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DESCRIPTION

[0001] The invention relates to the fields of biology, immunology, medicine and cancer therapy, in particular therapy against myeloproliferative or lymphoproliferative disorders. More in particular, the invention relates to antibodies against acute myeloid leukemia cells.

[0002] Acute myeloid leukemia (AML) is a high risk malignancy with five year survival rates of 40 - 50% in patients younger than 60 years of age. For patients over 65 years of age outcomes are even worse, with only less than 20% of patients obtaining durable remissions. Allogeneic stem cell transplantation is frequently applied in the treatment of acute leukemia. It was initially designed to rescue patients from otherwise lethal myeloablative chemotherapy but was subsequently found to be complicated by alloreactive immune response related complications (graft versus host disease; GvHD). T cell depletion of grafts before reinfusion averted GvHD but the observation that T cell depleted graft recipients, similar to monozygotic twin donor transplant recipients, experienced much higher rates of relapse made it increasingly clear that the success of allogeneic SCT is dependent on the induction of an anti-leukemic immune response (graft versus leukemia (GvL)). This has led to the development of strategies to apply allogeneic stem cell transplantation without myeloablative conditioning (reduced intensity stem cell transplantation, RIST), to reduce cytotoxicity and to allow allogeneic SCT in a larger group of patients including older patients and heavily pretreated patients. Preparative regimens in RIST are aimed at decimating the recipients adaptive immune system to prevent graft rejection, without complete ablation of the recipients bone marrow thereby reducing early SCT toxicity. Following transplantation, donor stem cells gradually replace stem cells of the recipient and full donor chimerism is usually achieved within three months after SCT. Although allogeneic SCT is curative in significant numbers of patients, and much progress has been made in the supportive care of SCT recipients, still 15-30% of patients die as a result of transplantation related complications such as GvHD and infectious complications (arising as a result of slow immune recovery following SCT or as a complication of immunosuppressive therapy of GvHD).

[0003] Hence, although SCT is potentially curative when potent graft versus leukemia (GvL) responses are induced, its therapeutic success is limited by anti-host immune responses leading to GvHD which causes high morbidity and mortality.

[0004] About 70% of SCT patients develop GvHD at one point following SCT, with target organs including the skin, liver, intestine and lung. GvHD is treated with local or systemic immunosuppressive therapy including corticosteroids. A significant number of GvHD patients is not responsive to steroid therapy, and about half of these patients also respond poorly to alternative (and partly still experimental) measures such as mesenchymal stromal cell (MSC) transplantation or T cell modulating therapy such as anti-tumor necrosis factor α (anti-TNF α ; infliximab). Extensive and long-term immunosuppressive therapy is undesirable, since it may hamper the development of therapeutic antileukemia responses. Indeed, when an AML relapse occurs while the patient is still on immunosuppressive therapy, the first step is to rapidly taper immunosuppressants. This may induce a curative GvL response, often at the expense of GvHD. In relapsed patients on immunosuppressive therapy who do not respond to tapering of immunosuppressants or relapsed patients in whom immunosuppressants were already phased out before relapse occurred but who had not developed GvHD, tumor load reduction by chemotherapy, followed by increasing doses of donor- lymphocyte infusions (DLI) may lead to durable remission of disease. While the absence of diagnostic tests to demonstrate the presence of a robust GvL makes it difficult to estimate exactly how often allogeneic SCT induce GvL responses in primary or relapsed AML, some studies provided compelling evidence of the induction of such a response in a considerable number of patients. For example, Schmid and colleagues demonstrated potent GvL responses by DLI in 50% of a small group of AML patients with disease relapse who were in second remission following chemotherapy (Schmid et al., 2007). Schlenk and colleagues convincingly showed the additive value of allogeneic SCT in primary AML, with a doubling of the 5-year disease free survival in patients with high risk AML who received an allogeneic SCT from a sibling, compared with patients who did not have a suitable sibling donor (Schlenk et al., 2008). Thus, GvL responses often occur at the cost of GvHD, and the observation that T cell depletion from the graft reduced GvHD incidence but increased disease relapse rates suggested that both are primarily mediated by T cell dependent immune

responses against recipient-antigens.

[0005] In view of the high GvHD incidence after allogeneic stem cell transplantation, resulting in death of 15-30% of the patients, as well as the fact that a suitable donor is not always available for a given patient, alternative treatment approaches are needed. It is an object of the present invention to provide alternative means and methods for counteracting and/or preventing AML.

[0006] The present invention relates to patient-derived, AML-specific, human antibodies that are able to bind intact AML cells. Provided is an isolated, synthetic or recombinant human antibody, or a functional part thereof, which is able to bind to snRNP200 of acute myeloid leukemia (AML) cells and which is able to diminish proliferation of AML cells by oncosis. Also provided is an isolated, synthetic or recombinant antibody, or a functional thereof capable of binding to snRNP200 of AML cells and diminishing proliferation of AML cells, comprising a heavy chain CDR1, CDR2 and CDR3 sequence and a light chain CDR1, CDR2 and CDR3 sequence as defined in claim 2. Importantly, the antibodies are derived from human AML patients that received an allogeneic SCT and are in complete remission indicating that the antibodies are effective against AML. Indeed, in the Examples it has been demonstrated that antibodies according to the present invention are able to bind intact AML cells. The AML-specific human antibodies according to the present invention are, therefore, particularly suitable for use in anti AML therapy. For instance, an antibody according to the invention is provided with a toxic moiety. After administration, AML cells will be bound and/or internalised and the toxic moiety will exert its toxic effect on the AML cell. Alternatively, in some embodiments antibody-dependent cell-mediated cytotoxicity (ADCC) or complement-dependent cytotoxicity (CDC) is induced using an antibody according to the present invention, optionally bound to an immunomodulatory compound. The fact that human antibodies are provided, or functional parts or functional equivalents of human antibodies, diminishes the chance of side effects in human beings, which is an important advantage. Hence, with the antibodies provided by the present invention, novel AML treatment options have become available which can be used in addition to existing AML therapy, or as an alternative.

[0007] An important embodiment of the present invention provides human AML-specific antibodies that are capable of diminishing proliferation of AML cells. Administration of such antibodies to an AML patient will counteract AML cells without the need to add additional (toxic) moieties to the antibody. A particularly preferred embodiment provides human AML-specific antibodies that are capable of diminishing proliferation of AML cells independently from antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC), apoptosis or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells. Preferably, such antibodies are capable of diminishing proliferation of AML cells (essentially) independently from any other immune cells, or complement or apoptosis. As shown in the Examples, such antibodies are capable of directly diminishing or inhibiting AML cell growth, or are even capable of killing AML cells, in the absence of immune cells like NK cells or macrophages, and in the absence of complement. This embodiment is in contrast to prior art approaches such as for instance described in Majeti et al., 2009 and Willingham et al., 2012, wherein a CD47-specific antibody is used in order to enable macrophage phagocytosis of tumor cells. WO 2009/051974 describes the use of C-type lectin-like molecule-1 (CLL-1)-specific antibodies, which are capable of inducing CDC against AML cells *in vitro* in the presence of rabbit complement. Bakker et al., 2004, however, does not envision that antibody-dependent cell-mediated cytotoxicity or complement-dependent cytotoxicity via CLL-1 will be an effective targeting mechanism, and proposes toxin-conjugated CLL-1 antibodies for use against AML. WO 2012/098407 discloses the use of antibodies specific for IL1RAP for inducing antibody-dependent cell-mediated cytotoxicity against AML cells, by recruiting NK cells which induce AML cell death. Hence, the above described prior art focuses on the use of antibodies in order to activate other immune cells, which may not provide the desired results in immune compromised individuals such as AML patients who have undergone chemotherapy with or without an allogeneic SCT.

[0008] WO 2013/071068 describes anti-CXCR4 antibodies that were raised in transgenic transchromosomal mice expressing human antibody genes. The obtained antibodies bind a broad range of hematopoietic cells and are capable of inhibiting growth of an AML cell line *in vitro*. These anti-CXCR4 antibodies induce apoptosis of various AML cell lines.

[0009] Anti-CD33 monoclonal antibody therapy against AML has also been described (Walther et al., 2012). For instance, CD33-specific antibodies coupled to a drug conjugate are described.

[0010] WO 2010/102244 describes a humanized anti-EphA3 antibody that is capable of inducing apoptosis of AML cells. Furthermore, Biernacki et al., 2010 and Wu et al., 2000 describe antibodies obtained from AML patients that are specific for intracellular antigens such as RAB38, TBCE, DUSP12 and RAFTK.

[0011] In conclusion, several publications describe AML antibodies that bind intracellular antigens. Such antibodies are not a first choice for combating living, intact AML cells *in vivo* due to the unreachability of such intracellular targets when the AML cells are intact. Other publications describe antibodies that bind a broad range of hematopoietic cells, for instance through CD33, CXCR4, CD47 or CLL-1. Antibodies which bind a broad range of (hematopoietic) cells involve the risk of severe side-effects.

[0012] Several antibodies described in the art act by inducing phagocytosis, ADCC or CDC, meaning that other immune cells or complement components are required for counteracting AML cells. The use of such antibodies is, therefore, limited in immune compromised individuals. Moreover, some of the described antibodies are not human, which involves a high risk of side effects. Other publications (such as WO 2013/071068 and WO 2010/102244) describe antibodies that induce apoptosis of AML cells.

[0013] In contrast to the above-mentioned publications, the present inventors have taken a different approach. Instead of artificially producing antibodies against a component that is present on, amongst other things, AML cells, the inventors have isolated antibodies from human AML patients who, after receiving an allogeneic SCT, mounted a potent graft versus leukemia response as they maintained in complete remission. These antibodies are capable of specifically binding snRNP200 of intact AML cells. Hence, instead of using artificially developed antibodies, the present inventors have elegantly taken advantage of the natural immune defenses elicited in human AML patients after receiving an allogeneic SCT. The humoral response found in nature results in a very adequate selection and outgrowth of B-cells that produce effective antibodies *in vivo*. The antibodies according to the present invention, or functional parts or functional derivatives thereof, are therefore particularly suitable for binding AML cells in AML patients. The fact that the antibodies are specific for intact AML cells, instead of intracellular antigens, makes them particularly suitable for AML therapy.

[0014] As described, an antibody or functional part thereof according to the invention can be coupled to a toxic moiety. Such toxic moiety will then be directed to AML cells *in vivo* through the binding of the antibody to AML cells. One embodiment of the present invention provides human antibodies, or functional parts thereof, which are able to bind intact AML cells and which are able to diminish proliferation of AML cells. Such antibody obviates the need of coupling the antibody to an additional, toxic component (although the use of a toxic moiety can still be useful for providing additional anti-AML effects). In one particularly preferred embodiment, human antibodies, or functional parts thereof, according to the invention are provided which are able to bind intact AML cells and which are able to diminish proliferation of AML cells independently from antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC) or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells. Preferably, such antibodies are capable of diminishing proliferation of AML cells independently from, or essentially independently from, other immune cells or complement components. The use of such antibodies, having a strong anti-AML activity, is preferred, especially in immune-compromised individuals. One preferred aspect of the present invention therefore provides an isolated, synthetic or recombinant human antibody, or a functional part thereof, which is able to bind snRNP of acute myeloid leukemia (AML) cells and which is able to diminish proliferation of AML cells independently from, or essentially independently from, antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC) or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells. Preferably, such antibodies are capable of diminishing proliferation of AML cells (essentially) independently from any other immune cells or complement. As shown in the Examples, at least antibodies AT12-023, AT12-025 and AT13-024 have these characteristics. These are, therefore, preferred antibodies according to the present invention.

[0015] In a further preferred embodiment, human antibodies, or functional parts thereof, according to the invention are provided which are able to bind intact AML cells and which are able to diminish proliferation of AML cells independently from apoptosis. As shown in the Examples, at least antibodies AT12-023, AT13-031 and AT13-037 have this characteristic. This is clear from the fact that these antibodies can induce death of AML cells in the presence of apoptosis inhibitors such as the pan caspase inhibitors Q-VD-OPh or Z-VAD-fmk, and from the fact that most of these antibodies (except antibody AT13-031) maintain their cytotoxic properties at 4°C. According to the present invention, antibodies such as AT12-023, AT13-031 and AT13-037 kill their AML target cells via necrosis (such as oncosis or necroptosis). This provides the advantage over currently known apoptosis-inducing antibodies that the necrosis-inducing antibodies according to the present invention will enhance a patient's immune response more than apoptosis-inducing antibodies. This is due to the fact that necrosis causes more exposure of the cell contents to an individual's immune system. Further provided is therefore an isolated, synthetic or recombinant human antibody, or a functional part or a functional equivalent thereof, which is able to bind a cell surface component of acute myeloid leukemia (AML) cells and which is able to diminish proliferation of AML cells independently from, or essentially independently from, apoptosis.

[0016] Disclosed are human antibodies, or functional parts or functional equivalents thereof, according to the invention are provided which are able to diminish proliferation of AML cells independently from both apoptosis and the above-mentioned immune cells and complement. Also disclosed is therefore an isolated, synthetic or recombinant human antibody, or a functional part or a functional equivalent thereof, which is able to bind a cell surface component of acute myeloid leukemia (AML) cells and which is able to diminish proliferation of AML cells essentially independently from antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC), apoptosis, or phagocytosis by macrophages or dendritic cells.

[0017] An antibody or functional part thereof according to the invention is capable of binding intact AML cells. Such antibody or functional part is able to bind a cell surface component that is specific for AML cells. This typically means that non-hematopoietic cells or non-malignant hematopoietic cells, such as for instance hepatocytes, colon cells, fibroblasts, endothelial cells, healthy peripheral blood mononuclear cells (PBMC) and healthy bone marrow cells, are not, or to a significantly lesser extent, recognized as compared to the binding affinity of an antibody or functional part or functional equivalent according to the invention for AML cells. This means that the binding of an antibody or functional part or functional equivalent according to the invention to non-hematopoietic cells or non-malignant hematopoietic cells is typically in the same range as binding of an irrelevant control antibody to these cells (wherein the control antibody is not specific for said cells). Some reactivity towards other types of malignant hematopoietic cells is, however, embraced within the term "AML-specific". For instance, it is shown in Table 4 and Figure 6 that antibodies AT13-031 and AT12-023 are capable of binding patient-derived B- non-Hodgkin lymphoma cells. A use of antibody AT13-031 or antibody AT12-023, or a functional part of any of these antibodies, for the preparation of a medicament or prophylactic agent against B- non-Hodgkin lymphoma is therefore also provided, as well as antibody AT13-031 or antibody AT12-023, or a functional part of any of these antibodies, for use in a method for at least in part treating or preventing B- non-Hodgkin lymphoma. Similarly, antibodies AT13-024, AT13-031 and AT12-019 are capable to bind lymphoma- and/or multiple myeloma cell lines (Table 4). A use of antibody AT13-024 or antibody AT13-031 or antibody AT12-019, or a functional part of any of these antibodies, for the preparation of a medicament or prophylactic agent against myeloid leukemia (AML) or B non-Hodgkin lymphoma (B-HNL) is therefore also provided, as well as antibody AT13-024 or antibody AT13-031 or antibody AT12-019, or a functional part or functional derivative of any of these antibodies, for use in a method for at least in part treating or preventing myeloid leukemia (AML) or B non-Hodgkin lymphoma (B-HNL).

[0018] As used herein, the term "AML cells" embraces natural AML cells, such as primary AML blasts that are present in AML patients, as well as AML cell lines such as for instance THP-1, Mono-Mac 6 and Molm13.

[0019] The term "antibody" as used herein, refers to an immunoglobulin protein comprising at least a heavy chain variable region (VH), paired with a light chain variable region (VL), that is specific for a target epitope.

[0020] A "functional part of an antibody" is defined herein as a part that has at least one shared property as said antibody in kind, not necessarily in amount. Said functional part is capable of binding the same antigen as said

antibody, albeit not necessarily to the same extent. In one embodiment a functional part of an antibody comprises at least a heavy chain variable domain (VH). Non-limiting examples of a functional part of an antibody are a single domain antibody, a single chain antibody, a nanobody, a unibody, a single chain variable fragment (scFv), a Fab fragment and a F(ab')₂ fragment.

[0021] As is well known by the skilled person, a heavy chain of an antibody is the larger of the two types of chains making up an immunoglobulin molecule. A heavy chain comprises a constant domain and a variable domain, which variable domain is involved in antigen binding. A light chain of an antibody is the smaller of the two types of chains making up an immunoglobulin molecule. A light chain comprises a constant domain and a variable domain. The variable domain is often, but not always, together with the variable domain of the heavy chain involved in antigen binding.

[0022] Complementary-determining regions (CDRs) are the hypervariable regions present in heavy chain variable domains and light chain variable domains. In case of whole antibodies, the CDRs 1-3 of a heavy chain and the CDRs 1-3 of the connected light chain together form the antigen-binding site.

[0023] As used herein, the term "an antibody or functional part according to the invention" is also referred to as "a binding compound according to the invention".

[0024] The term "cell surface component of AML cells" means any component that is at least in part present in or on the cell surface of AML cells, or a component that is attached to an AML cell surface. Non-limiting examples of cell surface components of AML cells are (trans)membrane proteins, glycoproteins, and any compound attached thereto.

[0025] The terms "specific for" and "capable of specifically binding" are used herein interchangeably and refer to the interaction between an antibody, or functional part or functional equivalent thereof, and its epitope. This means that said antibody, or functional part thereof, preferentially binds to said epitope over other antigens or amino acid sequences. Thus, although the antibody or functional part may non-specifically bind to other antigens or amino acid sequences, the binding affinity of said antibody or functional part for its epitope is significantly higher than the non-specific binding affinity of said antibody or functional part for other antigens or amino acid sequences.

[0026] An antibody or functional part according to the invention that is able to bind a particular epitope of AML cells can also be specific for other, non-AML cells if said epitope of AML cells is also present on other cells (for instance other leukemic cells, myeloma cells or lymphoma cells). In that case an antibody referred to herein as being specific for AML cells is also specific for said other cells comprising the same epitope. Preferably, human AML antibodies and functional parts thereof, as provided herewith, do not significantly bind non-hematopoietic cells and non-malignant hematopoietic cells.

[0027] "Binding affinity" refers to the strength of the total sum of the noncovalent interactions between a single binding site of an antibody or functional part or functional equivalent 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 can generally be represented by the equilibrium dissociation constant (K_D), which is calculated as the k_a to k_d ratio, see, e.g., Chen, Y., et al., (1999) J. Mol Biol 293:865-881. Affinity can be measured by common methods known in the art, such as for instance a surface plasmon resonance (SPR) assay such as BiaCore or IBIS-iSPR instrument at IBIS Technologies BV (Hengelo, the Netherlands) or solution phase assays, such as Kinexa. Preferably an antibody according to the invention has a binding affinity for an epitope at or on the cell surface of AML cells characterized by a dissociation constant (K_D) of at most 100 nM, more preferably at most 50 nM, more preferably at most 25 nM, more preferably at most 10 nM, more preferably at most 5 nM, more preferably at most 2 nM, more preferably at most 1 nM, more preferably at most 0.5 nM, more preferably at most 0.3 nM, more preferably at most 0.1 nM.

[0028] The percentage of identity of an amino acid or nucleic acid sequence, or the term "% sequence identity", is defined herein as the percentage of residues in a candidate amino acid or nucleic acid sequence that is identical with the residues in a reference sequence after aligning the two sequences and introducing gaps, if necessary, to achieve the maximum percent identity. Methods and computer programs for the alignment are well known in the art, for example "Align 2".

[0029] In a particularly preferred embodiment, an antibody or functional part according to the invention is provided which is able to induce death of primary AML blasts. Since primary AML blasts are directly derived from an AML patient, as opposed to commercially available cell lines, the activity of an antibody against such AML blasts is even more indicative for an *in vivo* situation. As shown in the Examples, at least antibodies AT13-024 and AT12-025 have this characteristic. These antibodies are, therefore, preferred. In a particularly preferred embodiment, an antibody or functional part according to the invention is provided which is able to induce death of primary AML blasts independently from, or essentially independently from, antibody-dependent cell-mediated cytotoxicity (ADCC), complement-dependent cytotoxicity (CDC), apoptosis, and/or phagocytosis by macrophages or dendritic cells. Preferably, such binding compounds are capable of inducing death of AML blasts essentially independently from other immune cells, or complement or apoptosis. Antibodies AT13-024 and AT12-025 also have this preferred characteristic.

[0030] As used herein, the term "essentially independently from ADCC, CDC or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells" means that ADCC, CDC or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells are not required for an anti-AML effect induced by a binding compound according to the present invention, even though in an *in vivo* situation ADCC, CDC or phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells may also occur. Hence, in this embodiment, ADCC, CDC and phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells is not excluded, but not essential either. Likewise, the term "essentially independently from other immune cells or complement" means that a binding compound according to the invention is, in principle, capable of exerting an anti-AML effect without the presence of other immune cells or complement, even though in an *in vivo* situation other immune cells or complement may also have an anti-AML activity. The term "essentially independently from apoptosis" means that the anti-AML effect is exerted by a binding compound according to the present invention via a mechanism other than apoptosis. Preferably, said anti-AML effect is exerted via necrosis.

[0031] In a further preferred embodiment, an antibody or functional part thereof according to the invention is provided which is able to diminish proliferation of AML cells *in vitro* within 7 days, preferably within 5 days, more preferably within 3 days and even more preferably within 1 day. This indicates a quick therapeutic effect.

[0032] The present invention provides isolated, synthetic and recombinant human antibodies, and functional parts thereof, which are able to bind intact AML cells. Said AML cells preferably belong to a French-American-British (FAB) classification selected from the group consisting of M5, M0, M1, M2, M3 and M4. More preferably, said AML cells belong to the FAB classification M5 or M1 or M0 or M4, preferably M5. These are the FAB classifications commonly found in AML patients. In a further preferred embodiment, isolated, synthetic and recombinant human antibodies, or functional parts or functional equivalents thereof, are provided which are able to bind different AML cells of at least two, preferably at least three, more preferably at least four different FAB classifications. Such antibodies are useful for different AML patients having different FAB classifications, so that these antibodies are broadly applicable. As shown in Table 3, antibody AT12-025 is capable of binding AML cells of at least two FAB classifications (M5 + M1). This is, therefore, a preferred antibody according to the invention. Antibody AT13-031 is also capable of binding AML cells of at least three FAB classifications (M5 + M1 + M4). These antibodies are, therefore, even more preferred. Furthermore, antibody AT12-023 is capable of binding AML cells of at least four FAB classifications (M5 + M0 + M1 + M4). This antibody is, therefore, even more broadly applicable and is, therefore, particularly preferred.

[0033] In one particularly preferred embodiment, an antibody or functional part according to the invention is of

the IgG isotype, preferably IgG1 or IgG3. This is beneficial for medical applications in humans.

[0034] Tables 1A and 1B, and Figure 1, provide an overview of the variable heavy and light chain sequences, as well as the individual CDR sequences, of antibodies AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016. These are preferred antibodies according to the invention, obtained from three human AML patients. The terms "AT12-023", "AT12-025", "AT13-024", "AT12-019", "AT13-022", "AT13-023", "AT13-031", "AT12-020", "AT13-033", "AT13-034", "AT13-035", "AT13-036", "AT13-037", "AT14-013", "AT14-014", "AT14-015" and "AT14-016" as used herein encompass all antibodies and functional parts and functional equivalents having at least the heavy and light chain CDR1-3 regions, preferably the variable heavy chain and light chain sequences, of these antibodies as depicted in Tables 1A and 1B and Figure 1, such as for instance isolated and/or purified antibodies or recombinantly produced antibodies.

[0035] As used herein, any reference to "Table 1" includes a reference to Table 1A and/or Table 1B.

[0036] Based on the antibodies depicted in Table 1 and Figure 1, it is possible to produce an antibody or functional part thereof comprising at least one CDR sequence of an antibody depicted in Table 1 or Figure 1, which is specific for AML cells. Disclosed is therefore an isolated, recombinant and/or synthetic antibody or a functional part or functional equivalent thereof comprising at least one CDR sequence of an antibody as depicted in Table 1. Said CDR sequence is preferably a CDR3 sequence of an antibody according to the present invention. Hence, preferably at least three CDRs of the heavy and light chains of antibody AT12-023, AT12-025, AT13-031, AT13-033, , AT13-035 or AT13-037 are jointly present in one binding compound according to the invention. Optionally, at least one of said CDR sequences is optimized, thereby generating a variant binding compound, preferably in order to improve binding efficacy, selectivity, or stability. This is for instance done by mutagenesis procedures where after the stability and/or binding efficacy of the resulting compounds are preferably tested and an improved AML-specific binding compound is selected. A skilled person is well capable of generating variants comprising at least one altered CDR sequence according to the invention. For instance, conservative amino acid substitution is applied. Examples of conservative amino acid substitution include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another hydrophobic residue, and the substitution of one polar residue for another polar residue, such as the substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for asparagine. Said binding compounds comprise heavy chain and light chain CDR 1-3 sequences which are at least 90% identical to the heavy and light chain CDR 1-3 sequences of the same antibody depicted in Table 1 or Figure 1. Preferably, the CDR sequences differ in no more than three, preferably in no more than two, preferably in no more than one amino acid from the original CDR sequences of an antibody according to the invention.

[0037] Besides optimizing CDR sequences in order to improve binding efficacy or stability, at least one sequence in at least one of the framework regions can be optimized. This is preferably done in order to improve binding efficacy or stability. Framework sequences are for instance optimized by mutating a nucleic acid molecule encoding such framework sequence where after the characteristics of the resulting antibody - or functional part or functional equivalent - are preferably tested. This way, it is possible to obtain improved binding compounds. In a preferred embodiment, human germline sequences are used for framework regions in antibodies according to the invention. The use of human germline sequences minimizes the risk of immunogenicity of said antibodies, because these sequences are less likely to contain somatic alterations which are unique to individuals from which the framework regions are derived, and may cause an immunogenic response when applied to another human individual. Further provided is therefore a synthetic or recombinant antibody or functional part according to the invention, comprising at least one non-natural mutation in a framework region. Additionally, or alternatively, a synthetic or recombinant antibody or functional part according to the invention is provided that comprises at least one non-natural mutation in a constant region. By a "non-natural mutation" is meant that the resulting amino acid sequence does not occur in nature. Instead, it has been artificially produced. In one embodiment, an IgG3 Fc region of antibody AT12-023 or AT12-025, is at least partly replaced by an IgG1 Fc region. This typically increases the stability and half life of the resulting immunoglobulin.

[0038] A binding compound according to the present invention preferably comprises a human variable region. More preferably, said binding compound comprises a human constant region and a human variable region. Most preferably, said binding compound is a human antibody. The use of human AML-specific antibodies is advantageous over the use of non-human antibodies. The *in vivo* use of non-human antibodies for diagnosis and/or treatment of human diseases is hampered by a number of factors. In particular, the human body may recognize non-human antibodies as foreign, which will result in an immunogenic response against the non-human antibodies, resulting in adverse side effects and/or rapid clearance of the antibodies from the circulation. A human antibody diminishes the chance of side-effects when administered to a human individual and often results in a longer half-life in the circulation because of reduced clearance when compared to non-human antibodies. In another embodiment a binding compound according to the invention is a humanized antibody. In another embodiment a binding compound according to the invention is a chimeric antibody. In a chimeric antibody, sequences of interest, such as for instance an additional binding site of interest, are included into a binding compound according to the invention.

[0039] Further, binding compounds according to the invention are preferably monoclonal antibodies. A monoclonal antibody is an antibody consisting of a single molecular species. Monoclonal antibodies can be produced in large quantities by monoclonal antibody-producing cells or recombinant DNA technology.

[0040] Hence, variant binding compounds based on the preferred antibodies depicted in Table 1 and Figure 1 can also be generated, using techniques known in the art such as for instance mutagenesis. Typically, sequence variations between 80 and 99% are tolerated while maintaining a certain antigen specificity. Binding compounds according to the invention comprising a sequence that has at least 80% sequence identity to at least a CDR sequence of any of the antibodies of Table 1 or Figure 1 are therefore also herein disclosed. Since the antigen specificity of an antibody is typically dominated by the CDR3 sequences, a variant antibody preferably comprises at least a heavy chain CDR3 sequence having at least 80% sequence identity with a heavy chain CDR3 sequence as depicted in Table 1 or Figure 1. Said variant antibody preferably comprises a heavy chain CDR3 sequence and a light chain CDR3 sequence having at least 80% sequence identity with the heavy and light chain CDR3 sequences of the same antibody, selected from the group consisting of AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016.

[0041] A preferred antibody according to the present invention is antibody AT12-023. This antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1, as shown in the Examples and Figures 7 and 8. This antibody is, therefore, particularly suitable for AML therapy and/or diagnosis. Interestingly, AT12-023 is of the IgG3 isotype and belongs to the VH4-34 family, which is a family of VH sequences known for their potential killing properties (Bhat et al, 1997). Antibody AT12-023 is also capable of efficiently binding primary AML blasts of at least four different FAB classifications (Table 3). The heavy chain CDR1, CDR2 and CDR3 sequences, and the light chain CDR1, CDR2 and CDR3 sequences of antibody AT12-023 are SEQ ID NOs 1, 14, 27, 40, 53 and 66, respectively, as depicted in Table 1. The invention therefore provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 1; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 14; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 27; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 40; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 53; and
- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 66. Preferably, said sequence identities are at least 91%, more preferably at least 92%, more

preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described herein before, at least 1, 2 or 3 amino acid residues in the recited CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, said heavy and light chain CDR 1, 2 and 3 sequences preferably contain antibody AT12-023-derived CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT12-023 CDR sequences.

[0042] Another preferred antibody according to the present invention is antibody AT12-025. This antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1, as well as patient-derived primary AML blasts, as shown in the Examples and Figures 8 and 10. This antibody is, therefore, particularly suitable for AML therapy and/or diagnosis. Interestingly, AT12-025 is of the IgG3 isotype and belongs to the VH4-34 family, which is a family of VH sequences known for their potential killing properties (Bhat et al, 1997). The heavy chain CDR1, CDR2 and CDR3 sequences and the light chain CDR1, CDR2 and CDR3 sequences of antibody AT12-025 are SEQ ID NOs 2, 15, 28, 41, 54 and 67, respectively, as depicted in Table 1. The invention therefore further provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 2; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 15; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 28; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 41; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 54; and
- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 67. Again, said sequence identities are preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described above, at least 1, 2 or 3 amino acid residues in the recited AT12-025 CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, the above mentioned heavy and light chain CDR 1, 2 and 3 sequences preferably contain CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT12-025 CDR sequences.

[0043] The invention further provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 7; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 20; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 33; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 46; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ

ID NO: 59; and

- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 72. These are the CDR sequences of antibody AT13-031. Interestingly, AT13-031 belongs to the VH4-34 family, which is a family of VH sequences known for their potential killing properties (Bhat et al, 1997). Antibody AT13-031, derived from a human AML patient in complete remission, is capable of specifically binding intact AML cells. Moreover, this antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1. Hence, a binding compound containing AT13-031-derived CDR sequences is particularly suitable for AML therapy and/or diagnosis. Such binding compound is for instance used as an antibody-drug conjugate (ADC), such that a toxic compound will be directed to AML cells, or it is used by inducing CDC and/or ADCC. Alternatively, or additionally, such binding compound can be used to mark AML cells for specific phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells, which cells can subsequently induce an AML specific immune response. Again, said sequence identities are preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described above, at least 1, 2 or 3 amino acid residues in the recited AT13-031 CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, the above mentioned heavy and light chain CDR 1, 2 and 3 sequences preferably contain CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT13-031 CDR sequences.

[0044] The invention further provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 9; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 22; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 35; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 48; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 61; and
- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 74. These are the CDR sequences of antibody AT13-033. Antibody AT13-033, derived from a human AML patient in complete remission, is capable of specifically binding intact AML cells. Moreover, this antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1. Hence, a binding compound containing AT13-033-derived CDR sequences particularly suitable for AML therapy and/or diagnosis. Such binding compound is for instance used as an antibody-drug conjugate (ADC), such that a toxic compound will be directed to AML cells, or it is used by inducing CDC and/or ADCC. Alternatively, or additionally, such binding compound can be used to mark AML cells for specific phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells, which cells can subsequently induce an AML specific immune response. Again, said sequence identities are preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described above, at least 1, 2 or 3 amino acid residues in the recited AT13-033 CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, the above mentioned heavy and light chain CDR 1, 2 and 3 sequences preferably contain CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT13-033

CDR sequences.

[0045] The invention further provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 11; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 24; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 37; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 50; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 63; and
- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 76. These are the CDR sequences of antibody AT13-035. Antibody AT13-035, derived from a human AML patient in complete remission, is capable of specifically binding intact AML cells. Moreover, this antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1. Hence, a binding compound containing AT13-035-derived CDR sequences particularly suitable for AML therapy and/or diagnosis. Such binding compound is for instance used as an antibody-drug conjugate (ADC), such that a toxic compound will be directed to AML cells, or it is used by inducing CDC and/or ADCC. Alternatively, or additionally, such binding compound can be used to mark AML cells for specific phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells, which cells can subsequently induce an AML specific immune response. Again, said sequence identities are preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described above, at least 1, 2 or 3 amino acid residues in the recited AT13-035 CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, the above mentioned heavy and light chain CDR 1, 2 and 3 sequences preferably contain CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT13-035 CDR sequences.

[0046] The invention further provides an isolated, synthetic or recombinant antibody, or a functional part thereof, which comprises:

- a heavy chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 13; and
- a heavy chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 26; and
- a heavy chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 39; and
- a light chain CDR1 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 52; and
- a light chain CDR2 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 65; and
- a light chain CDR3 sequence comprising a sequence which has at least 90% sequence identity with SEQ ID NO: 78. These are the CDR sequences of antibody AT13-037. Antibody AT13-037, derived from a human AML patient in complete remission, is capable of specifically binding intact AML cells. Moreover, this

antibody is preferred because it is capable of efficiently binding and killing cells of the AML cell line THP-1, as well as patient-derived primary AML blasts, as shown in the Examples. Hence, a binding compound containing AT13-037-derived CDR sequences particularly suitable for AML therapy and/or diagnosis. Such binding compound is for instance used as an antibody-drug conjugate (ADC), such that a toxic compound will be directed to AML cells, or it is used by inducing CDC and/or ADCC. Alternatively, or additionally, such binding compound can be used to mark AML cells for specific phagocytosis by tumor-associated myeloid cells such as macrophages or dendritic cells, which cells can subsequently induce an AML specific immune response. Again, said sequence identities are preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%. As described above, at least 1, 2 or 3 amino acid residues in the recited AT13-037 CDR sequences may vary while retaining the same kind of binding activity (in kind, not necessarily in amount). Hence, the above mentioned heavy and light chain CDR 1, 2 and 3 sequences preferably contain CDR sequences that deviate in no more than three, preferably no more than two, more preferably no more than one amino acid from the recited AT13-037 CDR sequences.

[0047] Preferably, an antibody according to the invention comprises a variable heavy chain sequence and/or a variable light chain sequence as depicted in Table 1 or Figure 1, or a sequence which has at least 90% sequence identity thereto. As shown in Table 1, the variable heavy chain sequences of antibodies AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016 are SEQ ID NOs 79-91 and 233-236, respectively. The variable light chain sequences of antibodies AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016 are SEQ ID NOs 92-104 and 237-240, respectively. Also provided is, therefore, an antibody or functional part thereof according to the invention, comprising a variable heavy chain sequence having at least 90% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 79, 80, 85, 87, 89 and 91, and/or comprising a variable light chain sequence having at least 90% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 92, 93, 98, 100, 102 and 104, or sequences that are at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, or even 100% identical to any one of these heavy chain or light chain sequences. The higher the identity, the more closely an antibody resembles an antibody depicted in Figure 1. Preferably, a binding compound according to the invention comprises the variable heavy chain sequence of any one of the antibodies depicted in Figure 1, together with the variable light chain sequence of the same antibody, or heavy and light chain sequences that are at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, thereto.

[0048] For instance, antibody AT12-023 has the variable heavy chain sequence of SEQ ID NO: 79 and the variable light chain sequence of SEQ ID NO: 92 as depicted in Table 1. A binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 79 is therefore preferably provided. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 92.

[0049] Antibody AT12-025 has the variable heavy chain sequence of SEQ ID NO: 80 and the variable light chain sequence of SEQ ID NO: 93 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 80. Preferably, said binding compound also comprises a

variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 93.

[0050] Antibody AT13-023 has the variable heavy chain sequence of SEQ ID NO: 84 and the variable light chain sequence of SEQ ID NO: 97 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 84. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 97.

[0051] Antibody AT13-031 has the variable heavy chain sequence of SEQ ID NO: 85 and the variable light chain sequence of SEQ ID NO: 98 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 85. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 98.

[0052] Antibody AT13-033 has the variable heavy chain sequence of SEQ ID NO: 87 and the variable light chain sequence of SEQ ID NO: 100 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 87. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 100.

[0053] Antibody AT13-035 has the variable heavy chain sequence of SEQ ID NO: 89 and the variable light chain sequence of SEQ ID NO: 102 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 89. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 102.

[0054] Antibody AT13-037 has the variable heavy chain sequence of SEQ ID NO: 91 and the variable light chain sequence of SEQ ID NO: 104 as depicted in Table 1. Further provided is therefore a binding compound according to the present invention, having a variable heavy chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, or 100% sequence identity with SEQ ID NO: 91. Preferably, said binding compound also comprises a variable light chain sequence having at least 90%, or at least 91%, or at least 92%, or at least 93%, or at least 94%, or at least 95%, or at least 96%, or at least 97%, or at least 98%, or at least 99%, sequence identity with SEQ ID NO: 104.

[0055] An antibody or functional part thereof according to the invention is able to bind snRNP200 of AML cells. snRNP200, also known as U5-snRNP, is a protein complex that is part of the spliceosome in all eukaryotic cells. Normally, snRNP200 is located in the nucleus. However, the present invention provides the surprising insight that snRNP200 is also present on the surface of AML cells. This antigen is bound by at least antibodies AT12-023,

AT13-031 and AT13-037, and functional parts thereof. Hence, snRNP200 is an important target for anti-AML therapy and snRNP200-specific antibodies according to the invention are therefore particularly suitable for counteracting these cells.

