treated as described above for Figure 6. The cells were analyzed by FACS using Ki-67 staining to mark proliferation (left panel). A shift in the FACS peak to the left indicates lower staining for Ki-67 and decreased proliferation, and conversely, a shift in the FACS peak to the right indicates higher staining for Ki-67 and increased proliferation. Based on this proliferation assay, HPB-ALL was sensitive to both DAPT and anti-NRR1, TALL-1 was sensitive to DAPT but not anti-NRR1, and P-12 Ichikawa cells were resistant to both. Again, these results are consistent with those from the other assays described above, as well

as apoptosis measurements shown in the right panel of Figure 8. That panel shows cell counts for Annexin V/7-AAD double negative (non-apoptotic) cells. Low cell counts (i.e., low numbers of Annexin V/7-AAD double negative (non-apoptotic) cells) indicate increased apoptosis, which in turn correlate with decreased proliferation in the left hand panel.

B. GSI-Responsive, Anti-NRR1 Resistant TALL-1 Cells Are Partially Sensitive to Anti-NRR3

As described above, two of the three classes of T-ALL, represented by HPB-ALL and TALL-1, are both sensitive to GSI but differ in that the former is sensitive to anti-NRR1, whereas the latter is not. Because sensitivity to GSI suggests a role for one or more Notch receptors, we asked whether a Notch receptor in addition to or in the alternative to Notch1 plays a role in the resistance of the latter class of T-ALL to anti-Notch1 NRR. To address this question, CCRF-CEM cells, HPB-ALL cells, and TALL-1 cells were treated as described for Figures 3-5, except that a Notch3-specific antagonist was also included at 10 μg/ml in a subset of the treatments to test whether growth depended on Notch3 signaling. The Notch3-specific antagonist used in these studies was mouse anti-human Notch3 monoclonal antibody 256A-4, the isolation and characterization of which are discussed in U.S. Patent Application Publication No. US 2008/0226621 A1. For convenience, 256A-4 is referred to herein as "anti-NRR3," and is also referred to as "α-N3" in the figures.

The results indicate that growth of TALL-1 is partially sensitive to anti-NRR3 and even more sensitive to anti-NRR1 plus anti-NRR3 (see Figure 9A-9F), suggesting that signaling through Notch3 as well as Notch1 explains why the line is sensitive to DAPT but not to anti-NRR1. Specifically, nearly 83% of TALL-1 cells were in G0/G1 after DAPT treatment, compared to about 53-54% for the control (DMSO- or α-gD-treated) cells. Treatment with anti-NRR3 resulted in about 61% of the cells in G0/G1, and addition of anti-NRR1 increased this figure to about 68%. In contrast, CCRF-CEM appears resistant to all of the tested treatments (Figure 10A-10F), each showing from about 52-57% of the cells in G0/G1. HBP-ALL appears sensitive to both DAPT and anti-NRR1 treatment (each showing about 67% of cells in G0/G1), but not anti-NRR3 treatment (showing about 37% of cells in G0/G1) (Figure 11A-11F).

The results of the above experiment in Figure 9B-9F are replotted in Figure 14. The TALL-1 cell cultures started with approximately $5x10^5$ cells/ml, and the y-axis is the number of cells/ml, in millions of cells, after treatment under the indicated conditions and as described for Figure 9B-9F. Figure 14 shows that anti-NRR1 and anti-NRR3 each

individually resulted in lower cell counts. However the combination of anti-NRR1 and anti-NRR3 had a more pronounced effect in lowering cell counts, approaching the levels seen with DAPT.

C. Notch3 Is Activated in Anti-NRR3-Sensitive Cells

To investigate the activation status of Notch3 in the three classes of T-ALL, a new anti-Notch3 ICD antibody was developed which recognizes cleaved (i.e., activated) Notch3 ICD. Using standard procedures, rabbit polyclonal antibodies were raised against a peptide corresponding to the N-terminus of the Notch3 ICD that is expected to result from gamma-secretase cleavage at the site S3. The peptide sequence used was: VMVARRKREHSTLW (SEQ ID NO:4). The peptide was conjugated to BSA for the immunizations. Polyclonal antibodies were purified on a protein A column and then used for immunoblotting, as shown in Figure 12. To test whether the antibody recognized nuclear, cleaved Notch3 ICD, the basal breast cancer cell line MDA-MB-468 was used. This line expresses high levels of Notch3. Cells were treated with immobilized Jag1 (R&D Systems) (or Fc as a control) to induce Notch signaling, and cytoplasmic (C) and nuclear (N) fractions were isolated at the indicated times following induction. As a control to examine the level of Notch3 ICD present without Jag1 induction, cells that were not induced were treated with DAPT (5 μM), DMSO (vehicle for DAPT) or the proteasome inhibitor MG132 to stabilize the Notch3 ICD, as indicated. CREB and tubulin served as markers for nuclear and cytoplasmic proteins, respectively. The results in Figure 12 show that the anti-Notch3 ICD antibody recognizes a band of the expected size that is localized to the nucleus and induced by Jag1.

This new anti-Notch3 ICD antibody was then used to investigate the activation status of Notch3 in the three classes of T-ALL. As shown in Figure 13, nuclear fractions of P12-Ichikawa, HPB-ALL, and TALL-1 cells were immunoblotted with anti-Notch1 Val1744, a commercially available polyclonal antibody that recognizes cleaved, activated Notch1 ICD (Cell Signaling Technologies) (upper panel), or with the anti-Notch3 ICD antibody (α-N3 ICD Y935, lower panel). 3T3 cells expressing Notch1 (3T3-N1) and MDA-MB-468 (MB468) cells were used as controls. Consistent with the growth inhibition studies described in the previous figures, TALL-1 expresses high levels of activated Notch3 but not activated Notch1 (compare TALL-1 lanes in lower and upper panels, respectively). Furthermore, production of activated Notch3 in TALL-1 could be blocked by DAPT but not anti-NRR1 (lower panel). Moreover, as expected, HPB-ALL cells express high levels of activated

Notch1, which can be blocked by DAPT or anti-NRR1 antibody (see HPB-ALL lanes in upper panel). As to the controls, activated Notch1 is seen as a lighter, up-shifted band in the 3T3-N1 cells treated with Jagged (+jag) (upper panel). Additionally, activated Notch3 is seen as a faint but detectable band in the MDA-MB-468 cells treated with an anti-Notch3 agonist antibody (A13, described in U.S. Patent Application Publication US 2008/0118520 A1 as 256A-13) in the absence of DAPT (lower panel).

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, the descriptions and examples should not be construed as limiting the scope of the invention. The disclosures of all patent and scientific literatures cited herein are expressly incorporated in their entirety by reference.

WHAT IS CLAIMED IS:

1. A method of treating a GSI-responsive T-cell leukemia that does not respond to a Notch1-specific antagonist, the method comprising administering to a patient having such leukemia an effective amount of a Notch3-specific antagonist.

2. The method of claim 1, wherein the T-cell leukemia is a lymphoblastic leukemia.

3. The method of claim 2, wherein the T-cell leukemia is T-ALL.

4. The method of claim 1, wherein the Notch3-specific antagonist is an anti-Notch3 antagonist antibody.

5. The method of claim 4, wherein the anti-Notch3 antagonist antibody is an anti-Notch3 NRR antibody.

6. The method of claim 5, wherein the anti-Notch3 NRR antibody binds to the LNR-A and HD-C domains of Notch3 NRR.

7. The method of claim 5, wherein the anti-Notch3 NRR antibody is a humanized form of antibody 256A-4 or 256A-8.

8. The method of claim 5, wherein the anti-Notch3 NRR antibody comprises the heavy and light chain variable region CDRs of antibody 256A-4 or 256A-8.

9. The method of claim 4, wherein the anti-Notch3 antagonist antibody is an anti-Notch3 antibody that binds to one or more EGF-like repeats of Notch3.

10. The method of claim 1, further comprising administering an effective amount of a Notch1-specific antagonist.

11. The method of claim 10, wherein the Notch1-specific antagonist is an anti-Notch1 antagonist antibody.

12. The method of claim 11, wherein the anti-Notch1 antagonist antibody is an anti-Notch1 NRR antibody.

13. The method of claim 12, wherein the anti-Notch1 NRR antibody binds to the LNR-A, LNR-B, and HD-C domains of Notch1 NRR.

14. The method of claim 12, wherein the anti-Notch1 NRR antibody is selected from Antibody A, A-1, A-2, and A-3.

15. The method of claim 12, wherein the anti-Notch1 NRR antibody comprises the heavy and light chain variable region CDRs of an antibody selected from Antibody A, A-1, A-2, and A-3.

16. The method of claim 11, wherein the anti-Notch1 antagonist antibody is an anti-Notch1 antibody that binds to one or more EGF-like repeats of Notch1.

17. An antibody that binds to activated Notch3 ICD.

18. The antibody of claim 17, wherein the antibody binds to the peptide of SEQ ID NO:4.

19. The antibody of claim 17, wherein the antibody is polyclonal.

20. The antibody of claim 17, wherein the antibody is monoclonal.

21. A method of identifying a cancer that is suitable for treatment with an antagonist of Notch3, the method comprising contacting a sample of the cancer with the antibody of claim 17, and determining whether significantly increased levels of activated Notch3 are present in the sample, wherein the presence of significantly increased levels of activated Notch3 indicates that the cancer is suitable for treatment with an antagonist of Notch3.

22. The method of claim 21, wherein the cancer is GSI-responsive.

90.7% identity in 2556 residues overlap; Score: 13215.0; Gap frequency: 1.0%

```
Human      1 MPPLLAPLLCLALLPALAARGPRCSQPGETCLNGGKCEAANGTEACVCGGAFVGPRCQDP
Mouse      1 MPRLLTPLLCLTLLPALAARGLRCSQPSGTCLNGGRCEVASGTEACVCSGAFVGQRCQDS
             ** ** ***** ********* *****  ****** ** * ******* ***** ****
             Signal Peptide          EGF1

Human     61 NPCLSTPCKNAGTCHVVDRRGVADYACSCALGFSGPLCLTPLDNACLTNPCRNGGTCDLL
Mouse     61 NPCLSTPCKNAGTCHVVDHGGTVDYACSCPLGFSGPLCLTPLDNACLANPCRNGGTCDLL
             ******************  *  ****** ****************** ************
             EGF2                                  EGF3

Human    121 TLTEYKCRCPPGWSGKSCQQADPCASNPCANGGQCLPFEASYICHCPPSFHGPTCRQDVN
Mouse    121 TLTEYKCRCPPGWSGKSCQQADPCASNPCANGGQCLPFESSYICRCPPGFHGPTCRQDVN
             ************************************ **** *** ***********
                                     EGF4

Human    181 ECGQKPGLCRHGGTCHNEVGSYRCVCRATHTGPNCERPYVPCSPSPCQNGGTCRPTGDVT
Mouse    181 ECSQNPGLCRHGGTCHNEIGSYRCACRATHTGPHCELPYVPCSPSPCQNGGTCRPTGDTT
             ** * ************* ***** ******** ** ********************** *
             EGF5                                  EGF6

Human    241 HECACLPGFTGQNCEENIDDCPGNNCKNGGACVDGVNTYNCRCPPEWTGQYCTEDVDECQ
Mouse    241 HECACLPGFAGQNCEENVDDCPGNNCKNGGACVDGVNTYNCRCPPEWTGQYCTEDVDECQ
             ********* ******* ****************************************
                                     EGF7                          EGF8

Human    301 LMPNACQNGGTCHNTHGGYNCVCVNGWTGEDCSENIDDCASAACFHGATCHDRVASFYCE
Mouse    301 LMPNACQNGGTCHNTHGGYNCVCVNGWTGEDCSENIDDCASAACFQGATCHDRVASFYCE
             ************************************************ **********
                                                 EGF9

Human    361 CPHGRTGLLCHLNDACISNPCNEGSNCDTNPVNGKAICTCPSGYTGPACSQDVDECSLGA
Mouse    361 CPHGRTGLLCHLNDACISNPCNEGSNCDTNPVNGKAICTCPSGYTGPACSQDVDECALGA
             ************************************************** ***
                          EGF10                                EGF11

Human    421 NPCEHAGKCINTLGSFECQCLQGYTGPRCEIDVNECVSNPCQNDATCLDQIGEFQCICMP
Mouse    421 NPCEHAGKCLNTLGSFECQCLQGYTGPRCEIDVNECISNPCQNDATCLDQIGEFQCICMP
             ********* ************************* ***********************
                                     EGF12

Human    481 GYEGVHCEVNTDECASSPCLHNGRCLDKINEFQCECPTGFTGHLCQYDVDECASTPCKNG
Mouse    481 GYEGVYCEINTDECASSPCLHNGHCMDKINEFQCQCPKGFNGHLCQYDVDECASTPCKNG
             ***** ** ************** * ******** ** ** ******************
                      EGF13                          EGF14

Human    541 AKCLDGPNTYTCVCTEGYTGTHCEVDIDECDPDPCHYGSCKDGVATFTCLCRPGYTGHHC
Mouse    541 AKCLDGPNTYTCVCTEGYTGTHCEVDIDECDPDPCHYGSCKDGVATFTCLCQPGYTGHHC
             ************************************************ ********
                                     EGF15

Human    601 ETNINECSSQPCRHGGTCQDRDNAYLCFCLKGTTGPNCEINLDDCASSPCDSGTCLDKID
Mouse    601 ETNINECHSQPCRHGGTCQDRDNSYLCLCLKGTTGPNCEINLDDCASNPCDSGTCLDKID
             ******* ************** *** ******************* ************
                EGF16                                 EGF17
```

