



- (51) **International Patent Classification:**
C12Q 1/68 (2006.01)
- (21) **International Application Number:**
PCT/EP2016/073055
- (22) **International Filing Date:**
28 September 2016 (28.09.2016)
- (25) **Filing Language:** English
- (26) **Publication Language:** English
- (30) **Priority Data:**
EP15306522.2 29 September 2015 (29.09.2015) EP
EP16305888.6 12 July 2016 (12.07.2016) EP
- (71) **Applicants:** INSERM (INSTITUT NATIONAL DE LA SANTÉ ET DE LA RECHERCHE MÉDICALE) [FR/FR]; 101, rue de Tolbiac, 75013 Paris (FR). UNIVERSITÉ PARIS DIDEROT - PARIS 7 [FR/FR]; 5, rue Thomas Mann, 75013 Paris (FR). UNIVERSITÉ PIERRE ET MARIE CURIE (PARIS 6) [FR/FR]; 4, place Jussieu, 75005 Paris (FR). UNIVERSITÉ PARIS DESCARTES [FR/FR]; 12, rue de l'Ecole de Médecine, 75006 Paris (FR). LIGUE NATIONALE CONTRE LE CANCER [FR/FR]; 14 rue Corvisart, 75013 Paris (FR). ASSISTANCE PUBLIQUE-HÔPITAUX DE PARIS (APHP) [FR/FR]; 3, avenue Victoria, 75004 Paris (FR).
- (72) **Inventors:** FRIDMAN, Wolf Herman; Centre de Recherche les Cordeliers / INSERM U1138, 15 rue de l'Ecole de Médecine, 75270 Paris (FR). DE REYNIES, Aurélien; Ligue Nationale Contre le Cancer, Programme CIT, 14 rue Corvisart, 75013 Paris (FR). BECHT, Etienne; INSERM
- UMRS1138, Equipe 13, 15 rue de l'Ecole de Médecine, 75006 Paris (FR).
- (74) **Agent:** COLLIN, Matthieu; Inserm Transfert 7 rue Watt, 75013 Paris (FR).
- (81) **Designated States** (unless otherwise indicated, for every kind of national protection available): AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JP, KE, KG, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.
- (84) **Designated States** (unless otherwise indicated, for every kind of regional protection available): ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM, TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).
- Published:**
— with international search report (Art. 21(3))



WO 2017/055324 A1

(54) **Title:** METHODS FOR QUANTIFYING THE POPULATION OF CELLS OF MONOCYTIC ORIGIN IN A TISSUE SAMPLE

(57) **Abstract:** The present invention relates to methods for quantifying the population of cells of monocytic origin in a tissue sample. In particular, the present invention relates to a method for quantifying the population of cells of monocytic origin in a tissue sample obtained from a subject comprising determining the expression level of at least one gene selected from the group consisting of CSF1R, ADAP2, RASSF4, FPR3, TFEC, PLA2G7 and KYNU.

METHODS FOR QUANTIFYING THE POPULATION OF CELLS OF MONOCYTIC ORIGIN IN A TISSUE SAMPLE

5 **FIELD OF THE INVENTION:**

The present invention relates to methods for quantifying the population of cells of monocytic origin in a tissue sample.

10 **BACKGROUND OF THE INVENTION:**

10 Tumors grow within a microenvironment composed of immune cells, endothelial cells, fibroblasts and adjacent normal tissue. The composition of the tumor microenvironment is of paramount importance during tumor development. Notably, infiltration by cells of the adaptive immune system helps control tumor growth and correlate with a favorable clinical outcome in most cancers. A consensual result is that infiltration with memory CD8⁺ T cells is associated
15 with a favorable patient's outcome. However, there are exceptions to this rule. Notably, in clear cell renal cell carcinoma (ccRCC), where angiogenesis is highly due to mutations disrupting the HIF pathway regulating the cellular response to hypoxia, tumor-infiltration by CD8⁺ T cells is associated with a poor prognosis for the patient. To understand this surprising result, the inventors recently performed a comprehensive characterization of the microenvironmental
20 components associated to CD8⁺ T cells' infiltration in ccRCC. It appeared that in this malignancy, CD8⁺ T cells infiltration is associated with a strong infiltration by other immune cells, including B cells and cells of monocytic origin. Conversely, in colorectal cancer (CRC), it is well known that infiltration by CD8⁺ T cells is associated with a favorable outcome. This disease is also highly heterogeneous in terms of tumor-cell phenotypes, as up to six molecular
25 subgroups have been described, which differ in carcinogenesis pathways, methylation profile, DNA mutational burden, and prognosis. The subgroup with the best prognosis featured a strong infiltration by cytotoxic lymphocytes. Surprisingly, the worst-prognosis subgroup also displayed a strong immune infiltration, with intermediate expression of lymphocytes' markers and a strong myeloid component, as well as a high signature of endothelial cells and fibroblasts.
30 Further analysis revealed an increased expression of pro-inflammatory and pro-angiogenic molecules in this subgroup, which appear to originate from microenvironment's fibroblasts. Altogether, these data underline the importance of a full characterization of the immune, endothelial and fibroblastic components of the microenvironment to decipher interactions

between these cell types and deliver therapies aimed at orienting inflammatory microenvironments towards a more immuneresponsive state.

SUMMARY OF THE INVENTION:

5 The present invention relates to methods for quantifying the population of cells of monocytic origin in a tissue sample. In particular, the present invention is defined by the claims.

DETAILED DESCRIPTION OF THE INVENTION:

10 The tumor microenvironment is a complex tissue which contains many distinct cell populations, and whose composition may predict prognosis and response to therapies. In the present disclosure, using samples of purified cell populations, the inventors defined specific and robust transcriptomic markers of the immune and stromal cell populations of the tumor microenvironment, and they quantitatively validated them in an in-vitro RNA mixture model.

15 For this purpose, they developed the ‘Microenvironment Cell Populations-counter’ (MCP-counter) method, which, using transcriptomic data, allows a robust quantification of the abundance of immune and stromal populations in cellularly heterogeneous tissues. They present in-vitro and ex-vivo data supporting the validity of this method’s estimates and they apply MCP-counter to draw a global picture of immune infiltrates across human healthy tissues and non-hematopoietic tumors, and to confirm recently-identified microenvironment-based cancer
20 stratifications associated with overall-survival in lung adenocarcinoma, colorectal, and breast cancers.

Accordingly a first object of the present invention relates to a method for quantifying the population of cells of monocytic origin in a tissue sample obtained from a subject
25 comprising determining the expression level of at least one gene selected from the group consisting of CSF1R, ADAP2, RASSF4, FPR3, TFEC, PLA2G7 and KYNU wherein the determined expression level indicates the quantity of the population of cells of monocytic origin in the tissue sample.

30 As used herein, the term “cells of monocytic origin” has its general meaning in the art. In particular, cells of monocytic origin include monocytes, macrophages and dendritic cells. Monocytes are immature myeloid cells which are mostly found in the blood. Upon stimulation by danger signals and/or cytokines, they differentiate into macrophages or myeloid dendritic cells. Macrophages are effector cells arising from monocytes upon entrance in tissues

from the peripheral blood. Their major function is phagocytosis, which is the internalization of cells, bacteria or other small bodies, which are then destroyed by acidification, action of proteases and reactive oxygen species. Macrophages are capable of low levels of antigen presentation to CD4+ T lymphocytes. Dendritic cells are specialized antigen-presenting cells (APC). Their names come from the long dendrites that extend from their bodies, which they use to sense surrounding molecular patterns. Dendritic cells are capable of phagocytosis, which enable them to present antigens originating from the extracellular milieu to CD4+ T lymphocytes, as well as to CD8+ T cells through a process known as antigen cross-presentation. Apart from phagocytosis, dendritic cells are also capable of macropynocytosis, which is the internalization of small volumes of extracellular fluids, whose antigenic content is subsequently processed and presented. Finally, dendritic cells can express co-stimulatory or co-inhibitory ligands, as well as a wide spectrum of cytokines, which depends on their state of maturation and the stimuli they received during maturation. These secondary signals will orientate the functionality of the dendritic cells-stimulated immune cells.

15

As used herein, the term "subject" denotes a mammal such as a rodent, a feline, a canine and a primate. Preferably, a subject according to the invention is a human.

As used herein, the term "tissue", when used in reference to a part of a body or of an organ, generally refers to an aggregation or collection of morphologically similar cells and associated accessory and support cells and intercellular matter, including extracellular matrix material, vascular supply, and fluids, acting together to perform specific functions in the body. There are generally four basic types of tissue in animals and humans including muscle, nerve, epithelial, and connective tissues.

25

In some embodiments, when the subject suffers from a cancer, the tissue sample is a tumor tissue sample. As used herein, the term "tumor tissue sample" means any tissue tumor sample derived from the patient. Said tissue sample is obtained for the purpose of the *in vitro* evaluation. In some embodiments, the tumor sample may result from the tumor resected from the patient. In some embodiments, the tumor sample may result from a biopsy performed in the primary tumour of the patient or performed in metastatic sample distant from the primary tumor of the patient. In some embodiments, the tumor tissue sample encompasses a global primary tumor (as a whole), a tissue sample from the center of the tumor, a tumor tissue sample collected prior surgery (for follow-up of patients after treatment for example), and a distant metastasis.

30

The tumor tissue sample can, of course, be subjected to a variety of well-known post-collection preparative and storage techniques (e.g., fixation, storage, freezing, etc.). The sample can be fresh, frozen, fixed (e.g., formalin fixed), or embedded (e.g., paraffin embedded).

5 In some embodiments, the subject suffers from a solid cancer selected from the group consisting of bile duct cancer (e.g. periphilar cancer, distal bile duct cancer, intrahepatic bile duct cancer), bladder cancer, bone cancer (e.g. osteoblastoma, osteochondroma, hemangioma, chondromyxoid fibroma, osteosarcoma, chondrosarcoma, fibrosarcoma, malignant fibrous histiocytoma, giant cell tumor of the bone, chordoma, lymphoma, multiple myeloma), brain
10 and central nervous system cancer (e.g. meningioma, astrocytoma, oligodendrogliomas, ependymoma, gliomas, medulloblastoma, ganglioglioma, Schwannoma, germinoma, craniopharyngioma), breast cancer (e.g. ductal carcinoma in situ, infiltrating ductal carcinoma, infiltrating, lobular carcinoma, lobular carcinoma in situ, gynecomastia), Castleman disease (e.g. giant lymph node hyperplasia, angiofollicular lymph node hyperplasia), cervical cancer,
15 colorectal cancer, endometrial cancer (e.g. endometrial adenocarcinoma, adenocanthoma, papillary serous adenocarcinoma, clear cell), esophagus cancer, gallbladder cancer (mucinous adenocarcinoma, small cell carcinoma), gastrointestinal carcinoid tumors (e.g. choriocarcinoma, chorioadenoma destruens), Hodgkin's disease, non-Hodgkin's lymphoma, Kaposi's sarcoma, kidney cancer (e.g. renal cell cancer), laryngeal and hypopharyngeal cancer,
20 liver cancer (e.g. hemangioma, hepatic adenoma, focal nodular hyperplasia, hepatocellular carcinoma), lung cancer (e.g. small cell lung cancer, non-small cell lung cancer), mesothelioma, plasmacytoma, nasal cavity and paranasal sinus cancer (e.g. esthesioneuroblastoma, midline granuloma), nasopharyngeal cancer, neuroblastoma, oral cavity and oropharyngeal cancer, ovarian cancer, pancreatic cancer, penile cancer, pituitary cancer, prostate cancer,
25 retinoblastoma, rhabdomyosarcoma (e.g. embryonal rhabdomyosarcoma, alveolar rhabdomyosarcoma, pleomorphic rhabdomyosarcoma), salivary gland cancer, skin cancer (e.g. melanoma, nonmelanoma skin cancer), stomach cancer, testicular cancer (e.g. seminoma, nonseminoma germ cell cancer), thymus cancer, thyroid cancer (e.g. follicular carcinoma, anaplastic carcinoma, poorly differentiated carcinoma, medullary thyroid carcinoma, thyroid
30 lymphoma), vaginal cancer, vulvar cancer, and uterine cancer (e.g. uterine leiomyosarcoma).

In the present specification, the name of each of the genes of interest refers to the internationally recognised name of the corresponding gene, as found in internationally recognised gene sequences and protein sequences databases, in particular in the database from

the HUGO Gene Nomenclature Committee, that is available notably at the following Internet address : <http://www.gene.ucl.ac.uk/nomenclature/index.html>. In the present specification, the name of each of the various biological markers of interest may also refer to the internationally recognised name of the corresponding gene, as found in the internationally recognised gene sequences and protein sequences databases ENTREZ ID, Genbank, TrEMBL or ENSEMBL. Through these internationally recognised sequence databases, the nucleic acid sequences corresponding to each of the gene of interest described herein may be retrieved by the one skilled in the art. For avoidance of doubt, each gene of the present invention is characterized with the probe set name available at the following Internet address <http://genecards.weizmann.ac.il/geneannot/index.shtml> and their access number available on <http://www.ncbi.nlm.nih.gov/gene/> : (see Table A).

| Probeset | Signature | Symbol | ENTREZ ID |
|--------------|-------------------------|--------------------------|-----------------------|
| 215784_at | Myeloid dendritic cells | CD1E | 913 |
| 206682_at | Myeloid dendritic cells | CLEC10A | 10462 |
| 213415_at | Myeloid dendritic cells | CLIC2 | 1193 |
| 210325_at | Myeloid dendritic cells | CD1A | 909 |
| 229566_at | Myeloid dendritic cells | WFDC21P | 645638 |
| 206749_at | Myeloid dendritic cells | CD1B | 910 |
| 217418_x_at | B cells | MS4A1 | 931 |
| 206398_s_at | B cells | CD19 | 930 |
| 1555779_a_at | B cells | CD79A | 973 |
| 221239_s_at | B cells | FCRL2 | 79368 |
| 205544_s_at | B cells | CR2 | 1380 |
| 221969_at | B cells | PAX5 | 5079 |
| 204581_at | B cells | CD22 | 933 |
| 1558662_s_at | B cells | BANK1 | 55024 |
| 216207_x_at | B cells | IGKC | 3514 |
| 1555691_a_at | Cytotoxic lymphocytes | KLRC4-KLRK1 /// KLRK1 | 100528032 // 22914 |
| 205758_at | Cytotoxic lymphocytes | CD8A | 925 |
| 210606_x_at | Cytotoxic lymphocytes | KLRD1 | 3824 |
| 37145_at | Cytotoxic lymphocytes | GNLY | 10578 |
| 231776_at | Cytotoxic lymphocytes | EOMES | 8320 |
| 207723_s_at | Cytotoxic lymphocytes | KLRC3 | 3823 |
| 210690_at | Cytotoxic lymphocytes | KLRC4 | 8302 |
| 223836_at | Cytotoxic lymphocytes | FGFBP2 | 83888 |
| 206785_s_at | Cytotoxic lymphocytes | KLRC1 /// KLRC2 | 3821 // 3822 |

| | | | |
|--------------|---------------------------|---------------------------|--------|
| 211813_x_at | Fibroblasts | DCN | 1634 |
| 209156_s_at | Fibroblasts | COL6A2 | 1292 |
| 212091_s_at | Fibroblasts | COL6A1 | 1291 |
| 201852_x_at | Fibroblasts | COL3A1 | 1281 |
| 202311_s_at | Fibroblasts | COL1A1 | 1277 |
| 213661_at | Fibroblasts | PAMR1 | 25891 |
| 205547_s_at | Fibroblasts | TAGLN | 6876 |
| 218468_s_at | Fibroblasts | GREM1 | 26585 |
| 207008_at | Neutrophils | CXCR2 | 3579 |
| 220528_at | Neutrophils | VNN3 | 55350 |
| 206515_at | Neutrophils | CYP4F3 | 4051 |
| 206643_at | Neutrophils | HAL | 3034 |
| 216782_at | Neutrophils | GENE 1 (*) (Hs.677385) | - |
| 204007_at | Neutrophils | FCGR3B | 2215 |
| 210119_at | Neutrophils | KCNJ15 | 3772 |
| 207094_at | Neutrophils | CXCR1 | 3577 |
| 220187_at | Neutrophils | STEAP4 | 79689 |
| 206222_at | Neutrophils | TNFRSF10C | 8794 |
| 203104_at | Cells of monocytic origin | CSF1R | 1436 |
| 219358_s_at | Cells of monocytic origin | ADAP2 | 55803 |
| 226436_at | Cells of monocytic origin | RASSF4 | 83937 |
| 230422_at | Cells of monocytic origin | FPR3 | 2359 |
| 232383_at | Cells of monocytic origin | TFEC | 22797 |
| 206214_at | Cells of monocytic origin | PLA2G7 | 7941 |
| 204385_at | Cells of monocytic origin | KYNU | 8942 |
| 210890_x_at | NK cells | KIR2DL1 | 3802 |
| 208179_x_at | NK cells | KIR2DL3 | 3804 |
| 217088_s_at | NK cells | NCR1 | 9437 |
| 211687_x_at | NK cells | KIR3DL1 | 3811 |
| 211389_x_at | NK cells | KIR3DS1 | 3813 |
| 207313_x_at | NK cells | KIR3DL2 | 3812 |
| 1553177_at | NK cells | SH2D1B | 117157 |
| 207840_at | NK cells | CD160 | 11126 |
| 237542_at | NK cells | GENE 2 (*) (Hs.607854) | - |
| 208426_x_at | NK cells | KIR2DL4 | 3805 |
| 217147_s_at | T cells | TRAT1 | 50852 |
| 213539_at | T cells | CD3D | 915 |
| 1558972_s_at | T cells | THEMIS | 387357 |
| 210439_at | T cells | ICOS | 29851 |
| 220485_s_at | T cells | SIRPG | 55423 |
| 206804_at | T cells | CD3G | 917 |
| 236341_at | T cells | CTLA4 | 1493 |
| 213958_at | T cells | CD6 | 923 |
| 230489_at | T cells | CD5 | 921 |
| 206545_at | T cells | CD28 | 940 |

| | | | |
|-------------|-------------------|---------|--------|
| 204677_at | Endothelial cells | CDH5 | 1003 |
| 222885_at | Endothelial cells | EMCN | 51705 |
| 231947_at | Endothelial cells | MYCT1 | 80177 |
| 219134_at | Endothelial cells | ELTD1 | 64123 |
| 226028_at | Endothelial cells | ROBO4 | 54538 |
| 226244_at | Endothelial cells | CLEC14A | 161198 |
| 202112_at | Endothelial cells | VWF | 7450 |
| 225369_at | Endothelial cells | ESAM | 90952 |
| 219091_s_at | Endothelial cells | MMRN2 | 79812 |
| 203934_at | Endothelial cells | KDR | 3791 |

Table A: correspondence between the gene name and the probe set name. (*) indicates that the probeset does not correspond to a known gene that is referenced in the present disclosure as GENE 1 and GENE 2

5

In some embodiments, the expression level of 2, 3, 4, 5, 6 or 7 genes is determined. Typically, the combination of genes is selected from the Table 1.

In some embodiments, the method of the present invention further comprises
10 quantifying at least one further population of cells in the tissue sample.

In some embodiments, the at least one population of cells is selected from the group consisting of B cells, T cells, NK cells, cytotoxic lymphocytes, neutrophils, myeloid dendritic cells, fibroblasts and endothelial cells (includes lymphatics and blood vessels).

15

In some embodiments, the method of the present invention further comprises determining the expression level of at least one gene representative of B cells selected from the group consisting of MS4A1, CD19, CD79A, FCRL2, CR2, PAX5, CD22, BANK1 and IGKC.

20 In some embodiments, the method of the present invention further comprises determining the expression level of at least one gene representative of T cells selected from the group consisting of TRAT1, CD3D, THEMIS, ICOS, SIRPG, CD3G, CTLA4, CD6, CD5 and CD28.

25 In some embodiments, the method of the present invention further comprises determining the expression level of at least one gene representative of NK cells selected from

the group consisting of KIR2DL1, KIR2DL3, NCR1, KIR3DL1, KIR3DS1, KIR3DL2, SH2D1B, CD160, GENE 2 and KIR2DL4.

In some embodiments, the method of the present invention further comprises
5 determining the expression level of at least one gene representative of cytotoxic lymphocytes selected from the group consisting of KLRC4-KLRK1 /// KLRK1, CD8A, KLRD1, GNLY, EOMES, KLRC3, KLRC4, FGFBP2 and KLRC1 /// KLRC2.

In some embodiments, the method of the present invention further comprises
10 determining the expression level of at least one gene representative of neutrophils selected from the group consisting of CXCR2, VNN3 CYP4F3, HAL, GENE 1, FCGR3B, KCNJ15, CXCR1, STEAP4 and TNFRSF10C.

In some embodiments, the method of the present invention further comprises
15 determining the expression level of at least one gene representative of myeloid dendritic cells selected from the group consisting of CD1E, CLEC10A, CLIC2, CD1A, WFDC21P and CD1B.

In some embodiments, the method of the present invention further comprises
20 determining the expression level of at least one gene representative of fibroblasts selected from the group consisting of DCN, COL6A2, COL6A1, COL3A1, COL1A1, PAMR1, TAGLN and GREM1.

In some embodiments, the method of the present invention further comprises
25 determining the expression level of at least one gene representative of endothelial cells selected from the group consisting of CDH5, EMCN, MYCT1, ELTD1, ROBO4, CLEC14A, VWF, ESAM, MMRN2 and KDR.

Typically, the expression level of a gene is determined by determining the quantity of mRNA. Methods for determining the quantity of mRNA are well known in the art. For example
30 the nucleic acid contained in the samples (e.g., cell or tissue prepared from the subject) is first extracted according to standard methods, for example using lytic enzymes or chemical solutions or extracted by nucleic-acid-binding resins following the manufacturer's instructions. The extracted mRNA is then detected by hybridization (e. g., Northern blot analysis, in situ hybridization) and/or amplification (e.g., RT-PCR). Other methods of Amplification include

ligase chain reaction (LCR), transcription-mediated amplification (TMA), strand displacement amplification (SDA) and nucleic acid sequence based amplification (NASBA).

5 Nucleic acids having at least 10 nucleotides and exhibiting sequence complementarity or homology to the mRNA of interest herein find utility as hybridization probes or amplification primers. It is understood that such nucleic acids need not be identical, but are typically at least about 80% identical to the homologous region of comparable size, more preferably 85% identical and even more preferably 90-95% identical. In some embodiments, it will be advantageous to use nucleic acids in combination with appropriate means, such as a detectable
10 label, for detecting hybridization.

Typically, the nucleic acid probes include one or more labels, for example to permit detection of a target nucleic acid molecule using the disclosed probes. In various applications, such as in situ hybridization procedures, a nucleic acid probe includes a label (e.g., a detectable
15 label). A “detectable label” is a molecule or material that can be used to produce a detectable signal that indicates the presence or concentration of the probe (particularly the bound or hybridized probe) in a sample. Thus, a labeled nucleic acid molecule provides an indicator of the presence or concentration of a target nucleic acid sequence (e.g., genomic target nucleic acid sequence) (to which the labeled uniquely specific nucleic acid molecule is bound or
20 hybridized) in a sample. A label associated with one or more nucleic acid molecules (such as a probe generated by the disclosed methods) can be detected either directly or indirectly. A label can be detected by any known or yet to be discovered mechanism including absorption, emission and/ or scattering of a photon (including radio frequency, microwave frequency, infrared frequency, visible frequency and ultra-violet frequency photons). Detectable labels
25 include colored, fluorescent, phosphorescent and luminescent molecules and materials, catalysts (such as enzymes) that convert one substance into another substance to provide a detectable difference (such as by converting a colorless substance into a colored substance or vice versa, or by producing a precipitate or increasing sample turbidity), haptens that can be detected by antibody binding interactions, and paramagnetic and magnetic molecules or
30 materials.

Particular examples of detectable labels include fluorescent molecules (or fluorochromes). Numerous fluorochromes are known to those of skill in the art, and can be selected, for example from Life Technologies (formerly Invitrogen), e.g., see, The Handbook—

A Guide to Fluorescent Probes and Labeling Technologies). Examples of particular fluorophores that can be attached (for example, chemically conjugated) to a nucleic acid molecule (such as a uniquely specific binding region) are provided in U.S. Pat. No. 5,866,366 to Nazarenko et al., such as 4-acetamido-4'-isothiocyanatostilbene-2,2'-disulfonic acid, acridine and derivatives such as acridine and acridine isothiocyanate, 5-(2'-aminoethyl) aminonaphthalene-1-sulfonic acid (EDANS), 4-amino-N-[3 vinylsulfonyl]phenyl]naphthalimide-3,5 disulfonate (Lucifer Yellow VS), N-(4-anilino-1-naphthyl)maleimide, antirranilamide, Brilliant Yellow, coumarin and derivatives such as coumarin, 7-amino-4-methylcoumarin (AMC, Coumarin 120), 7-amino-4-trifluoromethylcoumarin (Coumarin 151); cyanosine; 4',6-diaminidino-2-phenylindole (DAPI); 5',5''dibromopyrogallol-sulfonephthalein (Bromopyrogallol Red); 7-diethylamino-3-(4'-isothiocyanatophenyl)-4-methylcoumarin; diethylenetriamine pentaacetate; 4,4'-diisothiocyanatodihydro-stilbene-2,2'-disulfonic acid; 4,4'-diisothiocyanatostilbene-2,2'-disulfonic acid; 5-[dimethylamino] naphthalene-1-sulfonyl chloride (DNS, dansyl chloride); 4-(4'-dimethylaminophenylazo)benzoic acid (DABCYL); 4-dimethylaminophenylazophenyl-4'-isothiocyanate (DABITC); eosin and derivatives such as eosin and eosin isothiocyanate; erythrosin and derivatives such as erythrosin B and erythrosin isothiocyanate; ethidium; fluorescein and derivatives such as 5-carboxyfluorescein (FAM), 5-(4,6-dichlorotriazin-2-yl)aminofluorescein (DTAF), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein (JOE), fluorescein, fluorescein isothiocyanate (FITC), and QFITC (RITC); 2',7'-difluorofluorescein (OREGON GREEN®); fluorescamine; IR144; IR1446; Malachite Green isothiocyanate; 4-methylumbelliferone; ortho cresolphthalein; nitrotyrosine; pararosaniline; Phenol Red; B-phycoerythrin; o-phthalaldehyde; pyrene and derivatives such as pyrene, pyrene butyrate and succinimidyl 1-pyrene butyrate; Reactive Red 4 (Cibacron Brilliant Red 3B-A); rhodamine and derivatives such as 6-carboxy-X-rhodamine (ROX), 6-carboxyrhodamine (R6G), lissamine rhodamine B sulfonyl chloride, rhodamine (Rhod), rhodamine B, rhodamine 123, rhodamine X isothiocyanate, rhodamine green, sulforhodamine B, sulforhodamine 101 and sulfonyl chloride derivative of sulforhodamine 101 (Texas Red); N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA); tetramethyl rhodamine; tetramethyl rhodamine isothiocyanate (TRITC); riboflavin; rosolic acid and terbium chelate derivatives. Other suitable fluorophores include thiol-reactive europium chelates which emit at approximately 617 nm (Heyduk and Heyduk, *Analyt. Biochem.* 248:216-27, 1997; *J. Biol. Chem.* 274:3315-22, 1999), as well as GFP, Lissamine™, diethylaminocoumarin, fluorescein chlorotriazinyl, naphthofluorescein, 4,7-dichlororhodamine and xanthene (as described in U.S. Pat. No. 5,800,996 to Lee et al.) and derivatives thereof.

Other fluorophores known to those skilled in the art can also be used, for example those available from Life Technologies (Invitrogen; Molecular Probes (Eugene, Oreg.)) and including the ALEXA FLUOR® series of dyes (for example, as described in U.S. Pat. Nos. 5,696,157, 6, 130, 101 and 6,716,979), the BODIPY series of dyes (dipyrometheneboron difluoride dyes, for example as described in U.S. Pat. Nos. 4,774,339, 5,187,288, 5,248,782, 5,274,113, 5,338,854, 5,451,663 and 5,433,896), Cascade Blue (an amine reactive derivative of the sulfonated pyrene described in U.S. Pat. No. 5,132,432) and Marina Blue (U.S. Pat. No. 5,830,912).

10 In addition to the fluorochromes described above, a fluorescent label can be a fluorescent nanoparticle, such as a semiconductor nanocrystal, e.g., a QUANTUM DOT™ (obtained, for example, from Life Technologies (QuantumDot Corp, Invitrogen Nanocrystal Technologies, Eugene, Oreg.); see also, U.S. Pat. Nos. 6,815,064; 6,682,596; and 6,649, 138). Semiconductor nanocrystals are microscopic particles having size-dependent optical and/or
15 electrical properties. When semiconductor nanocrystals are illuminated with a primary energy source, a secondary emission of energy occurs of a frequency that corresponds to the bandgap of the semiconductor material used in the semiconductor nanocrystal. This emission can be detected as colored light of a specific wavelength or fluorescence. Semiconductor nanocrystals with different spectral characteristics are described in e.g., U.S. Pat. No. 6,602,671.
20 Semiconductor nanocrystals that can be coupled to a variety of biological molecules (including dNTPs and/or nucleic acids) or substrates by techniques described in, for example, Bruchez et al., Science 281 :20132016, 1998; Chan et al., Science 281:2016-2018, 1998; and U.S. Pat. No. 6,274,323. Formation of semiconductor nanocrystals of various compositions are disclosed in, e.g., U.S. Pat. Nos. 6,927, 069; 6,914,256; 6,855,202; 6,709,929; 6,689,338; 6,500,622;
25 6,306,736; 6,225,198; 6,207,392; 6,114,038; 6,048,616; 5,990,479; 5,690,807; 5,571,018; 5,505,928; 5,262,357 and in U.S. Patent Publication No. 2003/0165951 as well as PCT Publication No. 99/26299 (published May 27, 1999). Separate populations of semiconductor nanocrystals can be produced that are identifiable based on their different spectral characteristics. For example, semiconductor nanocrystals can be produced that emit light of
30 different colors based on their composition, size or size and composition. For example, quantum dots that emit light at different wavelengths based on size (565 nm, 655 nm, 705 nm, or 800 nm emission wavelengths), which are suitable as fluorescent labels in the probes disclosed herein are available from Life Technologies (Carlsbad, Calif.).

Additional labels include, for example, radioisotopes (such as ^3H), metal chelates such as DOTA and DPTA chelates of radioactive or paramagnetic metal ions like Gd^{3+} , and liposomes.

5 Detectable labels that can be used with nucleic acid molecules also include enzymes, for example horseradish peroxidase, alkaline phosphatase, acid phosphatase, glucose oxidase, beta-galactosidase, beta-glucuronidase, or beta-lactamase.

10 Alternatively, an enzyme can be used in a metallographic detection scheme. For example, silver in situ hybridization (SISH) procedures involve metallographic detection schemes for identification and localization of a hybridized genomic target nucleic acid sequence. Metallographic detection methods include using an enzyme, such as alkaline phosphatase, in combination with a water-soluble metal ion and a redox-inactive substrate of the enzyme. The substrate is converted to a redox-active agent by the enzyme, and the
15 redoxactive agent reduces the metal ion, causing it to form a detectable precipitate. (See, for example, U.S. Patent Application Publication No. 2005/0100976, PCT Publication No. 2005/003777 and U.S. Patent Application Publication No. 2004/0265922). Metallographic detection methods also include using an oxido-reductase enzyme (such as horseradish peroxidase) along with a water soluble metal ion, an oxidizing agent and a reducing agent, again to form a
20 detectable precipitate. (See, for example, U.S. Pat. No. 6,670,113).

Probes made using the disclosed methods can be used for nucleic acid detection, such as ISH procedures (for example, fluorescence in situ hybridization (FISH), chromogenic in situ hybridization (CISH) and silver in situ hybridization (SISH)) or comparative genomic
25 hybridization (CGH).

In situ hybridization (ISH) involves contacting a sample containing target nucleic acid sequence (e.g., genomic target nucleic acid sequence) in the context of a metaphase or interphase chromosome preparation (such as a cell or tissue sample mounted on a slide) with a
30 labeled probe specifically hybridizable or specific for the target nucleic acid sequence (e.g., genomic target nucleic acid sequence). The slides are optionally pretreated, e.g., to remove paraffin or other materials that can interfere with uniform hybridization. The sample and the probe are both treated, for example by heating to denature the double stranded nucleic acids. The probe (formulated in a suitable hybridization buffer) and the sample are combined, under

conditions and for sufficient time to permit hybridization to occur (typically to reach equilibrium). The chromosome preparation is washed to remove excess probe, and detection of specific labeling of the chromosome target is performed using standard techniques.

5 For example, a biotinylated probe can be detected using fluorescein-labeled avidin or avidin-alkaline phosphatase. For fluorochrome detection, the fluorochrome can be detected directly, or the samples can be incubated, for example, with fluorescein isothiocyanate (FITC)-conjugated avidin. Amplification of the FITC signal can be effected, if necessary, by incubation with biotin-conjugated goat antiavidin antibodies, washing and a second incubation with FITC-
10 conjugated avidin. For detection by enzyme activity, samples can be incubated, for example, with streptavidin, washed, incubated with biotin-conjugated alkaline phosphatase, washed again and pre-equilibrated (e.g., in alkaline phosphatase (AP) buffer). For a general description of in situ hybridization procedures, see, e.g., U.S. Pat. No. 4,888,278.

15 Numerous procedures for FISH, CISH, and SISH are known in the art. For example, procedures for performing FISH are described in U.S. Pat. Nos. 5,447,841; 5,472,842; and 5,427,932; and for example, in Pir1kel et al., Proc. Natl. Acad. Sci. 83:2934-2938, 1986; Pinkel et al., Proc. Natl. Acad. Sci. 85:9138-9142, 1988; and Lichter et al., Proc. Natl. Acad. Sci. 85:9664-9668, 1988. CISH is described in, e.g., Tanner et al., Am. J. Pathol. 157:1467-1472,
20 2000 and U.S. Pat. No. 6,942,970. Additional detection methods are provided in U.S. Pat. No. 6,280,929.

Numerous reagents and detection schemes can be employed in conjunction with FISH, CISH, and SISH procedures to improve sensitivity, resolution, or other desirable properties. As
25 discussed above probes labeled with fluorophores (including fluorescent dyes and QUANTUM DOTS®) can be directly optically detected when performing FISH. Alternatively, the probe can be labeled with a nonfluorescent molecule, such as a hapten (such as the following non-limiting examples: biotin, digoxigenin, DNP, and various oxazoles, pyrrazoles, thiazoles, nitroaryls, benzofurazans, triterpenes, ureas, thioureas, rotenones, coumarin, coumarin-based
30 compounds, Podophyllotoxin, Podophyllotoxin-based compounds, and combinations thereof), ligand or other indirectly detectable moiety. Probes labeled with such non-fluorescent molecules (and the target nucleic acid sequences to which they bind) can then be detected by contacting the sample (e.g., the cell or tissue sample to which the probe is bound) with a labeled detection reagent, such as an antibody (or receptor, or other specific binding partner) specific

for the chosen hapten or ligand. The detection reagent can be labeled with a fluorophore (e.g., QUANTUM DOT®) or with another indirectly detectable moiety, or can be contacted with one or more additional specific binding agents (e.g., secondary or specific antibodies), which can be labeled with a fluorophore.

5

In other examples, the probe, or specific binding agent (such as an antibody, e.g., a primary antibody, receptor or other binding agent) is labeled with an enzyme that is capable of converting a fluorogenic or chromogenic composition into a detectable fluorescent, colored or otherwise detectable signal (e.g., as in deposition of detectable metal particles in SISH). As indicated above, the enzyme can be attached directly or indirectly via a linker to the relevant probe or detection reagent. Examples of suitable reagents (e.g., binding reagents) and chemistries (e.g., linker and attachment chemistries) are described in U.S. Patent Application Publication Nos. 2006/0246524; 2006/0246523, and 2007/ 01 17153.

It will be appreciated by those of skill in the art that by appropriately selecting labelled probe-specific binding agent pairs, multiplex detection schemes can be produced to facilitate detection of multiple target nucleic acid sequences (e.g., genomic target nucleic acid sequences) in a single assay (e.g., on a single cell or tissue sample or on more than one cell or tissue sample). For example, a first probe that corresponds to a first target sequence can be labelled with a first hapten, such as biotin, while a second probe that corresponds to a second target sequence can be labelled with a second hapten, such as DNP. Following exposure of the sample to the probes, the bound probes can be detected by contacting the sample with a first specific binding agent (in this case avidin labelled with a first fluorophore, for example, a first spectrally distinct QUANTUM DOT®, e.g., that emits at 585 nm) and a second specific binding agent (in this case an anti-DNP antibody, or antibody fragment, labelled with a second fluorophore (for example, a second spectrally distinct QUANTUM DOT®, e.g., that emits at 705 nm). Additional probes/binding agent pairs can be added to the multiplex detection scheme using other spectrally distinct fluorophores. Numerous variations of direct, and indirect (one step, two step or more) can be envisioned, all of which are suitable in the context of the disclosed probes and assays.

Probes typically comprise single-stranded nucleic acids of between 10 to 1000 nucleotides in length, for instance of between 10 and 800, more preferably of between 15 and 700, typically of between 20 and 500. Primers typically are shorter single-stranded nucleic

acids, of between 10 to 25 nucleotides in length, designed to perfectly or almost perfectly match a nucleic acid of interest, to be amplified. The probes and primers are “specific” to the nucleic acids they hybridize to, i.e. they preferably hybridize under high stringency hybridization conditions (corresponding to the highest melting temperature T_m , e.g., 50 % formamide, 5x or 5 6x SCC. SCC is a 0.15 M NaCl, 0.015 M Na-citrate).

The nucleic acid primers or probes used in the above amplification and detection method may be assembled as a kit. Such a kit includes consensus primers and molecular probes. A preferred kit also includes the components necessary to determine if amplification has occurred. 10 The kit may also include, for example, PCR buffers and enzymes; positive control sequences, reaction control primers; and instructions for amplifying and detecting the specific sequences.

In some embodiments, the methods of the invention comprise the steps of providing total RNAs extracted from cumulus cells and subjecting the RNAs to amplification and 15 hybridization to specific probes, more particularly by means of a quantitative or semi-quantitative RT-PCR.

In some embodiments, the level is determined by DNA chip analysis. Such DNA chip or nucleic acid microarray consists of different nucleic acid probes that are chemically attached 20 to a substrate, which can be a microchip, a glass slide or a microsphere-sized bead. A microchip may be constituted of polymers, plastics, resins, polysaccharides, silica or silica-based materials, carbon, metals, inorganic glasses, or nitrocellulose. Probes comprise nucleic acids such as cDNAs or oligonucleotides that may be about 10 to about 60 base pairs. To determine the level, a sample from a test subject, optionally first subjected to a reverse transcription, is 25 labelled and contacted with the microarray in hybridization conditions, leading to the formation of complexes between target nucleic acids that are complementary to probe sequences attached to the microarray surface. The labelled hybridized complexes are then detected and can be quantified or semi-quantified. Labelling may be achieved by various methods, e.g. by using radioactive or fluorescent labelling. Many variants of the microarray hybridization technology 30 are available to the man skilled in the art (see e.g. the review by Hoheisel, Nature Reviews, Genetics, 2006, 7:200-210).

In some embodiments, the nCounter® Analysis system is used to detect intrinsic gene expression. The basis of the nCounter® Analysis system is the unique code assigned to each

nucleic acid target to be assayed (International Patent Application Publication No. WO 08/124847, U.S. Patent No. 8,415,102 and Geiss et al. Nature Biotechnology. 2008. 26(3): 317-325; the contents of which are each incorporated herein by reference in their entireties). The code is composed of an ordered series of colored fluorescent spots which create a unique barcode for each target to be assayed. A pair of probes is designed for each DNA or RNA target, a biotinylated capture probe and a reporter probe carrying the fluorescent barcode. This system is also referred to, herein, as the nanoreporter code system. Specific reporter and capture probes are synthesized for each target. The reporter probe can comprise at a least a first label attachment region to which are attached one or more label monomers that emit light constituting a first signal; at least a second label attachment region, which is non-over-lapping with the first label attachment region, to which are attached one or more label monomers that emit light constituting a second signal; and a first target-specific sequence. Preferably, each sequence specific reporter probe comprises a target specific sequence capable of hybridizing to no more than one gene and optionally comprises at least three, or at least four label attachment regions, said attachment regions comprising one or more label monomers that emit light, constituting at least a third signal, or at least a fourth signal, respectively. The capture probe can comprise a second target-specific sequence; and a first affinity tag. In some embodiments, the capture probe can also comprise one or more label attachment regions. Preferably, the first target-specific sequence of the reporter probe and the second target-specific sequence of the capture probe hybridize to different regions of the same gene to be detected. Reporter and capture probes are all pooled into a single hybridization mixture, the "probe library". The relative abundance of each target is measured in a single multiplexed hybridization reaction. The method comprises contacting the tumor tissue sample with a probe library, such that the presence of the target in the sample creates a probe pair - target complex. The complex is then purified. More specifically, the sample is combined with the probe library, and hybridization occurs in solution. After hybridization, the tripartite hybridized complexes (probe pairs and target) are purified in a two-step procedure using magnetic beads linked to oligonucleotides complementary to universal sequences present on the capture and reporter probes. This dual purification process allows the hybridization reaction to be driven to completion with a large excess of target-specific probes, as they are ultimately removed, and, thus, do not interfere with binding and imaging of the sample. All post hybridization steps are handled robotically on a custom liquid-handling robot (Prep Station, NanoString Technologies). Purified reactions are typically deposited by the Prep Station into individual flow cells of a sample cartridge, bound to a streptavidin-coated surface via the capture probe, electrophoresed to elongate the reporter

probes, and immobilized. After processing, the sample cartridge is transferred to a fully automated imaging and data collection device (Digital Analyzer, NanoString Technologies). The level of a target is measured by imaging each sample and counting the number of times the code for that target is detected. For each sample, typically 600 fields-of-view (FOV) are imaged (1376 X 1024 pixels) representing approximately 10 mm² of the binding surface. Typical imaging density is 100- 1200 counted reporters per field of view depending on the degree of multiplexing, the amount of sample input, and overall target abundance. Data is output in simple spreadsheet format listing the number of counts per target, per sample. This system can be used along with nanoreporters. Additional disclosure regarding nanoreporters can be found in International Publication No. WO 07/076129 and WO07/076132, and US Patent Publication No. 2010/0015607 and 2010/0261026, the contents of which are incorporated herein in their entireties. Further, the term nucleic acid probes and nanoreporters can include the rationally designed (e.g. synthetic sequences) described in International Publication No. WO 2010/019826 and US Patent Publication No.2010/0047924, incorporated herein by reference in its entirety.

Expression level of a gene may be expressed as absolute level or normalized level. Typically, levels are normalized by correcting the absolute level of a gene by comparing its expression to the expression of a gene that is not a relevant for determining the cancer stage of the subject, e.g., a housekeeping gene that is constitutively expressed. Suitable genes for normalization include housekeeping genes such as the actin gene ACTB, ribosomal 18S gene, GUSB, PGK1 and TFRC. This normalization allows the comparison of the level in one sample, e.g., a subject sample, to another sample, or between samples from different sources.

In some embodiments, the method of the present invention comprises comparing the determined expression level with a panel of predetermined reference values that correlate with the quantity of the population of cells of monocytic origin determined in a reference tissue sample.

According to the present invention, the predetermined references values are determined from reference samples wherein the expression level of the gene(s) was (were) determined and adjusted with the exact quantification of the population of cells. Typically, a set of reference samples characterized using both gene expression and another measurement technique such as immunohistochemistry, flow cytometry, or RNA can be used for defining the panel of the

predetermined reference value. Mixtures of known cellular proportions also can be suitable for determining the predetermined reference values.

5 The method of the present invention is particularly suitable for determining the proportion of the population of cells of monocytic origin in the tissue sample. Typically, when at least one further population of cells is quantified as above described the proportion is determined by any well-known method in the art that typically involves use of algorithm based e.g. on regression models.

10 The method of the present invention is thus suitable for characterizing the immune, endothelial and fibroblastic components of the microenvironment of a tumor to decipher interactions between these cell types that can impact the progression of the tumor and eventually the subject's survival time. The method of the present invention is thus particularly suitable for determining the survival time of a subject suffering from a cancer. The method is thus
15 particularly suitable for predicting the duration of the overall survival (OS), progression-free survival (PFS) and/or the disease-free survival (DFS) of the cancer subject. Those of skill in the art will recognize that OS survival time is generally based on and expressed as the percentage of people who survive a certain type of cancer for a specific amount of time. Cancer statistics often use an overall five-year survival rate. In general, OS rates do not specify whether
20 cancer survivors are still undergoing treatment at five years or if they've become cancer-free (achieved remission). DFS gives more specific information and is the number of people with a particular cancer who achieve remission. Also, progression-free survival (PFS) rates (the number of people who still have cancer, but their disease does not progress) includes people who may have had some success with treatment, but the cancer has not disappeared completely.
25 As used herein, the expression "short survival time" indicates that the subject will have a survival time that will be lower than the median (or mean) observed in the general population of subjects suffering from said cancer. When the subject will have a short survival time, it is meant that the subject will have a "poor prognosis". Inversely, the expression "long survival time" indicates that the subject will have a survival time that will be higher than the median (or
30 mean) observed in the general population of subjects suffering from said cancer. When the subject will have a long survival time, it is meant that the subject will have a "good prognosis".

The method of the present invention is also suitable for determining whether a subject suffering from a cancer is eligible or not to anti-cancer treatment. Typically, the treatment

includes chemotherapy, radiotherapy, and immunotherapy. In particular, subject having a short survival time would advantageously receive an anti-cancer treatment.

As used herein, the term "treatment" or "treat" refer to both prophylactic or preventive
5 treatment as well as curative or disease modifying treatment, including treatment of subjects at risk of contracting the disease or suspected to have contracted the disease as well as subjects who are ill or have been diagnosed as suffering from a disease or medical condition, and includes suppression of clinical relapse. The treatment may be administered to a subject having a medical disorder or who ultimately may acquire the disorder, in order to prevent, cure, delay
10 the onset of, reduce the severity of, or ameliorate one or more symptoms of a disorder or recurring disorder, or in order to prolong the survival of a subject beyond that expected in the absence of such treatment. By "therapeutic regimen" is meant the pattern of treatment of an illness, e.g., the pattern of dosing used during therapy. A therapeutic regimen may include an induction regimen and a maintenance regimen. The phrase "induction regimen" or "induction
15 period" refers to a therapeutic regimen (or the portion of a therapeutic regimen) that is used for the initial treatment of a disease. The general goal of an induction regimen is to provide a high level of drug to a subject during the initial period of a treatment regimen. An induction regimen may employ (in part or in whole) a "loading regimen", which may include administering a greater dose of the drug than a physician would employ during a maintenance regimen,
20 administering a drug more frequently than a physician would administer the drug during a maintenance regimen, or both. The phrase "maintenance regimen" or "maintenance period" refers to a therapeutic regimen (or the portion of a therapeutic regimen) that is used for the maintenance of a subject during treatment of an illness, e.g., to keep the subject in remission for long periods of time (months or years). A maintenance regimen may employ continuous
25 therapy (e.g., administering a drug at a regular intervals, e.g., weekly, monthly, yearly, etc.) or intermittent therapy (e.g., interrupted treatment, intermittent treatment, treatment at relapse, or treatment upon achievement of a particular predetermined criteria [e.g., disease manifestation, etc.]).