[0056] The invention further provides an isolated, synthetic or recombinant nucleic acid molecule, which encodes at least the variable heavy chain sequence and/or the variable light chain sequence of an antibody or functional part according to any one of claims 1-3, preferably wherein said nucleic acid molecule comprises a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 183, 184, 189, 191, 193 and 195, and/or comprising a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 196, 197, 202, 204, 206 and 208. A nucleic acid molecule according to the invention is for instance isolated from a B-cell which is capable of producing an antibody according to the invention. Said B-cell preferably produces antibody AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037 AT14-013, AT14-014, AT14-015, or AT14-016.

[0057] Nucleic acid sequences encoding heavy chain and light chain CDRs of antibodies AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016 are depicted in Table 1. Nucleic acid molecules encoding a heavy or light chain CDR of an antibody according to the invention which differ from the CDR nucleic acid sequences depicted in Table 1 but have nucleic acid codons which encode the same amino acids of said heavy or light chain CDR are also encompassed by the invention. Such nucleic acid molecules for instance comprise nucleic acid sequences that have been codon optimized for a producer cell, such as for instance *E.coli* or Chinese hamster ovary (CHO) cells, NSO cells (a mouse myeloma) or 293(T) cells, enabling high scale production of binding compounds according to the invention. It should be noted that antibody production can be done by any recombinant antibody production system; the four producer cell systems mentioned here are only a few examples of the many systems that are available to date. As used herein, the term "codon" means a triplet of nucleotides (or functional equivalents thereof) that encode a specific amino acid residue. The term "codon optimized" means that one or more codons from the original, human nucleic acid sequence are replaced by one or more codons that are preferred by a certain antibody production system. These replacement codons preferably encode the same amino acid residue as the original human codon that has been replaced. Alternatively, one or more replacement codons encode a different amino acid residue. This preferably results in conservative amino acid substitution, although this is not necessary. Typically, in constant regions and framework regions one or more amino acid substitutions are generally allowed. In CDR regions, preferably codons are used that encode the same amino acid residue as the original human codon that has been replaced.

[0058] Further provided is a vector comprising an isolated, synthetic or recombinant nucleic acid molecule, which encodes at least the variable heavy chain sequence and/or the variable light chain sequence of an antibody or functional part according to any one of claims 1-3, preferably wherein said nucleic acid molecule comprises a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 183, 184, 189, 191, 193 and 195, and/or comprising a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 196, 197, 202, 204, 206 and 208. Preferably, the resulting CDR differs in no more than three, preferably in no more than two, preferably in only one amino acid from the original CDR sequence of an antibody according to the invention.

[0059] Said sequence identities are preferably at least 85%, more preferably at least 90%, most preferably at least 95% sequence, most preferably 100%.

[0060] A preferred nucleic acid molecule or vector(s) according to the invention comprises a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 183, 184, 189, 191, 193 and 195, and/or comprising a sequence which has at least 80% sequence identity with a sequence selected from the group consisting of SEQ ID NOs: 196, 197, 202, 204, 206 and 208. Said sequence identities are preferably at least 85%, more preferably at least 86%, more preferably at least 87%, more preferably at least 88%, more preferably at least 89%, more preferably at least 90%, more preferably at least 91%, more preferably

at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, more preferably 100%.

[0061] More preferably, a nucleic acid molecule or one or more vectors according to the invention comprise(s) a variable heavy chain encoding sequence as well as a variable light chain encoding sequence which resemble the variable heavy and light chain encoding sequences of the same antibody depicted in Table 1. Thus, in a preferred embodiment a nucleic acid molecule or vector(s) according to the invention comprise(s) the variable heavy chain encoding sequence of antibody AT12-023, AT12-025, AT13-031, AT13-033, AT13-035 or AT13-036, , and the variable light chain encoding sequence of the same antibody, or sequences that are at least 80%, more preferably at least 85%, more preferably at least 86%, more preferably at least 87%, more preferably at least 88%, more preferably at least 89%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, more preferably at least 93%, more preferably at least 94%, more preferably at least 95%, more preferably at least 96%, more preferably at least 97%, more preferably at least 98%, more preferably at least 99%, identical thereto.

[0062] In some embodiments, nucleic acid molecules and vectors are provided that encode an antibody or functional part thereof according to the invention. Further provided is therefore a nucleic acid molecule, or one or more vectors, that encode(s) antibody AT12-023, AT12-025, AT13-031, AT13-033, AT13-035 or AT13-037, or functional part thereof. In some embodiments, said nucleic acid molecule or vector(s) is/are codon optimized for a non-human recombinant expression system.

[0063] Further provided is a vector comprising a nucleic acid molecule according to the invention. As used herein "a vector comprising a nucleic acid molecule according to the invention" is also referred to as "a vector according to the invention". These terms encompass one or more vector(s) according to the invention, comprising one or more nucleic acid molecule(s) according to the invention. As used herein, the singular term "a" encompasses the term "one or more".

[0064] Methods for constructing vectors comprising one or more nucleic acid molecule(s) according to the invention are well known in the art. Non-limiting examples of vectors suitable for generating a vector of the invention are retroviral and lentiviral vectors. Such vectors are suitable for a variety of applications. For instance, one or more vectors of the invention comprising a therapeutically beneficial nucleic acid sequence according to the invention is/are suitable for prophylactic or therapeutic applications against AML. Administration of such vector(s) to an individual, preferably a human, in need thereof results in expression of said prophylactic or therapeutic nucleic acid sequence *in vivo* resulting in at least partial treatment or prophylaxis against AML. Said vector(s) can also be used in applications involving *in vitro* expression of a nucleic acid molecule of interest, for instance for (commercial) production of antibodies or functional equivalents according to the invention. Also provided is therefore an isolated or recombinant cell, or a non-human animal, comprising at least one nucleic acid molecule or at least one vector, according to the invention.

[0065] A nucleic acid molecule or a vector according to the invention is particularly useful for generating antibodies or functional parts thereof according to the invention, which are specific for AML. This is for instance done by introducing such nucleic acid molecule or vector(s) into a cell so that the cell's nucleic acid translation machinery will produce the encoded antibodies or functional parts. In one embodiment, a nucleic acid molecule or vector encoding a heavy and/or light chain according to the invention is expressed in so called producer cells, such as for instance E.coli, CHO, NSO or 293(T) cells, some of which are adapted to commercial antibody production. Of note, any recombinant antibody production system is suitable; these four producer cell systems mentioned are only a few examples of the many systems that are available to date. As described herein before, in such cases it is preferred to use nucleic acid molecules wherein the original human sequences as provided herein are codon optimized for the producer cell. Proliferation of said producer cells results in a producer cell line capable of producing binding compounds according to the invention. Preferably, said producer cell line is suitable for producing antibodies for use in humans. Hence, said producer cell line is preferably free of pathogenic agents

such as pathogenic microorganisms. Most preferably, antibodies consisting of human sequences are generated using at least one nucleic acid molecule or vector according to the invention.

[0066] An isolated or recombinant antibody producing cell capable of producing a binding compound according to the invention is therefore also provided. Such cell typically comprises at least one nucleic acid molecule or vector according to the invention, which preferably contains a nucleic acid sequence that is codon optimized for said cell. An antibody producing cell is defined herein as a cell which is capable of producing and/or secreting antibodies or functional parts thereof, and/or which is capable of developing into a cell which is capable of producing and/or secreting antibodies or functional parts thereof. An antibody producing cell according to the invention is preferably a producer cell which is adapted to commercial antibody production. As explained above, said producer cell is preferably suitable for producing antibodies for use in humans. A method for producing an antibody or functional part according to the invention is therefore also provided, said method comprising providing a cell, preferably an antibody producing cell, with a nucleic acid molecule or a vector according to the invention, and allowing said cell to translate said nucleic acid molecule or vector, thereby producing said antibody or functional part according to the invention. A method according to the invention preferably further comprises a step of harvesting, purifying and/or isolating said antibody or functional part according to the invention. Obtained binding compounds according to the invention are preferably used in human therapy, optionally after additional purifying, isolation or processing steps.

[0067] Another aspect of the invention provides an antibody or functional part according to the invention, which is coupled to another compound. In one embodiment, it is coupled to another therapeutic moiety, such as a chemotherapeutic drug or other toxic compound or radioactive compound, to form a so called "antibody-drug conjugate". In another embodiment, a moiety that is coupled to a binding compound according to the invention is an immunomodulatory molecule such as for instance a CD3-specific antibody. Such CD3-specific antibody is capable of binding T cells and, if coupled to a binding compound according to the invention, it will target T cells to AML cells, thereby enhancing an anti-leukemic T-cell response. This provides an even stronger anti-AML effect. One preferred embodiment of the invention therefore provides a bispecific or multispecific binding compound, comprising an AML-specific binding compound according to the present invention and an immunomodulatory molecule, preferably a CD3-specific binding compound. Another preferred embodiment provides an anti-AML compound, said compound comprising a binding compound according to the present invention, which is specific for AML cells, and a toxic moiety. In some other embodiments, a binding compound according to the present invention is coupled to a label. This allows detection of myeloproliferative cells, such as AML cells, using such labeled binding compound. Other embodiments provide a binding compound according to the invention that is coupled to another AML-binding compound. In some embodiments, such other AML-binding compound is also a binding compound according to the present invention. Provided is therefore a compound comprising two binding compounds according to the invention that are coupled to each other. This is, however, not necessary since a binding compound according to the invention can also be coupled to other AML-binding compounds, such as currently known antibodies that bind AML cells. Bispecific compounds according to the invention allow, for instance, for increased binding of AML cells, especially when the two coupled binding compounds are specific for different epitopes on AML cells. Such bispecific compound is thus very suitable for therapeutic or diagnostic applications. It is also possible to use bispecific compounds according to the invention in assays wherein different AML cells are bound to the same bispecific binding compound.

[0068] In one embodiment, a synthetic or recombinant antibody is provided, or a functional part thereof, which comprises one Fab fragment of an antibody according to the present invention, and one Fab fragment of another antibody according to the invention. The resulting binding compound is specific for AML cells, but each Fab arm will typically bind its own epitope. In some embodiments, the epitopes recognized by the Fab fragments are different from each other. In another embodiment, the epitopes are the same. The Fab arms may bind the epitopes with different affinity. Alternatively, the Fab arms bind their epitopes with essentially the same affinity, meaning that the K_D of the Fab arms differ no more than 30%, preferably no more than 20% or no more than 10% from each other.

[0069] Said other moiety, for example a chemotherapeutic agent or a CD3-specific antibody, is preferably

coupled to a binding compound according to the invention via a linker such as for instance an acid-labile hydrazone linker, or via a peptide linker like citruline-valine, or through a thioether linkage, or by sortase catalized transamidation, which is described in detail in WO 2010/087994.

[0070] Sortase catalized transamidation involves engineering of a sortase recognition site (LPETGG) on the heavy chain of an antibody, preferably on the C-terminal part of the heavy chain, and on the moiety to be coupled to said antibody. The antibody and the moiety further typically contain a GGGGS sequence and a tag for purification purposes, such as a HIS tag. Subsequently sortase mediated transamidation is performed followed by click chemistry linkage. In a sortase catalized transaminidation, "click chemistry linkage" typically involves chemical coupling of, for instance, an alkyne-containing reagent and, for instance, an azide-containing reagent which are added by sortase through addition of glycines to the sortase motif on the heavy chain of the antibody and to a sortase motif on the moiety (such as a protein, peptide or antibody) to be coupled to the antibody. In one embodiment, the invention therefore provides an antibody according to the invention wherein a sortase recognition site (LPETGG) is engineered on the heavy chain of the antibody, preferably on the C-terminal part of the heavy chain, the antibody preferably further containing a GGGGS sequence and a purification tag, such as a HIS tag.

[0071] In another embodiment a binding compound according to the invention is coupled to another moiety via a thioether linkage. In such case, one or more cysteines are preferably incorporated into a binding compound according to the invention. Cysteines contain a thiol group and, therefore, incorporation of one or more cysteines into a binding compound according to the invention, or replacement of one or more amino acids by one or more cysteines of a binding compound according to the invention, enable coupling of said binding compound to another moiety. Said one or more cysteines are preferably introduced into a binding compound according to the invention at a position where it does not significantly influence folding of said binding compound, and does not significantly alter antigen binding or effector function. The invention therefore also provides a binding compound according to the invention wherein at least one amino acid other than cysteine has been replaced by a cysteine. In one embodiment, an AML-specific binding compound according to the present invention is coupled to at least one other AML-specific binding compound according to the present invention. Such bispecific or multispecific binding compound provides a stronger anti-AML effect.

[0072] Binding compounds according to the present invention are suitable for use against myeloproliferative disorders such as AML, or acute leukemia's that developed from myelodysplastic syndrome, chronic myeloid leukemia, myelofibrosis or other, non-malignant myeloproliferative syndromes. As some of the antibodies also bind to non-myeloid, lymphoproliferative malignancies such as multiple myeloma and B-non Hodgkin lymphoma (B-NHL), they are suitable for use against these disorders as well. Binding compounds according to the present invention are therefore particularly suitable for use as a medicine or prophylactic agent. Preferably, binding compounds according to the invention are used which consist of human sequences, in order to reduce the chance of adverse side effects when human individuals are treated. Such human sequences can be isolated from a human or synthetically or recombinantly produced based on the sequence of human antibodies, optionally using codon optimized nucleic acid sequences that encode the same amino acids as the original human nucleic acid sequence. Provided is therefore an antibody or functional part according to the invention for use as a medicament and/or prophylactic agent. Said antibody preferably comprises an antibody selected from the group consisting of AT12-023, AT12-025, AT13-031, AT13-033, AT13-035, and AT13-037. Also provided is a nucleic acid molecule according to the invention or a vector according to the invention comprising such nucleic acid, or a cell according to the invention, for use as a medicament and/or prophylactic agent. When (a vector comprising) one or more nucleic acid molecule(s) according to the invention is/are administered, the nucleic acid molecule(s) will be translated *in situ* by the host's machinery into a binding compound according to the invention. Produced binding compounds according to the invention are capable of preventing and/or counteracting myeloproliferative disorders such as AML and lymphoproliferative disorders such as for instance lymphoma, B-NHL and multiple myeloma. Further provided is therefore an antibody or functional part or functional equivalent according to the invention, or a nucleic acid molecule or functional equivalent according to the invention, or a vector or a cell according to the invention, for use in a method for at least in part treating or preventing myeloid leukemia (AML)

or B non-Hodgkin lymphoma (B-HNL). As described herein before, such disorder can be treated or prevented by using cytotoxic binding compounds according to the invention. As demonstrated in the Examples, at least antibodies AT13-033, AT13-035, AT13-036, AT13-037, AT12-023, AT12-025 and AT13-031 have cytotoxic activity. Further provided is therefore an antibody selected from the group consisting of antibodies AT13-033, AT13-035, AT13-037, AT12-023, AT12-025 and AT13-031, and functional parts thereof, or a nucleic acid molecule or one or more vectors encoding therefore, for use in a method for at least in part treating or preventing AML or B-HNL. Preferably, said disorder is AML.

[0073] In some embodiments, a binding compound according to the invention is coupled to a therapeutic moiety, such as a chemotherapeutic drug or other toxic compound or a radioactive compound or an immunomodulatory molecule such as for instance a CD3-specific antibody, to form a so called "antibody-drug conjugate" or a "chimeric antigen receptor (CAR) T cell", respectively, which is able to counteract a myeloproliferative or lymphoproliferative disorder.

[0074] In some embodiments, said lymphoproliferative disorder is treated with one or more antibodies selected from the group consisting of antibodies AT12-023, AT12-025, and AT13-031, and functional parts thereof. Further provided is therefore an antibody selected from the group consisting of antibodies AT12-023, AT12-025, and AT13-031, and functional parts thereof, or a nucleic acid molecule or one or more vectors encoding therefore, for use in a method for at least in part treating or preventing AML or B-HNL.

[0075] A binding compound according to the invention, or a nucleic acid molecule according to the invention, or at least one vector or cell according to the invention, is preferably used for at least in part treating and/or preventing AML. As used herein the term "at least in part treating and/or preventing AML" includes counteracting AML tumor growth and/or alleviating symptoms resulting from the presence of AML cells in a patient. Also provided is therefore a use of an antibody or functional part according to the invention, or of a nucleic acid molecule according to the invention, or of at least one vector or cell according to the invention, for the preparation of a medicament and/or prophylactic agent for at least in part treating and/or preventing AML. Further provided is an antibody or functional part according to the invention, or a nucleic acid molecule according to the invention, or at least one vector or cell according to the invention, for use in a method for at least in part treating and/or preventing AML.

[0076] Preferred antibodies for use in any of the recited methods are antibodies AT12-023, AT12-025, AT13-031, AT13-033, AT13-035 and AT13-037.

[0077] The invention further provides a composition comprising an antibody or functional part according to the invention. A composition comprising a nucleic acid molecule according to the invention is also provided, as well as a composition comprising a vector or a cell according to the invention. In some embodiments a composition according to the invention comprises at least two antibodies or functional parts thereof according to the invention.

[0078] A composition according to the present invention preferably comprises a pharmaceutical composition. Said pharmaceutical composition preferably also comprises a pharmaceutical acceptable carrier, diluent and/or excipient. Non-limiting examples of suitable carriers for instance comprise keyhole limpet haemocyanin (KLH), serum albumin (e.g. BSA or RSA) and ovalbumin. In one preferred embodiment said suitable carrier comprises a solution, like for example saline. A pharmaceutical composition according to the invention is preferably suitable for human use.

[0079] The invention further discloses a method for at least in part treating and/or preventing a myeloproliferative or lymphoproliferative disorder, comprising administering to an individual in need thereof a therapeutically effective amount of an antibody or functional part or functional equivalent according to the invention, and/or a nucleic acid molecule or functional equivalent thereof according to the invention, and/or a vector or cell according to the invention, and/or a composition according to the invention. As used herein, an "individual" or "subject" is a human or an animal, preferably a human AML patient. Said composition is preferably a pharmaceutical composition according to the invention.

[0080] A binding compound and/or composition according to the present invention is particularly suitable for administering to immune compromised individuals with an increased risk of complications, such as individuals that have undergone chemotherapy, particularly infants and elderly people. A binding compound, or a nucleic acid molecule, or a vector, and/or a pharmaceutical composition according to the invention is preferably administered via one or more injections. Typical doses of administration of a binding compound according to the invention are between 0.1 and 10 mg per kg body weight.

[0081] A binding compound according to the invention is also particularly suitable for diagnostic use. For instance, if an individual, preferably a human, is suspected of suffering from a myeloproliferative disorder such as AML or a lymphoproliferative disorder such as B-NHL or multiple myeloma, a sample, such as a blood or tissue sample, from said individual can be tested for the presence of myeloproliferative cells or lymphoproliferative cells, using a binding compound according to the invention. Preferably, said sample is mixed with a binding compound according to the invention, which will specifically bind to myeloproliferative cells. Myeloproliferative cells or lymphoproliferative cells bound to a binding compound according to the invention can be isolated from the sample and/or detected using any method known in the art, for example, but not limited to, isolation using magnetic beads, streptavidin-coated beads, or isolation through the use of secondary antibodies immobilized on a column. Alternatively, or additionally, a binding compound according to the invention is labeled in order to be able to detect said antibody, for instance, but not limited to, fluorescently labeled, enzymatically labeled, or radioactively labeled. Alternatively, a binding compound according to the invention is detected using a labeled secondary antibody which is directed against said binding compound. If binding of said antibody is detected, it is indicative for the presence of myeloproliferative or lymphoproliferative cells. The invention therefore provides an antibody or functional part according to the invention, or a nucleic acid molecule according to the invention, or a vector or a cell according to the invention, for use in detecting AML or B-HNL cells. Also provided is an antibody or functional part according to the invention, or a nucleic acid molecule according to the invention, or a vector or a cell according to the invention, for use in diagnosis of AML or B-HNL. Lymphoproliferative cells are preferably detected with one or more antibodies selected from the group consisting of AT12-023, AT12-025, and AT13-031, and functional parts thereof.

[0082] A use of an antibody or functional part according to the invention, or use of a nucleic acid molecule according to the invention, or use of a vector or a cell according to the invention, for determining whether a sample comprises AML or B-HNL cells is also provided, as well as a method for detecting AML or B-HNL cells using an antibody or functional part according to the invention. The invention further provides a method for determining whether AML or B-HNL cells are present in a sample comprising:

- contacting said sample with an antibody or functional part according to the invention, and
- allowing said antibody or functional part to bind myeloproliferative cells or lymphoproliferative cells, if present, and
- determining whether or not AML or B-HNL cells are bound to said antibody or functional part, thereby determining whether or not AML or B-HNL cells are present in said sample.

[0083] In a preferred embodiment, said myeloproliferative cells are AML cells. In another preferred embodiment, said lymphoproliferative cells are B-NHL. Lymphoproliferative cells are preferably detected with one or more antibodies selected from the group consisting of AT12-023, AT12-025 and AT13-031, and functional parts thereof.

[0084] In a embodiment relates to determining whether an individual is suffering from a myeloproliferative or lymphoproliferative disorder. Also provided is a method for determining whether an individual is suffering from a myeloproliferative disorder or a lymphoproliferative disorder, wherein said myeloproliferative disorder is AML and wherein said lymphoproliferative disorder is B non-Hodgkin lymphoma, comprising:

- contacting a sample from said individual with an antibody or functional part thereof according to the

invention, and

- allowing said antibody or functional part to bind myeloproliferative cells or lymphoproliferative cells, if present, and
- determining whether or not myeloproliferative cells or lymphoproliferative cells are bound to said antibody or functional part or functional equivalent, thereby determining whether or not said individual is suffering from a myeloproliferative disorder or a lymphoproliferative disorder. Preferably said individual is a human. In some embodiments, said myeloproliferative disorder is AML. In other embodiments, said lymphoproliferative disorder is lymphoma, B-NHL or multiple myeloma.

[0085] As described herein before, the present invention provides the surprising insight that snRNP200 is present on the surface of AML cells, whereas snRNP200 is normally located in the nucleus only. Hence, snRNP200 is an important target for anti-AML therapy. Moreover, antibodies AT12-023 and AT13-031, which are specific for snRNP200, also bind B-NHL cells and multiple myeloma cells. This indicates that surface expression of snRNP200 also occurs on B-NHL cells and multiple myeloma cells. Now that this insight has been provided, many applications have become possible. For instance, snRNP200-specific binding compounds can now be used for treating or preventing myeloproliferative or lymphoproliferative disorders. Disclosed is therefore a use of an snRNP200-specific binding compound for the preparation of a medicament for the treatment or prophylaxis of a myeloproliferative or lymphoproliferative disorder, such as AML, B-NHL or multiple myeloma. An snRNP200-specific binding compound for use in a method for at least in part treating or preventing a myeloproliferative or lymphoproliferative disorder is also disclosed, as well as a method for at least in part treating and/or preventing a myeloproliferative or lymphoproliferative disorder, comprising administering to an individual in need thereof a therapeutically effective amount of an snRNP200-specific binding compound.

[0086] Novel detection methods have also become available. Since snRNP200 is normally only present in the nucleus, but appears to be also present at the surface of myeloproliferative and lymphoproliferative cells, these cells can now be detected and distinguished from healthy cells by determining whether snRNP200 is present at their surface. Further disclosed is therefore a method for determining whether a myeloid cell or lymphoid cell is a myeloproliferative cell or lymphoproliferative cell, the method comprising determining whether snRNP200 is present on the surface of said cell, wherein the presence of snRNP200 on the surface of said cell indicates that said cell is myeloproliferative or lymphoproliferative. Also disclosed is a method for identifying myeloproliferative or lymphoproliferative cells, comprising detecting the presence of snRNP200 on the surface of said cells. As used herein, the expression "present at the surface of a cell" or "present on the surface of a cell" means that at least part of snRNP200 is present on, or within, the cell surface, or associated therewith.

[0087] In some embodiments, a cell-containing sample of an individual is typed. Such sample, which typically contains lymphoid cells and/or myeloid cells, is in some embodiments tested for the presence of snRNP200 on the surface of these cells. If snRNP200 appears to be present on the surface of cells, the sample is typed as containing myeloproliferative or lymphoproliferative cells. Further provided is therefore a method for typing a myeloid cell-containing sample or a lymphoid cell-containing sample of an individual, the method comprising determining whether snRNP200 is present on the surface of cells of said sample. If this is the case, it indicates that myeloproliferative cells or lymphoproliferative cells are present in said sample.

[0088] In some embodiments, the individual is suffering from, or suspected of suffering from, a myeloproliferative or lymphoproliferative disorder. This is however not necessary, since such typing method can also be part of a general screening test, for instance for health checks.

[0089] Said sample can be any sample that contains myeloid and/or lymphoid cells, such as for instance a bone marrow sample, a tissue sample or a lymph fluid sample. Preferably, said sample comprises peripheral blood mononuclear cells, since a blood sample is easily obtainable with little discomfort for the individual.

[0090] The present invention provides the insight that at least a subpopulation of patients who suffer from a

myeloproliferative or lymphoproliferative disorder produce antibodies that are specific for snRNP200. The presence of such antibodies in a sample from an individual is thus indicative for a myeloproliferative or lymphoproliferative disorder. Further provided is therefore a method for determining whether an individual is suffering from a myeloproliferative or lymphoproliferative disorder, wherein said myeloproliferative disorder is AML and wherein said lymphoproliferative disorder is B non-Hodgkin lymphoma, and comprising determining whether a sample from said individual comprises antibodies that are specific for snRNP200. In some embodiments such method comprises the steps of:

- contacting a sample from said individual with snRNP200 or an epitope thereof;
- allowing said snRNP200 or epitope to bind snRNP200-specific antibodies from said sample, if present, and
- determining whether or not said snRNP200 or epitope is bound to snRNP200-specific antibodies, wherein binding of said snRNP200 or epitope to snRNP200-specific antibodies indicates that said individual is suffering from a myeloproliferative or lymphoproliferative disorder.

[0091] Screening assays as provided herein can be performed using methods such as for instance enzyme-linked immunosorbent assays (ELISA), radio-immuno assays (RIA), Western Blot assays and immunohistochemical staining assays. These assays are well known in the art and therefore need no further explanation. Variations or adaptations of ELISA, RIA, Western blot assay and immunohistochemical staining assay are also known in the art.

[0092] Another aspect of the invention provides a method for determining whether a patient suffering from a myeloproliferative or lymphoproliferative disorder has an improved chance of a positive outcome of treatment with an snRNP200-specific antibody or functional part, as compared to the mean population of patients suffering from a myeloproliferative or lymphoproliferative disorder, the method comprising determining whether snRNP200 is present on the surface of myeloproliferative cells or lymphoproliferative cells of said patient. If this is the case, snRNP200-specific antibodies such as AT12-023, AT13-031 and AT13-037 are particularly suitable for counteracting such myeloproliferative or lymphoproliferative disorder. Therefore, if it is known that myeloproliferative or lymphoproliferative cells of an individual express snRNP200 at their surface, the chance of successful treatment is increased. A method according to the invention comprises the steps of:

- contacting a myeloproliferative cell- or lymphoproliferative cell-containing sample from said individual with an antibody or functional part that is specific for snRNP200;
- allowing said antibody or functional part to bind myeloproliferative cells or lymphoproliferative cells of said sample, and
- determining whether or not said a snRNP200-specific antibody or functional part is bound to myeloproliferative cells or lymphoproliferative cells of said sample, wherein binding of said snRNP200-specific antibody or functional part to myeloproliferative cells or lymphoproliferative cells of said sample indicates that said patient has an improved chance of a positive outcome of treatment with an antibody or functional part, as compared to the mean population of patients suffering from a myeloproliferative or lymphoproliferative disorder, wherein said myeloproliferative disorder is AML and wherein said myeloproliferative cells are AML cells, or wherein said lymphoproliferative disorder is B non-Hodgkin lymphoma and wherein said lymphoproliferative cells are B non-Hodgkin lymphoma cells. Said treatment preferably comprises the use of antibodies AT12-023, AT13-031 or AT13-037, or functional parts thereof, since at least these antibodies are able to bind snRNP200.

[0093] If the use of antibody AT12-023, AT13-031 and/or AT13-037 is contemplated, it is preferably determined beforehand if a certain patient contains malignant cells that express snRNP200 at their surface. Some embodiments therefore provide a method for determining whether a patient suffering from a myeloproliferative disorder or lymphoproliferative disorder is a candidate for treatment with antibody AT12-023, AT13-031 or AT13-037, or a functional part or a functional equivalent thereof, the method comprising determining whether

snRNP200 is present on the surface of myeloproliferative cells or lymphoproliferative cells of said patient.

[0094] In a method according to the invention, said myeloproliferative disorder is preferably AML and said myeloproliferative cells are preferably AML cells. Moreover, said lymphoproliferative disorder is preferably lymphoma, B- non-Hodgkin lymphoma or multiple myeloma and said lymphoproliferative cells are preferably lymphoma, B- non-Hodgkin lymphoma or multiple myeloma cells.

[0095] The above-mentioned procedures for detecting myeloproliferative or lymphoproliferative cells using binding compounds are for instance particularly suitable for determining whether a patient suffering from a myeloproliferative disorder or lymphoproliferative disorder who has received medical treatment, such as for instance an AML patient who has been treated against AML, for instance an AML patient who has received immunotherapy such as a stem cell transplantation or donor-lymphocyte infusion, has a GvL response. Until to date, there are no diagnostic tools to test for the presence of a potent GvL response in a treated patient. Such diagnostic tool is much needed, for instance because: 1) It will allow early identification of allogeneic SCT recipients at high risk for relapse, at a time-point before relapse has occurred thereby allowing earlier interventions such as tapering of immunosuppressants or donor-lymphocyte infusions; 2) It will allow titrating such donor lymphocyte infusions until anti-leukemia antibodies do appear; and 3) It will offer hope for allogeneic SCT recipients at a time they often suffer from one of many SCT-related complications when the presence of a potent GvL response can be demonstrated. Nowadays patients have to wait and see whether or not a relapse occurs, and there is no way to predict relapse of disease. The availability of a test for determining whether a patient has a GvL response will therefore greatly improve the clinical care of SCT patients, affecting prognosis and quality of life. Further provided is, therefore, a use of a binding compound according to the invention for determining whether a sample is indicative for a GvL response. Also provided is a use of an antibody according to any one of claims 1-4 for determining whether or not an AML patient has a GvL response. Also disclosed is a use of a binding compound according to the invention for determining whether a treatment against a myeloproliferative or lymphoproliferative disease, such as for instance anti-AML therapy, anti-B-NHL therapy or anti-multiple myeloma therapy, is efficacious. This is for instance done by determining whether a sample (for instance a blood or tissue sample) from a patient (that has for instance received a SCT or DLI or any other form of immunotherapy) contains myeloproliferative or lymphoproliferative cells, for instance AML cells, B-NHL cells or multiple myeloma cells. The absence of myeloproliferative or lymphoproliferative cells indicates that said patient has a GvL response. Further provided is, therefore, a method for determining whether a patient suffering from a myeloproliferative disorder or a lymphoproliferative disorder who has received immunotherapy against said disorder has a GvL response, the method comprising contacting a sample from said patient with an antibody or functional part thereof according to the invention, and allowing said antibody or functional part to bind myeloproliferative or lymphoproliferative cells, if present, and determining whether or not myeloproliferative cells or lymphoproliferative cells are bound to said antibody or functional part or functional equivalent, thereby determining whether or not said individual has a GvL response, whereby the absence of myeloproliferative or lymphoproliferative cells is indicative for a GvL response and the presence of myeloproliferative or lymphoproliferative cells is indicative for a lack of, or insufficient (ineffective), GvL response. In some embodiments, said lymphoproliferative disorder is lymphoma, B-NHL, or multiple myeloma. In some embodiments, said myeloproliferative disorder is AML. Also provided is, therefore, a method for determining whether an AML patient that has received anti-AML immunotherapy has a GvL response, the method comprising contacting a sample from said AML patient with an antibody or functional part or functional equivalent according to the invention, and allowing said antibody or functional part or functional equivalent to bind AML cells, if present, and determining whether or not AML cells are bound to said antibody or functional part or functional equivalent, thereby determining whether or not said individual has a GvL response, whereby the absence of AML cells is indicative for a GvL response and the presence of AML response is indicative for a lack of, or insufficient (ineffective), GvL response. Preferably said individual is a human. Alternatively, binding compounds according to the present invention that are labeled with a detectable moiety, such as for instance with a copper compound, are administered to an AML patient that has received anti-AML immunotherapy such as a SCT or DLI, and it is subsequently determined whether said labeled antibody is bound to AML cells of said patient *in vivo*, for instance using a PET scan. The absence of bound binding compounds is indicative for a GvL response and the presence of bound binding compounds is indicative for a lack of, or insufficient (ineffective), GvL response.

[0096] It is also possible to determine the amount of antibody belonging to the VH4-34 family before and after anti-AML immunotherapy. If the amount of antibody belonging to the VH4-34 family, which is a family of VH sequences known for their potential killing properties (Bhat et al, 1997), is significantly raised after immunotherapy, it indicates that a GvL response is present. Further disclosed is, therefore, a method for determining whether an AML patient that has received anti-AML immunotherapy has a GvL response, the method comprising determining the amount of antibody belonging to the VH4-34 family before and after anti-AML immunotherapy, and determining whether the amount of antibody belonging to the VH4-34 family is significantly raised after immunotherapy. If this is the case, it is concluded that a GvL response is present in said patient. If this is not the case, it is concluded that a GvL response is lacking, or not sufficient.

[0097] The invention is further explained in the following examples. These examples do not limit the scope of the invention, but merely serve to clarify the invention.

Brief description of the drawings

[0098]

Figure 1. Sequences of antibodies AT12-023, AT12-025, AT13-024, AT12-019, AT13-022, AT13-023, AT13-031, AT12-020, AT13-033, AT13-034, AT13-035, AT13-036, AT13-037, AT14-013, AT14-014, AT14-015 and AT14-016.

Figure 2. 36 year old patient with AML, who obtained complete remission after the first cycle of induction chemotherapy and received a myeloablative (MA) allogeneic stem cell transplantation (SCT) from her HLA-matched brother (sib) as consolidation therapy. AML relapse occurred however 5 months post-transplantation. Re-induction chemotherapy resulted again in complete remission and in severe, grade IV graft versus host disease (GvHD) of the liver and grade I GvHD of the skin. The observation that she has remained in complete remission for more than three years now implies that she has developed a potent graft versus leukemia response. B lymphocytes were isolated from a phlebotomy product obtained about 1,5 years after the one cycle of re-induction chemotherapy.

Figure 3. a) Supernatant of one of the minicultures (20 or 40 cells per well) binding to the AML cell line THP-1. b) B cells from this miniculture were plated into 1 cell/well solutions and supernatants again screened for binding to THP-1. THP-1 express HLA-DR, that was used in this screening experiment as a positive control. As a negative control an influenza-specific monoclonal antibody was used.

Figure 4. Two examples of the AML specific antibodies identified. AT12-023 (a) and AT13-031 (b) bind to AML cell lines THP-1 and MonoMac6, but not to healthy peripheral blood mononuclear cells (PBMC), endothelial cells (human umbilical vein endothelial cells: HUVEC), the T cell line Jurkat, primary fibroblasts, hepatocytes (liver hepatocellular carcinoma cell line: HepG2) or the colon adenocarcinoma cell line HT-29. The MRSA-mAb F1 is an in-house generated human IgG3 mAb that is used as control antibody.

Figure 5. Antibodies derived from donor 59 bind to the AML cell lines THP-1 and MonoMac6, and to primary leukemic blasts isolated from newly diagnosed AML patients (ranging from FAB classification M0-M4). See also table 3 for a more detailed overview.

Figure 6. Some of the antibodies also bind to other hematological malignancies. Here, binding of AT12-023 (antibodies isolated from supernatant of B cell clone) and AT 13-031 (recombinant antibody) to B-non Hodgkin lymphoma (B-NHL) cells that were freshly isolated from a lymphoma patient is shown. The antibodies did not bind to non-malignant B cells (not shown in this experiment). The RSV antibody Palivizumab was used as a negative control, and Rituximab, a CD20-antibody specifically binding B-cell lymphoma, as a positive control. See for more details of antibody binding to other hematologic malignancies table 4.

Figure 7. THP-1 cells were cultured in medium alone or with antibodies added at a concentration of 5 µg/ml at

day 0. In the presence of AT12-023, THP-1 cells showed significant growth inhibition. Depicted are total cell numbers in culture.

Figure 8. When added at day 0 of the culture, antibodies AT12-023 and AT12-025 strongly reduced the viability of THP-1 cells. Viability is depicted as the proportion of cells double-negative for cell-death markers Annexin V and 7AAD.

Figure 9. To quantify the amount of THP-1 cells specifically killed by AT12-023 we used a calcein AM release assay. Briefly, before THP-1 cells were incubated with AT12-023, the THP-1 cells were loaded with calcein AM, that is released when cells are dying and the cell membrane becomes instable. Lysis was read out after 4 hours of incubation and was related to the background death of calcein-loaded cells as measured with an irrelevant antibody.

Figure 10.

1. a) Besides killing of THP-1 cells, AT12-025 does also induce death of primary tumor cells, similar to AT13-024. Leukemic blasts, isolated from a patient with AML-M5 at diagnosis, were incubated with AT12-025 or AT13-024 (5 ug/ml) for 24 hours at 37°C, after which cells were stained with 7AAD and AnnexinV to determine the amount of dead cells (7AAD and Annexin V double-positive).
2. b) In addition, Lactate dehydrogenase (LDH) can be used as a marker to determine dying cells. Leukemic blasts, isolated from a patient with AML-M0, were incubated with AT13-024 or the RSV antibody palivizumab for 18 hrs, after which LDH release was measured. These two experiments show that AT13-024, but not palivizumab, induced death of leukemic blasts and that this property was not restricted to one type of AML but includes different FAB classifications (M0 to M5).

Figure 11. Donor 58 was diagnosed with AML-M5, for which she received three cycles of chemotherapy. She remained in complete remission for about a year, after which the AML relapsed. She received one cycle of re-induction chemotherapy, followed by an allogeneic reduced intensity stem cell transplantation (RIST) from a matched unrelated donor (MUD). She developed GvHD grade I of the liver and has remained in complete remission for almost 4 years now, implicating that she has developed a potent graft versus leukemia response. B cells were isolated from a phlebotomy product obtained from this patient about 3 years post-SCT.