FIG. 1A

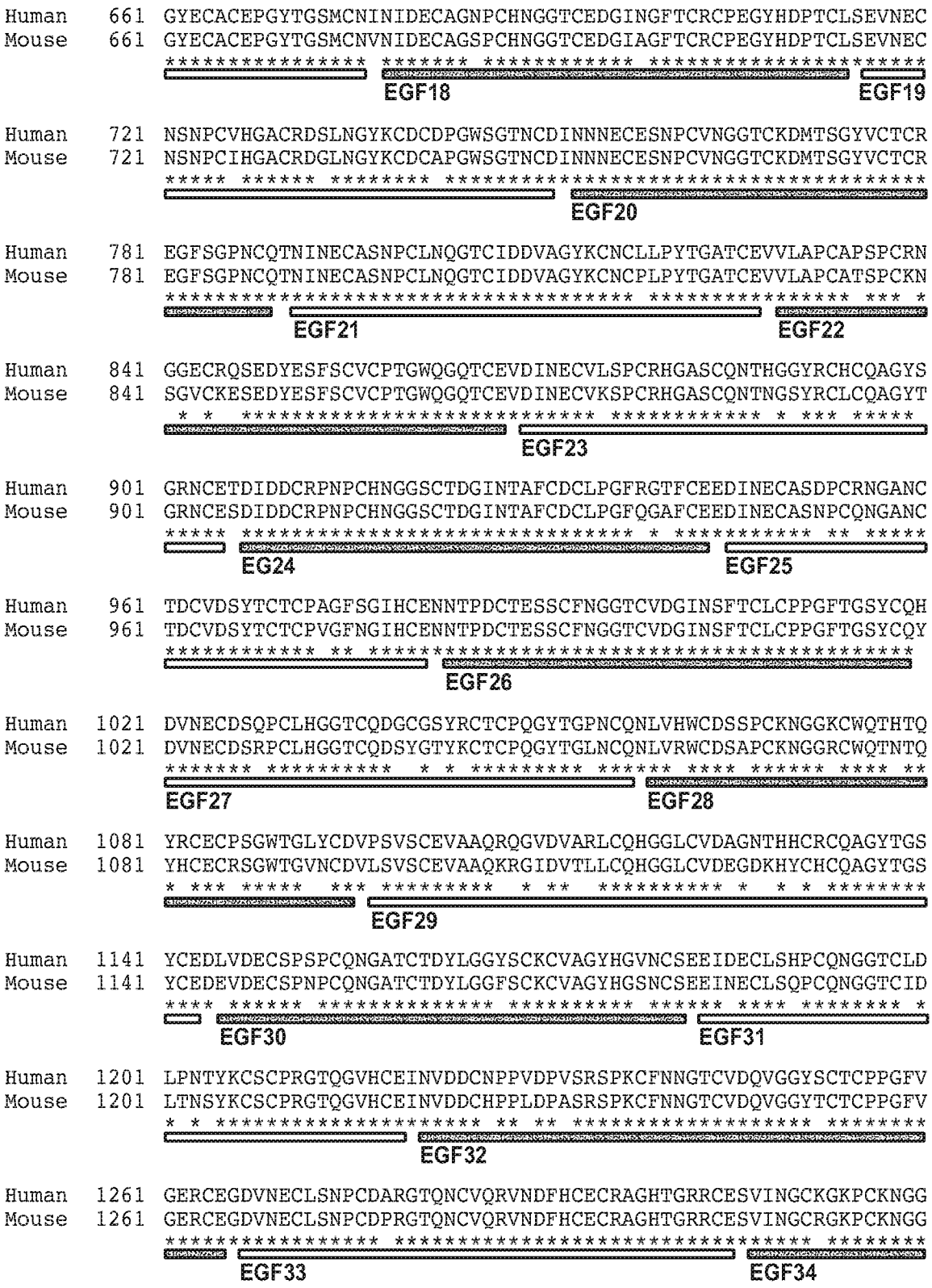

Human 661 GYECACEPGYTGSMCNINIDECAGNPCHNGGTCEDGINGFTCRCPEGYHDPTCLSEVNEC
Mouse 661 GYECACEPGYTGSMCNVNIDECAGSPCHNGGTCEDGIAGFTCRCPEGYHDPTCLSEVNEC
EGF18
EGF19
Human 721 NSNPCVHGACRDSLNGYKCDCDPGWSGTNCDINNNECESNPCVNGGTCKDMTSGYVCTCR
Mouse 721 NSNPCIHGACRDGLNGYKCDCAPGWSGTNCDINNNECESNPCVNGGTCKDMTSGYVCTCR
EGF20
Human 781 EGFSGPNCQTNINECASNPCLNQGTCIDDVAGYKCNCLLPYTGATCEVVLAPCAPSPCRN
Mouse 781 EGFSGPNCQTNINECASNPCLNQGTCIDDVAGYKCNCPLPYTGATCEVVLAPCATSPCKN
EGF21
EGF22
Human 841 GGECRQSEDYESFSCVCPTGWQGQTCEVDINECVLSPCRHGASCQNTHGGYRCHCQAGYS
Mouse 841 SGVCKESEDYESFSCVCPTGWQGQTCEVDINECVKSPCRHGASCQNTNGSYRCLCQAGYT
EGF23
Human 901 GRNCETDIDDCRPNPCHNGGSCTDGINTAFCDCLPGFRGTFCEEDINECASDPCRNGANC
Mouse 901 GRNCESDIDDCRPNPCHNGGSCTDGINTAFCDCLPGFQGAFCEEDINECASNPCQNGANC
EG24
EGF25
Human 961 TDCVDSYTCTCPAGFSGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPGFTGSYCQH
Mouse 961 TDCVDSYTCTCPVGFNGIHCENNTPDCTESSCFNGGTCVDGINSFTCLCPPGFTGSYCQY
EGF26
Human 1021 DVNECDSQPCLHGGTCQDGCGSYRCTCPQGYTGPNCQNLVHWCDSSPCKNGGKCWQTHTQ
Mouse 1021 DVNECDSRPCLHGGTCQDSYGTYKCTCPQGYTGLNCQNLVRWCDSAPCKNGGRCWQTNTQ
EGF27
EGF28
Human 1081 YRCECPSGWTGLYCDVPSVSCEVAAQRQGVDVARLCQHGGLCVDAGNTHHCRCQAGYTGS
Mouse 1081 YHCECRSGWTGVNCDVLSVSCEVAAQKRGIDVTLLCQHGGLCVDEGDKHYCHCQAGYTGS
EGF29
Human 1141 YCEDLVDECSPSPCQNGATCTDYLGGYSCKCVAGYHGVNCSEEIDECLSHPCQNGGTCLD
Mouse 1141 YCEDEVDECSPNPCQNGATCTDYLGGFSCKCVAGYHGSNCSEEINECLSQPCQNGGTCID
EGF30
EGF31
Human 1201 LPNTYKCSCPRGTQGVHCEINVDDCNPPVDPVSRSPKCFNNGTCVDQVGGYSCTCPPGFV
Mouse 1201 LTNSYKCSCPRGTQGVHCEINVDDCHPPLDPASRSPKCFNNGTCVDQVGGYTCTCPPGFV
EGF32
Human 1261 GERCEGDVNECLSNPCDARGTQNCVQRVNDFHCECRAGHTGRRCESVINGCKGKPCKNGG
Mouse 1261 GERCEGDVNECLSNPCDPRGTQNCVQRVNDFHCECRAGHTGRRCESVINGCRGKPCKNGG
EGF33
EGF34

FIG. 1B

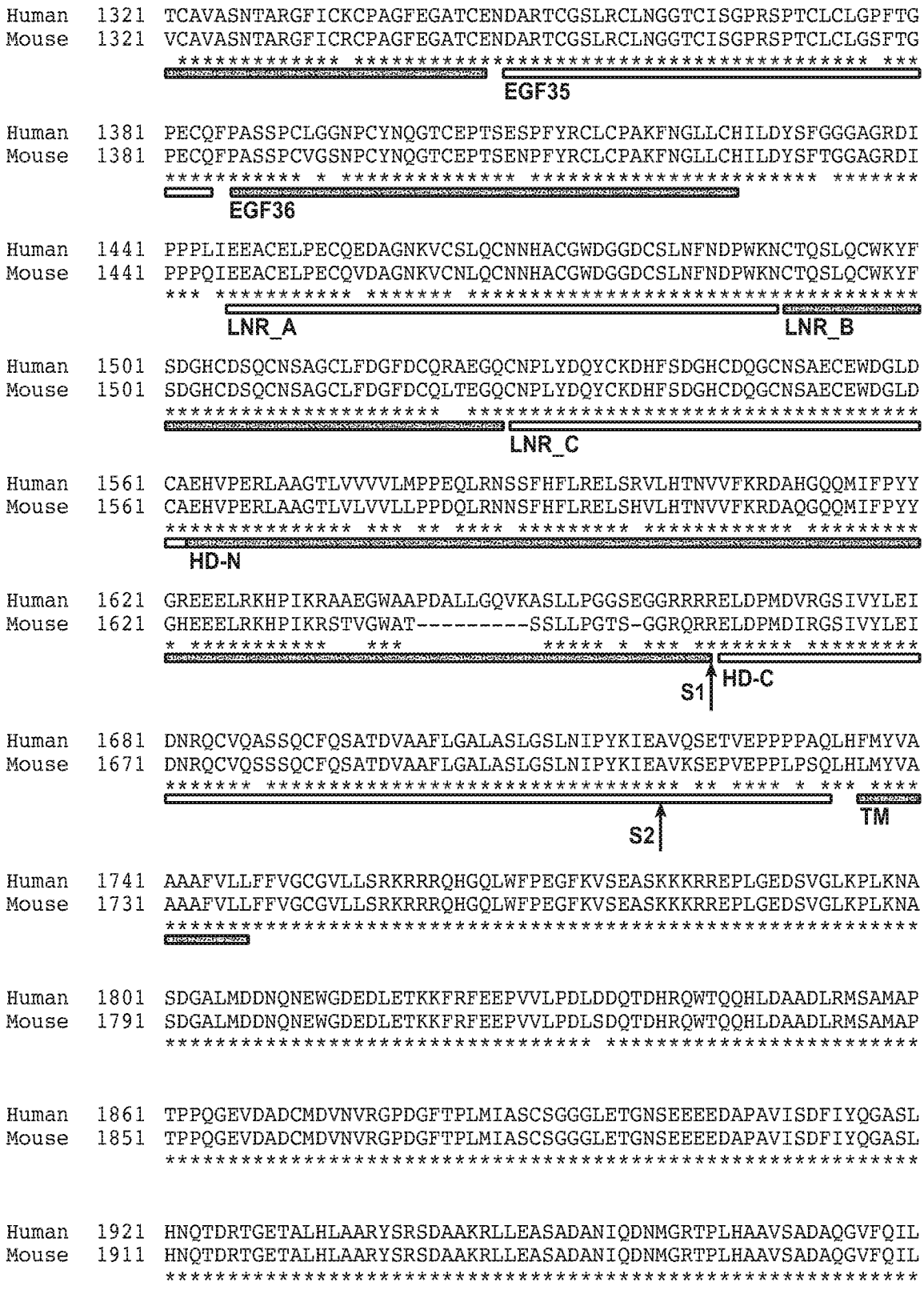

Human 1321 TCAVASNTARGFICKCPAGFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGPFTG
Mouse 1321 VCAVASNTARGFICRCPAGFEGATCENDARTCGSLRCLNGGTCISGPRSPTCLCLGSFTG
EGF35
Human 1381 PECQFPASSPCLGGNPCYNQGTCEPTSESPFYRCLCPAKFNGLLCHILDYSFGGGAGRDI
Mouse 1381 PECQFPASSPCVGSNPCYNQGTCEPTSENPFYRCLCPAKFNGLLCHILDYSFTGGAGRDI
EGF36
Human 1441 PPPLIEEACELPECQEDAGNKVCSLQCNNHACGWDGGDCSLNFNDPWKNCTQSLQCWKYF
Mouse 1441 PPPQIEEACELPECQVDAGNKVCNLQCNNHACGWDGGDCSLNFNDPWKNCTQSLQCWKYF
LNR_A
LNR_B
Human 1501 SDGHCDSQCNSAGCLFDGFDCQRAEGQCNPLYDQYCKDHFSDGHCDQGCNSAECEWDGLD
Mouse 1501 SDGHCDSQCNSAGCLFDGFDCQLTEGQCNPLYDQYCKDHFSDGHCDQGCNSAECEWDGLD
LNR_C
Human 1561 CAEHVPERLAAGTLVVVVLMPPEQLRNSSFHFLRELSRVLHTNVVFKRDAHGQQMIFPYY
Mouse 1561 CAEHVPERLAAGTLVLVVLLPPDQLRNNSFHFLRELSHVLHTNVVFKRDAQGQQMIFPYY
HD-N
Human 1621 GREEELRKHPIKRAAEGWAAPDALLGQVKASLLPGGSEGGRRRRELDPMDVRGSIVYLEI
Mouse 1621 GHEEELRKHPIKRSTVGWAT---------SSLLPGTS-GGRQRRELDPMDIRGSIVYLEI
S1
HD-C
Human 1681 DNRQCVQASSQCFQSATDVAAFLGALASLGSLNIPYKIEAVQSETVEPPPPAQLHFMYVA
Mouse 1671 DNRQCVQSSSQCFQSATDVAAFLGALASLGSLNIPYKIEAVKSEPVEPPLPSQLHLMYVA
S2
TM
Human 1741 AAAFVLLFFVGCGVLLSRKRRRQHGQLWFPEGFKVSEASKKKRREPLGEDSVGLKPLKNA
Mouse 1731 AAAFVLLFFVGCGVLLSRKRRRQHGQLWFPEGFKVSEASKKKRREPLGEDSVGLKPLKNA
Human 1801 SDGALMDDNQNEWGDEDLETKKFRFEEPVVLPDLDDQTDHRQWTQQHLDAADLRMSAMAP
Mouse 1791 SDGALMDDNQNEWGDEDLETKKFRFEEPVVLPDLSDQTDHRQWTQQHLDAADLRMSAMAP
Human 1861 TPPQGEVDADCMDVNVRGPDGFTPLMIASCSGGGLETGNSEEEEDAPAVISDFIYQGASL
Mouse 1851 TPPQGEVDADCMDVNVRGPDGFTPLMIASCSGGGLETGNSEEEEDAPAVISDFIYQGASL
Human 1921 HNQTDRTGETALHLAARYSRSDAAKRLLEASADANIQDNMGRTPLHAAVSADAQGVFQIL
Mouse 1911 HNQTDRTGETALHLAARYSRSDAAKRLLEASADANIQDNMGRTPLHAAVSADAQGVFQIL

FIG. 1C

```
Human   1981  IRNRATDLDARMHDGTTPLILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNN
Mouse   1971  LRNRATDLDARMHDGTTPLILAARLAVEGMLEDLINSHADVNAVDDLGKSALHWAAAVNN
              ************************************************************


Human   2041  VDAAVVLLKNGANKDMQNNREETPLFLAAREGSYETAKVLLDHFANRDITDHMDRLPRDI
Mouse   2031  VDAAVVLLKNGANKDMQNNKEETPLFLAAREGSYETAKVLLDHFANRDITDHMDRLPRDI
              ******************* ****************************************


Human   2101  AQERMHHDIVRLLDEYNLVRSPQLHGAPLGGTPTLSPPLCSPNGYLGSLKPGVQGKKVRK
Mouse   2091  AQERMHHDIVRLLDEYNLVRSPQLHGTALGGTPTLSPTLCSPNGYLGNLKSATQGKKARK
              ************************** ********* ********* **   **** **


Human   2161  PSSKGLACGSKEAKDLKARRKKSQDGKGCLLDSSGMLSPVDSLESPHGYLSDVASPPLLP
Mouse   2151  PSTKGLACGSKEAKDLKARRKKSQDGKGCLLDSSSMLSPVDSLESPHGYLSDVASPPLLP
              ** ******************************** ************************


Human   2221  SPFQQSPSVPLNHLPGMPDTHLGIGHLNVAAKPEMAALGGGGRLAFETGPPRLSHLPVAS
Mouse   2211  SPFQQSPSMPLSHLPGMPDTHLGISHLNVAAKPEMAALAGGSRLAFEPPPPRLSHLPVAS
              ******** ** ************ ************* ** *****  ***********


Human   2281  GTSTVLGSSSGGALNFTVGGSTSLNGQCEWLSRLQSGMVPNQYNPLRGSVAPGPLSTQAP
Mouse   2271  SASTVLSTNGTGAMNFTVGAPASLNGQCEWLPRLQNGMVPSQYNPLRPGVTPGTLSTQAA
                ****     ** *****   ********* *** **** ******  * ** *****


Human   2341  SLQHGMVGPLHSSLAASALSQMMSYQGLPSTRLATQPHLVQTQQVQPQNLQMQQQNLQPA
Mouse   2331  GLQHSMMGPLHSSLSTNTLSPII-YQGLPNTRLATQPHLVQTQQVQPQNLQLQPQNLQP-
               *** * *******    **    ***** ********************* * *****


Human   2401  NIQQQQSLQPPPPPPQPHLGVSSAASGHLGRSFLSGEPSQADVQPLGPSSLAVHTILPQE
Mouse   2389  --------------PSQPHLSVSSAANGHLGRSFLSGEPSQADVQPLGPSSLPVHTILPQE
                          * **** ***** ************************* ********


Human   2461  SPALPTSLPSSLVPPVTAAQFLTPPSQHSYSS-PVDNTPSHQLQVPEHPFLTPSPESPDQ
Mouse   2436  SQALPTSLPSSMVPPMTTTQFLTPPSQHSYSSSPVDNTPSHQLQVPEHPFLTPSPESPDQ
              * ********* *** *  ************* ***************************


Human   2520  WSSSSPHSNVSDWSEGVSSPPTSMQSQIARIPEAFK
Mouse   2496  WSSSSPHSNISDWSEGISSPPTTMPSQITHIPEAFK
              ********* ****** ***** * ***  ******
```

FIG. 1D

Amino Acid Sequence of Human Notch 3 (NP_000426)

```
   1 MGPGARGRRR RRRPMSPPPP PPPVRALPLL LLLAGPGAAA PPCLDGSPCA NGGRCTQLPS
  61 REAACLCPPG WVGERCQLED PCHSGPCAGR GVCQSSVVAG TARFSCRCPR GFRGPDCSLP
 121 DPCLSSPCAH GARCSVGPDG RFLCSCPPGY QGRSCRSDVD ECRVGEPCRH GGTCLNTPGS
 181 FRCQCPAGYT GPLCENPAVP CAPSPCRNGG TCRQSGDLTY DCACLPGFEG QNCEVNVDDC
 241 PGHRCLNGGT CVDGVNTYNC QCPPEWTGQF CTEDVDECQL QPNACHNGGT CFNTLGGHSC
 301 VCVNGWTGES CSQNIDDCAT AVCFHGATCH DRVASFYCAC PMGKTGLLCH LDDACVSNPC
 361 HEDAICDTNP VNGRAICTCP PGFTGGACDQ DVDECSIGAN PCEHLGRCVN TQGSFLCQCG
 421 RGYTGPRCET DVNECLSGPC RNQATCLDRI GQFTCICMAG FTGTYCEVDI DECQSSPCVN
 481 GGVCKDRVNG FSCTCPSGFS GSTCQLDVDE CASTPCRNGA KCVDQPDGYE CRCAEGFEGT
 541 LCDRNVDDCS PDPCHHGRCV DGIASFSCAC APGYTGTRCE SQVDECRSQP CRHGGKCLDL
 601 VDKYLCRCPS GTTGVNCEVN IDDCASNPCT FGVCRDGINR YDCVCQPGFT GPLCNVEINE
 661 CASSPCGEGG SCVDGENGFR CLCPPGSLPP LCLPPSHPCA HEPCSHGICY DAPGGFRCVC
 721 EPGWSGPRCS QSLARDACES QPCRAGGTCS SDGMGFHCTC PPGVQGRQCE LLSPCTPNPC
 781 EHGGRCESAP GQLPVCSCPQ GWQGPRCQQD VDECAGPAPC GPHGICTNLA GSFSCTCHGG
 841 YTGPSCDQDI NDCDPNPCLN GGSCQDGVGS FSCSCLPGFA GPRCARDVDE CLSNPCGPGT
 901 CTDHVASFTC TCPPGYGGFH CEQDLPDCSP SSCFNGGTCV DGVNSFSCLC RPGYTGAHCQ
 961 HEADPCLSRP CLHGGVCSAA HPGFRCTCLE SFTGPQCQTL VDWCSRQPCQ NGGRCVQTGA
1021 YCLCPPGWSG RLCDIRSLPC REAAAQIGVR LEQLCQAGGQ CVDEDSSHYC VCPEGRTGSH
1081 CEQEVDPCLA QPCQHGGTCR GYMGGYMCEC LPGYNGDNCE DDVDECASQP CQHGGSCIDL
1141 VARYLCSCPP GTLGVLCEIN EDDCGPGPPL DSGPRCLHNG TCVDLVGGFR CTCPPGYTGL
1201 RCEADINECR SGACHAAHTR DCLQDPGGGF RCLCHAGFSG PRCQTVLSPC ESQPCQHGGQ
1261 CRPSPGPGGG LTFTCHCAQP FWGPRCERVA RSCRELQCPV GVPCQQTPRG PRCACPPGLS
1321 GPSCRSFPGS PPGASNASCA AAPCLHGGSC RPAPLAPFFR CACAQGWTGP RCEAPAAAPE
1381 VSE***EPRCPRA ACQAKRGDQR CDRECNSPGC GWDGGDCSLS VGDPWRQCEA LQCWRLFNNS***
***1441*** ***RCDPACSSPA CLYDNFDCHA GGRERTCNPV YEKYCADHFA DGRCDQGCNT EECGWDGLDC***
***1501*** ***ASE***VPALLAR GVLVLTVLLP PEELLRSSAD FLQRLSAILR TSLRFRLDAH GQAMVFPYHR
1561 PSPGSEPRAR RELAPEVIGS VVMLEIDNRL CLQSPENDHC FPDAQSAADY LGALSAVERL
1621 DFPYPLRDVR GEPLEPPEPS VPLLPLLVAG AVLLLVILVL GVMVARRKRE HSTLWFPEGF
1681 SLHKDVASGH KGRREPVGQD ALGMKNMAKG ESLMGEVATD WMDTECPEAK RLKVEEPGMG
1741 AEEAVDCRQW TQHHLVAADI RVAPAMALTP PQGDADADGM DVNVRGPDGF TPLMLASFCG
1801 GALEPMPTEE DEADDTSASI ISDLICQGAQ LGARTDRTGE TALHLAARYA RADAAKRLLD
1861 AGADTNAQDH SGRTPLHTAV TADAQGVFQI LIRNRSTDLD ARMADGSTAL ILAARLAVEG
1921 MVEELIASHA DVNAVDELGK SALHWAAAVN NVEATLALLK NGANKDMQDS KEETPLFLAA
1981 REGSYEAAKL LLDHFANREI TDHLDRLPRD VAQERLHQDI VRLLDQPSGP RSPPGPHGLG
2041 PLLCPPGAFL PGLKAAQSGS KKSRRPPGKA GLGPQGPRGR GKKLTLACPG PLADSSVTLS
2101 PVDSLDSPRP FGGPPASPGG FPLEGPYAAA TATAVSLAQL GGPGRAGLGR QPPGGCVLSL
2161 GLLNPVAVPL DWARLPPPAP PGPSFLLPLA PGPQLLNPGT PVSPQERPPP YLAVPGHGEE
2221 YPVAGAHSSP PKARFLRVPS EHPYLTPSPE SPEHWASPSP PSLSDWSEST PSPATATGAM
2281 ATTTGALPAQ PLPLSVPSSL AQAQTQLGPQ PEVTPKRQVL A (SEQ ID NO 3)
```