30 In some embodiments, the treatment consists of administering to the subject a chemotherapeutic agent. The term "chemotherapeutic agent" refers to chemical compounds that are effective in inhibiting tumor growth. Examples of chemotherapeutic agents include alkylating agents such as thiotepa and cyclophosphamide; alkyl sulfonates such as busulfan, improsulfan and piposulfan; aziridines such as benzodopa, carboquone, meturedopa, and

uredopa; ethylenimines and methylamelamines including altretamine, triethylenemelamine, trietylenephosphoramidate, triethylenethiophosphoramide and trimethylolmelamine; acetogenins (especially bullatacin and bullatacinone); a camptothecin (including the synthetic analogue topotecan); bryostatin; calystatin; CC-1065 (including its adozelesin, carzelesin and bizelesin synthetic analogues); cryptophycins (particularly cryptophycin 1 and cryptophycin 8); dolastatin; duocarmycin (including the synthetic analogues, KW-2189 and CBI-TMI); eleutherobin; pancratistatin; a sarcodictyin; spongistatin; nitrogen mustards such as chlorambucil, chlornaphazine, cholophosphamide, estramustine, ifosfamide, mechlorethamine, mechlorethamine oxide hydrochloride, melphalan, novembichin, phenesterine, prednimustine, trofosfamide, uracil mustard; nitrosureas such as carmustine, chlorozotocin, fotemustine, lomustine, nimustine, ranimustine; antibiotics such as the enediyne antibiotics (e.g. calicheamicin, especially calicheamicin (11 and calicheamicin 211, see, e.g., Agnew Chem Intl. Ed. Engl. 33:183-186 (1994); dynemicin, including dynemicin A; an esperamicin; as well as neocarzinostatin chromophore and related chromoprotein enediyne antibiotic chromomorphores), aclacinomysins, actinomycin, anthramycin, azaserine, bleomycins, cactinomycin, carubicin, cinnomycin, carzinophilin, chromomycins, dactinomycin, daunorubicin, detorubicin, 6-diazo-5-oxo-L-norleucine, doxorubicin (including morpholino-doxorubicin, cyanomorpholino-doxorubicin, 2-pyrrolino-doxorubicin and deoxydoxorubicin), epirubicin, esorubicin, idarubicin, marcellomycin, mitomycins, mycophenolic acid, nogalarnycin, olivomycins, peplomycin, potfiromycin, puromycin, quelamycin, rodorubicin, streptomycin, streptozocin, tubercidin, ubenimex, zinostatin, zorubicin; anti-metabolites such as methotrexate and 5-fluorouracil (5-FU); folic acid analogues such as denopterin, methotrexate, pteropterin, trimetrexate; purine analogs such as fludarabine, 6-mercaptopurine, thiamiprine, thioguanine; pyrimidine analogs such as ancitabine, azacitidine, 6-azauridine, carmofur, cytarabine, dideoxyuridine, doxifluridine, enocitabine, floxuridine, 5-FU; androgens such as calusterone, dromostanolone propionate, epitostanol, mepitiostane, testolactone; anti-adrenals such as aminoglutethimide, mitotane, trilostane; folic acid replenisher such as frolinic acid; aceglatone; aldophosphamide glycoside; aminolevulinic acid; amsacrine; bestabucil; bisantrene; edatraxate; defofamine; demecolcine; diaziquone; elfornithine; elliptinium acetate; an epothilone; etoglucid; gallium nitrate; hydroxyurea; lentinan; lonidamine; maytansinoids such as maytansine and ansamitocins; mitoguazone; mitoxantrone; mopidamol; nitracrine; pentostatin; phenamet; pirarubicin; podophyllinic acid; 2-ethylhydrazide; procarbazine; PSK®; razoxane; rhizoxin; sizofiran; spirogennanium; tenuazonic acid; triaziquone; 2,2',2"-trichlorotriethylamine; trichothecenes (especially T-2 toxin, verrucarins A, roridin A and

anguidine); urethan; vindesine; dacarbazine; mannomustine; mitobromtol; mitolactol; pipobroman; gacytosine; arabinoside ("Ara-C"); cyclophosphamide; thiotepa; taxoids, e.g. paclitaxel (TAXOL®, Bristol-Myers Squibb Oncology, Princeton, N.J.) and doxorubicin (TAXOTERE®, Rhone-Poulenc Rorer, Antony, France); chlorambucil; gemcitabine; 6-thioguanine; mercaptopurine; methotrexate; platinum analogs such as cisplatin and carboplatin; 5 vinblastine; platinum; etoposide (VP-16); ifosfamide; mitomycin C; mitoxantrone; vincristine; vinorelbine; navelbine; novantrone; teniposide; daunomycin; aminopterin; xeloda; ibandronate; CPT-11; topoisomerase inhibitor RFS 2000; difluoromethylornithine (DMFO); retinoic acid; capecitabine; and pharmaceutically acceptable salts, acids or derivatives of any of the above.

10 Also included in this definition are antihormonal agents that act to regulate or inhibit hormone action on tumors such as anti-estrogens including for example tamoxifen, raloxifene, aromatase inhibiting 4(5)-imidazoles, 4-hydroxytamoxifen, toremifene, keoxifene, LY117018, onapristone, and toremifene (Fareston); and anti-androgens such as flutamide, nilutamide, bicalutamide, leuprolide, and goserelin; and pharmaceutically acceptable salts, acids or 15 derivatives of any of the above.

In some embodiments, the treatment consists of administering to the subject a targeted cancer therapy. Targeted cancer therapies are drugs or other substances that block the growth and spread of cancer by interfering with specific molecules ("molecular targets") that are 20 involved in the growth, progression, and spread of cancer. Targeted cancer therapies are sometimes called "molecularly targeted drugs," "molecularly targeted therapies," "precision medicines," or similar names. In some embodiments, the targeted therapy consists of administering the subject with a tyrosine kinase inhibitor. The term "tyrosine kinase inhibitor" refers to any of a variety of therapeutic agents or drugs that act as selective or non-selective 25 inhibitors of receptor and/or non-receptor tyrosine kinases. Tyrosine kinase inhibitors and related compounds are well known in the art and described in U.S. Patent Publication 2007/0254295, which is incorporated by reference herein in its entirety. It will be appreciated by one of skill in the art that a compound related to a tyrosine kinase inhibitor will recapitulate the effect of the tyrosine kinase inhibitor, e.g., the related compound will act on a different 30 member of the tyrosine kinase signaling pathway to produce the same effect as would a tyrosine kinase inhibitor of that tyrosine kinase. Examples of tyrosine kinase inhibitors and related compounds suitable for use in methods of embodiments of the present invention include, but are not limited to, dasatinib (BMS-354825), PP2, BEZ235, saracatinib, gefitinib (Iressa), sunitinib (Sutent; SU11248), erlotinib (Tarceva; OSI-1774), lapatinib (GW572016; GW2016),

canertinib (CI 1033), semaxinib (SU5416), vatalanib (PTK787/ZK222584), sorafenib (BAY 43-9006), imatinib (Gleevec; STI571), leflunomide (SU101), vandetanib (Zactima; ZD6474), MK-2206 (8-[4-aminocyclobutyl]phenyl)-9-phenyl-1,2,4-triazolo[3,4-f][1,6]naphthyridin-3(2H)-one hydrochloride) derivatives thereof, analogs thereof, and combinations thereof.

5 Additional tyrosine kinase inhibitors and related compounds suitable for use in the present invention are described in, for example, U.S. Patent Publication 2007/0254295, U.S. Pat. Nos. 5,618,829, 5,639,757, 5,728,868, 5,804,396, 6,100,254, 6,127,374, 6,245,759, 6,306,874, 6,313,138, 6,316,444, 6,329,380, 6,344,459, 6,420,382, 6,479,512, 6,498,165, 6,544,988, 6,562,818, 6,586,423, 6,586,424, 6,740,665, 6,794,393, 6,875,767, 6,927,293, and 6,958,340,

10 all of which are incorporated by reference herein in their entirety. In certain embodiments, the tyrosine kinase inhibitor is a small molecule kinase inhibitor that has been orally administered and that has been the subject of at least one Phase I clinical trial, more preferably at least one Phase II clinical, even more preferably at least one Phase III clinical trial, and most preferably approved by the FDA for at least one hematological or oncological indication. Examples of

15 such inhibitors include, but are not limited to, Gefitinib, Erlotinib, Lapatinib, Canertinib, BMS-599626 (AC-480), Neratinib, KRN-633, CEP-11981, Imatinib, Nilotinib, Dasatinib, AZM-475271, CP-724714, TAK-165, Sunitinib, Vatalanib, CP-547632, Vandetanib, Bosutinib, Lestaurtinib, Tandutinib, Midostaurin, Enzastaurin, AEE-788, Pazopanib, Axitinib, Motasenib, OSI-930, Cediranib, KRN-951, Dovitinib, Seliciclib, SNS-032, PD-0332991, MKC-I (Ro-

20 317453; R-440), Sorafenib, ABT-869, Brivanib (BMS-582664), SU-14813, Telatinib, SU-6668, (TSU-68), L-21649, MLN-8054, AEW-541, and PD-0325901.

In some embodiments, the treatment consists of administering to the subject an anti-VEGF agent. As used herein an "anti-VEGF agent" refers to a molecule that inhibits VEGF -

25 mediated angiogenesis, vasculogenesis, or undesirable vascular permeability. For example, an anti-VEGF therapeutic may be an antibody to or other antagonist of VEGF. An "anti-VEGF antibody" is an antibody that binds to VEGF with sufficient affinity and specificity to be useful in a method of the invention. An anti-VEGF antibody will usually not bind to other VEGF homologues such as VEGF- B or VEGF-C, or other growth factors such as P1GF, PDGF or

30 bFGF. A preferred anti- VEGF antibody is a monoclonal antibody that binds to the same epitope as the monoclonal anti-VEGF antibody A4.6.1 produced by hybridoma ATCC® HB 10709 and is a high-affinity anti-VEGF antibody. A "high-affinity anti-VEGF antibody" has at least 10-fold better affinity for VEGF than the monoclonal anti-VEGF antibody A4.6.1. Preferably the anti-VEGF antibody is a recombinant humanized anti-VEGF monoclonal antibody fragment

generated according to WO 98/45331, including an antibody comprising the CDRs or the variable regions of Y0317. More preferably, anti-VEGF antibody is the antibody fragment known as ranibizumab (LUCENTIS®). The anti-VEGF antibody ranibizumab is a humanized, affinity-matured anti-human VEGF Fab fragment. Ranibizumab is produced by standard recombinant technology methods in *E. coli* expression vector and bacterial fermentation. Ranibizumab is not glycosylated and has a molecular mass of -48,000 daltons. See W098/45331 and U.S. 2003/0190317. Anti-VEGF agents include but are not limited to bevacizumab (rhuMab VEGF, Avastin®, Genentech, South San Francisco Calif.), ranibizumab (rhuFAB V2, Lucentis®, Genentech), pegaptanib (Macugen®, Eyetech Pharmaceuticals, New York N.Y.), sunitinib maleate (Sutent®, Pfizer, Groton Conn.)

In some embodiments, the treatment consists of administering to the subject an immunotherapeutic agent. The term "immunotherapeutic agent," as used herein, refers to a compound, composition or treatment that indirectly or directly enhances, stimulates or increases the body's immune response against cancer cells and/or that decreases the side effects of other anticancer therapies. Immunotherapy is thus a therapy that directly or indirectly stimulates or enhances the immune system's responses to cancer cells and/or lessens the side effects that may have been caused by other anti-cancer agents. Immunotherapy is also referred to in the art as immunologic therapy, biological therapy biological response modifier therapy and biotherapy. Examples of common immunotherapeutic agents known in the art include, but are not limited to, cytokines, cancer vaccines, monoclonal antibodies and non-cytokine adjuvants. Alternatively the immunotherapeutic treatment may consist of administering the subject with an amount of immune cells (T cells, NK, cells, dendritic cells, B cells...).

Immunotherapeutic agents can be non-specific, i.e. boost the immune system generally so that the human body becomes more effective in fighting the growth and/or spread of cancer cells, or they can be specific, i.e. targeted to the cancer cells themselves immunotherapy regimens may combine the use of non-specific and specific immunotherapeutic agents.

Non-specific immunotherapeutic agents are substances that stimulate or indirectly improve the immune system. Non-specific immunotherapeutic agents have been used alone as a main therapy for the treatment of cancer, as well as in addition to a main therapy, in which case the non-specific immunotherapeutic agent functions as an adjuvant to enhance the effectiveness of other therapies (e.g. cancer vaccines). Non-specific immunotherapeutic agents

can also function in this latter context to reduce the side effects of other therapies, for example, bone marrow suppression induced by certain chemotherapeutic agents. Non-specific immunotherapeutic agents can act on key immune system cells and cause secondary responses, such as increased production of cytokines and immunoglobulins. Alternatively, the agents can themselves comprise cytokines. Non-specific immunotherapeutic agents are generally classified as cytokines or non-cytokine adjuvants.

A number of cytokines have found application in the treatment of cancer either as general non-specific immunotherapies designed to boost the immune system, or as adjuvants provided with other therapies. Suitable cytokines include, but are not limited to, interferons, interleukins and colony-stimulating factors.

Interferons (IFNs) contemplated by the present invention include the common types of IFNs, IFN-alpha (IFN- α), IFN-beta (IFN- β) and IFN-gamma (IFN- γ). IFNs can act directly on cancer cells, for example, by slowing their growth, promoting their development into cells with more normal behaviour and/or increasing their production of antigens thus making the cancer cells easier for the immune system to recognise and destroy. IFNs can also act indirectly on cancer cells, for example, by slowing down angiogenesis, boosting the immune system and/or stimulating natural killer (NK) cells, T cells and macrophages. Recombinant IFN-alpha is available commercially as Roferon (Roche Pharmaceuticals) and Intron A (Schering Corporation).

Interleukins contemplated by the present invention include IL-2, IL-4, IL-11 and IL-12. Examples of commercially available recombinant interleukins include Proleukin® (IL-2; Chiron Corporation) and Neumega® (IL-12; Wyeth Pharmaceuticals). Zymogenetics, Inc. (Seattle, Wash.) is currently testing a recombinant form of IL-21, which is also contemplated for use in the combinations of the present invention.

Colony-stimulating factors (CSFs) contemplated by the present invention include granulocyte colony stimulating factor (G-CSF or filgrastim), granulocyte-macrophage colony stimulating factor (GM-CSF or sargramostim) and erythropoietin (epoetin alfa, darbepoietin). Treatment with one or more growth factors can help to stimulate the generation of new blood cells in subjects undergoing traditional chemotherapy. Accordingly, treatment with CSFs can be helpful in decreasing the side effects associated with chemotherapy and can allow for higher

doses of chemotherapeutic agents to be used. Various-recombinant colony stimulating factors are available commercially, for example, Neupogen® (G-CSF; Amgen), Neulasta (pelfilgrastim; Amgen), Leukine (GM-CSF; Berlex), Procrit (erythropoietin; Ortho Biotech), Epogen (erythropoietin; Amgen), Arnesp (erythropoietin).

5

In addition to having specific or non-specific targets, immunotherapeutic agents can be active, i.e. stimulate the body's own immune response, or they can be passive, i.e. comprise immune system components that were generated external to the body.

10

Passive specific immunotherapy typically involves the use of one or more monoclonal antibodies that are specific for a particular antigen found on the surface of a cancer cell or that are specific for a particular cell growth factor. Monoclonal antibodies may be used in the treatment of cancer in a number of ways, for example, to enhance a subject's immune response to a specific type of cancer, to interfere with the growth of cancer cells by targeting specific cell growth factors, such as those involved in angiogenesis, or by enhancing the delivery of other anticancer agents to cancer cells when linked or conjugated to agents such as chemotherapeutic agents, radioactive particles or toxins.

15

In some embodiments, the immunotherapeutic agent is an immune checkpoint inhibitor. As used herein, the term "immune checkpoint inhibitor" refers to molecules that totally or partially reduce, inhibit, interfere with or modulate one or more checkpoint proteins. Checkpoint proteins regulate T-cell activation or function. Numerous checkpoint proteins are known, such as CTLA-4 and its ligands CD 80 and CD86; and PD1 with its ligands PDL1 and PDL2 (Pardoll, Nature Reviews Cancer 12: 252-264, 2012). These proteins are responsible for co-stimulatory or inhibitory interactions of T-cell responses. Immune checkpoint proteins regulate and maintain self-tolerance and the duration and amplitude of physiological immune responses. Immune checkpoint inhibitors include antibodies or are derived from antibodies. In some embodiments, the immune checkpoint inhibitor is an antibody selected from the group consisting of anti-CTLA4 antibodies (e.g. Ipilimumab), anti-PD1 antibodies, anti-PDL1 antibodies, anti-TIMP3 antibodies, anti-LAG3 antibodies, anti-B7H3 antibodies, anti-B7H4 antibodies, anti-BTLA antibodies, and anti-B7H6 antibodies. Examples of anti-CTLA-4 antibodies are described in US Patent Nos: 5,811,097; 5,811,097; 5,855,887; 6,051,227; 6,207,157; 6,682,736; 6,984,720; and 7,605,238. One anti-CDLA-4 antibody is tremelimumab, (ticilimumab, CP-675,206). In some embodiments, the anti-CTLA-4 antibody is ipilimumab

20

25

30

(also known as 10D1, MDX-D010) a fully human monoclonal IgG antibody that binds to CTLA-4. Another immune checkpoint protein is programmed cell death 1 (PD-1). Examples of PD-1 and PD-11 blockers are described in US Patent Nos. 7,488,802; 7,943,743; 8,008,449; 8,168,757; 8,217,149, and PCT Published Patent Application Nos: WO03042402, 5 WO2008156712, WO2010089411, WO2010036959, WO2011066342, WO2011159877, WO2011082400, and WO2011161699. In some embodiments, the PD-1 blockers include anti-PD-L1 antibodies. In certain other embodiments the PD-1 blockers include anti-PD-1 antibodies and similar binding proteins such as nivolumab (MDX 1106, BMS 936558, ONO 4538), a fully human IgG4 antibody that binds to and blocks the activation of PD-1 by its ligands PD-L1 and 10 PD-L2; lambrolizumab (MK-3475 or SCH 900475), a humanized monoclonal IgG4 antibody against PD-1 ; CT-011 a humanized antibody that binds PD-1 ; AMP-224 is a fusion protein of B7-DC; an antibody Fc portion; BMS-936559 (MDX- 1105-01) for PD-L1 (B7-H1) blockade. Other immune-checkpoint inhibitors include lymphocyte activation gene-3 (LAG-3) inhibitors, such as IMP321, a soluble Ig fusion protein (Brignone et al., 2007, J. Immunol. 179:4202- 15 4211). Other immune-checkpoint inhibitors include B7 inhibitors, such as B7-H3 and B7-H4 inhibitors. In particular, the anti-B7-H3 antibody MGA271 (Loo et al., 2012, Clin. Cancer Res. July 15 (18) 3834). Also included are TIM3 (T-cell immunoglobulin domain and mucin domain 3) inhibitors (Fourcade et al., 2010, J. Exp. Med. 207:2175-86 and Sakuishi et al., 2010, J. Exp. Med. 207:2187-94).

20 In some embodiments, the immunotherapeutic treatment consists of an adoptive immunotherapy as described by Nicholas P. Restifo, Mark E. Dudley and Steven A. Rosenberg "Adoptive immunotherapy for cancer: harnessing the T cell response, Nature Reviews Immunology, Volume 12, April 2012). In adoptive immunotherapy, the patient's circulating lymphocytes, or tumor infiltrated lymphocytes, are isolated in vitro, activated by lymphokines 25 such as IL-2 and readministered (Rosenberg et al., 1988; 1989). The activated lymphocytes are most preferably be the patient's own cells that were earlier isolated from a blood sample and activated (or "expanded") in vitro. In some embodiments, the subject is administered with host cells that express a chimeric antigen receptor. As used herein, the term "chimeric antigen receptor" or "CAR" has its general meaning in the art and refers to an artificially constructed 30 hybrid protein or polypeptide containing the antigen binding domains of an antibody (e.g., scFv) linked to T- cell signaling domains. Characteristics of CARs include their ability to redirect T-cell specificity and reactivity toward a selected target in a non-MHC-restricted manner, exploiting the antigen-binding properties of monoclonal antibodies. The non-MHC-restricted antigen recognition gives T cells expressing CARs the ability to recognize antigen independent

of antigen processing, thus bypassing a major mechanism of tumor escape. Moreover, when expressed in T-cells, CARs advantageously do not dimerize with endogenous T cell receptor (TCR) alpha and beta chains. While the host cell can be of any cell type, can originate from any type of tissue, and can be of any developmental stage, the host cell is a T cell, e.g. isolated from peripheral blood lymphocytes (PBL) or peripheral blood mononuclear cells (PBMC). In some 5 embodiments, the T cell can be any T cell, such as a cultured T cell, e.g., a primary T cell, or a T cell from a cultured T cell line, e.g., Jurkat, SupT1, etc., or a T cell obtained from a mammal. If obtained from a mammal, the T cell can be obtained from numerous sources, including but not limited to blood, bone marrow, lymph node, the thymus, or other tissues or fluids. T cells 10 can also be enriched for or purified. The T cell can be any type of T cell and can be of any developmental stage, including but not limited to, CD4+/CD8+ double positive T cells, CD4+ helper T cells, e.g., Th2 cells, CD8+ T cells (e.g., cytotoxic T cells), tumor infiltrating cells, memory T cells, naive T cells, and the like. The T cell may be a CD8+ T cell or a CD4+ T cell. The population of those T cells prepared as described above can be utilized in methods and 15 compositions for adoptive immunotherapy in accordance with known techniques, or variations thereof that will be apparent to those skilled in the art based on the instant disclosure. See, e.g., US Patent Application Publication No. 2003/0170238 to Gruenberg et al; see also US Patent No. 4,690,915 to Rosenberg. Adoptive immunotherapy of cancer refers to a therapeutic approach in which immune cells with an antitumor reactivity are administered to a tumor- 20 bearing host, with the aim that the cells mediate either directly or indirectly, the regression of an established tumor. Transfusion of lymphocytes, particularly T lymphocytes, falls into this category. Currently, most adoptive immunotherapies are autolymphocyte therapies (ALT) directed to treatments using the patient's own immune cells. These therapies involve processing the patient's own lymphocytes to either enhance the immune cell mediated response or to 25 recognize specific antigens or foreign substances in the body, including the cancer cells. The treatments are accomplished by removing the patient's lymphocytes and exposing these cells in vitro to biologics and drugs to activate the immune function of the cells. Once the autologous cells are activated, these ex vivo activated cells are reinfused into the patient to enhance the immune system to treat cancer. In some embodiments, the cells are formulated by first 30 harvesting them from their culture medium, and then washing and concentrating the cells in a medium and container system suitable for administration (a "pharmaceutically acceptable" carrier) in a treatment-effective amount. Suitable infusion medium can be any isotonic medium formulation, typically normal saline, Normosol R (Abbott) or Plasma-Lyte A (Baxter), but also 5% dextrose in water or Ringer's lactate can be utilized. The infusion medium can be

supplemented with human serum albumin. A treatment-effective amount of cells in the composition is dependent on the relative representation of the T cells with the desired specificity, on the age and weight of the recipient, on the severity of the targeted condition and on the immunogenicity of the targeted Ags. These amount of cells can be as low as approximately 10^3 /kg, preferably 5×10^3 /kg; and as high as 10^7 /kg, preferably 10^8 /kg. The number of cells will depend upon the ultimate use for which the composition is intended, as will the type of cells included therein. For example, if cells that are specific for a particular Ag are desired, then the population will contain greater than 70%, generally greater than 80%, 85% and 90-95% of such cells. For uses provided herein, the cells are generally in a volume of a liter or less, can be 500 ml or less, even 250 ml or 100 ml or less. The clinically relevant number of immune cells can be apportioned into multiple infusions that cumulatively equal or exceed the desired total amount of cells.

The immunotherapeutic treatment may consist of allografting, in particular, allograft with hematopoietic stem cell HSC. The immunotherapeutic treatment may also consist in an adoptive immunotherapy as described by Nicholas P. Restifo, Mark E. Dudley and Steven A. Rosenberg "Adoptive immunotherapy for cancer: harnessing the T cell response, Nature Reviews Immunology, Volume 12, April 2012). In adoptive immunotherapy, the subject's circulating lymphocytes, NK cells, are isolated amplified *in vitro* and readministered to the subject. The activated lymphocytes or NK cells are most preferably be the subject's own cells that were earlier isolated from a blood or tumor sample and activated (or "expanded") *in vitro*.

In some embodiments, the treatment consists of administering to the subject a radiotherapeutic agent. The term "radiotherapeutic agent" as used herein, is intended to refer to any radiotherapeutic agent known to one of skill in the art to be effective to treat or ameliorate cancer, without limitation. For instance, the radiotherapeutic agent can be an agent such as those administered in brachytherapy or radionuclide therapy. Such methods can optionally further comprise the administration of one or more additional cancer therapies, such as, but not limited to, chemotherapies, and/or another radiotherapy.

The invention will be further illustrated by the following figures and examples. However, these examples and figures should not be interpreted in any way as limiting the scope of the present invention.

EXAMPLES

Material and methods

5 1. Gene Expression Profiles (GEP) datasets

From public repositories, we curated transcriptomic profiles from several types of samples (Microenvironment Cell Populations (MCP), non-hematopoietic human tumors, non-diseased human tissues, in-vitro RNA mixtures) obtained from different gene expression platforms (mainly Affymetrix HGU 133 Plus 2.0, HGU 133A, HuGene 1.0 ST and Illumina
10 HiSeq 2000). For survival analysis, transcriptomic profiles of non-hematopoietic human tumors with Overall Survival annotations were also included. The table below lists the types of samples curated, stratified by gene expression platforms, and points to the identifiers of the included samples.

15 2. GEP normalization

Affymetrix Human Genome 133 Plus 2.0, Human Genome 133A, HuGene 1.0 ST arrays
MCP datasets and tumor datasets from Affymetrix Human Genome 133 Plus 2.0, Human Genome 133A, HuGene 1.0 ST arrays were normalized using the frozen robust
multiarray average (fRMA) method, implemented in the ‘fRMA’ R package (version 1.18.0).
20 Unlike RMA, fRMA uses fixed estimates of probe-specific effects and variances, allowing a consistent normalization of GEP from different series, provided that they were obtained on the same gene expression platform.

GEP obtained with the Affymetrix Human Genome 133 Plus 2.0, Human Genome 133A, HuGene 1.0 ST arrays platforms were thus normalized using the ‘frma’ function of the
25 ‘frma’ Bioconductor R package using the preprocessing input vectors provided respectively by the Bioconductor R packages ‘frmahgu133plus2frmavecs’ version 1.3.0, ‘frma133afrmavecs’ version 1.3.0 and ‘hugene.1.0.st.v1frmavecs’ version 1.0.0. The ‘frma’ method was called on batches of CEL files corresponding to individual series.

30 *The Cancer Genome Atlas gene expression data*

Gene expression data from non-currently-embargoed TCGA projects were obtained from the TCGA data portal (<https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm>). Only GEP obtained using Illumina HiSeq 2000 were retrieved. Already-normalized ‘level 3’ data

were downloaded separately for each project. The resulting ‘*.rsem.genes.normalized_results files’ were then merged into a single pan-cancer expression matrix.

Other gene expression platforms

5 For GEP obtained using other gene expression platforms, we used pre-processed GEP data as published by each studies’ authors and available from the corresponding public repositories.

3. Publicly available samples’ annotations

10 *MCP datasets - Discovery serie (Affymetrix 133 Plus 2.0 arrays)*

Samples were annotated according to the author-reported phenotypes yielding 344 distinct labels (data not shown). We recoded these labels into 63 categories, including 21 cancer cell phenotypes (42 immune and stromal labels).

15 *MCP datasets - Validation series (Affymetrix 133A and Affymetrix HuGene 1.0 ST arrays)*

Samples were annotated according to the 63 labels used to annotate the discovery MCP series. The previously-defined 63 categories did not fit the phenotype of a few samples and motivated the addition of 15 categories (data not shown). These newly-defined categories all
20 *refine some of the initial 63 labels.*

Non-diseased human tissues (GEO:GSE7307)

Samples’ annotations were retrieved from GEO:GSE7307. Samples corresponding to diseased tissues, cell lines or sorted immune cells were discarded, retaining only the non-
25 diseased cellularly-heterogeneous samples. For clarity, some tissues were regrouped in broader anatomical locations (data not shown). Anatomical systems were manually added.

Non-hematopoietic tumor samples series

From the three tumor datasets, only samples corresponding to primary tumors obtained
30 from tumor resections with no neoadjuvant treatments and that did not use laser capture microdissection were retained for analysis (data not shown).

Annotations for samples retrieved from GEO (respectively from ArrayExpress) were retrieved from the ‘Series matrix’ files (respectively from ‘sdrf’ files). Annotations for TCGA

samples were retrieved from the TCGA data portal (<https://tcga-data.nci.nih.gov/tcga/dataAccessMatrix.htm>).

Since annotations originated from many different groups, only a subset of the variables were retained for each series. The corresponding values were harmonized into a consistent ontology. The following list contains the final set of variables for which samples' annotations were retained:

- Sample identifiers
- Series identifiers
- Gene expression platform
- 10 • Cancer type
- Sample type (Autopsy, Biopsy, Cell culture, Surgery followed by laser capture microdissection, Surgery)
- Overall survival event and delay (months)

Non-hematopoietic tumor samples series (Other platforms)

15 Only sample identifiers, tumor types, sample status and Overall Survival were retained.

Removal of tumor samples duplicates

Some tumor GEP are present in multiple public datasets and correctly labeled as 'Reanalyzed'. In this case, only the original sample was considered for analysis. To avoid 20 unspecified duplicated GEP, we computed MD5 checksums for all uncompressed CEL files. Samples with identical MD5 checksums were considered duplicates. In this case, only the sample belonging to the oldest series was kept. Annotations present on the most recent sample instance and absent from the older sample instance were added to the older sample's annotation. Conflicting annotations were resolved by keeping the oldest annotation. These conflicts never 25 occurred for clinical follow-up variables.

4. Selection of the transcriptomic markers (TM)

Organization of the samples into a pyramidal graph of categories

We define as a pyramid a directed acyclic graph with a root node. Samples of 30 microenvironment purified cells were labeled according to their reported immune or stromal populations, resulting in 63 distinct labels in the MCP discovery series, with an addition of 15 labels for the MCP validation series, resulting in a total of 78 labels. We organized these labels in a pyramidal graph (data not shown) with nodes representing populations (categories), and

directed edges representing relations of inclusion. For instance, the labels “CD8+ T cells”, “CD4+ T cells”, “T $\gamma\delta$ cells”, “Memory T cells”, “Activated T cells” and “Naïve T cells”, and all labels included in them (for instance “Effector-memory CD8 T cells”), form the “T cells” category, which itself is included in the “T/NK lineage” category. Of these 78 labels of samples, some correspond to terminal leaves of this pyramid (ex. “Canonical CD4 Treg cells”), while some others do correspond to higher level nodes (ex. Peripheral-Blood Mononuclear Cells, “PBMC”). In addition to these 78 labels, 15 hematopoiesis or immunology-inspired categories that are not directly represented by samples but relevant for their organization in a structured pyramid (for instance “Lymphocytes”) or as potential cell population (for instance “antigen-experienced B cells”) were added (Supplementary Table S12). Categories corresponding to tumor samples were discarded for the identification of TM and only kept as negative controls, resulting in 68 categories available for screening.

Having defined this set of 78 labels and 68 categories (53 categories are directly represented by labels, with 15 additional categories not directly represented in the dataset), we exhaustively encoded the relationships between labels and categories using three possible relationships (data not shown). Relative to a category, we define three sets of samples:

C : ‘positive samples’ are those whose label is included in the category (all cells composing a sample which is in C are in the category)

C^- : ‘negative samples’ are those whose label is strictly non-overlapping with the category (all cells of a sample which is in C^- are not in the category)

-1 : ‘mixed samples’ are those whose label is partly overlapping with the category (some cells of the sample are in C and some are in C^-).

For instance, for CD8+ T cells, C is the set of samples whose label is “CD8 T cells” or “Effector memory CD8 T cells” (Supplementary Figure S1, Supplementary Table S12), mixed samples are for instance CD3+ T cells as they mix CD4+ and CD8+ T cells, or PBMC as they mix CD8+ T cells with e.g. monocytes. C^- is defined as all non-positive non-mixed samples.

Hence, strict exclusion or mixture relationships are not represented but are taken into account during the screening process (data not shown).

30

Selection of TMs for each category

We performed an exhaustive exploration of the categories’ pyramid to screen for the existence of potential transcriptomic markers at each node. Set of positive samples are C and negative samples are C^- (mixed samples are discarded for this node). Given this two sets of

samples, a triplet of probeset-level statistics was computed per probeset: the positive Area Under the ROC Curve (AUC), the fold-change (FC) and a specific fold-change (sFC), with the latter-two with the following definitions:

$$(1) \quad FC = X - X^-$$

$$5 \quad (2) \quad sFC = (X - X^-_{\min}) / (X^-_{\max} - X^-_{\min})$$

where we denote by X the centroid (i.e. average across all samples) of category C , X^- the centroid of C^- , X^-_j the centroid of any class j composing C^- ($j=1..k$), X^-_{\min} the min value across centroids of classes composing C^- ($X^-_{\min} = \min_{j \in 1..k} \{X^-_j\}$), X^-_{\max} the max value across centroids of classes composing C^- ($X^-_{\max} = \max_{j \in 1..k} \{X^-_j\}$). The specific fold-change both accounts for a high expression in C compared to C^- and a low variability within C^- .

For each non-root node of the pyramid, probesets with $AUC > 0.97$, $FC > 2$ and $sFC > 1.5$ were retained (data not shown).

15 *Selection of TM sets for 10 populations*

Having selected in an unbiased manner the markers for each level of the pyramid, we manually selected the most relevant TM sets: we discarded

very broad categories (such as ‘stromal cells’ which would, in a tumor, designate all non-malignant cells from the microenvironment)

20 categories with too few positive samples to reliably identify robust markers from high-dimensional data

those for which no appropriate controls were represented in the discovery series

those for which no markers were identified.

25 *Reduction of TM sets for four populations*

For four populations (Neutrophils, Endothelial cells, Fibroblasts and cells of the B lineage), the number of TM identified in the Discovery series was much higher (>90) than for the other cell populations (<25). To obtain more balanced marker sets, we performed the same selection process on the validation series, obtaining TM sets overlapping with those identified on the discovery series (Supplementary Table S3). To reduce the number of markers, we thus took the intersection of the markers across the three MCP series (B lineage, fibroblasts), or the discovery and the HuGene 1.0ST series (Endothelial cells), or the discovery and the Affymetrix

HGU 133A series (Neutrophils). Of note, this filtering step was not performed for the figures where data from the MCP validation series were used (data not shown).

5. Computation of MCP-counter scores

5 Given a set of transcriptomic markers of a given category, we computed a corresponding per-sample score, called hereafter a MCP-counter score, using the log₂ geometric mean of this set of markers.

10 6. Correlation profiles of transcriptomic markers in MCP and tumor datasets (Supplementary Fig S5-S7)

For a given set of TMs, corresponding features were subsetted from the expression matrices of the three MCP series and three primary tumor series (Affymetrix 133 Plus 2.0, 133A, and TCGA). On these six matrices, Pearson correlation coefficients were computed for each pair of features.

15

7. RNA mixture models

Peripheral blood immune cells sorting

Peripheral venous blood was extracted for 3 healthy donor using heparin vacuntainer tubes (BD Bioscience). Peripheral blood mononuclear (PBMC) or polymorphonuclear cells (PMN) were isolated using Ficoll-Paque PLUS (GE Healthcare Life Science) or Polymorph Prep (Axis-Shield) density gradient, respectively. PBMCs were stained with anti-CD3 FITC (Clone UCHT1), anti-CD14 APC (MΦP9), anti-CD19 ECD (J3-119) and anti-CD56 PE (B159); and PMNs with anti-CD66b FITC (G10F5), anti-CD19 ECD (J3-119), anti-CD3 PE (UCHT1), anti-CD56 PE (B159) and anti-CD14 APC (MΦP9). Cell sorting was done in a FACS Aria cytometer (BD Bioscience), and cell purity higher than 97% was always achieved. We sorted the following populations: T cells (DAPI-/CD3+/CD14-/CD19-/CD56-), monocytes (DAPI-/CD3-/CD14+/CD19-/CD56-), B cells (DAPI-/CD3-/CD14-/CD19+/CD56-) and NK cells (DAPI-/CD3-/CD14-/CD19-/CD56+) on PBMCs, and neutrophils (DAPI-/CD66b+/CD19-/CD3-/CD56-/CD14-) on PMNs.

30

Cell culture

HCT116 were purchased from ATCC and cultured according to vendor's instructions.

RNA extraction

Cells were lysed in RLT (QIAGEN)-1% mercaptoethanol buffer, and RNA was purified with a Maxwell 16 simplyRNA Kit (Promega) according to manufacturer's instructions. Genetic material quality and quantity were determined with a 2100 Bioanalyzer Instrument
5 (Agilent Technologies).

Mixtures of RNA solutions

A set of four 2-fold serial dilutions were performed on each aliquot of RNA extracted from sorted peripheral blood immune cells, yielding solutions of decreasing concentration S0
10 to S4 for each cell population. Ten aliquots were used to mix these solutions using two transposed latin squares layout.

The volume corresponding to ten nanograms of a solution of HCT116 colorectal-cancer cell line-extracted mRNA was then added to the Mixes 3 to 12. Two additional samples (Mixes
15 1 and 2) of pure HCT116 mRNA were also included.

Microarrays hybridization

Biotinylated double strand cDNA targets were prepared from 10 ng of total RNA using the NuGEN Ovation Pico WTA System V2 Kit (Cat # 3302) followed by the NuGEN Encore
20 Biotin Module Kit (Cat # 4200) according to manufacturer recommendations. Following fragmentation and labeling, 4.55 µg of cDNAs were hybridized for 16 hours at 45°C, 60 rpm on Human GeneChip HG-U133 plus 2.0 arrays (Affymetrix). The chips were washed and stained in the GeneChip Fluidics Station 450 (Affymetrix) using the FS450_0004 script and scanned with the GeneChip Scanner 3000 7G (Affymetrix) at a resolution of 1.56 µm. Raw
25 data (.CEL Intensity files) were extracted from the scanned images using the Affymetrix GeneChip Command Console (AGCC) version 4.0.

Correlation between MCP-counter scores and known mRNA proportions

MCP-counter scores were computed from the fRMA-normalized RNA-mixture
30 microarray dataset and plotted against the known mRNA log-proportions. Pearson correlation coefficients and the corresponding tests against the t distribution were performed.

Estimation of the limit of detection

For each of the five sorted cell populations (NK cells, B cells, T cells, Monocytes, Neutrophils), we fitted a least-square linear regression model of the known mRNA log-proportions with the corresponding MCP-counter score as predictive variable using the 10 mRNA mixture samples.

5 The MCP-counter scores for non-hematopoietic samples from the ‘MCP Discovery series’ were computed. The above-described linear fits were used to predict the mRNA fraction of the five sorted cell populations from the corresponding MCP-counter scores. The exponential of the mean of the estimated log-proportions across non-hematopoietic samples is reported as the estimate of the limit of detection for each immune cell population assayed.

10

Data deposition

The transcriptome data of the 12 mixture samples has been deposited in NCBI's Gene Expression Omnibus and are accessible through GEO Series accession number GSE64385.

15

8. Immunohistochemistry-based cellular densities estimates

Serial 5 μ m formalin-fixed paraffin-embedded (FFPE) tissue sections from colorectal cancer were stained using autostainerPlus Link 48 (Dako). Antigen retrieval and deparaffinization were carried out on a PT-Link (Dako) using the EnVision FLEX Target Retrieval Solutions (Dako). The antibodies used are listed in Supplementary Table S14. Peroxidase activity was detected using diaminobenzidine substrate (Dako). Slides stained with anti-CD3, anti-CD8A and anti-CD68 were digitalized with a NanoZoomer scanner (Hamamatsu). The densities of positive cells in the tumor core were measured using Calopix software (Tribvn, France).

20

25

9. Mapping of Affymetrix probesets to genes identifiers

For Affymetrix HGU 133 Plus 2.0, 133A, and HuGene 1.0 ST arrays, probesets were mapped to genes identifiers using annotations provided by Affymetrix version 35.

TCGA GEP are annotated with ENTREZ identifiers which were converted to HUGO symbols using

30

ftp://ftp.ncbi.nih.gov/gene/DATA/GENE_INFO/Mammalia/Homo_sapiens.gene_info.gz
(retrieved on 2015_05_20).

10. R implementation of the MCP-counter method

We implemented MCP-counter as an R package called ‘MCPcounter’. Users should call the ‘MCPcounter.estimate’ function, which takes a normalized gene expression matrix as its first argument, and the type of features that should be mapped to selected transcriptomic markers (probesets, HUGO symbols, ENTREZ ID) as its second argument.

5 We used mapped transcriptomic markers to ‘probesets’ to compute MCP-counter scores for ‘Affymetrix 133 Plus 2.0’ and ‘Affymetrix 133A’ samples, and HUGO symbols identifiers for samples obtained on ‘Affymetrix HuGene 1.0 ST’, ‘Illumina Hiseq’ and other gene expression platforms.

10 This package is available at the following URL: http://cit.ligue-cancer.net/?page_id=780&lang=en

11. Simulation of mRNA mixtures (data not shown)

Simulations were performed according to the following 5-steps procedure: 1) For each the following five immune cell populations (T cells, NK cells, B cells, Monocytic lineage, 15 Neutrophils), randomly choose one GEP from samples corresponding to the cell population of one of its cell subpopulations. In addition, choose a tumor cell line sample. 2) Create a vector of weights $w=(0.01/5, 0.02/5, 0.05/5, 0.1/5, 0.2/5, 0.5/5, 0.9/5)$ corresponding to the weight of each immune population in the simulated mixture. Tumor cells are given the complementary weight $1-5w$. 3) For each value of w , compute a linear combination of the randomly chosen 20 GEP with weights w for each of the five immune GEP and $1-5w$ for tumor cells. For CIBERSORT estimates, these mixtures were computed on the linear scale and in the log₂ scale for MCP-counter. 4) Add random noise drawn from the standard normal distribution to each gene expression feature of the simulated mixture. 5) Run CIBERSORT and MCP-counter algorithms on the simulated mixtures.

25 50 simulations were performed (leading to 350 estimates as 7 values of w per simulation run were used). Figure 4a represents, for each cell population, the mean MCP-counter scores or CIBERSORT estimates for a given value of w across the 50 simulations. For CIBERSORT, non-zero estimates of non-introduced cell populations (for instance Mast cells) were discarded, and the remaining estimates were re-normalized to sum to 1. Then, estimates for sub- 30 populations were summed (for instance, the ‘B cells’ CIBERSORT estimate sums the estimates corresponding to ‘B cells naïve’, ‘B cells memory’ and ‘Plasma cells’ subpopulations).

12. Comparison of MCP-counter TM sets with those from other methods (data not shown)

TM sets proposed by Bindea et al. (the “Immunome” TM set) and Yoshihara et al. (“ESTIMATE” TM set) were retrieved from the corresponding publication and the ESTIMATE R package, respectively. For the ‘Immunome’, probesets were used as TM for the Affymetrix 133 Plus 2.0 and 133A MCP series, and gene symbols for the HuGene 1.0 ST MCP series. For ESTIMATE, gene symbols were used for all three series. For each of the three MCP series, scores were computed (See Material and Methods, section 5) from the TM sets proposed herein, the ‘Immunome’ and ‘ESTIMATE’. For each TM set (columns), and each cell population represented in Figure 4b (rows), the average score for the TM set in this cell population was computed. This vector of averaged score, called the ‘Pred’ (for prediction) vector, was linearly mapped to a color code where the minimum value was affected to blue, the maximum to red, and the mean of the maximum and the minimum to white. A ‘Truce’ vector of colors, formed by the status of each cell population, was appended to each ‘Prediction’ vector (red, i.e. positive, if the cell population is supposed to express the genes in the TM set, blue, i.e. negative if the cell population should not express genes in the TM set, and white if the cell population mixes both positive and negative cells). An accurate TM set should thus produce blue values for ‘Pred’ when the ‘Truce’ is blue, and red values when the ‘Truce’ is red. White values of the ‘Truce’ column are less informative as expression of the TM set would then depend both on the accuracy of the TM set and on the proportion of the corresponding cell population in the sample.

13. Representative MCP-counter scores across cancers (data not shown)

In each of the three tumor series, samples were split according to their tumor type. The median MCP-counter score were computed for each cell population in each tumor type, yielding three “median matrices” (one per technological platform). Since MCP-counter scores are expressed in arbitrary units which depend on the gene expression platform used, we Z-transformed each column of these three matrices (the mean of each column was subtracted on each platform, and the resulting values were multiplied by the average of the three standard deviation observed across the three platform for this column) (Supplementary Figure S8). The resulting three matrices were averaged (omitting missing values in case of a cancer missing from one or two of the datasets) (data not shown).

30

14. Prognostic value of MCP-counter scores

For a given cancer type, several datasets, sometimes based on different platforms, were collected. MCP-counter estimates were first computed for each dataset individually. The

resulting scores were then Z-transformed for each dataset individually, leading to similar distributions of the scores across datasets. Then, univariate Cox proportional hazards models for Overall Survival (OS) were fitted separately in each dataset using the related Z-transformed MCP-counter scores. To aggregate the resulting estimates (beta values) across datasets, we used
5 the meta-analytical R package ‘meta’ (function ‘metagen’), using a fixed-effect model (as the scores in each series follow the same distribution). This function weights the independent estimates using an inverse-variance weighting.

15. Microenvironment-based tumor classifications

10 MCP-counter estimates were first computed for each dataset individually. The resulting scores were then Z-transformed for each dataset individually, leading to similar distributions of the scores across datasets. Datasets from the same cancer were then merged, and all MCP-counter variables were binarized using a median cut (leading to “High” and “Low” samples for each variable and for each cancer according to their relative position from the cancer’s median
15 value). We selected three tumor classifications from the literature (using B and T cells in lung adenocarcinoma, fibroblasts and cytotoxic lymphocytes in colorectal cancer, and macrophages and cytotoxic lymphocytes in breast cancer). For each of these three cancer, we concatenated the binarized scores for the two variables of interest, leading to four classes (High-High, High-Low, Low-High, Low-Low). The corresponding Kaplan-Meier curves for overall-survival were
20 then plotted and the p-value of the corresponding log-rank test is reported.