Figure 12. Antibodies derived from donor 58 bind to the AML cell lines THP-1 and MonoMac6. Palivizumab, the commercially available RSV specific antibody, was used as a negative control.

Figure 13. Clinical history of a third patient with a potent GvL response. Donor 101 was diagnosed with an intermediate-risk AML (no cytogenetic or molecular abnormalities; FAB classification AML-M5) at the age of 49 years. He received two courses of chemotherapy and one course of consolidation chemotherapy followed by an autologous HSCT, as there was no HLA-matched sibling stem cell donor available. Fourteen months after the first diagnosis his disease relapsed. He obtained complete remission after one cycle of high-dose cytarabine, after which he received a reduced-intensity allogeneic HSCT with a matched unrelated donor (RIST-MUD). Six weeks later he developed acute GvHD of skin, liver and intestine (stage 1; grade II) that responded well to corticosteroid therapy. B cells were isolated from a phlebotomy product obtained from this patient 38 months after the allogeneic HSCT. He has maintained durable remission until today.

Figure 14. Antibodies derived from donor 101 bind to the AML cell lines THP-1 and Molm13, but not to fibroblasts, monocytes, B cells and T cells. An in-house produced human antibody against CD30 was used as a negative control. AT14-013 showed minor reactivity with fibroblasts, compared to its high binding to the AML cell lines. See tables 7 and 8 for an overview of the binding capacities of the antibodies derived from donor 101.

Figure 15. AML-specific antibody AT14-013 (donor 101) binds primary leukemic blasts isolated from newly diagnosed AML patients (FAB classifications M0-M5).

Negative control: in-house generated CD30 antibody. See table 7 for an overview of the primary AML blast binding capacities of the antibodies derived from donor 101.

Figure 16. Antibody AT13-037 induces death of primary blasts. Leukemic blasts, isolated from an AML patient at diagnosis (BL-038; AML-M5), were incubated with antibodies purified from the supernatants of the parental B cell clone (sAT13-037) or with the recombinant antibody (rAT13-037) at a concentration of 5 ug/ml for 4 hours at 37°C, after which cells were stained with the death cell marker Dapi. To quantify death of cells a standard amount of beads was added. Recombinant influenza specific rAT10-002 was used as a negative control.

Figure 17. Cytotoxic antibodies induced a non-apoptotic death pathway.

a) Phase contrast imaging of THP-1 cells. THP-1 cells were incubated with the non-cytotoxic AML-specific antibody AT13-023 (left panel) or the cytotoxic antibody AML-specific AT13-037 (right panel). Interaction was visualized using time-lapse imaging and demonstrated swelling of target cells after which cells died. Stills were taken after 4 hours of incubation, with blue arrows indicating large cells that are dead. b) Double staining with DiOC6 and PI showed that cytotoxic antibodies do not induce apoptosis. THP-1 cells were incubated with the cytotoxic AML-specific antibody AT12-023, with diclofenac (that induces apoptosis in THP-1 cells) or with medium only. Cells undergoing apoptosis first lose their mitochondrial membrane potential (loss of DiOC6 stain) after which they become permeable (PI positive), as can be seen after incubation of THP-1 cells with diclofenac. THP-1 cells incubated with AT12-023 showed increased membrane permeability (PI+) but maintained mitochondrial membrane potential (DiOC6+), indicating the induction of a non-apoptotic cell death pathway. c) To confirm the non-apoptotic nature of the death pathway induced we tested the involvement of caspases in cell death induction. Cell death of THP-1 cells by AML-specific antibodies could not be prevented with the pan caspase inhibitors Q-VD-OPh (left panel) or Z-VAD-fmk (right panel).

Figure 18. Cell death induced by AML-specific antibodies also occurred at 4°C, suggesting the involvement of a passive process. This was true for all antibodies except AT13-031, which is cytotoxic at 37°C only (not shown). Negative controls included the AML-specific non-cytotoxic antibodies AT13-034, AT12-019, AT13-022, AT13-023 and AT13-024.

Figure 19. (a) Incubation of target cells with cytochalasin D did not inhibit binding of the antibodies. THP-1 cells were incubated with cytochalasin D, after which AML-specific antibodies AT12-023, AT13-031 and AT13-037 were added. (b) Preincubation of the target cells with the membrane stabilizing agent cytochalasin D did protect the THP-1 cells against cell death by the AML-specific cytotoxic antibodies.

Figure 20. Target verification of AT12-023, AT13-031 and AT13-037. a) THP-1 membrane lysate was incubated with AT12-023 and AT13-031, with the influenza-specific antibody AT10-002 or with marker alone. Western blot analysis including mouse-anti-human snRNP200 (and HMGB1 as a negative control) revealed specific binding of AT12-023 and AT13-031 to snRNP200. b) AML specific antibodies AT12-019, AT12-023, AT13-031 and AT13-037 or commercially available snRNP200-specific antibodies snRNP200 453 and snRNP200 454 were coated on an ELISA plate, incubated with a snRNP200-flag construct for capturing and with anti-flag HRP for detection. AT12-023, AT13-031 and AT13-037 specifically bound snRNP200, whereas negative controls and for example AT12-019 did not.

Figure 21. THP-1 cells express snRNP200 on their membrane. THP-1 cells and Jurkat cells were stained with a commercially available human-anti-mouse snRNP200 antibody. Intracellular staining of Jurkat cells and THP-1 cells showed nuclear staining, as expected (left panels). However, membrane staining of snRNP200 was restricted to THP-1 cells (right panels).

Examples

Example 1

MATERIALS & METHODS

Patient and healthy human materials

[0099] Study protocols were approved by the Medical Ethical Committee of the Academic Medical Centre. All participants signed informed consent. We selected two patients who had received an allogeneic stem cell transplantation (myeloablative sibling transplant for donor 59 and a matched unrelated donor- reduced intensity stem cell transplantation for donor 58) for AML and who, based on their clinical histories, can be assumed to have generated strong graft versus leukemia responses. These two SCT recipients donated 500 ml peripheral blood each, the products of one of many phlebotomies they underwent for post-transfusion hyperferritinemia. In addition, patients admitted to our clinic with newly diagnosed AML consented to donate 2-5 ml bone marrow or blood containing AML blasts to be used for antibody binding assays. Healthy bone marrow was donated by patients undergoing thoracotomy for cardiac surgery in our institute. B-non Hodgkin's lymphoma cells were obtained as rest material from biopsies of patients with newly diagnosed B-non Hodgkin's lymphoma. These B-non Hodgkin's lymphoma cells were used to test for binding of our antibodies as described below. Rest material of human umbilical vein endothelial cells (HUVECS), that were freshly isolated at the Department of Ophthalmology (AMC, Amsterdam, The Netherlands) were directly used for binding assays as described below. For purity, cells were co stained with and selected for anti human CD14+.

[0100] Mononuclear cells were isolated from peripheral blood and bone marrow of healthy individuals and AML patients by Ficoll separation. Extra markers like CD45, CD33, CD34, CD14, CD3 and CD19 were used to isolate specific cell populations (AML blasts, monocytes, T and B lymphocytes, respectively, obtained from blood bank donors).

Isolation of B cells

[0101] We obtained B cells from peripheral blood by Ficoll separation and CD22 MACS microbeads (Miltenyi Biotec). Subsequently we sorted these cells for CD27- or CD27+ CD19+CD3-IgM-IgA- (naive or memory IgG cells, respectively) and CD19+CD3-CD27+IgG-IgA- (memory IgM cells) on a FACSaria (Becton Dickinson).

Cell culture

[0102] We maintained B cells (2×10^5 cells/ml) in IMDM (Gibco) culture medium containing 8% FBS (HyClone) and penicillin/streptomycin (Roche), supplemented with recombinant mouse IL-21 (50 ng/ml, in house produced) and co-cultured them on γ -irradiated (50Gy) mouse L cell fibroblasts stably expressing CD40L (CD40L-L cells, 10^5 cells/ml). The cultures were tested routinely for the presence of mycoplasma by PCR (data not shown).

Retroviral transduction

[0103] Retroviral transduction was performed as described in Kwakkenbos et al, Nat Med 2010. Briefly, naive and memory IgG and memory IgM B cells were cultured and activated during 36 hours on CD40L-L cells in the presence of mIL-21. Then, BCL6 and Bcl-xL retroviral constructs that include the marker gene for GFP were used to transduce the B cells as described before (Diehl et al, J Immunol 2008), with the addition that we centrifuged cells and virus at room temperature for 60 min at $360 \times g$ (1800 RPM). Transduction efficiency ranged from 69-90%.

Culture of target cell lines

[0104] Target AML cell lines THP-1 (ATCC; density of 2×10^5 cells/ml to 1×10^6 cells/ml) and Mono-Mac6 (a kind gift from Dr. Hamann of the Experimental Immunology department, density of 2×10^5 cells/ml to 2×10^6 cells/ml) were maintained in RPMI 1640 (Gibco) culture medium, containing 10% FBS (HyClone) and penicillin/streptomycin (Roche). Culture medium of Mono-Mac6 was enriched with non-essential amino acids (Invitrogen), 1 mM sodium pyruvate (Invitrogen) and 10 µg/ml human insulin (Sigma). The AML cell line Molm13 was maintained at a density of 5×10^5 cells/ml to 1.5×10^6 cells/ml in RPMI 1640 (Gibco) culture medium, containing 20% FBS (HyClone) and penicillin/streptomycin (Roche). The liver cell lines HepG2 and Huh7 and the colon cell line HT29 (a kind gift from the Tytgat Institute, AMC, Amsterdam, The Netherlands) were cultured in DMEM (Gibco) culture medium, containing 8% FBS (HyClone) and penicillin/streptomycin (Roche). The acute T-cell leukemia cell line Jurkat (ATCC) was maintained in RPMI 1640 (Gibco) culture medium, containing 10% FBS (HyClone) and penicillin/streptomycin (Roche) at a density of 1×10^5 cells/ml to 2×10^6 cells/ml. Skin primary fibroblasts (a kind gift of the University of Leiden, The Netherlands) were cultured twice a week in DMEM (Gibco) culture medium, containing 10% FBS (HyClone) and penicillin/streptomycin (Roche). Cells were passaged no more than 10 times. The diffuse large cell B cell lymphoma (DLBCL) cell lines OCI-Ly1 and OCI-Ly7 (DSMZ and ATCC, respectively) were maintained in IMDM (Gibco) culture medium containing 8% FBS (HyClone) and penicillin/streptomycin (Roche). The cultures were maintained at 0.5×10^6 cells/ml. Finally, the multiple myeloma (MM) cell lines U266 and NCI-H929 were maintained and cultured as described for THP-1 cells.

Generation of AML-specific clones

[0105] Transduced naive and memory IgG and IgM B cells of each patient were seeded at concentrations of 20 or 40 cells per well (hereafter named microcultures) and expanded with IL-21 and CD40L. Supernatants of expanded B cell micro cultures were then screened for antibody binding to leukemia cell lines (THP-1, MonoMac6 and the cell lines depicted in Table 4), to liver- and colon cell lines, and some supernatants also to the primary blasts isolated from patients with AML- M0, M1, M4 and M5, by FACS, using human-IgG-PE (Southern Biotech) or human IgG H+L AF647 (Life Technologies) as a secondary antibody. Several in-house generated antibodies were used as negative control antibodies, such as anti-CD30 (expressed on activated B and T lymphocytes), anti-CD33 (expressed on monocytes, myeloid progenitor cells and myeloid leukaemias), D25 (against RSV; described in WO 2008/147196), AT10-002, AT10-004 (against influenza; described in WO 2013/081463), and F1 (against MRSA; described in WO 2011/008092). In addition, some commercially available antibodies were used, such as Rituximab (anti-CD20), Palivizumab (anti-RSV), Panitumumab (anti-EGFR) and HLA-DR. Microcultures binding to AML cell lines but not to liver- and colon cell lines were selected and seeded at a concentration of 1 cell/well and their supernatants tested again for specificity for AML cell lines. Clones with supernatants specifically binding AML cell lines and not liver- or colon cell lines, or healthy PBMC and bone marrow were selected for sequencing. Clones were expanded under normal culture conditions in the presence of FBS IgG low serum (Hyclone) and antibodies purified from the supernatants of these cultures as described below for the recombinant antibodies.

Cloning of AML-specific antibodies

[0106] To produce recombinant antibodies we isolated total RNA with the RNeasy® mini kit (Qiagen), generated cDNA, performed PCR and cloned the heavy and light chain variable regions into the pCR2.1 TA cloning vector (Invitrogen). To rule out reverse transcriptase or DNA polymerase induced mutations, we performed several independent cloning experiments. To produce recombinant mAb we cloned heavy and light variable regions of each antibody in frame with human IgG1 or IgG3 and Kappa constant regions into a pcDNA3.1 (Invitrogen) based vector and transiently transfected 293T cells. We purified recombinant antibodies from the culture supernatant with Protein A or G, depending on the Ig subtype of the clone.

***In vitro* activity of AML-specific antibodies**

[0107] To measure the *in vitro* effect of AML-specific antibodies on AML cells we used several approaches. First, THP-1 cells (2×10^4) were seeded in flat bottom 96 well plates (Costar). AML or control -antibodies were added on day 1, in a concentration of 5-10 $\mu\text{g/ml}$. Numbers of cells per well were counted daily. Induction of cell death on both THP-1 cells and primary leukemic cells by AML-specific antibodies was measured in parallel by costaining an aliquot of cells for Annexin V (BD Pharmingen) and 7-Aminoactinomycin D (7-AAD; Beckman Coulter), double-negative cells being the viable cells. In addition, we used a specific lysis assay. Target cells (THP-1) were labeled with Calcein AM (Becton Dickinson), a green fluorescent dye that is released from the cytoplasm when cells die. Briefly, 2 million THP-1 cells were incubated with 2 ml of 2 μM Calcein AM for 30 minutes at 37°C. AML or control antibodies were added for 4 hours, after which green fluorescence was measured using a fluorescence plate reader. The proportion of specific lysis was calculated as $(\text{experimental value} - \text{low control}) / (\text{high control} - \text{low control}) \times 100$, where low control means the spontaneous release of Calcein AM by unaffected cells and high control means the maximum amount of released Calcein AM when all cells are lysed. In addition to the Calcein AM release assay we applied the lactate dehydrogenase (LDH) release assay to measure the killing activity of AML specific antibodies. LDH is released by damaged cells, from the cytosol. Leukemic blasts, isolated at diagnosis from a patient with AML-M0, were incubated with AT13-024 at a maximum concentration of 10 $\mu\text{g/ml}$ per 10.000 blasts. LDH release is measured after adding Reaction mixture and Stop Solution (Roche Diagnostics/Applied Science) according to the manufacturer's protocol on an ELISA reader. The percent cytotoxicity is calculated as the $(\text{experimental value} - \text{low control}) / (\text{high control} - \text{low control}) \times 100$, where low control means the spontaneous release of LDH by unaffected cells and high control means the maximum amount of LDH when all cells are lysed. To quantify death of target cells induced by AML-specific antibodies we used a FACS-based leukemia cell lysis assay as previously described (Schmiedel et al, 2013). In brief, FACS calibration beads (Accudrop Fluorescent Beads, BD Biosciences) were added to the cells in a 50/50 ratio after which a standard amount of beads was acquired with FACS. As an equal assay volume was ascertained by the calibration beads, the amount of dead or vanished cells can then be calculated as follows: $100 - ((\text{Dapi negative cells in respective treatment} / \text{Dapi negative cells in control}) \times 100)$.

[0108] Finally, to discern between apoptotic and non-apoptotic pathways of cell death induced by our antibodies we co-stained target cells with DiOC6 and propidium iodide (PI). DiOC6 (3,3-dihexyloxacarbocyanine iodide) is a cell-permeant, green-fluorescent, lipophilic dye that is selective for the mitochondria of live cells, when used at low concentrations. Apoptotic cells will lose their mitochondrial membrane potential (loss of DiOC6 stain) before the cell membrane becomes permeable (PI positive); necrotic cells become PI positive before they lose their mitochondrial membrane potential (and become DiOC6-negative). The methods used for staining were adapted from Hugh J. M et al., 2004. In brief, THP-1 cells were stained with 40nM of DiOC6 (Invitrogen) for 20 minutes at 37°C. PI was added after which the samples were analyzed immediately by flow cytometry.

Flow cytometry

[0109] Stained cells were analyzed on FACS Aria (BD), FACSCanto (BD), FACS LSRFortessa X-20 (BD) and Guava (Millipore) flowcytometers and flow cytometry data were processed with FlowJo software (Tree Star).

Phase contrast imaging

[0110] THP-1 cells were added to a two chambered Cover glass system (LabTek). Using a phase contrast-imaging microscope (in-house manufactured), four fields of interest per chamber were chosen. The software was set to take a picture of every field of interest every other minute. Just prior to the run, the THP-1 binding, non-cytotoxic antibody AT13-023 and the THP-1 binding, cytotoxic antibody AT13-037 were added to their respective

wells at a concentration of 10 ug/ml.

Target verification: Immunoprecipitation and flow cytometry

[0111] THP-1 cells were lysed and precleared with an irrelevant antibody (in-house generated RSV antibody D25) and beads to remove non specific binding proteins. Precleared lysate was then incubated with bead-labeled AML-specific antibodies or with the influenza specific antibody AT10-002 as a negative control (3 hrs at 4°C). Antibody-incubated lysates were washed five times, bound proteins were eluted from the THP-1 lysate and then run on an SDS-PAGE gel. Proteins were blotted and stained with Ponceau S to reveal total protein. The blot was blocked with BSA and incubated with mouse-anti-snRNP200 (Millipore, clone 3B6.1) or Rabbit-anti-HMGB1 (Abcam) for Western blot analysis. Intracellular staining for snRNP200 was performed after fixing and permeabilizing THP-1 cells with methanol (Sigma) and permeabilization buffer containing triton X-100 (Sigma), EDTA (Gibco) and BSA (Roche), followed by incubation with rabbit-anti-human snRNP200 antibody (Sigma) overnight at 4°C.

Target conformation: snRNP200 ELISA

[0112] HEK 293T cells were transfected with an expression vector containing the full-length open reading frame of snRNP200 with an N-terminal FLAG tag. At 2 days after transfection cells were harvested and lysed in lysis buffer containing protease inhibitors. This lysate was cleared and protein concentration was measured. AML specific antibodies AT12-019, AT12-023, AT13-031 and AT13-037 or commercially available snRNP200 specific antibodies (Bethyl labs) were then coated on an ELISA plate. The lysate was added at a concentration of 3 µg/ml for capturing. After extensive washing, captured snRNP200-flag was detected with a monoclonal mouse anti-flag HRP antibody (Sigma-Aldrich, clone M2).

RESULTS

Generation of AML-specific antibodies

[0113] In our project we use a unique technology that was recently developed in our laboratory (WO 2007/067046; incorporated herein by reference) that allows for selection of naturally occurring leukemia-specific B cells and the antibodies produced by these cells. We employed this technology to generate leukemia-specific B cell lines from two AML patients who developed potent GvL responses in parallel with severe GvHD of the liver and skin. With our B cell immortalization technique, it became possible to identify B cell responses of leukemia patients and to create leukemia-specific B cell lines that allow functional studies of the antibodies these cell lines produce and allow generation of larger numbers of antibodies, as compared to other methods known in the art, with diagnostic and therapeutic potential.

[0114] First, we applied our technique as described in WO 2007/067046 to perform a set of pilot experiments, where we isolated and immortalized B lymphocytes from a carefully selected patient (donor 59) who developed a potent GvL response following extensive GvHD of liver and skin. This patient was diagnosed with AML at the age of 36 years. She obtained complete remission after the first of two courses induction chemotherapy after which she received a myeloablative, HLA-matched sibling donor SCT as consolidation therapy. Only 5 months after SCT, shortly after immunosuppressive therapy had been tapered, her AML relapsed. With one cycle of high-dose cytarabine she obtained complete remission again, after which she spontaneously, before the scheduled donor-lymphocyte infusion, developed stage III GvHD of the liver and stage II GvHD of the skin. She was successfully treated with high-dose corticosteroid therapy but during tapering of therapy hepatic GvHD relapsed twice. In the end, corticosteroid therapy was successfully phased out about 6 months before the current experiments were

started (1,5 yrs after AML relapse) and she has remained in complete remission from her leukemia for more than three years now (Figure 2).

[0115] From this patient, we generated B cell clones using our technique to immortalize B cells. Briefly, PBMC were isolated from the peripheral blood by ficoll centrifugation, and B lymphocytes sorted by FACS. Isolated B lymphocytes were then cultured with IL21 and CD40L and transduced with BCL6 and BCL-xL, with a transduction efficiency of around 70%. Using this technique, unique B cell clones that concurrently express the B cell receptor and secrete monoclonal antibodies were generated. Immortalized CD27- naive and CD27+ memory IgG+ B cells were seeded at concentrations of 20 or 40 cells per well and expanded with IL21 and CD40L. Supernatants of expanded B cell micro cultures were then screened for antibody binding to leukemia-, liver- and colon cell lines by FACS, using human-IgG-PE as a secondary detection antibody.

[0116] As the patient had been diagnosed with AML-M5 according to the French-American-British (FAB) classification (Bennett et al., 1976), we selected the THP-1 cell line that morphologically and phenotypically is roughly similar to AML-M5 for these screening essays (Tsuchiya et al., 1988). In addition, because the patient suffered from extensive GvHD of the liver we screened for the identification of liver-binding B cell clones using the liver cell line HepG2. As a negative control, and to select out cross-binding B cell clones we used the colon cell lines HT-29 and LSTR. Micro cultures with the highest binding to either of these cell lines were then sorted and single cells were deposited in 96 well formats, expanded and the supernatants of these expanded clones were again screened for binding against leukemia cell lines (Figure 3).

Properties of AML-specific antibodies

[0117] With this approach we generated eight B cell lines from this one patient, producing antibodies that bind to THP-1 (Figure 3) but not liver or colon cell lines, fibroblasts, endothelial cells (human umbilical vein endothelial cells or HUVEC), healthy PBMC or bone marrow (Table 2 and Figure 4). These are antibodies AT12-019, AT12-023, AT12-025, AT13-022, AT13-023, AT13-024, AT13-031 and AT12-020. The heavy and light chain variable regions of these antibodies are depicted in Table 1 and Figure 1.

[0118] Interestingly, the antibodies are of the IgG1 and IgG3 isotypes, and several of the DNA sequences showed somatic hypermutations. Antibodies AT12-023, AT12-025, AT13-023 and AT13-031 belong to the VH4-34 family, which is a family of VH sequences known for their potential killing properties (Bhat et al, 1997). The antibodies are of donor-origin, as confirmed by microchimerism analyses.

[0119] We then determined the breadth of binding within the spectrum of AML subtypes, and tested the generated AML-specific B cell clones for binding to other AML FAB classification types. Selected leukemia-specific clones also bound to the AML-M5 cell line MonoMac6 (Table 3) (see for review of AML cell lines (Drexler and Minowada, 1998)).

[0120] Our AML-specific antibodies also bound to freshly isolated AML blasts of newly diagnosed patients (Table 3 and Figure 5).

[0121] Furthermore, some antibodies also bound other hematopoietic malignancy -cell lines, such as the diffuse large cell B cell lymphoma cell lines OCI-Ly1 and OCI-Ly7 and the multiple myeloma cell lines U266 and NCI-H929, and/or patient-derived hematologic tumor cells (Table 4 and Figure 6).

In vitro activity of AML specific antibodies

[0122] While testing the specificity of the AML-binding antibodies, we made a striking observation. Three of the eight antibodies spontaneously induced death of the leukemic cells they were binding to. THP-1 cells were killed

by AT12-023 and AT12-025, and primary AML blasts isolated from patients diagnosed with AML were killed by AT12-025 and AT12-024 (Table 5 and Figures 7-10).

[0123] Figure 7 shows rapid killing of THP-1 cells by AT12-023. Dying blasts expressed 7-AAD and Annexin V. Strikingly, while co-culture of THP-1 with AT12-025 at first did not affect total cell numbers in the cultures (Figure 7), this antibody appeared to also induce death of THP-1 cells, albeit with a little delay compared to AT12-023 (Figure 8). The observation that some of the antibodies show direct killing activity against leukemic cells is highly exciting and has to the best of our knowledge not been reported before.

Confirmation of our findings by generating AML-specific B cell lines from a second patient

[0124] About 0.05 to 0.1% of the B cells that we screened from the first patient were found to be AML-specific. To confirm our findings, we selected a second patient with relapsed AML who obtained durable remission after an allogeneic SCT (donor 58; Figure 11). Also this patient developed GvHD of the skin and liver for which she was treated with oral steroids. After steroids were phased out, about one year after the SCT, PBMC were isolated, B cells immortalized, and B cell lines screened for binding to AML cell lines as described above. Five B cell clones have been generated from this patient that bind to the AML cell lines THP-1 and MonoMac6 (Figure 12), but not to liver or gut cell lines, fibroblasts or healthy PBMC (Table 6). These clones produce antibodies AT13-033, AT13-034, AT13-035, AT13-036 and AT13-037. Interestingly, all these antibodies are of the IgG3 isotype. The sequences of the heavy and light chain variable regions of these antibodies are also depicted in Table 1 and Figure 1. These data confirm the achievability of our project; despite the low frequencies of the B cells we are aiming at, we were able to isolate them and to generate robust antibody-producing B cell lines that were specific for AML.

Discussion

[0125] These preliminary data are highly exciting, as - to the best of our knowledge - we are the first to generate several human, non-chimeric, leukemia-specific B lymphocyte clones from patients that developed a robust, lasting GvL response against AML. The observation that some of these antibodies spontaneously show killing activity against leukemic blasts *in vitro* is highly exciting and very promising. In addition, the observation that some of the antibodies have a germline sequence and are of the IgG3 subclass, a type of antibody that can be induced without T cell help, warrants further attention as these findings demonstrate that 'natural' antibodies generated in a T-cell-independent way affect GvL responses in SCT patients. Importantly, these data offer proof of concept that using this technique, we can select leukemia-specific B cell clones.

Example 2

AML-specific antibodies from a third patient

[0126] To further confirm our approach and to show this anti-AML response is not only reserved for female patients, we selected a male patient as well. This patient (Figure 13), donor 101, was diagnosed with an intermediate-risk AML (no cytogenetic or molecular abnormalities; FAB classification AML-M5) at the age of 49 years. He received two courses of chemotherapy (cytarabine, idarubicine, amsacrine) and one course of consolidation chemotherapy (busulphan, cyclophosphamide) followed by an autologous HSCT, as there was no HLA-matched sibling stem cell donor available. Fourteen months after the first diagnosis his disease relapsed. He obtained complete remission after one cycle of high-dose cytarabine, after which he received a reduced intensity allogeneic HSCT of a matched, unrelated donor (RIST-MUD). Six weeks later he developed acute GvHD of skin,

liver and intestine (stage 1; grade II) that responded well to corticosteroid therapy. B cells were isolated from a phlebotomy product obtained from this patient 38 months post-SCT.

[0127] Using the same methods as described in Example 1, four B cell clones have been generated from this patient that bind to the AML cell lines THP-1 and/or Molm13 (Figure 14 and Table 7) but not to (fetal) liver or gut cell lines, fibroblasts or healthy PBMC (Table 8). These clones produce antibodies AT14-013 (IgG1), AT14-014 (IgG3), AT14-015 (IgG3) and AT14-016 (IgG3). Interestingly, again the majority of the antibodies is of the IgG3 isotype. The sequences of the heavy and light chain variable regions of these antibodies show high amounts of somatic hypermutations and are depicted in Table 1B and Figure 1. Clone AT14-013 shows very minor reactivity with the hepatocellular carcinoma cell line Huh7, but not to the hepatocellular carcinoma cell line HepG2 or healthy fetal liver cells. Also minor reactivity to fibroblasts is observed, however, the binding of this antibody to these tissue specific cells, compared to the binding to primary leukemic blasts is negligible (Figure 14).

[0128] It was also tested whether the four antibodies of donor 101 could bind primary AML blasts (Materials & Methods: see Example 1). Figure 15 and Table 7 show that antibody AT14-013 appears to bind primary blasts of at least three different FAB classifications (AML-M0, M4 and M5). Antibodies AT14-015 and AT14-016 are able to bind primary AML blasts of the M4 classification.

Example 3

In vitro activity of AML-specific antibodies of donors 59, 58 and 101

[0129] In Example 1, the breadth of binding of the antibodies of donor 59 within the spectrum of AML subtypes was determined (Table 3). Using the same methods, this has also been determined for the antibodies of donor 58. The results are shown in Table 9A: all five antibodies of donor 58 (AT13-033, AT13-034, AT13-035, AT 13-036 and AT 13-037) bound to the AML-M5 cell line THP-1, as well as to the AML-M5 cell line MonoMac6. These AML-specific antibodies did not significantly bind to freshly isolated AML blasts of newly diagnosed patients of FAB classification M0, M1 or M4. AT13-034 could only weakly bind M0 blasts. This indicates that these antibodies have a specificity for (at least) AML M5 blasts.

[0130] In Example 1, it was also determined that antibodies AT12-023 and AT12-025 of donor 59 killed THP-1 cells (Table 5 and Figures 7-9). Subsequently, we have tested whether the other antibodies of donor 59, as well as the antibodies of donor 58, could also kill THP-1 cells, using the same Materials & Methods as in Example 1. As shown in Tables 9B-10, in addition to AT12-023 and AT12-025 also antibody AT13-031 (donor 59), as well as antibodies AT13-033, AT13-035, AT13-036 and AT13-037 (donor 58) appear to be able to kill THP-1 cells.

[0131] The capability of inducing death of primary AML blasts was also tested (Materials & Methods: see Example 1). Similar to some of the antibodies obtained from donor 59, some of the antibodies derived from donor 58 are also capable of inducing cell death of primary AML cells. This is shown in Figure 16 for antibody AT13-037, in both forms (purified B cell supernatant (sAT13-037) and recombinant produced antibody (rAT13-037); both in the IgG3 confirmation). The leukemic cells are derived from the bone marrow of a newly diagnosed AML patient, FAB classification AML-M5.

Example 4

In vitro activity of AML antibodies is rapid and involves a non-apoptotic cell death pathway

[0132] To investigate the pathway through which several of the above-mentioned antibodies induced death of their target cells, we visualized death of target cells with time-lapse microscopy (Figure 17a). We observed that within a few minutes after incubation with antibody AT13-037, cells started to swell and then died. This suggested that antibodies according to the invention activated pathways other than the classical apoptosis pathways, as apoptotic cells shrink rather than swell. To further investigate this we performed double staining with the cell death markers DiOC6 and propidium iodide (PI). Cells engaged to undergo apoptosis first loose mitochondrial charge (which can be visualized by the loss of DiOC6 binding) before membrane permeability increases (visualized by propidium iodide (PI) staining), while cells undergoing necrosis loose their membrane integrity (PI positive) but not immediately the mitochondrial membrane potential. As diclofenac is known to induce apoptosis of THP-1 cells, we used diclofenac as a positive control. Diclofenac-treated, apoptotic THP-1 cells became DiOC6-negative (lost mitochondrial membrane potential), but maintained membrane integrity. Upon incubation with the AML-specific cytotoxic antibody AT12-023 mitochondrial membrane potential was maintained (DiOC6-positive) while the membrane permeability of THP-1 cells increased (PI-positive). Thus, AML-antibody treated THP-1 cells became PI-positive while maintaining mitochondrial membrane potential (Figure 17b, right panel) indicating the activation of a non-apoptotic death pathway. Indeed, death of THP-1 cells by cytotoxic AML-specific antibody treatment could not be prevented by incubating the cells with the pan caspase inhibitors Z-VAD-fmk or QVD-OPh (Figure 17c).

Cell death mediated through interference with the target cell membrane

[0133] Non-apoptotic death pathways include necroptosis and oncosis. Necroptosis is, similar to apoptosis, an active cell death pathway that depends on the activation of defined molecular pathways including the activation of receptor-interacting protein kinase 3 (RIPK3). To investigate whether AML-antibody-induced cell death was dependent on the activation of intracellular molecular pathways we tested whether antibody-induced cytotoxicity was dependent of temperature. We found that under these experimental conditions the cytotoxic activities of at least antibodies AT13-033, AT13-035, AT13-036, AT13-037, AT12-023 and AT12-025 were equally potent at 4°C as compared to their activities at 37°C (Figure 18), suggesting that at least these antibodies induced cell death by a passive process. Of note, the cytotoxic activity of antibody AT13-031 was significantly more potent at 37°C as compared to 4°C. However, since antibody AT13-031 does induce death of AML cells in the presence of apoptosis inhibitors (such as the pan caspase inhibitors Q-VD-OPh or Z-VAD-fmk), it is clear that antibody AT13-031 is also able to diminish proliferation of AML cells independently from apoptosis.

[0134] Oncosis is a mode of cell death characterized by swelling of the cell, through selective membrane injury, resulting in increased membrane permeability and ultimately cell death. Oncosis-inducing antibodies have been described that mediate cell death by forming large pores in the membrane through destabilization of the membrane (Hernandez et al, 2011). Cytochalasin D is an actin polymerization inhibitor that can stabilize the cytoskeleton. Treatment of the target cell line THP-1 with cytochalasin D did not prevent antibody binding to these cells (Figure 19a), however, it did prevent death of the target cells (Figure 19b). Thus, membrane stabilisation protects the target cells against the cytotoxic activity of our antibodies.

Example 5

One of the targets recognized by our antibodies is snRNP200

[0135] We then set out to determine the target recognized by several AML-specific antibodies. For this we used immunoprecipitation of cell membrane lysates of THP-1 cells with AT12-023 and AT13-031. We found a clear protein band at 250 kD that was sent for mass-spectrometry analysis which revealed snRNP200 as the target antigen which could be confirmed by Western blot analysis (Figure 20a). We developed an ELISA, to verify snRNP200 as the target of some of the AML antibodies. With this ELISA we found that in addition to AT12-023

and AT13-031, AT13-037 specifically recognizes snRNP200 (Figure 20b). Other AML specific antibodies like AT12-019 did not recognize snRNP200 as target antigen.

[0136] snRNP200 is part of the spliceosome in all eukaryotic cells and is therefore expected to be located in the nucleus. To confirm that AML cells express this protein on their cell surface we stained the cell membrane of THP-1 cells with a commercially available, anti-snRNP200 antibody. Figure 21 shows that the anti snRNP200 antibody is indeed binding to the membrane of the AML cells, but not to the Jurkat cell line. As expected, as snRNP200 is a nuclear protein, it did bind intracellularly to the Jurkat and THP-1 cell lines (Figure 21).

[0137] All eukaryotic cells have snRNP200 (also known as U5-snRNP) protein in the nucleus, as part of the spliceosome (Kattah, 2010). The spliceosome consists of a number of proteins. At least one of these proteins, U1-snRNP, has been described to be expressed on apoptotic cells in patients with systemic lupus erythematosus (SLE) and mixed connective tissue disease (MCTD) leading to auto-immune responses (Kattah, 2010).

[0138] We propose that snRNP200 expression by AML cells has triggered an allo-immune response (graft vs leukemia response) that has kept the patients in durable remission. Therefore, this protein can now be used as a new AML target. Moreover, since antibodies AT12-023 and AT13-031 specifically recognize snRNP200 and also recognize B-NHL cells, snRNP200 can now also be used as a target for B-NHL.