FIG. 2

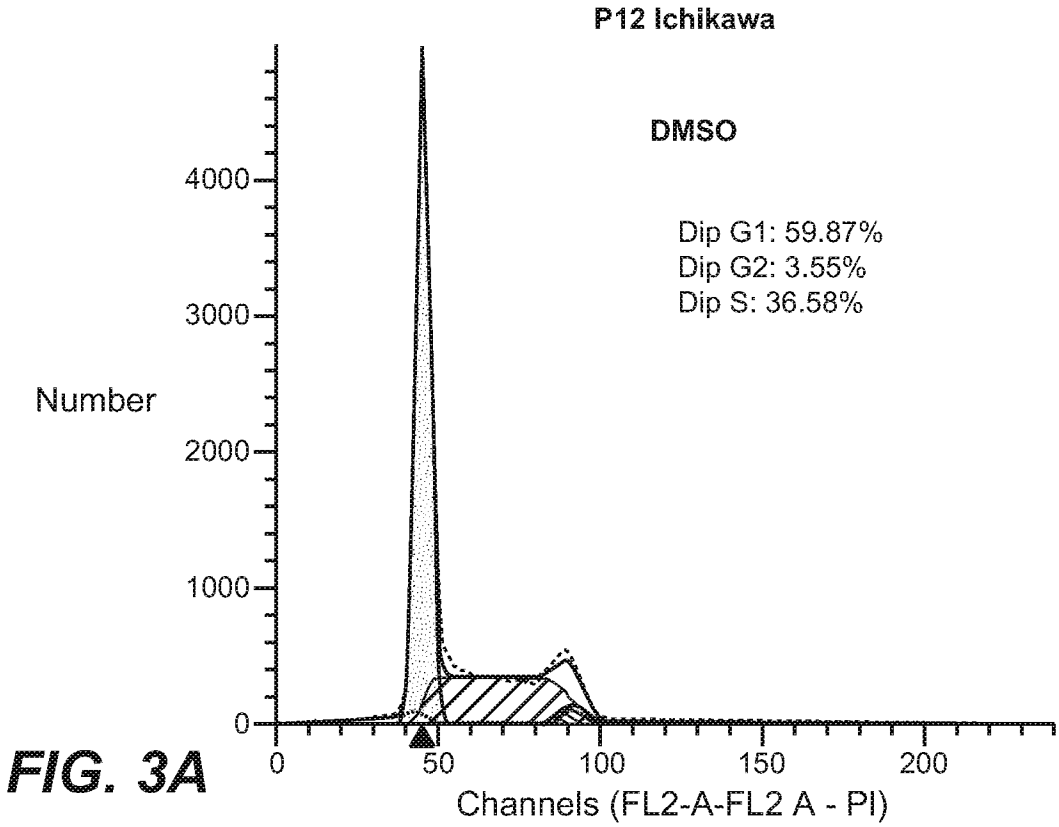

P12 Ichikawa
DMSO
Dip G1: 59.87%
Dip G2: 3.55%
Dip S: 36.58%
Number
4000
3000
2000
1000
0
0
50
100
150
200
Channels (FL2-A-FL2 A - PI)

FIG. 3A

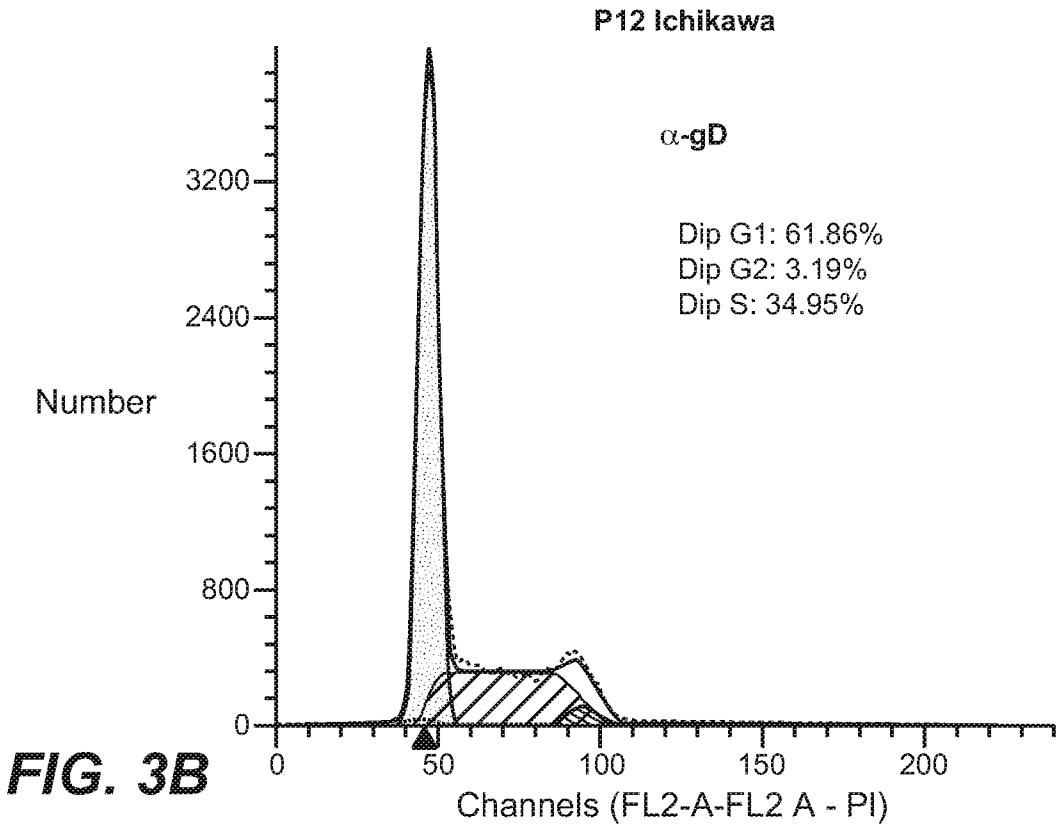

P12 Ichikawa
α-gD
Dip G1: 61.86%
Dip G2: 3.19%
Dip S: 34.95%
Number
3200
2400
1600
800
0
0
50
100
150
200
Channels (FL2-A-FL2 A - PI)

FIG. 3B

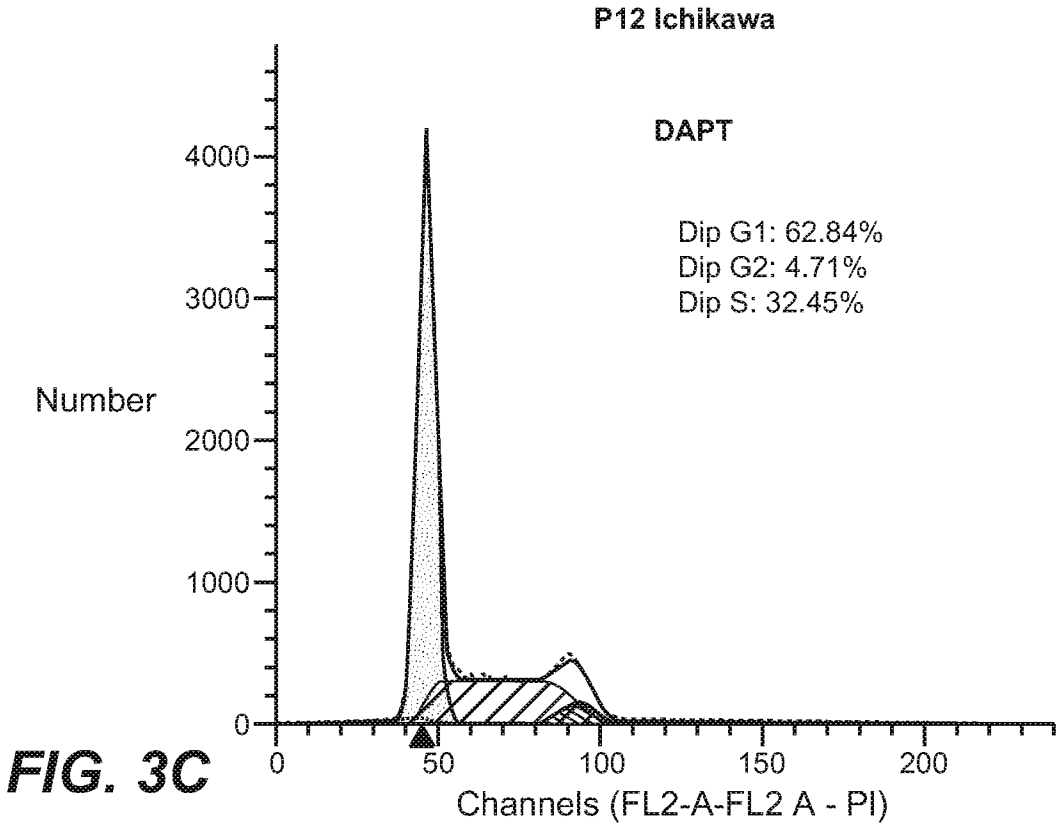

P12 Ichikawa
DAPT
Dip G1: 62.84%
Dip G2: 4.71%
Dip S: 32.45%
Number
4000
3000
2000
1000
0
0
50
100
150
200
Channels (FL2-A-FL2 A - PI)

FIG. 3C

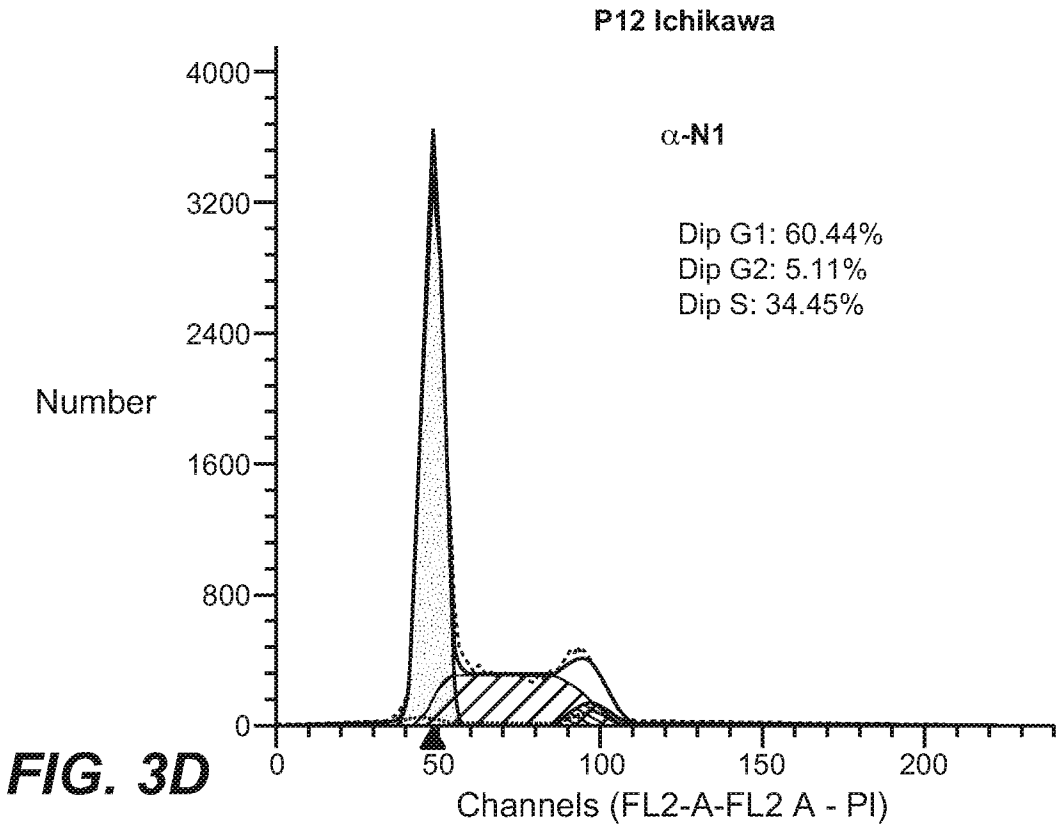

P12 Ichikawa
α-N1
Dip G1: 60.44%
Dip G2: 5.11%
Dip S: 34.45%
Number
4000
3200
2400
1600
800
0
0
50
100
150
200
Channels (FL2-A-FL2 A - PI)

FIG. 3D

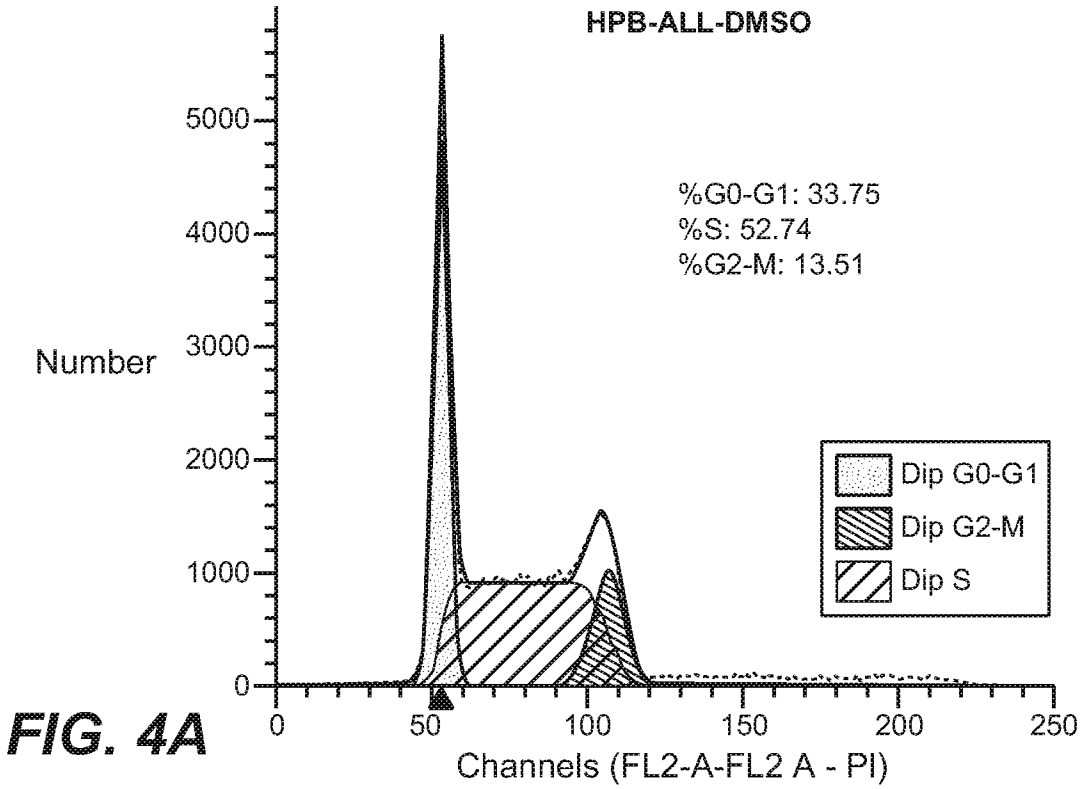

HPB-ALL-DMSO
%G0-G1: 33.75
%S: 52.74
%G2-M: 13.51
Number
5000
4000
3000
2000
1000
0
Dip G0-G1
Dip G2-M
Dip S
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)