Results:

Development and validation process of the MCP-counter method

25 We designed a method, called MCP-counter, which objective is to measure an inter-samples relative abundance of different microenvironment cell populations. To develop and validate our method, we set up a strategy in seven steps (data not shown). MCP-counter is based on the methodological framework of transcriptomic markers (TM), defined as gene-expression features expressed in one and only one cell population, and whose expression shows little
30 variation within the population of interest (step 1). It directly follows that within a sample composed of many different cell populations, the abundance of the population of interest is proportional to the sample’s expression of its related TM. Given their restrictive definition, TM are not guaranteed to exist for all populations. We set up a Discovery series by curating

Microenvironment Cell Populations (MCP) transcriptomes from 81 public datasets of ‘Affymetrix_HGU_133_Plus_2.0’ microarrays (step 2). These transcriptomes were normalized to allow their integration into a large meta-dataset which includes 1194 immune or non-immune microenvironment cell populations samples, and 742 non-hematopoietic tumor cell line samples as controls (Supplementary Table S1). After manual curation all the samples were annotated using 63 labels, of which 42 correspond to microenvironment cell populations and 21 represent cell lines from 21 non-hematopoietic cancer types (data not shown). We organized the 63 cell populations into a pyramidal graph according to rules of inclusions (Supplementary Figure S1). We added hematopoiesis-inspired (e.g. lymphoid and myeloid lineages) or functional (e.g. cytotoxic lymphocytes) categories to this pyramid, resulting in a total of 67 nodes corresponding to potential cellular populations of the tissue microenvironment (step 3) (data not shown). This organization was legitimated by its consistency with clusters obtained with transcriptome-based principal component analysis (step 4) (data not shown).

To identify TM of a given cell population (a node in our cell populations pyramid) (step 5), we defined as ‘positive’ the samples included in this population, and we defined as ‘negative’ the samples that do not contain this population. Samples containing both ‘positive’ and ‘negative’ cells are omitted from the analysis for this node. Three criteria were then calculated for each feature (probeset) within the Discovery set: a) the mean log₂-expression difference between positive and negative samples (a threshold of 2 was applied), b) the area under the ROC curve (AUC) of the feature for the identification of the positive samples (threshold of 0.97), and c) a measure of the signal to noise ratio between positive and negative samples (threshold of 1.5) (Material and methods, Supplementary Table S2). Gene-expression features that reached the defined thresholds simultaneously for all three criteria were retained as TM for the corresponding cell population.

Since we had no a priori on the populations for which TM could be identified, we applied our selection procedure exhaustively for each non-root node of the samples’ pyramid (data not shown) and selected a posteriori the most relevant TM sets. The number of identified markers at each level of this pyramidal graph is reported in Supplementary Table S3. From the 67 nodes, we retained TM for the most precise populations for which TM could be robustly identified. We thus discarded those for which appropriate ‘negative’ controls were not publically available (for instance, identifying TM for ‘Effector Memory CD4 T cells’ at least requires ‘negative’ controls such as ‘Central Memory CD4 T cells’ and ‘Effector Memory CD8 T cells’), those with few ‘positive’ samples, or those with no identified markers after the selection procedure. Nodes corresponding to more general populations (for instance

“Lymphocytes” or “Myeloid cells”) were discarded as TM for more precise daughter cell populations were available. We thus retained TMs specific for 10 distinct populations: 8 immune cell populations (T cells, CD8⁺ T cells, NK cells, cytotoxic lymphocytes, cells of the B lineage, of the monocytic lineage, myeloid dendritic cells, and neutrophils), and 2 non-immune stromal populations (endothelial cells and fibroblasts). The 81 datasets from the Discovery set spanned 344 different culture conditions, purifications methods and cell treatments, which ensures that the selection of TM was not sensitive to experimental conditions. MCP-counter scores were defined as the log₂ average expression of the TM for each population (step 6). We then validated MCP-counter (step 7).

10

Qualitative validation of the identified transcriptomic markers

The reproducibility of the identified TM was assessed on two validation series of 1596 samples hybridized on ‘Affymetrix_U133A’ arrays and 3208 samples hybridized on ‘Affymetrix_HuGene_1.0ST’ arrays (data not shown). For the 10 cell populations, the specific expression patterns obtained on the discovery series were consistently reproduced (data not shown), and the same selection criteria applied to MCP validation series identified significantly overlapping TM sets (data not shown). MCP-counter scores, exhibit a clear separation of the cell types on the discovery and two validation series (data not shown), with an AUC above 0.994 for each signature on the 4804 validation samples (data not shown).

20

Although their identification is data-driven, and not knowledge-driven, the selected TM largely overlap with known markers of the corresponding cell populations. They include for instance probesets mapping to CD3D and CD5 for T cells, CD8B for CD8⁺ T cells, EOMES and GNLY for cytotoxic lymphocytes, NCR1 (NKp46) and KIR genes for NK cells, CD19, CD79A and CD79B for B cells, CSF1R for monocytic cells, CD1 molecules for myeloid dendritic cells, FCGR3B and CEACAM3 (CD66b) for neutrophils, VWF (von Willebrand Factor) and CDH5 (VE-cadherin) for endothelial cells, and DCN and TAGLN for fibroblasts (data not shown). In contrast, the screening process excluded from TM some genes usually considered as specific for a given cell population, such as BLK that we found overexpressed not only in B cells but also at a lower level in plasmacytoid dendritic cells, a result which supports the relevance of a data-driven approach (data not shown).

30

Since for a given cell population, the TM are expected to be coordinately expressed, we examined the correlation matrices of the TM on the three MCP datasets. We observed highly positive correlation matrices for all populations in the MCP datasets (data not shown). Having assessed the reproducibility of this approach, we reduced the number of markers for four

populations (Neutrophils, Fibroblasts, Endothelial cells, B lineage) which had large (>90 markers) TM sets using information from the MCP validation series (Supplementary methods). We examined the correlation patterns of these final TM sets in 9408, 3548 and 6451 tumor transcriptomic samples (data not shown) obtained respectively using
5 'Affymetrix_HGU_133_Plus_2.0', 'Affymetrix_133A' and Illumina_HiSeq transcriptomic platforms (Supplementary Tables S7-S9). We observed largely positive-valued correlation matrices for all MCP in the three tumor datasets, both in pan-cancer (data not shown) and single-cancer (data not shown) datasets.

10 Quantitative validation of MCP-counter abundance estimates

We quantitatively validated the MCP-counter method. For this purpose, we designed an in-vitro RNA mixture experiment (data not shown). Immune populations were purified from healthy donors' peripheral blood; their RNAs were extracted and mixed in highly variable concentrations (from 0.7 to 46% of the sample's RNA). The RNA proportions of the
15 populations were arranged in two transposed latin squares to avoid collinearity and thus ensure specificity (data not shown). The mixtures were further diluted in a fixed amount of a solution containing mRNA extracted from HCT-116, a colorectal cancer cell line. Transcriptome analyses revealed that MCP-counter scores were highly correlated with the cells' proportions in the mixtures (data not shown), with Pearson's correlation coefficients ranging from 0.94 to
20 0.99. In addition, immunohistochemical (IHC) digital quantifications of CD3+, CD8 α + and CD68+ cell densities were performed on tissue sections from 38 colorectal-cancer tumors. The IHC-measured densities of each cell population was found to correlate with the corresponding MCP-counter score (data not shown).

Finally, we assessed the limit of detection of the technique for each cell population using
25 non-hematopoietic control samples. For each assayed population, we observed a limit of detection below 2% (depending on the population, from 1/950 to 1/50 of the sample's total RNA) (data not shown). Altogether, these results validate the use of the MCP-counter method to directly compare the abundance of the corresponding cell population across transcriptomic samples.

30

Comparison of MCP-counter with previously-published methods

MCP-counter differs from methods such as CIBERSORT, which aims to measure intra-sample, within leukocytes, proportions of immune cell populations, while MCP-counter outputs an abundance estimate per cell population that enables an inter-sample comparison, at the cost

of being expressed in arbitrary units. To illustrate these differences, we simulated mRNA mixtures where the within-leukocytes proportion of five immune cell populations was kept constant and equal, while the proportions of tumor cells varied (Figure 4a). In this setting, only MCP-counter was able to accurately reflect the difference in immune cells' abundances across simulated mixtures, while CIBERSORT (accurately) estimated stable proportions of each immune cell populations within the leukocytic fraction of the simulated mixtures.

To compare the robustness of TM sets used in MCP-counter and those identified in previously-published methods, we computed metagene scores on the three MCP series with TM sets reported by Bindea et al. or by Yoshihara et al.. We show that TM sets used in MCP-counter are better at discriminating between positive and negative MCP samples (Figure 4b). Notably, MCP-counter scores achieved high specificity and sensitivity for each of the corresponding cell populations, while some TM sets from other methods were sometimes highly expressed in negative samples (for instance, the 'T cells' TM set from Bindea et al. was highly expressed in NK cells) (data not shown).

15

Analysis of the microenvironment of normal and cancer tissues

We applied MCP-counter to a first dataset of 505 samples spanning 47 non-pathological anatomical locations[14]. Lymphoid organs (Spleen, lymph nodes, tonsils, bone marrow) were, as expected, found to harbor a high number of immune cells, while the thymus featured the highest MCP-counter score for CD3+ T cells (data not shown). On the other hand, known "immune sanctuaries" such as testes were correctly found to feature little abundance of immune cells.

Tumor immunology is one of the natural applications of MCP-counter. We estimated the abundance of immune and non-immune cell populations in 19,407 samples spanning 32 non-hematopoietic human tumors, thus proposing a global analysis of non-malignant cell populations' abundances across human cancers (data not shown). The MCP-scores obtained from the three underlying transcriptome platforms ('Affymetrix_HGU_133_Plus_2.0', 'Affymetrix_133A' and Illumina HiSeq) yielded reproducible patterns across cancer types (data not shown) and were thus averaged to produce a synthetic view (data not shown). We observed that kidney clear-cell carcinoma had the highest abundance of endothelial cells of all cancers, while uveal melanomas, which occur in the eye, an immune sanctuary, are poorly infiltrated by immune cells. Colorectal cancer samples were average in terms of immune cells abundance. Gliomas and glioblastomas appeared poorly-infiltrated by T cells. The often viral-

induced cervical squamous carcinoma is highly infiltrated by cytotoxic T and NK cells, but poorly by cells of monocytic origin.

Prognostic value associated with MCP-counter estimates

5 The three tumor series included respectively 2631, 1615 and 6047 Overall-Survival (OS)-annotated samples. We additionally curated 1591 tumor transcriptomes with OS annotations obtained using other transcriptomic platforms (data not shown). By performing a meta-analysis of univariate Cox models adjusted on each independent study, we assessed the correlation between the abundance of each microenvironment cell population, as estimated by
10 MCP-scores, and OS within cancer types (data not shown). Although this univariate analysis was not adjusted for variables potentially influencing OS, such as tumor stage or treatments received, it nonetheless appeared consistent with published literature, notably revealing an overall favorable prognosis associated with infiltration by T cells, except in kidney clear-cell carcinoma as previously reported and in low grade glioma. Fibroblasts were mostly associated
15 with poor outcome.

To assess whether MCP-counter was relevant to identify tumor subgroups based on their relative infiltration by multiple cell populations, we attempted to reproduce previously-reported prognostic classifications. In lung non-small cell adenocarcinoma, it was recently reported that infiltration by B or T cells independently predict favorable prognosis. In colorectal cancer,
20 extensive literature exists about the protective role of a high infiltration by T cells, while fibroblasts were reported to be associated with poor outcome. In breast cancer, a stratification relying on cytotoxic T cells (associated with favorable outcome) and macrophages (poor outcome) was proposed. Using MCP-counter, we were able to reproduce these clinically-relevant patterns (data not shown).

25

Discussion

Tissue-infiltrating immune and non-immune stromal cells contribute to the measured signal in gene expression experiments. Retrieving this information can yield estimates of the abundance of tissue-infiltrating cells, illustrated herein in cancer samples. To harness this
30 information, we developed the Microenvironment Cell Population (MCP)-counter method, implemented in an easy-to-use R package.

It produces a score for each of 10 distinct MCP. We validated that these scores are accurate abundance estimates in three different settings: a) transcriptomic profiles of 4804 validation MCP samples, in which MCP-counter score separated 'positive' and 'negative'

samples (relative to each of the 10 cell populations) with high specificity and sensitivity, b) in an in-vitro RNA mixture setting, where we showed that MCP-counter scores corresponding to the cell populations from which RNA were extracted highly correlated (Pearson's correlation coefficients ranging from 0.94 to 0.99) with the RNA fraction of the corresponding cell population in the mixture, and c) in an ex-vivo setting where we showed that MCP-counter estimates correlated with IHC measurements of the corresponding cells' densities. Using the in-vitro setting, we showed that MCP-counter's lower limit of detection for a population was below 2% of the sample's total RNA proportion when using 'Affymetrix_HGU_133_Plus_2.0' microarrays. This limit of detection might be lowered by using more sensitive gene expression techniques, such as rt-qPCR, Nanostring, or RNA-sequencing assays.

Other techniques to quantitatively characterize the cellular composition of a heterogeneous tissue notably include flow cytometry and enzymatic IHC. MCP-counter estimates are conceptually close to IHC-estimated cell densities (number of cells per surface unit on a tissue section), as the produced estimates can be used to compare the abundance of the corresponding cell populations across samples. However, unlike IHC, MCP-counter enables the simultaneous quantification of 10 cell populations with a single gene-expression experiment, while IHC quantifications are usually limited to a couple of markers. The information of the cells' spatial localization, which is available in IHC experiments, is however lost when using transcriptomic technologies.

MCP-counter is more sensitive and specific in the interpretation of its scores than other previously-published TM-based methods, through a rigorous, unbiased and conservative approach to define the TM sets on which it is based (data not shown). These methods were also limited to only two populations, or were not quantitatively validated. It conceptually differs from flow cytometry (FC) experiments or FC-inspired computational methods such as CIBERSORT, which aim at describing the relative proportions of various cell populations within a single sample (data not shown). In contrast, MCP-counter is specifically designed to compare the absolute abundance of a given cell population across multiple samples.

MCP-counter scores linearly correlate with the corresponding cell population's abundances across samples, but are expressed in arbitrary units. These arbitrary units are dependent on the gene expression platform used to produce the data and one can only compare samples produced with the same gene expression platforms. Nonetheless, we showed that the relative cellular abundance across three large tumor datasets, totaling more than 19,000 tumors, and obtained with three different gene expression platform, are largely consistent (data not

shown), legitimating the use of MCP-counter to assess which samples are most or least infiltrated by each characterized cell population.

We illustrated the use of MCP-counter on non-diseased human tissues where we observed abundance estimates consistent with known immunological status of the samples. We applied MCP-counter to describe the average MCP cellular abundances in 32 non-hematopoietic human malignancies. This analysis confirmed the very high vascularization of clear-cell renal-cell carcinoma, and showed that cervical squamous cell carcinoma tumors, which are often virally-induced, are highly infiltrated by T lymphocytes, and notably cytotoxic T cells, but only moderately by other immune subsets.

MCP-counter is most relevant to stratify a cohort of similar samples based on the composition of their immune and stromal microenvironments, or to follow the composition of the microenvironment over time. The use of MCP-counter confirmed that significant univariate association between OS and tumor infiltration by cytotoxic lymphocytes were mostly positive. In contrast, significant associations between prognosis and extensive abundance of non-immune stromal cell populations, and notably fibroblasts, are shown mostly negative using MCP-counter. These observations, largely consistent with published literature, validate the use of MCP-counter to assess the prognostic value of MCP in other cohorts of patients.

MCP-counter complements IHC approaches in that it enables the analysis of 10 cell populations using a single gene expression experiment. We notably illustrated its use to separately classify lung adenocarcinoma, colorectal, and breast tumors into microenvironment-defined subgroups. In this setting, we were able to confirm the prognostic impact of three previously-published microenvironment-based tumor classifications. These results suggest that MCP-counter may enable the identification of new multi-markers microenvironmental stratifications.

MCP-counter relies on TM which have been identified in a dataset containing GEP of cancer cell lines from 21 different anatomic locations among its negative controls, ensuring applicability in a wide range of samples. This large diversity of control samples may however discard TM which would be relevant in a specific setting: for instance, the screening procedure discarded NCAM1 (CD56), a widely-used marker of NK cells, as it is also expressed by nervous malignant cells, and is thus unsuitable to quantify NK cells in brain samples. The general framework that we developed herein could thus be tailored to identify additional TM for investigation in a more restricted set of organs.

MCP-counter can be incorporated in clinical routine to characterize immune infiltration in samples where IHC-based quantifications are impossible, such as for fine-needle aspiration

biopsies. In this setting, samples are typically collected one at a time. To complement the current multi-sample use of MCP-counter, designed for exploratory analyses, one could notably settle on a desired gene expression platform and use a set of calibrating samples. For instance, in-vitro RNA mixtures described herein could help mapping MCP-counter abundance scores to non-arbitrary units, such as the percentage of the corresponding cells within a sample.

To our knowledge, MCP-counter is the first validated computational method that enables a robust quantification of the abundance of multiple immune and non-immune stromal populations in the transcriptome of cellularly-heterogeneous tissues such as normal or malignant tissues. It might be relevant in a clinical setting, as immune biomarkers can help predict patient's prognosis or response to therapies, most notably to immunotherapies. Its retrospective and prospective application to study inflammatory profiles through transcriptomics should help unraveling the role of immune and stromal populations in cancers and other diseases, and help decipher the interplay between these populations.

Table 1: Gene signatures for quantifying the population of cells of monocytic origin and others cells in a tissue sample.

Complete gene signatures were obtained based on the methodology described in EXAMPLE. In this example, it is shown that the complete signatures are able to predict corresponding cell types' proportions in a heterogeneous tissue.

5 Let S be a signature, composed of n probesets $f_{1 \leq i \leq n}$.
 9697 tumor transcriptomes from multiple cancer types were obtained from public repositories. Expression values for each probesets were mean-centered across samples (row centering). The expression values from probesets within S were then averaged to obtain a single representative value for each sample : $mean_{1 \leq i \leq n}(f)$.

We then computed, for each combination f_{sub} of length from 1 and up to 10 probesets of S , the average expression $mean(f_{sub})$ for each 10 sample.

We then correlated $mean(f_{sub})$ to $mean_{1 \leq i \leq n}(f)$.

When available, we correlated the true-proportions of mRNA from the corresponding cell type in the *in-vitro* RNA-mixture validation model described in EXAMPLE to $mean(f_{sub})$.

Combinations were ranked according to their ability to correlate with *in-vitro* RNA proportions, if available or with their ability to correlate 15 to the summarized expression of the complete set of marker.

Table 1: combination of genes

Combination of genes for identification of B cells

20

| | | | | | | | | | | | | |
|----------|----|----|----|----|----|----|----|----|----|-----|------------|------------|
| Nb Genes | S1 | S2 | S3 | S4 | S5 | S6 | S7 | S8 | S9 | S10 | r_metagene | r_melanges |
|----------|----|----|----|----|----|----|----|----|----|-----|------------|------------|

| | | | | | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|----|----|----|----|----|----|----|----|------------|----|------------|
| 3 | MS4A1 | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93563326 | NA | 0,99626798 |
| 4 | MS4A1 | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93326143 | NA | 0,99534292 |
| 4 | MS4A1 | CD19 | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9550717 | NA | 0,9953207 |
| 2 | MS4A1 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92281625 | NA | 0,99530783 |
| 4 | MS4A1 | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94797522 | NA | 0,99481924 |
| 3 | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87288207 | NA | 0,99406149 |
| 5 | MS4A1 | CD19 | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95131115 | NA | 0,99397741 |
| 2 | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86624957 | NA | 0,99388892 |
| 1 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7391599 | NA | 0,99384517 |
| 4 | MS4A1 | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94452501 | NA | 0,99363876 |
| 5 | MS4A1 | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94359934 | NA | 0,99337142 |
| 1 | MS4A1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91226624 | NA | 0,99333527 |
| 3 | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89896886 | NA | 0,99331135 |
| 3 | MS4A1 | CD19 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95471648 | NA | 0,99322704 |
| 5 | MS4A1 | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94578471 | NA | 0,99310143 |
| 5 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9603499 | NA | 0,99305263 |
| 3 | MS4A1 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91796041 | NA | 0,99280505 |
| 3 | CD19 | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91829543 | NA | 0,9924966 |
| 3 | MS4A1 | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9062648 | NA | 0,99249446 |
| 3 | MS4A1 | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93733292 | NA | 0,99236082 |
| 5 | MS4A1 | CD19 | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95894958 | NA | 0,99234037 |
| 5 | MS4A1 | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95488479 | NA | 0,99224518 |
| 4 | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89269044 | NA | 0,9922331 |
| 3 | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88419484 | NA | 0,99205412 |
| 6 | MS4A1 | CD19 | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9571508 | NA | 0,99200751 |
| 3 | MS4A1 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94298914 | NA | 0,99183484 |
| 4 | CD19 | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9149227 | NA | 0,99183066 |
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95795815 | NA | 0,99168854 |
| 6 | MS4A1 | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95399996 | NA | 0,99154148 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|------|----|----|----|----|------------|------------|
| 4 | MS4A1 | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91790571 | 0,99142212 |
| 4 | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,90135266 | 0,99131979 |
| 4 | MS4A1 | CD19 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,94661979 | 0,99113852 |
| 3 | MS4A1 | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92594051 | 0,99084195 |
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,96384824 | 0,99078303 |
| 5 | MS4A1 | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,96798904 | 0,99074951 |
| 3 | MS4A1 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,93586662 | 0,99057309 |
| 4 | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91059616 | 0,9905674 |
| 4 | MS4A1 | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,92532405 | 0,99048103 |
| 4 | CD19 | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,92952112 | 0,990438 |
| 2 | MS4A1 | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92135589 | 0,99041176 |
| 4 | MS4A1 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,93365311 | 0,99039564 |
| 6 | MS4A1 | CD19 | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,97614328 | 0,99038639 |
| 4 | MS4A1 | CD19 | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93265131 | 0,99031979 |
| 7 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,96293755 | 0,99027657 |
| 5 | MS4A1 | CD19 | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,96930951 | 0,99027205 |
| 5 | CD19 | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,92394658 | 0,99015921 |
| 5 | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,91540357 | 0,98998209 |
| 4 | MS4A1 | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,94066403 | 0,98995897 |
| 3 | MS4A1 | CD19 | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94532322 | 0,98992465 |
| 2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79184882 | 0,98992361 |
| 4 | CD19 | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92261967 | 0,98989298 |
| 4 | MS4A1 | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,95836094 | 0,98987365 |
| 4 | MS4A1 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93789227 | 0,98980658 |
| 4 | MS4A1 | CD19 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,96095618 | 0,98975014 |
| 5 | MS4A1 | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,93390717 | 0,98942868 |
| 5 | CD19 | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,92828861 | 0,98930985 |
| 4 | MS4A1 | CD19 | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | 0,9511751 | 0,98924644 |
| 5 | MS4A1 | CD19 | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,93816482 | 0,98924072 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|------|----|----|----|----|------------|------------|
| 4 | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93855636 | 0,98912211 |
| 4 | MS4A1 | CD19 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95822052 | 0,98909381 |
| 6 | MS4A1 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,97367789 | 0,98907717 |
| 5 | MS4A1 | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,96534493 | 0,98897845 |
| 5 | MS4A1 | CD19 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,95412426 | 0,98897416 |
| 6 | MS4A1 | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,98019213 | 0,98884669 |
| 4 | MS4A1 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95194273 | 0,98881967 |
| 2 | MS4A1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87197667 | 0,98864823 |
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | 0,97302681 | 0,98864191 |
| 4 | MS4A1 | CD19 | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,9451123 | 0,98859083 |
| 3 | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82398562 | 0,98856023 |
| 7 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,97934183 | 0,98855111 |
| 5 | CD19 | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,95495608 | 0,98846685 |
| 7 | MS4A1 | CD19 | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,98507187 | 0,98843678 |
| 5 | CD19 | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,93351767 | 0,98842369 |
| 5 | MS4A1 | CD19 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,95574241 | 0,98838583 |
| 5 | MS4A1 | CD19 | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | 0,94235766 | 0,98836113 |
| 5 | MS4A1 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94937805 | 0,98836093 |
| 2 | CD19 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89004555 | 0,98829046 |
| 6 | CD19 | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,93546846 | 0,98826137 |
| 2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84099684 | 0,9882253 |
| 3 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83638655 | 0,9878484 |
| 2 | MS4A1 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93665178 | 0,98783606 |
| 4 | MS4A1 | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,94861702 | 0,98772438 |
| 7 | MS4A1 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,98425082 | 0,98769964 |
| 4 | CD19 | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,9409771 | 0,98767821 |
| 6 | MS4A1 | CD19 | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,97945512 | 0,98767447 |
| 5 | MS4A1 | CD19 | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | 0,95168985 | 0,98762994 |
| 5 | MS4A1 | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,97273142 | 0,98761494 |

| | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|------|------|----|----|------------|------------|
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | 0,94689658 | 0,98759884 |
| 5 | MS4A1 | CD19 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,96425538 | 0,98735291 |
| 8 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | 0,98727506 | 0,98720099 |
| 5 | MS4A1 | CD19 | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,96077108 | 0,98718849 |
| 6 | MS4A1 | CD19 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,96184143 | 0,9871467 |
| 6 | MS4A1 | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,97760869 | 0,98712009 |
| 3 | MS4A1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,89237448 | 0,98711845 |
| 3 | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,91707241 | 0,98707494 |
| 3 | CD19 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,8845682 | 0,9870749 |
| 2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,79792646 | 0,98704302 |
| 5 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,94944549 | 0,98702949 |
| 5 | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,9575633 | 0,98700465 |
| 7 | MS4A1 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | 0,98195468 | 0,98678206 |
| 6 | CD19 | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,96793387 | 0,98640876 |
| 4 | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,93202706 | 0,98639497 |
| 4 | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,86704657 | 0,98639097 |
| 6 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,96090204 | 0,98631774 |
| 2 | MS4A1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90971678 | 0,98620615 |
| 3 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,85624311 | 0,98615995 |
| 5 | MS4A1 | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,95734596 | 0,9860997 |
| 3 | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,8655927 | 0,98606824 |
| 5 | MS4A1 | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,96336206 | 0,98604253 |
| 2 | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86214574 | 0,98595174 |
| 5 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | 0,94868775 | 0,98592479 |
| 2 | MS4A1 | CD19 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94960466 | 0,9858662 |
| 5 | MS4A1 | CD19 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,96647529 | 0,98584596 |
| 3 | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,84809113 | 0,98576805 |
| 4 | MS4A1 | CD19 | CR2 | IGKC | NA | NA | NA | NA | NA | NA | 0,95301933 | 0,98573656 |
| 6 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,96525917 | 0,9857326 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|------|------|------|----|----|----|----|------------|------------|
| 4 | CD19 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,90007337 | 0,98568803 |
| 2 | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79277849 | 0,98566369 |
| 4 | MS4A1 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,95246454 | 0,98556824 |
| 4 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,88304022 | 0,98547845 |
| 6 | MS4A1 | CD19 | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,9711505 | 0,98547325 |
| 3 | MS4A1 | CD19 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92005584 | 0,98545944 |
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,96581706 | 0,98539803 |
| 3 | MS4A1 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90706276 | 0,98534467 |
| 3 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86683129 | 0,98534125 |
| 4 | MS4A1 | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,94766315 | 0,98513308 |
| 7 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97208761 | 0,98510101 |
| 4 | CD19 | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,88159827 | 0,98505472 |
| 6 | MS4A1 | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,96982432 | 0,9850303 |
| 4 | MS4A1 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92003739 | 0,98491998 |
| 5 | CD19 | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,95665677 | 0,98485672 |
| 2 | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81306738 | 0,98484643 |
| 3 | MS4A1 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,93482697 | 0,98483162 |
| 3 | CD19 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91084648 | 0,98476827 |
| 5 | MS4A1 | CD19 | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | 0,95881036 | 0,98472749 |
| 4 | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,94127473 | 0,984724 |
| 4 | MS4A1 | CD19 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92731117 | 0,984704 |
| 4 | MS4A1 | CD19 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,95419459 | 0,98462229 |
| 3 | MS4A1 | CR2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,93693495 | 0,98461057 |
| 5 | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,95164541 | 0,98456665 |
| 3 | CD19 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89473925 | 0,98452596 |
| 7 | MS4A1 | CD19 | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97487891 | 0,9843861 |
| 5 | MS4A1 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,96206758 | 0,98437053 |
| 6 | MS4A1 | CD19 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,97888851 | 0,98432698 |
| 6 | MS4A1 | CD19 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,97178589 | 0,98430027 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|------|----|----|----|----|------------|------------|
| 5 | MS4A1 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,97023122 | 0,98429406 |
| 4 | CD19 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,90897621 | 0,98425791 |
| 6 | CD19 | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,96196929 | 0,98415697 |
| 5 | CD19 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,91998267 | 0,98388955 |
| 5 | CD19 | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,90222881 | 0,98384808 |
| 3 | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89931683 | 0,98368166 |
| 5 | MS4A1 | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,96229407 | 0,98365708 |
| 6 | MS4A1 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,97698788 | 0,98357058 |
| 5 | MS4A1 | CD19 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,96107127 | 0,98356341 |
| 5 | MS4A1 | CD19 | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,96486755 | 0,98354662 |
| 3 | MS4A1 | CD19 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95369624 | 0,98354153 |
| 7 | MS4A1 | CD19 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,98253411 | 0,98340134 |
| 4 | CD19 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91535662 | 0,98326758 |
| 4 | MS4A1 | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,9545773 | 0,98326295 |
| 6 | MS4A1 | CD19 | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,96903096 | 0,98325637 |
| 4 | MS4A1 | CD19 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93485975 | 0,98320303 |
| 5 | MS4A1 | CD19 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94034571 | 0,98316078 |
| 3 | MS4A1 | CD19 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94172605 | 0,98315805 |
| 4 | MS4A1 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,94694587 | 0,98314638 |
| 3 | CD19 | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87072221 | 0,98290259 |
| 3 | MS4A1 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,93391049 | 0,98286657 |
| 4 | CD19 | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,89439966 | 0,98286129 |
| 4 | CD19 | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,92664517 | 0,98282004 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | 0,96695517 | 0,98275563 |
| 5 | MS4A1 | CD19 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,96908174 | 0,9825981 |
| 4 | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92481613 | 0,98252549 |
| 4 | CD19 | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,90360172 | 0,98252071 |
| 4 | MS4A1 | CD19 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,94990986 | 0,9824086 |
| 6 | MS4A1 | CD19 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,973755 | 0,98227573 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|----|----|----|------------|------------|
| 5 | MS4A1 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,96524212 | 0,98209551 |
| 4 | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,91809393 | 0,98206113 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,97169449 | 0,98205935 |
| 5 | CD19 | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94311014 | 0,98174925 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | 0,96974089 | 0,98172364 |
| 4 | MS4A1 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95620009 | 0,98171334 |
| 5 | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,93852849 | 0,98169936 |
| 4 | CD19 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,92981205 | 0,98166161 |
| 8 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | 0,9740553 | 0,98139656 |
| 5 | MS4A1 | CD79A | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,95915221 | 0,98136485 |
| 6 | MS4A1 | CD79A | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,966518 | 0,98128874 |
| 3 | CD19 | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88473797 | 0,98126912 |
| 5 | CD19 | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,93701638 | 0,98121322 |
| 5 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | 0,96903417 | 0,98111856 |
| 3 | CD19 | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90631527 | 0,98104223 |
| 3 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89725776 | 0,98098966 |
| 7 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,97100663 | 0,98097514 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | 0,96467057 | 0,98095127 |
| 6 | CD19 | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95080332 | 0,98092806 |
| 5 | CD19 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,95004811 | 0,98068731 |
| 2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,66715922 | 0,98066017 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | 0,97045527 | 0,98059006 |
| 4 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92887121 | 0,98048437 |
| 5 | CD19 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,9413525 | 0,98031944 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,97262371 | 0,98026497 |
| 4 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,91896451 | 0,98017742 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | 0,97395376 | 0,98011868 |
| 5 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94407234 | 0,98011372 |
| 6 | CD19 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95811598 | 0,98003583 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|------|----|----|------------|------------|
| 4 | MS4A1 | CD19 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,94318027 | 0,98003574 |
| 5 | MS4A1 | CD19 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,95854665 | 0,97954565 |
| 4 | MS4A1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,94380945 | 0,97927855 |
| 5 | MS4A1 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,95531605 | 0,97925659 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,97160337 | 0,97921314 |
| 5 | MS4A1 | CD19 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,95205318 | 0,97918206 |
| 6 | MS4A1 | CD19 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,96502514 | 0,97918094 |
| 3 | MS4A1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92070233 | 0,97913025 |
| 3 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78166002 | 0,97905618 |
| 5 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | 0,9660653 | 0,97905604 |
| 4 | MS4A1 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93653115 | 0,97899145 |
| 3 | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,89343488 | 0,97894926 |
| 4 | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91971045 | 0,97880719 |
| 4 | CD19 | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,92092762 | 0,97877418 |
| 5 | MS4A1 | CD79A | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,9681436 | 0,97854414 |
| 5 | CD19 | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,93764622 | 0,97849641 |
| 6 | CD19 | CD79A | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95127079 | 0,97828268 |
| 5 | CD19 | CD79A | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,94504848 | 0,97818186 |
| 4 | CD19 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,91795311 | 0,97815532 |
| 3 | CD19 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,90100089 | 0,97804456 |
| 4 | MS4A1 | CD79A | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,96186986 | 0,97803321 |
| 7 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,95566884 | 0,97794305 |
| 3 | CD19 | CR2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,90732523 | 0,97782841 |
| 5 | CD19 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,93936416 | 0,97780132 |
| 9 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | 0,98671507 | 0,97778275 |
| 8 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,98534791 | 0,97767455 |
| 8 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | 0,97940489 | 0,9776293 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,97726667 | 0,97758106 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | 0,95009381 | 0,97754956 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|----|----|----|------------|------------|
| 4 | CD19 | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92778329 | 0,97751791 |
| 4 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91641146 | 0,97724451 |
| 6 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,9485502 | 0,97721888 |
| 4 | CD19 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92759362 | 0,97717095 |
| 5 | CD79A | CR2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,93988497 | 0,97701512 |
| 3 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,88253236 | 0,97698073 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95629669 | 0,97696982 |
| 3 | CD19 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8187019 | 0,97695123 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | 0,96027221 | 0,97694566 |
| 4 | CD19 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,86259045 | 0,97687255 |
| 8 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,98507623 | 0,97679198 |
| 5 | MS4A1 | CD19 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,95410459 | 0,9766764 |
| 4 | MS4A1 | CD19 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,93852251 | 0,97658303 |
| 3 | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90084353 | 0,97650179 |
| 5 | MS4A1 | CD19 | CD79A | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | 0,95172964 | 0,97629875 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | 0,95612126 | 0,97620897 |
| 7 | MS4A1 | CD79A | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,98252299 | 0,97619048 |
| 5 | CD79A | CR2 | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,93946147 | 0,97619012 |
| 7 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,97571901 | 0,97618297 |
| 2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74212781 | 0,97617417 |
| 7 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | 0,97391176 | 0,97615119 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95532684 | 0,97613424 |
| 4 | MS4A1 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,93988517 | 0,97606642 |
| 6 | MS4A1 | CD19 | CD79A | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,97107887 | 0,97602441 |
| 4 | CD79A | CR2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,92872989 | 0,97573149 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,9536605 | 0,97564217 |
| 8 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | 0,98068003 | 0,97563609 |
| 5 | MS4A1 | CD79A | CR2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94817273 | 0,9755111 |
| 4 | MS4A1 | CD19 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,94586319 | 0,97546455 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|----|----|----|------------|------------|
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | 0,96860583 | 0,975427 |
| 6 | MS4A1 | CD79A | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,97197232 | 0,97534228 |
| 5 | MS4A1 | CD19 | CD79A | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,96512853 | 0,97532057 |
| 3 | MS4A1 | CD19 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,92699652 | 0,97532005 |
| 3 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89310271 | 0,97528639 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | 0,97244881 | 0,97523829 |
| 3 | MS4A1 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,91615027 | 0,97522226 |
| 2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72943062 | 0,97511138 |
| 6 | MS4A1 | CD79A | FCRL2 | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,97007996 | 0,9750289 |
| 5 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | 0,94972197 | 0,97502351 |
| 5 | CD19 | CD79A | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,95087491 | 0,97494793 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,9790282 | 0,9747407 |
| 5 | MS4A1 | CD79A | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | 0,94882001 | 0,97465164 |
| 4 | CD19 | CD79A | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,94728838 | 0,97434564 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | 0,96218803 | 0,97434051 |
| 5 | MS4A1 | CD79A | BANK1 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,96399178 | 0,9742211 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | 0,96985889 | 0,97415347 |
| 8 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,97288041 | 0,97412091 |
| 5 | CD79A | CR2 | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,94710864 | 0,97408636 |
| 7 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,97793601 | 0,97398602 |
| 2 | CR2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86681086 | 0,97394642 |
| 2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84885578 | 0,9737535 |
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,9739847 | 0,9736447 |
| 5 | MS4A1 | CD79A | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | 0,96167674 | 0,97355679 |
| 7 | CD19 | CD79A | CR2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97021925 | 0,97349447 |
| 5 | CD19 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,92425149 | 0,97343512 |
| 4 | MS4A1 | CD79A | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,94038371 | 0,9733746 |
| 3 | MS4A1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92431357 | 0,97326718 |
| 7 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,96292453 | 0,97323663 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|------|------|------|----|----|----|------------|------------|
| 5 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | 0,96005737 | 0,97317365 |
| 3 | CD19 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84704201 | 0,97309499 |
| 4 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,89755162 | 0,97309259 |
| 1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,55670562 | 0,97308261 |
| 8 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,97429393 | 0,97308215 |
| 5 | MS4A1 | CD19 | CD79A | CR2 | CD22 | NA | NA | NA | NA | NA | NA | 0,96007687 | 0,97307024 |
| 3 | CD19 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85860543 | 0,97300676 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,9671637 | 0,97278351 |
| 7 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,96872754 | 0,97268061 |
| 5 | MS4A1 | CD79A | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | 0,95931106 | 0,97260058 |
| 5 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | 0,96992168 | 0,97253764 |
| 4 | CD19 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,90854879 | 0,97252836 |
| 6 | CD19 | CD79A | CR2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,95895989 | 0,97245996 |
| 5 | MS4A1 | CD19 | CD79A | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,97279629 | 0,97243255 |
| 8 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,98136312 | 0,9723154 |
| 1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,49124845 | 0,97228258 |
| 4 | CD79A | CR2 | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,9398039 | 0,97217371 |
| 4 | MS4A1 | CD79A | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,95377549 | 0,97215688 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97168222 | 0,97214909 |
| 6 | MS4A1 | CD79A | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,97477367 | 0,9721214 |
| 4 | CD79A | CR2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,93992666 | 0,97191919 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | 0,96594349 | 0,97188759 |
| 5 | MS4A1 | CD79A | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | 0,97131136 | 0,97161625 |
| 1 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74508284 | 0,97158098 |
| 7 | MS4A1 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97100347 | 0,97152032 |
| 3 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86829048 | 0,97141972 |
| 4 | MS4A1 | CD19 | CD79A | CR2 | NA | NA | NA | NA | NA | NA | NA | 0,95842652 | 0,9713712 |
| 4 | CD19 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,90177063 | 0,97134167 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,93053719 | 0,97130274 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|----|----|----|------------|------------|
| 7 | MS4A1 | CD19 | CD79A | BANK1 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,97890412 | 0,97130237 |
| 6 | CD79A | CR2 | BANK1 | IGKC | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | 0,96394968 | 0,97129264 |
| 7 | MS4A1 | CD19 | CD79A | FCRL2 | BANK1 | BANK1 | IGKC | PAX5 | NA | NA | NA | 0,97170296 | 0,97108718 |
| 6 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | IGKC | PAX5 | NA | NA | NA | NA | 0,95540805 | 0,97103888 |
| 4 | MS4A1 | CD19 | CD79A | BANK1 | BANK1 | NA | NA | NA | NA | NA | NA | 0,96874678 | 0,97091887 |
| 6 | CD19 | CD79A | FCRL2 | BANK1 | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | 0,94720138 | 0,9708394 |
| 7 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | BANK1 | IGKC | CD22 | NA | NA | NA | 0,96253043 | 0,97083217 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | IGKC | IGKC | PAX5 | NA | NA | NA | NA | 0,96232531 | 0,97061993 |
| 7 | MS4A1 | CD79A | FCRL2 | BANK1 | IGKC | IGKC | PAX5 | CD22 | NA | NA | NA | 0,97785227 | 0,97058695 |
| 5 | CD19 | CD79A | CR2 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | 0,92181348 | 0,97015069 |
| 2 | CD19 | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89180868 | 0,97014801 |
| 2 | CD19 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79165949 | 0,97012304 |
| 3 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86181803 | 0,97006497 |
| 5 | MS4A1 | CD79A | CR2 | BANK1 | IGKC | IGKC | NA | NA | NA | NA | NA | 0,96249088 | 0,97001551 |
| 4 | MS4A1 | CD79A | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | 0,95546463 | 0,96987568 |
| 3 | CD19 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88029201 | 0,96987253 |
| 2 | MS4A1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89417939 | 0,96984535 |
| 5 | CD79A | CR2 | FCRL2 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | 0,91699959 | 0,96973209 |
| 6 | MS4A1 | CD19 | CD79A | BANK1 | IGKC | IGKC | PAX5 | NA | NA | NA | NA | 0,96800436 | 0,96972953 |
| 6 | MS4A1 | CD79A | CR2 | IGKC | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | 0,96664528 | 0,96972295 |
| 5 | CD19 | CD79A | BANK1 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | 0,94019805 | 0,96967196 |
| 4 | MS4A1 | CD79A | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95441585 | 0,96956861 |
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | 0,95575629 | 0,96956853 |
| 7 | MS4A1 | CD19 | CD79A | CR2 | FCRL2 | FCRL2 | IGKC | CD22 | NA | NA | NA | 0,96728341 | 0,96947444 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | IGKC | IGKC | PAX5 | NA | NA | NA | NA | 0,96005782 | 0,96946621 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | BANK1 | BANK1 | IGKC | NA | NA | NA | NA | 0,95081491 | 0,96924026 |
| 4 | MS4A1 | CD79A | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,96411787 | 0,96908191 |
| 5 | CD79A | FCRL2 | BANK1 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | 0,9349252 | 0,96892933 |
| 5 | CD79A | CR2 | BANK1 | IGKC | PAX5 | PAX5 | NA | NA | NA | NA | NA | 0,94847687 | 0,96892383 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-------|------|------|----|----|----|------------|------------|
| 7 | MS4A1 | CD19 | CD79A | CD79A | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | 0,97205676 | 0,96888691 |
| 4 | MS4A1 | CD79A | BANK1 | CD22 | CD22 | NA | NA | NA | NA | NA | NA | 0,96690309 | 0,96883976 |
| 6 | CD19 | CD79A | CR2 | BANK1 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,95895669 | 0,9688355 |
| 6 | MS4A1 | CD79A | BANK1 | IGKC | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,97344244 | 0,96874823 |
| 5 | CD19 | CD79A | CR2 | FCRL2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | 0,92455066 | 0,96854853 |
| 6 | MS4A1 | CD79A | FCRL2 | BANK1 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | 0,96509234 | 0,96853511 |
| 5 | CD19 | CD79A | FCRL2 | BANK1 | BANK1 | PAX5 | NA | NA | NA | NA | NA | 0,93920754 | 0,96845593 |
| 6 | CD79A | CR2 | FCRL2 | BANK1 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,95576899 | 0,96833643 |
| 3 | CD79A | CR2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,93161313 | 0,96812098 |
| 4 | CD19 | FCRL2 | IGKC | CD22 | CD22 | NA | NA | NA | NA | NA | NA | 0,89648348 | 0,96809997 |
| 2 | CD19 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80950487 | 0,96805325 |
| 5 | MS4A1 | CD19 | CD79A | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95018765 | 0,96792573 |
| 5 | MS4A1 | CD79A | FCRL2 | PAX5 | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,94844566 | 0,96749048 |
| 7 | CD19 | CD79A | CR2 | FCRL2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,95298142 | 0,96748392 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | 0,95781313 | 0,96738437 |
| 4 | CD79A | CR2 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | NA | 0,90029962 | 0,96728417 |
| 7 | CD19 | CD79A | FCRL2 | BANK1 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | 0,95993342 | 0,96697427 |
| 6 | MS4A1 | CD19 | CD79A | CR2 | CR2 | IGKC | CD22 | NA | NA | NA | NA | 0,96421671 | 0,9669454 |
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | 0,96075536 | 0,96686648 |
| 6 | MS4A1 | CD79A | CR2 | FCRL2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | 0,96252164 | 0,96675139 |
| 5 | MS4A1 | CD19 | CD79A | FCRL2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | 0,95046498 | 0,96664793 |
| 5 | MS4A1 | CD79A | CR2 | IGKC | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,95408652 | 0,96663479 |
| 4 | CD19 | CD79A | BANK1 | PAX5 | PAX5 | NA | NA | NA | NA | NA | NA | 0,93080338 | 0,96656002 |
| 6 | MS4A1 | CD19 | CD79A | BANK1 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | 0,96874913 | 0,96650951 |
| 4 | CD79A | BANK1 | PAX5 | CD22 | CD22 | NA | NA | NA | NA | NA | NA | 0,91934165 | 0,96649097 |
| 4 | CD19 | CD79A | CR2 | PAX5 | PAX5 | NA | NA | NA | NA | NA | NA | 0,91497037 | 0,96643706 |
| 5 | CD19 | CD79A | CR2 | BANK1 | BANK1 | IGKC | NA | NA | NA | NA | NA | 0,94553432 | 0,96641746 |
| 5 | CD19 | CD79A | FCRL2 | BANK1 | BANK1 | CD22 | NA | NA | NA | NA | NA | 0,94270097 | 0,96633461 |
| 2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82114181 | 0,9663097 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|------|------|------|----|----|----|----|------------|------------|
| 5 | CD19 | CD79A | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | 0,92981325 | 0,96630389 |
| 6 | MS4A1 | CD79A | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,96623323 | 0,96609579 |
| 3 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85302786 | 0,96605271 |
| 2 | CD19 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87512244 | 0,9660193 |
| 5 | MS4A1 | CD79A | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,95870064 | 0,96576482 |
| 7 | MS4A1 | CD19 | CD79A | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | 0,96433433 | 0,96566981 |
| 4 | CD79A | CR2 | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,90618535 | 0,96528207 |
| 6 | CD19 | CD79A | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,94768795 | 0,9652759 |
| 5 | CD79A | CR2 | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,93960271 | 0,96527281 |
| 6 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,94486592 | 0,96501847 |
| 4 | CD79A | FCRL2 | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,92016058 | 0,96501619 |
| 6 | CD19 | CD79A | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95456375 | 0,964815 |
| 5 | CD79A | CR2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,94922608 | 0,96468916 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,94089451 | 0,96459409 |
| 5 | MS4A1 | CD19 | CD79A | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | 0,95862731 | 0,96457489 |
| 6 | CD79A | FCRL2 | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95090436 | 0,96437618 |
| 4 | MS4A1 | CD79A | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,93733797 | 0,96437425 |
| 6 | CD19 | CD79A | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,94569477 | 0,96426477 |
| 3 | MS4A1 | CD79A | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95845726 | 0,96411196 |
| 4 | MS4A1 | CD19 | CD79A | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,94418505 | 0,963839 |
| 3 | MS4A1 | CD79A | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95047375 | 0,96374817 |
| 3 | CD19 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | 0,86642719 | 0,96365921 |
| 5 | MS4A1 | CD19 | CD79A | CR2 | IGKC | NA | NA | NA | NA | NA | NA | 0,95350448 | 0,96361397 |
| 5 | MS4A1 | CD19 | CD79A | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,955841 | 0,96344972 |
| 6 | MS4A1 | CD19 | CD79A | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95967772 | 0,96306329 |
| 5 | MS4A1 | CD79A | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | 0,94976617 | 0,9629642 |
| 6 | MS4A1 | CD79A | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,95763319 | 0,96287314 |
| 3 | CD19 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87319211 | 0,96281525 |
| 4 | MS4A1 | CD79A | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,93924174 | 0,96281185 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|------|------|----|----|----|----|----|------------|------------|
| 4 | CD79A | CR2 | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,91862521 | 0,96277307 |
| 4 | CD19 | CD79A | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,93785151 | 0,96274173 |
| 4 | CD79A | FCRL2 | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92981775 | 0,96267336 |
| 5 | MS4A1 | CD79A | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,9508874 | 0,96257034 |
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | 0,95280004 | 0,96249251 |
| 5 | MS4A1 | CD79A | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,95720343 | 0,96233033 |
| 4 | CD19 | CD79A | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | 0,93711341 | 0,96230814 |
| 5 | MS4A1 | CD79A | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,96022713 | 0,96207872 |
| 4 | CD19 | CD79A | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,92397341 | 0,96197831 |
| 6 | CD19 | CD79A | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,93960472 | 0,96159795 |
| 6 | CD19 | CD79A | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,94253209 | 0,96159362 |
| 4 | CD19 | CD79A | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | 0,92823933 | 0,96132356 |
| 5 | CD79A | CR2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,93603227 | 0,96126822 |
| 5 | CD19 | CD79A | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,9337243 | 0,96115513 |
| 5 | CD19 | CD79A | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,93796735 | 0,96104149 |
| 5 | CD79A | BANK1 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94144229 | 0,96081423 |
| 4 | MS4A1 | CD79A | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95508562 | 0,96053954 |
| 5 | CD19 | CD79A | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,90773872 | 0,96051076 |
| 5 | CD79A | CR2 | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,92814666 | 0,96048179 |
| 3 | CD79A | BANK1 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89934544 | 0,96023416 |
| 5 | CD79A | FCRL2 | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,93100971 | 0,9601859 |
| 4 | MS4A1 | CD19 | CD79A | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,95626558 | 0,96002015 |
| 6 | MS4A1 | CD19 | CD79A | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | 0,95264669 | 0,95981001 |
| 3 | CD79A | CR2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88600241 | 0,95968698 |
| 4 | MS4A1 | CD19 | CD79A | FCRL2 | NA | NA | NA | NA | NA | NA | NA | 0,9568748 | 0,95957529 |
| 4 | CD79A | CR2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,9300985 | 0,95918669 |
| 5 | MS4A1 | CD79A | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,94987129 | 0,95868499 |
| 5 | MS4A1 | CD19 | CD79A | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,94641501 | 0,95849152 |
| 2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8017488 | 0,95810302 |

| | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|------|------|----|----|----|----|----|------------|------------|
| 5 | MS4A1 | CD79A | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | 0,94193109 | 0,95802889 |
| 6 | CD19 | CD79A | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | 0,93014867 | 0,95723021 |
| 5 | CD79A | FCRL2 | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,92752808 | 0,95716729 |
| 5 | CD79A | CR2 | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,92739378 | 0,95702276 |
| 5 | CD19 | CD79A | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | 0,92484191 | 0,95698851 |
| 5 | CD19 | CD79A | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,93460988 | 0,9568771 |
| 3 | MS4A1 | CD79A | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92549158 | 0,95649481 |
| 4 | CD79A | FCRL2 | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,87924174 | 0,95648687 |
| 5 | CD19 | CD79A | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | 0,92509771 | 0,95636047 |
| 5 | CD19 | CD79A | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,93265817 | 0,956217 |
| 4 | MS4A1 | CD79A | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,94220342 | 0,95605219 |
| 2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80634342 | 0,95594253 |
| 3 | CD19 | CD79A | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,93305792 | 0,95591415 |
| 4 | CD19 | CD79A | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | 0,89086699 | 0,95571302 |
| 3 | CD79A | BANK1 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91487251 | 0,95566576 |
| 4 | MS4A1 | CD79A | CR2 | IGKC | NA | NA | NA | NA | NA | NA | NA | 0,94235709 | 0,95531016 |
| 3 | CD79A | FCRL2 | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91711174 | 0,95519691 |
| 5 | MS4A1 | CD79A | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,94248612 | 0,95499586 |
| 5 | MS4A1 | CD19 | CD79A | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | 0,93891904 | 0,95438797 |
| 4 | CD79A | BANK1 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,91749719 | 0,95426132 |
| 5 | MS4A1 | CD19 | CD79A | IGKC | CD22 | NA | NA | NA | NA | NA | NA | 0,94655998 | 0,95426123 |
| 3 | CD79A | CR2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90521944 | 0,95409317 |
| 4 | CD79A | CR2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,91608093 | 0,95380675 |
| 3 | CD79A | CR2 | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91479532 | 0,95336818 |
| 4 | CD19 | CD79A | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | 0,8974084 | 0,95301774 |
| 5 | CD79A | FCRL2 | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | 0,91275391 | 0,95263552 |
| 3 | CD19 | CD79A | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92464784 | 0,95246193 |
| 2 | CD19 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83388936 | 0,95198197 |
| 3 | MS4A1 | CD79A | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94821999 | 0,9519337 |

| | | | | | | | | | | | | | | | |
|---|-------|-------|-------|------|------|----|----|----|----|----|----|----|----|------------|------------|
| 5 | CD19 | CD79A | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91958419 | 0,95189769 |
| 3 | MS4A1 | CD79A | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95112497 | 0,95144854 |
| 3 | MS4A1 | CD19 | CD79A | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95592077 | 0,95093265 |
| 4 | MS4A1 | CD79A | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93129778 | 0,95089188 |
| 5 | CD19 | CD79A | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91174455 | 0,95062975 |
| 4 | CD19 | CD79A | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90173912 | 0,95059051 |
| 4 | CD79A | FCRL2 | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90184624 | 0,94953493 |
| 4 | CD79A | BANK1 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91325141 | 0,94934749 |
| 4 | CD19 | CD79A | BANK1 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91357035 | 0,94926208 |
| 3 | CD79A | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84157134 | 0,94811484 |
| 4 | CD79A | CR2 | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90652648 | 0,94804069 |
| 4 | CD79A | CR2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91532533 | 0,94776953 |
| 5 | CD19 | CD79A | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90567888 | 0,94729674 |
| 4 | CD19 | CD79A | CR2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91560673 | 0,94689009 |
| 4 | MS4A1 | CD79A | FCRL2 | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92314232 | 0,94609559 |
| 4 | MS4A1 | CD79A | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93199211 | 0,94588963 |
| 4 | MS4A1 | CD19 | CD79A | IGKC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93052407 | 0,94499541 |
| 3 | CD79A | FCRL2 | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85683343 | 0,94444187 |
| 4 | CD79A | IGKC | PAX5 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89474296 | 0,94415373 |
| 3 | CD19 | CD79A | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87762003 | 0,94289464 |
| 4 | CD79A | FCRL2 | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88594471 | 0,94254636 |
| 1 | CR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80302115 | 0,94237086 |
| 3 | CD79A | FCRL2 | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87176333 | 0,94181899 |
| 4 | CD19 | CD79A | IGKC | PAX5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89750387 | 0,94129789 |
| 2 | CD79A | BANK1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89852152 | 0,9390774 |
| 4 | CD79A | FCRL2 | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87794757 | 0,93869974 |
| 3 | CD19 | CD79A | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88768 | 0,93762591 |
| 4 | CD19 | CD79A | IGKC | CD22 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89031085 | 0,9355648 |
| 3 | CD19 | CD79A | FCRL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89918968 | 0,93538769 |

| | | | | | | | | | | | | |
|---|--------------------------|-------|-------|--------------------|--------------------|-------|--------|--------|----|----|------------|----|
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC4 | FGFBP2 | NA | NA | 0,98640948 | NA |
| 8 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,98090553 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | NA | NA | 0,98011097 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | NA | NA | NA | 0,97975409 | NA |
| 7 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | 0,97956756 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | FGFBP2 | NA | NA | NA | 0,97838768 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | 0,97830428 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | 0,97739418 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,97727865 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | 0,97685843 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | 0,97653839 | NA |
| 7 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | 0,97608674 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,97551181 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | KLRC4 | FGFBP2 | NA | NA | NA | 0,97507423 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC4 | NA | NA | NA | 0,97463883 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,97449377 | NA |

| | | | | | | | | | | | | |
|---|--------------------------|-------|-------------------|-------------------|-------------------|--------|--------|--------|----|----|------------|----|
| 7 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | 0,97331621 | NA |
| 7 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | KLRC4 | NA | NA | NA | 0,97207271 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | FGFBP2 | NA | NA | NA | NA | 0,9719625 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | KLRC3 | FGFBP2 | NA | NA | NA | 0,97153412 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | 0,97094866 | NA |
| 6 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | NA | NA | NA | NA | 0,97070135 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | FGFBP2 | NA | NA | NA | NA | 0,96937171 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLR2 | EOMES | FGFBP2 | NA | NA | NA | NA | 0,96922791 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,96895651 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | FGFBP2 | NA | NA | NA | NA | 0,96874368 | NA |
| 6 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | NA | 0,96784754 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | NA | NA | NA | NA | 0,96768575 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | KLRC3 | NA | NA | NA | NA | 0,96741077 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | KLRC4 | NA | NA | NA | NA | 0,96709106 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | 0,96702014 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | EOMES | KLRC3 | KLRC4 | NA | NA | NA | 0,96697943 | NA |

| | | | | | | | | | | | | |
|---|--------------------------|-------|-------------------|-------------------|-------------------|--------|--------|--------|----|----|------------|----|
| 7 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | 0,96696895 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLR2 | EOMES | KLRC4 | NA | NA | NA | NA | 0,96622326 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | KLRC4 | NA | NA | NA | 0,9662044 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | KLRC4 | NA | NA | NA | NA | 0,96602043 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC3 | KLRC4 | NA | NA | NA | NA | 0,96592429 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | NA | NA | NA | NA | 0,96585275 | NA |
| 6 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC4 | NA | NA | NA | NA | 0,96582163 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC4 | NA | NA | NA | NA | 0,96489177 | NA |
| 6 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | NA | 0,96475244 | NA |
| 6 | CD8A | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | FGFBP2 | NA | NA | NA | NA | 0,96466781 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLR2 | KLRC4 | FGFBP2 | NA | NA | NA | NA | 0,96447757 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLR2 | EOMES | KLRC3 | KLRC4 | NA | NA | NA | 0,96427071 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | 0,96404936 | NA |
| 7 | CD8A | KLRD1 | GPLY | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | 0,96375624 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC3 | FGFBP2 | NA | NA | NA | NA | 0,96372759 | NA |
| 8 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLR2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | 0,96319254 | NA |

| | | | | | | | | | | | | | | |
|---|--------------------------|-------|--------------------|--------------------|--------------------|--------|--------|----|----|----|----|----|------------|----|
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | KLRC3 | NA | NA | NA | NA | NA | NA | 0,96315232 | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLRK2 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | 0,96314544 | NA |
| 7 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | 0,96244425 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | 0,96238285 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | KLRC1 /// KLRK2 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | 0,96114694 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | 0,96107269 | NA |
| 5 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | KLRC4 | NA | NA | NA | NA | NA | NA | NA | 0,96030102 | NA |
| 7 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | KLRC3 | KLRC4 | NA | NA | NA | NA | NA | 0,9602309 | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | NA | NA | NA | NA | NA | NA | NA | 0,96022686 | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | KLRC1 /// KLRK2 | EOMES | NA | NA | NA | NA | NA | NA | NA | 0,96018753 | NA |
| 6 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | 0,96012208 | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | NA | NA | NA | NA | NA | NA | NA | 0,95999771 | NA |
| 7 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | 0,95977332 | NA |
| 6 | CD8A | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | FGFBP2 | NA | NA | NA | NA | NA | NA | 0,95976623 | NA |
| 6 | CD8A | KLRD1 | GPLY | KLRC1 /// KLRK2 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | 0,9596332 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLRK2 | EOMES | KLRC3 | KLRC4 | NA | NA | NA | NA | NA | 0,95887071 | NA |

| | | | | | | | | | | | | | | | | |
|---|--------------------------|--------------------|--------------------|--------------------|--------|--------|----|----|----|----|----|----|----|------------|-----------|----|
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9108215 | NA |
| 4 | CD8A | GPLY | KLRC3 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,910677 | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | EOMES | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | 0,90921946 | NA | NA |
| 3 | CD8A | KLRC1 /// KLRC2 | KLRC4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90911222 | NA | NA |
| 4 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRC1 /// KLRC2 | KLRC3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90832511 | NA | NA |
| 3 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | KLRC1 /// KLRC2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90807598 | NA | NA |
| 6 | CD8A | KLRD1 | GPLY | EOMES | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | 0,90780154 | NA | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC1 /// KLRC2 | KLRC3 | KLRC4 | NA | NA | NA | NA | NA | NA | NA | 0,90768374 | NA | NA |
| 2 | CD8A | KLRC3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90673128 | NA | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRD1 | GPLY | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90638933 | NA | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | CD8A | GPLY | EOMES | KLRC4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90582226 | NA | NA |
| 3 | KLRC4-KLRK1 /// KLRK1 | KLRC1 /// KLRC2 | EOMES | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90484148 | NA | NA |
| 5 | KLRC4-KLRK1 /// KLRK1 | KLRD1 | GPLY | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90481931 | NA | NA |
| 3 | KLRC4-KLRK1 /// KLRK1 | GPLY | KLRC1 /// KLRC2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90427726 | NA | NA |
| 6 | KLRC4-KLRK1 /// KLRK1 | CD8A | KLRC1 /// KLRC2 | KLRC3 | KLRC4 | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | 0,90361268 | NA | NA |
| 3 | GPLY | KLRC1 /// KLRC2 | EOMES | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90359784 | NA | NA |
| 4 | GPLY | KLRC1 /// KLRC2 | EOMES | FGFBP2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90348314 | NA | NA |

| | | | | | | | | | | | | | |
|----|-------|---------|---------|-------|-------|-------|-------|-------|------|-----|------|------------|----|
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | 0,95784257 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,95783516 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,9575579 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | 0,95754319 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | 0,95752418 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,95700372 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | 0,95691538 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | NA | NA | NA | NA | 0,95686558 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | 0,95683616 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | 0,95647575 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,95632336 | NA |
| 7 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95629537 | NA |
| 6 | MYCT1 | CLEC14A | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,95616531 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | 0,9561248 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | 0,95551279 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,95543829 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | KDR | NA | NA | NA | NA | NA | 0,95528518 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,955271 | NA |
| 6 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95503027 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | NA | NA | NA | NA | 0,95500482 | NA |
| 8 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,95496222 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95495155 | NA |
| 5 | MYCT1 | CLEC14A | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | NA | 0,9549135 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | 0,95483027 | NA |
| 10 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | ESAM | 0,95480261 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ESAM | NA | NA | NA | NA | NA | 0,95475525 | NA |
| 9 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,95410255 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95395613 | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,95391269 | NA |

| | | | | | | | | | | | | | |
|---|-------|---------|---------|-------|-------|-------|-------|-------|------|----|----|------------|----|
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | 0,95391191 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | 0,95390138 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,95386259 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | NA | NA | NA | NA | NA | 0,95376966 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ESAM | KDR | NA | NA | NA | NA | 0,95370792 | NA |
| 7 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95368727 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | 0,95351568 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | 0,9534452 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | EMCN | VWF | NA | NA | NA | NA | NA | NA | 0,95344091 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95334655 | NA |
| 7 | CDH5 | MYCT1 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95324277 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | 0,9529976 | NA |
| 6 | CDH5 | MYCT1 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,95280465 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | KDR | NA | NA | NA | NA | 0,9527461 | NA |
| 8 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,95273556 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | NA | NA | NA | NA | NA | 0,95273527 | NA |
| 6 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,95268357 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,95268343 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | 0,95256609 | NA |
| 6 | CDH5 | MYCT1 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95253046 | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,95240229 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | 0,95236093 | NA |
| 5 | CDH5 | MYCT1 | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | NA | 0,95234614 | NA |
| 8 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,95231961 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,95228094 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,95225264 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | 0,95210181 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | EMCN | ESAM | NA | NA | NA | NA | NA | NA | 0,95208494 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95197494 | NA |

| | | | | | | | | | | | | | |
|---|-------|---------|---------|-------|-------|-------|-------|------|-----|----|----|------------|----|
| 6 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95192702 | NA |
| 6 | MYCT1 | ROBO4 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,95183685 | NA |
| 5 | MYCT1 | CLEC14A | EMCN | VWF | KDR | NA | NA | NA | NA | NA | NA | 0,95172462 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,95160252 | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ESAM | NA | NA | NA | NA | NA | NA | 0,95146531 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95127385 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | 0,95123484 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,9511948 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | 0,95107194 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | 0,95104637 | NA |
| 7 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,95098809 | NA |
| 6 | MYCT1 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,95088459 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | 0,95082226 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | ESAM | KDR | NA | NA | NA | NA | NA | 0,95078198 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | 0,95077017 | NA |
| 7 | CDH5 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95074895 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | NA | 0,95064184 | NA |
| 9 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,95062874 | NA |
| 9 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,95060483 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | 0,95050868 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,95045217 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | 0,95042186 | NA |
| 7 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | NA | NA | 0,9503705 | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95035744 | NA |
| 6 | CDH5 | CLEC14A | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,9502555 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95017625 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,9501157 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | 0,9501067 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,95007926 | NA |

| | | | | | | | | | | | | | |
|---|---------|---------|---------|-------|-------|-------|-------|-------|-----|----|----|------------|----|
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | ESAM | KDR | NA | NA | NA | NA | NA | 0,9500687 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | KDR | NA | NA | NA | NA | NA | 0,95006706 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,95001376 | NA |
| 9 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,94997195 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | ESAM | KDR | NA | NA | NA | NA | 0,94992421 | NA |
| 6 | MYCT1 | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94986953 | NA |
| 7 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94985459 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94976502 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | 0,94973531 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94963952 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | NA | NA | NA | NA | NA | NA | 0,94963275 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | KDR | NA | NA | NA | 0,94962595 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94961937 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,94958891 | NA |
| 6 | CDH5 | MYCT1 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94958119 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,94955273 | NA |
| 5 | MYCT1 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | NA | 0,94952574 | NA |
| 8 | CDH5 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94948784 | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | EMCN | VWF | NA | NA | NA | NA | NA | NA | 0,94947062 | NA |
| 8 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94940878 | NA |
| 5 | MYCT1 | ROBO4 | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | NA | 0,94926077 | NA |
| 5 | MYCT1 | CLEC14A | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | 0,94923424 | NA |
| 5 | MYCT1 | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | 0,94920562 | NA |
| 8 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94911799 | NA |
| 5 | MYCT1 | CLEC14A | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | NA | 0,94908914 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94903521 | NA |
| 8 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94901943 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | 0,94891904 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | 0,9488437 | NA |

| | | | | | | | | | | | | | |
|---|-------|---------|---------|-------|-------|-------|-------|------|----|----|----|------------|----|
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | KDR | NA | NA | NA | NA | NA | 0,94883447 | NA |
| 8 | CDH5 | MYCT1 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94883288 | NA |
| 8 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,94881796 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | NA | 0,94879526 | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | EMCN | MMRN2 | NA | NA | NA | NA | NA | NA | 0,948658 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94843787 | NA |
| 5 | CDH5 | MYCT1 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | NA | 0,94837585 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94832 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | VWF | KDR | NA | NA | NA | NA | NA | NA | 0,94828991 | NA |
| 8 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,94826962 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94826436 | NA |
| 8 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,94825447 | NA |
| 6 | MYCT1 | CLEC14A | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94825248 | NA |
| 7 | MYCT1 | CLEC14A | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94823728 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94817364 | NA |
| 5 | MYCT1 | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | 0,94814563 | NA |
| 6 | CDH5 | CLEC14A | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94807556 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,94806073 | NA |
| 6 | CDH5 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,94805378 | NA |
| 7 | CDH5 | ROBO4 | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94803833 | NA |
| 5 | CDH5 | MYCT1 | ROBO4 | EMCN | ESAM | NA | NA | NA | NA | NA | NA | 0,94799564 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | KDR | NA | NA | NA | NA | 0,94799011 | NA |
| 7 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,94797913 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,94796442 | NA |
| 8 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,9479478 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | 0,94793438 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | NA | 0,9479319 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | ESAM | KDR | NA | NA | NA | 0,94791939 | NA |
| 6 | MYCT1 | CLEC14A | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94781719 | NA |

| | | | | | | | | | | | | |
|---|---------|---------|---------|-------|-------|-------|-------|------|----|----|------------|----|
| 8 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | 0,9477904 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | ESAM | NA | NA | NA | NA | 0,94778431 | NA |
| 6 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | NA | 0,94772241 | NA |
| 8 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | 0,94772185 | NA |
| 4 | MYCT1 | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | NA | 0,94766941 | NA |
| 5 | CDH5 | MYCT1 | ROBO4 | EMCN | VWF | NA | NA | NA | NA | NA | 0,94765919 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | ESAM | KDR | NA | NA | NA | NA | 0,94759027 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | ESAM | KDR | NA | NA | 0,94757787 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | KDR | NA | NA | 0,94755517 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | NA | NA | NA | NA | 0,94751924 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | MMRN2 | KDR | NA | NA | NA | NA | 0,94747353 | NA |
| 6 | CLEC14A | ROBO4 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | 0,94741722 | NA |
| 7 | CDH5 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,94740687 | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | MMRN2 | KDR | NA | NA | NA | NA | 0,94736678 | NA |
| 6 | MYCT1 | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94734794 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | 0,94734621 | NA |
| 5 | CDH5 | CLEC14A | ROBO4 | EMCN | ESAM | NA | NA | NA | NA | NA | 0,94730652 | NA |
| 5 | CDH5 | CLEC14A | EMCN | VWF | KDR | NA | NA | NA | NA | NA | 0,94728042 | NA |
| 5 | MYCT1 | CLEC14A | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,94727197 | NA |
| 7 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94726031 | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | KDR | NA | NA | 0,94723648 | NA |
| 7 | CDH5 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,94721796 | NA |
| 5 | CDH5 | CLEC14A | EMCN | VWF | ESAM | NA | NA | NA | NA | NA | 0,94721365 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | EMCN | ESAM | KDR | NA | NA | NA | NA | 0,94718768 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | EMCN | MMRN2 | NA | NA | NA | NA | NA | 0,94716372 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | 0,94710882 | NA |
| 5 | CDH5 | MYCT1 | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | 0,94709624 | NA |
| 7 | CDH5 | MYCT1 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | 0,9470815 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | 0,94706952 | NA |

| | | | | | | | | | | | | | | | | | |
|---|---------|---------|---------|-------|-------|-------|-------|-----|----|----|----|----|----|----|------------|------------|----|
| 4 | MYCT1 | CLEC14A | EMCN | VWF | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94699689 | NA |
| 6 | CLEC14A | EMCN | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94699278 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | KDR | NA | NA | NA | NA | NA | NA | NA | 0,946912 | NA | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94688992 | NA | NA |
| 8 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | NA | 0,94688504 | NA | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94684423 | NA | NA |
| 6 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | NA | NA | NA | 0,94680083 | NA | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94679558 | NA | NA |
| 5 | MYCT1 | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94677222 | NA | NA |
| 6 | CLEC14A | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | NA | 0,94674454 | NA | NA |
| 8 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | 0,94664295 | NA | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | NA | 0,94662256 | NA | NA |
| 7 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94661046 | NA | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94660035 | NA | NA |
| 7 | MYCT1 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94656173 | NA | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | NA | 0,94654882 | NA | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | KDR | NA | NA | NA | NA | NA | NA | NA | NA | 0,94646686 | NA | NA |
| 6 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94637698 | NA | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | VWF | KDR | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94630134 | NA | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | NA | NA | NA | NA | NA | NA | NA | 0,9462891 | NA | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94623815 | NA | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94623738 | NA | NA |
| 7 | CDH5 | MYCT1 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94617713 | NA | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | VWF | ESAM | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94614155 | NA | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94609267 | NA | NA |
| 5 | CDH5 | CLEC14A | ROBO4 | EMCN | MMRN2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94608006 | NA | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94604726 | NA | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94594875 | NA | NA |
| 5 | CDH5 | MYCT1 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,94594515 | NA | NA |

| | | | | | | | | | | | | |
|---|---------|---------|---------|-------|-------|-------|-------|-----|----|----|------------|----|
| 6 | MYCT1 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | NA | 0,94408752 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | EMCN | KDR | NA | NA | NA | NA | NA | 0,94408504 | NA |
| 7 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | KDR | NA | NA | NA | 0,94407754 | NA |
| 7 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | 0,94407037 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | 0,94406554 | NA |
| 6 | CDH5 | ROBO4 | EMCN | MMRN2 | ESAM | KDR | NA | NA | NA | NA | 0,94406317 | NA |
| 5 | MYCT1 | CLEC14A | EMCN | ESAM | KDR | NA | NA | NA | NA | NA | 0,94404444 | NA |
| 6 | MYCT1 | CLEC14A | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | 0,94401294 | NA |
| 7 | CDH5 | MYCT1 | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | 0,94400471 | NA |
| 6 | CLEC14A | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | NA | 0,94398762 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | ESAM | NA | NA | NA | 0,94397123 | NA |
| 4 | CDH5 | CLEC14A | EMCN | ESAM | NA | NA | NA | NA | NA | NA | 0,94389966 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | ESAM | KDR | NA | NA | NA | 0,94389461 | NA |
| 6 | MYCT1 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,94387427 | NA |
| 6 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | 0,94386288 | NA |
| 5 | CDH5 | CLEC14A | ROBO4 | EMCN | KDR | NA | NA | NA | NA | NA | 0,94385661 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | ESAM | NA | NA | NA | NA | 0,94385244 | NA |
| 5 | CDH5 | EMCN | VWF | ESAM | KDR | NA | NA | NA | NA | NA | 0,94379729 | NA |
| 6 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | 0,94379507 | NA |
| 6 | CDH5 | CLEC14A | EMCN | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | 0,94377567 | NA |
| 5 | CDH5 | ROBO4 | EMCN | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,94376782 | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | NA | NA | NA | 0,94373482 | NA |
| 5 | MYCT1 | CLEC14A | ROBO4 | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,9437334 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | NA | NA | NA | 0,94369447 | NA |
| 7 | CDH5 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94367113 | NA |
| 7 | CDH5 | CLEC14A | ROBO4 | EMCN | ELTD1 | MMRN2 | KDR | NA | NA | NA | 0,94363962 | NA |
| 6 | CDH5 | MYCT1 | EMCN | ELTD1 | VWF | ESAM | NA | NA | NA | NA | 0,94363842 | NA |
| 7 | MYCT1 | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | 0,94361023 | NA |
| 8 | CDH5 | CLEC14A | ROBO4 | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | 0,94360301 | NA |

| | | | | | | | | | | | | | | |
|---|---------|---------|---------|-------|-------|-------|------|----|----|----|----|----|------------|----|
| 6 | CDH5 | MYCT1 | CLEC14A | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | NA | 0,94354541 | NA |
| 5 | CDH5 | CLEC14A | EMCN | VWF | MMRN2 | NA | NA | NA | NA | NA | NA | NA | 0,94353061 | NA |
| 4 | CDH5 | MYCT1 | CLEC14A | EMCN | NA | NA | NA | NA | NA | NA | NA | NA | 0,94351862 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | VWF | MMRN2 | NA | NA | NA | NA | NA | NA | NA | 0,94345847 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | EMCN | ELTD1 | ESAM | NA | NA | NA | NA | NA | NA | 0,94345113 | NA |
| 5 | CDH5 | CLEC14A | ROBO4 | EMCN | VWF | NA | NA | NA | NA | NA | NA | NA | 0,94340946 | NA |
| 5 | CLEC14A | ROBO4 | EMCN | VWF | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94340373 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ELTD1 | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94339569 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,9433847 | NA |
| 6 | CDH5 | MYCT1 | ROBO4 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | 0,94322186 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ELTD1 | VWF | KDR | NA | NA | NA | NA | NA | NA | 0,94320846 | NA |
| 7 | CDH5 | MYCT1 | ROBO4 | EMCN | ELTD1 | VWF | KDR | NA | NA | NA | NA | NA | 0,94320592 | NA |
| 5 | CDH5 | MYCT1 | VWF | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94317872 | NA |
| 7 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94314706 | NA |
| 7 | CDH5 | MYCT1 | ELTD1 | VWF | MMRN2 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94313311 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | ROBO4 | KDR | NA | NA | NA | NA | NA | NA | NA | 0,9430895 | NA |
| 4 | CDH5 | MYCT1 | CLEC14A | VWF | NA | NA | NA | NA | NA | NA | NA | NA | 0,9430482 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,94301461 | NA |
| 5 | CDH5 | MYCT1 | CLEC14A | ROBO4 | VWF | NA | NA | NA | NA | NA | NA | NA | 0,94300589 | NA |
| 5 | CDH5 | CLEC14A | EMCN | ESAM | KDR | NA | NA | NA | NA | NA | NA | NA | 0,94296402 | NA |
| 5 | MYCT1 | CLEC14A | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | NA | 0,94283637 | NA |
| 7 | CDH5 | ROBO4 | EMCN | ELTD1 | VWF | MMRN2 | ESAM | NA | NA | NA | NA | NA | 0,94281143 | NA |
| 6 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | ESAM | NA | NA | NA | NA | NA | NA | 0,94280113 | NA |
| 7 | CDH5 | CLEC14A | EMCN | ELTD1 | VWF | MMRN2 | KDR | NA | NA | NA | NA | NA | 0,9427626 | NA |
| 6 | CDH5 | CLEC14A | EMCN | ELTD1 | VWF | KDR | NA | NA | NA | NA | NA | NA | 0,94269565 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | EMCN | ELTD1 | KDR | NA | NA | NA | NA | NA | 0,94263224 | NA |
| 6 | MYCT1 | EMCN | ELTD1 | VWF | ESAM | KDR | NA | NA | NA | NA | NA | NA | 0,94254749 | NA |
| 6 | CDH5 | MYCT1 | CLEC14A | ELTD1 | MMRN2 | ESAM | NA | NA | NA | NA | NA | NA | 0,94251689 | NA |
| 7 | CDH5 | MYCT1 | CLEC14A | ROBO4 | ELTD1 | ESAM | KDR | NA | NA | NA | NA | NA | 0,94249949 | NA |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|-------|----|----|----|----|------------|----|
| 5 | COL3A1 | DCN | GREM1 | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | NA | 0,98055719 | NA |
| 7 | COL3A1 | DCN | COL6A2 | COL1A1 | TAGLN | GREM1 | PAMR1 | NA | NA | NA | NA | 0,98045963 | NA |
| 4 | COL3A1 | DCN | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97967789 | NA |
| 6 | COL3A1 | DCN | COL6A2 | COL1A1 | GREM1 | COL6A1 | NA | NA | NA | NA | NA | 0,97900842 | NA |
| 5 | DCN | COL6A2 | COL1A1 | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | 0,97886714 | NA |
| 6 | COL3A1 | DCN | COL6A2 | TAGLN | GREM1 | PAMR1 | NA | NA | NA | NA | NA | 0,97847942 | NA |
| 5 | COL3A1 | DCN | COL6A2 | GREM1 | PAMR1 | NA | NA | NA | NA | NA | NA | 0,97833602 | NA |
| 5 | DCN | COL6A2 | COL1A1 | TAGLN | GREM1 | NA | NA | NA | NA | NA | NA | 0,97732209 | NA |
| 5 | DCN | COL1A1 | GREM1 | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | NA | 0,97716968 | NA |
| 4 | DCN | COL6A2 | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97708011 | NA |
| 6 | DCN | COL6A2 | TAGLN | GREM1 | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | 0,97686705 | NA |
| 5 | COL3A1 | DCN | COL6A2 | TAGLN | GREM1 | NA | NA | NA | NA | NA | NA | 0,97662971 | NA |
| 5 | DCN | COL6A2 | COL1A1 | GREM1 | PAMR1 | NA | NA | NA | NA | NA | NA | 0,97653712 | NA |
| 4 | DCN | COL1A1 | TAGLN | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97628668 | NA |
| 6 | COL3A1 | DCN | COL6A2 | COL1A1 | GREM1 | PAMR1 | NA | NA | NA | NA | NA | 0,97627316 | NA |
| 6 | COL3A1 | DCN | COL6A2 | COL1A1 | TAGLN | GREM1 | NA | NA | NA | NA | NA | 0,97591219 | NA |
| 5 | COL3A1 | DCN | COL1A1 | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | 0,97564524 | NA |
| 4 | COL3A1 | DCN | COL6A2 | GREM1 | NA | NA | NA | NA | NA | NA | NA | 0,9743702 | NA |
| 6 | COL3A1 | DCN | COL1A1 | TAGLN | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | 0,97431503 | NA |
| 4 | COL3A1 | DCN | TAGLN | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97428815 | NA |
| 5 | COL3A1 | DCN | COL1A1 | TAGLN | COL6A1 | NA | NA | NA | NA | NA | NA | 0,97412009 | NA |
| 4 | DCN | COL1A1 | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97352977 | NA |
| 5 | DCN | COL6A2 | GREM1 | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | NA | 0,97286973 | NA |
| 4 | DCN | TAGLN | GREM1 | COL6A1 | NA | NA | NA | NA | NA | NA | NA | 0,97133746 | NA |
| 7 | COL3A1 | DCN | COL6A2 | COL1A1 | TAGLN | COL6A1 | PAMR1 | NA | NA | NA | NA | 0,97114255 | NA |
| 6 | COL3A1 | DCN | COL1A1 | TAGLN | GREM1 | PAMR1 | NA | NA | NA | NA | NA | 0,97060549 | NA |
| 4 | DCN | COL6A2 | COL1A1 | GREM1 | NA | NA | NA | NA | NA | NA | NA | 0,97052176 | NA |
| 7 | COL3A1 | COL6A2 | COL1A1 | TAGLN | GREM1 | COL6A1 | PAMR1 | NA | NA | NA | NA | 0,97046408 | NA |
| 6 | COL3A1 | DCN | COL6A2 | COL1A1 | TAGLN | COL6A1 | NA | NA | NA | NA | NA | 0,97031481 | NA |

| | | | | | | | | | | | | | | | | | |
|---|--------|-------|----|----|----|----|----|----|----|----|----|----|----|----|----|------------|----|
| 1 | GREM1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71888174 | NA |
| 1 | COL6A1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6911634 | NA |
| 2 | COL6A1 | PAMR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,58159652 | NA |
| 1 | PAMR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,08455272 | NA |

Combination of genes for identification of cells of monocytic origin

| | | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 2 | CSF1R | FPR3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87165335 | 0,9890985 |
| 3 | ADAP2 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79500676 | 0,98865004 |
| 3 | CSF1R | ADAP2 | FPR3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89320392 | 0,988532 |
| 4 | CSF1R | ADAP2 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88070275 | 0,98658863 |
| 2 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6978311 | 0,98333583 |
| 3 | CSF1R | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84348522 | 0,98287389 |
| 3 | CSF1R | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85697068 | 0,98050743 |
| 5 | CSF1R | ADAP2 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87708908 | 0,97966598 |
| 2 | CSF1R | ADAP2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86106378 | 0,97909297 |
| 4 | CSF1R | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83666996 | 0,97869136 |
| 4 | CSF1R | ADAP2 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89137636 | 0,97738861 |
| 3 | CSF1R | ADAP2 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89301648 | 0,97694438 |
| 3 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70257538 | 0,97569667 |
| 4 | ADAP2 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79222991 | 0,97562069 |
| 2 | ADAP2 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76325543 | 0,97474965 |
| 1 | CSF1R | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80084571 | 0,97451763 |
| 5 | CSF1R | ADAP2 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90713273 | 0,96983322 |
| 4 | CSF1R | ADAP2 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88572286 | 0,96919054 |
| 2 | CSF1R | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,838643 | 0,96903113 |
| 4 | CSF1R | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88163015 | 0,96705239 |
| 3 | CSF1R | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82363724 | 0,96490587 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|------|----|----|----|------------|------------|
| 6 | CSF1R | ADAP2 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | 0,9047556 | 0,96417377 |
| 5 | CSF1R | ADAP2 | RASSF4 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | 0,96346089 | 0,96405942 |
| 3 | CSF1R | ADAP2 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,87490749 | 0,9636965 |
| 5 | CSF1R | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,87627421 | 0,96226059 |
| 4 | CSF1R | ADAP2 | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | 0,91862941 | 0,96137073 |
| 4 | CSF1R | ADAP2 | RASSF4 | FPR3 | NA | NA | NA | NA | NA | NA | 0,96106023 | 0,9610462 |
| 2 | CSF1R | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,8000538 | 0,96090087 |
| 4 | CSF1R | ADAP2 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,9249639 | 0,96063761 |
| 6 | CSF1R | ADAP2 | RASSF4 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | 0,96360464 | 0,96058524 |
| 4 | ADAP2 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,8415891 | 0,95952886 |
| 3 | ADAP2 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,75753273 | 0,95876217 |
| 3 | CSF1R | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | NA | 0,90463501 | 0,95856471 |
| 1 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,5376277 | 0,95661878 |
| 5 | CSF1R | ADAP2 | RASSF4 | FPR3 | KYNU | NA | NA | NA | NA | NA | 0,96905506 | 0,95573502 |
| 4 | CSF1R | RASSF4 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,95495888 | 0,95539042 |
| 3 | CSF1R | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | 0,89332119 | 0,95517274 |
| 6 | CSF1R | ADAP2 | RASSF4 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | 0,9710615 | 0,95476541 |
| 5 | CSF1R | ADAP2 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,92097386 | 0,95469869 |
| 5 | CSF1R | ADAP2 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | 0,91925853 | 0,95463094 |
| 5 | CSF1R | RASSF4 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,9517327 | 0,95460707 |
| 3 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | 0,77676194 | 0,95391603 |
| 4 | ADAP2 | RASSF4 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,93686931 | 0,95279024 |
| 4 | CSF1R | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | 0,89760987 | 0,95256031 |
| 5 | ADAP2 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,83886295 | 0,95216775 |
| 4 | CSF1R | ADAP2 | RASSF4 | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,96460973 | 0,95156684 |
| 7 | CSF1R | ADAP2 | RASSF4 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | 0,97253139 | 0,95153358 |
| 4 | CSF1R | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | 0,88286922 | 0,95050792 |
| 2 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,57778973 | 0,94989903 |
| 3 | CSF1R | ADAP2 | TFEC | NA | NA | NA | NA | NA | NA | NA | 0,90833099 | 0,94972407 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|------|----|----|----|----|----|------------|------------|
| 3 | ADAP2 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,8167454 | 0,94965034 |
| 5 | ADAP2 | RASSF4 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | 0,93249315 | 0,94920381 |
| 3 | CSF1R | RASSF4 | FPR3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,95895418 | 0,94916314 |
| 5 | CSF1R | ADAP2 | RASSF4 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | 0,970852 | 0,94899215 |
| 2 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70823929 | 0,94896645 |
| 5 | CSF1R | RASSF4 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,96418404 | 0,94843671 |
| 4 | CSF1R | RASSF4 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,96332578 | 0,94815677 |
| 4 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,77612661 | 0,94815204 |
| 5 | CSF1R | ADAP2 | RASSF4 | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | 0,96886588 | 0,9475721 |
| 2 | ADAP2 | FPR3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83502288 | 0,94682916 |
| 6 | CSF1R | RASSF4 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,96339854 | 0,94658595 |
| 3 | ADAP2 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83683401 | 0,94534352 |
| 5 | CSF1R | ADAP2 | RASSF4 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,97488781 | 0,94421261 |
| 3 | CSF1R | ADAP2 | RASSF4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91396178 | 0,94375159 |
| 6 | CSF1R | ADAP2 | RASSF4 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | 0,97712758 | 0,9436109 |
| 2 | CSF1R | TFEC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88053612 | 0,94238726 |
| 4 | CSF1R | ADAP2 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,9200644 | 0,94210103 |
| 5 | ADAP2 | RASSF4 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | 0,94670945 | 0,9416126 |
| 6 | CSF1R | ADAP2 | RASSF4 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,9816282 | 0,9415775 |
| 4 | CSF1R | ADAP2 | RASSF4 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,94436447 | 0,94009861 |
| 4 | CSF1R | RASSF4 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,9525739 | 0,94008226 |
| 4 | CSF1R | RASSF4 | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | NA | 0,96626573 | 0,93906018 |
| 3 | CSF1R | RASSF4 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94869765 | 0,93896879 |
| 6 | ADAP2 | RASSF4 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | 0,9453955 | 0,93855061 |
| 4 | RASSF4 | FPR3 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,90116119 | 0,93808954 |
| 4 | ADAP2 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,83126553 | 0,93774644 |
| 1 | ADAP2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79466903 | 0,9375616 |
| 5 | CSF1R | RASSF4 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | 0,97258664 | 0,937114 |
| 3 | CSF1R | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,88354615 | 0,93605557 |

| | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|------|----|----|----|----|----|----|----|------------|------------|
| 4 | CSF1R | RASSF4 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | 0,96335243 | 0,93533878 |
| 3 | RASSF4 | FPR3 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90922117 | 0,93495258 |
| 5 | CSF1R | RASSF4 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,9687047 | 0,93460084 |
| 3 | ADAP2 | RASSF4 | FPR3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,95738414 | 0,93429048 |
| 4 | CSF1R | ADAP2 | RASSF4 | TFEC | NA | NA | NA | NA | NA | NA | NA | NA | 0,93838817 | 0,93363118 |
| 2 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71513867 | 0,93302004 |
| 3 | ADAP2 | RASSF4 | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93214072 | 0,93236046 |
| 4 | ADAP2 | RASSF4 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,95629549 | 0,93191512 |
| 4 | ADAP2 | RASSF4 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,9329197 | 0,93144735 |
| 5 | CSF1R | ADAP2 | RASSF4 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,96280022 | 0,93071475 |
| 4 | RASSF4 | FPR3 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9251673 | 0,93001398 |
| 5 | RASSF4 | FPR3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,92158396 | 0,92995861 |
| 3 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72158999 | 0,92859415 |
| 3 | CSF1R | RASSF4 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91766392 | 0,92719649 |
| 4 | ADAP2 | RASSF4 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | 0,94572755 | 0,92582426 |
| 5 | ADAP2 | RASSF4 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,94972994 | 0,92429187 |
| 2 | CSF1R | RASSF4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87870297 | 0,92393834 |
| 4 | CSF1R | RASSF4 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,94583934 | 0,9208856 |
| 3 | CSF1R | RASSF4 | TFEC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91642923 | 0,92066165 |
| 4 | ADAP2 | RASSF4 | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | NA | NA | 0,95907943 | 0,92062717 |
| 4 | ADAP2 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,86391711 | 0,92039091 |
| 5 | ADAP2 | RASSF4 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | 0,96275672 | 0,91942951 |
| 3 | ADAP2 | FPR3 | TFEC | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87188675 | 0,91832319 |
| 2 | ADAP2 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74723243 | 0,91713722 |
| 3 | RASSF4 | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87690005 | 0,91389502 |
| 4 | RASSF4 | TFEC | PLA2G7 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | 0,91105188 | 0,91181434 |
| 3 | RASSF4 | FPR3 | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93497686 | 0,91097564 |
| 3 | RASSF4 | TFEC | PLA2G7 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90672296 | 0,90884053 |
| 3 | FPR3 | TFEC | KYNU | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79807777 | 0,90617639 |