Table 1A. Preferred anti-AML antibodies according to the invention (CDR numbering according to Kabat *et al.* 1991)

SEQ ID NO.	Antibody	Identity	Sequence
1	AT12-023	Heavy chain CDR1	GYWWS
2	AT12-025	Heavy chain CDR1	GYWWS
3	AT13-024	Heavy chain CDR1	SYGMH
4	AT12-019	Heavy chain CDR1	SYAMS
5	AT13-022	Heavy chain CDR1	SYGMH
6	AT13-023	Heavy chain CDR1	GYFWT
7	AT13-031	Heavy chain CDR1	GYWWS
8	AT12-020	Heavy chain CDR1	TYSMN
9	AT13-033	Heavy chain CDR1	NYGMH
10	AT13-034	Heavy chain CDR1	SHAIH

SEQ ID NO.	Antibody	Identity	Sequence
11	AT13-035	Heavy chain CDR1	SYGMH
12	AT13-036	Heavy chain CDR1	SYSMN
13	AT13-037	Heavy chain CDR1	TYGMH
14	AT12-023	Heavy chain CDR2	EINHSGSTNYNPSLKS
15	AT12-025	Heavy chain CDR2	EINHSGSTNYNPSLKS
16	AT13-024	Heavy chain CDR2	FIRYDGSNKYFADSVRG
17	AT12-019	Heavy chain CDR2	TIRASGGSTSYADSVKG
18	AT13-022	Heavy chain CDR2	ISYDGSNKYYADSVKG
19	AT13-023	Heavy chain CDR2	ETVHSGGTNYNPSLKS
20	AT13-031	Heavy chain CDR2	EINHSGSTNYNPSLKS
21	AT12-020	Heavy chain CDR2	SISSSSGYIYYADSVKG
22	AT13-033	Heavy chain CDR2	VISHDGSKTYYGHSVKG
23	AT13-034	Heavy chain CDR2	LIWYDGSNNYYADSVKG
24	AT13-035	Heavy chain CDR2	VISYDGSNKYYADSVKG
25	AT13-036	Heavy chain CDR2	SISSSSTYIYYADSVKG
26	AT13-037	Heavy chain CDR2	VIWYDGSNTYYADSVKG
27	AT12-023	Heavy chain CDR3	GRSTSPLDYYYYYMDV

SEQ ID NO.	Antibody	Identity	Sequence
28	AT12-025	Heavy chain CDR3	GSMARPKPFDY
29	AT13-024	Heavy chain CDR3	DPQERIYYSDTSGYLDY
30	AT12-019	Heavy chain CDR3	SPAMIRGVRGGDYFDY
31	AT13-022	Heavy chain CDR3	DGKGIVVIYYYYGMDV
32	AT13-023	Heavy chain CDR3	GLNSPFDY
33	AT13-031	Heavy chain CDR3	GPRGMYSSSSGDY
34	AT12-020	Heavy chain CDR3	DGTFSYYYMDV
35	AT13-033	Heavy chain CDR3	AGLNYYGNLLSNFYFYGMDV
36	AT13-034	Heavy chain CDR3	ARDGCTGGSCCYFDN
37	AT13-035	Heavy chain CDR3	AKDSYYYGSGRRWGYYFDY
38	AT13-036	Heavy chain CDR3	ARRREVGRDGYSLYPRGYHYGMDV
39	AT13-037	Heavy chain CDR3	ARGRGYSAQGNNRAYYFDY
40	AT12-023	Light chain CDR1	QGDFLRSYYAS
41	AT12-025	Light chain CDR1	RASQSISRYLN
42	AT13-024	Light chain CDR1	RASQSISSWLA
43	AT12-019	Light chain CDR1	RASQAFSSYLV
44	AT13-022	Light chain	SGDKLGDKYAC

SEQ ID NO.	Antibody	Identity	Sequence
		CDR1	
45	AT13-023	Light chain CDR1	RASQGIRNVLG
46	AT13-031	Light chain CDR1	RASQGIRNDLG
47	AT12-020	Light chain CDR1	RASQDISSSLA
48	AT13-033	Light chain CDR1	TGTSSDIGGYNYVS
49	AT13-034	Light chain CDR1	RASQSISSNLLG
50	AT13-035	Light chain CDR1	QGDSLRSYYAS
51	AT13-036	Light chain CDR1	TGTSSDVGGYNYVS
52	AT13-037	Light chain CDR1	RASQSVSSNLA
53	AT12-023	Light chain CDR2	GKNKRPS
54	AT12-025	Light chain CDR2	AASSLQS
55	AT13-024	Light chain CDR2	KASSLES
56	AT12-019	Light chain CDR2	ATSTLQG
57	AT13-022	Light chain CDR2	QDSKRPS
58	AT13-023	Light chain CDR2	AASSLQS
59	AT13-031	Light chain CDR2	AAVSLQS
60	AT12-020	Light chain CDR2	AASTLQS
61	AT13-033	Light	EVTKRPS

SEQ ID NO.	Antibody	Identity	Sequence
		chain CDR2	
62	AT13-034	Light chain CDR2	GASTRAT
63	AT13-035	Light chain CDR2	GKNNRPS
64	AT13-036	Light chain CDR2	DVNRPS
65	AT13-037	Light chain CDR2	GAFTRVT
66	AT12-023	Light chain CDR3	NSRDRSGNHLV
67	AT12-025	Light chain CDR3	QQSYSTPRT
68	AT13-024	Light chain CDR3	QQYNTYPYT
69	AT12-019	Light chain CDR3	QQYYSYPPT
70	AT13-022	Light chain CDR3	QAWDSSTVVF
71	AT13-023	Light chain CDR3	LQHNSHPRT
72	AT13-031	Light chain CDR3	LQHNSYPRT
73	AT12-020	Light chain CDR3	QQYYSYPPT
74	AT13-033	Light chain CDR3	SSYAGSNDLL
75	AT13-034	Light chain CDR3	QQYNNWPRLT
76	AT13-035	Light chain CDR3	NSRDSSGNHVV
77	AT13-036	Light chain CDR3	SSYTRSNTVI

SEQ ID NO.	Antibody	Identity	Sequence
78	AT13-037	Light chain CDR3	QQYNDRPPYT
79	AT12-023	Heavy chain	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLKSRVTISV DTSKNQFSLKLSSVTAADTAVYYCARGRSTSPLDYYYYYMDVWAKGTTTVTVSS
80	AT12-025	Heavy chain	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLKSRVTISV DTSKNQFSLKLSSVTAADTAVYYCARGSMARPKPFDYWGQGLTVTVSS
81	AT13-024	Heavy chain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYFADSVRGRFTIS RDNSKNTLFLQMNSLRAEDTAVYYCAKDPQERIIYSDTSGYLDYWGGQGLTATVSS
82	AT12-019	Heavy chain	EVHLLSFGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTIRASGGSTSYADSVKGRFTISR DNSQSRLYLQMNSLTAEDTAVYYCAKSPAMIRGVRGGDYFDYWGGQGLTVTVSS
83	AT13-022	Heavy chain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCAKDGKGIIVIIYGGMDVWGGQGTTVTVSS
84	AT13-023	Heavy chain	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYFWTWIRQPPGKGLEWIGETVHSGGTNYPNPSLKSRVTISV DTSKNQFSLRLNSVTAADTAVYYCVRGLNSPFDDYWGGQGLTATVSS
85	AT13-031	Heavy chain	QVQLQQWGAGLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKGLEWIGEINHSGSTNYPNPSLKSRVTISV DTSKKQFSLKLSSVTAADTAVYYCARGPRGMYSSSSGDIWGGQGLTVTVSS
86	AT12-020	Heavy chain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSTYSMNWVRQAPGKGLEWVSSISSSSGYIYADSVKGRFTISR DNAKNSLYLQMNSLRAEDTAVYYCARDGTFSYIIYMDVWGGKGTTVTVSS
87	AT13-033	Heavy chain	QVQLVESGGGVVQPGRSLRLSCAVSGLSFRNYGMHWVRQAPGKGLEWVAVISHDGSKTYIGHSVKGRFTI SRDKSKTMLFLQMNSLRPEDTAVYYCAKACILNYCNIISNYFYGMIDVWGGQGTTVTVSS
88	AT13-034	Heavy chain	QVHLLVESGGGVVQPGTSLRLSCAASEFTFSSHAHWVRQAPGKGLEWVALIWDGSSNNYADSVKGRFTIS RDSSKNTVILQMNSLRVEDTAVYYCARDGCTGGSCCYFDNWGGQGLTVTVSS
89	AT13-035	Heavy chain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTIS RDNSKNTLYLQMNSLRAEDTAVYYCAKDSYYGSGRRWGYFDYWGGQGLTVTVSS
90	AT13-036	Heavy chain	EVQLVESGGGLVQPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSTIYIYADSVKGRFTISR DNARNSLYLQMNSLRAEDTAVYYCARRREVGRDGYSLYPRCYHYGMDVWGGQGTTVTVSS
91	AT13-037	Heavy chain	QVQLVESGGGVVQPGRSLRLSCAASGFTFSTYGMHWVRQAPGKGLEWVAVIWDGSSNTYYADSVKGRFTI SRDNSKNTLYLQIKSLRAEDTAVYYCARGRGYSAQCNRNRAYFDYWGGQGLTVTVSS
92	AT12-023	Light	

SEQ ID NO.	Antibody	Identity	Sequence
		chain	SSELTQDPAVSVALGQTVRITCQGDFLRSYASWYQQKPGQAPVLFVFGKNKRPISGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDRSGNIILATGGGKLTVL
93	AT12-025	Light chain	DIQMTQSPSSLSASVGDRTTITCRASQSISSRYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLPEDFATYYCQQSYSTPRTFGPGTKVEIK
94	AT13-024	Light chain	DIQMTQSPSTLSASVGDRTTITCRASQSISSRLAWYQQKPGKAPKLLIYKASSLESQGVPSRFSGTSGSGTEFTLTISLQPDDEFATYYCQYNTYPYTFGGGKLEIK
95	AT12-019	Light chain	AIRLTQSPSSVSASTGDRVTITCRASQAFSSYLWYQQKPGKAPNLLIYATSTLQGGVPSRFSGSGSGTDFTLTISNLQSEDFATYYCQQYSYPPTFGGKLEIK
96	AT13-022	Light chain	SYELTQPPSVSVSPGQTASITCSGDKLGDYACWYQQKPGQSPVLVIYQDSKRPSCHPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSTVVFGGGKLTVL
97	AT13-023	Light chain	DIQMTQSPSSLSASVGDRTTITCRASQGIRNVLGWYQQKPGKAPKCLIIYAASSLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSHPRTFGGKVEIK
98	AT13-031	Light chain	DIQMTQSPSSLSASVGDRTTITCRASQGIRNDLGWYQQKPGKAPKRLIYAASLQSGVPSRFSGSGSGTEFTLTISLQPEDFATYYCLQHNSYPRTFGGKLEIK
99	AT12-020	Light chain	AIRMTQSPSSFSASTGDRVTITCRASQDISSSLAWYQQKPGKAPKLLIYAASLTQSGVPSRFSGSGSGTDFTLTISCLQSEDFATYYCQQYSYPPTFGGKTRLEIK
100	AT13-033	Light chain	QSALTQPPSASGSPGQSVTISCTGTSSDIGCYNYSWYQHHPGKAPKLMIEVTKRPSGVDPDRFSGSKSGNTASLTVSGLQAEDEAHYCCSYAGSNDLLFGGGKLTVL
101	AT13-034	Light chain	EVVMTQSPATLSVSPGERATLSCRASQSISSNLCWYQQKPGQAPRLIYGASTRATGIPCRFSGSGSGTEFTLTITSLQSEDFAVYYCQQYNNWPRLTFGGGKVEIK
102	AT13-035	Light chain	SSELTQDPAVSVALGQTVRITCQGDSLRSYASWYQQKPGQAPVLFVYGKNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSCNHVVFGGKLTVL
103	AT13-036	Light chain	QSALTQPASVSGSPRQSITISCTGTSSDVGCYNYSWYQQLPKGKAPKLMIDVNDRPSGVSIIRFSGSKSGNTASLTISGLQAEDEADYYCSSYTRSNVIFGGGKLTVL
104	AT13-037	Light chain	EIVMTQSPATLSVSPGERVILSCRASQSVSSNLAWYQQKPGQPPRLIYGAPTRVTGVDPARFSGSGSGTEFTLTISLQSEDFAVYYCQQYNDRPPYTFGGGKLEIK
105	AT12-023	Heavy chain CDR1	ggt tac tac tgg agc
106	AT12-025	Heavy chain CDR1	ggt tat tac tgg agc
107	AT13-024	Heavy	agc tat ggc atg cac

SEQ ID NO.	Antibody	Identity	Sequence
		chain CDR1	
108	AT12-019	Heavy chain CDR1	agc tat gcc atg agt
109	AT13-022	Heavy chain CDR1	agc tat ggc atg cac
110	AT13-023	Heavy chain CDR1	ggg tac ttc tgg acc
111	AT13-031	Heavy chain CDR1	ggg tac tac tgg agc
112	AT12-020	Heavy chain CDR1	acc tat agc atg aac
113	AT13-033	Heavy chain CDR1	aat tat ggc atg cac
114	AT13-034	Heavy chain CDR1	tcc cat gcc ata cac
115	AT13-035	Heavy chain CDR1	agc tat ggc atg cac
116	AT13-036	Heavy chain CDR1	agt tat agc atg aac
117	AT13-037	Heavy chain CDR1	acc tat ggc atg cac
118	AT12-023	Heavy chain CDR2	gaa atc aat cat agt gga agc acc aac tac aac ccg tcc ctc aag agt
119	AT12-025	Heavy chain CDR2	gaa atc aat cat agt gga agc acc aac tac aac ccg tcc ctc aag agt
120	AT13-024	Heavy chain CDR2	ttt ata cgg tat gat gga agt aat aaa tac ttt gca gac tcc gtg agg ggc
121	AT12-019	Heavy chain CDR2	act att agg gct agt ggt ggt agc aca agc tac gca gac tcc gtg aag ggc
122	AT13-022	Heavy chain CDR2	ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg aag ggc
123	AT13-023	Heavy chain CDR2	gaa acc gtt cat agt gga ggc acc aac tac aac ccg tcc ctc aag agt

SEQ ID NO.	Antibody	Identity	Sequence
124	AT13-031	Heavy chain CDR2	gaa atc aat cat agt gga agc acc aac tac aac ccg tcc ctc aag agt
125	AT12-020	Heavy chain CDR2	tcc att agt agt agt agt ggt tac ata tac tac gca gac tca gtg aag ggc
126	AT13-033	Heavy chain CDR2	gtc att tcg cat gat gga agt aag aca tac tat gga cac tcc gtg aag ggc
127	AT13-034	Heavy chain CDR2	ctt ata tgg tat gat gga agt aat aat tat tat gca gac tcc gtg aag ggc
128	AT13-035	Heavy chain CDR2	ggt ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg aag ggc
129	AT13-036	Heavy chain CDR2	tcc att agt agt agt agt act tac ata tac tac gca gac tca gtg aag ggc
130	AT13-037	Heavy chain CDR2	ggt ata tgg tat gat gga agt aat aca tac tat gca gac tcc gtg aag ggc
131	AT12-023	Heavy chain CDR3	ggc cgt agt acc agc ccg ctc gac tac tac tac tac atg gac gtc
132	AT12-025	Heavy chain CDR3	ggc tca atg gca aga ccc aag cca ttt gac tac
133	AT13-024	Heavy chain CDR3	gcg aaa gat ccc caa gag cgt att tat tac tct gat act agt ggt tac ctt gac tac
134	AT12-019	Heavy chain CDR3	tct cct gct atg att cgg gga gtt agg ggg ggt gac tac ttt gac tac
135	AT13-022	Heavy chain CDR3	gat ggg aag ggg att gta gtt att tac tac tac tac ggt atg gac gtc
136	AT13-023	Heavy chain CDR3	ggc ctt aac agc ccc ttt gac tac
137	AT13-031	Heavy chain CDR3	ccc cgg ggc atg tat agc agc tcg tcc ggg gac tac
138	AT12-020	Heavy chain CDR3	gat ggg act ttc tcc tac tac tac tac atg gac gtc
139	AT13-033	Heavy chain CDR3	gcc ggg ttg aac tac tat gga aac cta tta tca aac tac ttc tac tac gga atg gac gtc
140	AT13-034	Heavy chain CDR3	gcg aga gat ggt tgt act ggt ggt agc tgc tgc tat ttt gac aac

SEQ ID NO.	Antibody	Identity	Sequence
141	AT13-035	Heavy chain CDR3	gcg aaa gac tcg tat tac tat ggt tcg ggg aga cga tgg ggc tac tac ttt gac tac
142	AT13-036	Heavy chain CDR3	gcg aga agg agg gag gtc ggt aga gat ggc tac agt ttg tac ccc cgg ggg tac cac tac ggt atg gac gtc
143	AT13-037	Heavy chain CDR3	gcg aga ggc cgt gga tat agt gcc caa ggg aat cgg aat agg gct tac tac ttt gac tac
144	AT12-023	Light chain CDR1	caa gga gac ttc ctc aga agc tat tat gca agc
145	AT12-025	Light chain CDR1	cgg gca agt cag agc att agc agg tat tta aat
146	AT13-024	Light chain CDR1	cgg gcc agt cag agt att agt agc tgg ttg gcc
147	AT12-019	Light chain CDR1	cgg gcg agt cag gct ttt agc agt tat tta gtc
148	AT13-022	Light chain CDR1	tct gga gat aaa ttg ggg gat aaa tat gct tgc
149	AT13-023	Light chain CDR1	cgg gca agt cag ggc att aga aat gtt tta ggc
150	AT13-031	Light chain CDR1	cgg gca agt cag ggc att aga aat gat tta ggc
151	AT12-020	Light chain CDR1	cgg gcg agt cag gat att agc agt tct tta gcc
152	AT13-033	Light chain CDR1	act ggg acc agc agt gac att ggt ggt tat aac tat gtc tcc
153	AT13-034	Light chain CDR1	agg gcc agt cag agc att agc aac aac tta ggc
154	AT13-035	Light chain CDR1	caa gga gac agc ctc aga agc tat tat gca agc
155	AT13-036	Light chain CDR1	act gga acc agc agt gac gtt ggt ggt tat aac tat gtc tcc
156	AT13-037	Light chain CDR1	agg gcc agt cag agt gtt agc agc aac tta gcc
157	AT12-023	Light chain	ggt aaa aac aag cgg ccc tca

SEQ ID NO.	Antibody	Identity	Sequence
		CDR2	
158	AT12-025	Light chain CDR2	gct gca tcc agt ttg caa agt
159	AT13-024	Light chain CDR2	aag gcg tct agt tta gaa agt
160	AT12-019	Light chain CDR2	gct aca tcc act ttg caa ggt
161	AT13-022	Light chain CDR2	caa gat agc aag cgg ccc tca
162	AT13-023	Light chain CDR2	gct gca tcc agt ttg caa agt
163	AT13-031	Light chain CDR2	gct gca gtc agt ttg caa agt
164	AT12-020	Light chain CDR2	gct gca tcc act ttg caa agt
165	AT13-033	Light chain CDR2	gag gtc act aag cgg ccc tca
166	AT13-034	Light chain CDR2	ggg gca tcc acc agg gcc act
167	AT13-035	Light chain CDR2	ggg aaa aac aac cgg ccc tca
168	AT13-036	Light chain CDR2	gat gtc aat gat cgg ccc tca
169	AT13-037	Light chain CDR2	ggg gca ttc acg agg gtc act
170	AT12-023	Light chain CDR3	aac tcc cgg gac cgc agt ggt aac cac ctg gtg
171	AT12-025	Light chain CDR3	caa cag agt tac agt acc cct cgc act
172	AT13-024	Light chain CDR3	caa cag tat aat act tac ccg tac act
173	AT12-019	Light chain CDR3	caa cag tat tat agt tac cct ccg act
174	AT13-022	Light	cag gcg tgg gac agc agc act gtg gta ttc

SEQ ID NO.	Antibody	Identity	Sequence
		chain CDR3	
175	AT13-023	Light chain CDR3	cta cag cat aat agt cac ccc cgg acg
176	AT13-031	Light chain CDR3	cta cag cat aat agt tac cct cgg act
177	AT12-020	Light chain CDR3	caa cag tat tat agt tac cct ccg acg
178	AT13-033	Light chain CDR3	agc tca tat gca ggc agc aac gat ttg cta
179	AT13-034	Light chain CDR3	caa caa tat aat aac tgg cct cgg ctc act
180	AT13-035	Light chain CDR3	aac tcc cgg gac agc agt ggt aac cat gtg gta
181	AT13-036	Light chain CDR3	agc tca tat aca aga agc aac act gtg ata
182	AT13-037	Light chain CDR3	cag cag tac aat gac cgg ccc ccg tac act
183	AT12-023	Heavy chain	cag gtg cag cta cag cag tgg ggc gca gga elg ttg aag cct tgg gag ace elg tcc etc ace tgc gct gtc lat ggt ggg tcc ttc agt ggt tac tac tgg age tgg ate cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg gaa atc aat cat agt gga age ace aac tac aac cgg tcc etc aag agt cga gtc acc ata tea gla gac acg tcc aag aac cag ttc tcc ctg aag ctg age tct gtg acc ggc ggg gac aeg gct gtg tat tac tgt ggc agg ggc cgt agt acc age cgg etc gac tac tac tac tac atg gac gtc tgg ggc aaa ggg acc acg gtc acc gtc tcc tea
184	AT12-025	Heavy chain	cag gtg cag cta cag cag tgg ggc gca gga elg ttg aag cct tgg gag ace elg tcc etc ace tgc gct gtc tat ggt ggg tcc ttc agt ggt tat tac tgg age tgg ate cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg gaa atc aat cat agt gga age ace aac tac aac cgg tcc etc aag agt cga gtc acc ata tea gla gac acg tcc aag aac cag ttc tcc ctg aag ctg age tct gtg acc ggc ggg gac aeg gct gtg tat tac tgt ggc aga ggc tea atg gca aga ccc aag cca ttt gac tac tgg ggc cag gga ace ctg gtc acc gtc tcc tea
185	AT13-024	Heavy chain	cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg tcc ctg aga etc tcc tgt gca ggc tct gga ttc ace ttc agt age tat ggc atg cag tgg gtc cgc cag cct cca ggg aag ggg ctg gag tgg gtg gca ttt ata cgg tat gat gga agt aat aaa tac ttt gca gac tcc gtg agg ggc cga ttc acc ate tcc aga gac aat tcc aag aac acg ctg ttt ctg caa atg aac age ctg aga gct gag gac acg gct gtg tat tac tgt ggc aaa gat ccc cca gag cgt att tat tac tct gat act agt ggt tac ett gac tac tgg ggc cag gga ace ctg gtc acc gtc tcc tea
186	AT12-019	Heavy chain	gag gtg cag ctg ttg gag tct ggg gga ggc ttg gta cag cct ggg ggg tcc ctg aga etc tcc tgl gca ggc tct gga ttc ace ttt age age tat ggc atg agt tgg gtc cgc cag cct cca ggg aag ggg ctg gag tgg gtc tea act att agg gct agt ggt agt age aca age tac gca gac tcc gtg aag ggc cgg ttc acc ate tcc aga gac aat tcc cag age agg ttg lat ctg caa atg aac agt ctg aca goc gag gac acg ggc gta tat tac tgt ggc aaa tct cct gct atg att cgg gga gtt agg ggg ggt gac ttt gac tac tgg ggc cag gga ace ctg gtc acc gtc tcc tea
187	AT13-022	Heavy chain	cag gtg cag ctg gtg gag tct ggg gga ggc gtg gtc cag cct ggg agg tcc ctg aga etc tcc tgt gca ggc tct gga ttc ace ttc agt age tat ggc atg cag tgg gtc cgc cag cct cca ggg aag ggg ctg gag tgg gtg gca ttt ata tea tat gat gga agt aat aaa

SEQ ID NO.	Antibody	Identity	Sequence
			tac tat gca gac tcc gta aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg caa atg aac age ctg aga gct gag gac acg gct gta tat tac tgt ggc aaa gat ggg aag ggg att gta gtt att tac tac tac tac ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tea
188	AT13-023	Heavy chain	cag gta cag cta cag cag tgg ggc gca gga ctg ttg aag cct tgg gag acc ctg tcc etc acc tgc gct gtc tat ggt ggg tcc ttc agt ggt tac ttc tgg acc tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg gaa acc gtt cat agt gga ggc acc aac tac aac cgg tcc etc aag agt cga gtc acc ata tca gtc gac acg tcc aag aac cag ttc tcc ctg agg ctg aac tct gta acc ggc ggc gac acg gct gta tat tat tgt ggc aga ggc ccc cgg ggc atg tat age age tgc tcc ggg gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tea
189	AT13-031	Heavy chain	cag gta cag cta cag cag tgg ggc gca gga ctg ttg aag cct tgg gag acc ctg tcc etc acc tgc gct gtc tat ggt ggg tcc ttc agt ggt tac tac tgg acc tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg gaa atc aat cat agt gga age acc aac tac aac cgg tcc etc aag agt cga gtc acc ata tca gta gac acg tcc aag aag cag ttc tcc ctg aag ctg age tct gta acc ggc ggc gac acg gct gta tat tat tgt ggc aga ggc ccc cgg ggc atg tat age age tgc tcc ggg gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tea
190	AT12-020	Heavy chain	gag gta cag ctg gta gag tct ggg gga ggc ctg gtc aag cct ggg ggg tcc ctg aga etc tcc tgt gca ggc tct gga ttc acc ttc agt acc tat age atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca tcc att agt agt agt agt ggt tac ata tac tac gca gac tca gta aag ggc cga ttc acc atc tcc aga gac aac ggc aag aac tca ctg tat ctg caa atg aac age ctg aga ggc gag gac acg gct gta tat tac tgt ggc aga ggc ccc cgg ggc atg tat age age tgc tcc ggg gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tea
191	AT13-033	Heavy chain	cag gta cag ctg gta gag tct ggg gga ggc gta gtc cag cct ggg agg tcc ctg aga etc tcc tgt gca gtc tct gga etc agt ttc agg aat tat ggc atg cac tgg gtc cgc cag gct ccc ggc aag ggg ctg gag tgg gta gca gtc att tgg cat gat gga agt aag aca tac tat gga cac tcc gta aag ggc cga ttc acc ata tcc aga gac aac tcc aag acc atg ttg ttt etc caa atg aac age ctg aga cct gag gac acg gct gtt tat tac tgt ggc aaa ggc ggg ttg aac tac tat gga aac cta tta tca aac tac ttc tac tac gga atg gac gtc tgg ggc caa ggg acc aca gtc acc gtc tgg tea
192	AT13-034	Heavy chain	cag gta cag ctg gta gag tct ggg gga ggc gta gtc cag cct ggg acc tcc ctg aga etc tcc tgt gca ggc tct gga ttc acc ttc agt tcc cct ggc aca cag tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gta gca ctt ata tgg tat gat gga agt aat aat tat tat gca gac tcc gta aag ggc cga ttc acc atc tcc aga gac agt tcc aag aac acg gta cat ctg caa atg aac age ctg aga gtc gag gac acg gct gta tat tac tgt ggc aga gat ggt tgt act ggt ggt age tgc tgc tat ttt gac aac tgg ggc cag gga acc cta gtc acc gtc tcc tea
193	AT13-035	Heavy chain	cag gta cag ctg gta gag tct ggg gga ggc gta gtc cag cct ggg agg tcc ctg aga etc tcc tgt gca ggc tct gga ttc acc ttc agt age tat ggc atg cac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gta gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc gta aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg caa atg aac age ctg aga gct gag gac acg gct gta tat tac tgt ggc aag ggc cgt gga tat agt ggc caa ggg aat cgg aat agg gct tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tea
194	AT13-036	Heavy chain	gag gta cag ctg gta gag tct ggg gga ggc ctg gtc aag cct ggg ggg tcc ctg aga etc tcc tgt gca ggc tct gga ttc acc ttc agt agt tat age atg aac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gta gca gtt ata tca tat gat gga agt aat aat tac tac gca gac tca gta aag ggc cga ttc acc atc tcc aga gac aac ggc agg aac tca ctg tat ctg caa atg aac age ctg aga ggc gag gac acg gct gta tat tat tgt ggc aga agg agg gag gtc ggt aga gat ggc tac agt ttg tac ccc cgg ggc tac cac tac
			ggg atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tea
195	AT13-037	Heavy chain	cag gta cag ctg gta gag tct ggg gga ggc gta gtc cag cct ggg agg tcc ctg aga etc tcc tgt gca ggc tct gga ttc acc ttc agt acc tat ggc atg cac tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gta gca gtt ata tca tat gat gga agt aat aca tac tat gca gac tcc gta aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat ctg caa atg aac age ctg aga ggc gag gac acg gct gta tat tac tgt ggc aga ggc cgt gga tat agt ggc caa ggg aat cgg aat agg gct tac tac ttt gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tea
196	AT12-023	Light chain	tct tct gag ctg act cag gac cct gct gta tct gta ggc ttg gga cag aca gtc agt atc aca tgc caa gga gac ttc etc aga age tat tat gca age tgg tac cag cag aag cca gga cag ggc cct gta ctt gtc atc ttt ggt aaa aac aag cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc age tca gga aac aca gct tcc ttg acc atc act ggg gct cag ggc gaa gat gag gct gac tat tac tgt aac tcc cgg gac cgc agt ggt aac cag ctg gta ttc ggc gga ggg acc aag ctg acc gtc cta

SEQ ID NO.	Antibody	Identity	Sequence
197	AT12-025	Light chain	gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt cag age att age agg tat tta aat tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat get gca tcc agt ttg caa agt ggg gtc cca tca agg ttc agt ggc agt gga tct ggg aca gat ttc act ete acc atc age agt ctg caa cct gaa gat ttt gca act tac tac tgt caa cag agt tac agt acc cct cgc act ttc ggc cct ggg acc aaa gtg gat atc aaa
198	AT13-024	Light chain	gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gcc agt cag agt att agt age tgg ttg gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat aag ggc tct agt tta gaa agt ggg gtc cca tca agg ttc age ggc act gga tct ggg aca gaa ttc act ete acc atc age age ctg cag cct gat gat ttt gca act tat tac tgc caa cag tat aat act tac cgc tac act ttt ggc cag ggg acc aag ctg gag atc aaa
199	AT12-019	Light chain	gcc atc cgg ttg acc cag tct cca tcc tca gtc tct gca tct aca gga gac aga gtc acc atc act tgt cgg ggc agt cag get ttt age agt tat tta gtc tgg tat cag cag aaa cca ggg aaa gcc cct aac ctg ctg atc tac get aca tcc act ttg caa agt ggg gtc cca tca agg ttc age ggc agt gga tct ggg aca gat ttc act ete acc atc age aac ctg cag tct gaa gat ttt gca act tat tac tgt caa cag tat tat agt tac cct cgc act ttt ggc cag ggg acc aag ttg gag atc aaa
200	AT13-022	Light chain	tcc tat gag ctg act cag cca ccc tca gtg tcc gtg tcc cca gga cag aca gcc age atc acc tgc tct gga gat aaa ttg ggg gat aaa tat get tgc tgg tat cag cag aag cca ggc cag tcc cct gtg ctg gtc atc tat caa gat age aag cgg ccc tca ggg atc cct gag cga ttc tct ggc tcc aac tct ggg aac aca gcc act ctg acc atc age ggg acc cag get atg gat gag get gac tat tac tgt cag ggc tgg gac age age act ggg gta ttc ggc gga ggc acc aag ctg acc gtc cta
201	AT13-023	Light chain	gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt cag ggc att
			aga aat gtt tta ggc tgg tat cag cag aaa cca ggg aaa gcc cct aag tgc ctg atc tat get gca tcc agt ttg caa agt ggg gtc cca tca agg ttc age ggc agt gga tct ggg aca gaa ttc act ete acc atc age age ctg cag cct gaa gat ttt gca act tat tac tgt cta cag cat aat agt cac ccc cgg aeg ttc ggc caa ggg acc aag gtg gaa atc aaa
202	AT13-031	Light chain	gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act tgc cgg gca agt cag ggc att aga aat gat tta ggc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat get gca gtc agt ttg caa agt ggg gtc cca tca agg ttc age ggc agt gga tct ggg aca gaa ttc act ete acc atc age age ctg cag cct gaa gat ttt gca act tat tac tgt cta cag cat aat agt tac cct cgc act ttt ggc cag ggg acc aag ctg gag atc aaa
203	AT12-020	Light chain	gcc atc cgg atg acc cag tct cca tcc tca ttc tct gca tct aca gga gac aga gtc acc atc act tgt cgg ggc agt cag gat att age agt tct tta gcc tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat get gca tcc act ttg caa agt gga gtc cca tca agg ttc age ggc agt gga tct ggg aca gac ttc act ete acc atc age tgc ctg cag tct gaa gat ttt gca act tat tac tgt caa cag tat tat agt tac cct cgc aeg ttc ggc caa ggg acc agg ttg gaa atc aaa
204	AT13-033	Light chain	cag tct gcc ctg act cag cct ccc tcc ggc tcc gga tct cct ggt cag tca gtc acc atc tcc tgt act ggg acc age agt gac att ggt ggt tat aac tat gtc tcc tgg tac caa cac cac cca ggc aaa gcc ccc aaa ttg atg att tat gag gtc act aag cgg ccc tca ggg gtc cct gat cgt ttc tct ggc tcc aag tct ggc aac aeg gcc tcc ctg acc gtc tct gga ctg cag get gag gat gag get cat tat tac tgc age tca tat gca ggc age aac gat ttg cta ttc ggc gga ggg acc aag ctg acc gtc ctg
205	AT13-034	Light chain	gaa gta gtg atg acc cag tct cca gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctg tcc tgc agg gcc agt cag age att age aac aac tta ggc tgg tat cag cag aaa cct ggc cag get ccc agg ctg ctg atc tac ggt gca tcc acc agg gcc act ggt atc cca ggc agg ttc agt ggc agt gga tct ggg aca gag ttc act ete acc atc tae age ctg cag tct gaa gat ttt gca act tat tac tgt caa caa tat aat aac tgg cct cgg ctg act ttc ggc gga ggg acc aag gtg gag atc aaa
206	AT13-035	Light chain	tct tct gag ctg act cag gac cct get gtg tct gtg gcc ttg gga cag aca gtc agg atc aca tgc caa gga gac age ctg aga age tat tat gca age tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc age tca gga aac aca get tcc ttg acc atc act ggg gct cag ggc gaa gat gag get gac tat tac tgt aac tcc cgg gac age agt ggt aac cat gtg gta ttc ggc gga ggg acc aag ctg acc gtc cta
207	AT13-036	Light chain	cag tct gcc ctg act cag cct gcc tcc gtg tct ggg tct cct aga cag tgc atc acc atc tcc tgc act gga acc age agt gac gtt ggt ggt tat aac tat gtc tcc tgg tac caa caa ctc cca ggc aaa gcc ccc aaa ctg att tat gat gtc aat gat cgg ccc tca ggg gtt tct att cgc ttc tct ggc tcc aag tct ggc aac aeg gcc tcc ctg acc atc tct ggg ctg cag get gag gac gag get gat tat tac tgc age tca tat aca aga age aac act gtg ata ttc ggc gga ggg acc aaa ctg acc gtc cta

SEQ ID NO.	Antibody	Identity	Sequence
208	AT13-037	Light chain	gaa ata gtg atg acg cag tet cca gcc acc ctg tet gtg tet cca ggg gaa agg gtc atc etc tcc tgc agg gcc agt cag agt gtt
			aga agc aac tta gcc tgg tac cag cag aaa cct ggc cag cct ccc agg etc etc atc tat ggt gca ttc acg agg gle act ggt gtc cca gcc agg ttc agt ggc agt ggg tet ggg aca gaa ttc act etc acc atc agc agc ctg cag tet gaa gat ttt gca gtu tat tac tgt cag cag tac aat gac cgg ccc cgg tac act ttt ggc cag ggg acc aag ctg gag atc aaa

Table 1B. Preferred anti-AML antibodies according to the invention (CDR numbering according to Kabat *et al.* 1991)

SEQ ID NO.	Antibody	Identity	Sequence
209	AT14-013	Heavy chain CDR1	SPNWWT
210	AT 14-014	Heavy chain CDR1	DAWMS
211	AT14-015	Heavy chain CDR1	DFAMS
212	AT 14-016	Heavy chain CDR1	SYAMT
213	AT 14-013	Heavy chain CDR2	EIYYGGRVSYNSALRS
214	AT 14-014	Heavy chain CDR2	HINTKVDGGTTEYAAPVKG
215	AT 14-015	Heavy chain CDR2	FIRTKANDGTTEYAASVKG
216	AT14-016	Heavy chain CDR2	SISGSGGSTYYADSVRG
217	AT14-013	Heavy chain CDR3	AGQKNIGCGYSSCFISWFD
218	AT14-014	Heavy chain CDR3	TTEAIYDSSGYFHDY
219	AT14-015	Heavy chain CDR3	ASDPFMTTDYYYYYMDV
220	AT 14-016	Heavy chain CDR3	AKGYVGCSSGNCYSGGAFDI
221	AT 14-	Light	KSSQTILQRSNHLNYLA

SEQ ID NO.	Antibody	Identity	Sequence
	013	chain CDR1	
222	AT14-014	Light chain CDR1	KSSRSVLYSSNNKNYLA
223	AT14-015	Light chain CDR1	TGTSSDVGGYNSVS
224	AT14-016	Light chain CDR1	GGNNIGSESVH
225	AT14-013	Light chain CDR2	WASTRES
226	AT14-014	Light chain CDR2	WASIRES
227	AT14-015	Light chain CDR2	EVYKRPL
228	AT 14-016	Light chain CDR2	YDTRPS
229	AT 14-013	Light chain CDR3	HQYYTTPQT
230	AT14-014	Light chain CDR3	QQYSRPPT
231	AT14-015	Light chain CDR3	SSYGGTVLF
232	AT14-016	Light chain CDR3	QVWDNTSDHPVVF
233	AT14-013	Heavy chain	QGRLQESGPGIARPSETLTITCAVSGGSSVSSPNWWTWVRQAPGKGLEWIGETIYGGRVSYNSALRSRVTI SSDRSKKEEESLKLRSVTAADTAIYYCAGQKNIGCGYSSCFISWFDTWGQGIATVSS
234	AT14-014	Heavy chain	EVQLVESGGGLVAPGGSRLRLSCAASGFTFSDAWMSWVRQAPGKGLEWVGHINTKVDGGTTEYAAPVKGR FTISRDDSKNSLYLIIMDSLKTEDTAVYYCTEAIYDSSGYFIDYWGGQSLVTVSS
235	AT14-015	Heavy chain	EVQLVESGGGLVAPGGSRLRLSCTASGFRFGDFAMSWVRQAPGKGLEWVGFIKTRANDGTTEYAASVKGRF HSRDDSKSLAYLQMNSLKTEDTAVYYCASDPFMTTDYIIYMDVWGKGTITVTVSS
236	AT14-016	Heavy chain	EVQVLESGGDSVQPGGSRLRLSCAASGFTFSSYAMTWVRQAPGKGLKVVSSISGSGGSTYYADSVRGRFTISR DNSKNTLYVQMNSLRAEDTAVYYCAKGYVGCSCGNCYSGGAFDIWGGQGTIVTVSS
237	AT14-013	Light chain	DIVMTQSPDLSAVSLGERATIACKSSQTILQRSNHLNYLAWYQQKPGQPPKVLIIWASTRESGVPDRFSGSG SGTDFTLTINSLSQAEDVAVYYCHQYYTTPQTFGQGTKVEIK

SEQ ID NO.	Antibody	Identity	Sequence
238	AT14-014	Light chain	DIVMTQSPDSLAVSLGERATINCKSSRSVLYSSNNKNYLAWYQQKPGQPPKLLIYWASIRESGVPDRFSGSGSGTDFTLTINSLQAEDVAVYYCQQYSRPTFGQGTKVEIK
239	AT14-015	Light chain	QSALTQPPSASGSPGQSVTISCTGTSSDVGGYNSVSWYQHHPGKAPKLMIEVYKRPLGVDPDRFSGSKSGNTASLTIVSGLQAEDVAVYYCQSSYGGTVLFGGGTKLTVL
240	AT 14-016	Light chain	SYVLTQPPSVSVAPGKTARITCGGNNIGSESVHWYQQKPGQAPVVVITYDTRPSGIPERFSGSNSGNTATLTISRVEAGDEADYYCQVWDNTSDHPVVFVGGGTKLTVL
241	AT14-013	Heavy chain CDR1	agt cct aac tgg tgg act
242	AT14-014	Heavy chain CDR1	gac gcc tgg atg agc
243	AT14-015	Heavy chain CDR1	gat ttt gct atg agt
244	AT14-016	Heavy chain CDR1	agc tat gcc atg acc
245	AT14-013	Heavy chain CDR2	gaa atc tat tat ggt ggg aga gtg agc tac aac tcg gcc ctc agg agt
246	AT14-014	Heavy chain CDR2	cat att aac acc aaa gtt gat ggt ggg aca aca gag tac gct gca ccc gtg aaa ggc
247	AT14-015	Heavy chain CDR2	ttc att aga acc aaa gct aat gat ggg aca aca gaa tac gcc gcg tct gtg aaa ggc
248	AT14-016	Heavy chain CDR2	agt att agt ggt agt ggt ggt agc aca tac tac gca gac tcc gtg agg ggc
249	AT14-013	Heavy chain CDR3	gcg ggt caa aaa aat att ggc tgt ggt tac agc agt tgc ttt atc agt tgg ttc gac acc
250	AT14-014	Heavy chain CDR3	acc aca gag gcg ata tat gat agt agt ggt tat ttc cat gac tat
251	AT14-015	Heavy chain CDR3	gct agc gat ccc ttc atg act aca gac tat tac tac tac tac atg gac gtc
252	AT14-016	Heavy chain CDR3	gcg aaa gga tat gtg ggg tgt agt ggt ggg aac tgc tac tcg ggg ggt gct ttt gat atc
253	AT14-013	Light chain CDR1	aag tcc agc cag act att tta caa agg tcc aac cat ttg aac tac tta gct

SEQ ID NO.	Antibody	Identity	Sequence
254	AT14-014	Light chain CDR1	aag tcc agc cgg agt gtt tta tac agc tcc aac aat aag aac tac tta gct
255	AT14-015	Light chain CDR1	act ggg acc agc agt gac gtt ggt ggt tat aac tct gtc tcc
256	AT14-016	Light chain CDR1	ggg ggg aac aac att gga agt gaa agt gtt cac
257	AT14-013	Light chain CDR2	tgg gca tct acc cgg gaa tcc
258	AT14-014	Light chain CDR2	tgg gca tct atc cgg gaa tcc
259	AT14-015	Light chain CDR2	gag gtc tat aag cgg ccc tta
260	AT14-016	Light chain CDR2	tat gat acc gac cgg ccc tca
261	AT14-013	Light chain CDR3	cac caa tat tat act act ccg cag act
262	AT14-014	Light chain CDR3	cag caa tat tct cgt cct ccg acg
263	AT14-015	Light chain CDR3	age tca tat gga ggc acc gtg cta ttc
264	AT14-016	Light chain CDR3	cag gtg tgg gat aac act agt gat cat cct gtg gta ttc
265	AT14-013	Heavy chain	cag ggg cga ctg cag gag tgg ggc cca gga ctg gtg aag cct tgg gag acc ctg acc ctc aag tgc gct gtg tcc ggt ggc tcc tcc gtc age agt cct aac tgg tgg act tgg gtc cgc cag gcc ccc ggg aag ggg ctg gag tgg att gga gaa atc tat tat ggt ggg aga gtg age tac aac tgg gcc ctc agg agt cga gtc acc att tea tea gac agg tcc aaa gag gag ttc tcc ctg aaa ctg agg tet gtg acc gcc ggg gac aeg gcc ata tat tat tgt ggg ggt caa aaa aat att ggc tgt ggt tac age agt tgc ttt ate agt tgg ttc gac acc tgg gga cag gga att ggg gtc acc gtc tcc tea
266	AT14-014	Heavy chain	gag gfg cag ctg gfg gag tct ggg gga ggt ttg gta aag cct ggg ggg tcc ctt aga ctc tcc tgt gca gcc tct gga ttc act ttc agt gac gcc tgg atg age tgg gtc cgc cag get cca ggg aag ggg ctg gag tgg gtt ggc cat att aac acc aaa gtt gat ggt ggg aca aca gag tac get gca ccc gtg aaa ggc aga ttc acc atc tea aga gat gat tea aaa aat tgg ctg tat ctg cac atg gac age ctg aaa acc gag gac aca gcc gfg tat tac tgt acc aca gag gog ala tat gat agt agt ggt tat ttc cat gac tat tgg ggc cag gga tcc ctg gtc acc gtc tcc tea
267	AT14-015	Heavy chain	gag gfg cag ctg gfg gag tgg ggg gga ggc ttg gca cag cca ggg cgg tcc ctg aga ctc tcc tgt aca get tet gga ttc agg ttt ggt gat ttt get atg agt tgg gtc cgc cag get cca ggg aag gga ctg gag tgg gta ggt ttc att aga acc aaa get aat gat ggg aca aca gaa tac gcc gog tct gtg aaa ggc aga ttc atc atc tea aga gat gat tcc aaa agt atc gcc tai ctg caa atg aac age ctg aaa acc gag gac aca gcc gtt tat tac tgt get age gat ccc ttc atg act aca gac tat tac tac tac tac atg gac gtc tgg ggc aaa ggg acc aeg gtc acc gtc tcc tea
268	AT14-016	Heavy chain	gag gfg caa gfg ttg gag tet ggg gga gac tgg gta cag cct ggg ggg tcc ctg aga ctc tcc tgt gca gcc tet gga ttc acc ttt age age tat gcc atg acc tgg gtc cgc cag get cca ggg aag ggg ctg aaa tgg gtc tea agt att agt ggt agt ggt ggt age aca taa taa gaa gaa taa atg cag gga acc tta gaa ctc taa gaa gaa aat taa gaa gaa gaa atg tat ctg ggt atg gaa gaa atg gaa

[illegible]

Tabel 2

mAb are specific for AML															
mAbs					Cell lines									Prim cells	
Name	Ig class	Mel ¹	Mel ²	Mel ³	BJ	FB	Col ¹	Col ²	Col ³	Vero	HUVEC	HepG2		PBMC	BM
AT12-019	IgG1 κ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT13-023	IgG1 κ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT13-031	IgG1 κ					-				-	-	-		-	-
AT12-020	IgG3 κ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT12-023	IgG3 λ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT12-025	IgG3 κ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT13-022	IgG3 λ	-	-	-	-	-	-	-	-	-	-	-		-	-
AT13-024	IgG3 κ	-	-	-	-	-	-	-	-	-	-	-		-	-

Mel¹: Mel 126.2; Mel²: Mel BLM; Mel³: Mel WBO; BJ: Fibroblast cell line; FB: primary fibroblasts (skin); Col¹: Colo205; Col²: Caco-2; Col³: HT29; Vero: non-human kidney; PBMC: peripheral blood mononuclear cells; BM: bone marrow.