FIG. 4A

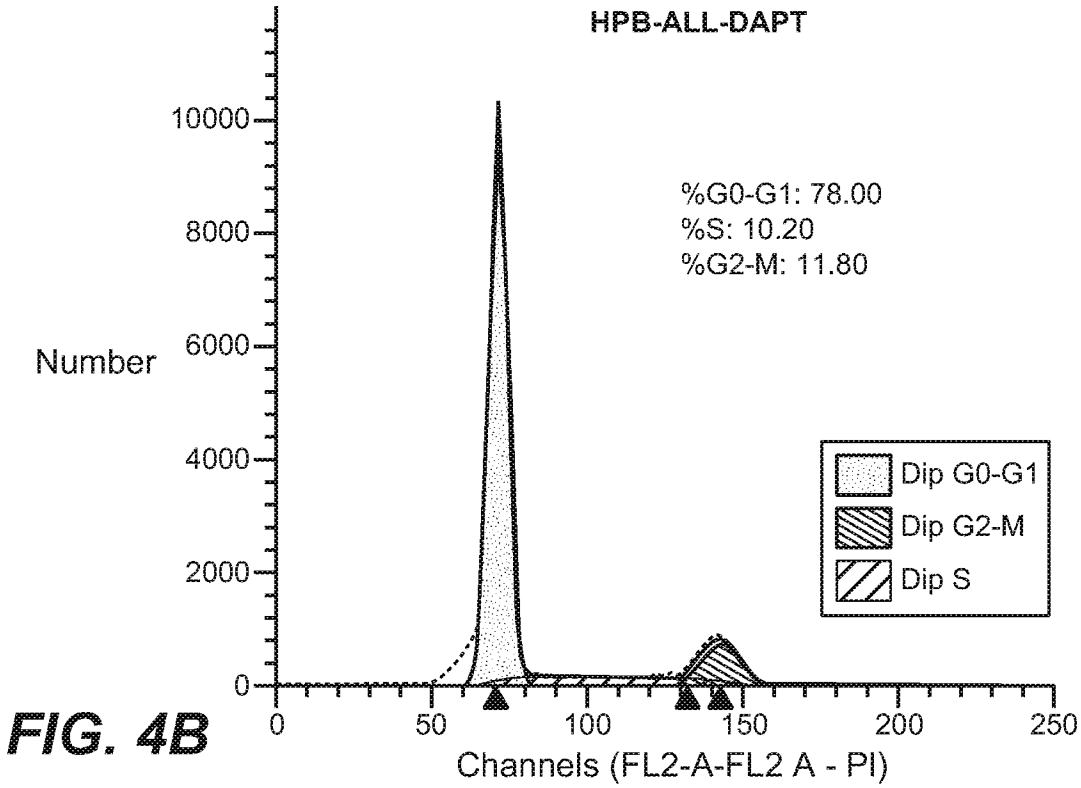

HPB-ALL-DAPT
%G0-G1: 78.00
%S: 10.20
%G2-M: 11.80
Number
10000
8000
6000
4000
2000
0
Dip G0-G1
Dip G2-M
Dip S
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)

FIG. 4B

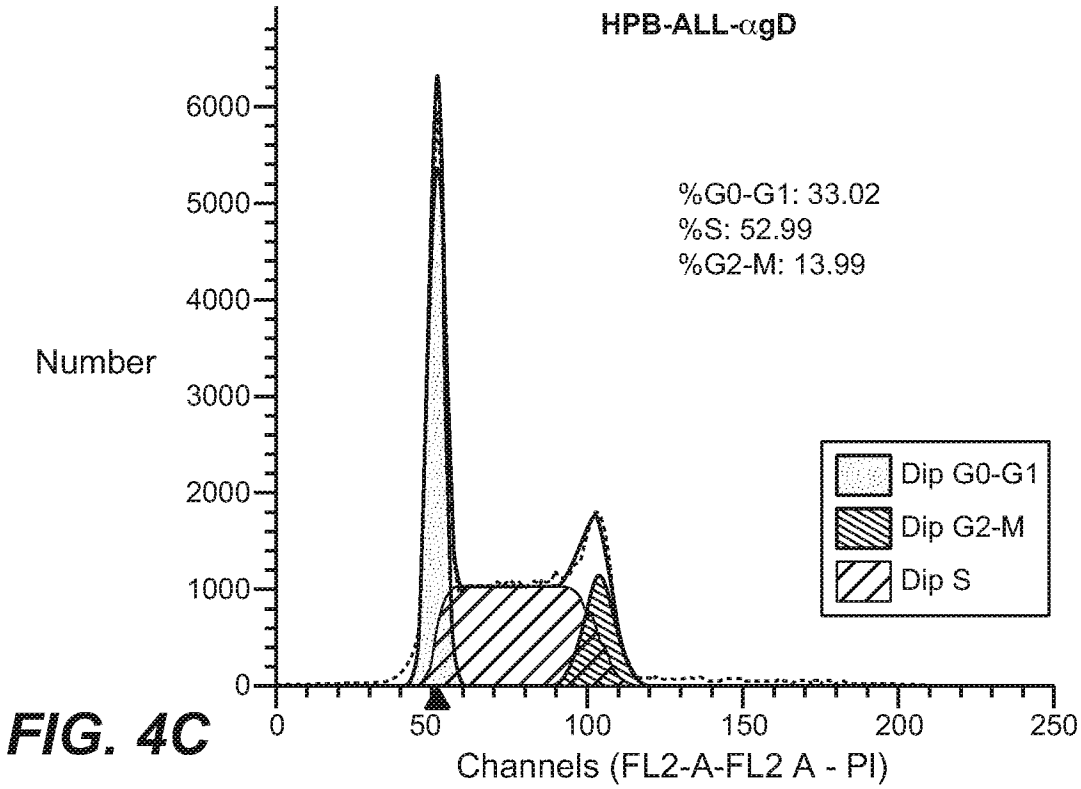

HPB-ALL-αgD
%G0-G1: 33.02
%S: 52.99
%G2-M: 13.99
Number
6000
5000
4000
3000
2000
1000
0
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 4C

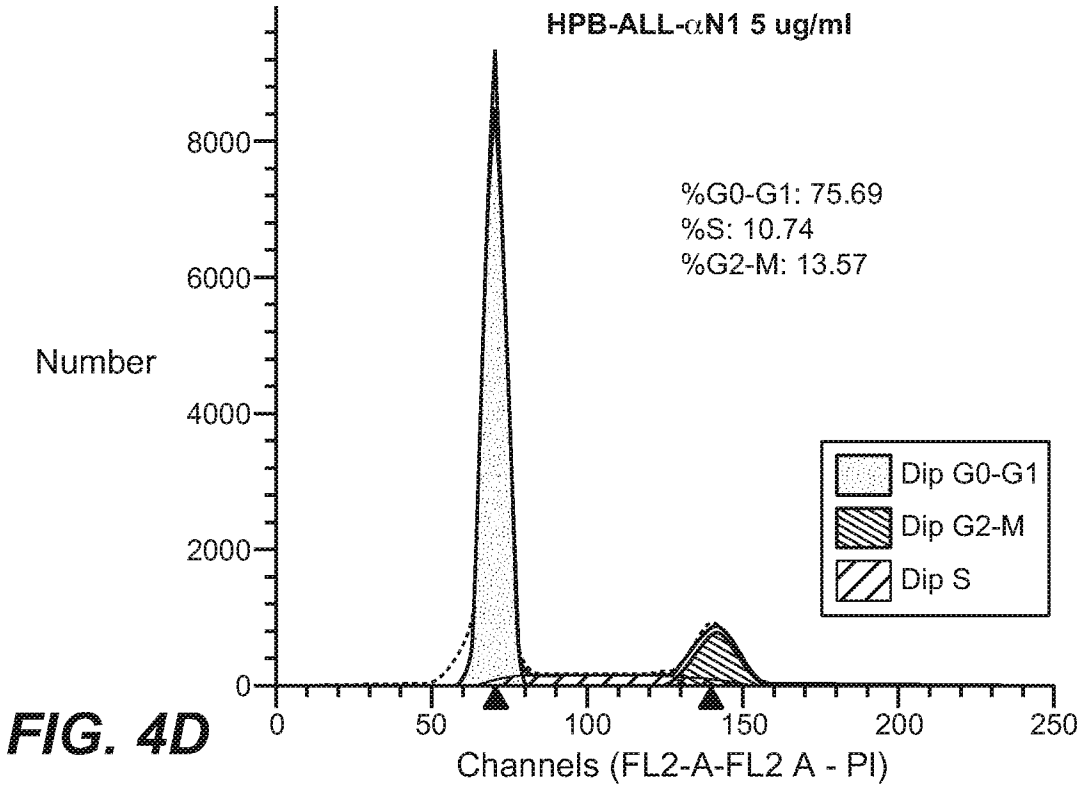

HPB-ALL-αN1 5 ug/ml
%G0-G1: 75.69
%S: 10.74
%G2-M: 13.57
Number
8000
6000
4000
2000
0
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 4D

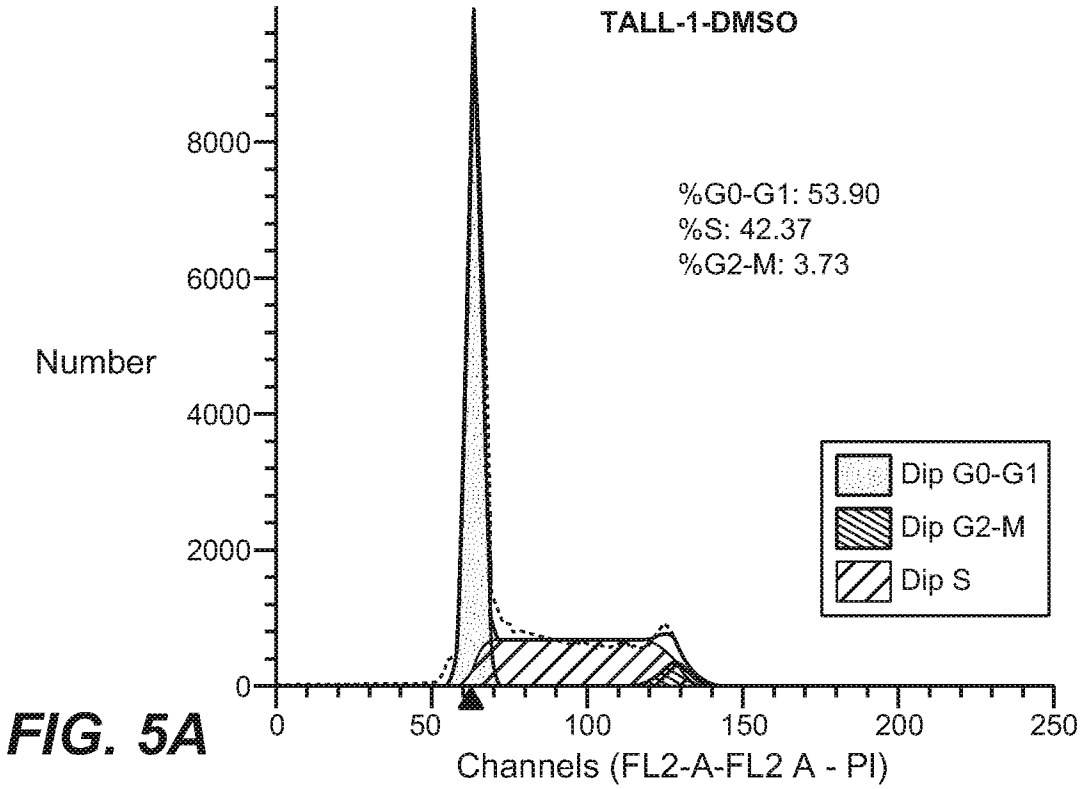

TALL-1-DMSO
%G0-G1: 53.90
%S: 42.37
%G2-M: 3.73
Number
8000
6000
4000
2000
0
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 5A

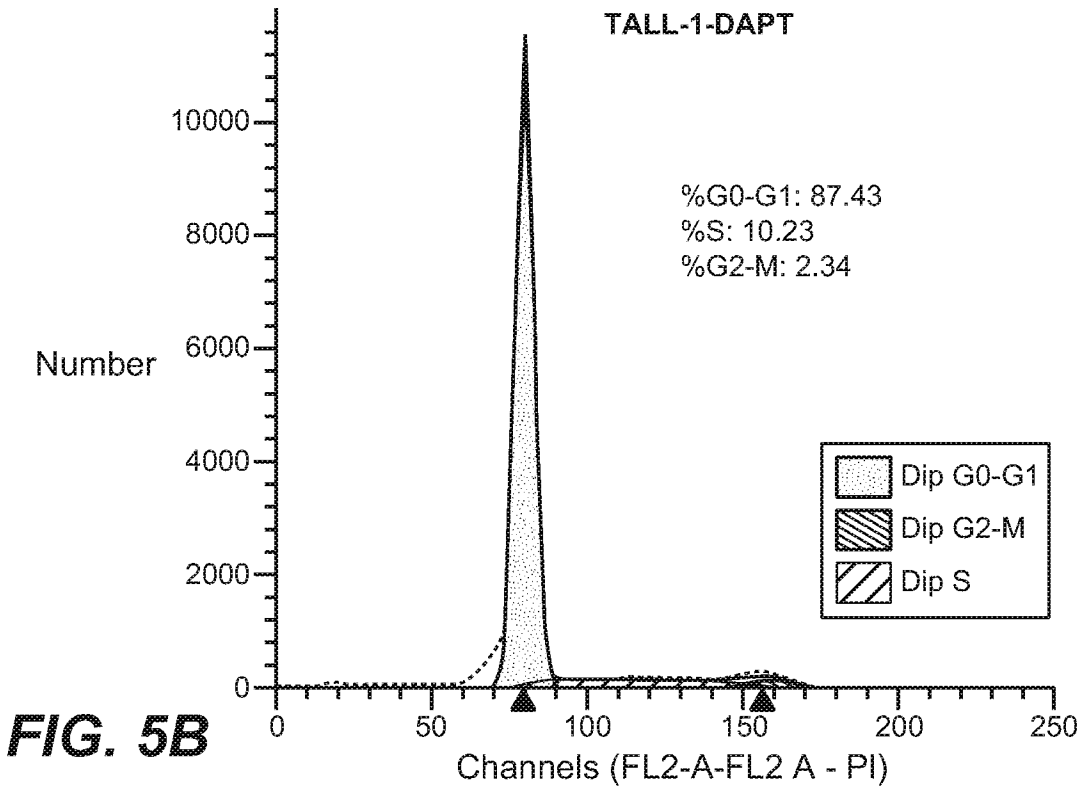

TALL-1-DAPT
%G0-G1: 87.43
%S: 10.23
%G2-M: 2.34
Number
10000
8000
6000
4000
2000
0
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 5B

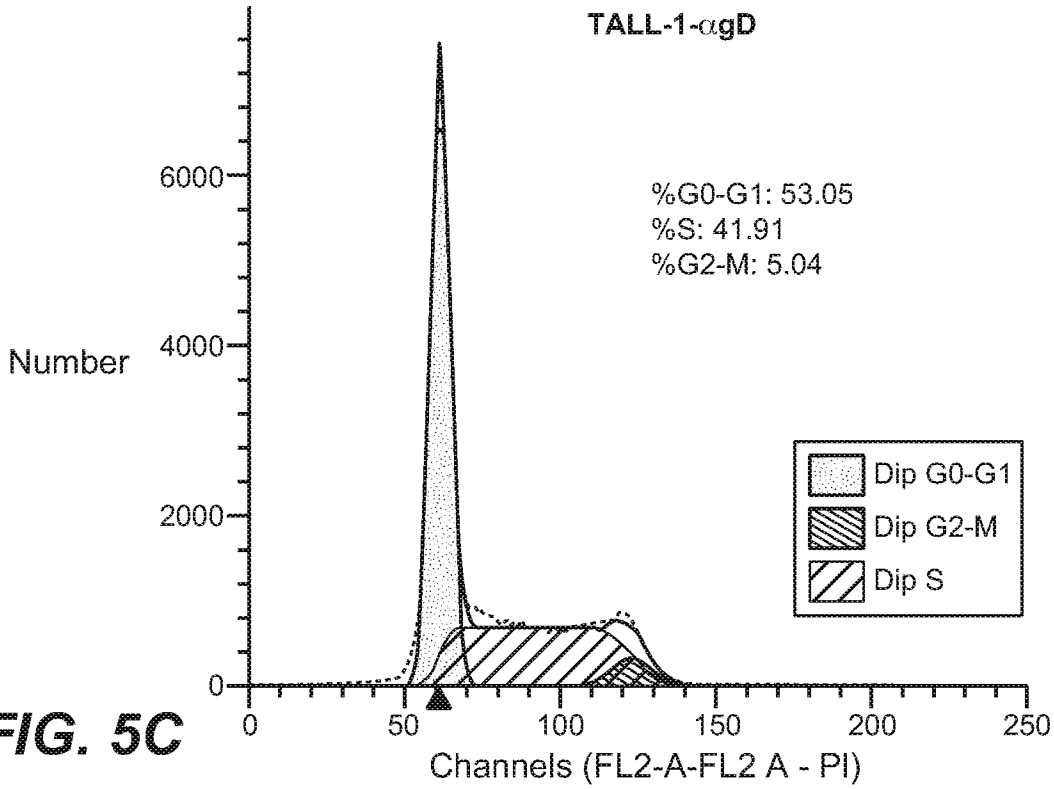

TALL-1-αgD
%G0-G1: 53.05
%S: 41.91
%G2-M: 5.04
Number
6000
4000
2000
0
Dip G0-G1
Dip G2-M
Dip S
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)