Combination of genes for identification of cells of neutrophils

| | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|-------|-------|----|----|----|----|----|------------|------------|
| 2 | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,49562347 | 0,99464199 |
| 3 | NA | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70025625 | 0,99316259 |
| 1 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,47602408 | 0,99309484 |
| 4 | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,59500868 | 0,9926376 |
| 3 | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,66672387 | 0,99243056 |
| 5 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,74300917 | 0,99236083 |
| 2 | NA | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75157864 | 0,99202913 |
| 3 | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,52633156 | 0,99193577 |
| 4 | NA | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,72847342 | 0,99189598 |
| 4 | NA | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81270778 | 0,99187086 |
| 1 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,41264532 | 0,99186557 |
| 3 | CXCR2 | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,63309894 | 0,99168841 |
| 3 | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,56769155 | 0,99167315 |
| 4 | NA | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,73482751 | 0,99159683 |
| 4 | NA | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,71735678 | 0,99157952 |
| 5 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,71496494 | 0,991562 |
| 6 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | NA | NA | NA | NA | NA | 0,83128742 | 0,99151845 |
| 3 | KCNJ15 | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82329073 | 0,99149094 |
| 2 | NA | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,65361118 | 0,9913653 |
| 3 | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57306049 | 0,99133749 |
| 5 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,68697221 | 0,99131095 |
| 4 | CXCR2 | NA | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78924075 | 0,99127753 |
| 6 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | NA | NA | NA | NA | NA | 0,80909562 | 0,99125773 |
| 4 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,68005631 | 0,99115726 |
| 5 | KCNJ15 | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,84864837 | 0,99110223 |
| 5 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,8007367 | 0,99110161 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|-------|----|----|----|----|------------|------------|
| 4 | KCNJ15 | NA | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,84761446 | 0,99109118 |
| 6 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,88426252 | 0,99106533 |
| 5 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,8248917 | 0,99098437 |
| 5 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,81796651 | 0,99098425 |
| 3 | NA | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,71590437 | 0,99090453 |
| 4 | KCNJ15 | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,83445705 | 0,99081147 |
| 4 | CXCR2 | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,67280044 | 0,99080103 |
| 5 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,83124021 | 0,99064834 |
| 5 | KCNJ15 | NA | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,85759418 | 0,99059667 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,85597731 | 0,99054399 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,92577474 | 0,99046265 |
| 4 | NA | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,79656462 | 0,99045427 |
| 4 | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,70420012 | 0,99042814 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,75853108 | 0,99042417 |
| 3 | NA | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81676382 | 0,9904189 |
| 4 | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,70318126 | 0,99040072 |
| 3 | NA | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,77185084 | 0,99039929 |
| 5 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,87588681 | 0,99037306 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,91615468 | 0,99037081 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,896285 | 0,99036747 |
| 4 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,87580527 | 0,9903508 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,88666836 | 0,99032884 |
| 5 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,83635652 | 0,99031178 |
| 5 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,89715372 | 0,99030864 |
| 5 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,81032241 | 0,99029466 |
| 5 | KCNJ15 | NA | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,87577919 | 0,99026966 |
| 4 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,71979062 | 0,99025764 |
| 6 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,85224093 | 0,99024013 |
| 4 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,86929391 | 0,99022405 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|--------|-------|----|----|------------|------------|
| 5 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,8804988 | 0,99015459 |
| 5 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,79690353 | 0,99013407 |
| 4 | KCNJ15 | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,84424966 | 0,99013101 |
| 3 | NA | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,78661387 | 0,99012 |
| 2 | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,53200447 | 0,99011539 |
| 5 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,88831792 | 0,99011413 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,90190197 | 0,9901051 |
| 4 | CXCR2 | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,67603087 | 0,99006422 |
| 4 | CXCR2 | NA | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,79951842 | 0,99002831 |
| 2 | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,64948592 | 0,99000226 |
| 4 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,64989844 | 0,98999416 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | 0,91098641 | 0,98998935 |
| 4 | NA | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,82245978 | 0,98989503 |
| 4 | NA | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,82272561 | 0,98985942 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | 0,93502717 | 0,98982068 |
| 4 | KCNJ15 | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,83859041 | 0,98980961 |
| 5 | NA | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,86735977 | 0,98980457 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | 0,92157256 | 0,98978145 |
| 5 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,75084097 | 0,98977822 |
| 2 | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,62303304 | 0,98974805 |
| 3 | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,66677854 | 0,98968327 |
| 6 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,83908826 | 0,98967299 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | 0,90688084 | 0,98966632 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,89412636 | 0,98964962 |
| 5 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,88069831 | 0,98964271 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,91981747 | 0,98962084 |
| 5 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,87507039 | 0,98960829 |
| 3 | CXCR2 | NA | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,8482567 | 0,98960128 |
| 5 | CXCR2 | NA | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,8689723 | 0,98957132 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|--------|----|----|----|------------|------------|
| 6 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,85645437 | 0,98954278 |
| 3 | KCNJ15 | NA | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,81187958 | 0,9895375 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,91172316 | 0,98950201 |
| 5 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,72785047 | 0,98945189 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | 0,90791548 | 0,98942681 |
| 2 | KCNJ15 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78744764 | 0,98939205 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | 0,93234305 | 0,98937711 |
| 2 | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,53944218 | 0,98933493 |
| 5 | KCNJ15 | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,89353139 | 0,98932419 |
| 4 | KCNJ15 | NA | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,86471169 | 0,98932021 |
| 3 | NA | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,67935574 | 0,98931814 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,88467673 | 0,98927519 |
| 5 | KCNJ15 | CXCR2 | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,88647978 | 0,98927201 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | 0,91093672 | 0,98922452 |
| 5 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | NA | 0,89143032 | 0,98921044 |
| 3 | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,60203253 | 0,98920827 |
| 3 | CXCR2 | NA | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,76489412 | 0,98919825 |
| 5 | KCNJ15 | NA | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,88371283 | 0,98917237 |
| 4 | KCNJ15 | NA | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,80756758 | 0,98916869 |
| 3 | CXCR2 | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,65804633 | 0,98916021 |
| 4 | NA | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,79616979 | 0,98913201 |
| 5 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,75195396 | 0,98912893 |
| 5 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | 0,85134807 | 0,98907273 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,88763436 | 0,98907234 |
| 4 | KCNJ15 | NA | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,82629856 | 0,98901211 |
| 5 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | NA | NA | NA | NA | NA | 0,90466321 | 0,98897922 |
| 2 | CXCR2 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,69598594 | 0,98897317 |
| 6 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | 0,87757073 | 0,98894865 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | NA | NA | NA | NA | 0,9037816 | 0,98893731 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|-------|----|----|----|----|------------|------------|
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | 0,93008186 | 0,98892943 |
| 3 | NA | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8028427 | 0,98890431 |
| 3 | KCNJ15 | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83390061 | 0,98890113 |
| 4 | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,73444257 | 0,98882538 |
| 3 | KCNJ15 | NA | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,7893318 | 0,98881161 |
| 4 | KCNJ15 | NA | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,87020617 | 0,98880948 |
| 1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,61632959 | 0,98879878 |
| 5 | KCNJ15 | NA | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,85293536 | 0,98878821 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,9174336 | 0,98875815 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,91961573 | 0,98875349 |
| 4 | CXCR2 | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,72938377 | 0,98870818 |
| 5 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,9138491 | 0,98869955 |
| 5 | KCNJ15 | NA | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,87794761 | 0,98868059 |
| 3 | KCNJ15 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,804617 | 0,98867955 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,90423346 | 0,98857176 |
| 4 | CXCR2 | NA | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,85046836 | 0,9885631 |
| 4 | KCNJ15 | CXCR2 | NA | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,86231446 | 0,98853898 |
| 4 | CXCR2 | NA | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,82249887 | 0,98852048 |
| 3 | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,68914121 | 0,98850803 |
| 4 | KCNJ15 | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,85263094 | 0,98842962 |
| 3 | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,64274473 | 0,9884242 |
| 5 | NA | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,79708393 | 0,98841249 |
| 2 | CXCR2 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,5880959 | 0,98839125 |
| 4 | CXCR2 | NA | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,81616063 | 0,98838773 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | 0,92608069 | 0,98832888 |
| 3 | KCNJ15 | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84941405 | 0,98830617 |
| 4 | KCNJ15 | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,85772866 | 0,98830177 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | 0,92508265 | 0,9882996 |
| 4 | NA | FCGR3B | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,86731865 | 0,98829092 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|--------|----|----|----|----|------------|------------|
| 4 | KCNJ15 | NA | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,84297122 | 0,98827893 |
| 4 | KCNJ15 | CXCR2 | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,87841599 | 0,98827584 |
| 4 | NA | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,78002779 | 0,98825031 |
| 4 | KCNJ15 | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,88593951 | 0,98824412 |
| 5 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,82653812 | 0,98823274 |
| 6 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,86950965 | 0,9882151 |
| 4 | KCNJ15 | CXCR2 | NA | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,84677138 | 0,98820364 |
| 5 | KCNJ15 | CXCR2 | NA | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,8578191 | 0,98820281 |
| 3 | KCNJ15 | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83092286 | 0,98818801 |
| 2 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,45629978 | 0,98813493 |
| 3 | KCNJ15 | CXCR2 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84541741 | 0,98812182 |
| 6 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,80229722 | 0,98810505 |
| 5 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,77088741 | 0,98810082 |
| 5 | KCNJ15 | CXCR2 | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,92016779 | 0,98808922 |
| 5 | KCNJ15 | CXCR2 | NA | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,87132918 | 0,98807515 |
| 4 | CXCR2 | FCGR3B | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | 0,74220036 | 0,98807127 |
| 6 | KCNJ15 | NA | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,89406513 | 0,98805181 |
| 4 | CXCR2 | NA | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,86156045 | 0,98796587 |
| 7 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,87271815 | 0,98794261 |
| 5 | KCNJ15 | FCGR3B | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,90931464 | 0,98793958 |
| 4 | CXCR2 | NA | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,88459917 | 0,98793892 |
| 4 | CXCR2 | NA | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,77729697 | 0,98792487 |
| 5 | NA | FCGR3B | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86263836 | 0,98792207 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | 0,8860428 | 0,98791458 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | 0,86758383 | 0,98785668 |
| 7 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,92797454 | 0,98784364 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | 0,89128043 | 0,98778899 |
| 5 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,82170994 | 0,98778884 |
| 7 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,91397247 | 0,98777862 |

| | | | | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|-------------|--------|--------|----|----|----|----|----|------------|----|------------|
| 4 | KCNJ15 | NA | HAL | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85947031 | NA | 0,98776777 |
| 7 | CXCR2 | NA | HAL | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85500759 | NA | 0,98773616 |
| 4 | KCNJ15 | CXCR2 | VNN3 | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8753944 | NA | 0,98768704 |
| 4 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,63647112 | NA | 0,98765311 |
| 4 | KCNJ15 | FCGR3B | HAL | CYP4F3 | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88673182 | NA | 0,98765087 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | HAL | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,91122666 | NA | 0,98762051 |
| 8 | KCNJ15 | NA | FCGR3B | HAL | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,9474518 | NA | 0,98761712 |
| 5 | KCNJ15 | NA | VNN3 | CYP4F3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88306664 | NA | 0,98759719 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86079106 | NA | 0,98759122 |
| 5 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,75169271 | NA | 0,98756715 |
| 2 | KCNJ15 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81435276 | NA | 0,98754865 |
| 5 | KCNJ15 | VNN3 | CYP4F3 | CXCR1 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87786862 | NA | 0,98754269 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | HAL | HAL | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89973498 | NA | 0,98754202 |
| 8 | KCNJ15 | CXCR2 | NA | HAL | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,93987638 | NA | 0,98754177 |
| 5 | CXCR2 | NA | FCGR3B | HAL | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87410325 | NA | 0,98753924 |
| 4 | KCNJ15 | CXCR2 | CYP4F3 | CXCR1 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8550842 | NA | 0,98752939 |
| 8 | CXCR2 | NA | FCGR3B | HAL | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,8897327 | NA | 0,98752828 |
| 6 | CXCR2 | NA | VNN3 | CYP4F3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,85491367 | NA | 0,98752204 |
| 3 | CXCR2 | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70450573 | NA | 0,9875173 |
| 5 | CXCR2 | NA | VNN3 | CYP4F3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84596552 | NA | 0,9874588 |
| 6 | NA | HAL | VNN3 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | NA | 0,77834002 | NA | 0,98745431 |
| 7 | KCNJ15 | CXCR2 | NA | VNN3 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,92260015 | NA | 0,9874539 |
| 3 | KCNJ15 | CXCR2 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86594044 | NA | 0,98744262 |
| 5 | KCNJ15 | NA | FCGR3B | HAL | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89807637 | NA | 0,98741022 |
| 5 | KCNJ15 | CXCR2 | NA | HAL | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90342852 | NA | 0,98740268 |
| 4 | NA | FCGR3B | HAL | VNN3 | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86107167 | NA | 0,98738375 |
| 5 | CXCR2 | NA | FCGR3B | HAL | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87397758 | NA | 0,98737178 |
| 3 | CXCR2 | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,68878445 | NA | 0,98736403 |
| 7 | CXCR2 | NA | FCGR3B | VNN3 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,88001133 | NA | 0,98735994 |

| | | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|--------|-----------|--------|--------|--------|----|----|------------|------------|
| 4 | CXCR2 | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70369802 | 0,98735343 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,92191325 | 0,98735194 |
| 6 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,91057394 | 0,98734693 |
| 3 | CXCR2 | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,69265575 | 0,98734558 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | 0,95361413 | 0,98734087 |
| 5 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91187445 | 0,98731309 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85688312 | 0,98728168 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86319731 | 0,98726085 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | 0,93312252 | 0,9872577 |
| 2 | NA | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74023309 | 0,98724336 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86871339 | 0,98722551 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,91551349 | 0,98718274 |
| 3 | KCNJ15 | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84309248 | 0,98716441 |
| 6 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,87576059 | 0,9871459 |
| 3 | NA | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77708536 | 0,98708772 |
| 7 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,85497837 | 0,98705349 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | VNN3 | NA | NA | NA | NA | NA | NA | 0,92051041 | 0,98701346 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,90920909 | 0,9869838 |
| 6 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,76951229 | 0,98695353 |
| 7 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,90313201 | 0,98693327 |
| 3 | NA | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75910919 | 0,98692824 |
| 6 | KCNJ15 | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8843707 | 0,98691718 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | 0,92890605 | 0,98690872 |
| 5 | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,67143658 | 0,98690577 |
| 6 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,9079149 | 0,98689624 |
| 3 | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,60868055 | 0,98688427 |
| 7 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | 0,92178975 | 0,98685478 |
| 7 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | STEAP4 | NA | NA | NA | NA | NA | 0,91461743 | 0,98683007 |
| 4 | FCGR3B | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,73845963 | 0,9868004 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|--------|-----------|--------|-----------|-----------|----|----|------------|-------------|
| 7 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,83518954 | 0,98680034 |
| 6 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,74692547 | 0,98677408 |
| 4 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | 0,70076915 | 0,98676951 |
| 5 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | NA | NA | NA | NA | NA | 0,91058525 | 0,98675383 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,91314166 | 0,98670823 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | 0,92856345 | 0,98667414 |
| 5 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,73037467 | 0,9866673 |
| 7 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,8023891 | 0,98667158 |
| 4 | KCNJ15 | NA | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | 0,80220091 | 0,986666925 |
| 8 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,93885439 | 0,9866507 |
| 4 | KCNJ15 | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86517604 | 0,98664421 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | NA | NA | NA | NA | NA | NA | 0,85043617 | 0,98664398 |
| 4 | KCNJ15 | NA | HAL | VNN3 | NA | NA | NA | NA | NA | NA | 0,87086587 | 0,98664024 |
| 5 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,64209542 | 0,98663487 |
| 3 | KCNJ15 | NA | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,73891147 | 0,98663255 |
| 6 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,78295949 | 0,98660143 |
| 3 | CXCR2 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,61228503 | 0,98660136 |
| 6 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,84595632 | 0,98656842 |
| 8 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,93034896 | 0,98654722 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | 0,93369509 | 0,9865142 |
| 6 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,87359693 | 0,98649571 |
| 5 | NA | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,79855291 | 0,98648549 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | 0,88498349 | 0,98648377 |
| 5 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,90405255 | 0,98648346 |
| 6 | KCNJ15 | NA | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,90588583 | 0,98647997 |
| 8 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,87408842 | 0,98647412 |
| 6 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,86539504 | 0,98645881 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,94122334 | 0,986415 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | 0,94992324 | 0,98640064 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|-----------|-----------|-----------|--------|-----------|----|----|------------|------------|
| 5 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,90027688 | 0,98637284 |
| 5 | KCNJ15 | NA | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8653526 | 0,98636487 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,94218192 | 0,98633367 |
| 6 | KCNJ15 | NA | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,90531371 | 0,98632996 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,93515937 | 0,98632142 |
| 5 | NA | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,78771851 | 0,98630638 |
| 6 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,90476356 | 0,98629429 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,94540756 | 0,98628732 |
| 4 | CXCR2 | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,71425633 | 0,98627824 |
| 5 | NA | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85103166 | 0,98627676 |
| 6 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,85775665 | 0,98622806 |
| 6 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,74810743 | 0,98621182 |
| 6 | KCNJ15 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,8737422 | 0,9862076 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,94831408 | 0,98619203 |
| 4 | KCNJ15 | CXCR2 | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,91493653 | 0,98615669 |
| 7 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,89043377 | 0,9861461 |
| 2 | NA | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,67392652 | 0,98613227 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,9086425 | 0,98611511 |
| 4 | NA | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76873917 | 0,98611406 |
| 3 | FCGR3B | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,72380099 | 0,98610888 |
| 5 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,77437671 | 0,9860723 |
| 5 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,75931407 | 0,98603223 |
| 6 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,72309325 | 0,98596026 |
| 3 | KCNJ15 | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8746979 | 0,98595725 |
| 6 | KCNJ15 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,87743952 | 0,9859474 |
| 4 | KCNJ15 | FCGR3B | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,89581793 | 0,98593049 |
| 7 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,91350231 | 0,98592071 |
| 6 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,84276236 | 0,98591985 |
| 3 | CXCR2 | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,73883915 | 0,98591929 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|-----------|----|----|----|------------|------------|
| 5 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,76805335 | 0,98591482 |
| 7 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,90535497 | 0,98585602 |
| 7 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,91491157 | 0,98582581 |
| 6 | KCNJ15 | CXCR2 | NA | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,90112322 | 0,98582516 |
| 4 | KCNJ15 | CXCR2 | NA | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,80702412 | 0,98581199 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | 0,89895263 | 0,98580671 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | 0,82750846 | 0,9857829 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,91428999 | 0,98577643 |
| 6 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,83012609 | 0,9857079 |
| 2 | KCNJ15 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71285006 | 0,98566649 |
| 6 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,85161006 | 0,9856542 |
| 2 | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57934013 | 0,98565231 |
| 4 | CXCR2 | FCGR3B | HAL | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,76048457 | 0,98564941 |
| 4 | NA | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,83975715 | 0,98563821 |
| 7 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,7840174 | 0,98563114 |
| 3 | KCNJ15 | NA | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | 0,78702028 | 0,98562464 |
| 4 | KCNJ15 | NA | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,8501858 | 0,98560625 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,92043566 | 0,98558934 |
| 5 | KCNJ15 | NA | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,89637451 | 0,98556946 |
| 4 | NA | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,74916961 | 0,98554827 |
| 2 | CXCR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78650347 | 0,98554444 |
| 3 | NA | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,74357105 | 0,98554295 |
| 6 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,89718355 | 0,98552295 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,92708078 | 0,98551498 |
| 3 | KCNJ15 | CXCR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79007976 | 0,98551025 |
| 5 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,77635266 | 0,98549651 |
| 6 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,86452199 | 0,98546131 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,87257253 | 0,98542105 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | NA | NA | NA | NA | NA | NA | 0,90681159 | 0,98540957 |

| | | | | | | | | | | | |
|---|--------|--------|--------|--------|-----------|-----------|-----------|-----------|----|------------|------------|
| 7 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,90827113 | 0,98540932 |
| 4 | KCNJ15 | CXCR2 | HAL | VNN3 | NA | NA | NA | NA | NA | 0,91287666 | 0,98537063 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | 0,93640349 | 0,98536857 |
| 5 | KCNJ15 | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,88895172 | 0,98535232 |
| 5 | KCNJ15 | CXCR2 | NA | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,89094149 | 0,98534263 |
| 5 | CXCR2 | NA | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,83943772 | 0,98533088 |
| 6 | KCNJ15 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,89707886 | 0,9853167 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | 0,92108421 | 0,98531643 |
| 4 | KCNJ15 | CXCR2 | NA | HAL | NA | NA | NA | NA | NA | 0,89208101 | 0,98530741 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | 0,94408168 | 0,98530376 |
| 5 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,84165313 | 0,98527828 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | 0,92430694 | 0,9852737 |
| 3 | CXCR2 | NA | HAL | NA | NA | NA | NA | NA | NA | 0,87340718 | 0,98526449 |
| 3 | KCNJ15 | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | 0,79562738 | 0,9852634 |
| 4 | CXCR2 | NA | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | 0,77991315 | 0,98526225 |
| 6 | KCNJ15 | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,91839412 | 0,98525426 |
| 6 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,85805098 | 0,98524877 |
| 4 | KCNJ15 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,85084355 | 0,98523384 |
| 6 | KCNJ15 | CXCR2 | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,9136837 | 0,98522563 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | 0,90790585 | 0,98522421 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | 0,90745124 | 0,98522416 |
| 5 | KCNJ15 | NA | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,87059682 | 0,98520474 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | 0,92529893 | 0,98520394 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | 0,86397561 | 0,98519575 |
| 6 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,82483656 | 0,98517839 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | NA | NA | NA | NA | 0,90223566 | 0,98517644 |
| 4 | CXCR2 | NA | FCGR3B | HAL | NA | NA | NA | NA | NA | 0,86783917 | 0,98517291 |
| 4 | CXCR2 | FCGR3B | HAL | VNN3 | NA | NA | NA | NA | NA | 0,76209907 | 0,98516474 |
| 4 | KCNJ15 | CXCR2 | NA | FCGR3B | NA | NA | NA | NA | NA | 0,81691104 | 0,98516381 |

| | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|-----------|----|------------|------------|
| 7 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,8573051 | 0,98514436 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,93436738 | 0,98514077 |
| 5 | KCNJ15 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,86137974 | 0,9851147 |
| 5 | KCNJ15 | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,88016727 | 0,98511296 |
| 3 | CXCR2 | NA | FCGR3B | NA | NA | NA | NA | NA | NA | 0,76852055 | 0,98510151 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | 0,91227212 | 0,98505528 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,92748724 | 0,98501465 |
| 6 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,89770555 | 0,98501377 |
| 5 | CXCR2 | NA | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,85731352 | 0,98496898 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | 0,94322933 | 0,98496632 |
| 4 | CXCR2 | NA | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,82562246 | 0,98496457 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | 0,79429084 | 0,98495893 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | STEAP4 | NA | NA | NA | 0,92700919 | 0,98495083 |
| 5 | NA | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,83026545 | 0,98494596 |
| 6 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,84002793 | 0,98492315 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | 0,87769479 | 0,98491111 |
| 4 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,58940124 | 0,98489106 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | 0,91568245 | 0,98486642 |
| 5 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,71932057 | 0,98486399 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | 0,90479343 | 0,98485806 |
| 5 | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,76255737 | 0,98485344 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | 0,93035785 | 0,98485075 |
| 5 | KCNJ15 | NA | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,82423052 | 0,98485068 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | 0,94149698 | 0,98484872 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,89495099 | 0,98480104 |
| 6 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | 0,79781438 | 0,98478462 |
| 5 | CXCR2 | NA | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,82190354 | 0,98475718 |
| 4 | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,72237917 | 0,98474321 |
| 7 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,87648581 | 0,98474182 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|-----------|-----------|----|----|----|------------|------------|
| 5 | KCNJ15 | CXCR2 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,8889502 | 0,98473948 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,86786889 | 0,98473928 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,9341181 | 0,98471568 |
| 3 | CXCR2 | NA | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,80314669 | 0,98471233 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | 0,919639 | 0,98471057 |
| 5 | CXCR2 | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,73300406 | 0,98470976 |
| 2 | KCNJ15 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,7524258 | 0,98470261 |
| 3 | CXCR2 | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | 0,71229196 | 0,98469986 |
| 6 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | 0,88405986 | 0,98469751 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | 0,92434241 | 0,98467608 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | 0,92263411 | 0,98466033 |
| 5 | CXCR2 | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,74093585 | 0,98461415 |
| 6 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,85735407 | 0,9845972 |
| 5 | CXCR2 | NA | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,84601442 | 0,98454597 |
| 6 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,89374816 | 0,98452384 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | 0,88784328 | 0,98451123 |
| 4 | KCNJ15 | NA | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | 0,88791968 | 0,98447532 |
| 6 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,83998113 | 0,98447089 |
| 5 | KCNJ15 | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,87338609 | 0,9844692 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,90094801 | 0,98446828 |
| 5 | KCNJ15 | NA | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,89398419 | 0,98444939 |
| 5 | NA | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,86388589 | 0,98438685 |
| 5 | FCGR3B | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,75768699 | 0,98437159 |
| 4 | HAL | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,65357435 | 0,98436384 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | 0,81330426 | 0,98430769 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,90186489 | 0,98429928 |
| 3 | NA | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | NA | 0,85687959 | 0,98426895 |
| 6 | NA | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,87688788 | 0,98426587 |
| 6 | KCNJ15 | NA | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,89238921 | 0,98423503 |

| | | | | | | | | | | | | | | | |
|----|--------|--------|--------|--------|-----------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 4 | KCNJ15 | FCGR3B | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90257898 | 0,98418041 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,91903972 | 0,98416244 |
| 6 | CXCR2 | NA | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,87738156 | 0,98412767 |
| 4 | NA | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77292477 | 0,98412738 |
| 5 | CXCR2 | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,71282392 | 0,98412562 |
| 9 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,95770896 | 0,98407691 |
| 5 | KCNJ15 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,87295686 | 0,98404545 |
| 3 | KCNJ15 | CXCR2 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82154976 | 0,98403815 |
| 10 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,96177406 | 0,98403775 |
| 9 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,95099874 | 0,98399417 |
| 3 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,58621299 | 0,98398975 |
| 5 | CXCR2 | NA | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84593271 | 0,98398912 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,91090867 | 0,98398646 |
| 6 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,75630372 | 0,98398609 |
| 8 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,92889712 | 0,98397391 |
| 5 | KCNJ15 | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,8669387 | 0,98397108 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,77903651 | 0,98396843 |
| 5 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,7603474 | 0,98395281 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,92446647 | 0,98395135 |
| 6 | KCNJ15 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,91275732 | 0,98394972 |
| 2 | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57409036 | 0,98392546 |
| 4 | KCNJ15 | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87887513 | 0,98392322 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,9303282 | 0,98392033 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,92668733 | 0,98391766 |
| 6 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,8790553 | 0,98390101 |
| 5 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,69386529 | 0,9838901 |
| 5 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,73995934 | 0,98387759 |
| 8 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89111414 | 0,98387389 |
| 6 | KCNJ15 | CXCR2 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,90735439 | 0,98387308 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|-----------|-----------|--------|----|------------|------------|
| 6 | KCNJ15 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,89561791 | 0,9838535 |
| 4 | HAL | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,62480608 | 0,98385202 |
| 4 | KCNJ15 | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,8548462 | 0,98383972 |
| 3 | KCNJ15 | NA | HAL | NA | NA | NA | NA | NA | NA | NA | 0,84144018 | 0,98382149 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,88789564 | 0,98382123 |
| 4 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,62428758 | 0,98379859 |
| 4 | NA | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,77960603 | 0,9837966 |
| 3 | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,5672645 | 0,9837881 |
| 9 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | 0,90385089 | 0,98377857 |
| 4 | KCNJ15 | CXCR2 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,87738654 | 0,98377149 |
| 5 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,82109038 | 0,98376903 |
| 5 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,89587228 | 0,98376786 |
| 8 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,93755146 | 0,98376317 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,91914561 | 0,98376243 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,88613642 | 0,98371143 |
| 5 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,74268102 | 0,98370011 |
| 7 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,83029595 | 0,98369508 |
| 8 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,87534173 | 0,98367485 |
| 6 | CXCR2 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,88074568 | 0,98367102 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | 0,86913169 | 0,98363758 |
| 5 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,89119905 | 0,98361573 |
| 7 | KCNJ15 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90881855 | 0,98361313 |
| 4 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,71162283 | 0,9836124 |
| 6 | KCNJ15 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,89335202 | 0,98360007 |
| 3 | KCNJ15 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,83247235 | 0,98359669 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,92267724 | 0,9835783 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | 0,94064257 | 0,98352587 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,90002946 | 0,9835237 |
| 5 | KCNJ15 | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,85607217 | 0,98352331 |

| | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|--------|----|------------|------------|
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | 0,93907392 | 0,98351985 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | 0,86373908 | 0,98348666 |
| 4 | HAL | VNN3 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,65058509 | 0,98346143 |
| 5 | NA | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,81685454 | 0,98344472 |
| 4 | CXCR2 | CYP4F3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,70293423 | 0,98342996 |
| 7 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,88675219 | 0,98342468 |
| 8 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | 0,932953 | 0,98340921 |
| 5 | KCNJ15 | NA | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,84989178 | 0,98338784 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | 0,93045854 | 0,98337836 |
| 5 | CXCR2 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,71835788 | 0,98336541 |
| 5 | KCNJ15 | NA | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,88890209 | 0,98331146 |
| 6 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,78079015 | 0,98331004 |
| 5 | KCNJ15 | NA | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | 0,85208843 | 0,98330539 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | 0,91949611 | 0,98329549 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | 0,9144177 | 0,98327816 |
| 5 | KCNJ15 | CXCR2 | NA | VNN3 | STEAP4 | NA | NA | NA | NA | 0,85466609 | 0,98326616 |
| 5 | CXCR2 | NA | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,83342541 | 0,98325419 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | 0,9031503 | 0,98324496 |
| 6 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | 0,87408836 | 0,98321008 |
| 5 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,8533419 | 0,98316495 |
| 6 | NA | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,82698923 | 0,9831428 |
| 4 | NA | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,76292483 | 0,98307399 |
| 6 | KCNJ15 | CXCR2 | NA | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,88800116 | 0,98306789 |
| 8 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | 0,89293638 | 0,98306309 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,86039857 | 0,98303979 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | 0,91337735 | 0,98301838 |
| 5 | KCNJ15 | CXCR2 | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,8716254 | 0,9829968 |
| 3 | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,70319676 | 0,98298887 |
| 4 | CXCR2 | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,68345542 | 0,98298785 |

| | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|-----------|-----------|-----------|-----------|-----------|--------|----|----|------------|------------|
| 3 | FCGR3B | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7197283 | 0,98298673 |
| 5 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,75197529 | 0,98297777 |
| 5 | KCNJ15 | CXCR2 | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,90423422 | 0,98295983 |
| 5 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,82563653 | 0,9829578 |
| 5 | CXCR2 | NA | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,83055992 | 0,9829443 |
| 9 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,93930865 | 0,98292861 |
| 7 | CXCR2 | NA | VNN3 | CYP4F3 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,87429978 | 0,98281969 |
| 3 | KCNJ15 | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87188171 | 0,9828164 |
| 8 | KCNJ15 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93534237 | 0,98280978 |
| 2 | KCNJ15 | CXCR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80270188 | 0,98278585 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,92399289 | 0,98278244 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,87308767 | 0,98278157 |
| 8 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92927966 | 0,98276713 |
| 4 | CXCR2 | FCGR3B | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,74794026 | 0,98276592 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,91789401 | 0,98276082 |
| 3 | KCNJ15 | CXCR2 | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80170481 | 0,98273732 |
| 5 | KCNJ15 | NA | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,82060409 | 0,98270112 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,95932647 | 0,98266431 |
| 5 | KCNJ15 | NA | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,81676786 | 0,98262003 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,91006322 | 0,9826051 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,83974168 | 0,98259071 |
| 4 | KCNJ15 | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8302639 | 0,98258657 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,90596913 | 0,98257493 |
| 5 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,82684542 | 0,98256073 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,90201031 | 0,98254775 |
| 2 | NA | HAL | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77284334 | 0,98253926 |
| 4 | NA | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81558495 | 0,98253285 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,86473119 | 0,98253025 |
| 7 | KCNJ15 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,90416201 | 0,98252996 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|-----------|--------|----|------------|------------|
| 7 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92314661 | 0,98252033 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | 0,93786556 | 0,98250626 |
| 7 | KCNJ15 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93338938 | 0,98247723 |
| 8 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | 0,94653432 | 0,98246103 |
| 5 | KCNJ15 | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,91017925 | 0,98245778 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | 0,95729158 | 0,98242558 |
| 6 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,84282217 | 0,98242434 |
| 4 | NA | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,73115126 | 0,98242418 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | 0,91791227 | 0,98242147 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | 0,89177992 | 0,98241141 |
| 4 | KCNJ15 | NA | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80462594 | 0,98238851 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,92304068 | 0,98236754 |
| 8 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,8230547 | 0,98235852 |
| 8 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | 0,95402437 | 0,98232848 |
| 8 | KCNJ15 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,95262392 | 0,98232213 |
| 7 | KCNJ15 | CXCR2 | NA | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92795878 | 0,98231394 |
| 5 | KCNJ15 | NA | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,88810783 | 0,98229274 |
| 5 | CXCR2 | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | 0,7875391 | 0,98224958 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,89976359 | 0,98224382 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,79383978 | 0,98223765 |
| 5 | CXCR2 | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,73368828 | 0,98223041 |
| 7 | FCGR3B | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,79635336 | 0,98222875 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,92802434 | 0,98222713 |
| 8 | KCNJ15 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,94747129 | 0,98222502 |
| 3 | CXCR2 | FCGR3B | CXCR1 | NA | NA | NA | NA | NA | NA | NA | 0,64110903 | 0,98220698 |
| 6 | KCNJ15 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,89741079 | 0,98219984 |
| 4 | FCGR3B | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,69857041 | 0,98218951 |
| 6 | KCNJ15 | NA | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90060453 | 0,98217424 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | 0,91445405 | 0,98216379 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|------------|------------|
| 8 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | 0,90106676 | 0,98216322 |
| 2 | KCNJ15 | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | 0,77819637 | 0,98215376 |
| 3 | CXCR2 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,68001016 | 0,98215152 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,91786785 | 0,98214828 |
| 7 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92139086 | 0,98211945 |
| 6 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | 0,87847531 | 0,98208566 |
| 4 | CXCR2 | NA | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,82963649 | 0,98206444 |
| 7 | CXCR2 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,77628559 | 0,98204961 |
| 5 | KCNJ15 | CXCR2 | NA | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,88176435 | 0,98204608 |
| 6 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,8319223 | 0,98203281 |
| 7 | KCNJ15 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92265974 | 0,98201615 |
| 5 | KCNJ15 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,87808214 | 0,98198896 |
| 5 | KCNJ15 | CXCR2 | NA | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,82043778 | 0,98198818 |
| 4 | KCNJ15 | NA | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,83918632 | 0,9819772 |
| 5 | CXCR2 | NA | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,81053126 | 0,98195735 |
| 6 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,88338676 | 0,98195405 |
| 7 | KCNJ15 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,9218655 | 0,98195356 |
| 4 | NA | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,77768144 | 0,98192779 |
| 7 | CXCR2 | NA | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,89109795 | 0,98190451 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | 0,92731574 | 0,98187728 |
| 7 | CXCR2 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,86917531 | 0,98182795 |
| 6 | CXCR2 | NA | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | 0,88064652 | 0,98182496 |
| 8 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,90584075 | 0,98180004 |
| 7 | NA | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,88643531 | 0,98176329 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | 0,91558602 | 0,98175305 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | 0,91666259 | 0,98174521 |
| 6 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,78111365 | 0,98173982 |
| 6 | HAL | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,71050084 | 0,98173866 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,88418867 | 0,98173748 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 5 | KCNJ15 | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,89995465 | 0,98170945 |
| 7 | NA | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,89406319 | 0,98169344 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,91377961 | 0,98169308 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,79002264 | 0,98168335 |
| 5 | KCNJ15 | NA | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86674517 | 0,98168005 |
| 3 | KCNJ15 | CXCR2 | HAL | NA | NA | NA | NA | NA | NA | NA | NA | 0,90333397 | 0,98167352 |
| 4 | KCNJ15 | NA | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76216087 | 0,9816296 |
| 2 | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,54709233 | 0,98158667 |
| 5 | KCNJ15 | CXCR2 | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,90231923 | 0,98158095 |
| 6 | CXCR2 | NA | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,86933593 | 0,98155168 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,92132352 | 0,98154095 |
| 7 | KCNJ15 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,91686782 | 0,98153085 |
| 5 | KCNJ15 | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8854537 | 0,98151967 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,90674951 | 0,98151523 |
| 7 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,80456594 | 0,98149905 |
| 4 | NA | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,8214352 | 0,9814979 |
| 4 | KCNJ15 | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,86584255 | 0,98149696 |
| 5 | CXCR2 | NA | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,84668654 | 0,98149116 |
| 4 | KCNJ15 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,83705354 | 0,98148844 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,91196477 | 0,98148074 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92325439 | 0,98146987 |
| 5 | NA | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8157824 | 0,98145264 |
| 7 | CXCR2 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,88043804 | 0,98144756 |
| 5 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,76187495 | 0,9814202 |
| 4 | CXCR2 | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,72326923 | 0,98136862 |
| 5 | NA | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86671648 | 0,98134965 |
| 5 | KCNJ15 | CXCR2 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87710907 | 0,98133561 |
| 5 | CXCR2 | NA | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,84074202 | 0,98127272 |
| 5 | CXCR2 | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,75915813 | 0,9812673 |

| | | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|-----------|-----------|--------|----|----|------------|-------------|
| 5 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85434067 | 0,98122979 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,86812061 | 0,98119171 |
| 6 | NA | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,83081208 | 0,98118326 |
| 6 | CXCR2 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,88524576 | 0,981117861 |
| 6 | NA | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,81946211 | 0,98117202 |
| 5 | CXCR2 | NA | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,87609687 | 0,98116948 |
| 5 | CXCR2 | NA | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,79471932 | 0,9811682 |
| 4 | NA | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76915296 | 0,98113553 |
| 5 | KCNJ15 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,90868608 | 0,98113114 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,91973855 | 0,9811272 |
| 5 | CXCR2 | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,75826357 | 0,98112157 |
| 5 | FCGR3B | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,76258687 | 0,98111234 |
| 5 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,68514249 | 0,9811071 |
| 7 | KCNJ15 | CXCR2 | NA | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,91351867 | 0,98108882 |
| 5 | KCNJ15 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,85957666 | 0,98105113 |
| 6 | KCNJ15 | NA | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,88312125 | 0,98104851 |
| 5 | KCNJ15 | NA | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87406944 | 0,98103468 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,86284352 | 0,98099978 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93658473 | 0,98099613 |
| 6 | CXCR2 | VNN3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,76326779 | 0,98098736 |
| 9 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,93430074 | 0,98091169 |
| 6 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,88277133 | 0,98090143 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,92036444 | 0,98086611 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93706974 | 0,98086238 |
| 4 | CXCR2 | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,7149063 | 0,9808519 |
| 5 | KCNJ15 | NA | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,85299835 | 0,98084118 |
| 4 | FCGR3B | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,74745265 | 0,98083699 |
| 3 | NA | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,71461174 | 0,9808326 |
| 4 | CXCR2 | NA | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,8043435 | 0,98076405 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 5 | KCNJ15 | CXCR2 | NA | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,85660385 | 0,98074146 |
| 5 | CXCR2 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,77438677 | 0,9807265 |
| 5 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87907319 | 0,98068992 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,89928565 | 0,98065336 |
| 5 | CXCR2 | NA | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86436909 | 0,98064396 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,95364332 | 0,98063652 |
| 4 | KCNJ15 | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,863662 | 0,98061556 |
| 4 | HAL | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,65542935 | 0,98061337 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | 0,82783009 | 0,98061226 |
| 5 | CXCR2 | NA | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87796288 | 0,9806071 |
| 6 | KCNJ15 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,91912884 | 0,98055098 |
| 7 | KCNJ15 | CXCR2 | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,92430589 | 0,98053375 |
| 6 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,87143651 | 0,98049951 |
| 7 | KCNJ15 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,9334276 | 0,98048483 |
| 7 | KCNJ15 | CXCR2 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,92990301 | 0,98044008 |
| 3 | NA | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,73863429 | 0,98043802 |
| 5 | KCNJ15 | CXCR2 | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87892947 | 0,98043509 |
| 6 | KCNJ15 | CXCR2 | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,91656127 | 0,98043506 |
| 4 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,69022249 | 0,98042498 |
| 7 | CXCR2 | NA | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87950208 | 0,98041299 |
| 8 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,9279819 | 0,98040899 |
| 8 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92964947 | 0,98040255 |
| 1 | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,53484838 | 0,98039138 |
| 5 | CXCR2 | NA | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,89401824 | 0,98038234 |
| 5 | KCNJ15 | NA | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,87776869 | 0,98037115 |
| 5 | KCNJ15 | NA | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,88609364 | 0,98035901 |
| 4 | CXCR2 | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,70542247 | 0,98030732 |
| 3 | CXCR2 | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | NA | NA | 0,74785543 | 0,98028396 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,8816968 | 0,9802622 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|------------|------------|
| 7 | KCNJ15 | FCGR3B | HAL | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93123941 | 0,9802609 |
| 4 | KCNJ15 | VNN3 | CXCR1 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,84319554 | 0,98025942 |
| 5 | NA | FCGR3B | HAL | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,87672389 | 0,98022077 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,94133834 | 0,9801782 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | 0,90466969 | 0,98017223 |
| 5 | NA | FCGR3B | HAL | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,86571551 | 0,98013932 |
| 5 | CXCR2 | FCGR3B | CYP4F3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,73411407 | 0,98010872 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,8221733 | 0,9801087 |
| 5 | CXCR2 | NA | FCGR3B | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,83070962 | 0,98010725 |
| 4 | KCNJ15 | CXCR2 | VNN3 | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85685852 | 0,98009156 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,88112115 | 0,98007343 |
| 4 | KCNJ15 | NA | VNN3 | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80665958 | 0,98002058 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,91855095 | 0,98000948 |
| 7 | KCNJ15 | NA | FCGR3B | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,86948579 | 0,98000213 |
| 7 | KCNJ15 | NA | FCGR3B | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,94736965 | 0,97999949 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | 0,90742205 | 0,97996609 |
| 8 | CXCR2 | NA | FCGR3B | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,89397652 | 0,97994393 |
| 7 | CXCR2 | FCGR3B | HAL | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,81733799 | 0,97993357 |
| 2 | CXCR2 | FCGR3B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6196135 | 0,97993108 |
| 4 | FCGR3B | HAL | CYP4F3 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,73225216 | 0,97989636 |
| 5 | KCNJ15 | VNN3 | CYP4F3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,88866743 | 0,97987177 |
| 4 | NA | FCGR3B | VNN3 | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,82546291 | 0,97986642 |
| 1 | KCNJ15 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71751313 | 0,97986355 |
| 4 | NA | HAL | CXCR1 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,82868699 | 0,97985677 |
| 4 | KCNJ15 | FCGR3B | VNN3 | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,84262651 | 0,97984375 |
| 6 | KCNJ15 | HAL | CYP4F3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90254172 | 0,97984271 |
| 6 | CXCR2 | NA | CYP4F3 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,8622009 | 0,9797102 |
| 4 | CXCR2 | NA | CXCR1 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,79010298 | 0,97968739 |
| 7 | CXCR2 | FCGR3B | HAL | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,82088121 | 0,97968721 |