Tabel 3

Overview AML-specific mAbs derived from a patient with a potent GvL response (donor 59)															
mAbs					AML				Primary AML*						
Name	Ig class		CD27	SHM V _H /V _L		THP-1		MM6		M0	M1	M1		M1	M4
AT12-019	IgG1 κ		+	10/9		++		+		+	+	++		+/-	-
AT13-023	IgG1 κ		+	8/4		++				++	+				
AT13-031	IgG1 κ		+	1/1		++		+		-	+	-		-	+/-
AT12-020	IgG3 κ		+	4/2		++									
AT12-023	IgG3 λ		-	Germline/6		+++		++		+	++	++		+/-	++
AT12-025	IgG3 κ		-	1/1		++		++		-	+/-	+		-	-
AT13-022	IgG3 λ		+	Germline		++				++	++				
AT13-024	IgG3 κ		-	6/3		++		++		++	++	++			
MM6: MonoMac6; M0: donor 77; M1 donor 69, 79, 86 respectively; M4 donor 78															
* AML according to the FAB classification; SHM: number of somatic hypermutations															

Tabel 4

Some mAb bind other hematologic tumors							
mAbs		Other hematologic tumor cell lines				Primary tumors	
Name	Ig class	OCI-Ly1	OCI-Ly7	U266	NCI-H929	NHL pt	ALL pt
AT12-019	IgG1 κ	+	-	-	-	-	-
AT13-023	IgG1 κ						
AT13-031	IgG1 κ	++	+	-	+/-	++	-
AT12-020	IgG3 κ						
AT12-023	IgG3 λ	-	-	+/-	-	++	-
AT12-025	IgG3 κ	-	-	+	-	-	-
AT13-022	IgG3 λ						
AT13-024	IgG3 κ	++	+	-	-	-	-

OCI-Ly1 and OCI-Ly7: diffuse large B cell lymphoma cell lines; U266 and NCI-H929: multiple myeloma cell lines; NHL pt: B-non Hodgkin lymphoma cells freshly isolated from a newly diagnosed patient ; ALL pt: B-acute lymphatic leukemia cells freshly isolated from a newly diagnosed patient.

Tabel 5

Some mAb show <i>in vitro</i> activity					
mAbs				Killing	
Name	Ig class	CD27	SHM V _H /V _L	THP-1	M0/5
AT12-019	IgG1 κ	+	10/9	no	no
AT13-023	IgG1 κ	+	8/4		
AT13-031	IgG1 κ	+	1/1		
AT12-020	IgG3 κ	+	4/2		
AT12-023	IgG3 λ	-	Germline/6	yes	
AT12-025	IgG3 κ	-	1/1	yes	yes
AT13-022	IgG3 λ	+	Germline		
AT13-024	IgG3 κ	-	6/3	no	yes

Some mAb show <i>in vitro</i> activity					
mAbs				Killing	
Name	Ig class	CD27	SHM V _H /V _L	THP-1	M0/5
AT13-023, AT13-031, AT12-020 and AT13-022 were not yet tested for <i>in vitro</i> activity					

Tabel 6

2nd AML patient with GvL response (donor 58)									
mAbs				AML		Not binding to			
Clone	CD27	Ig class	SHM V _H /V _L	THP-1	MM6	PBMC	Caco	HT-29	HepG2
AT13-033	+	IgG3 λ	18/5	++	++	-	-	-	-
AT13-034	+	IgG3 κ	14/6	++	++	-	-	-	-
AT13-035	-	IgG3 λ	0/0	++	++	-	-	-	-
AT13-036	-	IgG3 λ	4/9	++	++	-	-	-	-
AT13-037	+	IgG3 κ	4/8	++	++	-	-	-	-
SHM: number of somatic hypermutations									

Table 7

Overview of AML-specific mAbs derived from a 3 rd patient with a potent GvL response (donor 101)									
mAbs				AML		Primary AML*			
Name	Ig class	CD27	SHM V _H /V _L	THP-1	Molm13	M0	M4	M5 ¹	M5 ²
AT14-013	IgG1 κ	+	26/11	+++	+++	+++	++	+/-	+
AT14-014	IgG3 κ	+	9/6	++	++	-	-	-	-
AT14-015	IgG3 λ	+	9/9	++	-	-	+	-	-
AT14-016	IgG3 λ	+	9/5	++	++	-	+	-	-
M1: donor 77; M4: donor BL-046; M5 ¹ : donor BL-034, M5 ² : donor BL-038 * AML according to the FAB classification; SHM: number of somatic hypermutations									

Table 8

mAb are specific for AML (donor 101)										
mAbs		Cell lines				PBMCs				Primary cells
Name	Ig class	FB	Col	Liv ¹	Liv ²	CD3	CD14	CD19	CD56	Fetal liver cells
AT14-013	IgG1 κ	+/-	-	+/-	-	-	-	-	-	-
AT14-014	IgG3 κ	-	-	-	-	-	-	-	-	-
AT14-015	IgG3 λ	-	-	-	-	-	-	-	-	-
AT14-016	IgG3 λ	-	-	-	-	-	-	-	-	-
FB: primary fibroblasts (skin); Col: Caco-2; Liv ¹ : Huh7 liver cell line; Liv ² : HepG2 liver cell line PBMC: peripheral blood mononuclear cells;										

Tabel 9A

Overview of AML-specific mAbs derived from a 2 nd patient with a potent GvL response (donor 58)									
mAbs				AML		Primary AML*			
Clone	CD27	Ig class	SHM V _H /V _L	THP-1	MM6	M0	M0	M1	M4
AT13-033	+	IgG3 λ	18/5	++	++	-	-	-	-
AT13-034	+	IgG3 κ	14/6	++	++	+/-	-	-	-

Overview of AML-specific mAbs derived from a 2 nd patient with a potent GvL response (donor 58)									
mAbs				AML		Primary AML*			
Clone	CD27	Ig class	SHM V _H /V _L	THP-1	MM6	M0	M0	M1	M4
AT13-035	-	IgG3 λ	0/0	++	++	-	-	-	-
AT13-036	-	IgG3 λ	4/9	++	++	-	-	-	-
AT13-037	+	IgG3 κ	4/8	++	++	-	-	-	-
MM6: MonoMac6; M0: donor 77, BL-030; M1 donor 69, respectively; M4 donor 78									
* AML according to the FAB classification; SHM: number of somatic hypermutations									

Tabel 9B

Some mAb show <i>in vitro</i> activity (donor 59)					
mAbs				Killing	
Name	Ig class	CD27	SHM V _H /V _L	THP-1	M1
AT12-019	IgG1 κ	+	10/9	no	no
AT13-023	IgG1 κ	+	8/4	no	nd
AT13-031	IgG1 κ	+	1/1	yes*	nd
AT12-020	IgG3 κ	+	4/2	nd	nd
AT12-023	IgG3 λ	-	Germline/6	yes	nd
AT12-025	IgG3 κ	-	1/1	yes	yes
AT13-022	IgG3 λ	+	Germline	no	nd
AT13-024	IgG3 κ	-	6/3	no	yes
*Only at 37 C; nd = not determined					

Tabel 10

Some mAb show <i>in vitro</i> activity (donor 58)				
mAbs				Killing
Clone	CD27	Ig class	SHM V _H /V _L	THP-1
AT13-033	+	IgG3 λ	18/5	yes
AT13-034	+	IgG3 κ	14/6	no
AT13-035	-	IgG3 λ	0/0	yes
AT13-036	-	IgG3 λ	4/9	yes
AT13-037	+	IgG3 κ	4/8	yes

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PATENTKRAV

1. Isoleret, syntetisk eller rekombinant humant antistof, eller en funktionel del deraf, der er i stand til at binde snRNP200 fra akut myeloid leukæmi- (AML) celler, og der er i stand til at reducere proliferation af AML-celler ved onkose.
- 5 2. Isoleret, syntetisk eller rekombinant antistof, eller en funktionel del deraf, der er i stand til at binde til snRNP200 af AML-celler og reducere proliferation af AML-celler, som omfatter:
 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 1, 14, 27, 40, 53 og 66, eller sekvenser, der udviser mindst 90 % identitet dermed;
 - 10 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 2, 15, 28, 41, 54 og 67, eller sekvenser, der udviser mindst 90 % identitet dermed;
 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 7, 20, 33, 46, 59 og 15 72, eller sekvenser, der udviser mindst 90 % identitet dermed;
 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 9, 22, 35, 48, 61 og 74, eller sekvenser, der udviser mindst 90 % identitet dermed;
 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 11, 24, 37, 50, 63 og 20 76, eller sekvenser, der udviser mindst 90 % identitet dermed; or
 - en CDR1-, CDR2- og CDR3-sekvens af en tungkæde og en CDR1-, CDR2- og CDR3-sekvens af en letkæde som defineret ved henholdsvis SEQ ID NO: 13, 26, 39, 52, 65 og 78, eller sekvenser, der udviser mindst 90 % identitet dermed.
- 25 3. Antistof eller funktionel del deraf ifølge krav 2, der omfatter en variabel tungkædesekvens med mindst 90 % sekvensidentitet med en sekvens udvalgt fra gruppen bestående af SEQ ID NO: 79, 80, 85, 87, 89 og 91, og/eller der omfatter en variabel letkædesekvens med mindst 90 % sekvensidentitet med en sekvens udvalgt fra gruppen bestående af SEQ ID NO: 92, 93, 98, 100, 102 og 104.
- 30 4. Antistof eller funktionel del deraf ifølge et hvilket som helst af krav 1-3, der er koblet til en anden forbindelse, fortrinsvis hvor den anden forbindelse er en detekterbar markør, et kemoterapeutisk lægemiddel, en toksisk del, et immunmodulatorisk molekyle, en anden AML-specifik bindende forbindelse eller en radioaktiv forbindelse.
5. Isoleret, syntetisk eller rekombinant nukleinsyremolekyle, der koder for mindst den

variable tungkædesekvens og/eller den variable letkædesekvens af et antistof eller en funktionel del deraf ifølge et hvilket som helst af krav 1-3, fortrinsvis hvor nukleinsyremolekylet omfatter en sekvens, der har mindst 80 % sekvensidentitet med en sekvens udvalgt fra gruppen bestående af SEQ ID NO: 183, 184, 189, 191, 193 og 195, og/eller en sekvens, der har mindst 80 % sekvensidentitet med en sekvens udvalgt fra gruppen bestående af SEQ ID NO: 196, 197, 202, 204, 206 og 208.

6. Vektor, der omfatter et nukleinsyremolekyle ifølge krav 5.

7. Isoleret eller rekombinant celle, eller et ikke-humant dyr, der omfatter et nukleinsyremolekyle ifølge krav 5 eller en vektor ifølge krav 6.

8. Sammensætning, der omfatter antistof eller funktionel del deraf ifølge et hvilket som helst af krav 1-4, eller et nukleinsyremolekyle ifølge krav 5, eller en vektor ifølge krav 6, eller en celle ifølge krav 7, fortrinsvis hvor sammensætningen er en farmaceutisk sammensætning, der omfatter en farmaceutisk acceptabel bærer, fortynder eller excipients, mere fortrinsvis hvor den farmaceutiske sammensætning omfatter mindst to antistoffer eller funktionelle dele deraf ifølge et hvilket som helst af krav 1-4.

9. Antistof eller funktionel del ifølge et hvilket som helst af krav 1-4, eller et nukleinsyremolekyle ifølge krav 5, eller en vektor ifølge krav 6, eller en celle ifølge krav 7, til anvendelse som et lægemiddel eller profylaktisk middel.

10. Antistof eller funktionel del ifølge et hvilket som helst af krav 1-4, eller et nukleinsyremolekyle ifølge krav 5, eller en vektor ifølge krav 6, eller en celle ifølge krav 7, til anvendelse i en fremgangsmåde til mindst delvis behandling eller forebyggelse af myeloid leukæmi (AML) eller B-ikke-Hodgkins lymfom (B-HNL) eller til anvendelse i diagnosticering af AML eller B-HNL.

11. Anvendelse af et antistof eller en funktionel del ifølge et hvilket som helst af krav 1-4, eller et nukleinsyremolekyle ifølge krav 5, eller en vektor ifølge krav 6, eller en celle ifølge krav 7, til bestemmelse af, om en prøve omfatter AML-celler eller B- ikke-Hodgkin lymfomceller.

12. Fremgangsmåde til fremstilling af et antistof eller en funktionel del ifølge et hvilket som helst af krav 1-3, hvilken fremgangsmåde omfatter tilvejebringelse af en celle med et nukleinsyremolekyle eller en vektor ifølge krav 5 eller 6, og at lade cellen omdanne nukleinsyremolekylet eller vektoren, hvorved der fremstilles antistoffet eller den funktionelle del ifølge et hvilket som helst af krav 1-3, hvor fremgangsmåden fortrinsvis endvidere omfatter høstning, oprensning og/eller isolering af antistoffet eller den funktionelle del.

13. Fremgangsmåde til bestemmelse af, om en myeloid celle eller lymfoid celle er en myeloid leukæmi- (AML) eller B-ikke-Hodgkins lymfom- (B-HNL) celle, hvilken fremgangsmåde

omfatter bestemmelse af, om snRNP200 er til stede på cellens overflade, hvor tilstedeværelse af snRNP200 på cellens overflade indikerer, at cellen er en AML- eller B-HNL-celle.

14. Fremgangsmåde til bestemmelse af, om AML- eller B-HNL-celler er til stede i en prøve, der omfatter:

- 5 - etablering af kontakt mellem prøven og et antistof eller en funktionel del ifølge et hvilket som helst af krav 1-4, og
- at lade antistoffet eller den funktionelle del binde myeloproliferative celler eller lymfoproliferative celler, hvis de er til stede, og
- bestemmelse af, om AML- eller B-HNL-celler er bundet til antistoffet eller den
- 10 funktionelle del eller ej for derved at bestemme, om AML- eller B-HNL-celler er til stede i prøven eller ej.

15. Fremgangsmåde til bestemmelse af, om et individ lider af en myeloproliferativ eller lymfoproliferativ forstyrrelse, hvor den myeloproliferative forstyrrelse er AML, og hvor den lymfoproliferative forstyrrelse er B-ikke-Hodgkins lymfom, og omfatter bestemmelse af, om en

15 prøve fra individet omfatter antistoffer, der er specifikke for snRNP200, fortrinsvis hvor fremgangsmåden omfatter:

- etablering af kontakt mellem en prøve fra individet og snRNP200 eller en epitop deraf;
- at lade snRNP200 eller epitopen binde snRNP200-specifikke antistoffer fra
- 20 prøven, hvis de er til stede, og
- bestemmelse af, om snRNP200 eller epitopen er bundet til snRNP200-specifikke antistoffer eller ej, hvor binding af snRNP200 eller epitopen til snRNP200-specifikke antistoffer indikerer, at individet lider af den myeloproliferative eller lymfoproliferative forstyrrelse.

16. Fremgangsmåde til bestemmelse af, om en patient, der lider af en myeloproliferativ eller

25 lymfoproliferativ forstyrrelse, har en bedre chance for et positivt behandlingsresultat med et snRNP200-specifikt antistof eller en funktionel del, sammenlignet med middelpopulationen af patienter, der lider af en myeloproliferativ eller lymfoproliferativ forstyrrelse, hvilken fremgangsmåde omfatter bestemmelse af, om snRNP200 er til stede på overfladen af patientens myeloproliferative celler eller lymfoproliferative celler, hvilken fremgangsmåde omfatter:

- 30 - etablering af kontakt mellem en myeloproliferativ celle- eller lymfoproliferativ celleholdig prøve fra individet og et antistof eller en funktionel del, der er specifik for snRNP200;
- at lade antistoffet eller den funktionelle del binde prøvens myeloproliferative celler eller lymfoproliferative celler, og
- bestemmelse af, om det snRNP200-specifikke antistof eller den funktionelle del

er bundet til prøvens myeloproliferative celler eller lymfoproliferative celler eller ej, hvor binding af det snRNP200-specifikke antistof eller den funktionelle del til prøvens myeloproliferative celler eller lymfoproliferative celler indikerer, at patienten har en bedre chance for et positivt behandlingsresultat med et snRNP200-specifikt antistof eller en funktionel del, sammenlignet med middelpopulationen af patienter, der lider af en myeloproliferativ eller lymfoproliferativ forstyrrelse, hvor den myeloproliferative forstyrrelse is AML, og hvor de myeloproliferative celler er AML-celler, eller hvor den lymfoproliferative forstyrrelse er B-ikke-Hodgkins lymfom, og hvor de lymfoproliferative celler er B-ikke-Hodgkin-lymfomceller.

- 5 17. Anvendelse af et antistof eller en funktionel del ifølge et hvilket som helst af krav 1-4 til
10 bestemmelse af, om en AM- patient har et graft-versus-leukæmirespons.

DRAWINGS

FIG. 1

AIMM Therapeutics AML antibody panel

NR: CDR numbering according to Kabat et al (1991)

AT12-023 (11C9-22C11)

Heavy chain

Recombined from gene segments:

IGHV4-34*01 F

IGHD2-2*01 F

IGHJ6*03 F

AMINO ACID:

Fw1 QVQLQQWGAGLLKPSSETLSLTCAYVGGSF

CDR1 GYYWS

Fw2 WIRQPPGKGLIEWIG

CDR2 EINHSGSTNYNPSLKS

Fw3 RVTISVDTSKNQFSLKISSVTAADTAVYYCAR

CDR3 GRSTSPLDYNYMDV

Fw4 WAKGTTIVSS

NUCLEOTIDE:

Fw1 cag gtc cag cta cag cag tgg ggc gca gga ctg ttg aag cct tgc gag acc ctg tcc ctc acc tgc
gct gtc tat ggt ggg tcc ttc agt

CDR1 ggt tac tac tgg agc

Fw2 tgg atc ggc cag ccc cca ggg aag ggg ctg gag tgg att ggg

CDR2 gaa atc aat cat agt gga agc acc aac tac aac cgc tcc ctc aag agt

Fw3 cga gtc acc ata tca gta gac agc tcc aag aac cag ttc tcc ctg aag ctg agc tat gtg acc gac
ggg gac agc gct gtg tat tac tgt cgc agc

CDR3 ggc cgt agt acc agc cgc ctc gac tac tac tac tac tac atg gac gtc

Fw4 tgg gcc aaa ggg acc acg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGLV3-13*01 F

IGLJ3*02 F

AMINO ACID:

Fw1 SSELTDPAVSVALGQTVRITC

CDR1 QGDFLRSYYAS

Fw2 WYQQKPGQAPVLVIF

CDR2 GKNKRPS

Fw3 GIPDRFSGSSSGNTASLTITGAQAEDEADYYC

CDR3 NSRDRSGNHLV

Fw4 FGGGTKITVI

NUCLEOTIDE:

Fw1 tct tct gag ctg act gag gac cct gct gtg tct ctg gcc ttg gga gag aca gtc agg atc aca tgc

CDR1 caa gca gac ttc ctc aga agc tat tat gca agc

Fw2 tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc ttt

CDR2 ggt aaa aac aag ggg ccc tca

Fw3 ggg atc cca gac cga ttc tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg gct
cag ggc gaa gat gag gct gac tat tac tct

CDR3 aac tcc ggg gac ggc agt ggt aac cag ctg gtg

Fw4 ttc gcc gga ggg acc aag ctg acc gtc cta

AT12-025 (14D3-12D5)**Heavy chain**

Recombined from gene segments:

IGHV4-34*01 F

IGHD1 1*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLQQWGAGLLKFSETLSLTCAVYGGSF5

CDR1 GYYWS

Fw2 WIRQPPGKGLEWIG

CDR2 EINHSGSTNYNPSLK5

Fw3 FVTISVDTSKNQFSLKLSSVTAADTAVYYCAR

CDR3 GSMARPKPFDY

Fw4 WGQGLTVTVSS

NUCLEOTIDE:

Fw1 cag gtg cag cta cag cag tgg ggc gca gga ctg ttg aag cct tgg cag acc ctg tcc ctc acc tgc
ggt gtc tat ggt ggg tcc ttc agt

CDR1 ggt tat taa tgg agc

Fw2 tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg

CDR2 gaa atc aat cat agt gca agc acc aac tac aac cgg tcc ctc aag agt

Fw3 cga gtc acc ata tca gta gac acg tgg aag aac cag ttc tcc ctg aag ctg agc tct ctg acc gcc
ggg gac acc gct gtc tat tac tgt cgg aga

CDR3 ggc tca atg gca aga ccc aag cca ttt gac taa

Fw4 tgg ggc cag gga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-33*01 F

IGKJ3*01 F

AMINO ACID:

Fw1 DIQMTQSFSSLSASVGDRTITC

CDR1 RASQISRYLN

Fw2 WYQQKPGKAPKLLIY

CDR2 AASSLQS

Fw3 GVPSRFGSGSGTLEFTLTISSLQFEDFATYYC

CDR3 QQSYSTPRT

Fw4 FPGGTKVDIK

NUCLEOTIDE:

Fw1 gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act
tga

CDR1 cgg gca agt cag agc att agc agg tat tta aat

Fw2 tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat

CDR2 gct gca tcc agt ttg caa agt

Fw3 ggg gtc cca tca agg ttc agt ggc agt gga tct cgg aca gat ttc act ctc acc atc agc agt ctg
caa cct gaa gat ttt gca act tac tac tct

CDR3 caa cag agt tac agt acc cct cgc act

Fw4 ttc ggc cct ggg acc aaa gtg cat atc aaa

AT13-024 (15H3-10F7)**Heavy chain**

Recombined from gene segments:

IGHV3-30*02 F

IGHD3 22*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLVESGGGVVQFGRSLRLSCAASGFTFS

CDR1 SYGMH

Fw2 WVRQAPGKGLEWVA

CDR2 FIRYDGSNKYFACSVRG

Fw3 RFTISRDN SKNTLFLQMNSLR AEDTAVYYCAK

CDR3 DPQERIYYSDTSGYLDY

Fw4 WGQGLVTVSS

NUCLEOTIDE:

Fw1 cag gtg cag ctg gtg gag tct ggg gga ggc gtg ctg cag cct .ggg agg tcc ctg aga ctg tcc tgt
gga ggc tct gga ttg acc ttc agt

CDR1 aga tat ggc atg cac

Fw2 tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca

CDR2 ttt ata cgg tat gat gca agt aat aaa tac ttt gca gac tcc gtg agg ggg

Fw3 cga ttc acc atg tcc aga gac aat tgg aag aac acg ctg ttt ctg caa atg aac agc ctg aga gct
gag gac acc gct ctg tat tac tgt

CDR3 cgg aaa gat cgc cga gag cgt att tat tac tct gat act agt ggt tac ctt gag tac

Fw4 tgg ggc cag gga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-5*03 F

IGKJ2*01 F

AMINO ACID:

Fw1 DIQMTQSFSTLSASVGDRTITC

CDR1 RASQSISSWLA

Fw2 WYQQKPGKAPKLLIY

CDR2 KASSLES

Fw3 GVPSRFSGTGSGTEFTLTISSLQFDDFATYYC

CDR3 QQYNTYPT

Fw4 FGQGTKLEIK

NUCLEOTIDE:

Fw1 gac atc cag atg acc cag tct cct tcc acc ctg tct gca tct gta gga gac aga gtc acc atc act
tga

CDR1 cgg gcc agt cag agt att agt agc tgg ttg gcc

Fw2 tgg tat cag cag aaa cca ggg aaa gcc cct aag ctg ctg atc tat

CDR2 aag gcg tct agt tta gaa agt

Fw3 ggg gtc cca tca agg ttc agc ggc act gga tct cgg aca gaa ttc act ctg acc atc agc agc ctg
cag cct gat gat ttt gca act tat tac tgc

CDR3 caa cag tat aat act tac cgc tac act

Fw4 ttt gcc cag ggg acc aag ctg cag atc aaa

AT12-019 (1B3-15E2)**Heavy chain**

Recombined from gene segments:

IGHV3-23*01 F

IGHD3 10*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 EVHLLSEGGGLVQFGGSLRLSCAASGFTFS

CDR1 SYAMS

Fw2 WVRQAPGKGLEWVS

CDR2 TIRASGGSTSYACSVKG

Fw3 RFTISRDNSSQSRLLYLQMNSLTAEDTAVYYCAK

CDR3 SPAMIRGVRRGGDYFDY

Fw4 WGQGLVTVSS

NUCLEOTIDE:

Fw1 qag gtg caa ctg ttg gag tct ggg gga ggc ttg cta caa cct .ggg ggg tcc ctg aga ctc tcc tgt
gaa gcc tct gga ttg acc ttt agc

CDR1 aga tat gcc atg agt

Fw2 tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca

CDR2 act att agg gct aqt gct ggt agc aca aac tac gca gac tcc gtg aag ggg

Fw3 cgg ttc acc atc tcc aga gac aat tcc cag agc agg ttg tat ctg caa atg aac agt ctg aca gcc
cag gac acc gcc cta tat tac tgt cgg aaa

CDR3 tct cct gct atg att cgg gga gtt agg ggg ggt gac tac ttt gac tac

Fw4 tgg ggc cag gga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-8*01 F

IGKJ2*01 F

AMINO ACID:

Fw1 AIRLTQSPSSVSASTGDRVITTC

CDR1 RASQAFSSYL

Fw2 WYQQKPGKAPNLLIY

CDR2 ATSTLQG

Fw3 GVPSRFSGSGSGTFTLTISNLSQSEDFATYYC

CDR3 QQYYSPPT

Fw4 FGQGTKLEIK

NUCLEOTIDE:

Fw1 gcc atc cgg ttg acc cag tct cca tcc tca gtc tct gca tct aca gga gac aga gtc acc atc act
tgt

CDR1 cgg ggg agt cag gct ttt agc agt tat tta gtc

Fw2 tgg tat cag caa aaa cca ggg aaa gcc cct aac ctg ctg atc tac

CDR2 gct aca tcc act ttg caa ggt

Fw3 ggg gtc cca tca agg ttc agc ggc act gga tct cgg aca gat ttc act ctg acc atc agc aac ctg
cag tct gaa gat ttt gca act tat tac tgt

CDR3 caa cag tat tat agt tac cct cgg act

Fw4 ttt ggc cag ggg acc aag ttg cag atc aaa

AT13-022 (8H11-6P4)**Heavy chain**

Recombined from gene segments:

IGHV3-30*03 F
IGHD2-15*01 F
IGHJ6*02 F

AMINO ACID:

Fw1 QVQLVESGGGVVQFGRSLRLSCAASGFTFS
CDR1 SYGMH
Fw2 WVRQAPGKGLEWVAV
CDR2 ISYDGSNKYYADSVKG
Fw3 RFTISRDN SKNTLYLQMNSLRAEDTAVYYCAK
CDR3 DGKGIVVIYIYYGMDV
Fw4 WGQGTIVIVSS

NUCLEOTIDE:

Fw1 cag gtc cag ctg gtg gag tct cgg gca gcc gtg ctg cac cct cgg agg tcc ctg aga ctg tcc tgt
gca gcc tct gga ttc acc ttc agt

CDR1 agc tat gcc atg cac

Fw2 tgg gtc cgc cag gct cca gcc aag cgg ctg gag tgg gtg gca gtt

CDR2 ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg aag gcc

Fw3 cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg caa atg aac ago ctg aga gct
gag gac aag gct gtg tat tac tgt cag aaa

CDR3 gat cgg aag cgg att gta gtt att tac tac tac tac ggt atg gac gtc

Fw4 tgg gcc aaa cgg acc acg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGLV3-1*01 F
IGLJ2*01 F

AMINO ACID:

Fw1 SYELTOPFSVSVSFGQTASITC
CDR1 SGDGLGKRYAC
Fw2 WYQQKPGQSPVLVIY
CDR2 QDSKRPS
Fw3 GIPERFSGSNSGNTATLTISGTQAMDEADYYC
CDR3 QAWDSSTVVF
Fw4 GGSTKLTVL

NUCLEOTIDE:

Fw1 tcc tat gag ctg act cag cca ccc tca gtg tcc ctg tcc cca gga cag aca gcc agc atc acc tgc

CDR1 tct gca gat aaa ttg cgg gat aaa tat gct tgc

Fw2 tgg tat cag cag aag cca gcc cag tcc cct gtg ctg gtc atc tat

CDR2 caa gat agc aag cgg ccc tca

Fw3 gcc atc cct gag cga ttc tct gcc tcc aac tct cgg aac aca gcc act ctg acc atc agc gcc acc
cag gct atg gat gag gct gac tat tac tgt

CDR3 cag gcg tgg gac agc agc act gly gta ttc

Fw4 gcc gga cgg acc aag ctg acc ctg cta

AT13-023 (19G7-8L15)**Heavy chain**

Recombined from gene segments:

IGHV4-34*12 F

IGHD2 2*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLQQWGAGLLKFSETLSLTCAVYGGSF5

CDR1 GYFWT

Fw2 WIRQPPGKGLEWIG

CDR2 EIVHSGGTNYNPSLK5

Fw3 FVTISVDTSKNQFSLRLNSVTAADTAVYYCVR

CDR3 GLNSPFDY

Fw4 WGQGLVTVSS

NUCLEOTIDE:

Fw1 cag gta cag cta cag cag tgg ggc gca gga ctg ttg aag cct tgg cag acc ctg tcc ctg acc tgc
ggt gtc tat ggt ggg tcc ttc agt

CDR1 ggt tac ttc tgg acc

Fw2 tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att ggg

CDR2 gaa acc gtt sat agt gca ggc acc aac tac aac cgg tcc ctg aag agt

Fw3 cga gtc acc ata tca gtc gac acg tgg aag aac cag ttc tcc ctg agg ctg aac tct ctg acc gcc
ggg gac acc gct ctg tat tac tgt ctg aga

CDR3 ggc ctt aac agc ccc ttt gac tac

Fw4 tgg ggc cag gga acc cta gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-17*01 F

IGKJ1*01 F

AMINO ACID:

Fw1 DIQMTQSFSSLSASVGDRTITC

CDR1 RASQGIKRVLG

Fw2 WYQQKPGKAPKCLIIY

CDR2 AASSLQS

Fw3 GVPSRFGSGSGTEFTLTISSLQFEDFATYYC

CDR3 LQHNSEFRT

Fw4 FGQGTKVEIK

NUCLEOTIDE:

Fw1 gac atc cag atg acc cag tct cca tcc tcc ctg tct gca tct gta gga gac aga gtc acc atc act
tga

CDR1 cgg gca agt cag ggc att aga aat gtt tta ggc

Fw2 tgg tat cag cag aaa cca ggg aaa gcc cct aag tgc ctg atc tat

CDR2 gct gca tcc agt ttg caa agt

Fw3 ggg gtc cca tca agg ttc agc ggc agt gga tct cgg aca gaa ttc act ctg aca atc agg agc ctg
cag cct gaa gat ttt gca act tat tac tct

CDR3 cta cag cat aat agt cag ccc cgg acg

Fw4 ttc ggc caa ggg acc aag gtg gaa atc aaa

AT13-031 (6G6-2I10)**Heavy chain**

Recombined from gene segments:

IGHV4-34*01 F

IGHD6 6*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLQQWCGALLKPSSETLSLTCAVYGGSF3

CDR1 GYYWS

Fw2 WIRQPPGKGLEWIG

CDR2 EINHSGSTNYKPSLK5

Fw3 RVTISYDTSKKQFSLKLSSVTAADTAVYYCAR

CDR3 GPRGMYSSSSGDY

Fw4 WQGTLVIVSS

NUCLEOTIDE:

Fw1 cag gtc caa cta cag caa tgg ggc gca gga ctg ttg aag cct tgg gag acc ctg tcc ctg acc tgc
ggt ctg tat ggt ggg tcc ttc agt

CDR1 ggt tac tac tgg agc

Fw2 tgg atc cgc cag ccc cca ggg aag ggg ctg gag tgg att cgg

CDR2 gaa atc aat cat agt cga agc acc aac tac aac ccc tcc ctg aag agt

Fw3 cga gtc acc ata tca gta gac aag tcc aag aag cag ttc tcc ctg aag ctg agc tct gtc acc ggc
ggg cag acc gct gtc tat tat tgt ggc aga ggc

CDR3 ccc cgg ggc atg tat agc agc tgg tcc cgg gag tac

Fw4 tgg ggc cag gga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-17*01 F

IGKJ2*02 F

AMINO ACID:

Fw1 DIQMTQSFSSLSASVGDRTITC

CDR1 SASQGIKNDLG

Fw2 WYQQKPGKAPKRLIY

CDR2 AAVSLQS

Fw3 GVPSRFSGSGTEFTLTISSLQPEDFATYYC

CDR3 LQHNSYFRT

Fw4 FGQGTKLEIK

NUCLEOTIDE:

Fw1 cag atc cag atg acc cag tct cca tcc tcc ctg tct gaa tct gta gga gac aga gtc acc atc act
tgc

CDR1 cgg gca agt cag ggc att aga aat gat tta gcc

Fw2 tgg tat cag cag aaa cca ggg aaa gcc cct aag cgc ctg atc tat

CDR2 gat gca gtc agt ttg caa agt

Fw3 cgg gtc cca tca agg ttc agc ggc agt cga tct ggg acc gaa ttc act ctg acc atc agc agc ctg
cag cct gaa gat ttt cca act tat tac tgt

CDR3 cta cag cat aat agt tac cct cgg act

Fw4 ttt ggc cag ggg acc aag ctg gag atc aaa

AT12-020 (1B3-13C8)**Heavy chain**

Recombined from gene segments:

IGHV3-21*01 F

IGHD1-25*01 F

IGHJ6*03 F

AMINO ACID:

Fw1 EVQLVESGGGLVKFGGSLRLSCAASGFTFS

CDR1 TYSMN

Fw2 WVRQAPGKGLEWVS

CDR2 SSSSSGYIYYACSVKG

Fw3 RFTISRDNAKNSLYLQMNSLRAEETAVYYCAR

CDR3 DGTFSYYYMDV

Fw4 WGRGTTVTVSS

NUCLEOTIDE:

Fw1 gag gtg cag ctg gtg gag tct ggg gga ggc ctg gtc aag cct ggg ggg tcc ctg aga ctc tcc tgt
gca gcc tct gga ttc acc ttc agt

CDR1 acc tat agc atg aac

Fw2 tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtc tca

CDR2 tcc att agt agt agt agt ggt tac ata tac tac gca cac tca gtg aag ggc

Fw3 cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg tat ctg caa atg aac agc ctg aga gcc
cag gac acc gct ctg tat tac tgt ccg aga

CDR3 gat ggg act ttc tcc tac tac tac tac atg gac gtc

Fw4 tgg ggc aaa ggg acc acg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV1-8*01 F

IGKJ1*01 F

AMINO ACID:

Fw1 AIRMTQSPSSFSASTGDRVTITC

CDR1 RASQDISSSLA

Fw2 WYQQKPGKAPKLLIY

CDR2 AASTLQS

Fw3 GVPSRFSGSGSGTEFTLTISCLQSEDFATYYC

CDR3 QQYYSVPPT

Fw4 FGQGTREIK

NUCLEOTIDE:

Fw1 gcc atc egg atg acc cag tct cca tcc tca ttc tct gca tct aca gga gac aga gtc acc atc act
tgt

CDR1 egg ggg agt cag cat att agc agt tct tta gcc

Fw2 tgg tat cag caa aaa cca ggg aaa gcc cct aag ctg ctg atc tat

CDR2 cct gca tcc act ttg caa agt

Fw3 gca gtc cca tca agg ttc aga gga agt gga tct ggg aca gac ttc act ctg acc atc aga tgc ctg
cag tct gaa gat ttt gca act tat tac tct

CDR3 caa cag tat tat agt tac cct ccg acg

Fw4 ttc ggc caa ggg acc agc ttg caa atc aaa

AT13-033 (7H10-2A4)**Heavy chain**

Recombined from gene segments:

IGHV3-30*03 F
IGHD1-23*01 ORF
IGHJ6*02 F

AMINO ACID:

Fw1 QVQLVESGGGVVQFGRSLRLSCAVSGLSFR
CDR1 NYGMH
Fw2 WVRQAPGKGLEWVA
CDR2 VISHDGSKTTYGHSVKG
Fw3 RFTISRDKSKTMLFLQMNSLRPEDTAVYYCAK
CDR3 AGLNYYGNLLSNFYFYGMQV
Fw4 WGQGTIVIVSS

NUCLEOTIDE:

Fw1 cag gtg cag ctg gtg gag tct cgg gca gcc gtg ctg caa cct cgg agg tcc ctg aga ctg tcc tgt
gca gtc tct gga ctg agt ttc agg

CDR1 aat tat gcc atg cac

Fw2 tgg gtc cgc cag gct ccc gcc aag ggg ctg gag tgg gtc gca

CDR2 gtc att tcg cat gat gga agt aag aca tac tat gga cac tcc gtg aag gcc

Fw3 cga ttc acc ata tcc aga gac aaa tcc aag act atg ttg ttt ctg caa atg aac ago ctg aga cct
gag gac aag gct gtt tat tac tgt cgg aaa

CDR3 gcc ggg ttg aac tac tat gga aac cta tta tca aac tac ttc tac tac gca atg gac gtc

Fw4 tgg gcc caa cgg acc aca gtc acc gtc tcg tca

Light chain

Recombined from gene segments:

IGLV2-8*01 F
IGLJ2*01 F

AMINO ACID:

Fw1 QSALTQPPFSASGSFQSVTISC
CDR1 TGTSSDIGGYNYS
Fw2 WYQHHPGKAPKLMY
CDR2 EVTKRPS
Fw3 GVPDRFSGSKSGNTASLTIVSGLOAEDEAEYYC
CDR3 SSYAGSNDLL
Fw4 FGGGTRLTIVL

NUCLEOTIDE:

Fw1 cag tct gcc ctg act cag cct ccc tcg gcc tcc cgg tct cct ggt cag tca gtc acc atc tcc tgt

CDR1 act cgg acc agc agt gac att ggt cgt tat aac tat gtc tcc

Fw2 tgg tac caa cac cac cca gcc aaa gcc ccc aaa ttg atg att tat

CDR2 gag gtc act aag cgg ccc tca

Fw3 gcc gtc cct gat cgt ttc tct gcc tcc aag tct gcc aac acg gcc tcc ctg acc gtc tct gga ctg
cag gct gag gat gag gct cat tat tac tgc

CDR3 agc tca tat gca cgc agc aac gal ttg cta

Fw4 ttc gcc gga cgg acc aag ctg acc gtc ctg

AT13-034 (7H10-4F9)**Heavy chain**

Recombined from gene segments:

IGHV3-33*01 F

IGHD2 15*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVHLVESGGGVVQFGTSLRLSCAASEFTFS

CDR1 SHAIH

Fw2 WVRQAPGKGLEWVA

CDR2 LIWYDGSNNYYAGSVKG

Fw3 RFTISRDSKNTVHLMNSLRVEDTAVYYC

CDR3 ARDGCTGGSCCYFDN

Fw4 WGQGLTVTSS

NUCLEOTIDE:

Fw1 cag gtg cac ctg gtg gag tct ggg gga ggc gtg ctg caa cct ggg acg tcc ctg aga ctg tcc tgt
gaa gag tct gaa ttc acc ttc agt

CDR1 tcc cat gcc ata cac

Fw2 tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gaa

CDR2 ctt ata tgg tat gat gca agt aat aat tat tat gca gac tcc gtg aag ggg

Fw3 cga ttc acc atc tcc aga gac agt tcc aag aac acg gtg cat ctg caa atg aac agc ctg aga gtc
gag gac acc gct gtg tat tac tgt

CDR3 ggg aga gat ggt tgt acg ggt ggt agc tgc tgc tat ttt gac aac

Fw4 tgg ggc cag gga acc cta gtc acc gtc tcc tgg

Light chain

Recombined from gene segments:

IGKV3-15*01 F

IGKJ4*01 F

AMINO ACID:

Fw1 EVVMTQSPATLSVSPGERATLSC

CDR1 RASQISNNLG

Fw2 WYQQKPGQAPRLLIY

CDR2 GASTRAT

Fw3 GIPGRFSGSGSGTEFTLTITISLQSEDFAVYYC

CDR3 QQYNNWPRLT

Fw4 FGGGTKVEIK

NUCLEOTIDE:

Fw1 gaa gta gtg atg acg cag tct cca gcc acc ctg tct gtg tct cca ggg gaa aga gcc acc ctg tcc
tga

CDR1 agg gcc agt cag agc att agc aac aac tta ggc

Fw2 tgg tat cag cag aaa cct gcc cag gct ccc agg ctg ctg atc tac

CDR2 ggt gca tcc acc agg gcc act

Fw3 ggt atc cca ggc agg ttc agt ggc act ggg tct ggg aca gag ttc act ctg acc atc tac agc ctg
cag tct gag gat ttt gca gtt tat tac tgt

CDR3 caa caa tat aat aac tgg cct ggg ctg act

Fw4 ttc ggc gga ggg acc aag gtg cag atc aaa

AT13-035 (19C7-2F8)**Heavy chain**

Recombined from gene segments:

IGHV3-30*03 F

IGHD3-10*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLVESGGGVVQFGRSLRLSCAASGFTFS

CDR1 SYGMH

Fw2 WVRQAPGKGLEWVA

CDR2 VISYDGSNKYYACSVKG

Fw3 RFTISRDN SKNTLYLQMNSLRAEDTAVYYC

CDR3 AKDSYYYGSGRRWGYFDCY

Fw4 WGQGLVTVSS

NUCLEOTIDE:

Fw1 cag gtg cag ctg gtg gag tct ggg gca ggc gtg ctg caq cct ggg agg tcc ctg aga ctg tcc tgt
gca gcc tct gga ttc acc ttc agt

CDR1 agc tat ggc atg cac

Fw2 tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg gca

CDR2 gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg aag gcc

Fw3 cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat ctg caa atg aac ago ctg aga gct
gag gac aag gct gtg tat tac tgt

CDR3 cgg aaa gac tgg tat tac tat ggt tgg ggg aga cga tgg ggc tac tac ttt gac tac

Fw4 tgg ggc caq cga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGLV3-19*01 F

IGLJ2*01 F

AMINO ACID:

Fw1 SSELTDFAVSVALGQTVRITC

CDR1 QGDSLRSYYAS

Fw2 WYQKPGQAPVLVIY

CDR2 GKNNRPS

Fw3 GIPDRFSGSSSGNTASLTITGAQAEDEADYYC

CDR3 NSRDSSGNHVV

Fw4 FGGGTRLTVL

NUCLEOTIDE:

Fw1 tct tct gag ctg act cag gac cct gct gtg tct ctg gcc ttg gga cag acc gtc agg atc acc tgc

CDR1 caa gca gac agc ctg aga agc tat tat gca agc

Fw2 tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat

CDR2 ggt aaa aac aac cgg ccc tca

Fw3 cgg atc cca gac cga ttc tct ggc tcc agc tca cga aac acc gct tcc ttg acc atc act ggg gct
cag gcg gaa gat gag gct gac tat tac tgt

CDR3 aac tcc cgg gac agc agt ggt aac cat gtc gla

Fw4 ttc ggc gga cgg acc aag ctg acc gtc cta

AT13-036 (12C2-5F6)**Heavy chain**

Recombined from gene segments:

IGHV3-21*01 F
IGHD5 24*01 QRF
IGHJ6*02 F

AMINO ACID:

Fw1 EVQLVESGGGLVKPGGSLRLSCAASGFTFS
CDR1 SYSMN
Fw2 WVRQAPGKGLEWVS
CDR2 SISSSSYIYYADSVKG
Fw3 RFTISRDNARNSLYLQMNSLRAEDTAVYYC
CDR3 ARPREVGRDGYSLYPRGYHYGMDV
Fw4 WGQGTIVIVSS

NUCLEOTIDE:

Fw1 cag gtc cag ctg ctg gag tct ggg gga ggc ctg gtc aag cct ggg ggg tcc ctg aga ctc tcc tgt
gga gcc tct gga ttc acc ttc agt

CDR1 agt tat agc atg aac

Fw2 tgg gtc cgc sag cct cca ggg aag ggg ctg gag tgg gtc tca

CDR2 tcc att agt agt agt agt act tac ata tac tac gca gac tca ctg aag ggc

Fw3 cga ttc acc atc tcc aga gac aac gcc agg aac tca ctg tat ctg caa atg aac agc ctg aga gcc
gag gac acc gct ctg tat tat tgt

CDR3 ggc aga agg agg gag gtc ggt aga gat ggc taa agt ttg tac ccc cgg ggc tac cac tac ggt atg
gac ctg

Fw4 tgg gcc caa ggg aac acg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGLV2-14*01 F
IGLJ2*01 F

AMINO ACID:

Fw1 QSALTQPAASVSGSPRQSITISQ
CDR1 TGTSSDVGGYNYVS
Fw2 WYQQLPGKAPKLMY
CDR2 DVNDRPS
Fw3 GVSIRFSGSKSGNTASLTISGLQAEDADYYC
CDR3 SSYTRSNTVI
Fw4 FGGGTKLTVL

NUCLEOTIDE:

Fw1 cag tct gcc ctg act cag cct gcc tcc ctg tct ggg tct cct aga cag tgg atc acc atc tcc tgc

CDR1 act gga acc agc agt gac gtt ggt ggt tat aac tat gtc tcc

Fw2 tgg tac caa caa ctg cca ggc aaa gcc ccc aaa ctg atg att tat

CDR2 gat gtc aat gat cgg ccc tca

Fw3 cgg gtt tct att cgc ttc tct ggc tcc aag tct ggc aac acg gcc tcc ctg acc atc tct ggg ctg
cag cct gag gac gag cct gat tat tac tgc

CDR3 agc tca tat aca aga agc aac act gtg ata

Fw4 ttc gcc gga ggg acc aaa ctg acc gtc cta

AT13-037 (3G11-5E3)**Heavy chain**

Recombined from gene segments:

IGHV3-33*01 F

IGHD5-12*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 QVQLVESGGGVVQPGRSLRLSCAASGFTFS

CDR1 TYGMH

Fw2 WVRQAPGKGLEWVA

CDR2 VIWYDGSNTYYADSVKG

Fw3 RFTISRDN SKNTLYLQIKSLRAEDTAVFYC

CDR3 ARGRGYSAQGNRN RAYFYFY

Fw4 WQQGTIVTVSS

NUCLEOTIDE:

Fw1 cag ctg cag atg gtg gag tct ggg gga gcc gtg gtc aag cct ggg agg tcc ctg aga ctc tcc tgt
aca ggg tct gca ttc acc ttc agt

CDR1 acc tat gcc atg cac

Fw2 tgg gtc ccg cag gct cca gcc aag ggg ctt gag tgg gtg gca

CDR2 gtt ata tgg tat gat gga agt aat aca tac tat gca gac tcc gtg aag ggc

Fw3 cga ttc acc atc tcc aga gac aat tcc aag aac aca ctg tat ctg caa ata aag agc ctg aga gcc
gag gac acg gct gtc tat tac tgt

CDR3 ggg aga ggc cgt gca tat agt gcc caa ggg aat ggg aat agg gct tac tac ttt gac tac

Fw4 tgg cga cag gga acc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV3-15*01 F

IGKJ2*01 F

AMINO ACID:

Fw1 EIVMTQSPATLSVSPGERVILSC

CDR1 RASQSVSSNLA

Fw2 WYQQKPGQPRLLIY

CDR2 GAFTRVT

Fw3 GVPARFSGSGSTEFTLTISSLQSEDFAVYYC

CDR3 QQYNDRPPYT

Fw4 FGQGTKLEIK

NUCLEOTIDE:

Fw1 gaa ata gtg atg acc aag tct cca gcc acc ctg tct gtg tct cca ggg gaa agg gtc atc ctc tcc
tgc

CDR1 agg gcc agt cag aet gtt agc agc aac tta gcc

Fw2 tgg tac cag cag aaa cct gcc cag cct ccc agg ctg ctg atc tat

CDR2 ggt gca ttc acg agg gtc act

Fw3 ggt gtc cca gcc agg ttc agt ggc agt ggc tct ggg aca gaa ttc act ctg acc atc agg agc ctg
cag tct gaa gat ttt gca gtt tat tac tgt

CDR3 cag cag tac aat gac cgc gcc ccg tac act

Fw4 ttt gcc cag ggg acc aag ctg gag atc aaa

AT14-013 (2K23-1K13)**Heavy chain**

Recombined from gene segments:

IGHV4-4*02 F
IGHD6 19*01 F
IGHJ5*02 F

AMINO ACID:

Fw1 QGRLLQESGPGGLVKFSETLTILTCAVSGGSSVS
CDR1 SPNWWT
Fw2 WVRQAPGKGLEWIG
CDR2 EIYYGGRVGYNSALRS
Fw3 FVTISSDRSKEEFSLKLRSVTAADTAIYYC
CDR3 AGQKNIGCGYSSCFISWFDT
Fw4 WGQGIAVTSS

NUCLEOTIDE:

Fw1 cag ggg cga ctg cag gag tgg ggc cca gga ctg ctg aag cct tgg gag acc ctg acc ctg acg tgc
gct gtg tcc ggt ggc tcc tcc gtc agc

CDR1 agt cct aac tgg tgg act

Fw2 tgg gtc cgc cag gcc ccc ggg aag ggg ctg gag tgg att gga

CDR2 gaa atc tat tat ggt ggc aga gtg agc tac aac tgg gcc ctg agc agt

Fw3 cga gtc acc att tca tca gac agg tgg aaa gag gag ttc tcc ctg aaa ctg agc tct ctg acc gcc
ggg gac acc gcc ata tat tat tgt

CDR3 ggc ggt caa aaa aat att ggc tgt cgt tac agc agt tgc ttt atc agt tgg ttc gac acc

Fw4 tgg gga cag gga att gcc gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV4-1*01 F
IGKJ2*01 F

AMINO ACID:

Fw1 DIVMTQSPFDSLAVSLGERATIA
CDR1 KSSQTIHQRSNELNYLA
Fw2 WYQQKPGQPPKVLII
CDR2 WASTRES
Fw3 GVPDRFSGSGSTLTFTLTINSLOAEDVAVYYC
CDR3 EQYYTTPQT
Fw4 FGQGTKVEIK

NUCLEOTIDE:

Fw1 gac atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agc gcc acc atc gcc
tgc

CDR1 aag tcc agc gag act att tta caa agc tcc aac cat ttg aac tac tta gct

Fw2 tgg tac cag cag aaa cca gga cag cct cct aaa gtg ctg att tat

CDR2 tgg gca tct acc cgg gaa tcc

Fw3 ggg gtc cct cag cga ttc agt ggc acc ggg tct cgg aca gat ttc act ctg acc atc aac agc ctg
cag gct gag gat gtg gca gtt tat tac tct

CDR3 cag caa tat tat act act cgg cag act

Fw4 ttt gcc cag ggg acc aag gtg gag atc aaa

AT14-014 (6P13-5H5)**Heavy chain**

Recombined from gene segments:

IGHV3-15*01 F

IGHD3 22*01 F

IGHJ4*02 F

AMINO ACID:

Fw1 EVQLVESGGGLVKFGGSLRLSCAASGFTFS

CDR1 DAWMS

Fw2 WVRQAPGKGLEWVG

CDR2 EINTKVEGGTTEYAAPVKG

Fw3 RFTISRDESKNSLYLHMDSLKTEDTAVYYC

CDR3 TTEAIYDSSGYFHDY

Fw4 WGQGLVTSS

NUCLEOTIDE:

Fw1 gaa gtc cag ctg gtg gag tct ggg gga ggt ttg cta aag cct ggg ggg tcc att aga ctc tcc tgt
gaa gcc tct gga ttc act ttc agt

CDR1 gaa gcc tgg atg agc

Fw2 tgg gtc cgc cag gct cca ggg aag ggg ctg gag tgg gtt ggc

CDR2 cat att aac acc aaa gtt gat ggt cgg aca aca gag tac gct gaa ccc ctg aaa ggc

Fw3 aga ttc acc atc tca aga gat gat tca aaa aat tgg ctg tat ctg cac atg gac agc ctg aaa acc
gag gac aca gcc ctg tat tac tgt

CDR3 acc aca gag ggg ata tat gat agt agt ggt tat ttc cat gac tat

Fw4 tgg ggc cag gga tcc ctg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGKV4-1*01 F

IGKJ1*01 F

AMINO ACID:

Fw1 DIVMTQSPFDSLAVSLGERATINC

CDR1 KSSRSVLYSSNNKNYLA

Fw2 WYQQKPGQPPKLLIY

CDR2 WASIRES

Fw3 GVPDRFSGSGSGTFTLTINSLOAEDVAVYYC

CDR3 QQYSRPPT

Fw4 FGQGTKVEIK

NUCLEOTIDE:

Fw1 gaa atc gtg atg acc cag tct cca gac tcc ctg gct gtg tct ctg gga gag agg gcc acc atc aac
tga

CDR1 aag tcc agc cgg agt gll tta tac agc tcc aac aat aag aac tac tta gcl

Fw2 tgg tac cag cag aaa cca gga cag cct cct aag ctg ctg att tac

CDR2 tgg gca tct atc cgg gaa tcc

Fw3 ggg gtc ccl cag cga ttc agt ggc acc ggg tcl cgg aca gat ttc act ctg acc atc aac agc ctg
cag gcl gaa gat ctg gca gtt tat tac tgt

CDR3 cag caa tat tct cgt cct cgg acc

Fw4 ttc ggc caa ggg acc aag gtg caa atc aaa

AT14-015 (1L18-7H16)**Heavy chain**

Recombined from gene segments:

IGHV3-43*04 F

IGHD4-11*01 F

IGHJ6*03 F

AMINO ACID:

Fw1 EVQLVESGGGLAQFGRSLRLSCTASGFRFG

CDR1 DFAMS

Fw2 WVRQAPGKGLEWVG

CDR2 FIRTKANDGTTEYAASVKG

Fw3 RFIISRDESKSIAYLQMNSLKTEDTAVYYC

CDR3 ASDPFMTTDYYYVYMDV

Fw4 WGKGTTIVVSS

NUCLEOTIDE:

Fw1 gag gtc cag ctg gtc gag tcg cgg gca gcc ttg cca cac cca cgg cgg tcc ctg aga ctc tcc tgt
aca gct tct gga ttc acg ttt ggt

CDR1 gat ttt gct atg agt

Fw2 tcg gtc cgc cag gct cca cgg aag gca ctg gag tcg gta ggt

CDR2 ttc att aga acc aaa gct aat gat cgg aca aca gaa tac gcc gcg tct gtg aaa gcc

Fw3 aga ttc atc atc tca aga gat gat tcc aaa agt atc gcc tat ctg caa atg aac ago ctg aaa acc
cag gac aca gcc gtt tat tac tgt

CDR3 gct acc gat ccc ttc atg act aba gac tat tac tac tac tac atg gac gtc

Fw4 tcg gcc aaa cgg acc acg gtc acc gtc tcc tca

Light chain

Recombined from gene segments:

IGLV2-8*01 F

IGLJ2*01 F

AMINO ACID:

Fw1 QSALTQPPFSASGSFQSVTISC

CDR1 TGTSSDVGGYNSVS

Fw2 WYQHHPGKAPKLMY

CDR2 EVYKRPL

Fw3 GVPDRFSGSKSGNTASLTVSGLOAEDEAYYYC

CDR3 SSYGGTVLF

Fw4 GGSTKLTVL

NUCLEOTIDE:

Fw1 cag tct gcc ctg act cag cct ccc tcc gcg tcc cgg tct cct gga cag tca gtc acc atc tcc tgc

CDR1 act gcg acc agc agt gac gtt ggt cgt tat aac tct gtc tcc

Fw2 tcg tac caa cat cac cca gcc aaa gcc ccc aaa ctc atg att tat

CDR2 gag gtc tat aag cgg ccc tta

Fw3 gcg gtc cct gat cgc ttc tct gcc tcc aag tct gcc aac acg gcc tcc ctg acc gtc tct gcg ctc
cag gct gag gat gag gct tat tat tac tgc

CDR3 agc tca tat gga cgc acc gly cta ttc

Fw4 gcc gga cgg acc aag ctg acc gtc cta

AT14-016 (1P22-8F16)**Heavy chain**

Recombined from gene segments:

IGHV3-23*01 F

IGHD2-15*01 F

IGHJ3*02 F

AMINO ACID:

Fw1 EVGVLESGGDSVQFGGSLRLSCAASGFTFS

CDR1 SYAMT

Fw2 WVRQAPGKGLKWS

CDR2 SISGGSTYYACSVRG

Fw3 RFTISRDN SKNTLYVQMNSLRAEDTAVYYC

CDR3 AKGYVGCSSGNCYSGGAFDI

Fw4 WGGTVVTVSS

NUCLEOTIDE:

Fw1 gag gtc caa ctg ttg gag tct cgg gca gac tgg cta cac cct cgg cgg tcc ctg aga ctc tcc tgt
gca gcc tct gga ttc acc ttt agc

CDR1 agc tat gcc atg acc

Fw2 tgg gtc cgc cag gct cca cgg aag cgg ctg aaa tgg gtc tca

CDR2 agt att agt ggt agt ggt ggt agc aca tac tac gca gac tcc gtg agg gcc

Fw3 cgg ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat gtg cag atc aac ago ctg aga gcc
gag gac aag gcc gta tat tac tgt

CDR3 cgg aaa gga tat ctg cgg tgt agt cgt ggg aac tgc tac tcc ggg ggt gct ttt gat atc

Fw4 tgg gcc aaa cgg aca gtg gtc acc gtc tct tca

Light chain

Recombined from gene segments:

IGLV3-21*01 F

IGLJ2*01 F

AMINO ACID:

Fw1 SYVLTOPFSVSVAFGKTARITC

CDR1 GGNIGSESVH

Fw2 WYQQKPGQAPVVVIY

CDR2 YETDRPS

Fw3 GIPERFSGSNSGNTATLTISRVEAGDEADYYC

CDR3 QVWDNTSDHPVVF

Fw4 GGSTKLTVL

NUCLEOTIDE:

Fw1 tcc tat gtg ctg act cag cca ccc tca gtg tca ctg gcc cca gga aag acg gcc cgg att acc tgt

CDR1 cgg cgg aac aac att gga agt gaa agt gtt cac

Fw2 tgg tac cag cag aag cca gcc cag gcc cct gtg ctg gtc atc tat

CDR2 tat gat acc gac cgg ccc tca

Fw3 cgg atc cct gag cgc ttc tct gcc tcc aac tct cgg aac acg gcc acc ctg acc atc agc agc gtc
gaa gcc ggg gat gag gcc gac tat tac tgt

CDR3 cag gtg tgg gat aac act agt gat cat cct glg gta ttc

Fw4 gcc gga cgg acc aag ctg acc ctg cta

Clinical history of donor 59

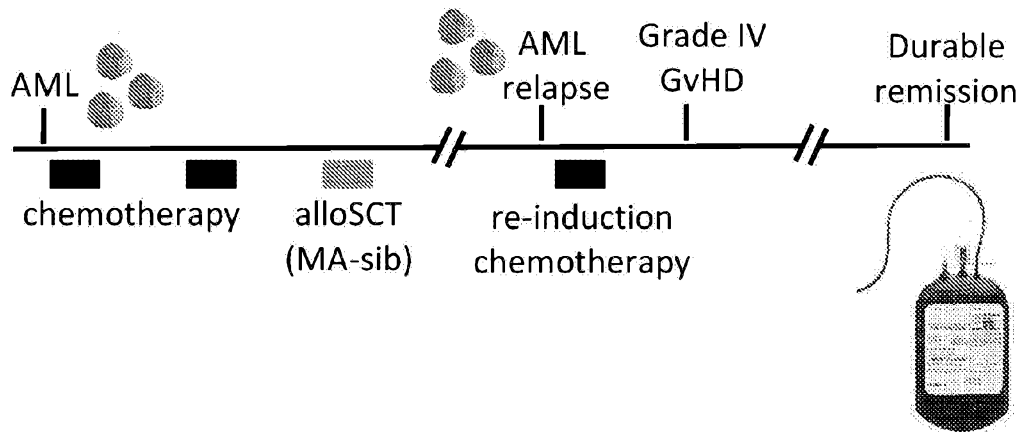
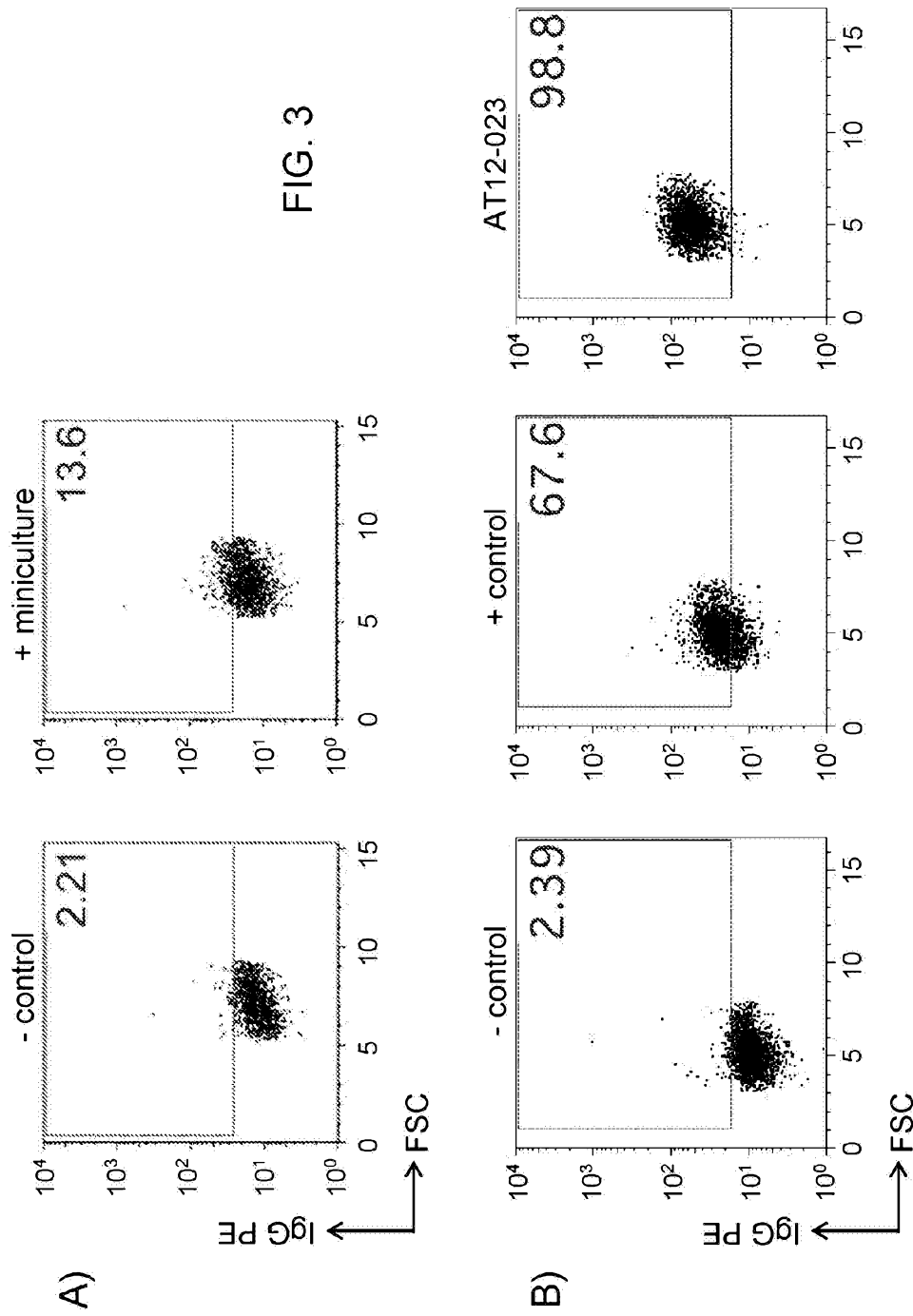