FIG. 5C

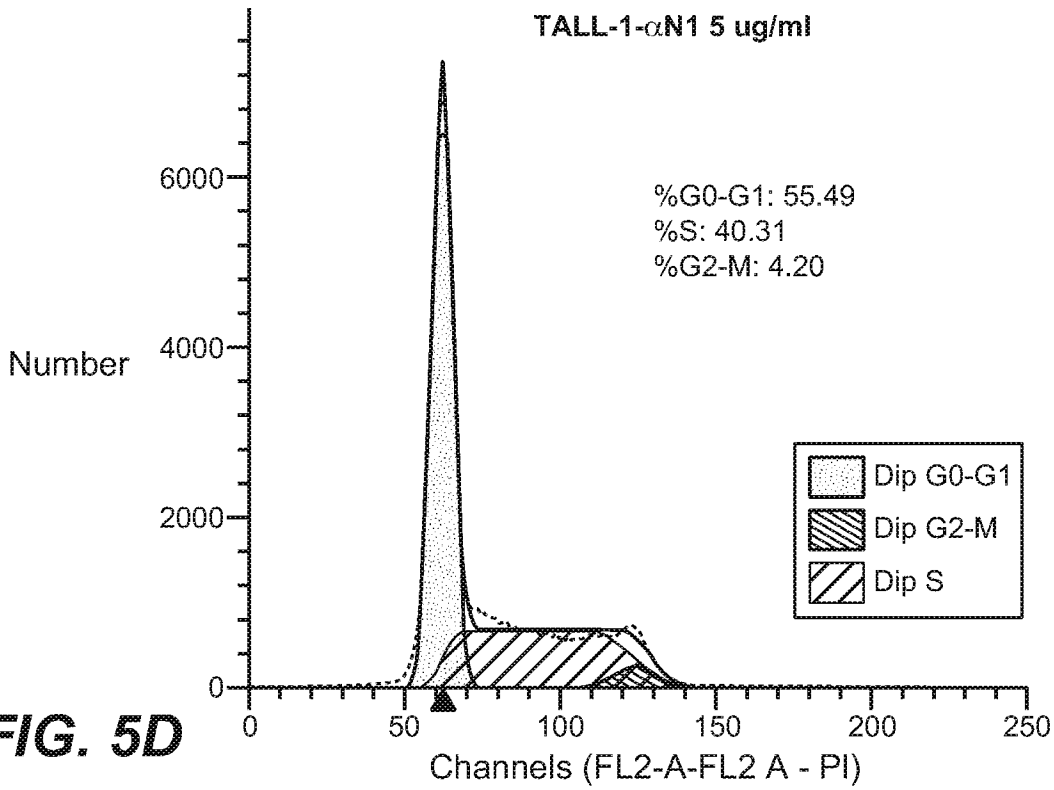

TALL-1-αN1 5 ug/ml
%G0-G1: 55.49
%S: 40.31
%G2-M: 4.20
Number
6000
4000
2000
0
Dip G0-G1
Dip G2-M
Dip S
0
50
100
150
200
250
Channels (FL2-A-FL2 A - PI)

FIG. 5D

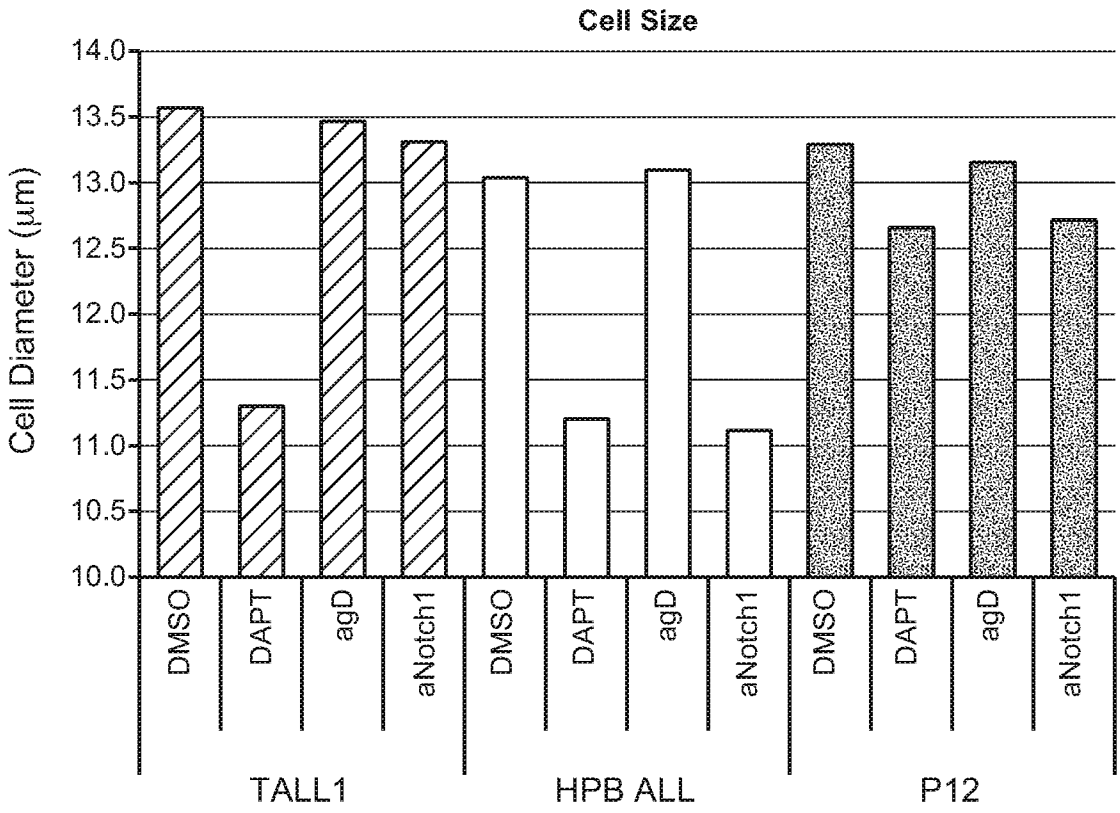

Cell Size
Cell Diameter (µm)
14.0
13.5
13.0
12.5
12.0
11.5
11.0
10.5
10.0
DMSO
DAPT
agD
aNotch1
DMSO
DAPT
agD
aNotch1
DMSO
DAPT
agD
aNotch1
TALL1
HPB ALL
P12

FIG. 6

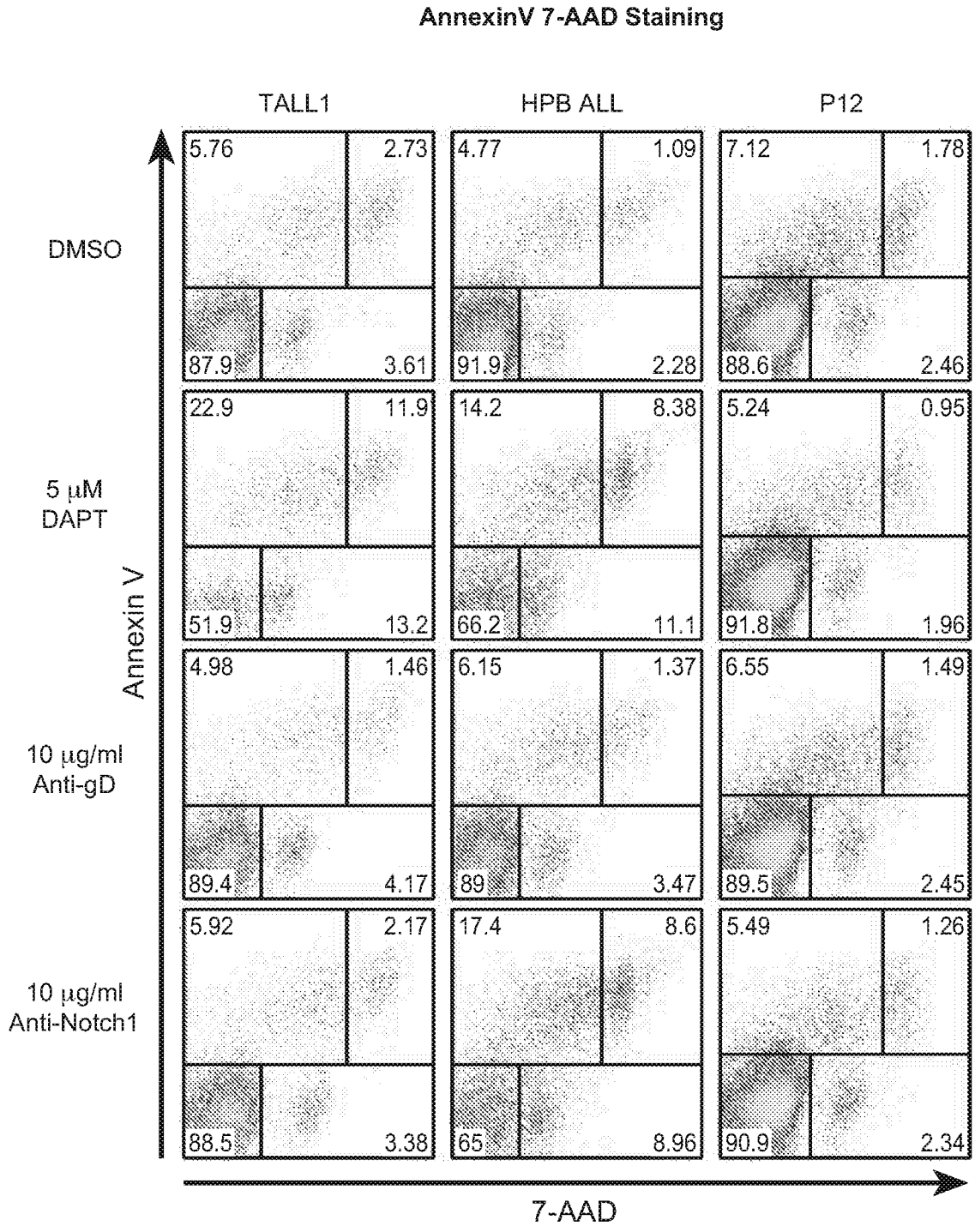

AnnexinV 7-AAD Staining
TALL1
HPB ALL
P12
DMSO
5 μM DAPT
10 μg/ml Anti-gD
10 μg/ml Anti-Notch1
Annexin V
7-AAD
5.76
2.73
87.9
3.61
4.77
1.09
91.9
2.28
7.12
1.78
88.6
2.46
22.9
11.9
51.9
13.2
14.2
8.38
66.2
11.1
5.24
0.95
91.8
1.96
4.98
1.46
89.4
4.17
6.15
1.37
89
3.47
6.55
1.49
89.5
2.45
5.92
2.17
88.5
3.38
17.4
8.6
65
8.96
5.49
1.26
90.9
2.34

FIG. 7

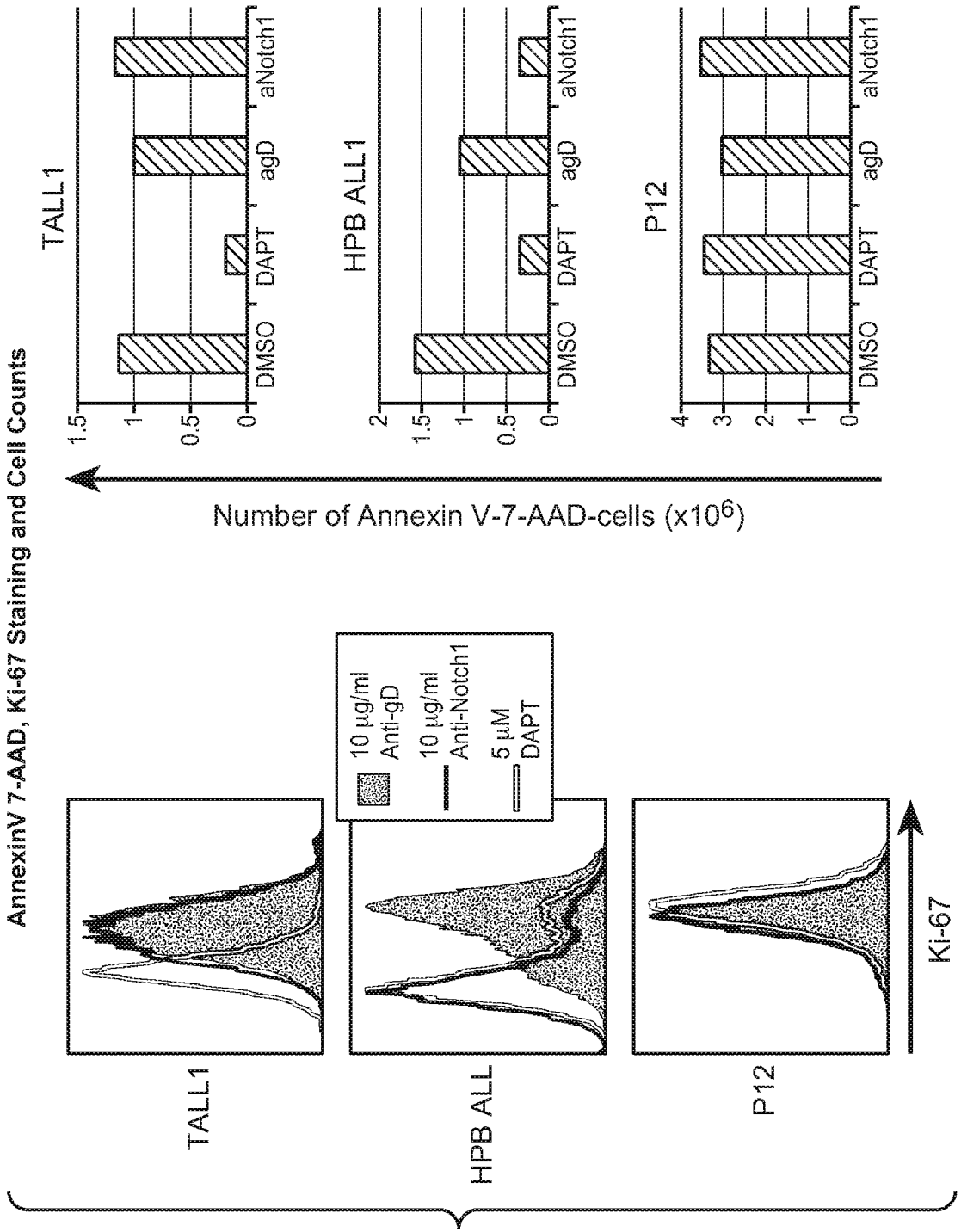

AnnexinV 7-AAD, Ki-67 Staining and Cell Counts
TALL1
HPB ALL
P12
Ki-67
10 µg/ml Anti-gD
10 µg/ml Anti-Notch1
5 µM DAPT
Number of Annexin V-7-AAD-cells (x10^6)
TALL1
HPB ALL1
P12
DMSO
DAPT
agD
aNotch1

FIG. 8

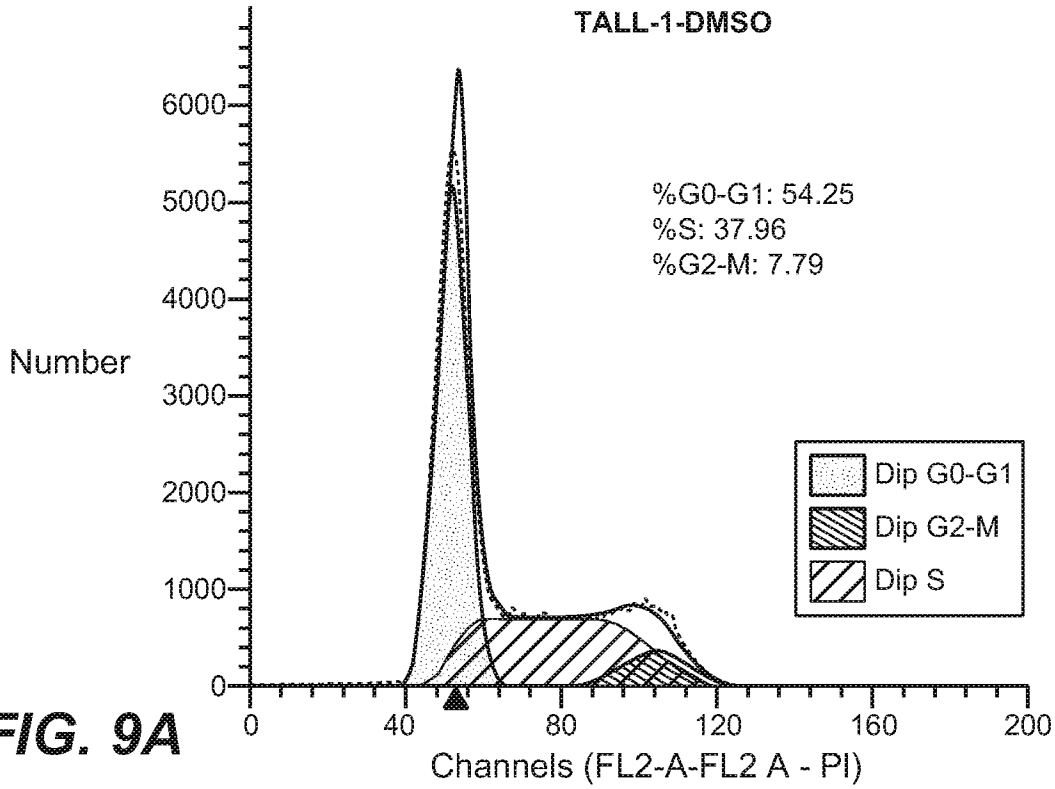

TALL-1-DMSO
%G0-G1: 54.25
%S: 37.96
%G2-M: 7.79
Number
6000
5000
4000
3000
2000
1000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9A

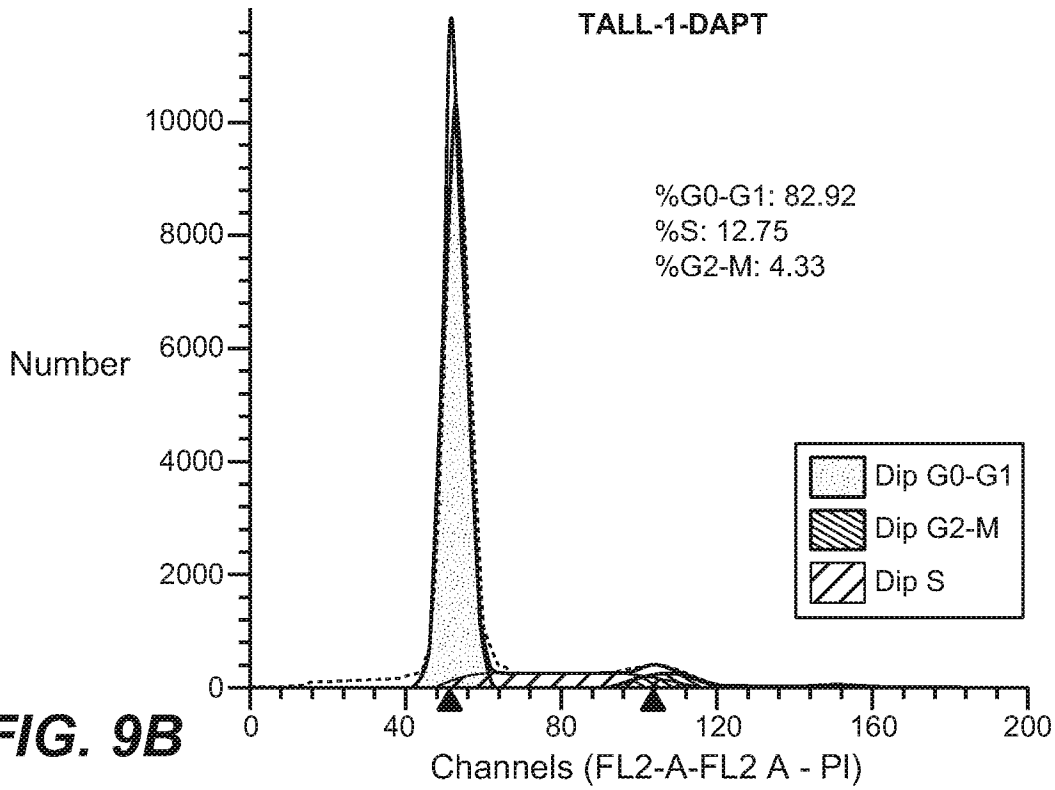

TALL-1-DAPT
%G0-G1: 82.92
%S: 12.75
%G2-M: 4.33
Number
10000
8000
6000
4000
2000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9B