| | | | | | | | | | | | | |
|---|--------|--------|--------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 4 | KCNJ15 | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87326686 | 0,9796871 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90658774 | 0,97968324 |
| 6 | KCNJ15 | NA | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,91016285 | 0,97964725 |
| 3 | KCNJ15 | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | NA | 0,88504544 | 0,97964306 |
| 7 | KCNJ15 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90149094 | 0,97963811 |
| 6 | CXCR2 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,79915525 | 0,97962242 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,8358722 | 0,97961608 |
| 5 | NA | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,80518522 | 0,97961564 |
| 7 | KCNJ15 | CXCR2 | NA | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,8728584 | 0,97960482 |
| 7 | CXCR2 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90183772 | 0,97958483 |
| 4 | NA | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80449821 | 0,97956502 |
| 4 | KCNJ15 | NA | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80047039 | 0,97956373 |
| 5 | KCNJ15 | CXCR2 | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,90509552 | 0,97955439 |
| 4 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,69246123 | 0,97952846 |
| 4 | KCNJ15 | CXCR2 | NA | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80228691 | 0,97952541 |
| 3 | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,57701415 | 0,97952379 |
| 6 | KCNJ15 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90398198 | 0,97951186 |
| 4 | KCNJ15 | CXCR2 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87144764 | 0,97950293 |
| 4 | KCNJ15 | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80276735 | 0,97946851 |
| 6 | KCNJ15 | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,89602732 | 0,97945208 |
| 6 | KCNJ15 | CXCR2 | NA | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90581378 | 0,97944592 |
| 5 | KCNJ15 | NA | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,81380716 | 0,97941761 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | 0,90668411 | 0,97939374 |
| 2 | CXCR2 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,65134471 | 0,97935244 |
| 5 | CXCR2 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,72264283 | 0,97932128 |
| 5 | KCNJ15 | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,89217702 | 0,97931575 |
| 7 | NA | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,88531438 | 0,97926993 |
| 6 | KCNJ15 | NA | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,91332895 | 0,97925009 |
| 4 | CXCR2 | NA | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,84848266 | 0,9792402 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|-----------|--------|----|----|------------|------------|
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | 0,91548623 | 0,97921983 |
| 5 | FCGR3B | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,77256923 | 0,97921472 |
| 6 | FCGR3B | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,79320549 | 0,97914219 |
| 6 | CXCR2 | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,76579791 | 0,97913446 |
| 7 | CXCR2 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,88574991 | 0,97912912 |
| 6 | KCNJ15 | NA | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,83390911 | 0,97909073 |
| 4 | CXCR2 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,66609534 | 0,97901713 |
| 3 | CYP4F3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,53584713 | 0,97901578 |
| 6 | KCNJ15 | CXCR2 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90488721 | 0,97899486 |
| 5 | KCNJ15 | CXCR2 | NA | HAL | STEAP4 | NA | NA | NA | NA | NA | 0,89264287 | 0,97896931 |
| 7 | CXCR2 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,84342472 | 0,97893076 |
| 6 | CXCR2 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,77468603 | 0,9789208 |
| 4 | NA | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80956111 | 0,97890613 |
| 6 | FCGR3B | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,78770467 | 0,97890049 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | 0,91049205 | 0,97886249 |
| 4 | CXCR2 | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,71812011 | 0,97885074 |
| 3 | HAL | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,6020042 | 0,97883115 |
| 5 | KCNJ15 | NA | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,87123334 | 0,97882698 |
| 6 | CXCR2 | NA | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87231027 | 0,97882108 |
| 5 | CXCR2 | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,75248143 | 0,97878118 |
| 4 | HAL | VNN3 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,65853338 | 0,97875474 |
| 8 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,91961231 | 0,97875037 |
| 3 | KCNJ15 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,82566244 | 0,97874096 |
| 5 | KCNJ15 | CXCR2 | NA | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,81832095 | 0,97872516 |
| 6 | NA | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,88762406 | 0,97871712 |
| 4 | KCNJ15 | CXCR2 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81945601 | 0,97868529 |
| 5 | KCNJ15 | CXCR2 | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,92341303 | 0,97865972 |
| 3 | NA | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,67805072 | 0,97861103 |
| 5 | KCNJ15 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,87446102 | 0,97860001 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|-----------|--------|----|----|------------|------------|
| 6 | CXCR2 | NA | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87527661 | 0,97858141 |
| 6 | NA | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,83366253 | 0,97856995 |
| 2 | HAL | VNN3 | NA | NA | NA | NA | NA | NA | NA | NA | 0,56504539 | 0,97853281 |
| 5 | KCNJ15 | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,90583627 | 0,97852322 |
| 3 | HAL | CYP4F3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,62684976 | 0,97850689 |
| 5 | KCNJ15 | CXCR2 | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,90683775 | 0,97844669 |
| 3 | NA | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,76842078 | 0,97843959 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | 0,91837326 | 0,97842713 |
| 5 | CXCR2 | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | 0,77871825 | 0,97834529 |
| 4 | CXCR2 | NA | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | 0,77878161 | 0,97833199 |
| 8 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | 0,92939221 | 0,97830672 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,85873583 | 0,97829936 |
| 5 | KCNJ15 | NA | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | 0,89002796 | 0,9782908 |
| 5 | KCNJ15 | CXCR2 | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,92397296 | 0,97826138 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,93306541 | 0,97824441 |
| 4 | KCNJ15 | NA | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,75865784 | 0,97816112 |
| 5 | NA | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,86462564 | 0,97808303 |
| 5 | CXCR2 | NA | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | 0,86789617 | 0,97806613 |
| 6 | NA | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,83424287 | 0,97802148 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,87484261 | 0,97801225 |
| 5 | HAL | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,69976948 | 0,97797946 |
| 5 | KCNJ15 | CXCR2 | NA | HAL | TNFRSF10C | NA | NA | NA | NA | NA | 0,90356652 | 0,97796619 |
| 4 | CXCR2 | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,71901746 | 0,97795812 |
| 4 | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,66478849 | 0,97792062 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,86825969 | 0,97791329 |
| 7 | KCNJ15 | CXCR2 | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,92405905 | 0,97780552 |
| 6 | CXCR2 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,78548339 | 0,97780392 |
| 4 | CXCR2 | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,72682024 | 0,97779974 |
| 6 | CXCR2 | NA | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,84495869 | 0,97778806 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 7 | KCNJ15 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,91676973 | 0,97770342 |
| 3 | VNN3 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,58388353 | 0,97769008 |
| 5 | CXCR2 | NA | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,85353795 | 0,97754609 |
| 4 | NA | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,79341525 | 0,97752008 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,91265096 | 0,97751378 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90884909 | 0,9775085 |
| 5 | KCNJ15 | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,90011692 | 0,97750558 |
| 5 | HAL | VNN3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,69386704 | 0,97748983 |
| 5 | CXCR2 | NA | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,78950151 | 0,97746409 |
| 5 | NA | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,81662579 | 0,97745923 |
| 5 | FCGR3B | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,75753349 | 0,97745697 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,90170311 | 0,97741571 |
| 5 | KCNJ15 | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,91396679 | 0,9774103 |
| 5 | CXCR2 | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | 0,78211407 | 0,97737304 |
| 5 | CXCR2 | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,78182687 | 0,97736227 |
| 5 | KCNJ15 | NA | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | NA | 0,89918556 | 0,9773573 |
| 6 | KCNJ15 | CXCR2 | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,92309632 | 0,97730998 |
| 7 | KCNJ15 | CXCR2 | NA | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,9219202 | 0,97727589 |
| 2 | CXCR2 | HAL | NA | NA | NA | NA | NA | NA | NA | NA | 0,7150884 | 0,97725675 |
| 3 | KCNJ15 | NA | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,73630869 | 0,97722872 |
| 5 | CXCR2 | FCGR3B | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | 0,78496767 | 0,97722452 |
| 4 | KCNJ15 | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,89090918 | 0,97720131 |
| 6 | KCNJ15 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,86158673 | 0,97715632 |
| 3 | FCGR3B | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,67784861 | 0,97714464 |
| 4 | KCNJ15 | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86535469 | 0,97712113 |
| 4 | NA | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,77048718 | 0,97712024 |
| 4 | KCNJ15 | CXCR2 | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,87345527 | 0,97711584 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,84623973 | 0,97705565 |
| 3 | KCNJ15 | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,80591083 | 0,97698084 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 5 | CXCR2 | NA | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | NA | 0,87996062 | 0,97697579 |
| 4 | KCNJ15 | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,85353117 | 0,97697419 |
| 5 | KCNJ15 | CXCR2 | NA | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | 0,8275053 | 0,97696705 |
| 5 | NA | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,78101432 | 0,97695968 |
| 6 | KCNJ15 | NA | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,85993783 | 0,97694301 |
| 6 | KCNJ15 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,92760371 | 0,97692708 |
| 7 | CXCR2 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,80835627 | 0,97691997 |
| 7 | KCNJ15 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,9210634 | 0,97691068 |
| 6 | KCNJ15 | CXCR2 | NA | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,86231085 | 0,97689231 |
| 3 | KCNJ15 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,75638352 | 0,97684409 |
| 6 | KCNJ15 | CXCR2 | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87492373 | 0,97671685 |
| 7 | CXCR2 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,8851392 | 0,97665214 |
| 4 | CXCR2 | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,67604782 | 0,97663874 |
| 1 | CXCR2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,62447666 | 0,97662399 |
| 1 | CXCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,3685264 | 0,97660463 |
| 4 | NA | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,78765863 | 0,97657167 |
| 7 | CXCR2 | NA | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,88916415 | 0,9765488 |
| 5 | CXCR2 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,74243908 | 0,97642492 |
| 5 | KCNJ15 | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89693428 | 0,97642156 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | 0,82284524 | 0,97634579 |
| 5 | KCNJ15 | CXCR2 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89681976 | 0,97628986 |
| 3 | NA | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,7438576 | 0,97627968 |
| 6 | KCNJ15 | NA | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,82579783 | 0,97626127 |
| 6 | KCNJ15 | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,89639591 | 0,97621877 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | 0,80832754 | 0,97621344 |
| 3 | CXCR2 | CYP4F3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,6504626 | 0,9762005 |
| 6 | CXCR2 | FCGR3B | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,81350786 | 0,97617267 |
| 6 | KCNJ15 | NA | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87816507 | 0,97613807 |
| 4 | FCGR3B | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,75523555 | 0,97595811 |

| | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|-----------|--------|----|----|----|------------|------------|
| 6 | CXCR2 | NA | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,83687077 | 0,97593255 |
| 3 | FCGR3B | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,67360798 | 0,97582462 |
| 4 | CXCR2 | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,74963038 | 0,97582457 |
| 4 | KCNJ15 | NA | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | 0,84747688 | 0,97578854 |
| 4 | CXCR2 | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,77058895 | 0,9757769 |
| 4 | FCGR3B | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,74359932 | 0,97575332 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | 0,88945972 | 0,97575091 |
| 6 | KCNJ15 | CXCR2 | NA | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,82913625 | 0,97574589 |
| 3 | CXCR2 | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,68663342 | 0,97558884 |
| 4 | CXCR2 | NA | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85714186 | 0,97557367 |
| 4 | KCNJ15 | NA | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,86017116 | 0,97556877 |
| 4 | CYP4F3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,64684575 | 0,97556196 |
| 4 | KCNJ15 | NA | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80176676 | 0,97553696 |
| 2 | KCNJ15 | HAL | NA | NA | NA | NA | NA | NA | NA | NA | 0,85328114 | 0,97552682 |
| 3 | CXCR2 | NA | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76076368 | 0,97552628 |
| 4 | CXCR2 | NA | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80145351 | 0,97552135 |
| 4 | KCNJ15 | CXCR2 | NA | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80502337 | 0,97543927 |
| 6 | CXCR2 | FCGR3B | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,74741263 | 0,97540752 |
| 5 | KCNJ15 | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,83855367 | 0,97538552 |
| 4 | CXCR2 | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,71637199 | 0,97535774 |
| 5 | KCNJ15 | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89169243 | 0,97535356 |
| 4 | KCNJ15 | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,80817248 | 0,97533342 |
| 6 | FCGR3B | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,78293215 | 0,97531136 |
| 4 | KCNJ15 | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,89087843 | 0,97529947 |
| 4 | CXCR2 | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,74936861 | 0,97528386 |
| 6 | CXCR2 | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,77994019 | 0,97527991 |
| 6 | NA | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | 0,87592845 | 0,97527844 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | 0,90554123 | 0,97527693 |
| 4 | CXCR2 | NA | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | 0,88928979 | 0,9752695 |

| | | | | | | | | | | | | |
|---|--------|-------------|-----------------|-----------------|-----------------|-----------------|----|----|----|----|------------|------------|
| 6 | KCNJ15 | NA | HAL | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,88977955 | 0,97523447 |
| 5 | KCNJ15 | NA | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,81802029 | 0,97516431 |
| 6 | CXCR2 | NA | HAL | CXCR1 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,88406469 | 0,97511345 |
| 7 | KCNJ15 | CXCR2 | NA | FCGR3B | HAL | TNFRSF10CSTEAP4 | NA | NA | NA | NA | 0,91139202 | 0,97486938 |
| 6 | CXCR2 | NA | HAL | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,8768347 | 0,9748469 |
| 7 | KCNJ15 | CXCR2 | FCGR3B | HAL | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | 0,91445165 | 0,9748234 |
| 4 | NA | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8502935 | 0,97474613 |
| 4 | KCNJ15 | CYP4F3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,86094711 | 0,97465793 |
| 3 | FCGR3B | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,61617696 | 0,97464856 |
| 4 | NA | FCGR3B | HAL | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | 0,87403149 | 0,9746102 |
| 3 | KCNJ15 | VNN3 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | NA | 0,83065611 | 0,97460696 |
| 5 | CXCR2 | FCGR3B | CYP4F3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,77701234 | 0,97459535 |
| 2 | CYP4F3 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | NA | NA | 0,50322931 | 0,9745212 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | HAL | TNFRSF10CNA | NA | NA | NA | NA | NA | 0,90197643 | 0,97451472 |
| 6 | NA | FCGR3B | HAL | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,87766677 | 0,97448217 |
| 5 | CXCR2 | HAL | CYP4F3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,76137505 | 0,97446849 |
| 4 | KCNJ15 | CXCR2 | CXCR1 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | 0,83052695 | 0,97444269 |
| 6 | CXCR2 | NA | FCGR3B | CXCR1 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,80190407 | 0,97440324 |
| 5 | KCNJ15 | NA | CXCR1 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,77728984 | 0,97439204 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,86106247 | 0,97429431 |
| 5 | NA | FCGR3B | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,82353865 | 0,97428034 |
| 3 | NA | CXCR1 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | NA | 0,69376755 | 0,97425456 |
| 4 | KCNJ15 | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86794576 | 0,97420706 |
| 4 | FCGR3B | HAL | VNN3 | TNFRSF10CNA | NA | NA | NA | NA | NA | NA | 0,7531681 | 0,97420154 |
| 5 | FCGR3B | HAL | CYP4F3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,7820711 | 0,9740947 |
| 5 | FCGR3B | VNN3 | CXCR1 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,7172923 | 0,97408606 |
| 4 | CXCR2 | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | 0,7374257 | 0,97406324 |
| 5 | CXCR2 | NA | VNN3 | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | NA | 0,83404725 | 0,9739128 |
| 6 | KCNJ15 | CXCR2 | NA | FCGR3B | TNFRSF10CSTEAP4 | NA | NA | NA | NA | NA | 0,83635938 | 0,97367914 |

| | | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|--------|----|----|----|----|----|------------|------------|
| 6 | KCNJ15 | CXCR2 | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,91232365 | 0,97356323 |
| 4 | CXCR2 | NA | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,78232161 | 0,97353635 |
| 6 | KCNJ15 | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,90039583 | 0,9733947 |
| 2 | FCGR3B | HAL | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70238883 | 0,97336613 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,82979211 | 0,97327895 |
| 6 | KCNJ15 | CXCR2 | NA | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,901941 | 0,97307726 |
| 5 | CXCR2 | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,72930411 | 0,97307317 |
| 3 | FCGR3B | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,68370508 | 0,97305886 |
| 5 | NA | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,7787785 | 0,97303202 |
| 3 | KCNJ15 | CXCR2 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,79716548 | 0,97301536 |
| 3 | HAL | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,64807884 | 0,97298346 |
| 5 | NA | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,82407018 | 0,97287171 |
| 6 | KCNJ15 | CXCR2 | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,9159039 | 0,97283332 |
| 4 | FCGR3B | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,74434827 | 0,97282629 |
| 3 | KCNJ15 | NA | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,73775064 | 0,97279199 |
| 4 | FCGR3B | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,74461991 | 0,97275955 |
| 4 | KCNJ15 | CXCR2 | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,88954572 | 0,97271677 |
| 5 | HAL | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,69613868 | 0,97260683 |
| 6 | KCNJ15 | NA | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89918408 | 0,97255429 |
| 3 | KCNJ15 | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78296027 | 0,97248712 |
| 3 | CXCR2 | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,71801953 | 0,97243601 |
| 3 | CXCR2 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,63860637 | 0,97234585 |
| 3 | KCNJ15 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,77228388 | 0,9723019 |
| 4 | CXCR2 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,72650148 | 0,97223329 |
| 4 | KCNJ15 | CXCR2 | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,91607502 | 0,97217534 |
| 6 | KCNJ15 | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,90936965 | 0,97212216 |
| 5 | KCNJ15 | CXCR2 | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86389529 | 0,97202252 |
| 5 | CXCR2 | NA | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,7942375 | 0,97194485 |
| 6 | CXCR2 | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,79507831 | 0,9719084 |

| | | | | | | | | | | | | | |
|---|--------|--------|-----------|-----------|-----------|--------|----|----|----|----|----|------------|------------|
| 5 | KCNJ15 | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,85134355 | 0,9718565 |
| 6 | CXCR2 | NA | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,87759702 | 0,97167814 |
| 4 | CXCR2 | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,66757757 | 0,97158251 |
| 5 | NA | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81714064 | 0,97156207 |
| 5 | KCNJ15 | NA | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81227385 | 0,97144197 |
| 5 | KCNJ15 | CXCR2 | NA | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81417711 | 0,97141618 |
| 5 | KCNJ15 | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81294445 | 0,97136641 |
| 6 | CXCR2 | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,79982958 | 0,97131284 |
| 4 | KCNJ15 | CXCR2 | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,81427801 | 0,97127775 |
| 4 | KCNJ15 | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,87822392 | 0,97121383 |
| 4 | HAL | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,6783907 | 0,97105928 |
| 3 | NA | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,81101126 | 0,9709009 |
| 3 | NA | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,75899876 | 0,97089903 |
| 4 | NA | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,75723381 | 0,97086529 |
| 4 | KCNJ15 | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,8986973 | 0,97078584 |
| 5 | KCNJ15 | CXCR2 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,82751428 | 0,97078005 |
| 5 | KCNJ15 | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,87864833 | 0,97063824 |
| 4 | VNN3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,61656151 | 0,97037871 |
| 3 | HAL | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,62654984 | 0,9701952 |
| 4 | CXCR2 | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76256034 | 0,97016216 |
| 3 | CXCR2 | NA | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,79285885 | 0,9699381 |
| 5 | CXCR2 | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,73605899 | 0,96988858 |
| 6 | KCNJ15 | CXCR2 | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | 0,89794709 | 0,96957842 |
| 5 | KCNJ15 | NA | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8624141 | 0,96957469 |
| 4 | CXCR2 | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | 0,77414733 | 0,96956938 |
| 3 | HAL | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,63048085 | 0,9694152 |
| 5 | CXCR2 | NA | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,78987124 | 0,96933988 |
| 4 | NA | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,69952027 | 0,96927698 |
| 2 | NA | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,62151689 | 0,96925868 |

| | | | | | | | | | | | | | |
|---|--------|-----------|-----------|-----------|--------|----|----|----|----|----|----|------------|------------|
| 3 | CXCR2 | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,65186583 | 0,96903713 |
| 3 | FCGR3B | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,61454421 | 0,96898689 |
| 3 | NA | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,77042069 | 0,96898234 |
| 3 | CYP4F3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,61733804 | 0,96882074 |
| 5 | CXCR2 | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,77357948 | 0,96867189 |
| 5 | KCNJ15 | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,88306856 | 0,96866735 |
| 5 | FCGR3B | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,76711329 | 0,96864808 |
| 5 | CXCR2 | NA | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,8707226 | 0,96845848 |
| 5 | CXCR2 | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,69568067 | 0,96807244 |
| 5 | NA | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,86418381 | 0,96786306 |
| 4 | KCNJ15 | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,82010903 | 0,96783039 |
| 4 | KCNJ15 | NA | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,75575579 | 0,96766945 |
| 5 | CXCR2 | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,76485234 | 0,96760676 |
| 4 | KCNJ15 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,77285509 | 0,96740308 |
| 5 | KCNJ15 | CXCR2 | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,81866673 | 0,96734855 |
| 3 | KCNJ15 | CXCR2 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,81736713 | 0,96719183 |
| 3 | KCNJ15 | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,79542787 | 0,96675397 |
| 5 | FCGR3B | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,76980288 | 0,96670142 |
| 2 | VNN3 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,55919657 | 0,96645831 |
| 3 | CXCR2 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,66471352 | 0,9663203 |
| 5 | KCNJ15 | CXCR2 | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,90046167 | 0,96592379 |
| 2 | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,51514046 | 0,9657588 |
| 3 | KCNJ15 | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | 0,8762787 | 0,96554697 |
| 4 | FCGR3B | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,69956156 | 0,96514123 |
| 4 | NA | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,76001236 | 0,96513967 |
| 4 | CXCR2 | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,71016279 | 0,96498165 |
| 5 | KCNJ15 | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | 0,88960578 | 0,96482132 |
| 2 | CXCR1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,42370895 | 0,96476881 |
| 4 | CXCR2 | NA | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | 0,77319957 | 0,96467731 |

| | | | | | | | | | | | | | | | |
|---|--------|-----------|-----------|-----------|--------|----|----|----|----|----|----|----|----|------------|------------|
| 3 | HAL | VNN3 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,62279691 | 0,96458987 |
| 3 | KCNJ15 | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8410868 | 0,96419313 |
| 4 | FCGR3B | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,64564148 | 0,96399882 |
| 3 | CXCR2 | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75802434 | 0,9638347 |
| 2 | KCNJ15 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72129633 | 0,96377477 |
| 2 | NA | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,66022453 | 0,96345285 |
| 4 | HAL | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,67289003 | 0,96293099 |
| 5 | CXCR2 | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78304262 | 0,96290575 |
| 4 | CXCR2 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,66275689 | 0,96250092 |
| 3 | CXCR2 | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7200711 | 0,96233865 |
| 4 | KCNJ15 | CXCR2 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81007088 | 0,96230893 |
| 4 | NA | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79901982 | 0,96199172 |
| 4 | KCNJ15 | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79714284 | 0,96190517 |
| 3 | FCGR3B | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74245329 | 0,96160846 |
| 3 | CXCR2 | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,65310781 | 0,9615743 |
| 3 | FCGR3B | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71835032 | 0,95976708 |
| 4 | HAL | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6689673 | 0,95954703 |
| 2 | CXCR1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,44896197 | 0,95853973 |
| 4 | KCNJ15 | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85976787 | 0,95804955 |
| 4 | CXCR2 | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,67718598 | 0,957286 |
| 2 | KCNJ15 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74727494 | 0,95713786 |
| 2 | CXCR2 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,58931625 | 0,95652272 |
| 2 | FCGR3B | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57601257 | 0,95643304 |
| 3 | NA | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6586713 | 0,95616395 |
| 4 | CXCR2 | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75223003 | 0,95511506 |
| 3 | VNN3 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57425548 | 0,95484861 |
| 3 | CXCR1 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,49495687 | 0,95357497 |
| 4 | FCGR3B | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74841561 | 0,95343735 |
| 3 | KCNJ15 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74520811 | 0,95178388 |

| | | | | | | | | | | | | | | | | | |
|---|-----------|-----------|--------|----|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 1 | HAL | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,52091783 | 0,9507591 |
| 2 | FCGR3B | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,59015901 | 0,94686739 |
| 2 | CXCR2 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,65147504 | 0,94641357 |
| 2 | HAL | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,61103242 | 0,94479043 |
| 3 | CXCR2 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,62828006 | 0,94347311 |
| 3 | FCGR3B | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,61578023 | 0,94320001 |
| 2 | HAL | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,57460017 | 0,93626681 |
| 3 | HAL | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,63361718 | 0,93610287 |
| 2 | TNFRSF10C | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,42311976 | 0,90272515 |
| 1 | STEAP4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,32180583 | 0,88772051 |
| 1 | TNFRSF10C | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,36301142 | 0,86997082 |

Combination of genes for identification of NK cells

| | | | | | | | | | | | | | | | | | |
|---|-------------|---------|--------|-------|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6206794 | 0,99737312 |
| 3 | KIR2DL4 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76998378 | 0,99481562 |
| 3 | KIR2DL3 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79169128 | 0,99436778 |
| 3 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75505304 | 0,99389824 |
| 1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,53413718 | 0,99351725 |
| 1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,49935826 | 0,99291315 |
| 4 | KIR2DL4 | KIR2DL3 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84820203 | 0,99281843 |
| 3 | KIR3DL1 /// | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77734996 | 0,99264364 |
| 2 | KIR2DL3 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77545278 | 0,99241191 |
| 4 | KIR2DL4 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83615744 | 0,99230083 |
| 2 | KIR2DL4 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7580131 | 0,99199984 |
| 4 | KIR2DL3 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85021874 | 0,99192893 |
| 3 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80854997 | 0,99180458 |

| | | | | | | | | | | | | | | | | |
|---|---------|----------------|----------------|--------|-------|----|----|----|----|----|----|----|----|----|------------|------------|
| 2 | KIR2DL4 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75574228 | 0,9917317 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | |
| 4 | KIR2DL4 | KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85385468 | 0,99127529 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88168833 | 0,99097815 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | |
| 4 | KIR2DL3 | KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85624124 | 0,99087799 |
| 4 | KIR2DL4 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85643053 | 0,99064719 |
| 2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72520187 | 0,99059921 |
| 2 | KIR2DL3 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76971888 | 0,99045612 |
| 3 | KIR2DL4 | KIR2DL3 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84568452 | 0,99043856 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | |
| 4 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84245756 | 0,99042659 |
| 4 | KIR2DL3 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85640503 | 0,99018134 |
| | | | KIR3DL1 /// | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88992051 | 0,99010088 |
| 2 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72718152 | 0,98994505 |
| 3 | KIR2DL4 | KIR2DL3 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83528596 | 0,98988195 |
| 4 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85661991 | 0,98969298 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88783565 | 0,98965533 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8797961 | 0,98955444 |
| 3 | KIR2DL4 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82664504 | 0,9895539 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8862551 | 0,98932116 |
| 3 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76425196 | 0,98931684 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88443469 | 0,98908253 |

| | | | | | | | | | | | | | |
|---|-------------|---------|---------|---------|--------|-------|----|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR2DL3 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87236267 | 0,98903878 |
| 4 | KIR2DL4 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,84211505 | 0,98893322 |
| 3 | KIR2DL3 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84455027 | 0,98892954 |
| 3 | KIR2DL4 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83747814 | 0,98891117 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90818251 | 0,98887216 |
| 2 | KIR3DL1 /// | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74592027 | 0,98877464 |
| 4 | KIR3DL1 /// | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87135503 | 0,988759 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,88100316 | 0,98870378 |
| 3 | KIR2DL3 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,82710506 | 0,98863802 |
| 4 | KIR2DL4 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,80431909 | 0,98840039 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,89655646 | 0,98837214 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86534584 | 0,98832441 |
| 4 | KIR2DL3 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,84645769 | 0,98832091 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89805887 | 0,98831984 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89825122 | 0,98828321 |
| 5 | KIR2DL4 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,8552704 | 0,98827533 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88018432 | 0,98827378 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,87990732 | 0,98816057 |
| 2 | KIR3DL1 /// | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76571826 | 0,98795489 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,88788636 | 0,98788976 |

| | | | | | | | | | | | | | | | |
|---|---------------------------|--------------------------------------|---------------------------|---------|--------|-------|----|----|----|----|----|----|----|------------|------------|
| 3 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85492283 | 0,98779889 |
| 3 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85419953 | 0,98779211 |
| 3 | KIR2DL3 | KIR3DL2 /// KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84194483 | 0,9877435 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90464098 | 0,98766604 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89360169 | 0,98746427 |
| 4 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83634246 | 0,98745203 |
| 5 | KIR2DL4 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8800988 | 0,98744211 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR3DL1 /// KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90379732 | 0,98742301 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89877704 | 0,98734392 |
| 5 | KIR2DL3 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86750377 | 0,98731943 |
| 5 | KIR2DL4 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87580866 | 0,98729359 |
| 4 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR3DL1 /// KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88563415 | 0,98728229 |
| 6 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,912112 | 0,98726205 |
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86829305 | 0,98723572 |

| | | | | | | | | | | | | | | | | | | |
|---|---------------------------|---------|----------------|---------|---------|--------|-------|----|----|----|----|----|----|----|----|----|------------|------------|
| 3 | KIR2DL4 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8385572 | 0,98706316 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90074043 | 0,98702406 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87853714 | 0,98699412 |
| 5 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87995604 | 0,98696846 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90100204 | 0,98693183 |
| 4 | KIR2DL3 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,823192 | 0,98690898 |
| 2 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78089081 | 0,98690475 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91387487 | 0,98686038 |
| 3 | KIR2DL3 | KIR3DL2 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83876217 | 0,9868507 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91828663 | 0,98685022 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89599081 | 0,98681974 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89769918 | 0,98670324 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91129225 | 0,98668168 |
| 4 | KIR2DL4 | KIR3DL2 | KIR3DL1 /// | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88097462 | 0,98664379 |
| 3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82773241 | 0,98662702 |

| | | | | | | | | | | | | | | | |
|---|------------------------|----------------|---------|---------|--------|-------|-------|----|----|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88787007 | 0,98662251 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84183785 | 0,98649604 |
| 3 | KIR2DL4 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84628698 | 0,98642049 |
| 3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82931821 | 0,98638443 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85430277 | 0,98635546 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | CD160 | NA | NA | NA | NA | NA | NA | 0,90385178 | 0,98630149 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86507329 | 0,98628899 |
| 4 | KIR2DL4 | KIR3DL2 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88838236 | 0,98627428 |
| 2 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78178861 | 0,98627339 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87108074 | 0,98627048 |
| 5 | KIR2DL3 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87703689 | 0,98625216 |
| 3 | KIR2DL3 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8313366 | 0,98624943 |
| 4 | KIR2DL4 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84594186 | 0,98620156 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89235232 | 0,98616142 |
| 5 | KIR2DL4 | KIR2DL3 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88110093 | 0,98613512 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87917204 | 0,98613509 |

| | | | | | | | | | | | | | | |
|---|--------------------|---------------------------|---------|---------|--------|-------|----|----|----|----|----|----|------------|------------|
| 6 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89534014 | 0,98612208 |
| 4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87372227 | 0,98610542 |
| 5 | KIR2DL4 | KIR2DL3 KIR3DL2 | KIR3DL2 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90265381 | 0,98609741 |
| 4 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78319951 | 0,98605483 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88859599 | 0,98600725 |
| 3 | KIR2DL3 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82011589 | 0,98598958 |
| 4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86344892 | 0,98597899 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86284003 | 0,98597285 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89573749 | 0,98595736 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 | KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91735555 | 0,98595194 |
| 6 | KIR2DL4 | KIR3DL2 /// KIR3DL1 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90827944 | 0,98587642 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89557389 | 0,9857704 |
| 6 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90811024 | 0,98573321 |
| 3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8252254 | 0,98572133 |
| 4 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86248819 | 0,98568853 |
| 5 | KIR3DL1 KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85043171 | 0,98559495 |

| | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|-------|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87001894 | 0,98558385 |
| | | | KIR3DL1 /// | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91598028 | 0,98558064 |
| 5 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,86866223 | 0,98551979 |
| | | | KIR3DL1 /// | | | | | | | | | | |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92429087 | 0,98548778 |
| | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,87816076 | 0,98547711 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,87887434 | 0,98546857 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91961237 | 0,98543187 |
| 4 | KIR2DL3 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,85327222 | 0,98540808 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,89818886 | 0,9853371 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90336585 | 0,98531163 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88257686 | 0,98528067 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88651856 | 0,98526948 |
| 5 | KIR2DL4 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,8849546 | 0,98526333 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,84421614 | 0,98523667 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87521568 | 0,98522419 |
| 4 | KIR2DL4 | KIR2DL3 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,8655584 | 0,98520627 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9048109 | 0,98517869 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90040914 | 0,98512386 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90659853 | 0,98509696 |
| 4 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,831019 | 0,98509226 |

| | | | | | | | | | | | | | | | |
|---|------------------------|----------------|---------|----------------|--------|-------|----|----|----|----|----|----|----|------------|------------|
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85902484 | 0,98498451 |
| 2 | KIR2DL4 | KIR2DL3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81552172 | 0,98494614 |
| 4 | KIR3DL1 /// KIR3DL2 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79874306 | 0,98485411 |
| 7 | KIR2DL3 | KIR3DL2 /// | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,91078571 | 0,98485213 |
| 3 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78033848 | 0,98481883 |
| 3 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83829521 | 0,98479051 |
| 5 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88763861 | 0,9847777 |
| 4 | KIR2DL4 | KIR3DL2 /// | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88393888 | 0,98475832 |
| 3 | KIR2DL4 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83508502 | 0,98475451 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89415554 | 0,9847474 |
| 5 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88757701 | 0,98468111 |
| 1 | KIR2DL4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7474446 | 0,98459233 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,8823933 | 0,98459111 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86244382 | 0,98457827 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87941213 | 0,98457213 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89850325 | 0,98454151 |
| 6 | KIR2DL4 | KIR3DL2 /// | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,91229028 | 0,98451727 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 /// | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89024532 | 0,98451508 |

| | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|-------|----|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | 0,91101663 | 0,98449922 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90722722 | 0,98449809 |
| 4 | KIR2DL4 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,8477192 | 0,98448138 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88937681 | 0,98438105 |
| 5 | KIR2DL4 | KIR3DL2 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,89351667 | 0,98431998 |
| 4 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,8506936 | 0,9843032 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | 0,89306385 | 0,98424068 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 /// | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | 0,89016894 | 0,98418062 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90198316 | 0,98413324 |
| 3 | KIR3DL1 /// | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85108477 | 0,98412632 |
| 4 | KIR2DL3 | KIR3DL2 /// | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | 0,86416688 | 0,98411084 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91726239 | 0,98409249 |
| 6 | KIR2DL3 | KIR3DL2 /// | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,89650659 | 0,98407718 |

| | | | | | | | | | | | | | | | | |
|---|-------------|---------|---------|---------|---------|--------|-------|----|----|----|----|----|----|----|------------|------------|
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8904381 | 0,98380393 |
| 5 | KIR2DL4 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8837396 | 0,98380005 |
| 3 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84494199 | 0,98374497 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,901866 | 0,9837383 |
| 5 | KIR2DL3 | KIR3DL2 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88779316 | 0,98372309 |
| 4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86651436 | 0,98368962 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86879489 | 0,98367338 |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90554203 | 0,98364809 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89584594 | 0,98362233 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87116687 | 0,98361695 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90508002 | 0,98359167 |
| 6 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90606355 | 0,9835277 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87881556 | 0,98347762 |
| 3 | KIR2DL3 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82027504 | 0,98340603 |
| 1 | KIR2DL3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72111231 | 0,98338255 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91875895 | 0,98336823 |

| | | | | | | | | | | | | | |
|---|---------------------------|---------------------------|---------------------------|---------|---------|--------|-------|----|----|----|----|------------|-------------|
| 6 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90705229 | 0,983336265 |
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88909894 | 0,98333474 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90271012 | 0,9833337 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92778765 | 0,98332076 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,880897 | 0,98331379 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89660315 | 0,98327723 |
| 2 | KIR2DL4 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81748431 | 0,98318603 |
| 4 | KIR3DL1 /// KIR3DL2 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,85699967 | 0,98317027 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91427006 | 0,98316269 |
| 5 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,8764187 | 0,98314494 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87453591 | 0,98314187 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92184187 | 0,98308093 |
| 4 | KIR2DL4 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86331757 | 0,98305095 |
| 2 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74091682 | 0,98302896 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,89213925 | 0,98300791 |
| 4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85098017 | 0,98296529 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91013458 | 0,98292936 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89231446 | 0,98292745 |

| | | | | | | | | | | | | | | | |
|---|---------|---------|----------------|---------|---------|---------|--------|--------|-------|----|----|----|----|------------|------------|
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,91230869 | 0,98292146 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88550073 | 0,98289378 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89417063 | 0,98282901 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89976443 | 0,98278535 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,9047331 | 0,9827655 |
| 4 | KIR2DL4 | KIR3DL2 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86757424 | 0,9827456 |
| 5 | KIR2DL4 | KIR3DS1 | SH2D1B | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86762709 | 0,98273579 |
| 7 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91788108 | 0,98270096 |
| 4 | KIR2DL3 | KIR3DL1 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84942015 | 0,98269863 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91794587 | 0,98269079 |
| 3 | KIR2DL4 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79797706 | 0,98269022 |
| 4 | KIR2DL4 | KIR2DL3 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87029441 | 0,98264053 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | NA | 0,89607771 | 0,98263394 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89890893 | 0,98262372 |

| | | | | | | | | | | | | | | |
|---|---------|----------------|----------------|---------|---------|---------|--------|-------|----|----|----|----|------------|------------|
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89956405 | 0,98260579 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 4 | KIR2DL4 | KIR3DL2 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,88038299 | 0,98259777 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91097077 | 0,98259213 |
| 3 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81477877 | 0,98256776 |
| 4 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85920186 | 0,98249892 |
| | | | KIR3DL1 /// | | | | | | | | | | | |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92481419 | 0,98247381 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90180343 | 0,98246756 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91852889 | 0,98246555 |
| | | | KIR3DL1 /// | | | | | | | | | | | |
| 9 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92917281 | 0,98243665 |
| 3 | KIR2DL4 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83666131 | 0,98240484 |
| 6 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89763934 | 0,98240444 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8871531 | 0,98240024 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9212051 | 0,9823726 |
| 2 | KIR2DL3 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78451394 | 0,98235791 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89456431 | 0,9823313 |
| 5 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88779287 | 0,98230645 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90658528 | 0,98229697 |

| | | | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|-------|----|----|----|----|----|----|------------|------------|
| | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90374049 | 0,98227629 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86872486 | 0,98226836 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | | |
| | | | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89243795 | 0,98223446 |
| | | KIR3DL1 /// | | | | | | | | | | | | | |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87625165 | 0,98219007 |
| 4 | KIR2DL4 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87728583 | 0,98210354 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8669948 | 0,98207903 |
| | | KIR3DL1 /// | | | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89748361 | 0,9820749 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,87927581 | 0,98207458 |
| | | KIR3DL1 /// | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89672005 | 0,98207296 |
| | | KIR3DL1 /// | | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,91026064 | 0,98203739 |
| | | | KIR3DL1 /// | | | | | | | | | | | | |
| 3 | KIR2DL4 | KIR2DL3 | KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85723149 | 0,98198916 |
| | | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90440349 | 0,98197469 |
| | | KIR3DL1 /// | | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90796114 | 0,98195213 |
| 3 | KIR2DL3 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82626967 | 0,98194537 |

| | | | | | | | | | | | | | | | |
|---|---------|----------------|----------------|---------|---------|---------|--------|-------|----|----|----|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | 0,91159561 | 0,98192933 |
| 8 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9301973 | 0,98191014 |
| 3 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,68527828 | 0,98188007 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DS1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86817279 | 0,98185565 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87016434 | 0,98185181 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90490346 | 0,981813 |
| 7 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,92394719 | 0,98179701 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91026959 | 0,98176449 |
| 4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8638054 | 0,98170246 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,85322891 | 0,98169232 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88116276 | 0,98167666 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86993064 | 0,98166621 |
| 6 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,895587 | 0,98159015 |
| 4 | KIR2DL4 | KIR2DL3 | NCR1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86162866 | 0,98157914 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88235546 | 0,98156 |

| | | | | | | | | | | | | | |
|---|-------------|---------|---------|---------|---------|--------|-------|----|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87286159 | 0,98148527 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,89647275 | 0,98146065 |
| | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89465948 | 0,98144488 |
| | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9094281 | 0,98143032 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91175343 | 0,98142982 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89172595 | 0,98139999 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88428495 | 0,98138926 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89954837 | 0,981364 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 8 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9176034 | 0,98135143 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,8775913 | 0,9813401 |
| | | | KIR3DL1 | | | | | | | | | | |
| | | | /// | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,88671111 | 0,98127367 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 4 | KIR2DL4 | KIR3DL2 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,8813796 | 0,98126323 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | 0,89262458 | 0,98125838 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | 0,88955675 | 0,98122542 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91932024 | 0,98119669 |

| | | | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|--------|-------|----|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90092814 | 0,9811937 |
| 4 | KIR2DL3 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85057094 | 0,98112715 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88825715 | 0,98109676 |
| 7 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91115539 | 0,98109224 |
| 4 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,85588385 | 0,98106122 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85659812 | 0,9809619 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,85694899 | 0,98095908 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,93142131 | 0,98095118 |
| 3 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86691945 | 0,98093443 |
| 3 | KIR3DL1 /// | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82538667 | 0,98090941 |
| 6 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90906846 | 0,98088071 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84134022 | 0,98086636 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,87585336 | 0,98083474 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8564718 | 0,98083382 |

| | | | | | | | | | | | | |
|---|---------------------------|---------------------------|---------------------------|---------|---------|---------|--------|-------|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | 0,87786158 | 0,98083137 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | 0,92217765 | 0,98082615 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | 0,83581158 | 0,98081902 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,88769115 | 0,98080582 |
| 6 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | 0,89870567 | 0,98079328 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 /// KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,91262015 | 0,98076768 |
| 4 | KIR2DL4 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,85140528 | 0,98076254 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,92025966 | 0,9807572 |
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,89311365 | 0,98073974 |
| 4 | KIR2DL4 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87111977 | 0,98066022 |
| 3 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | 0,81564306 | 0,98065241 |
| 2 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84951163 | 0,98061935 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 /// KIR3DL1 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | 0,90040867 | 0,9806152 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | 0,8932446 | 0,98060086 |

| | | | | | | | | | | | | | |
|---|---------|----------------|----------------|---------|---------|--------|--------|-------|----|----|----|------------|------------|
| 6 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,90047915 | 0,98059679 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88105686 | 0,98058196 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90540968 | 0,98057427 |
| 6 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,9007596 | 0,98053646 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,9025494 | 0,98049739 |
| 4 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,84253449 | 0,98046458 |
| 9 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,92945071 | 0,98046107 |
| 7 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91458027 | 0,98044426 |
| 5 | KIR3DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,8555263 | 0,98043653 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92152805 | 0,98040487 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88941819 | 0,9803967 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,90998326 | 0,98038252 |
| 4 | KIR3DL2 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,83288366 | 0,98038172 |
| 5 | KIR2DL4 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,88122045 | 0,98033828 |
| 6 | KIR2DL4 | KIR2DL3 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90261613 | 0,98030362 |
| 5 | KIR3DL2 | KIR2DL1 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,8749699 | 0,98029123 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90050413 | 0,98028516 |

| | | | | | | | | | | | | | | |
|---|---------|---------|---------|---------|---------|--------|-------|----|----|----|----|----|------------|------------|
| 3 | KIR2DL3 | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81978627 | 0,98028373 |
| 1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,66688616 | 0,9802761 |
| 3 | KIR2DL4 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83474708 | 0,98027583 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91082799 | 0,98026554 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89133381 | 0,98025544 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87236326 | 0,98022935 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89856764 | 0,98022695 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89076013 | 0,98022167 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87637521 | 0,98019939 |
| 4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,85419485 | 0,98019287 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,91205606 | 0,98010006 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92384481 | 0,98009886 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87712297 | 0,98009024 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87515157 | 0,98008194 |
| | | KIR3DL1 | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92223829 | 0,98007828 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89073143 | 0,98006388 |

| | | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|---------|--------|--------|-------|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86322125 | 0,98001311 |
| 6 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89862681 | 0,97997198 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | 0,85995235 | 0,97996781 |
| 9 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,91870218 | 0,97996637 |
| 3 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83346405 | 0,9798594 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86372672 | 0,97985337 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,90000999 | 0,97985031 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,86839792 | 0,97983958 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90840833 | 0,97983538 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91263989 | 0,97982672 |
| 6 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90427914 | 0,97979983 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90599816 | 0,9797924 |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,90104497 | 0,97971609 |
| 4 | KIR2DL4 | KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86298083 | 0,97968537 |

| | | | | | | | | | | | | | | | | | | |
|---|-------------|----------------|---------|---------|--------|--------|--------|-------|----|----|----|----|----|----|----|----|------------|------------|
| | | KIR3DL1 /// | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78928646 | 0,97967522 |
| 2 | KIR2DL3 | KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82017937 | 0,97966084 |
| 3 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86610425 | 0,97965533 |
| 4 | KIR2DL4 | KIR2DL3 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | | |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | CD160 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92335936 | 0,97964794 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84954605 | 0,9796343 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89146526 | 0,97960872 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90950338 | 0,97959234 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89791343 | 0,97958713 |
| 4 | KIR2DL4 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86592314 | 0,97958589 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91278482 | 0,97957191 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85017012 | 0,97956657 |
| 4 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85913162 | 0,97955865 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90653297 | 0,97955597 |
| | KIR3DL1 /// | | | | | | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85855512 | 0,97954106 |
| 5 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87633117 | 0,97953828 |
| 4 | KIR2DL3 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85722922 | 0,97952376 |
| 3 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82911185 | 0,97951609 |

| | | | | | | | | | | | | |
|---|--------------------|---------------------------|----------------|---------|---------|---------|--------|-------|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | 0,89294079 | 0,97950739 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | 0,90847462 | 0,97950435 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | KIR3DL2 | NA | NA | NA | NA | NA | 0,90611787 | 0,97948364 |
| 5 | KIR3DL1 KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | KIR3DL1 | NA | NA | NA | NA | NA | 0,875287 | 0,97948043 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | KIR3DL1 | CD160 | NA | NA | NA | NA | 0,91660835 | 0,97947273 |
| 8 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,9306221 | 0,97946815 |
| 4 | KIR3DL1 KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,85861362 | 0,97945038 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | 0,88035934 | 0,97943354 |
| 5 | KIR2DL1 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,88159389 | 0,97936394 |
| 3 | KIR2DL3 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,80856734 | 0,97934997 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | 0,87925772 | 0,97931776 |
| 6 | KIR2DL4 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90060943 | 0,97931244 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,89401243 | 0,9792882 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90037797 | 0,97927791 |
| 8 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | 0,92426742 | 0,97924971 |

| | | | | | | | | | | | | | |
|---|---------|---------------------------|---------------------------|--------------------|---------|--------|-------|----|----|----|----|------------|------------|
| 6 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,89568563 | 0,97922508 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL2 KIR3DL1 /// | KIR2DL1 KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,88523393 | 0,97919669 |
| 4 | KIR2DL4 | KIR3DL2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88494178 | 0,97919117 |
| 5 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL2 KIR3DL1 /// | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,89256384 | 0,97917438 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,86905187 | 0,97915568 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87740045 | 0,97913498 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,8997433 | 0,97905475 |
| 4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86571963 | 0,97905218 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL2 KIR3DL1 /// | KIR2DL1 KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,90530975 | 0,97904243 |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91713277 | 0,97896371 |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88014325 | 0,97892641 |
| 4 | KIR3DL2 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,8606584 | 0,97888822 |

| | | | | | | | | | | | | | |
|---|---------|----------------|---------|---------|---------|--------|--------|-------|----|----|----|------------|------------|
| 7 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91779825 | 0,97887918 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,88500792 | 0,97884707 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | 0,86359358 | 0,97884042 |
| 8 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91964615 | 0,97883497 |
| 8 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,90851774 | 0,97882008 |
| 3 | KIR3DL2 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81582647 | 0,97880118 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,90715007 | 0,97878788 |
| 3 | KIR3DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75567006 | 0,97876166 |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92276278 | 0,97874279 |
| 3 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78591918 | 0,9787323 |
| 5 | KIR2DL4 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88824529 | 0,97868994 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | 0,91777736 | 0,97867262 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91010252 | 0,97866189 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,89865238 | 0,97863288 |

| | | | | | | | | | | | | | |
|---|---------|----------------|---------|---------|---------|---------|-------|----|----|----|----|------------|------------|
| 6 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,88716442 | 0,97862322 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | 0,89902332 | 0,97858922 |
| 4 | KIR2DL4 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85960246 | 0,97857456 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,90032352 | 0,97855338 |
| 2 | KIR2DL4 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80168487 | 0,97854454 |
| 3 | KIR2DL3 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,82580407 | 0,97850041 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,91220975 | 0,97846036 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90041001 | 0,97844101 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 4 | KIR2DL3 | KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85470478 | 0,97842838 |
| 5 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,88373359 | 0,97842361 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90655387 | 0,97842189 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90457227 | 0,97840056 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,91057338 | 0,97838969 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | 0,91441278 | 0,97835173 |
| 6 | KIR2DL4 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,9022263 | 0,97834244 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,8696596 | 0,97834109 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,85660136 | 0,97828559 |

| | | | | | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|-------------------|------------------|--------|--------|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 2 | KIR3DL1 /// KIR3DL2 | KIR3DL1 NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77929773 | 0,97827866 |
| 6 | KIR2DL3 KIR2DL4 | KIR3DL1 NCR1 | SH2D1B KIR3DL1 | CD160 KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90387981 | 0,97827175 |
| 7 | | KIR2DL3 KIR3DL1 /// | KIR2DL1 | | | | | | | | | | | | | | 0,90782405 | 0,97826891 |
| 4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82044577 | 0,9782455 |
| 4 | KIR2DL3 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85586286 | 0,97818276 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88179028 | 0,97814933 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8897259 | 0,97814397 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87802134 | 0,97813512 |
| 4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86454405 | 0,97811217 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88617479 | 0,97810255 |
| 4 | KIR2DL3 | KIR3DL2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86275123 | 0,97807487 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89021378 | 0,97807016 |
| 3 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85405797 | 0,97801913 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87506368 | 0,97798301 |

| | | | | | | | | | | | | | |
|----|---------------------------|---------------------------|---------------------------|---------|---------|---------|--------|--------|-------|----|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90421079 | 0,97794482 |
| 7 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91187187 | 0,97792892 |
| 2 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72385922 | 0,97792774 |
| 9 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,9347991 | 0,97783335 |
| 4 | KIR2DL4 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87574772 | 0,97778934 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | 0,87893317 | 0,97778469 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | 0,86260632 | 0,97778218 |
| 6 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88781717 | 0,97777769 |
| 7 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,91316609 | 0,97777092 |
| 6 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,90109113 | 0,9777653 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,85203454 | 0,9777392 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86947122 | 0,97771877 |
| 10 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | 0,93110225 | 0,97771356 |
| 7 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | 0,89023202 | 0,97765751 |

| | | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|--------|-------|-------|----|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90986493 | 0,97763833 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90933802 | 0,97763131 |
| 6 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,90904837 | 0,97761681 |
| 5 | KIR3DL1 /// | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88245886 | 0,97758923 |
| 9 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | CD160 | NA | NA | NA | 0,925556 | 0,97757705 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,92832461 | 0,97755628 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88095989 | 0,97748719 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88495037 | 0,97747579 |
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,89670467 | 0,97747148 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,86833048 | 0,97743814 |
| 4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86730134 | 0,97741372 |
| 4 | KIR3DS1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80171769 | 0,97741176 |
| 6 | KIR2DL3 | KIR3DL1 /// | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90274129 | 0,97737809 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88795163 | 0,9773754 |
| 4 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,83722246 | 0,97735939 |