FIG. 2

Binding of miniculture supernatant to AML cells



Antibodies do not bind to irrelevant cell lines

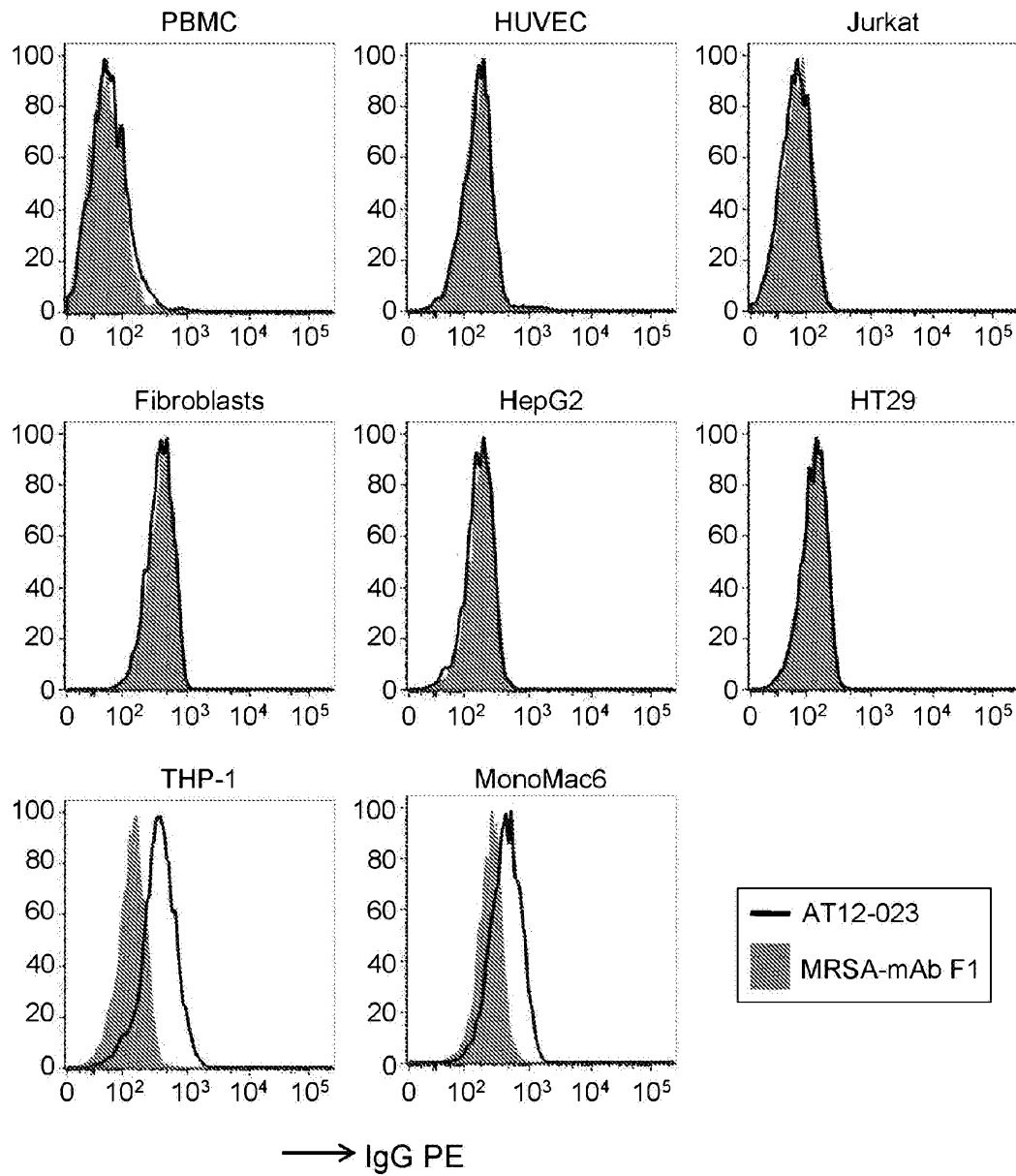


FIG. 4A

Antibodies do not bind to irrelevant cell lines

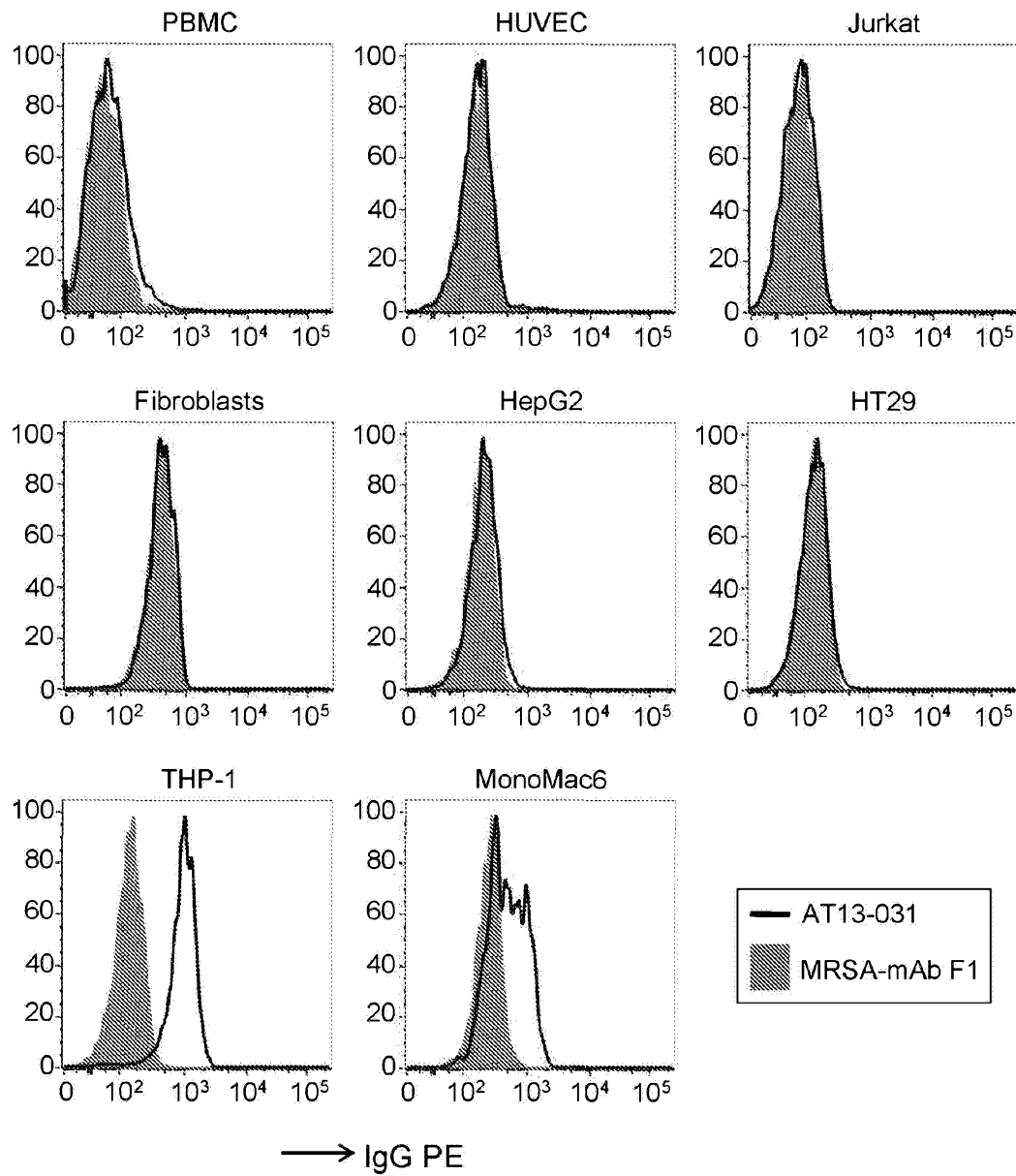


FIG. 4B

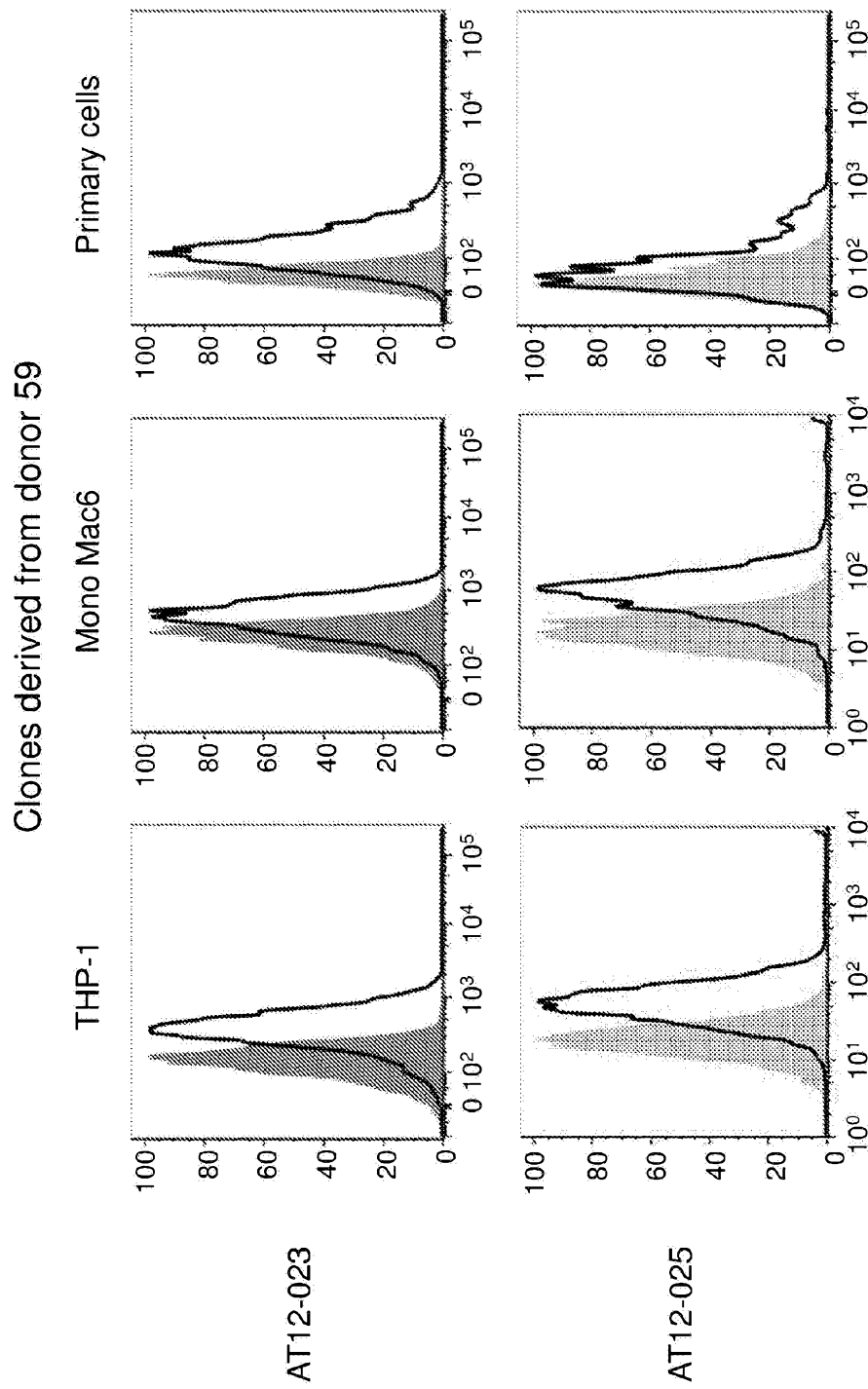


FIG. 5

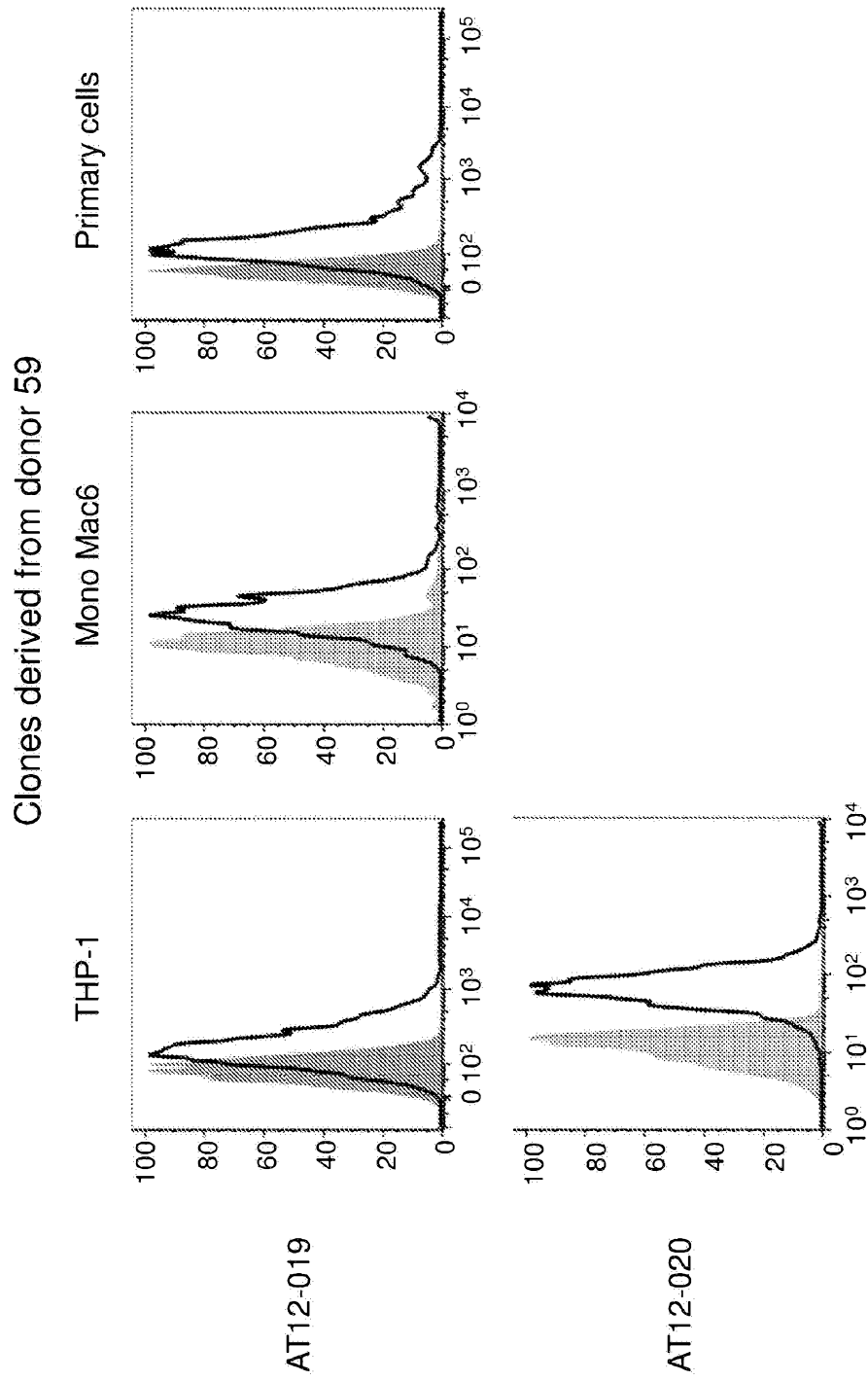


FIG. 5, Cont'd

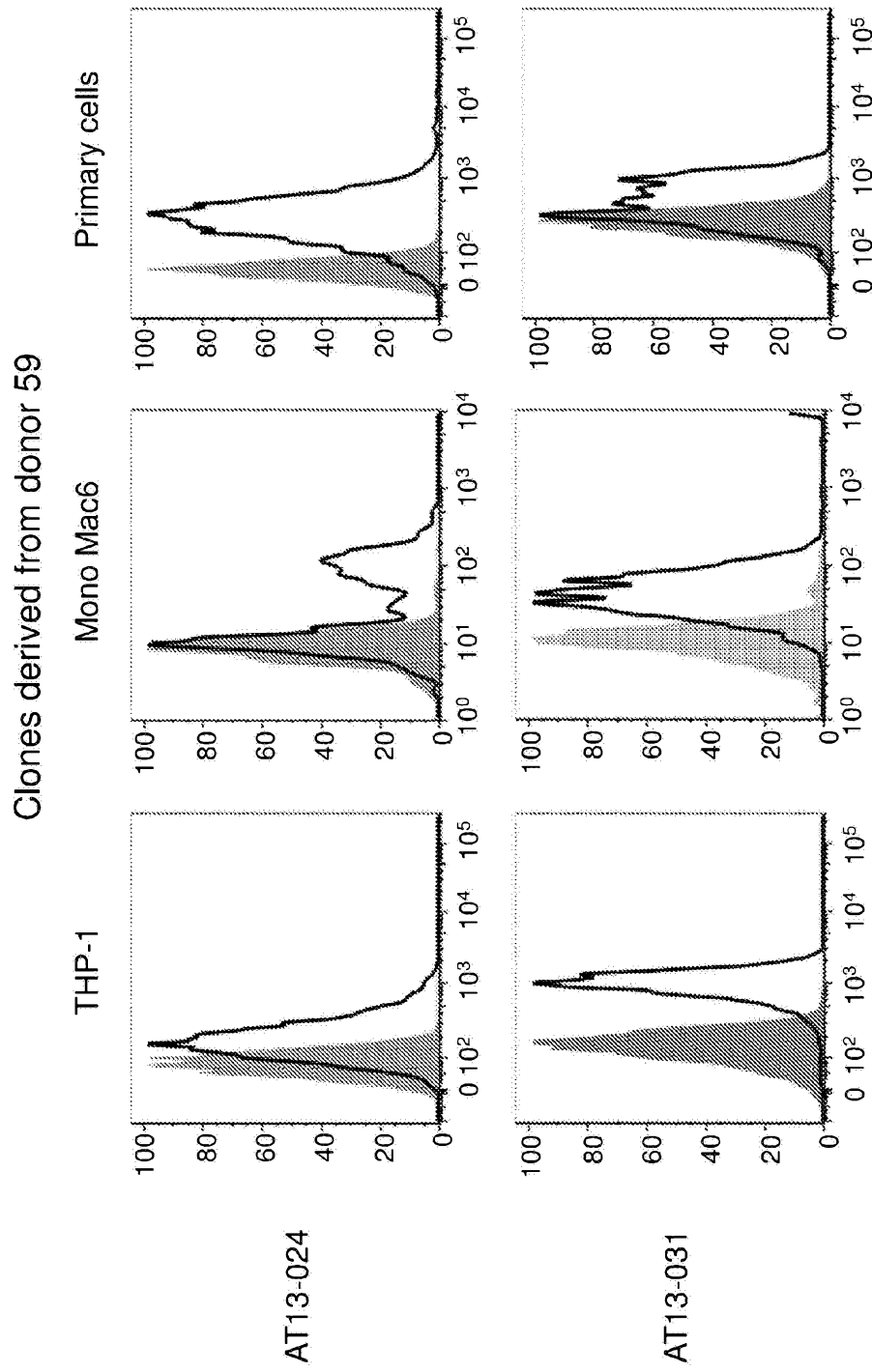


FIG. 5, Cont'd

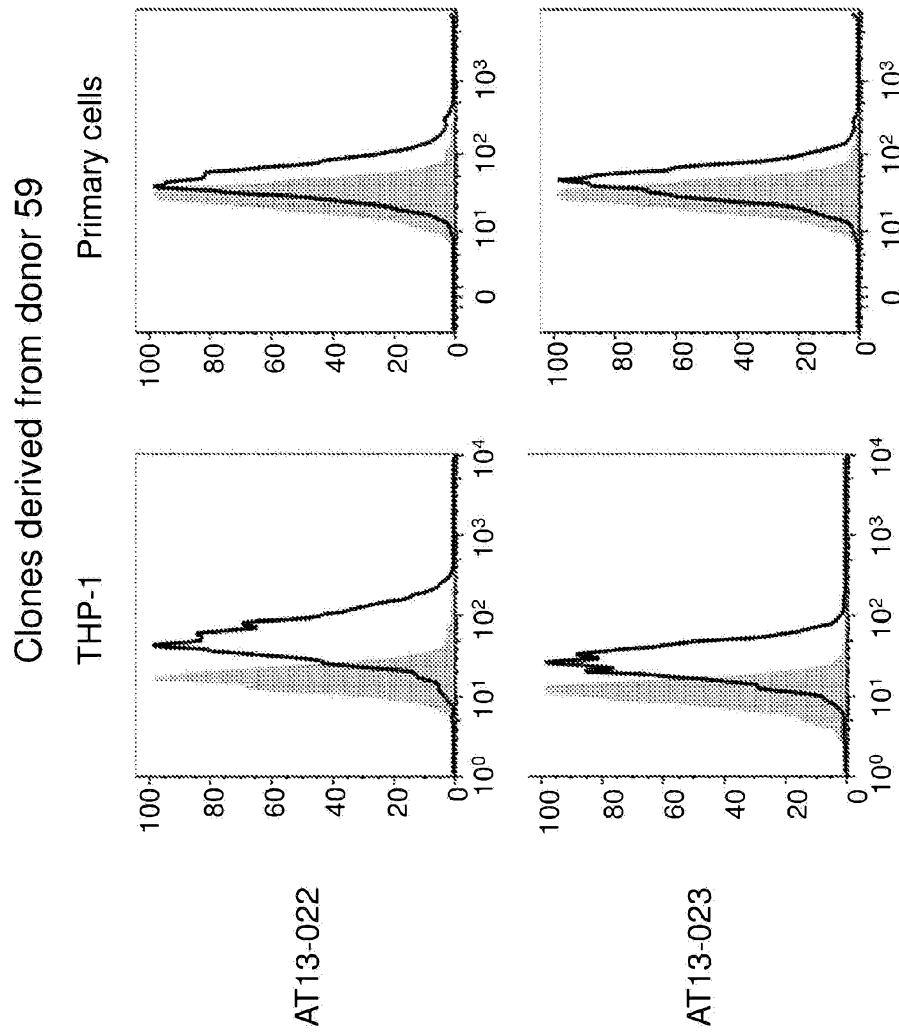


FIG. 5, Cont'd

Binding to B - non Hodgkin's lymphoma

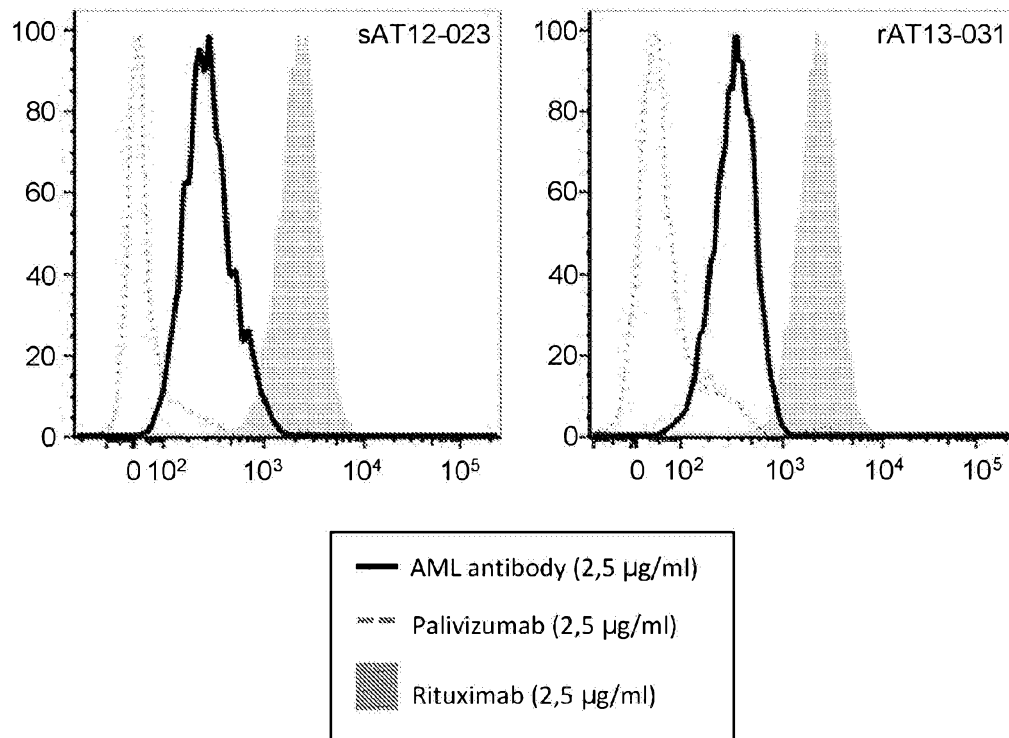


FIG. 6

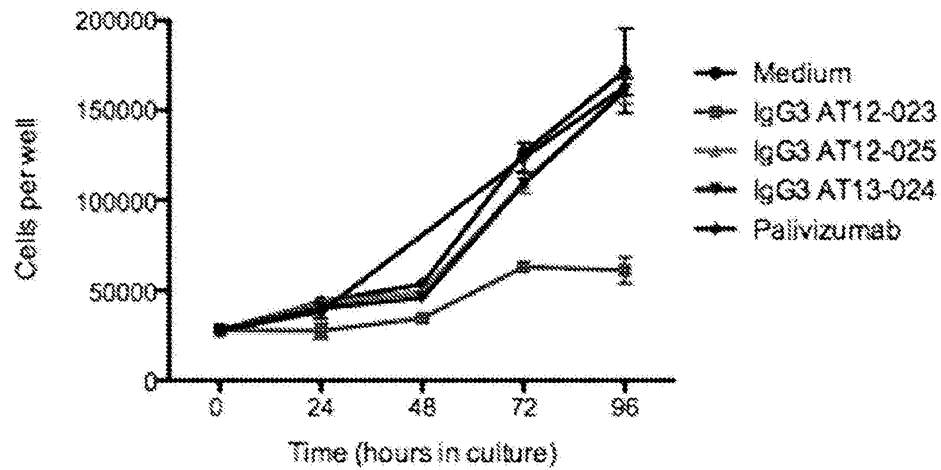
In vitro activity of AT12-023

FIG. 7

AT12-023 and AT12-025 reduce viability of THP-1

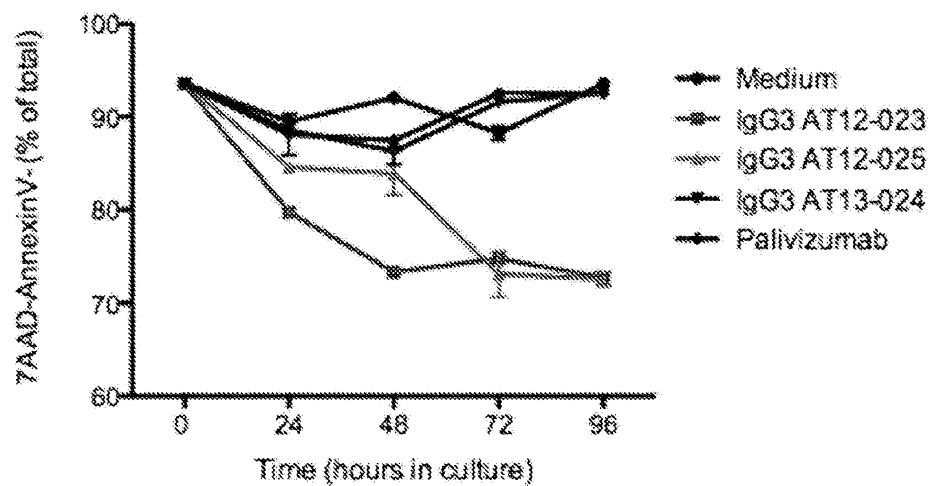


FIG. 8

Cytotoxicity of AT12-023 against THP-1

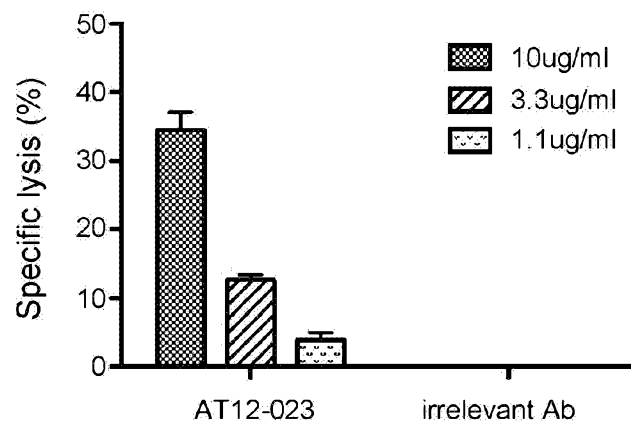


FIG. 9

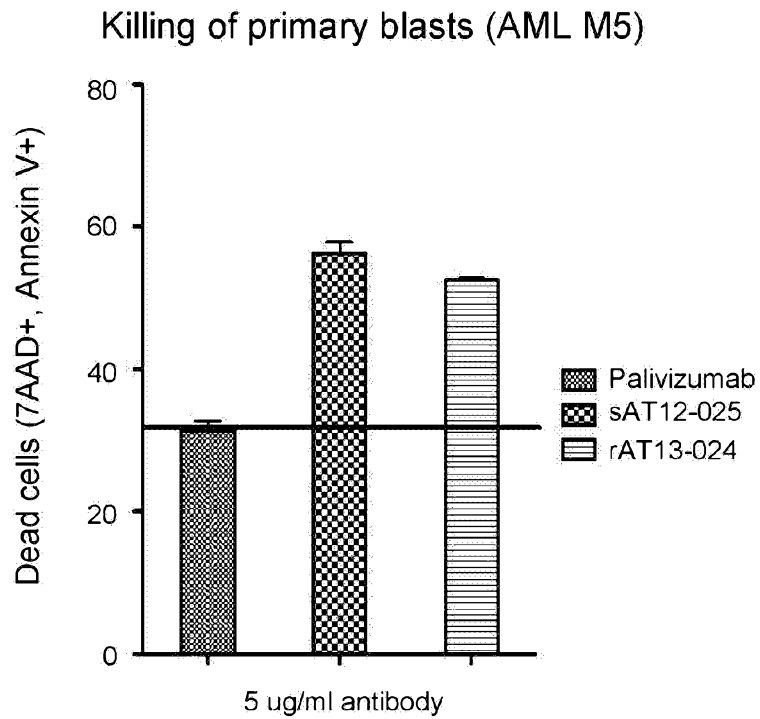


FIG. 10A

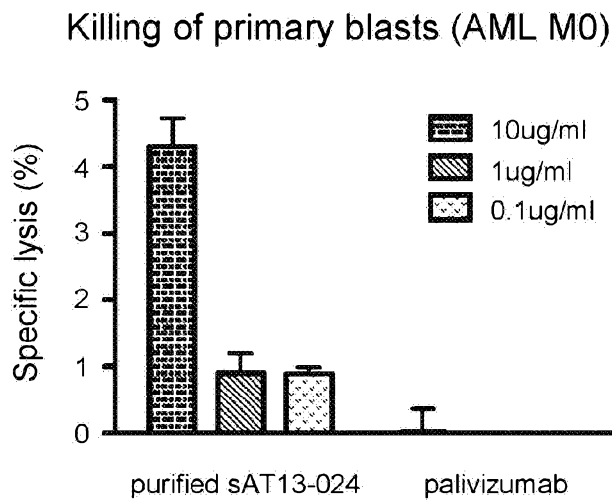


FIG. 10B

Clinical history of donor 58

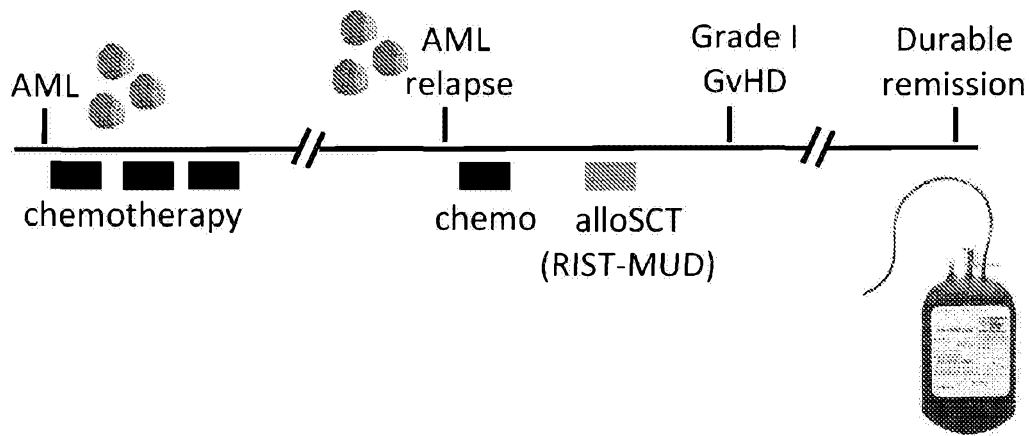


FIG. 11

Antibodies derived from donor 58

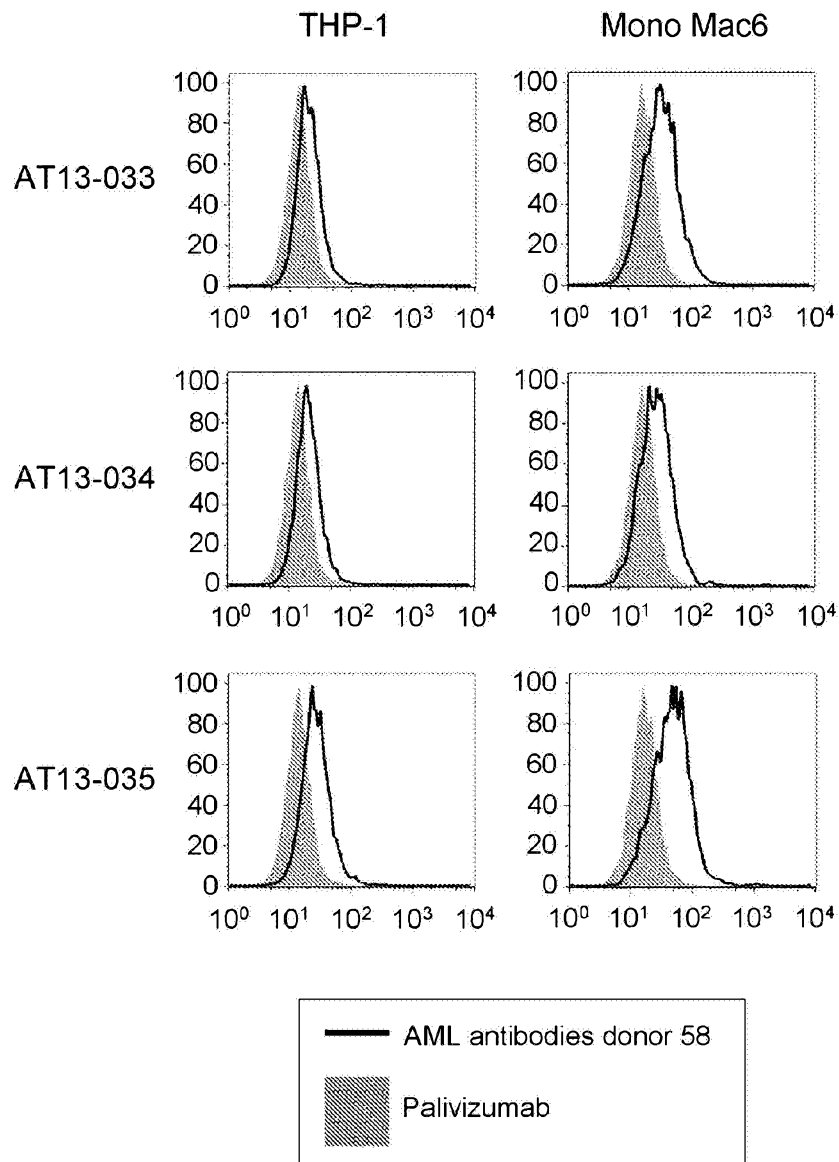


FIG. 12

Antibodies derived from donor 58

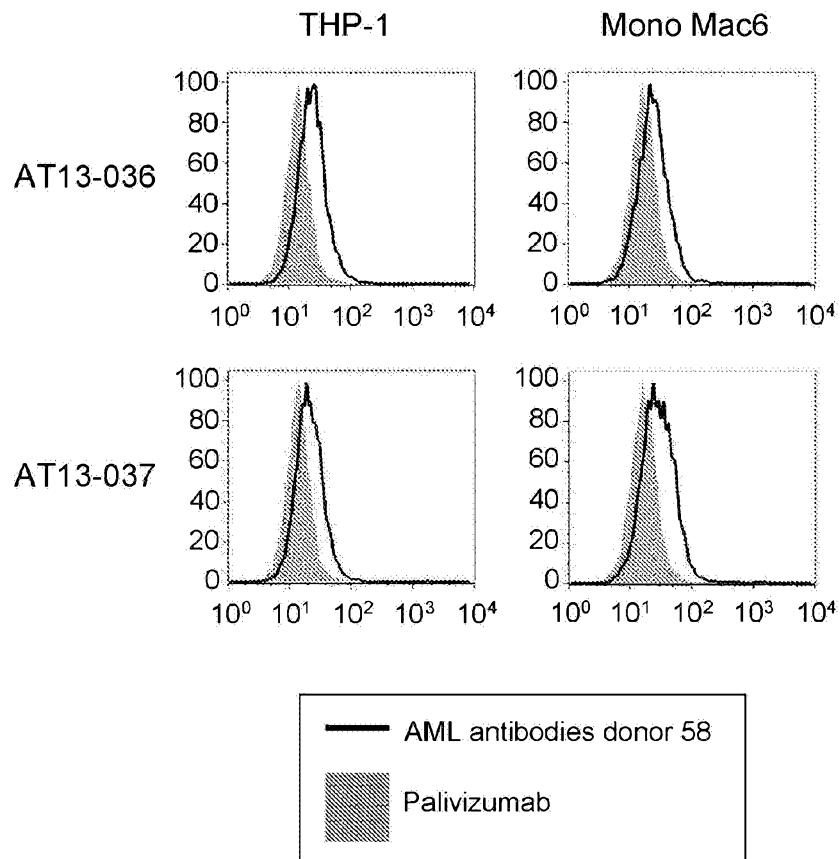


FIG. 12, Cont'd

Clinical history of donor 101

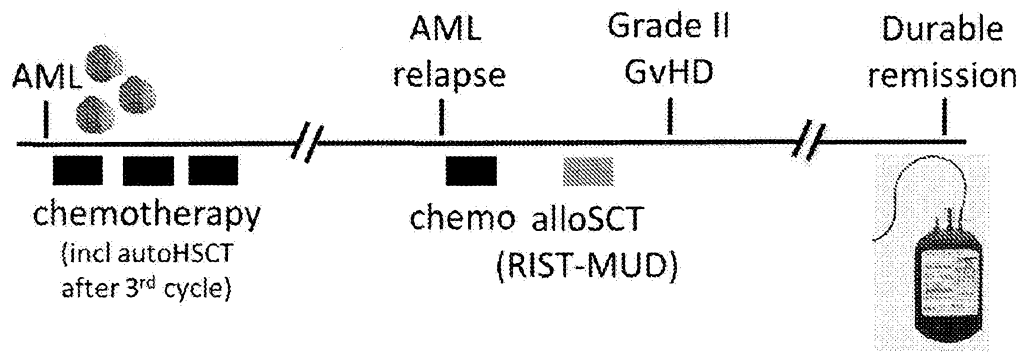
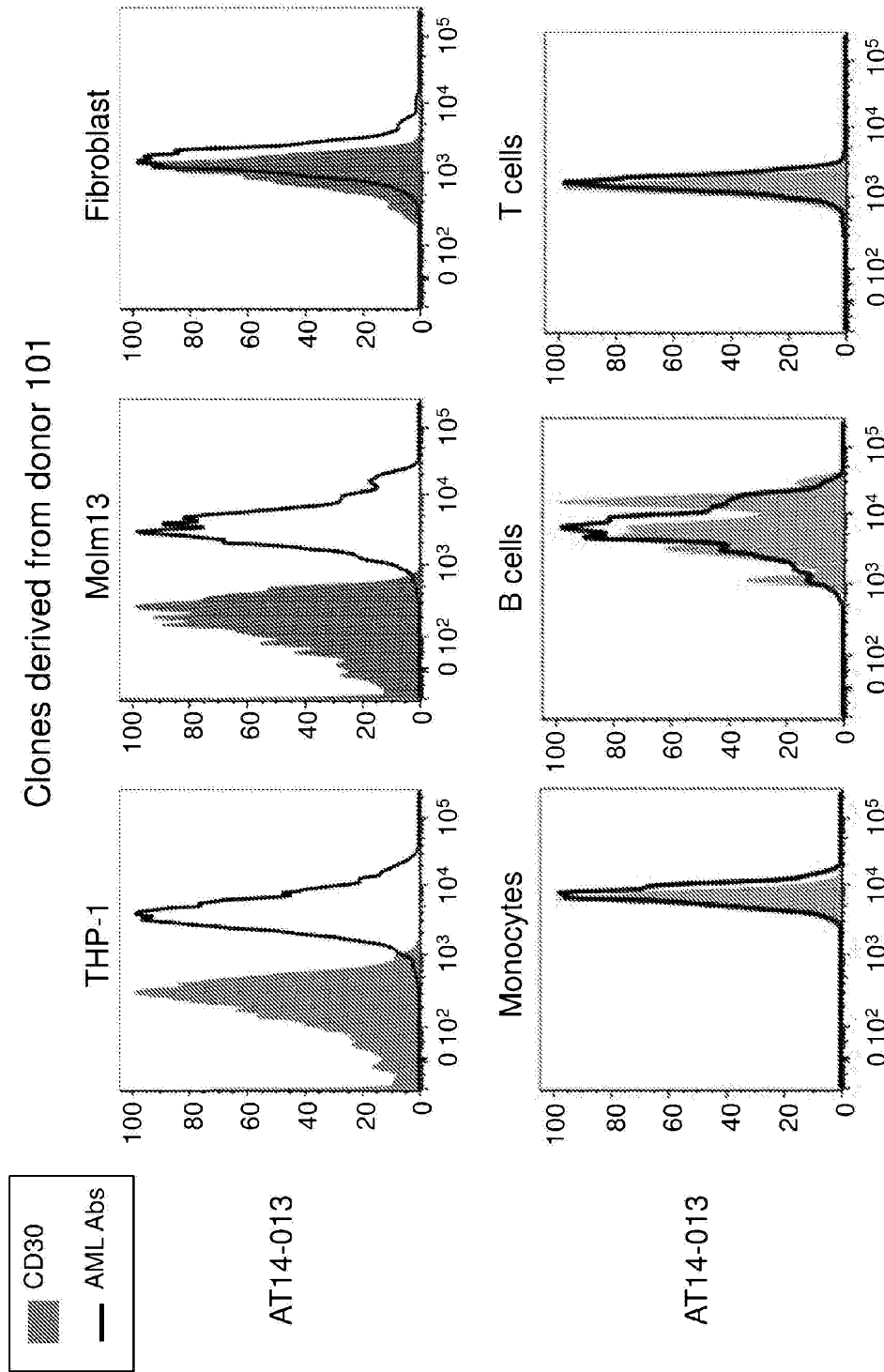