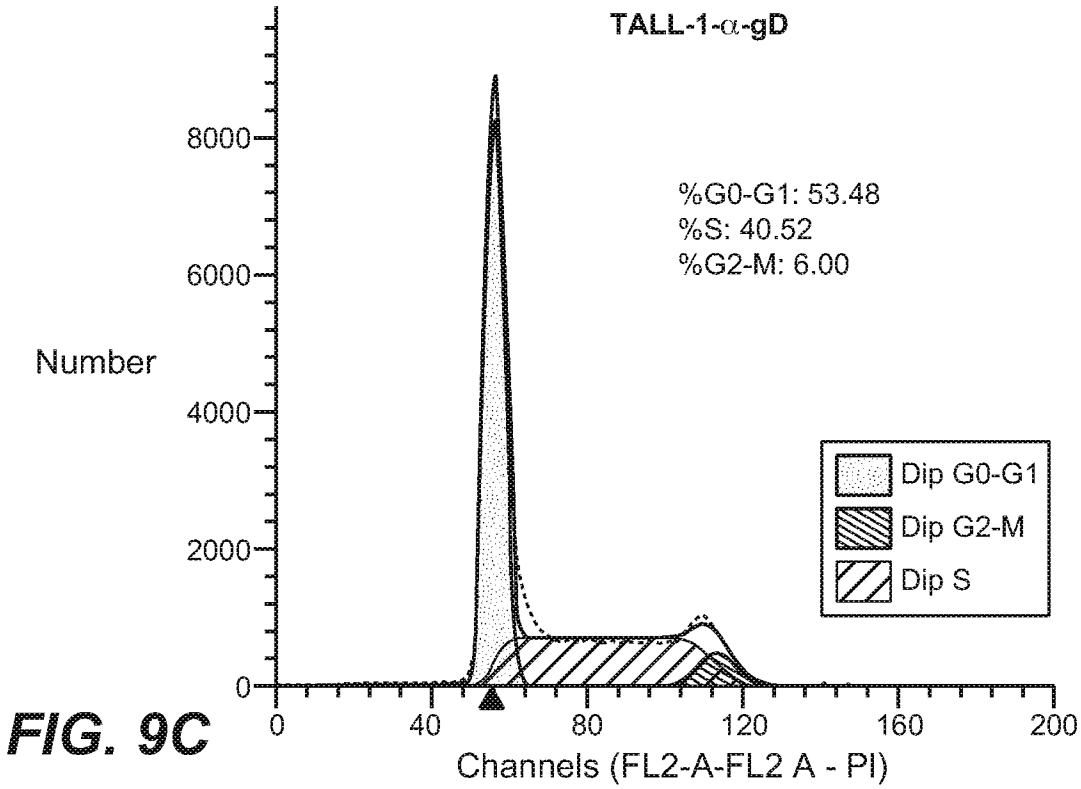

TALL-1-α-gD
%G0-G1: 53.48
%S: 40.52
%G2-M: 6.00
Number
8000
6000
4000
2000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9C

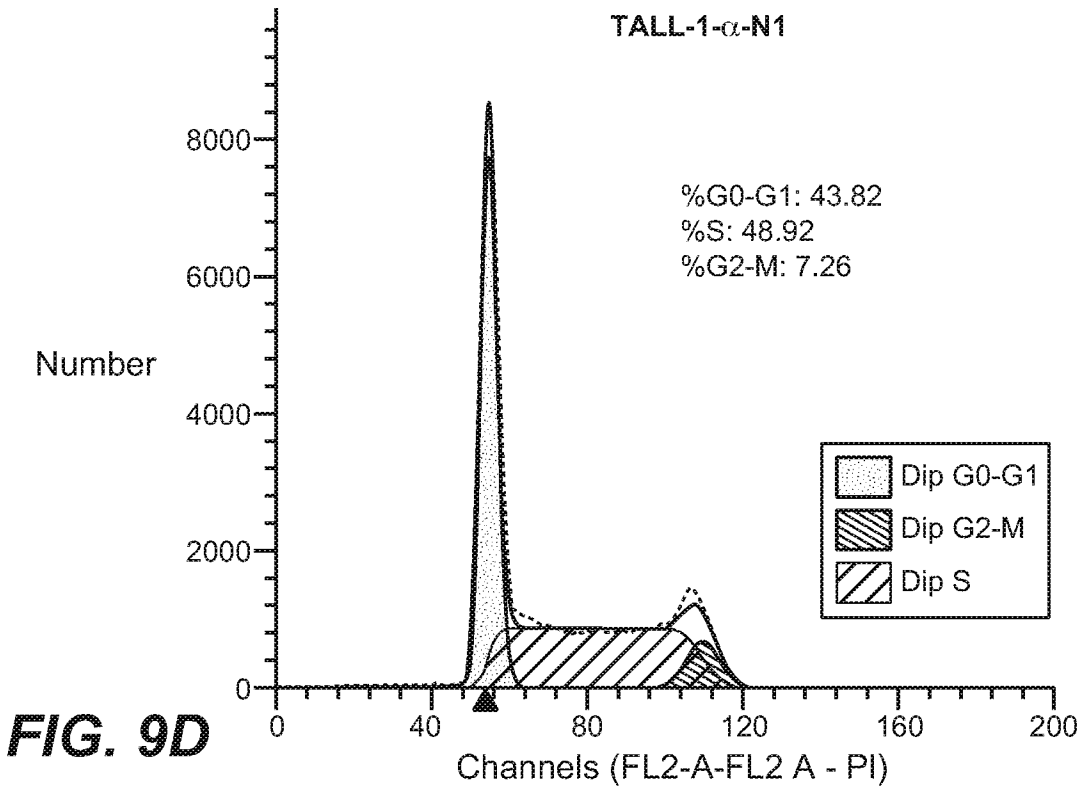

TALL-1-α-N1
%G0-G1: 43.82
%S: 48.92
%G2-M: 7.26
Number
8000
6000
4000
2000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9D

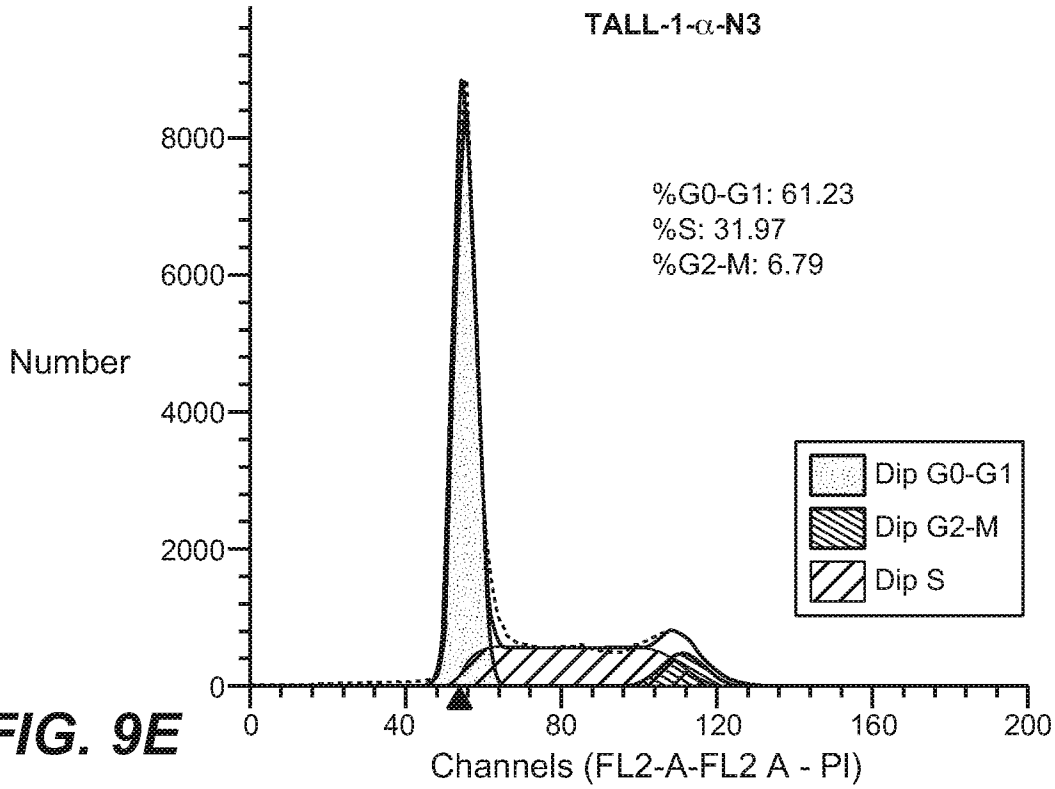

TALL-1-α-N3
%G0-G1: 61.23
%S: 31.97
%G2-M: 6.79
Number
8000
6000
4000
2000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9E

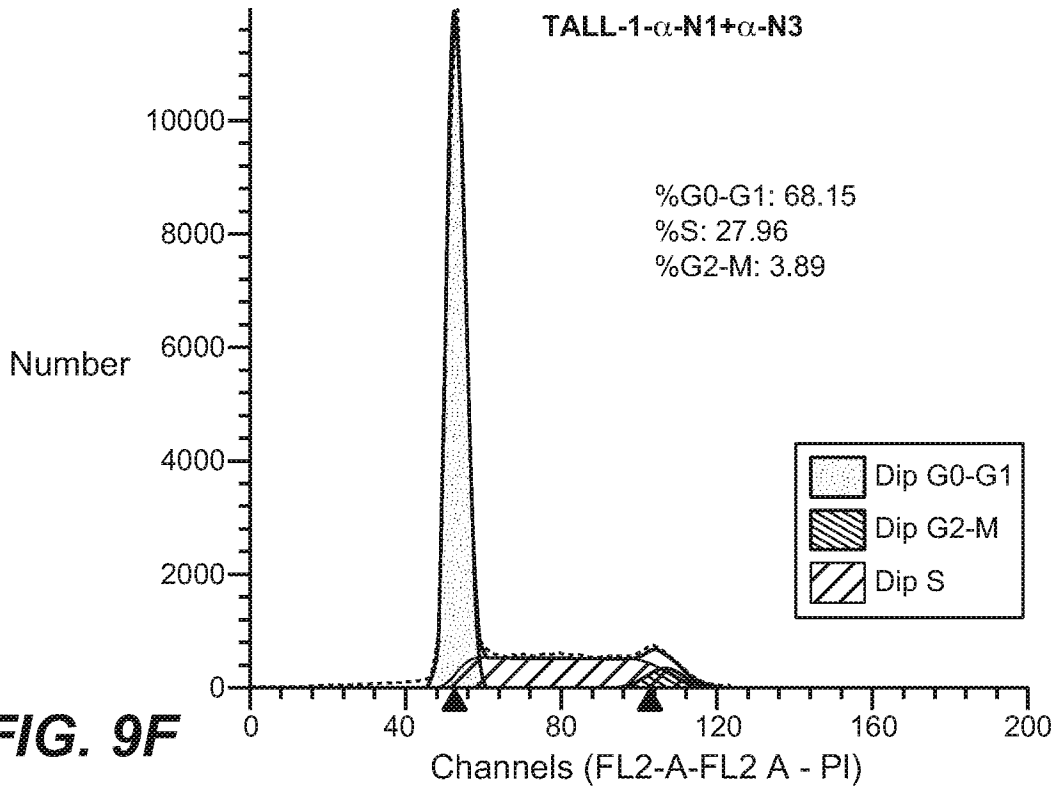

TALL-1-α-N1+α-N3
%G0-G1: 68.15
%S: 27.96
%G2-M: 3.89
Number
10000
8000
6000
4000
2000
0
0
40
80
120
160
200
Channels (FL2-A-FL2 A - PI)
Dip G0-G1
Dip G2-M
Dip S