FIG. 13



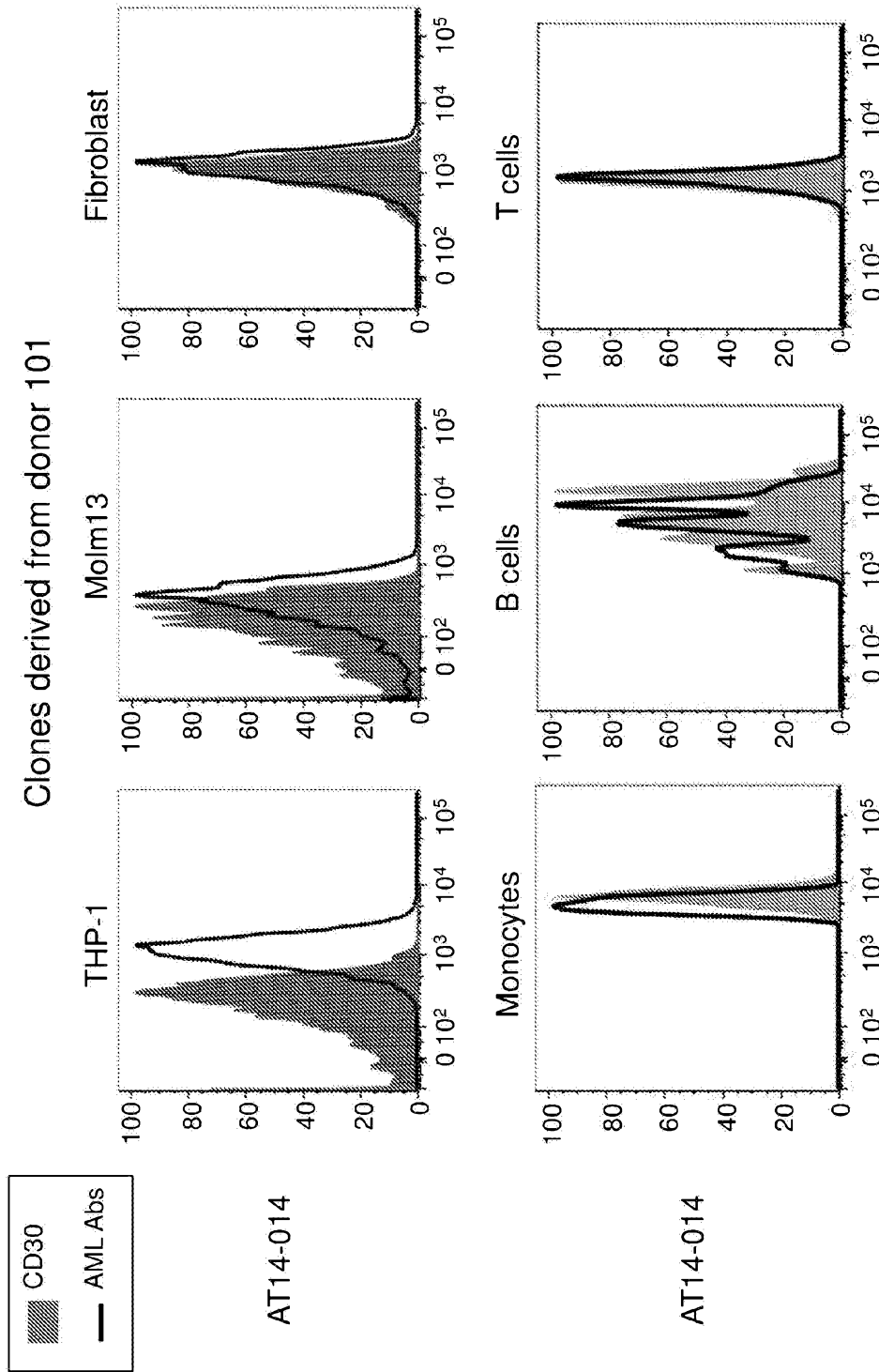


FIG. 14, Cont'd

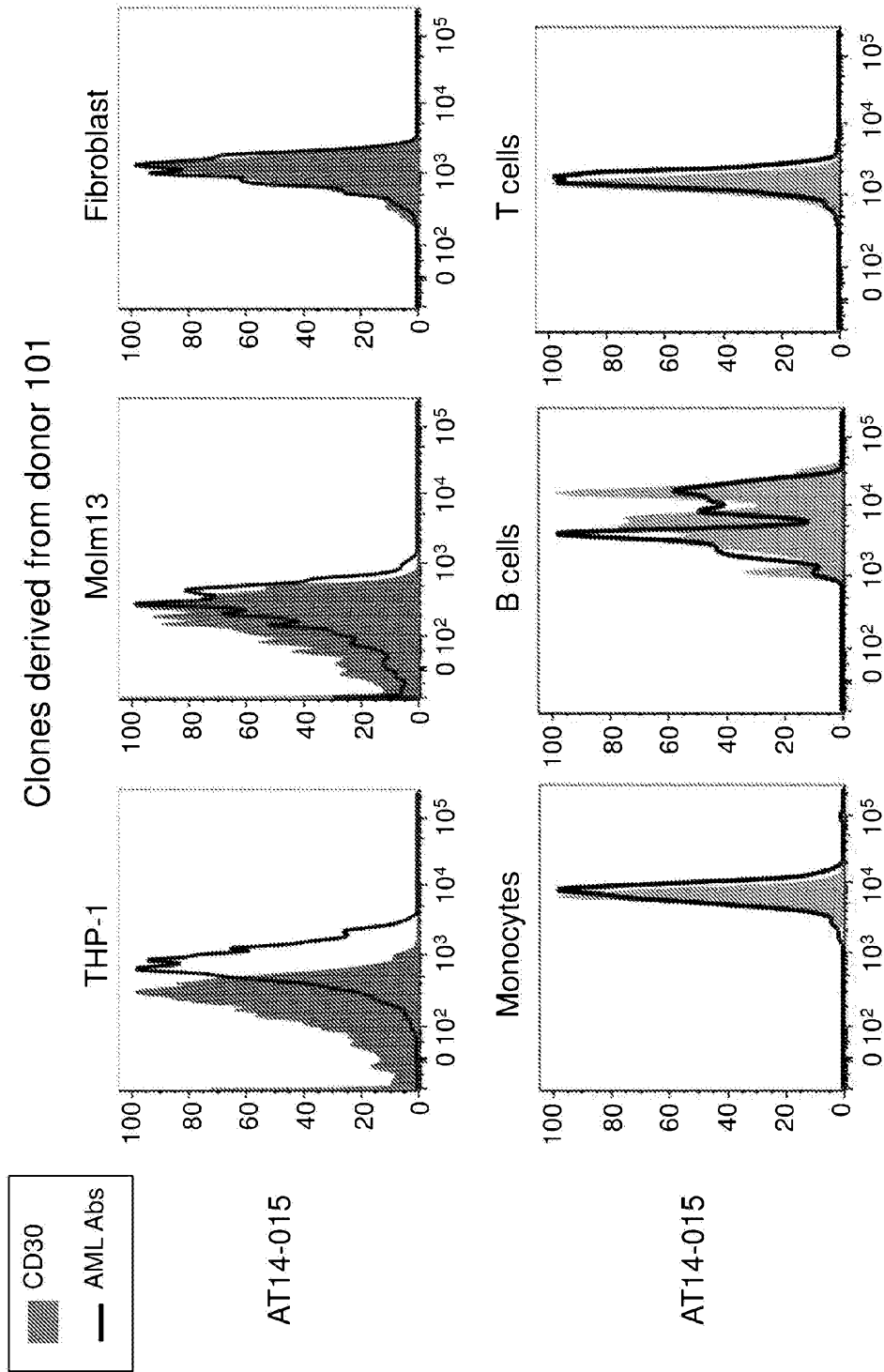


FIG. 14, Cont'd

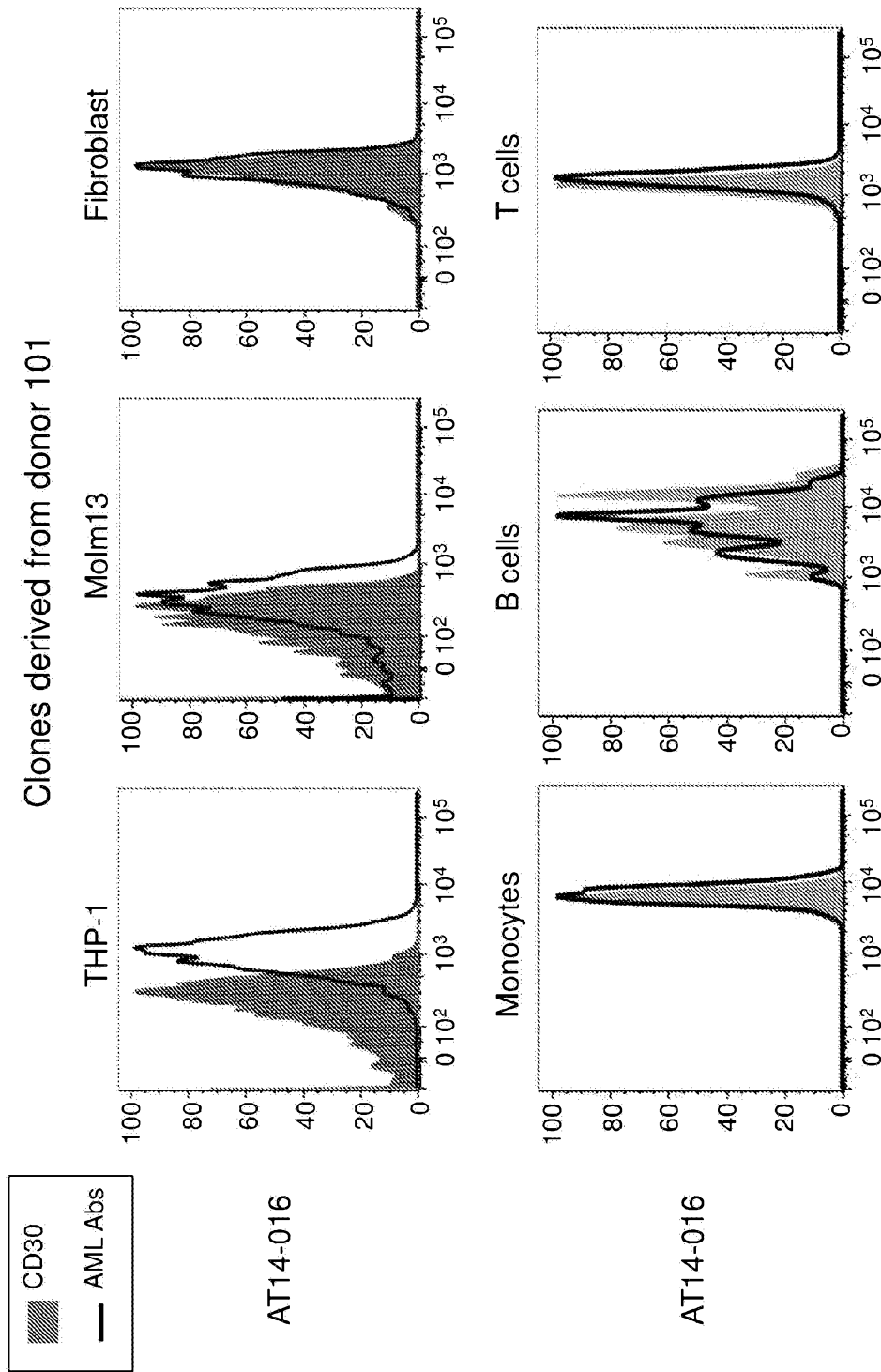


FIG. 14, Cont'd

AT14-013 binds primary AML blasts

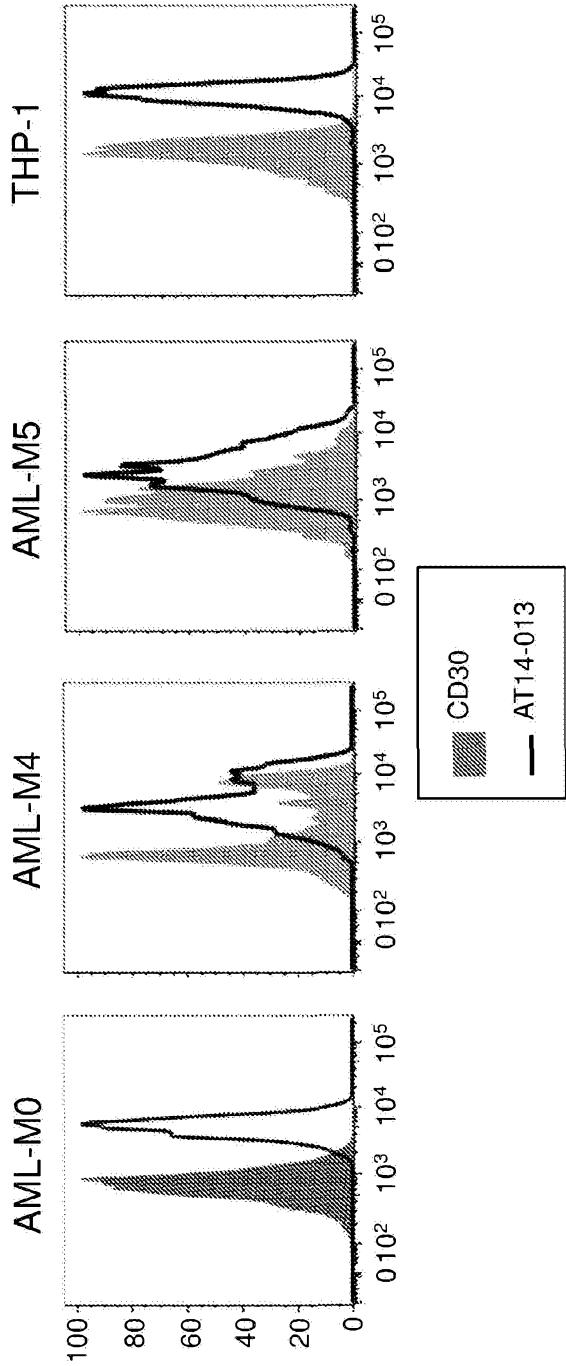


FIG. 15

Killing of primary blasts (AML M5)

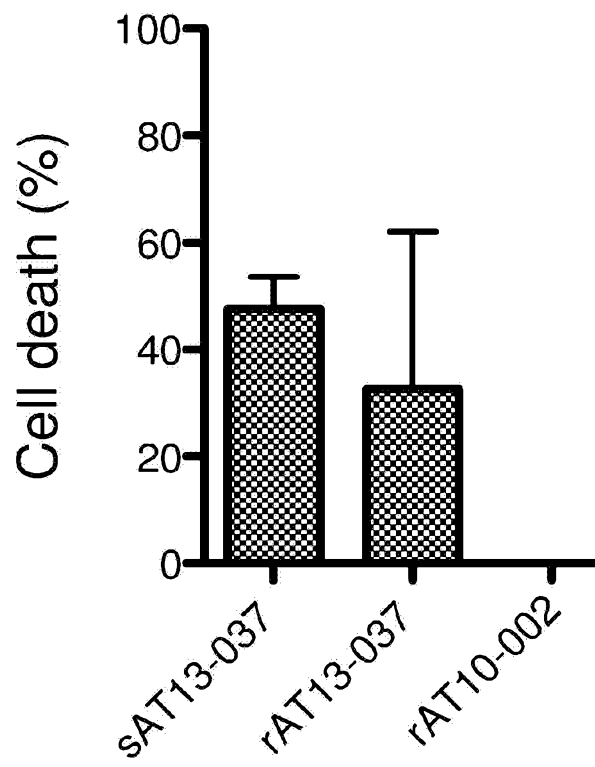
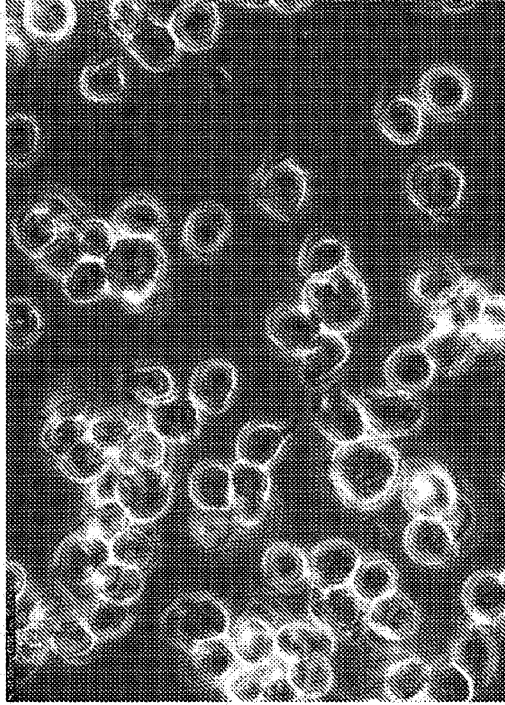


FIG. 16

Cytotoxic AML-specific antibodies induce death of THP-1 cells
(phase-contrast imaging)

AT13-023 (non-cytotoxic)



AT13-037 (cytotoxic)

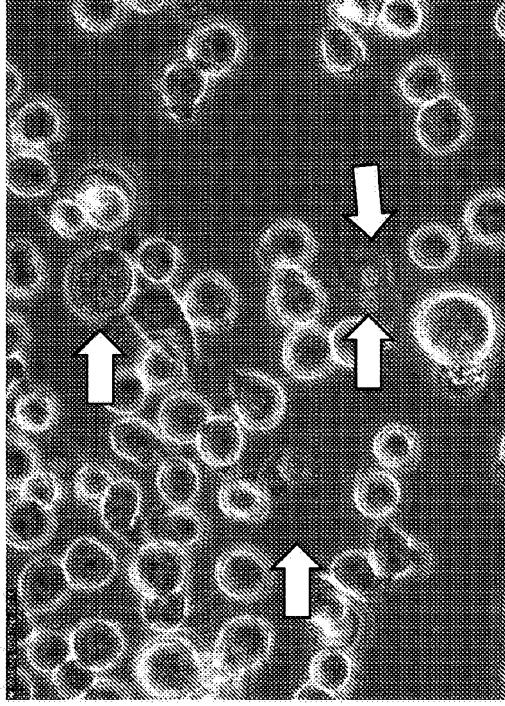


FIG. 17A

Cytotoxic antibodies do not induce apoptosis

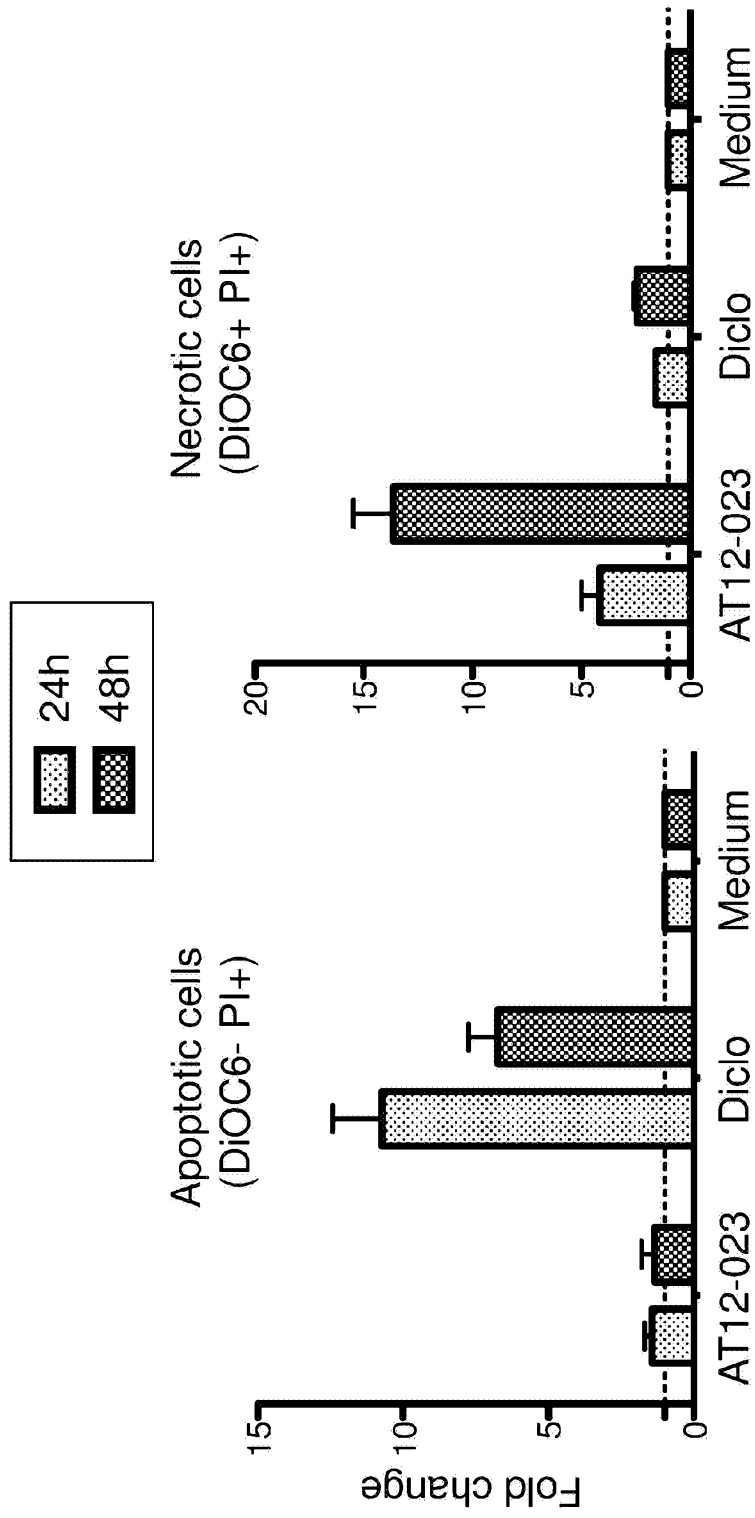
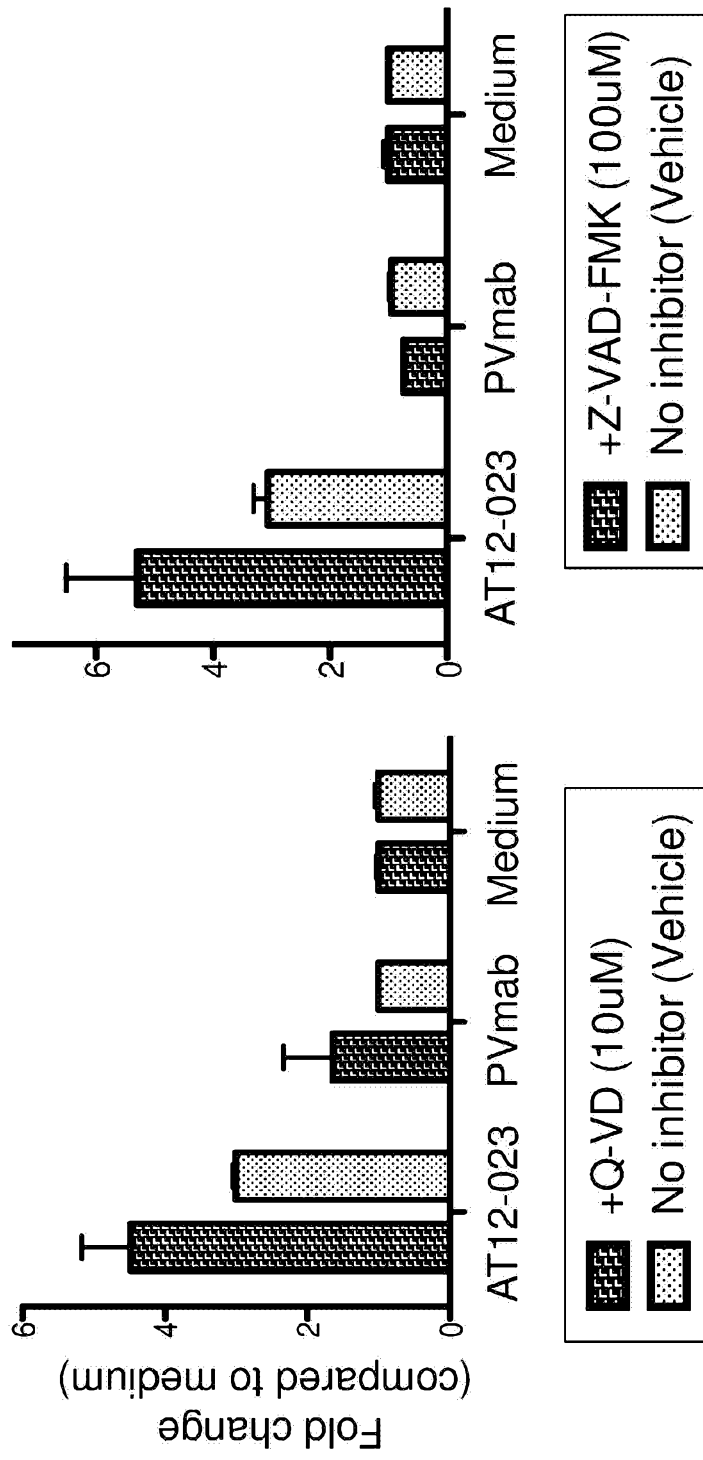


FIG. 17B

Inhibition of caspases does not block cell death



PVmab: palivizumab

FIG. 17C

Cell death is passive: also occurs at 4°C

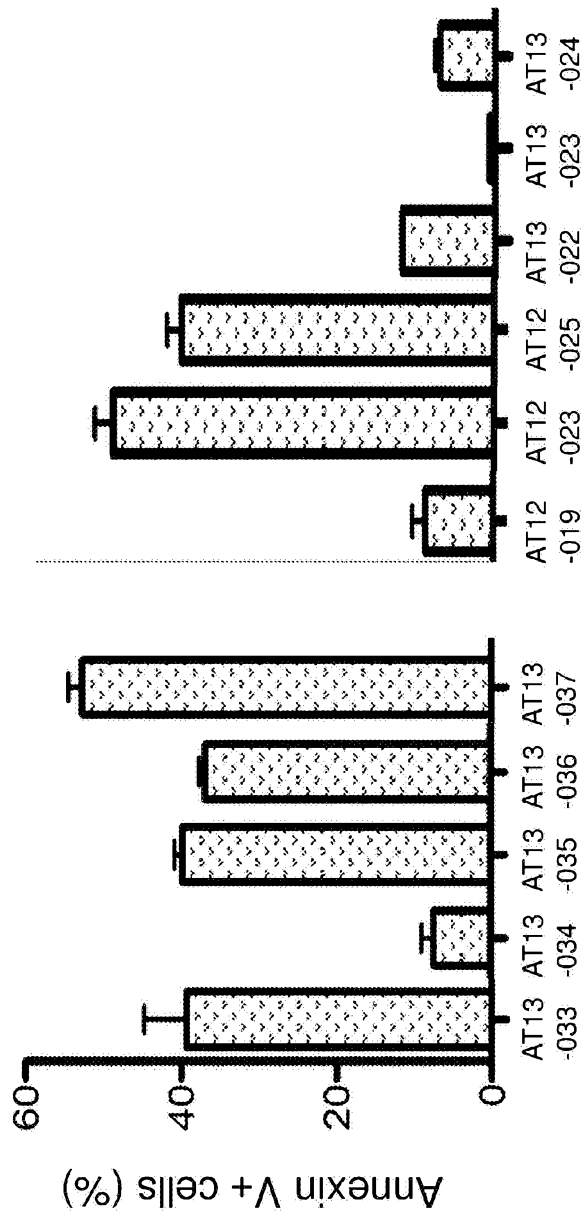


FIG. 18

Cytochalasin D does not prevent binding of the antibodies to the target cell membrane

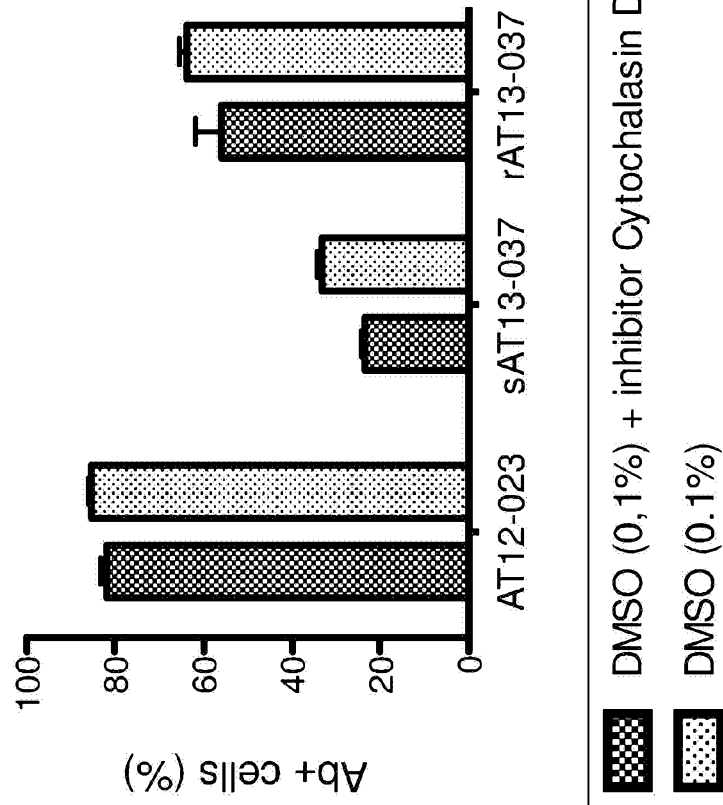


FIG. 19A

Cell death is prevented by stabilising
the target cell membrane

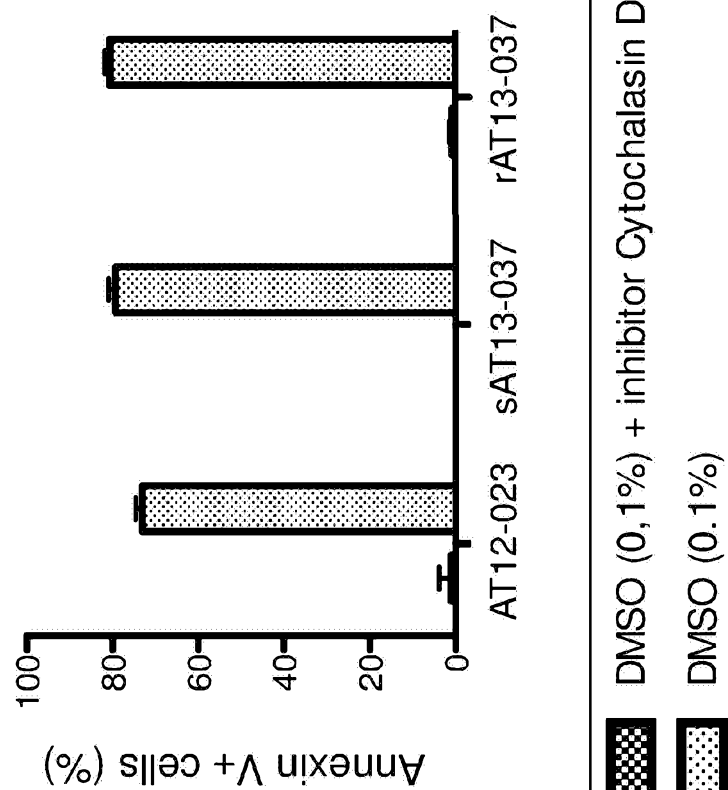


FIG. 19B

snRNP200:
the target of AT12-023 and AT13-031

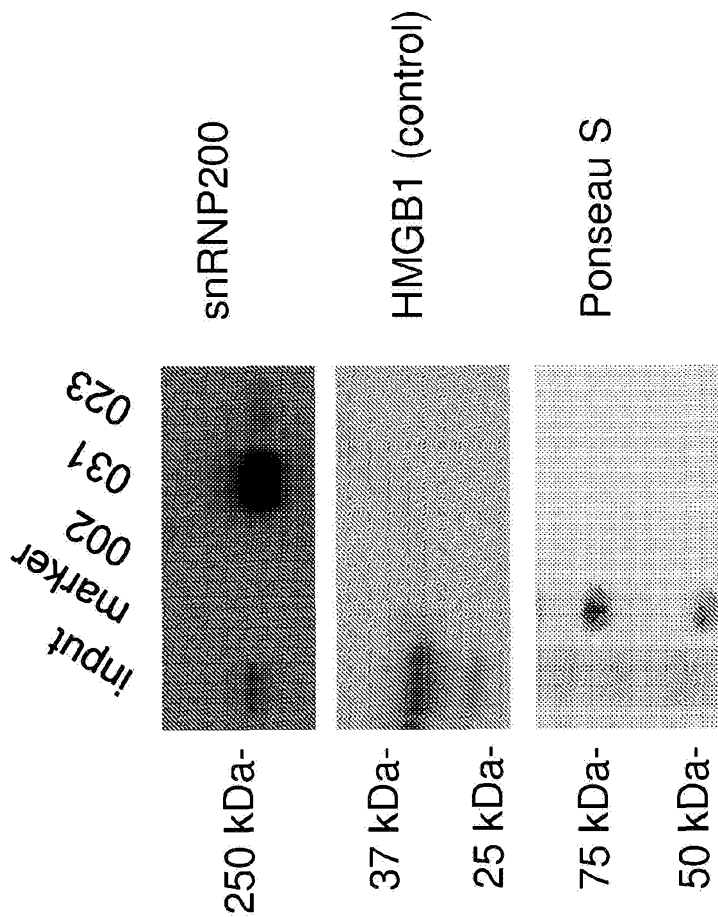


FIG. 20A

AT12-023, AT13-031 and AT13-037 bind
snRNP200 (snRNP200-ELISA)

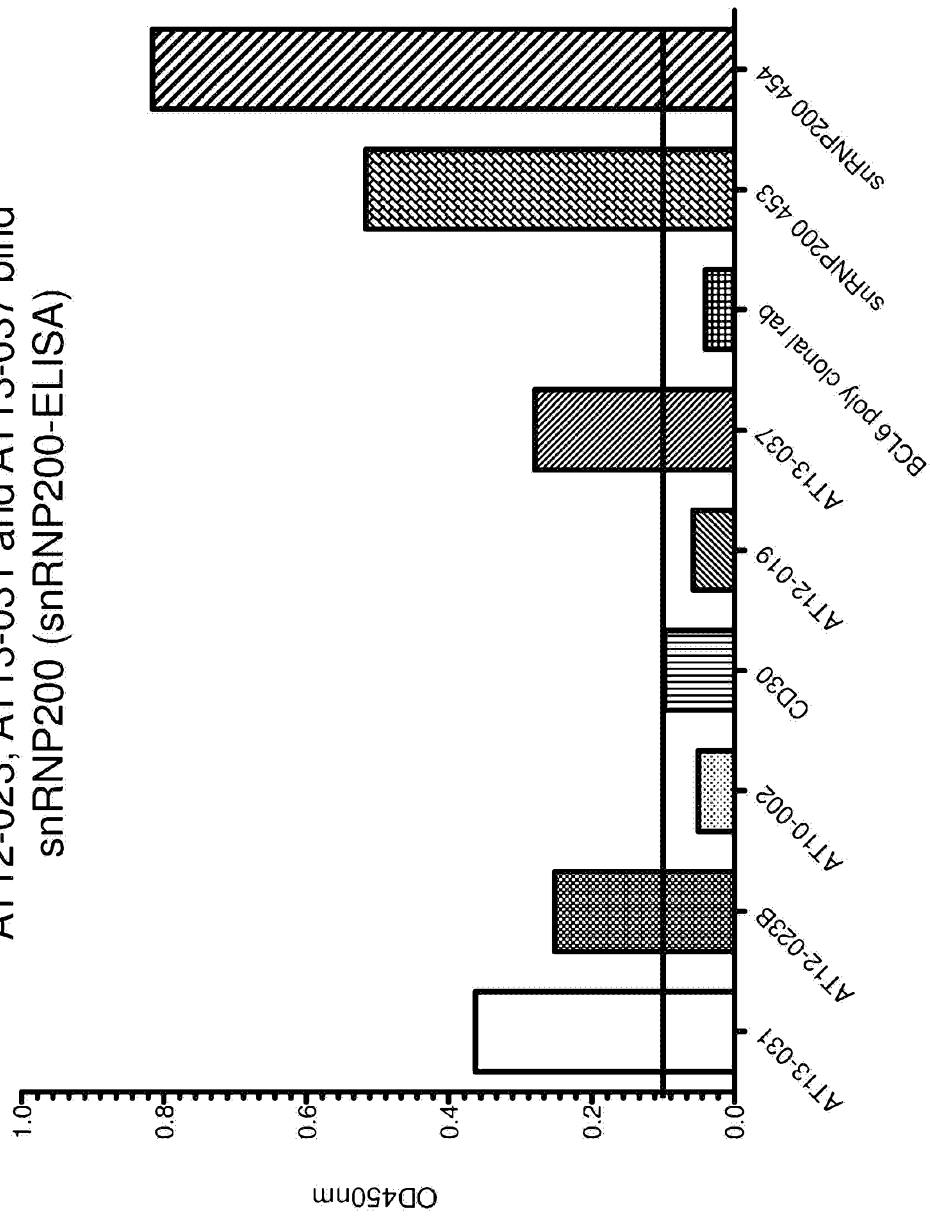


FIG. 20B

snRNP200 is a nuclear protein that is not expressed on the membrane of non-AML cells

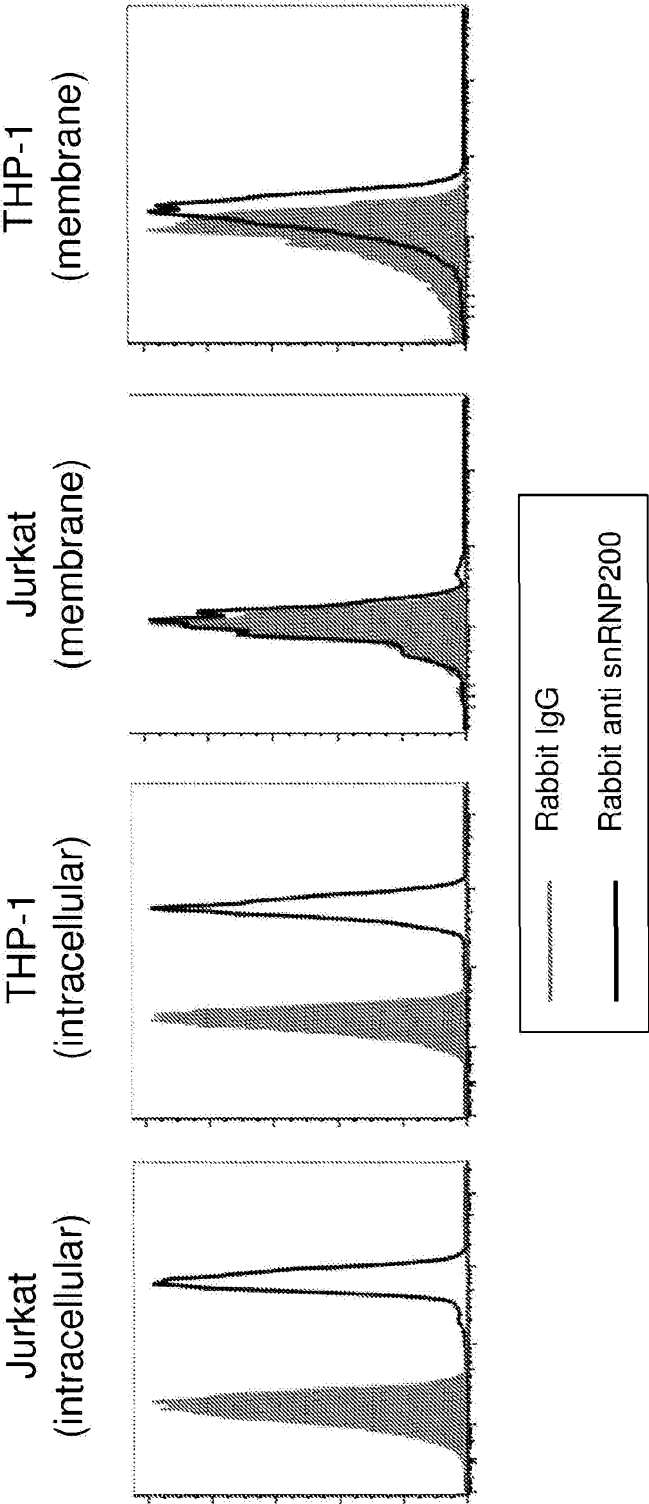


FIG. 21