FIG. 9F

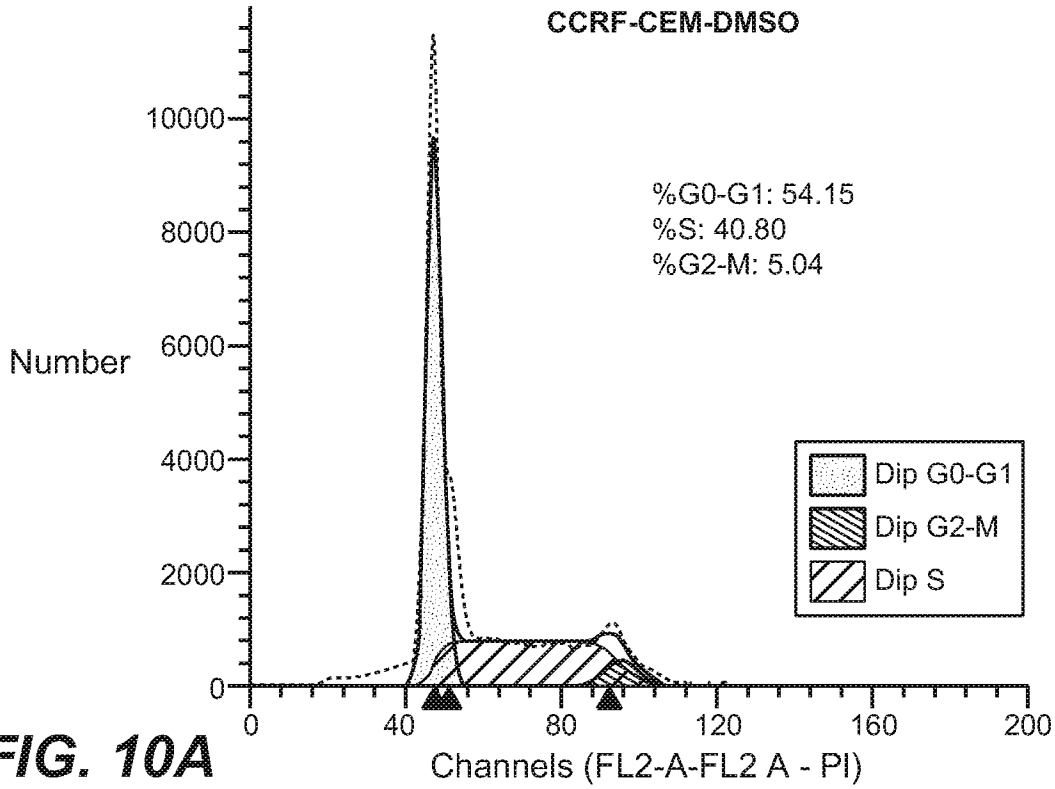


FIG. 10A

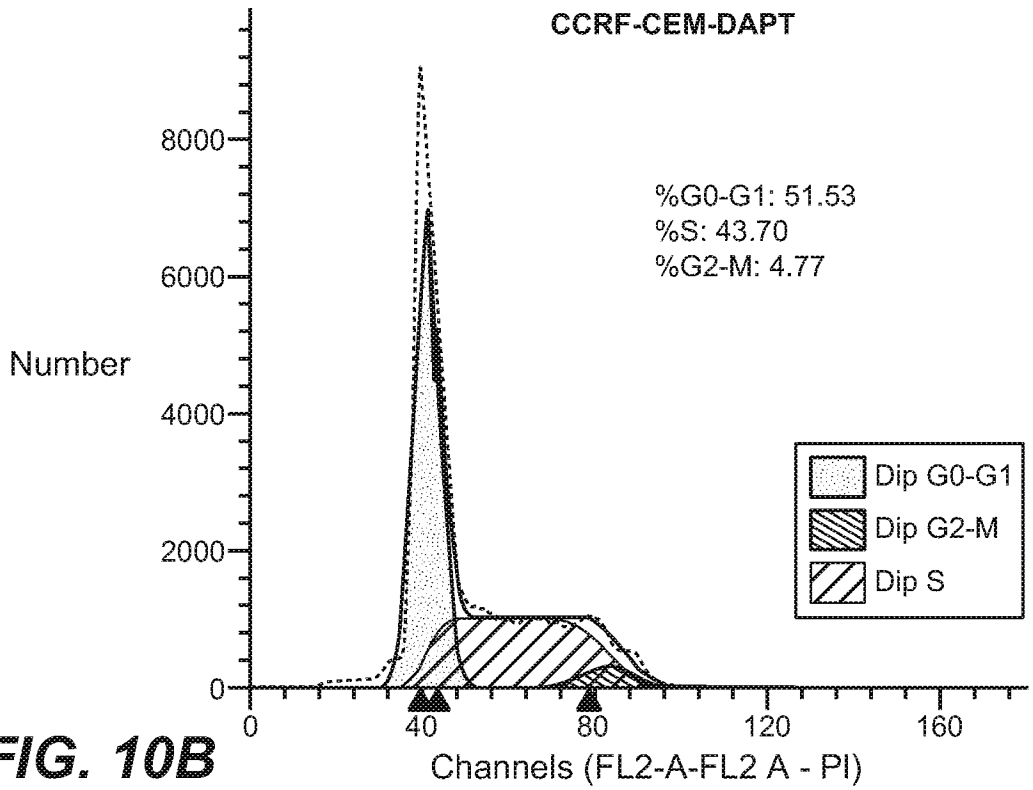


FIG. 10B

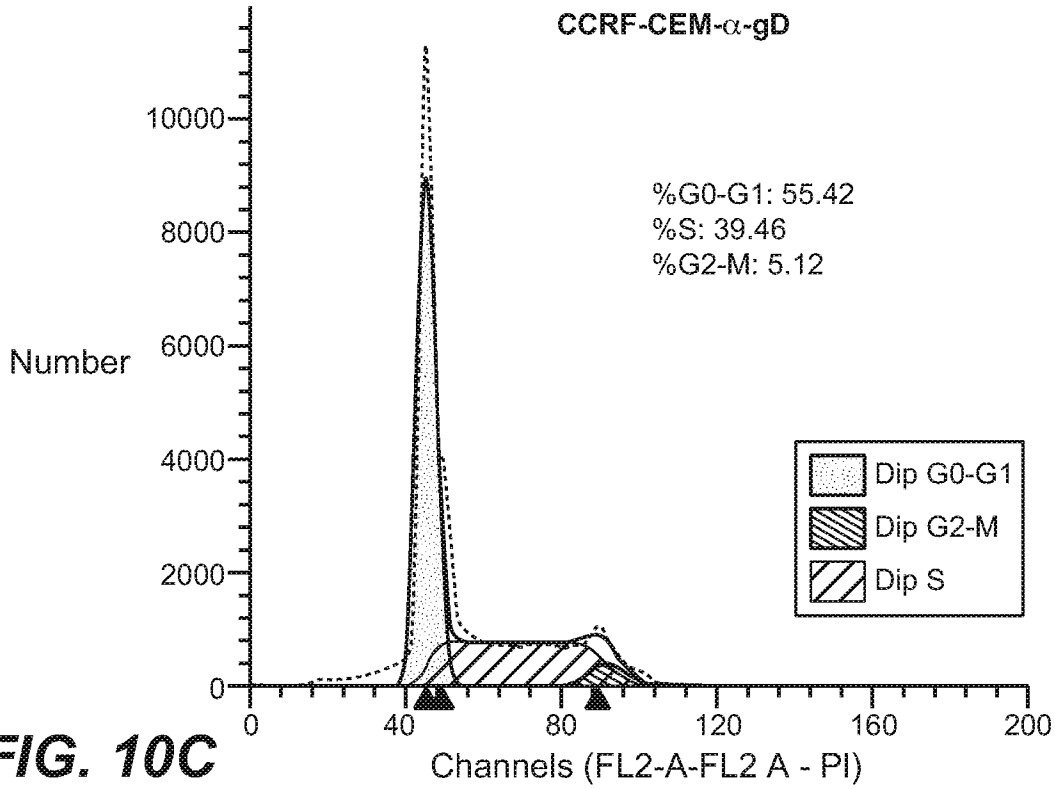


FIG. 10C

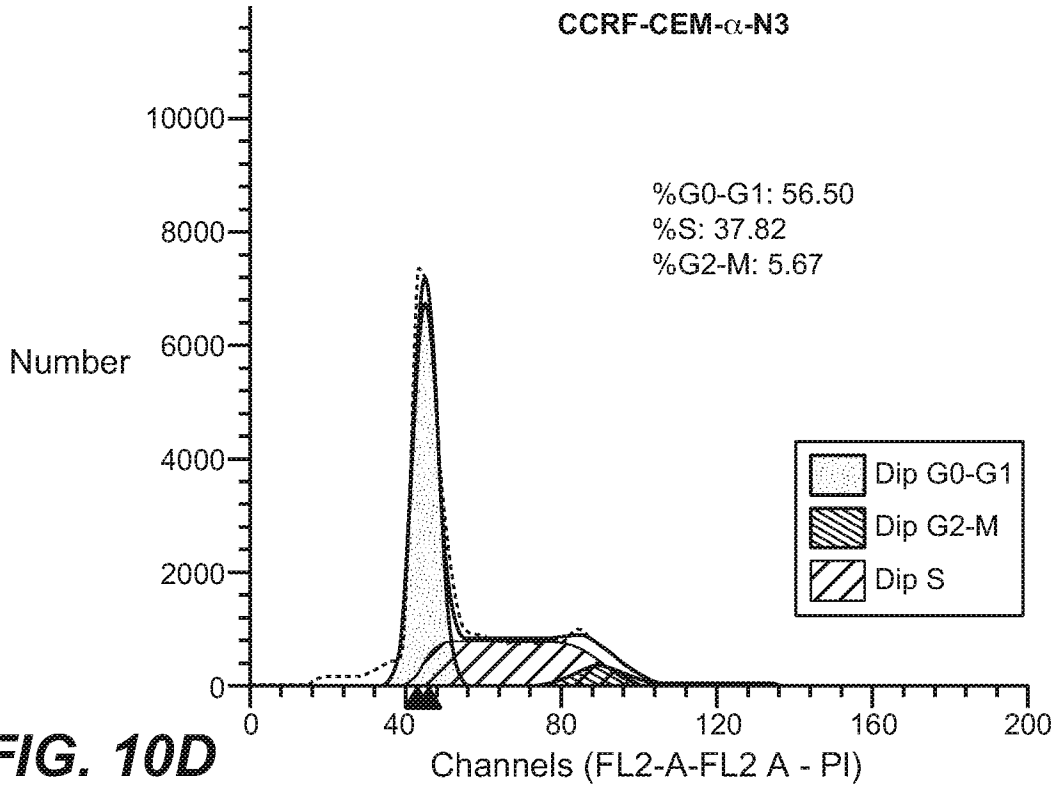


FIG. 10D

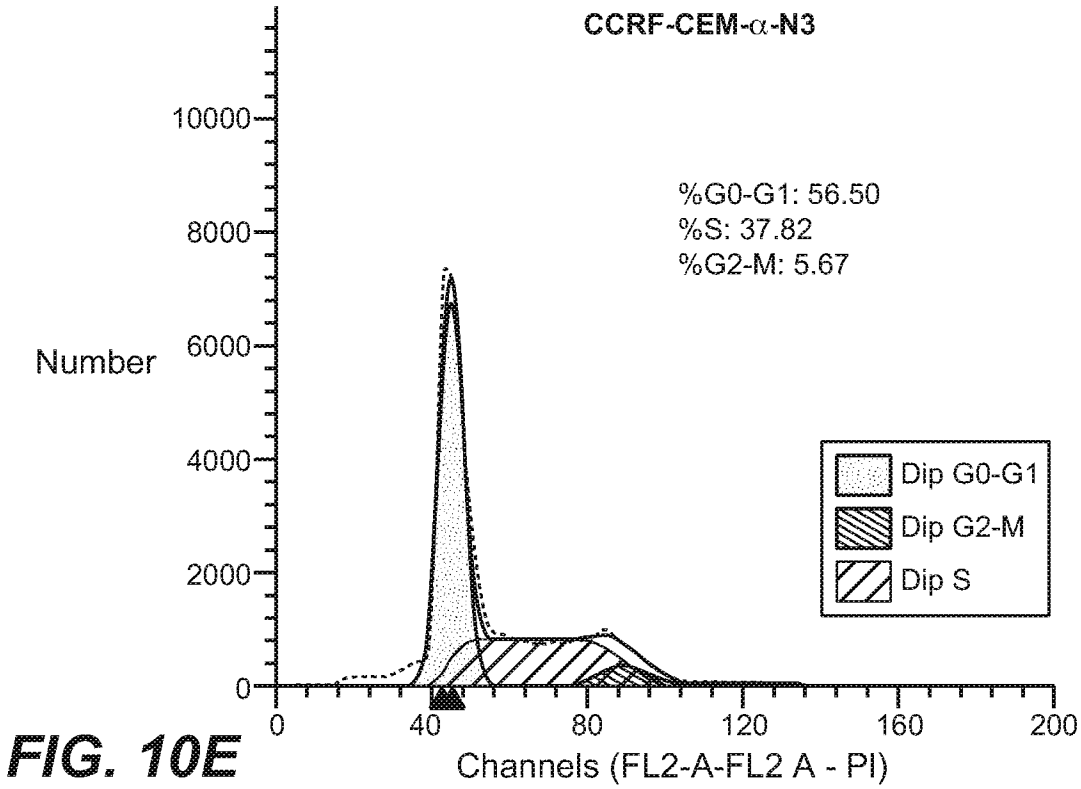


FIG. 10E

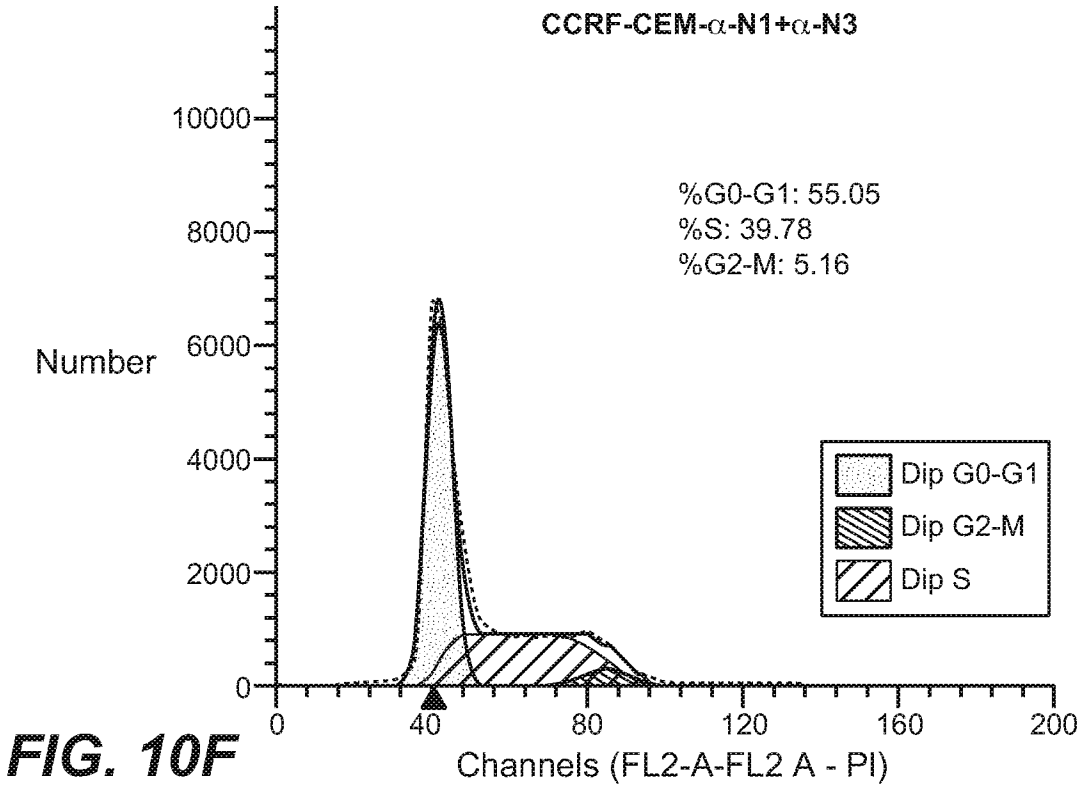


FIG. 10F

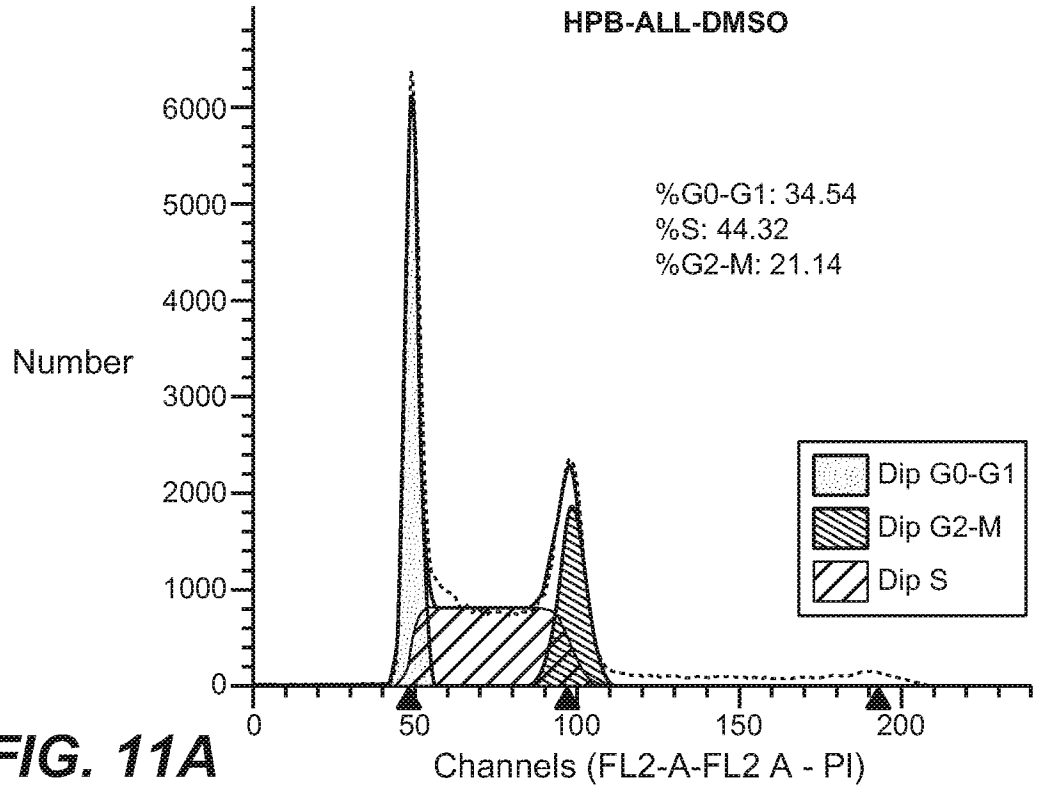


FIG. 11A

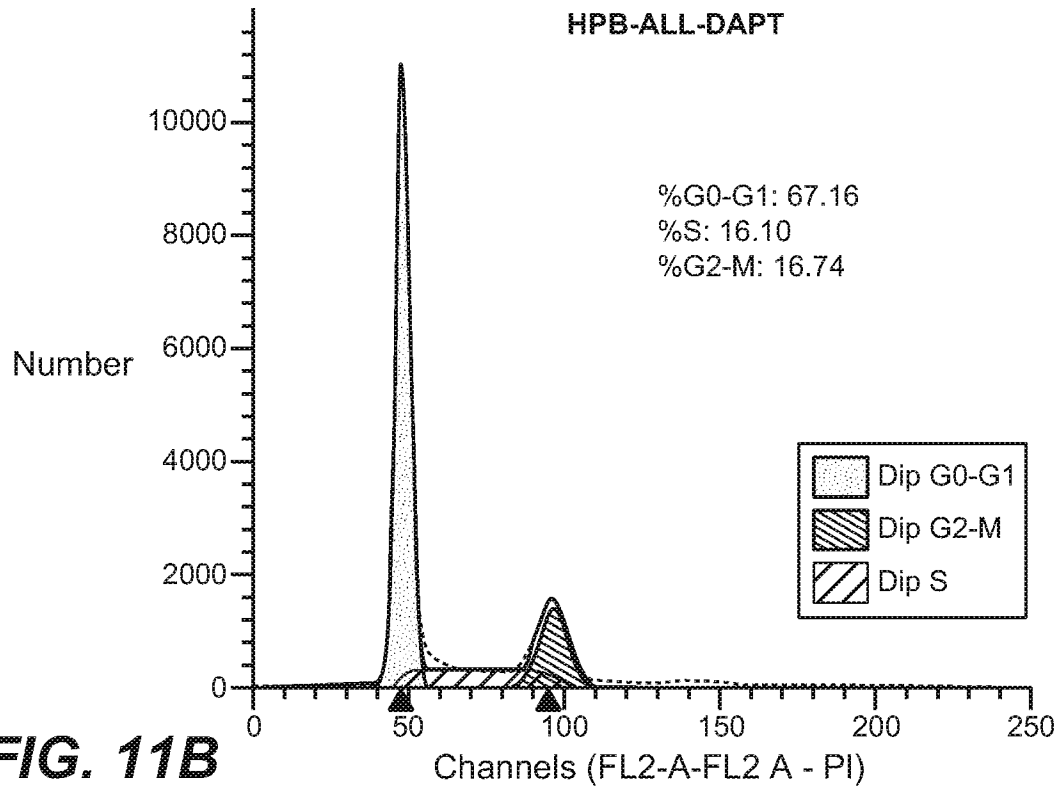


FIG. 11B

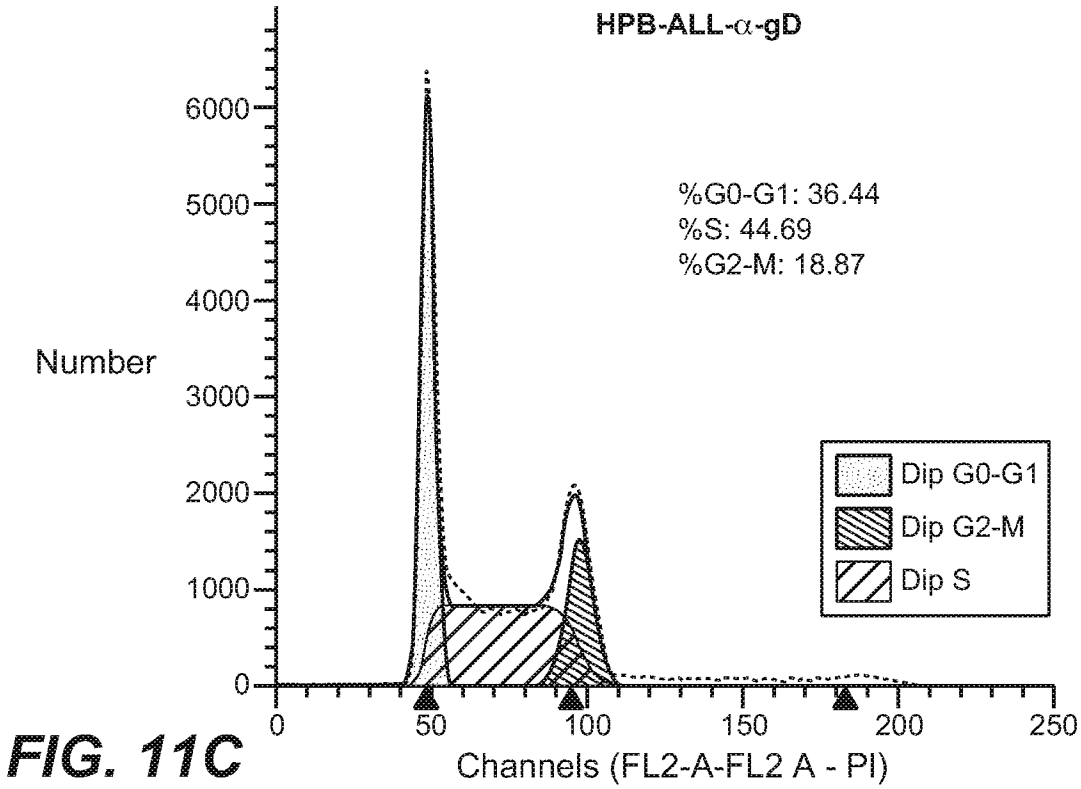


FIG. 11C

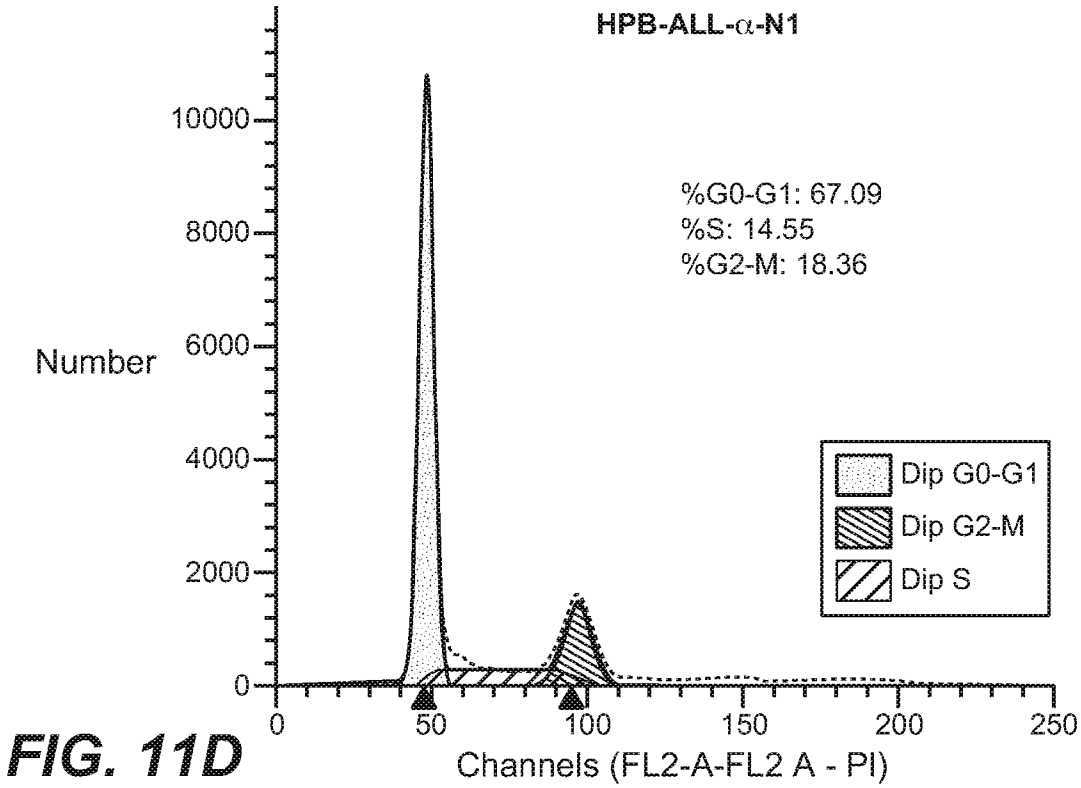


FIG. 11D

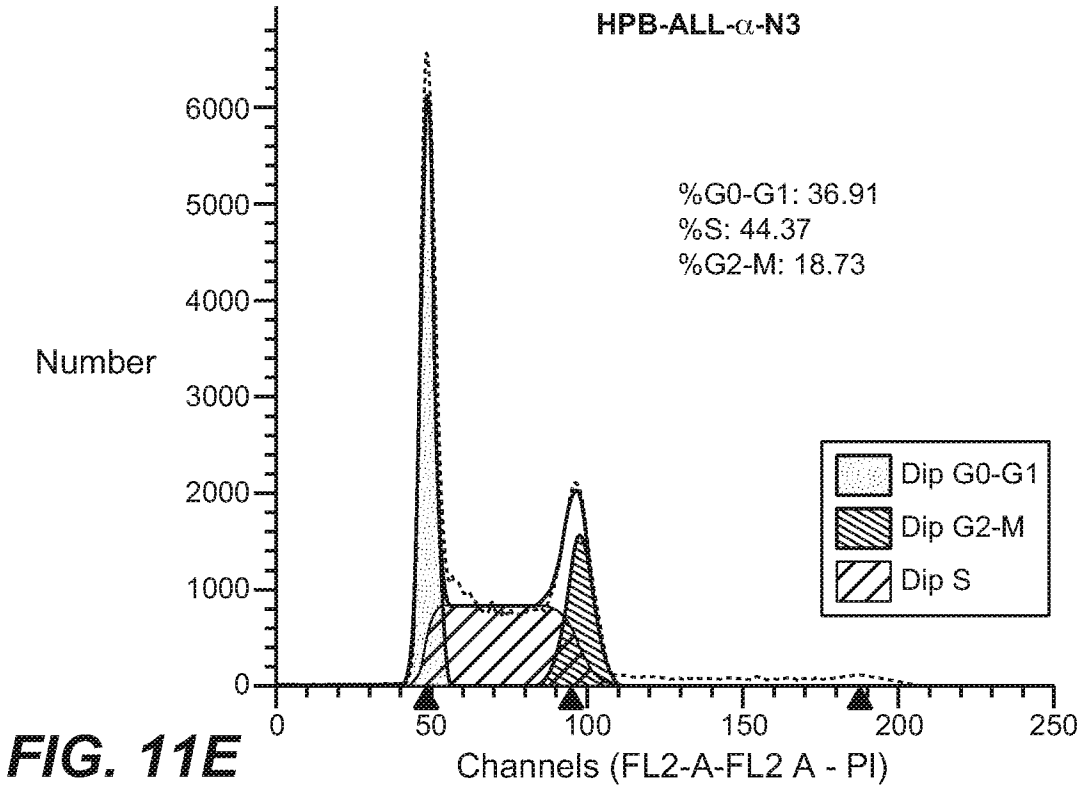


FIG. 11E

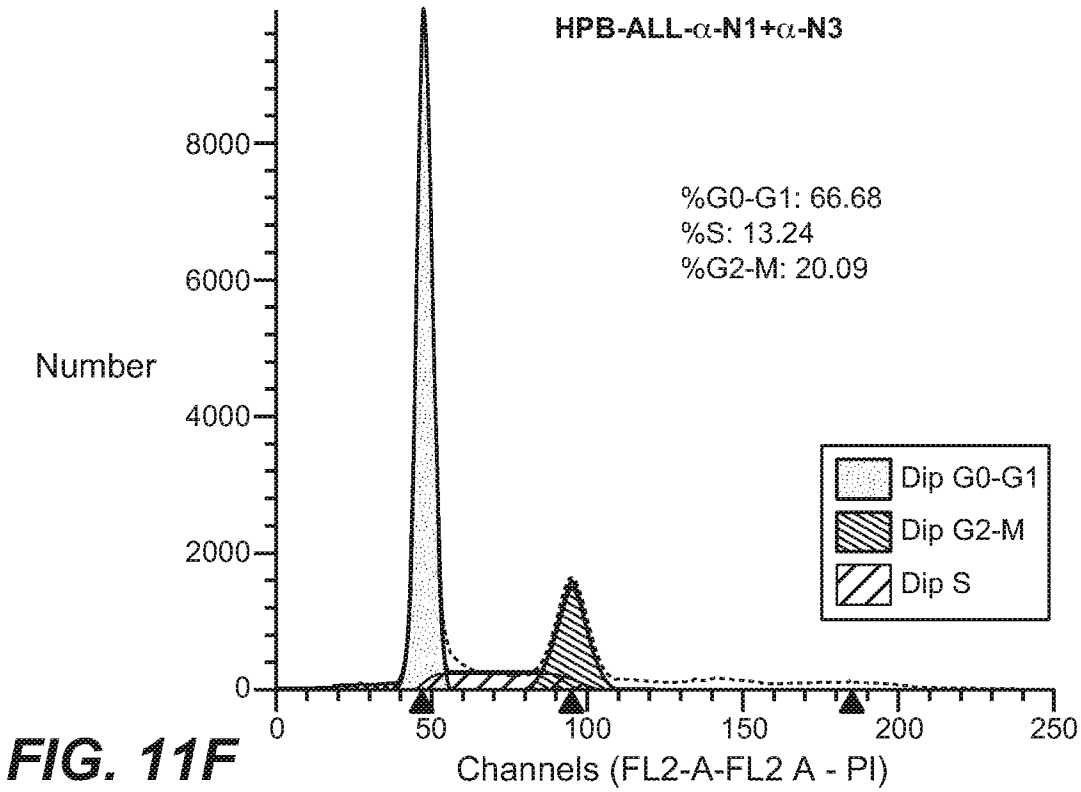


FIG. 11F

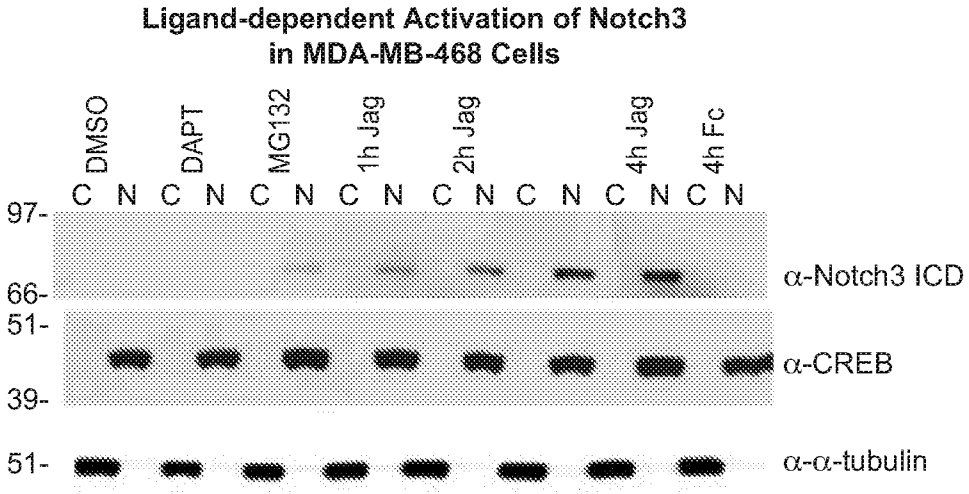
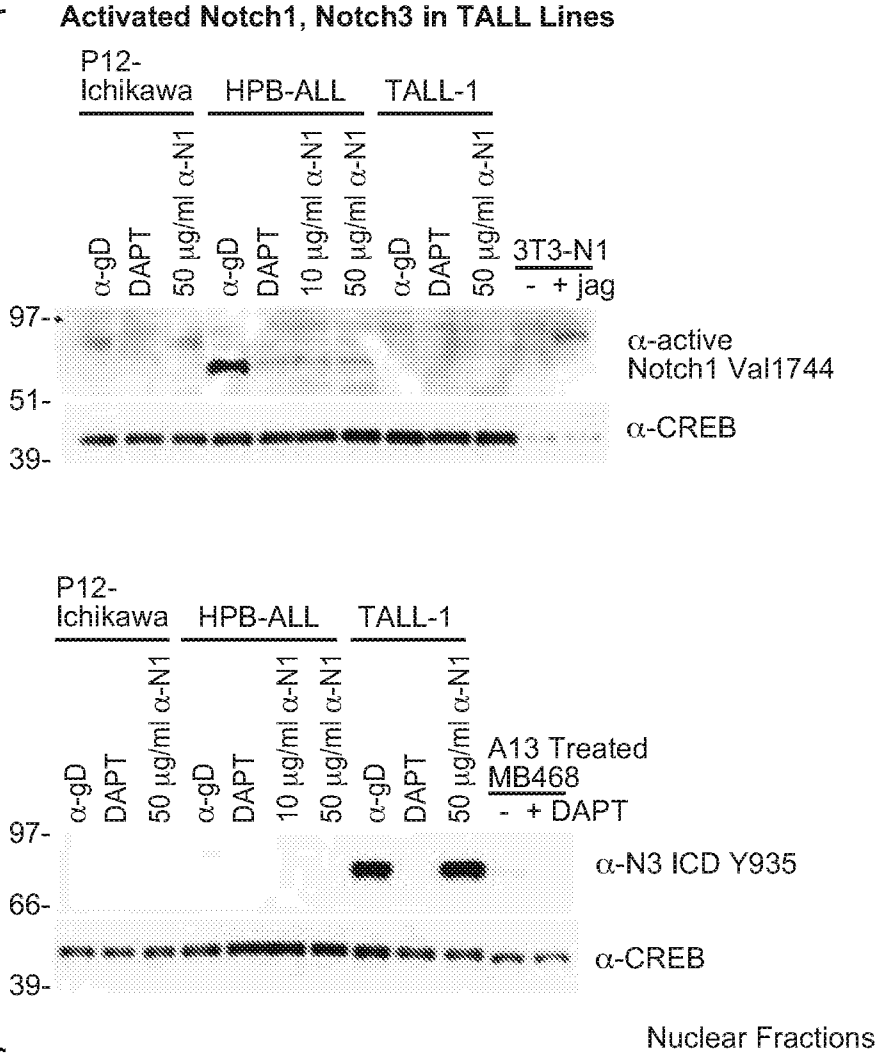

Ligand-dependent Activation of Notch3
in MDA-MB-468 Cells
DMSO
DAPT
MG132
1h Jag
2h Jag
4h Jag
4h Fc
C N C N C N C N C N C N C N C N
97-
66-
51-
39-
51-
α-Notch3 ICD
α-CREB
α-α-tubulin

FIG. 12

FIG. 13


Activated Notch1, Notch3 in TALL Lines
P12-Ichikawa
HPB-ALL
TALL-1
α-gD
DAPT
50 μg/ml α-N1
10 μg/ml α-N1
3T3-N1
- + jag
97-
51-
39-
α-active Notch1 Val1744
α-CREB
A13 Treated MB468
- + DAPT
66-
α-N3 ICD Y935
Nuclear Fractions

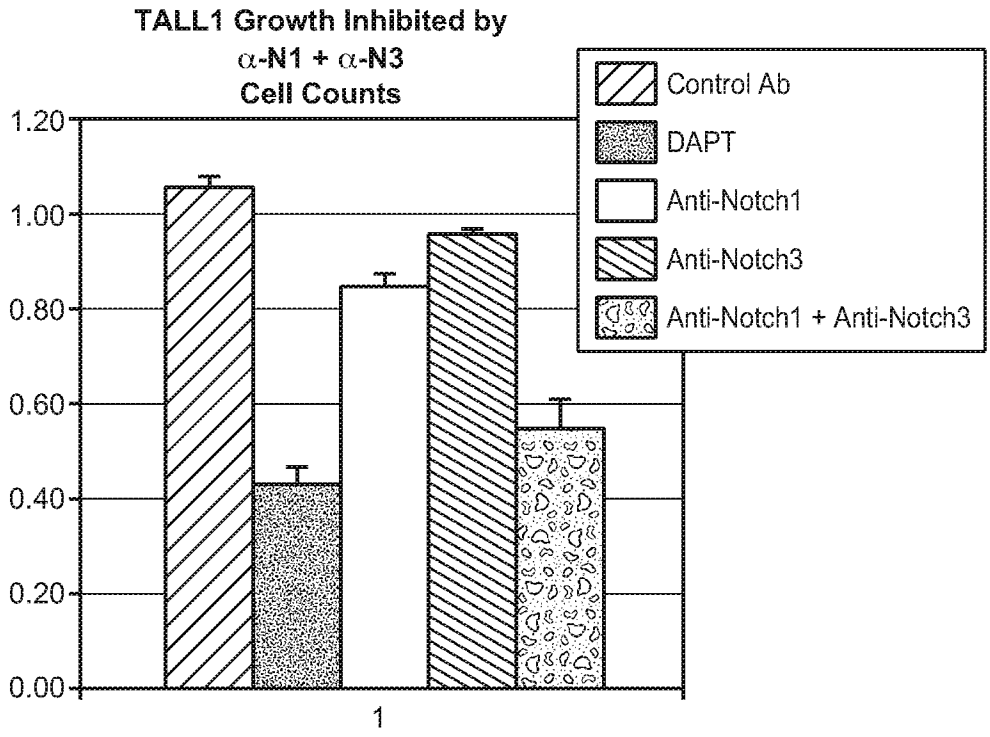

TALL1 Growth Inhibited by
α-N1 + α-N3
Cell Counts
1.20
1.00
0.80
0.60
0.40
0.20
0.00
1
Control Ab
DAPT
Anti-Notch1
Anti-Notch3
Anti-Notch1 + Anti-Notch3

FIG. 14