| | | | | | | | | | | | | | | |
|---|-------------|---------|---------|---------|---------|-------|--------|-------|----|----|----|----|------------|------------|
| 3 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83099332 | 0,97734789 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,89242006 | 0,97734636 |
| 2 | KIR2DL3 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74785725 | 0,97730058 |
| 4 | KIR3DL1 /// | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,8728892 | 0,9772754 |
| 5 | KIR2DL3 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,87653507 | 0,97725167 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,89986335 | 0,97724014 |
| 6 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89713819 | 0,97723452 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90020528 | 0,97722259 |
| 4 | KIR2DL3 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86677538 | 0,97721356 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90360723 | 0,97721213 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86393297 | 0,97721175 |
| 3 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80062161 | 0,97719454 |
| 7 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91757839 | 0,97719441 |
| 3 | KIR2DL1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80821173 | 0,97716794 |
| 4 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84365868 | 0,97716548 |
| 6 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90309452 | 0,97709355 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88411579 | 0,97705483 |
| 9 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92708624 | 0,97702858 |

| | | | | | | | | | | | | | |
|---|---------|---------|----------------|---------|---------|---------|---------|--------|--------|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | 0,91569562 | 0,97702035 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | 0,90853217 | 0,97701932 |
| 5 | KIR2DL4 | NCR1 | SH2D1B | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,8705 | 0,97698674 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,92798901 | 0,9769153 |
| 3 | KIR2DL1 | KIR3DS1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,83662891 | 0,97690466 |
| 5 | KIR2DL1 | KIR3DS1 | NCR1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,88351577 | 0,97685923 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | 0,89770838 | 0,97682514 |
| 4 | KIR2DL4 | KIR3DL2 | NCR1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88198141 | 0,97679679 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | 0,88082423 | 0,9767773 |
| 4 | KIR3DL2 | KIR3DL1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,82874007 | 0,97677304 |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | 0,91700265 | 0,97673411 |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | 0,88186001 | 0,97672619 |
| 3 | KIR2DL4 | KIR2DL3 | KIR3DS1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,83173482 | 0,97670267 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | 0,8932361 | 0,97670239 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,91914097 | 0,97667207 |

| | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|--------|--------|-------|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | 0,8724537 | 0,97657338 |
| | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,878659 | 0,97656672 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89625198 | 0,97655951 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,90385931 | 0,97655319 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,8846918 | 0,97654947 |
| | | | KIR3DL1 /// | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | 0,86160555 | 0,97653174 |
| | | | KIR3DL1 /// | | | | | | | | | | |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,85674858 | 0,97653173 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,8646558 | 0,97652473 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | 0,84467646 | 0,97650845 |
| 4 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85262229 | 0,97650171 |
| | | | KIR3DL1 /// | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,89108828 | 0,97647971 |
| | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89946878 | 0,97647452 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | 0,91012114 | 0,97647246 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87339252 | 0,97647005 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 9 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,93525561 | 0,97640014 |

| | | | | | | | | | | | | | | | | | | |
|---|-------------|-------------|---------|---------|---------|--------|--------|----|----|----|----|----|----|----|----|----|------------|------------|
| 3 | KIR3DL1 /// | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78180006 | 0,9763912 |
| 4 | KIR3DL1 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84732611 | 0,97637916 |
| 4 | KIR2DL4 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86564708 | 0,97633213 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89216245 | 0,97628715 |
| 6 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90102829 | 0,97627759 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91746222 | 0,97622713 |
| | | KIR3DL1 /// | | | | | | | | | | | | | | | | |
| 3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81158966 | 0,97622224 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 4 | KIR2DL3 | KIR3DL2 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86199985 | 0,97619009 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 8 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,93318815 | 0,97616682 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89577402 | 0,97608701 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87627891 | 0,9760341 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90695634 | 0,97601158 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88683062 | 0,97600583 |
| | | KIR3DL1 | | | | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | | | | |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87700372 | 0,97600496 |

| | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|---------------------------|---------|---------|--------|--------|-------|----|----|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,90368563 | 0,97594515 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | 0,87172628 | 0,97590854 |
| 8 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | CD160 | NA | NA | NA | NA | 0,92743101 | 0,97589562 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88930657 | 0,97588403 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85018713 | 0,97587023 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,90495219 | 0,97584645 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,87176652 | 0,97581796 |
| 9 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92177816 | 0,97580376 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | 0,90374961 | 0,97575001 |
| 2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75535809 | 0,97574475 |
| 5 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,8670056 | 0,97574048 |
| 4 | KIR2DL4 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86229873 | 0,97569014 |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89219293 | 0,97567704 |
| 3 | KIR2DL4 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83028014 | 0,97564235 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,85262779 | 0,97561491 |

| | | | | | | | | | | | | | | |
|---|---------------------------|---------------------------|---------|---------------------------|---------|---------|---------|---------|---------|--------|--------|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | 0,87754212 | 0,97555273 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | NCR1 | CD160 | NA | 0,89843848 | 0,97552497 |
| 5 | KIR2DL4 | KIR3DL1 | KIR3DS1 | KIR3DS1 | NCR1 | SH2D1B | SH2D1B | SH2D1B | SH2D1B | NA | NA | NA | 0,88667528 | 0,97550115 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | CD160 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85677331 | 0,97550096 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | NCR1 | SH2D1B | SH2D1B | SH2D1B | SH2D1B | SH2D1B | NA | NA | NA | 0,90564853 | 0,9754716 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR2DL1 | KIR3DL1 | KIR3DL1 | NCR1 | CD160 | NA | 0,91301264 | 0,97547007 |
| 8 | KIR2DL3 | KIR3DL2 | KIR3DL2 | KIR3DL1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | SH2D1B | CD160 | NA | 0,92283271 | 0,97545569 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 /// KIR3DL2 | NCR1 | SH2D1B | SH2D1B | SH2D1B | SH2D1B | NA | NA | NA | 0,90832951 | 0,9754384 |
| 5 | KIR2DL3 | NCR1 | SH2D1B | SH2D1B | CD160 | CD160 | CD160 | CD160 | CD160 | NA | NA | NA | 0,87811412 | 0,97543525 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DL1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | CD160 | NA | NA | 0,89486283 | 0,97543487 |
| 7 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | 0,90005084 | 0,97540422 |
| 4 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DL1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | NA | NA | NA | 0,86897415 | 0,97537147 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR2DL1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | NA | NA | NA | 0,82983821 | 0,97536342 |
| 6 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR2DL1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | KIR3DS1 | CD160 | NA | NA | 0,91124128 | 0,97534666 |

| | | | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|---------|---------|---------|--------|--------|--------|----|----|----|----|----|------------|------------|------------|
| 3 | KIR3DL1 /// KIR3DL2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84307011 | 0,97534168 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR2DL1 | NCR1 | SH2D1B | NA | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88903995 | 0,97532453 |
| 8 | KIR2DL4 | KIR3DL2 KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,93029937 | 0,97530392 | |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | SH2D1B | NA | NA | NA | NA | NA | 0,91207643 | 0,9752857 | |
| 7 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,92132244 | 0,97526982 | |
| 5 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86874398 | 0,97522456 | |
| 4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86570201 | 0,97517436 | |
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88851894 | 0,97516651 | |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88883246 | 0,97515801 | |
| 8 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91671217 | 0,97515136 | |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | SH2D1B | NA | NA | NA | NA | NA | 0,8861782 | 0,97514886 | |
| 1 | KIR3DL1 /// KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70638337 | 0,97505912 | |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,87936191 | 0,97500663 | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | CD160 | NA | CD160 | NA | NA | NA | NA | NA | 0,91952554 | 0,97500634 | |
| 4 | KIR2DL3 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84173691 | 0,97498145 | |
| 5 | KIR2DL1 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87476684 | 0,97494894 | |
| 5 | KIR2DL4 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89271853 | 0,97489056 | |
| 3 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84481611 | 0,97486655 | |
| 3 | KIR2DL3 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82502146 | 0,97483677 | |

| | | | | | | | | | | | | |
|---|--------------------|--------------------------------------|---------|---------|---------|--------|--------|----|----|----|------------|------------|
| 7 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | 0,87556973 | 0,97478444 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR3DL2 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | 0,89396315 | 0,97475058 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | 0,86655207 | 0,97474622 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | 0,90351659 | 0,97464399 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,91261272 | 0,97463726 |
| 4 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | 0,87079515 | 0,97460928 |
| 4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | 0,82168516 | 0,97460871 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 /// KIR3DL2 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | 0,89073729 | 0,97459896 |
| 7 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | 0,92267971 | 0,97457368 |
| 8 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | 0,91622265 | 0,97455815 |
| 5 | KIR3DL1 KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,88192416 | 0,97455288 |
| 5 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,86604134 | 0,97450675 |

| | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|---------|---------|---------|--------|--------|----|----|----|----|----|------------|------------|
| 4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 KIR3DL1 /// | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87090545 | 0,97449994 |
| 6 | KIR2DL3 | KIR3DL2 KIR3DL2 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,8879186 | 0,97448781 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89687344 | 0,97447542 |
| 3 | KIR2DL4 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79086068 | 0,97447295 |
| 3 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82453122 | 0,97446907 |
| 5 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89275154 | 0,97444185 |
| 5 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8434446 | 0,97441088 |
| 7 | KIR2DL3 | KIR3DL2 /// | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,89237887 | 0,97436984 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,86260355 | 0,97436046 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85225938 | 0,97434785 |
| 7 | KIR2DL3 | KIR3DL1 KIR3DL1 /// | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91657445 | 0,97434405 |
| 6 | KIR2DL4 | KIR3DL2 /// | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,89367101 | 0,97432684 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,91868761 | 0,97432463 |
| 5 | KIR3DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86706468 | 0,97419732 |
| 9 | KIR2DL4 | KIR2DL3 KIR3DL2 /// | KIR3DL1 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,90952973 | 0,97419632 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84545513 | 0,9741427 |

| | | | | | | | | | | | | | | | |
|---|----------------|----------------|---------|---------|---------|---------|---------|----|----|----|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82559248 | 0,97410861 |
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89460187 | 0,97410635 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87058218 | 0,97403408 |
| 4 | KIR2DL3 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85669093 | 0,97402646 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | 0,88199806 | 0,97400959 |
| 5 | KIR2DL4 | KIR2DL3 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89011578 | 0,97400173 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90652265 | 0,97395955 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87683992 | 0,97394901 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87746398 | 0,97388106 |
| 5 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88238326 | 0,97384601 |
| 8 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,92416546 | 0,97382923 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,86025852 | 0,97382138 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,91673232 | 0,97380905 |
| 3 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79736934 | 0,97377025 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,87436724 | 0,97375938 |

| | | | | | | | | | | | | | |
|---|---------|----------------|---------|---------|---------|--------|--------|----|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88352816 | 0,97375905 |
| 2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75678843 | 0,97371916 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | 0,90434086 | 0,97371342 |
| 4 | KIR2DL4 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86530487 | 0,9736918 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 2 | KIR3DL2 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7880112 | 0,97365097 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,91267331 | 0,97364678 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89567252 | 0,9736438 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,90673155 | 0,9736198 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | 0,88890637 | 0,97354918 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,86624629 | 0,97353373 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | 0,902441 | 0,97352542 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90915858 | 0,97347238 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,89626583 | 0,97345585 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,90645138 | 0,97344777 |

| | | | | | | | | | | | | | | |
|---|------------------------|----------------|---------|---------|---------|-------|-------|----|----|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86558126 | 0,97344089 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89244515 | 0,97336419 |
| 3 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85550505 | 0,97335412 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90815955 | 0,97334996 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,80197501 | 0,9732907 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84940282 | 0,97325109 |
| 7 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,88038563 | 0,9732432 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88024897 | 0,97322959 |
| 5 | KIR3DL1 /// KIR3DL2 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87085762 | 0,97322074 |
| 4 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85767575 | 0,97319409 |
| 5 | KIR2DL1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8790249 | 0,97315305 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,83965896 | 0,97314348 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85853525 | 0,97309981 |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88336944 | 0,97308385 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,87165667 | 0,97308028 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83754248 | 0,9729758 |

| | | | | | | | | | | | | | |
|---|------------------------|----------------|----------------|---------|---------|--------|--------|----|----|----|----|------------|------------|
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87605257 | 0,97296857 |
| 3 | KIR2DL4 | KIR2DL3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85026071 | 0,97295516 |
| 7 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,91496333 | 0,97294381 |
| 5 | KIR2DL4 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89097378 | 0,97291734 |
| 4 | KIR3DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,83814758 | 0,97291529 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8699983 | 0,97285055 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,88061685 | 0,97283326 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | 0,90580273 | 0,97282031 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,89193646 | 0,97277689 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,9101624 | 0,9727766 |
| 7 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | 0,9153447 | 0,97275769 |
| 6 | KIR2DL4 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90329249 | 0,97271041 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,84815028 | 0,97268942 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,9092814 | 0,97264731 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82012697 | 0,97256455 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87796251 | 0,97256267 |

| | | | | | | | | | | | | | |
|---|----------------|----------------|---------|---------|---------|--------|--------|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,89145666 | 0,97156171 |
| 5 | KIR2DL4 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88484027 | 0,97155799 |
| 2 | KIR2DL4 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81378762 | 0,97145575 |
| 5 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,86727089 | 0,97145142 |
| 6 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,892214 | 0,97143764 |
| 4 | KIR3DL2 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,84438566 | 0,97142881 |
| 6 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,90061863 | 0,97142143 |
| 8 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | 0,89414136 | 0,97133268 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,91308191 | 0,97132606 |
| 4 | KIR2DL1 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86066106 | 0,97130906 |
| 8 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | 0,90753667 | 0,97123232 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | 0,88473639 | 0,97119236 |
| 5 | KIR2DL3 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88287618 | 0,97117492 |
| 4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,82112312 | 0,97113282 |
| 7 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,91868267 | 0,97111683 |

| | | | | | | | | | | | | | |
|---|--------------------|----------------|---------|---------|---------|---------|-------|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,86360302 | 0,97110747 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8295882 | 0,97106424 |
| 4 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85677254 | 0,97098791 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90079675 | 0,97090995 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,86571987 | 0,97085714 |
| 3 | KIR3DL1 KIR3DL2 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82742214 | 0,97083297 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,90635887 | 0,97081205 |
| 5 | KIR3DL1 KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87066797 | 0,97081063 |
| 5 | KIR2DL1 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87974252 | 0,97080144 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | 0,86105057 | 0,97078672 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,88224729 | 0,9707826 |
| 4 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,82039282 | 0,97073381 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | 0,90844048 | 0,97068377 |
| 3 | KIR3DL1 KIR3DL2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,79864971 | 0,97062372 |
| 3 | KIR2DL4 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83003445 | 0,97055984 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,87719326 | 0,97051603 |

| | | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|---------|----------------|---------|---------|--------|----|----|----|----|----|----|------------|------------|
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 KIR3DL1 /// | KIR3DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88356596 | 0,97049273 |
| 4 | KIR2DL4 | KIR3DL2 KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87170202 | 0,97043493 |
| 3 | KIR2DL3 | KIR2DL1 KIR3DL1 /// | KIR3DS1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77518419 | 0,97036868 |
| 6 | KIR2DL3 | KIR3DL2 KIR3DL1 /// | KIR3DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89814192 | 0,97035827 |
| 5 | KIR2DL3 | KIR3DL2 KIR3DL1 /// | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,82684991 | 0,97033616 |
| 6 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL2 | KIR3DL1 /// | KIR3DL1 | | | | | | | | | | |
| 5 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,86816915 | 0,97031763 |
| 6 | KIR3DL1 | KIR3DS1 KIR3DL1 /// | KIR2DL3 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86342097 | 0,97030559 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DS1 | KIR3DL1 /// | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90048578 | 0,97023835 |
| 6 | KIR2DL4 | KIR3DL2 KIR3DL1 /// | KIR3DL2 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,88046431 | 0,97020912 |
| 6 | KIR2DL4 | KIR3DL2 KIR3DL1 /// | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90638675 | 0,9701913 |
| 6 | KIR2DL3 | KIR3DL2 KIR3DL1 /// | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,85074102 | 0,97017986 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 KIR3DL1 /// | KIR3DS1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88073044 | 0,97015583 |
| 7 | KIR2DL3 | KIR3DL2 KIR3DL1 /// | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,89861732 | 0,97009083 |

| | | | | | | | | | | | | | |
|---|----------------|-------------|---------|---------|---------|--------|-------|----|----|----|----|------------|------------|
| | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,91162751 | 0,97002244 |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,90134101 | 0,96996335 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88540713 | 0,96987466 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | | |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 5 | KIR2DL3 | KIR3DL2 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,88387631 | 0,96983271 |
| 3 | KIR2DL4 | KIR2DL3 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82265993 | 0,96976475 |
| 4 | KIR2DL4 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86273699 | 0,96975525 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82668014 | 0,96975349 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 8 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | 0,91793444 | 0,9697441 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,85210859 | 0,96973907 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,88663475 | 0,96973827 |
| 5 | KIR2DL3 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,86761943 | 0,96971227 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 4 | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,85834543 | 0,96969576 |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,91486603 | 0,96968838 |
| | | KIR3DL1 /// | | | | | | | | | | | |
| 6 | KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | 0,89804117 | 0,96950608 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | 0,8455528 | 0,96947662 |
| 2 | KIR2DL3 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75340539 | 0,96946303 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,8844281 | 0,96945857 |
| | | KIR3DL1 | | | | | | | | | | | |
| | | /// | | | | | | | | | | | |
| 4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,83059049 | 0,96945716 |

| | | | | | | | | | | | | | | |
|---|------------------------|----------------|---------|---------|---------|--------|-------|----|----|----|----|----|------------|------------|
| 5 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87749737 | 0,96938046 |
| 1 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,68978701 | 0,96937337 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83616335 | 0,96924113 |
| 6 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,9035411 | 0,9691772 |
| 5 | KIR2DL4 | KIR2DL3 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89158975 | 0,96916196 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88598656 | 0,9691525 |
| 3 | KIR3DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74888385 | 0,96913426 |
| | | KIR3DL1 /// | KIR3DL1 | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,91266974 | 0,9690534 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 8 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,89742817 | 0,96903358 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88838238 | 0,9689499 |
| 3 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82097286 | 0,96894348 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,90806421 | 0,96890495 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87125984 | 0,96890162 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,88244552 | 0,96888572 |
| 4 | KIR2DL4 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86363502 | 0,9688031 |
| 4 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,84677734 | 0,96872394 |
| | | KIR3DL1 /// | KIR3DL1 | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,85098962 | 0,96870688 |
| 5 | KIR2DL1 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,87356025 | 0,96868979 |
| 3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78895089 | 0,96866267 |

| | | | | | | | | | | | | | |
|---|---------------------------|---------------------------|---------------------------|---------|--------|--------|----|----|----|----|----|------------|------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,89986564 | 0,9685871 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,85287972 | 0,96854555 |
| 3 | KIR2DL4 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83290311 | 0,96850132 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,89056465 | 0,96846705 |
| 3 | KIR3DL1 /// KIR3DL2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76244941 | 0,96843313 |
| 3 | KIR2DL4 | KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85086116 | 0,96828792 |
| 3 | KIR2DL1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80225692 | 0,9682697 |
| 5 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,86905803 | 0,96819834 |
| 7 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | 0,89742582 | 0,96817551 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,7986266 | 0,96815729 |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,84793595 | 0,9680955 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,86664087 | 0,96803768 |
| 4 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,8507539 | 0,96803294 |
| 6 | KIR2DL4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,91149497 | 0,96792851 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,88022095 | 0,9678889 |
| 4 | KIR2DL3 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85696105 | 0,96788239 |

| | | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|-----------------|------------------|------------|-------------|------|----|----|----|----|----|----|--------------------------|--------------------------|
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 KIR3DL1 /// | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8928449 | 0,96787396 |
| 7 | KIR2DL4 | KIR3DL2 KIR3DS1 | KIR3DL1 NCR1 | KIR3DS1 CD160 | NCR1 NA | CD160 NA | NA | NA | NA | NA | NA | NA | NA | 0,91965544 0,84415804 | 0,96786875 0,96780752 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,86498323 | 0,96773486 |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,89934806 | 0,96764735 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86961572 | 0,96759858 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85545545 | 0,96755937 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89208582 | 0,96748522 |
| 6 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,88255509 | 0,9674799 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83654306 | 0,96744158 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80978824 | 0,96742969 |
| 3 | KIR2DL3 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80207594 | 0,96742125 |
| 3 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83863716 | 0,96739516 |
| 3 | KIR2DL4 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91004754 | 0,96735461 |
| 7 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,88166424 | 0,96732943 |
| 8 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,89177384 | 0,96721441 |
| 5 | KIR2DL4 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87294399 | 0,9670689 |
| 6 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87294399 | 0,9670689 |

| | | | | | | | | | | | | | |
|---|---------|----------------|---------|---------|---------|-------|----|----|----|----|----|------------|------------|
| 6 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | 0,83005343 | 0,96699347 |
| 7 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,90056324 | 0,96698684 |
| 4 | KIR2DL4 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86509232 | 0,96694474 |
| 4 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,80734389 | 0,96693253 |
| 4 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86970346 | 0,96689532 |
| 7 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,91208197 | 0,96679805 |
| 4 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81398181 | 0,96671274 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,83038576 | 0,9665158 |
| 6 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,88971226 | 0,96651315 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | 0,84019669 | 0,96642984 |
| 7 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | 0,8911517 | 0,96642251 |
| 5 | KIR2DL4 | KIR3DL1 /// | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89540019 | 0,96638464 |
| 2 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75121716 | 0,9663692 |
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,87022104 | 0,9662761 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | 0,87789075 | 0,96615779 |

| | | | | | | | | | | | | | | |
|---|---------|----------------|---------|---------|---------|-------|----|----|----|----|----|----|------------|------------|
| 5 | KIR2DL4 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88485613 | 0,96597364 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,88207104 | 0,96593625 |
| 3 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81837875 | 0,96591891 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,88959142 | 0,96586491 |
| 3 | KIR2DL3 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80070606 | 0,96585414 |
| 5 | KIR2DL3 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88598855 | 0,96576417 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 4 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82179919 | 0,96560057 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 3 | KIR2DL4 | KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85250053 | 0,96558462 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 6 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89419279 | 0,96555443 |
| 4 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85662415 | 0,96551869 |
| 4 | KIR3DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83634159 | 0,96548267 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,90321007 | 0,96547938 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,83031915 | 0,96534764 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,89005609 | 0,96533489 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,84600405 | 0,96517676 |
| | | KIR3DL1 /// | | | | | | | | | | | | |
| 3 | KIR2DL3 | KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81229153 | 0,96517545 |

| | | | | | | | | | | | | | | | |
|---|------------------------|---------------------------|--------------------|--------------------|-----------------|-------------|----------|----------|----------|----------|----------|----------|----------|--------------------------|--------------------------|
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 KIR3DL1 | KIR3DL1 KIR3DS1 | KIR3DS1 NCR1 | NA SH2D1B | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,84370866 0,88766471 | 0,96516859 0,96514647 |
| 3 | KIR2DL3 | KIR2DL1 KIR3DL1 /// | NA KIR3DL1 | NA CD160 | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,7955252 0,88057089 | 0,96502712 0,96493308 |
| 5 | KIR2DL3 | KIR3DL2 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83273208 | 0,96486739 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86839156 | 0,96484841 |
| 4 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84946991 | 0,96483385 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87190114 | 0,96481558 |
| 7 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR2DL1 KIR3DL1 | KIR3DL1 KIR3DS1 | NCR1 KIR3DS1 | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,85144625 | 0,96473782 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89845114 | 0,96471468 |
| 7 | KIR3DL1 /// KIR3DL2 | KIR2DL1 KIR3DL1 | KIR3DL1 KIR3DS1 | KIR3DS1 NCR1 | NCR1 NA | CD160 NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,8778062 | 0,96456259 |
| 5 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DL1 KIR3DS1 | NCR1 NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,85923488 | 0,96440477 |
| 5 | KIR2DL3 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75345221 | 0,96437814 |
| 2 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85427523 | 0,96432089 |
| 5 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89113188 | 0,96426959 |
| 6 | KIR3DL1 /// KIR3DL2 | KIR2DL1 /// | KIR3DS1 NCR1 | NCR1 SH2D1B | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,87055454 | 0,96423715 |
| 5 | KIR3DS1 | NCR1 | SH2D1B | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83266357 | 0,96420845 |
| 4 | KIR2DL4 | KIR2DL3 KIR3DL1 /// | KIR3DS1 KIR3DL1 | NCR1 KIR3DS1 | NA NCR1 | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | NA NA | 0,80918771 | 0,96417474 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85863603 | 0,96408309 |
| 4 | KIR2DL1 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85863603 | 0,96408309 |

| | | | | | | | | | | | | | | |
|---|----------------|----------------|----------------|---------|---------|---------|------|----|----|----|----|----|------------|-------------|
| 7 | KIR2DL4 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | 0,87534332 | 0,96408274 |
| 3 | KIR2DL3 | KIR3DL1 /// | KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,80253041 | 0,96401071 |
| 4 | KIR2DL3 | NCR1 | SH2D1B | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | 0,86044735 | 0,96400006 |
| 3 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,81055647 | 0,96392332 |
| 6 | KIR2DL4 | KIR3DL1 | KIR3DS1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90962832 | 0,963883913 |
| 3 | KIR3DS1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78641216 | 0,96371949 |
| 5 | KIR2DL4 | KIR3DS1 | NCR1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | 0,89424209 | 0,9635404 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR3DL2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87442503 | 0,96350414 |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,8136683 | 0,96331214 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,88117622 | 0,96330543 |
| 3 | KIR3DL1 /// | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77786614 | 0,96326794 |
| 6 | KIR2DL4 | KIR3DL2 | KIR3DS1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | 0,90843518 | 0,96322199 |
| 4 | KIR2DL1 | KIR3DS1 | NCR1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,84559247 | 0,96319894 |
| 5 | KIR3DL1 /// | KIR3DL1 | NCR1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87752662 | 0,96317928 |
| 7 | KIR2DL4 | KIR3DL2 | KIR2DL1 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | 0,88519659 | 0,96304401 |

| | | | | | | | | | | | | | | | |
|---|-------------|---------|---------|---------|---------|------|----|----|----|----|----|----|----|------------|------------|
| 4 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86200564 | 0,9629158 |
| 5 | KIR2DL4 | KIR2DL3 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85426991 | 0,96287431 |
| 3 | KIR2DL1 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78297431 | 0,9628426 |
| 4 | KIR3DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85073669 | 0,96267174 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90012354 | 0,96262725 |
| 4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83486151 | 0,96261811 |
| 6 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89517452 | 0,9626029 |
| 5 | KIR2DL1 | KIR3DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87472488 | 0,96253503 |
| 4 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8495898 | 0,96227504 |
| 3 | KIR2DL3 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76591851 | 0,96213487 |
| | KIR3DL1 /// | | | | | | | | | | | | | | |
| 5 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82721445 | 0,96208627 |
| | | KIR3DL1 | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | |
| 7 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,85510587 | 0,96199947 |
| | | KIR3DL1 | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | |
| 6 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88794215 | 0,96198682 |
| 3 | KIR3DL1 /// | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81421846 | 0,9619785 |
| | KIR3DL2 | | | | | | | | | | | | | | |
| 5 | KIR3DL1 /// | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87789823 | 0,96187312 |
| | | KIR3DL1 | | | | | | | | | | | | | |
| | | /// | | | | | | | | | | | | | |
| 5 | KIR2DL4 | KIR3DL2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8868715 | 0,9617781 |
| 5 | KIR2DL3 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87824541 | 0,9613934 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88207483 | 0,96134932 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87976776 | 0,96131252 |
| 2 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,6323044 | 0,96130681 |

| | | | | | | | | | | | | | | | |
|---|----------------|----------------|---------|---------|-------|----|----|----|----|----|----|----|----|------------|------------|
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83075429 | 0,96129263 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86310794 | 0,96124597 |
| 4 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85474563 | 0,96114747 |
| 4 | KIR3DL1 /// | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85822939 | 0,96105794 |
| 4 | KIR2DL1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85381747 | 0,96104105 |
| 3 | KIR3DL1 /// | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80439584 | 0,96102454 |
| 2 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75278215 | 0,96099733 |
| 4 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80843617 | 0,96090974 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82071985 | 0,96051598 |
| 6 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89145187 | 0,96047784 |
| 6 | KIR2DL4 | KIR2DL3 | KIR3DL2 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88231354 | 0,96045883 |
| 2 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7302413 | 0,96034289 |
| 5 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87351479 | 0,96015533 |
| 5 | KIR2DL3 | KIR3DL2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8550289 | 0,96009602 |
| 5 | KIR3DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88093098 | 0,9600758 |
| 3 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78061583 | 0,95994695 |
| 6 | KIR2DL4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86249107 | 0,95985822 |

| | | | | | | | | | | | | | | | |
|---|-------------|----------------|---------|---------|-------|----|----|----|----|----|----|----|----|------------|------------|
| 4 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80706885 | 0,95977265 |
| 6 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88937584 | 0,95972995 |
| 4 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82776043 | 0,95966292 |
| 4 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81931693 | 0,95951215 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83292496 | 0,95944673 |
| 6 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88834247 | 0,95922298 |
| 6 | KIR2DL4 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89055732 | 0,95911333 |
| 5 | KIR3DL1 /// | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88012023 | 0,95899351 |
| 4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82240108 | 0,95859156 |
| 5 | KIR2DL1 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87667713 | 0,95855576 |
| 3 | KIR3DL1 /// | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79670195 | 0,95849112 |
| 6 | KIR2DL4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87324574 | 0,95844716 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83815566 | 0,95836302 |
| 4 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78443589 | 0,95815897 |
| 4 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81900576 | 0,958043 |
| 6 | KIR2DL3 | KIR3DL1 /// | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85780147 | 0,95772742 |

| | | | | | | | | | | | | | |
|---|-------------|----------------|---------|---------|------|----|----|----|----|----|----|------------|------------|
| 6 | KIR2DL4 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,87869888 | 0,95767043 |
| 4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,83024679 | 0,95751342 |
| 6 | KIR2DL3 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,84227045 | 0,95698221 |
| 5 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,84430131 | 0,95691447 |
| 4 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,79977009 | 0,95633747 |
| 6 | KIR2DL3 | KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,84421345 | 0,95621089 |
| 2 | KIR2DL4 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79280673 | 0,95613871 |
| 4 | KIR2DL4 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85790431 | 0,95599091 |
| 3 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,80448662 | 0,95558079 |
| 4 | KIR3DL1 /// | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,80725039 | 0,95542074 |
| 5 | KIR2DL4 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,89018892 | 0,95520515 |
| 6 | KIR3DL1 /// | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | 0,85234008 | 0,95492233 |
| 4 | KIR2DL4 | KIR2DL3 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86127695 | 0,95423433 |
| 4 | KIR2DL3 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | 0,85589194 | 0,95339009 |
| 5 | KIR2DL3 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87612511 | 0,95326892 |
| 5 | KIR2DL4 | KIR2DL3 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,87026509 | 0,95290581 |
| 2 | KIR2DL3 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,74804569 | 0,95278866 |
| 3 | KIR2DL4 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82075822 | 0,95235745 |
| 4 | KIR2DL4 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86404371 | 0,9518104 |
| 5 | KIR3DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | 0,87734854 | 0,95104187 |
| 5 | KIR2DL4 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | 0,87881516 | 0,95094899 |

| | | | | | | | | | | | | | | | | | | |
|---|-------------|----------------|---------|-------|----|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 5 | KIR3DL1 /// | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87001346 | 0,95062743 |
| 4 | KIR3DL2 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84355331 | 0,95055981 |
| 4 | KIR2DL4 | KIR3DL1 /// | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87260992 | 0,95042885 |
| 3 | KIR2DL4 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84753965 | 0,95030017 |
| 4 | KIR3DL1 /// | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84237593 | 0,95008931 |
| 5 | KIR2DL4 | KIR3DL1 /// | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8807196 | 0,95004049 |
| 3 | KIR2DL3 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7710152 | 0,94996026 |
| 4 | KIR2DL4 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84642293 | 0,9497987 |
| 5 | KIR2DL1 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8730616 | 0,94959879 |
| 5 | KIR2DL4 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86231116 | 0,94917636 |
| 4 | KIR2DL1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84726203 | 0,94917576 |
| 4 | KIR2DL3 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83703731 | 0,94888072 |
| 5 | KIR2DL3 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84663033 | 0,94880936 |
| 2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75675657 | 0,94847946 |
| 5 | KIR2DL3 | KIR3DL1 /// | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84256954 | 0,94791779 |
| 4 | KIR2DL3 | KIR3DL1 /// | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83563903 | 0,9475306 |
| 3 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78456843 | 0,94701058 |
| 5 | KIR2DL3 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82652192 | 0,94691262 |
| 4 | KIR3DS1 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85524404 | 0,94674973 |
| 4 | KIR2DL3 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81163687 | 0,9466551 |

| | | | | | | | | | | | | | | | | | |
|---|------------------------|---------|---------|------|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 5 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84558123 | 0,94617638 |
| 2 | KIR3DL1 /// KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76603657 | 0,94616701 |
| 3 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78418379 | 0,94585249 |
| 3 | KIR2DL3 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80882961 | 0,94569372 |
| 3 | KIR3DS1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7675957 | 0,94568834 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83174 | 0,94547097 |
| 5 | KIR2DL1 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83519151 | 0,94506473 |
| 4 | KIR2DL1 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81582567 | 0,94440771 |
| 5 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8390395 | 0,94435518 |
| 2 | KIR2DL4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77416238 | 0,94429958 |
| 1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,64441569 | 0,94393288 |
| 4 | KIR3DL1 /// KIR3DL2 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82616251 | 0,94335615 |
| 3 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,76577262 | 0,94306138 |
| 3 | KIR3DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78210742 | 0,94260114 |
| 2 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,72928506 | 0,94220637 |
| 3 | NCR1 | SH2D1B | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79805285 | 0,94189877 |
| 3 | KIR3DL1 /// KIR3DL2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7834259 | 0,94146373 |
| 3 | KIR2DL1 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79907024 | 0,93995161 |
| 2 | KIR2DL3 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75983711 | 0,9342681 |
| 4 | KIR2DL4 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86146988 | 0,93195221 |
| 2 | KIR3DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,67104577 | 0,9308818 |
| 2 | KIR3DL1 /// KIR3DL2 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70222981 | 0,92917851 |

| | | | | | | | | | | | | | | | | | | |
|---|-------------|---------|-------|----|----|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 2 | KIR2DL1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,73107306 | 0,9284614 |
| 4 | KIR3DS1 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84009401 | 0,92832666 |
| 4 | KIR2DL3 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82408471 | 0,92808082 |
| 4 | KIR3DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82497251 | 0,92538818 |
| | KIR3DL1 /// | | | | | | | | | | | | | | | | | |
| 4 | KIR3DL2 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82150016 | 0,92487851 |
| 4 | KIR2DL1 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81391125 | 0,92294678 |
| 3 | KIR2DL4 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83315011 | 0,9203775 |
| 2 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,60229015 | 0,91539667 |
| 3 | KIR2DL3 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80388117 | 0,91358387 |
| 2 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,7167987 | 0,9120559 |
| 3 | KIR3DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78866404 | 0,91014085 |
| | KIR3DL1 /// | | | | | | | | | | | | | | | | | |
| 3 | KIR3DL2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79397066 | 0,90971314 |
| 3 | NCR1 | CD160 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77327884 | 0,90746482 |
| 3 | KIR2DL1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78163382 | 0,90714012 |
| 3 | KIR3DS1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78285921 | 0,86348366 |
| 2 | KIR3DS1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70596942 | 0,86325686 |
| 1 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,62614327 | 0,85198674 |
| 2 | NCR1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,70377843 | 0,71840551 |
| 1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,43670266 | 0,26130817 |

Combination of genes for identification of T cells

| | | | | | | | | | | | | | | | | | | |
|---|-------|-------|------|------|----|----|----|----|----|----|----|----|----|----|----|----|------------|------------|
| 4 | TRAT1 | SIRPG | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8798215 | 0,99738871 |
| 2 | TRAT1 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79861814 | 0,99724241 |
| 3 | TRAT1 | SIRPG | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86632136 | 0,99723586 |
| 3 | TRAT1 | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88277553 | 0,99687047 |

| | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|-------|------|------|------|------|------------|------------|
| 4 | CD3D | TRAT1 | ICOS | CD28 | NA | NA | NA | NA | NA | NA | 0,89191247 | 0,99661201 |
| 4 | TRAT1 | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | NA | 0,88327837 | 0,9965735 |
| 5 | TRAT1 | SIRPG | ICOS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,8836644 | 0,99643474 |
| 5 | TRAT1 | SIRPG | ICOS | CD6 | CD28 | CD28 | NA | NA | NA | NA | 0,91386967 | 0,99641004 |
| 3 | TRAT1 | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,84244075 | 0,99605627 |
| 4 | TRAT1 | SIRPG | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91009568 | 0,99601113 |
| 5 | CD3D | TRAT1 | SIRPG | ICOS | CD28 | CD28 | NA | NA | NA | NA | 0,90542062 | 0,99599501 |
| 4 | TRAT1 | SIRPG | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,880905 | 0,99595475 |
| 4 | TRAT1 | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,89738039 | 0,99595393 |
| 5 | TRAT1 | CD3G | ICOS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,88749215 | 0,99572014 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,91213091 | 0,99571113 |
| 5 | CD3D | TRAT1 | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | 0,91312836 | 0,99563004 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,90701484 | 0,99546212 |
| 5 | CD3D | TRAT1 | ICOS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,89440382 | 0,99542518 |
| 5 | TRAT1 | CD3G | ICOS | CD6 | CD28 | CD28 | NA | NA | NA | NA | 0,91212158 | 0,99540253 |
| 4 | TRAT1 | SIRPG | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,87386529 | 0,99528204 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD28 | CD28 | NA | NA | NA | 0,90306128 | 0,99525895 |
| 5 | TRAT1 | SIRPG | CD6 | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,91434605 | 0,99514609 |
| 3 | CD3D | TRAT1 | ICOS | NA | NA | NA | NA | NA | NA | NA | 0,89363942 | 0,99514409 |
| 4 | TRAT1 | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,85522959 | 0,99509717 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,90341823 | 0,99504812 |
| 5 | TRAT1 | CD3G | ICOS | THEMIS | CD28 | CD28 | NA | NA | NA | NA | 0,88658294 | 0,99503048 |
| 5 | TRAT1 | SIRPG | CD3G | ICOS | CD28 | CD28 | NA | NA | NA | NA | 0,90127003 | 0,99500803 |
| 5 | TRAT1 | ICOS | CD6 | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,89637189 | 0,9949748 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD28 | CD28 | CD28 | CD28 | 0,90699669 | 0,99497129 |
| 3 | TRAT1 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,84058339 | 0,99497068 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CD28 | CD28 | NA | NA | NA | 0,92087181 | 0,99493582 |
| 4 | TRAT1 | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,89366921 | 0,99488334 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,91244318 | 0,99488107 |

| | | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|--------|-------|------|----|----|----|----|----|------------|------------|
| 4 | TRAT1 | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8691429 | 0,99487041 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,908657 | 0,99485178 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91393984 | 0,9947783 |
| 3 | TRAT1 | SIRPG | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88141023 | 0,99476459 |
| 5 | TRAT1 | SIRPG | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90973013 | 0,9947279 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,9218713 | 0,99465175 |
| 5 | CD3D | TRAT1 | SIRPG | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90487829 | 0,99464426 |
| 5 | TRAT1 | SIRPG | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8884824 | 0,99461052 |
| 1 | TRAT1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81700729 | 0,99460459 |
| 3 | TRAT1 | SIRPG | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87728197 | 0,9945767 |
| 6 | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89322564 | 0,9945532 |
| 6 | TRAT1 | SIRPG | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91095415 | 0,99454757 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91119851 | 0,99451542 |
| 5 | TRAT1 | SIRPG | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89408053 | 0,99450831 |
| 5 | TRAT1 | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91425353 | 0,99450573 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,92181882 | 0,99446783 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91222378 | 0,99441838 |
| 4 | TRAT1 | SIRPG | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88410996 | 0,99436635 |
| 4 | TRAT1 | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88886777 | 0,99434602 |
| 3 | CD3D | TRAT1 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88475957 | 0,99433173 |
| 8 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,9236679 | 0,99432542 |
| 6 | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90467274 | 0,99428798 |
| 7 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92733425 | 0,994263 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,92345385 | 0,99422769 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,92179748 | 0,99421078 |
| 5 | TRAT1 | SIRPG | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88721206 | 0,99420588 |
| 6 | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91627342 | 0,99419907 |
| 6 | CD3D | TRAT1 | SIRPG | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91153386 | 0,99416777 |
| 7 | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91282286 | 0,99416054 |

| | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|--------|-------|------|------|----|----|----|------------|------------|
| 5 | TRAT1 | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88669521 | 0,99415757 |
| 6 | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | NA | 0,89255223 | 0,99410389 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CD28 | CD28 | NA | NA | NA | NA | NA | 0,90523464 | 0,9940855 |
| 5 | TRAT1 | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,9019252 | 0,99407875 |
| 7 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,91492627 | 0,99407615 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,92126262 | 0,99401665 |
| 4 | SIRPG | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87008023 | 0,99401634 |
| 8 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,9249025 | 0,99401041 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,91568695 | 0,9939863 |
| 4 | CD3D | TRAT1 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88771712 | 0,99394298 |
| 6 | TRAT1 | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91843162 | 0,99394218 |
| 8 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | 0,92809142 | 0,99392359 |
| 2 | TRAT1 | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85332591 | 0,99387156 |
| 7 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91639175 | 0,99387 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,92131375 | 0,99386195 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | 0,90939501 | 0,99385592 |
| 5 | TRAT1 | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89544172 | 0,99385552 |
| 5 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,90935609 | 0,99384767 |
| 4 | TRAT1 | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,89124304 | 0,99384177 |
| 6 | TRAT1 | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91421281 | 0,99383084 |
| 5 | TRAT1 | SIRPG | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90655404 | 0,99382433 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | 0,91725029 | 0,99381848 |
| 6 | TRAT1 | SIRPG | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90702869 | 0,99379599 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD28 | CD28 | NA | NA | NA | NA | 0,91396759 | 0,99376835 |
| 5 | CD3D | TRAT1 | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89619764 | 0,99375648 |
| 5 | TRAT1 | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89069669 | 0,99374771 |
| 4 | CD3D | TRAT1 | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90912077 | 0,99369135 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92356614 | 0,99367827 |
| 3 | CD3D | TRAT1 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89130327 | 0,99365616 |

| | | | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|--------|--------|-------|------|------|------|----|----|----|------------|------------|
| 4 | CD3D | TRAT1 | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8958562 | 0,99364313 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9164043 | 0,99362481 |
| 6 | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91212583 | 0,99360679 |
| 7 | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,92388926 | 0,99360154 |
| 7 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,92329998 | 0,99358757 |
| 7 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,92618153 | 0,99358018 |
| 4 | CD3D | TRAT1 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89398087 | 0,99355672 |
| 5 | CD3D | TRAT1 | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91076254 | 0,99353352 |
| 5 | SIRPG | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90645411 | 0,99352229 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91574636 | 0,99351389 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91282441 | 0,99350228 |
| 4 | TRAT1 | SIRPG | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89397388 | 0,99348306 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90936742 | 0,99347756 |
| 6 | CD3D | TRAT1 | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9001827 | 0,99346821 |
| 5 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90450633 | 0,99345859 |
| 7 | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,91964725 | 0,99343549 |
| 3 | SIRPG | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86450947 | 0,99341924 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,91901498 | 0,99339942 |
| 5 | TRAT1 | SIRPG | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90434273 | 0,99337599 |
| 6 | TRAT1 | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89937189 | 0,99337572 |
| 5 | CD3D | TRAT1 | SIRPG | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90926298 | 0,99335881 |
| 5 | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89750338 | 0,99332409 |
| 8 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | THEMIS | CTLA4 | CD28 | CD28 | CD28 | NA | NA | NA | 0,92214483 | 0,99330573 |
| 4 | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87502843 | 0,99329762 |
| 5 | CD3D | TRAT1 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89801934 | 0,99328424 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90632181 | 0,99328021 |
| 7 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,91761233 | 0,99325953 |
| 6 | TRAT1 | SIRPG | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92322751 | 0,99323755 |
| 5 | TRAT1 | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90942534 | 0,99323137 |

| | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|-------|--------|-------|------|----|----|----|------------|------------|
| 5 | TRAT1 | SIRPG | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9134268 | 0,99322722 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | 0,92758745 | 0,99321318 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92108371 | 0,99320027 |
| 5 | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91302684 | 0,99318663 |
| 4 | CD3D | TRAT1 | SIRPG | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,90538525 | 0,99317908 |
| 5 | CD3D | TRAT1 | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91536266 | 0,99314557 |
| 8 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92294698 | 0,99314299 |
| 6 | CD3D | TRAT1 | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91351623 | 0,99313483 |
| 5 | CD3D | SIRPG | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90248236 | 0,99312827 |
| 4 | SIRPG | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90918898 | 0,99312202 |
| 6 | TRAT1 | SIRPG | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91245898 | 0,99311885 |
| 4 | CD3D | TRAT1 | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,89965015 | 0,99309706 |
| 5 | CD3D | TRAT1 | SIRPG | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90638977 | 0,99306341 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | 0,92484855 | 0,99306083 |
| 3 | TRAT1 | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87112694 | 0,99302974 |
| 4 | TRAT1 | SIRPG | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91393985 | 0,99302775 |
| 4 | TRAT1 | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9028124 | 0,99302403 |
| 4 | CD3D | TRAT1 | SIRPG | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90349588 | 0,99301919 |
| 6 | CD3D | TRAT1 | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91742329 | 0,99301712 |
| 4 | TRAT1 | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88635832 | 0,99301676 |
| 7 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92489681 | 0,99300901 |
| 6 | TRAT1 | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90929404 | 0,99300012 |
| 3 | TRAT1 | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90700861 | 0,99299467 |
| 7 | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92903244 | 0,99298913 |
| 4 | TRAT1 | SIRPG | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,91289021 | 0,99295885 |
| 5 | CD3D | TRAT1 | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90295801 | 0,99294164 |
| 7 | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91258648 | 0,99293178 |
| 6 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,90669487 | 0,99292645 |
| 5 | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,89599899 | 0,99291901 |

| | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|------|------|----|----|----|------------|------------|
| 3 | TRAT1 | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85683535 | 0,99291841 |
| 4 | TRAT1 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88033536 | 0,99291126 |
| 8 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD5 | CD28 | CD28 | NA | NA | NA | NA | 0,92997957 | 0,99290552 |
| 6 | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91577159 | 0,99289165 |
| 4 | TRAT1 | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88189754 | 0,99288332 |
| 4 | TRAT1 | SIRPG | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89120149 | 0,99288318 |
| 9 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | 0,9319578 | 0,99287916 |
| 7 | CD3D | TRAT1 | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91574756 | 0,99287082 |
| 4 | CD3D | TRAT1 | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91140118 | 0,99285313 |
| 8 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | NA | 0,9212912 | 0,99285082 |
| 5 | SIRPG | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89773294 | 0,99283591 |
| 7 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,9238924 | 0,9928061 |
| 8 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | NA | 0,92698392 | 0,99276364 |
| 4 | CD3D | TRAT1 | SIRPG | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9027907 | 0,99274699 |
| 8 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | NA | 0,92634885 | 0,99274666 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92466112 | 0,99274273 |
| 5 | TRAT1 | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92201329 | 0,99272409 |
| 5 | CD3D | TRAT1 | SIRPG | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91426331 | 0,99271342 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,92283391 | 0,9926715 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91976658 | 0,99265775 |
| 5 | TRAT1 | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89902428 | 0,99264937 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,92574491 | 0,99264225 |
| 6 | TRAT1 | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91828556 | 0,9926381 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91884042 | 0,9926356 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92728591 | 0,99263344 |
| 3 | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86817411 | 0,99262357 |
| 5 | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90608797 | 0,99258064 |
| 9 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | NA | NA | NA | 0,93209436 | 0,99257025 |
| 5 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,91546874 | 0,99255893 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|------------|------------|
| 5 | CD3D | TRAT1 | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,90350479 | 0,99254931 |
| 5 | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,92144708 | 0,99253522 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | 0,92536983 | 0,99251956 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | 0,9147101 | 0,99249409 |
| 4 | TRAT1 | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,89064664 | 0,99248833 |
| 4 | TRAT1 | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90050848 | 0,99245638 |
| 7 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92971427 | 0,99245601 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,91863151 | 0,99245081 |
| 5 | TRAT1 | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91123736 | 0,99245042 |
| 6 | CD3D | SIRPG | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91888252 | 0,992419 |
| 3 | SIRPG | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86316774 | 0,99241492 |
| 5 | CD3D | TRAT1 | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91417373 | 0,99241077 |
| 4 | CD3D | SIRPG | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90056906 | 0,99240116 |
| 5 | TRAT1 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,89495368 | 0,9923987 |
| 6 | CD3D | TRAT1 | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,90753957 | 0,99239666 |
| 5 | SIRPG | CD3G | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,90346977 | 0,99239522 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,91988657 | 0,99239257 |
| 3 | TRAT1 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82875213 | 0,99237286 |
| 7 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,92501515 | 0,9923712 |
| 8 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | 0,92990725 | 0,99235565 |
| 5 | CD3D | TRAT1 | SIRPG | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91981414 | 0,9923423 |
| 4 | CD3D | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88537661 | 0,99232128 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,91108042 | 0,99229261 |
| 4 | TRAT1 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,85892543 | 0,99229155 |
| 4 | TRAT1 | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,89214346 | 0,9922856 |
| 5 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | 0,90569101 | 0,99227717 |
| 5 | TRAT1 | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,90486346 | 0,99226763 |
| 5 | CD3D | TRAT1 | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,89813319 | 0,99226214 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | 0,91683737 | 0,9922428 |

| | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|--------|-------|------|----|----|----|----|------------|------------|
| 5 | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,91916855 | 0,99223587 |
| 3 | TRAT1 | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86397842 | 0,9922228 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | 0,92206727 | 0,9922198 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91707146 | 0,99220749 |
| 5 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,9174144 | 0,99219442 |
| 4 | CD3D | TRAT1 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90302692 | 0,99217582 |
| 6 | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,90316661 | 0,99217545 |
| 6 | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92358417 | 0,99212738 |
| 4 | SIRPG | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90804876 | 0,99211046 |
| 6 | CD3D | SIRPG | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91143269 | 0,99207839 |
| 5 | CD3D | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90838448 | 0,99205657 |
| 6 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91883722 | 0,99203906 |
| 2 | TRAT1 | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89722732 | 0,99197493 |
| 4 | CD3D | TRAT1 | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,91173603 | 0,99197199 |
| 5 | TRAT1 | SIRPG | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90292093 | 0,99196629 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,92006394 | 0,99196386 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,91760667 | 0,99193513 |
| 5 | TRAT1 | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90059338 | 0,9919318 |
| 4 | TRAT1 | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90187072 | 0,99192903 |
| 7 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,92133183 | 0,99192835 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | 0,92537556 | 0,99192233 |
| 5 | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90792052 | 0,99191118 |
| 4 | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90444084 | 0,99190911 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | 0,92028228 | 0,99189488 |
| 7 | CD3D | TRAT1 | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,923021 | 0,99185454 |
| 3 | TRAT1 | SIRPG | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88519704 | 0,99184401 |
| 5 | CD3G | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88933409 | 0,99184354 |
| 3 | TRAT1 | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88899338 | 0,99183051 |
| 6 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,92374729 | 0,99181663 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|------------|------------|
| 7 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92935925 | 0,99180506 |
| 3 | CD3D | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88165987 | 0,9917973 |
| 6 | CD3D | TRAT1 | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91136405 | 0,99177658 |
| 7 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,92599806 | 0,99177119 |
| 6 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91305625 | 0,9917683 |
| 5 | TRAT1 | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,87079149 | 0,9917653 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | 0,91383453 | 0,99170083 |
| 4 | CD3D | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90604889 | 0,99169554 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | 0,92789505 | 0,99168781 |
| 7 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,91755058 | 0,99167436 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,92755961 | 0,99167375 |
| 5 | CD3D | TRAT1 | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91502494 | 0,99167309 |
| 5 | CD3D | SIRPG | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91680779 | 0,99167104 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | 0,9100072 | 0,9916665 |
| 6 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91457397 | 0,99164503 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92064035 | 0,99163484 |
| 5 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | 0,91985596 | 0,99160393 |
| 4 | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88286614 | 0,99158512 |
| 3 | SIRPG | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86137403 | 0,99157323 |
| 5 | SIRPG | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,9039855 | 0,99156351 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,91924397 | 0,99153732 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | 0,91176413 | 0,99153448 |
| 6 | SIRPG | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92930739 | 0,9915121 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,92311371 | 0,99150763 |
| 5 | CD3D | SIRPG | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,90975765 | 0,99148377 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92361035 | 0,99148079 |
| 8 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92837524 | 0,99146751 |
| 2 | TRAT1 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83179274 | 0,99145714 |
| 6 | CD3D | TRAT1 | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,91810727 | 0,9914536 |

| | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|------------|------------|
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | 0,92289091 | 0,99143229 |
| 5 | CD3D | TRAT1 | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,90989077 | 0,99138929 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | NA | NA | NA | NA | 0,91267859 | 0,99135834 |
| 5 | CD3D | TRAT1 | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,92085639 | 0,99134144 |
| 5 | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | 0,91452279 | 0,99133879 |
| 4 | TRAT1 | SIRPG | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | 0,89396218 | 0,99133108 |
| 6 | CD3D | CD3G | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,90838222 | 0,99132969 |
| 5 | SIRPG | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91294403 | 0,99132417 |
| 3 | TRAT1 | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,8944801 | 0,99128991 |
| 7 | CD3D | TRAT1 | SIRPG | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92430594 | 0,99128979 |
| 4 | SIRPG | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | NA | 0,89528132 | 0,99127362 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | 0,92387432 | 0,99126309 |
| 5 | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,91665251 | 0,99123812 |
| 8 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | 0,92094519 | 0,99123519 |
| 6 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | 0,92495674 | 0,99123337 |
| 3 | TRAT1 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,88710646 | 0,99122727 |
| 4 | TRAT1 | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | 0,90305076 | 0,99122649 |
| 8 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | 0,93330268 | 0,99122443 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | THEMIS | CD5 | NA | NA | NA | NA | 0,92016086 | 0,99122067 |
| 5 | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | 0,903864 | 0,99121676 |
| 4 | TRAT1 | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91096521 | 0,99119813 |
| 7 | CD3D | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | 0,92780877 | 0,99117473 |
| 5 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | NA | NA | NA | NA | NA | 0,91629523 | 0,99117455 |
| 6 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,91746671 | 0,99117136 |
| 7 | CD3D | TRAT1 | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92738812 | 0,99116414 |
| 4 | TRAT1 | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,85901269 | 0,99115921 |

| | | | | | | | | | | | | |
|---|-------|--------|--------|--------|-------|--------|--------|-------|------|----|------------|------------|
| 8 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | 0,92812469 | 0,99115696 |
| 5 | SIRPG | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91789507 | 0,99114345 |
| 4 | CD3G | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,8822139 | 0,99113582 |
| 9 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | 0,92927319 | 0,99112228 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | 0,92718175 | 0,99112123 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | 0,91803017 | 0,99111941 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | 0,92184257 | 0,99110889 |
| 6 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,91875344 | 0,99110616 |
| 5 | CD3D | SIRPG | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91242363 | 0,99109485 |
| 8 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | 0,93145379 | 0,99108916 |
| 6 | CD3D | TRAT1 | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | 0,92098087 | 0,99108871 |
| 5 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,90786384 | 0,99107874 |
| 5 | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | 0,91232682 | 0,99107769 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | 0,92622882 | 0,99104584 |
| 6 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,9246289 | 0,99104185 |
| 6 | CD3D | TRAT1 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,91572715 | 0,99101666 |
| 4 | SIRPG | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,88424663 | 0,99101094 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | 0,92250571 | 0,99099847 |
| 2 | TRAT1 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,84682548 | 0,99097411 |
| 5 | SIRPG | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,8893757 | 0,99096413 |
| 5 | TRAT1 | SIRPG | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,9170253 | 0,99095739 |

| | | | | | | | | | | | | | |
|----|-------|-------|--------|--------|--------|-------|--------|-------|-----|------|------|------------|------------|
| 7 | CD3D | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,92189584 | 0,99095693 |
| 7 | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,9236027 | 0,99093123 |
| 3 | SIRPG | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89902066 | 0,99090917 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,92543329 | 0,99090126 |
| 5 | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90441163 | 0,9909 |
| 10 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | CD28 | 0,93310568 | 0,99087587 |
| 5 | TRAT1 | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91404169 | 0,9908744 |
| 5 | SIRPG | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,89950887 | 0,99086853 |
| 7 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | 0,92804883 | 0,99085564 |
| 6 | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,91612596 | 0,99085345 |
| 6 | CD3D | TRAT1 | SIRPG | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91895894 | 0,99084412 |
| 5 | CD3D | TRAT1 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90866312 | 0,9908304 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | 0,92582712 | 0,9908089 |
| 6 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | 0,91410687 | 0,99080653 |
| 6 | CD3D | SIRPG | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,9277799 | 0,99080159 |
| 4 | TRAT1 | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90752118 | 0,99079567 |
| 5 | CD3D | SIRPG | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91181059 | 0,99078213 |
| 4 | TRAT1 | SIRPG | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90614669 | 0,99077957 |
| 4 | TRAT1 | SIRPG | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91774217 | 0,99077011 |
| 6 | TRAT1 | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,90915943 | 0,99076813 |
| 5 | TRAT1 | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,91481599 | 0,99076467 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|------|------|----|----|----|------------|------------|
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | 0,92734818 | 0,99076118 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | 0,91764989 | 0,99076111 |
| 3 | TRAT1 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86572037 | 0,99075587 |
| 7 | CD3D | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92380825 | 0,99074226 |
| 7 | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92494371 | 0,99073871 |
| 6 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91905416 | 0,99072651 |
| 3 | TRAT1 | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90266892 | 0,99071821 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91753956 | 0,99071778 |
| 6 | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,93130324 | 0,99071553 |
| 8 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | 0,92589481 | 0,99070429 |
| 8 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,93257549 | 0,9907017 |
| 6 | TRAT1 | SIRPG | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92628419 | 0,99063984 |
| 4 | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,87991921 | 0,99062302 |
| 5 | SIRPG | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91749706 | 0,99061379 |
| 5 | TRAT1 | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92349844 | 0,99061168 |
| 6 | TRAT1 | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,90984606 | 0,99060886 |
| 4 | TRAT1 | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91235322 | 0,99059547 |
| 7 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92819432 | 0,9905844 |
| 5 | CD3D | CD3G | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,90383761 | 0,99057348 |
| 3 | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,82394716 | 0,99055753 |
| 4 | TRAT1 | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,89347178 | 0,99053978 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|--------|------|----|----|----|------------|------------|
| 7 | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,9209175 | 0,99052343 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92273491 | 0,99052284 |
| 3 | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88279762 | 0,99052068 |
| 5 | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,91053697 | 0,99051345 |
| 7 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92227294 | 0,9905064 |
| 8 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,93223637 | 0,99050581 |
| 4 | TRAT1 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90294688 | 0,99048567 |
| 5 | TRAT1 | SIRPG | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,9213695 | 0,99047636 |
| 4 | TRAT1 | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90393207 | 0,99043513 |
| 5 | TRAT1 | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91223395 | 0,99043453 |
| 8 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,93307922 | 0,99042744 |
| 2 | TRAT1 | SIRPG | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87069197 | 0,99040781 |
| 4 | SIRPG | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89072646 | 0,99039988 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | 0,92251677 | 0,99039379 |
| 5 | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91853218 | 0,99036174 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | 0,92325648 | 0,9903557 |
| 7 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92636889 | 0,99034847 |
| 5 | TRAT1 | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,90918448 | 0,99034269 |
| 3 | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,87354046 | 0,99034073 |
| 8 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92956496 | 0,99031143 |
| 4 | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89999242 | 0,99031022 |

| | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|--------|--------|-----|------|----|----|------------|------------|
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | 0,92129663 | 0,99030602 |
| 5 | TRAT1 | SIRPG | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,90675134 | 0,99030324 |
| 2 | SIRPG | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,834124 | 0,99030204 |
| 4 | SIRPG | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91115019 | 0,99029753 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | 0,92488559 | 0,99029722 |
| 6 | CD3D | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91749144 | 0,9902757 |
| 4 | TRAT1 | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | 0,91342347 | 0,99027476 |
| 4 | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,89270105 | 0,99027195 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,91855677 | 0,99024934 |
| 6 | TRAT1 | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91622549 | 0,99024851 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | 0,9299533 | 0,99024752 |
| 6 | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,921982 | 0,99024426 |
| 6 | CD3D | CD3G | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | 0,91811539 | 0,99023353 |
| 6 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91189759 | 0,99021974 |
| 8 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | 0,93224702 | 0,99020787 |
| 7 | CD3D | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92683996 | 0,99020471 |
| 4 | SIRPG | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90051623 | 0,99019327 |
| 5 | SIRPG | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,91916269 | 0,99018052 |
| 3 | CD3D | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88129112 | 0,99017631 |
| 4 | TRAT1 | SIRPG | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89327858 | 0,99017166 |
| 6 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,93053559 | 0,99016907 |

| | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|-------|------|----|----|----|----|----|----|------------|------------|
| 4 | CD3D | SIRPG | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90525912 | 0,99016761 |
| 5 | TRAT1 | SIRPG | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90862751 | 0,99016489 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9238703 | 0,9901489 |
| 5 | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91453957 | 0,99012579 |
| 5 | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89586446 | 0,99011031 |
| 5 | CD3D | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90086445 | 0,99008021 |
| 7 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,93012405 | 0,99007916 |
| 3 | TRAT1 | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89528191 | 0,99007567 |
| 6 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92514153 | 0,99007052 |
| 5 | SIRPG | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91590245 | 0,99004905 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92163104 | 0,99003104 |
| 5 | TRAT1 | SIRPG | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91671137 | 0,99002347 |
| 5 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,91495622 | 0,99001909 |
| 4 | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87469038 | 0,98999428 |
| 6 | CD3D | SIRPG | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92223714 | 0,98999264 |
| 6 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92521955 | 0,98998974 |
| 4 | TRAT1 | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87568926 | 0,98998825 |
| 5 | CD3D | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89807492 | 0,9899847 |
| 5 | CD3D | SIRPG | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92199117 | 0,98998298 |
| 5 | SIRPG | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91585331 | 0,98995916 |
| 4 | CD3D | SIRPG | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89723062 | 0,98994142 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|------|------|----|----|----|----|------------|------------|
| 6 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,92878111 | 0,98993344 |
| 6 | CD3D | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91544616 | 0,98993199 |
| 5 | TRAT1 | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,89887526 | 0,98993103 |
| 4 | CD3D | SIRPG | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,90826756 | 0,9898575 |
| 4 | TRAT1 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88721275 | 0,98985397 |
| 5 | SIRPG | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91309143 | 0,98980935 |
| 2 | CD3D | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87350288 | 0,98975062 |
| 4 | SIRPG | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,90267303 | 0,98974233 |
| 6 | CD3D | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91556181 | 0,98973089 |
| 7 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | 0,92551359 | 0,98969218 |
| 3 | SIRPG | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,86547947 | 0,98967297 |
| 6 | CD3D | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,9242016 | 0,98967218 |
| 4 | TRAT1 | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,9089831 | 0,98965104 |
| 6 | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92330692 | 0,98961364 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | 0,91863284 | 0,98960342 |
| 4 | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89600804 | 0,98960044 |
| 5 | CD3D | TRAT1 | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,9097367 | 0,98956437 |
| 6 | TRAT1 | SIRPG | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91326145 | 0,98954287 |
| 5 | TRAT1 | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90776443 | 0,98952349 |
| 4 | SIRPG | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,88532927 | 0,98952027 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,91161269 | 0,98951038 |

| | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|------|----|----|----|----|----|------------|------------|
| 5 | TRAT1 | SIRPG | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91957353 | 0,98950802 |
| 5 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91701015 | 0,98950276 |
| 7 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,93042895 | 0,9895005 |
| 3 | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85375915 | 0,98942985 |
| 6 | SIRPG | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,9201824 | 0,98940888 |
| 5 | CD3D | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91606632 | 0,9893953 |
| 5 | SIRPG | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92267717 | 0,98936713 |
| 3 | SIRPG | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88950025 | 0,98935352 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | 0,92774527 | 0,98934173 |
| 5 | CD3D | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91723803 | 0,98932463 |
| 4 | SIRPG | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91290738 | 0,98929175 |
| 4 | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89306622 | 0,98929113 |
| 5 | CD3D | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90866119 | 0,98924669 |
| 5 | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90887697 | 0,98924613 |
| 4 | SIRPG | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89801405 | 0,98923846 |
| 6 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91639379 | 0,9892071 |
| 4 | SIRPG | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89172333 | 0,98918509 |
| 5 | SIRPG | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92464094 | 0,98917738 |
| 5 | CD3D | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91360102 | 0,98915488 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,92274162 | 0,98914904 |
| 3 | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88608725 | 0,98913743 |

| | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|-------|------|-------|----|----|----|----|----|------------|------------|
| 3 | TRAT1 | SIRPG | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90954506 | 0,98910672 |
| 5 | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91985892 | 0,98909373 |
| 4 | CD3D | SIRPG | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90505797 | 0,98907072 |
| 6 | CD3D | SIRPG | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91744655 | 0,98906176 |
| 5 | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91662333 | 0,98905022 |
| 4 | CD3D | SIRPG | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91403877 | 0,98902846 |
| 5 | CD3D | SIRPG | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9216379 | 0,98902662 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | NA | CTLA4 | NA | NA | NA | NA | NA | 0,91767219 | 0,98902621 |
| 5 | CD3D | TRAT1 | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90630128 | 0,98902449 |
| 5 | TRAT1 | SIRPG | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91724583 | 0,98901611 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92727636 | 0,98900247 |
| 2 | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83986171 | 0,98898905 |
| 5 | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92100182 | 0,98895314 |
| 4 | TRAT1 | SIRPG | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90016281 | 0,98893517 |
| 3 | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87143696 | 0,98891347 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | NA | CTLA4 | NA | NA | NA | NA | NA | 0,92213208 | 0,98889098 |
| 5 | CD3D | SIRPG | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,92127744 | 0,98888419 |
| 4 | CD3D | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89546525 | 0,988847 |
| 4 | CD3D | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90325726 | 0,98882028 |
| 3 | TRAT1 | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86644133 | 0,988811 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91992564 | 0,98879216 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|------------|------------|
| 7 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | 0,92834634 | 0,98879152 |
| 4 | SIRPG | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92223739 | 0,98874414 |
| 4 | TRAT1 | SIRPG | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90413892 | 0,9887005 |
| 5 | CD3D | TRAT1 | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,90579722 | 0,98869343 |
| 2 | SIRPG | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84976106 | 0,98869282 |
| 4 | CD3D | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89466203 | 0,98869218 |
| 3 | CD3D | TRAT1 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89841489 | 0,98869167 |
| 5 | CD3D | CD3G | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,90595078 | 0,98869109 |
| 5 | CD3D | SIRPG | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | 0,9127209 | 0,98865443 |
| 4 | CD3D | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90864617 | 0,98863973 |
| 6 | CD3D | CD3G | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,92056078 | 0,98862642 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91698154 | 0,98861977 |
| 4 | SIRPG | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90369456 | 0,98857884 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92168329 | 0,98857784 |
| 5 | SIRPG | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | 0,92074118 | 0,98856547 |
| 4 | CD3D | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90042847 | 0,98853591 |
| 6 | CD3D | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91758807 | 0,98852753 |
| 6 | CD3D | SIRPG | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,92276397 | 0,98851335 |
| 8 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | 0,92875018 | 0,98849613 |
| 7 | CD3D | SIRPG | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92483635 | 0,98849389 |
| 8 | CD3D | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92876395 | 0,98848736 |

| | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|------|----|----|----|----|----|------------|------------|
| 4 | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90039246 | 0,98848227 |
| 6 | CD3D | TRAT1 | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92845911 | 0,98847074 |
| 9 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,93314986 | 0,98846726 |
| 6 | CD3D | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92086031 | 0,98846239 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92595356 | 0,98843278 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92737963 | 0,98843074 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91843511 | 0,98842648 |
| 3 | TRAT1 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87176308 | 0,98840825 |
| 8 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92668027 | 0,98840627 |
| 4 | CD3D | TRAT1 | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89729839 | 0,98840577 |
| 5 | CD3D | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91848066 | 0,98840231 |
| 4 | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9179505 | 0,98839528 |
| 8 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92880838 | 0,98837912 |
| 6 | CD3D | TRAT1 | SIRPG | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92554461 | 0,98836688 |
| 7 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92994757 | 0,98836267 |
| 4 | TRAT1 | SIRPG | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90111325 | 0,98836258 |
| 7 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,93277755 | 0,98835141 |
| 3 | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86833607 | 0,98834712 |
| 5 | CD3D | TRAT1 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91918872 | 0,98829374 |
| 7 | CD3D | CD3G | ICOS | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,9206846 | 0,98828523 |
| 4 | CD3D | TRAT1 | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91682768 | 0,98825376 |

| | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|--------|-------|------|----|------------|------------|
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | 0,92573444 | 0,98823241 |
| 4 | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90286152 | 0,98822903 |
| 4 | CD3D | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | 0,90866802 | 0,98821854 |
| 4 | SIRPG | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,90586295 | 0,98820076 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | 0,93343737 | 0,98818879 |
| 8 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | 0,9262978 | 0,98818332 |
| 5 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | 0,91784154 | 0,98817771 |
| 4 | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | 0,9129697 | 0,98816222 |
| 7 | CD3D | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,9340145 | 0,98814876 |
| 2 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,78751656 | 0,98812669 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | 0,93165128 | 0,98812314 |
| 5 | CD3D | SIRPG | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,92719963 | 0,98811159 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | 0,92658586 | 0,98811055 |
| 6 | CD3D | SIRPG | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,91571016 | 0,98809994 |
| 6 | CD3D | TRAT1 | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | 0,92092872 | 0,98808489 |
| 7 | CD3D | TRAT1 | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,9203438 | 0,98808473 |
| 5 | ICOS | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | 0,90065964 | 0,98808407 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | 0,91582679 | 0,98807629 |
| 6 | CD3D | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92548767 | 0,98805242 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | 0,9266633 | 0,98801619 |
| 4 | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | 0,90174871 | 0,98801451 |

| | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|--------|-------|-----|------|----|----|----|------------|------------|
| 4 | CD3D | TRAT1 | SIRPG | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91018186 | 0,98800852 |
| 5 | CD3D | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91630297 | 0,9879173 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91308206 | 0,98790812 |
| 3 | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88404827 | 0,98787855 |
| 4 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88927497 | 0,98785242 |
| 4 | CD6 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89455311 | 0,9878358 |
| 3 | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87773465 | 0,98782339 |
| 3 | CD3D | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88319364 | 0,98782157 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91816854 | 0,98779356 |
| 6 | CD3D | SIRPG | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92573015 | 0,987755 |
| 5 | CD3D | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90525422 | 0,98774405 |
| 5 | CD3D | TRAT1 | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9112925 | 0,98772261 |
| 5 | CD3D | TRAT1 | CD6 | THEMIS | CD5 | THEMIS | NA | NA | NA | NA | NA | NA | 0,91832713 | 0,98771952 |
| 9 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,93023059 | 0,9877178 |
| 5 | CD3D | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,9102596 | 0,98770347 |
| 6 | CD3D | TRAT1 | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92433404 | 0,98769778 |
| 4 | CD3D | CD3G | ICOS | THEMIS | NA | THEMIS | NA | NA | NA | NA | NA | NA | 0,90153229 | 0,98766604 |
| 4 | CD3D | CD3G | ICOS | CD28 | NA | CD28 | NA | NA | NA | NA | NA | NA | 0,89563595 | 0,98761463 |
| 5 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CD6 | NA | NA | NA | NA | NA | NA | 0,91121231 | 0,98759832 |
| 4 | CD3G | ICOS | CD6 | CTLA4 | NA | CTLA4 | NA | NA | NA | NA | NA | NA | 0,90218129 | 0,98758956 |
| 5 | CD3D | TRAT1 | SIRPG | CD6 | CTLA4 | CD6 | NA | NA | NA | NA | NA | NA | 0,92347873 | 0,98756214 |

| | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|----|----|----|------------|------------|
| 2 | SIRPG | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86647858 | 0,98755735 |
| 7 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92500836 | 0,9875343 |
| 3 | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90106435 | 0,98753287 |
| 6 | CD3D | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92693894 | 0,9875309 |
| 7 | CD3D | TRAT1 | SIRPG | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,93056172 | 0,98752491 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,92279687 | 0,98749374 |
| 5 | SIRPG | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9193498 | 0,98746396 |
| 6 | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92598499 | 0,98744672 |
| 6 | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91781469 | 0,98743506 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92360163 | 0,98742778 |
| 2 | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79257089 | 0,98738248 |
| 3 | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86312932 | 0,98737324 |
| 6 | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92200216 | 0,98737051 |
| 4 | CD3D | TRAT1 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90960367 | 0,98736508 |
| 7 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,93291862 | 0,98733521 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92311003 | 0,98733166 |
| 3 | SIRPG | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89489411 | 0,98732881 |
| 5 | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9140799 | 0,98732807 |
| 7 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,93098174 | 0,98732721 |
| 4 | SIRPG | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89281629 | 0,98732486 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91726906 | 0,98732332 |

| | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|------|------|----|----|----|----|----|------------|------------|
| 3 | CD3D | SIRPG | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90228266 | 0,98730192 |
| 5 | SIRPG | CD3G | THEMIS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92461843 | 0,98727861 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91662785 | 0,9872645 |
| 4 | SIRPG | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89598055 | 0,98724649 |
| 5 | CD3D | SIRPG | CD3G | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,9099605 | 0,98719299 |
| 7 | CD3D | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92417272 | 0,98717575 |
| 6 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92388295 | 0,98714616 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,90756801 | 0,98712763 |
| 4 | SIRPG | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92105369 | 0,9871235 |
| 7 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92145156 | 0,98712016 |
| 3 | CD3D | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88262123 | 0,98708798 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92391723 | 0,98708733 |
| 7 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92609126 | 0,98707216 |
| 6 | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92686231 | 0,9870597 |
| 4 | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91309946 | 0,98705618 |
| 8 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92899186 | 0,98704084 |
| 6 | CD3D | SIRPG | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92355586 | 0,98698641 |
| 5 | CD3D | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91888256 | 0,98697314 |
| 5 | CD3D | SIRPG | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91806682 | 0,98695965 |
| 4 | CD3D | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91494978 | 0,98695501 |
| 6 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92042071 | 0,98694943 |

| | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|--------|------|------|--------|-----|----|------------|------------|
| 5 | CD3D | SIRPG | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90872378 | 0,9869455 |
| 5 | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92982001 | 0,98693913 |
| 2 | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,80811825 | 0,9869172 |
| 5 | CD3D | CD3G | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91028894 | 0,98690917 |
| 5 | CD3D | TRAT1 | SIRPG | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91719725 | 0,9868947 |
| 6 | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92189715 | 0,986881 |
| 3 | SIRPG | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90990737 | 0,98687366 |
| 3 | CD3D | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89323929 | 0,98687351 |
| 3 | CD3D | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89992408 | 0,98687205 |
| 3 | CD3D | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89698279 | 0,98687072 |
| 6 | CD3D | TRAT1 | SIRPG | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92207289 | 0,98681211 |
| 5 | CD3D | CD3G | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,91366582 | 0,98676506 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | 0,92715386 | 0,98676114 |
| 5 | CD3D | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91194348 | 0,98674147 |
| 7 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92316604 | 0,98673819 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91804005 | 0,98673485 |
| 7 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,93222052 | 0,98671942 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD28 | THEMIS | CD5 | NA | 0,92623451 | 0,98668829 |
| 4 | CD3D | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91892559 | 0,98668129 |
| 5 | TRAT1 | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91431468 | 0,98667764 |
| 6 | CD3D | CD3G | ICOS | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,9167512 | 0,9866762 |

| | | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|-------|--------|--------|--------|-----|------|-----|-----|-----|-----|-----|------------|------------|
| 3 | CD3D | SIRPG | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88900399 | 0,98667613 |
| 5 | CD3D | SIRPG | CD3G | ICOS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90735111 | 0,98665267 |
| 5 | CD3D | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91549209 | 0,98664193 |
| 3 | SIRPG | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88930268 | 0,98663016 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | THEMIS | CD5 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,92076687 | 0,986624 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | NA | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,91808459 | 0,98661259 |
| 4 | CD3D | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91223475 | 0,98660851 |
| 6 | CD3D | SIRPG | CD6 | THEMIS | CD5 | CD28 | NA | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92680687 | 0,98660109 |
| 4 | CD3D | CD3G | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89360165 | 0,98660033 |
| 5 | CD3D | TRAT1 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91296067 | 0,98659126 |
| 4 | ICOS | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85948033 | 0,98654824 |
| 4 | SIRPG | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91634555 | 0,98654169 |
| 5 | CD3G | ICOS | CTLA4 | CD5 | CD28 | CD28 | NA | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90189864 | 0,98653018 |
| 5 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | NA | NA | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91318308 | 0,98651899 |
| 6 | CD3D | TRAT1 | CD3G | THEMIS | CD5 | CD28 | CD28 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91267839 | 0,98651562 |
| 6 | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CTLA4 | CD5 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,92281058 | 0,98649178 |
| 5 | CD3D | TRAT1 | CD3G | CD6 | CD28 | CD28 | NA | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91164874 | 0,98648727 |
| 2 | CD3D | TRAT1 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88838699 | 0,98648186 |
| 6 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | CD28 | CD28 | ICOS | CD5 | NA | NA | NA | NA | NA | NA | 0,91478165 | 0,98647637 |
| 6 | CD3D | SIRPG | ICOS | CD6 | CD5 | CD28 | CD28 | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91982733 | 0,98646246 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CD6 | CD6 | THEMIS | CD3G | CD6 | CD6 | CD6 | CD6 | CD6 | CD6 | CD6 | 0,91932901 | 0,98644988 |

| | | | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|------|------|------|----|----|----|----|----|------------|------------|
| 4 | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89514407 | 0,98641211 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92223545 | 0,98640666 |
| 5 | CD3D | TRAT1 | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91458609 | 0,98636587 |
| 5 | SIRPG | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90926411 | 0,98633839 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92035037 | 0,98632209 |
| 5 | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90798983 | 0,98631462 |
| 4 | CD3D | TRAT1 | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90079989 | 0,98622786 |
| 3 | CD3D | TRAT1 | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90566512 | 0,98612309 |
| 4 | CD3D | SIRPG | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91557641 | 0,98610727 |
| 5 | SIRPG | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91967329 | 0,98608689 |
| 4 | CD3D | SIRPG | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91299319 | 0,98604948 |
| 3 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8673642 | 0,9860216 |
| 5 | CD3D | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91767172 | 0,98600211 |
| 3 | CD3D | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89584524 | 0,98595199 |
| 5 | CD3D | TRAT1 | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91235004 | 0,98593917 |
| 4 | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9188876 | 0,98592791 |
| 3 | THEMIS | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,840143 | 0,98583793 |
| 6 | TRAT1 | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92313077 | 0,98580986 |
| 6 | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9227211 | 0,98577192 |
| 4 | ICOS | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90006993 | 0,98576539 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92627622 | 0,98575157 |

| | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|-------|------|----|----|----|----|----|------------|------------|
| 5 | CD3D | SIRPG | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91932239 | 0,98573269 |
| 4 | CD3D | TRAT1 | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89633828 | 0,98566983 |
| 5 | CD3D | TRAT1 | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91639903 | 0,98565433 |
| 4 | SIRPG | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89124905 | 0,98560773 |
| 5 | CD3G | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91841011 | 0,98560099 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91495356 | 0,98553416 |
| 2 | SIRPG | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85511354 | 0,98551874 |
| 7 | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,93064826 | 0,98551614 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | 0,91970461 | 0,98543655 |
| 4 | CD3D | SIRPG | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90322972 | 0,98543138 |
| 2 | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84731245 | 0,9854145 |
| 5 | CD3D | SIRPG | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91256672 | 0,98539394 |
| 3 | CD6 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87626805 | 0,98539291 |
| 4 | CD3D | TRAT1 | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90760245 | 0,98537011 |
| 4 | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89942641 | 0,98530967 |
| 6 | CD3D | TRAT1 | SIRPG | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | 0,91842802 | 0,98525171 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,9238548 | 0,9852327 |
| 5 | TRAT1 | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9133932 | 0,9851734 |
| 7 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,92683241 | 0,98516278 |
| 6 | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,92374991 | 0,98515811 |
| 6 | SIRPG | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92337172 | 0,98515533 |

| | | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|----|----|----|----|------------|------------|
| 2 | CD3D | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88349129 | 0,98508639 |
| 4 | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90899859 | 0,98504341 |
| 5 | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91060095 | 0,98504299 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92035261 | 0,98504286 |
| 3 | SIRPG | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90183961 | 0,98503186 |
| 4 | CD3D | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90189877 | 0,98499509 |
| 4 | TRAT1 | CD3G | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91474854 | 0,98496976 |
| 5 | TRAT1 | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91079442 | 0,98494086 |
| 4 | ICOS | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90612186 | 0,98493104 |
| 7 | CD3D | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92605212 | 0,98490667 |
| 3 | CD3D | SIRPG | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89658074 | 0,98490056 |
| 8 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92964124 | 0,98481848 |
| 5 | SIRPG | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9163971 | 0,98479904 |
| 3 | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86636783 | 0,98478216 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90855681 | 0,98475915 |
| 4 | SIRPG | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91158175 | 0,9847304 |
| 3 | CD3D | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90418811 | 0,98472926 |
| 3 | SIRPG | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88487557 | 0,98461691 |
| 8 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,93315487 | 0,98460867 |
| 5 | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91205494 | 0,98458813 |
| 7 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92437928 | 0,98456653 |

| | | | | | | | | | | | | | |
|---|--------|--------|--------|--------|--------|-------|------|----|----|----|----|------------|------------|
| 6 | CD3D | CD3G | ICOS | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,91963725 | 0,9845197 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,91750752 | 0,98451626 |
| 6 | TRAT1 | SIRPG | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,91976779 | 0,98446959 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | 0,91661125 | 0,98446569 |
| 3 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89674037 | 0,9844551 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | 0,92106013 | 0,98444308 |
| 5 | CD3D | TRAT1 | SIRPG | ICOS | CD5 | NA | NA | NA | NA | NA | NA | 0,91227282 | 0,98444046 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | NA | NA | NA | NA | NA | NA | 0,90725888 | 0,98438406 |
| 7 | CD3D | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92762552 | 0,98436829 |
| 5 | TRAT1 | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90794616 | 0,98436812 |
| 3 | TRAT1 | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88806514 | 0,98434305 |
| 4 | CD3D | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90648417 | 0,98433571 |
| 5 | CD3D | SIRPG | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91615561 | 0,98432979 |
| 3 | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90298159 | 0,98430422 |
| 3 | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,88889045 | 0,98428172 |
| 4 | SIRPG | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,89979693 | 0,98423492 |
| 4 | TRAT1 | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,89972558 | 0,98422053 |
| 4 | CD3D | CD3G | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90633476 | 0,98419723 |
| 3 | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89208219 | 0,98417976 |
| 5 | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | 0,9230114 | 0,98414301 |
| 6 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | 0,92550361 | 0,98413633 |

| | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|--------|-------|------|----|----|----|------------|------------|
| 5 | TRAT1 | SIRPG | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92449387 | 0,98409688 |
| 4 | TRAT1 | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9158244 | 0,98407087 |
| 5 | CD3D | CD3G | CD6 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | 0,91889706 | 0,98406984 |
| 5 | SIRPG | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91202321 | 0,98406877 |
| 6 | SIRPG | CD3G | ICOS | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92104287 | 0,98405267 |
| 7 | CD3D | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92178736 | 0,98404771 |
| 7 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | 0,92793083 | 0,98401653 |
| 6 | CD3D | SIRPG | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,93069329 | 0,98401107 |
| 4 | SIRPG | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,90783124 | 0,98394229 |
| 4 | CD3D | TRAT1 | SIRPG | CD6 | NA | NA | NA | NA | NA | NA | NA | 0,91311542 | 0,98394054 |
| 8 | CD3D | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | 0,92699202 | 0,9839367 |
| 7 | CD3D | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | 0,92709307 | 0,98391846 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | 0,93155565 | 0,98387307 |
| 5 | CD3D | TRAT1 | SIRPG | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91637808 | 0,98369477 |
| 5 | TRAT1 | SIRPG | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91127465 | 0,98369308 |
| 4 | TRAT1 | SIRPG | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,90494087 | 0,98363684 |
| 2 | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87694884 | 0,98361925 |
| 3 | SIRPG | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89940757 | 0,98352304 |
| 3 | CD3D | TRAT1 | SIRPG | NA | NA | NA | NA | NA | NA | NA | NA | 0,90044565 | 0,98348223 |
| 3 | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88049062 | 0,98342215 |
| 4 | CD3D | TRAT1 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90597597 | 0,98341405 |

| | | | | | | | | | | | | | | | |
|---|------|--------|--------|--------|--------|-------|------|----|----|----|----|----|----|------------|------------|
| 5 | CD3D | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90975301 | 0,98340934 |
| 4 | CD3D | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89646985 | 0,98340345 |
| 5 | CD3D | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92502853 | 0,98339636 |
| 6 | CD3D | CD3G | THEMIS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91967972 | 0,98336455 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92609573 | 0,98332598 |
| 4 | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89235938 | 0,9833079 |
| 5 | CD3D | SIRPG | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92493736 | 0,98330098 |
| 6 | CD3D | TRAT1 | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92122502 | 0,98329852 |
| 3 | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87298791 | 0,98309436 |
| 5 | CD3D | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91428973 | 0,98309056 |
| 2 | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86306233 | 0,98308666 |
| 6 | CD3D | SIRPG | CD3G | CD6 | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92330184 | 0,98306227 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92071856 | 0,98303991 |
| 6 | CD3D | CD3G | ICOS | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91378023 | 0,98285384 |
| 3 | ICOS | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86259817 | 0,98284931 |
| 5 | CD3D | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90961735 | 0,98281024 |
| 6 | CD3D | SIRPG | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91655908 | 0,98280161 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91628149 | 0,98275586 |
| 2 | CD3D | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86681292 | 0,98271456 |
| 2 | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8674238 | 0,98267119 |
| 5 | CD3D | SIRPG | CD3G | ICOS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90612894 | 0,98260142 |

| | | | | | | | | | | | | | | | | | |
|---|-------|--------|-------|--------|--------|--------|-----|-----|--------|------|------|------|------|------|------|------------|------------|
| 3 | ICOS | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84398968 | 0,98259836 |
| 4 | SIRPG | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90718887 | 0,98256455 |
| 3 | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89244442 | 0,98254779 |
| 5 | SIRPG | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91174843 | 0,98247349 |
| 7 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CTLA4 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | 0,92323837 | 0,98240996 |
| 5 | TRAT1 | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91287119 | 0,98235801 |
| 4 | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89841247 | 0,98235753 |
| 4 | TRAT1 | SIRPG | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9105026 | 0,98232683 |
| 5 | TRAT1 | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91663161 | 0,98225199 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | CD5 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | 0,93100208 | 0,98224932 |
| 6 | CD3D | SIRPG | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92624712 | 0,98222058 |
| 7 | CD3D | TRAT1 | CD3G | CD6 | CTLA4 | CD5 | CD5 | CD5 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | 0,9262948 | 0,98221818 |
| 4 | SIRPG | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89229354 | 0,98214027 |
| 8 | CD3D | TRAT1 | SIRPG | CD3G | CD3G | ICOS | CD6 | CD6 | CTLA4 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | 0,92631722 | 0,98212852 |
| 6 | CD3D | CD3G | ICOS | CD6 | THEMIS | CD5 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91731564 | 0,98210571 |
| 5 | CD3D | SIRPG | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91239996 | 0,98206288 |
| 4 | CD3D | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9172572 | 0,98205565 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | CD5 | CD28 | CD5 | CD5 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | CD28 | 0,92250385 | 0,98203073 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | THEMIS | CD5 | CD5 | THEMIS | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | 0,92167734 | 0,98194246 |
| 6 | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | CD5 | 0,92969334 | 0,98187405 |
| 3 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8633604 | 0,98175744 |

| | | | | | | | | | | | | | | | | |
|---|--------|-------|--------|--------|--------|--------|------|-----|----|----|----|----|----|----|------------|------------|
| 4 | SIRPG | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90315173 | 0,98174942 |
| 2 | THEMIS | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84429563 | 0,98174584 |
| 7 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92452281 | 0,98169497 |
| 5 | CD3D | SIRPG | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90888438 | 0,98164362 |
| 4 | CD3D | CD3G | CTLA4 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8989301 | 0,98158861 |
| 5 | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92232215 | 0,98155754 |
| 6 | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92002 | 0,98141344 |
| 5 | CD3D | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91720317 | 0,98140382 |
| 6 | CD3D | CD3G | CD6 | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91710262 | 0,98133237 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91672498 | 0,98122756 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | 0,92081844 | 0,98116758 |
| 6 | CD3D | SIRPG | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91735722 | 0,98113029 |
| 3 | TRAT1 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89452415 | 0,98109757 |
| 2 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8680035 | 0,98107824 |
| 5 | CD3D | CD3G | ICOS | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91223132 | 0,9810543 |
| 4 | CD3D | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89952339 | 0,98105386 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91667556 | 0,98099102 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92494529 | 0,98093819 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | THEMIS | CD5 | CD5 | NA | NA | NA | NA | NA | NA | 0,92173267 | 0,98079313 |
| 5 | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,9214964 | 0,98074673 |
| 2 | THEMIS | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78573271 | 0,980736 |

| | | | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|-------|-------|------|------|----|----|----|----|----|----|------------|------------|
| 4 | SIRPG | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90306406 | 0,9805973 |
| 3 | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86815478 | 0,98054875 |
| 6 | CD3D | TRAT1 | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91859187 | 0,98052135 |
| 5 | CD3D | SIRPG | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91653475 | 0,98040891 |
| 4 | CD3D | SIRPG | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91423901 | 0,98034416 |
| 3 | ICOS | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91018252 | 0,98032748 |
| 5 | CD3D | TRAT1 | CD3G | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91839195 | 0,98028319 |
| 6 | CD3D | SIRPG | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,918856 | 0,98028117 |
| 1 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,64119745 | 0,9802757 |
| 6 | CD3D | TRAT1 | SIRPG | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92662014 | 0,98026879 |
| 3 | SIRPG | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87975777 | 0,98019991 |
| 5 | CD3D | SIRPG | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91850137 | 0,98015163 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | CD5 | CD28 | CD28 | NA | NA | NA | NA | NA | NA | 0,92048091 | 0,98012877 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD6 | NA | NA | NA | NA | NA | NA | NA | 0,92354979 | 0,98009925 |
| 6 | CD3D | CD3G | ICOS | CD6 | CD5 | CD28 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91447101 | 0,98008686 |
| 4 | TRAT1 | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90812811 | 0,98002523 |
| 5 | CD3D | TRAT1 | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,92197935 | 0,97991586 |
| 4 | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,910482 | 0,97985721 |
| 4 | CD3D | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90751647 | 0,97977668 |
| 5 | TRAT1 | SIRPG | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91198843 | 0,97977425 |
| 3 | SIRPG | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88326079 | 0,97972348 |

| | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|--------|------|----|----|----|----|----|----|------------|------------|
| 5 | TRAT1 | SIRPG | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91251808 | 0,97964377 |
| 5 | CD3D | SIRPG | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | 0,91166072 | 0,97958986 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,91644627 | 0,97956481 |
| 3 | CD3D | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90251505 | 0,97955445 |
| 6 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,9256934 | 0,97952272 |
| 6 | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,91765713 | 0,97952227 |
| 5 | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91004777 | 0,97949835 |
| 4 | CD3D | CD3G | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,90164949 | 0,97949084 |
| 5 | CD3D | TRAT1 | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91010163 | 0,97944642 |
| 2 | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82366156 | 0,97939624 |
| 5 | CD3D | CD3G | THEMIS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90926611 | 0,97935139 |
| 2 | CD6 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88057346 | 0,97931256 |
| 4 | TRAT1 | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8971309 | 0,97925709 |
| 3 | SIRPG | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8774974 | 0,97923339 |
| 3 | CD3D | SIRPG | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90030442 | 0,9791635 |
| 3 | TRAT1 | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89535412 | 0,97886531 |
| 4 | CD3D | SIRPG | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | 0,90165171 | 0,97884721 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | 0,91437554 | 0,97884501 |
| 5 | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91421028 | 0,97881219 |
| 4 | TRAT1 | SIRPG | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90785396 | 0,97870678 |
| 4 | CD3D | TRAT1 | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90654437 | 0,97866801 |

| | | | | | | | | | | | | | | | |
|---|-------|-------|--------|--------|--------|-------|------|----|----|----|----|----|----|------------|------------|
| 3 | CD3D | CD3G | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88740937 | 0,9785716 |
| 4 | CD3D | SIRPG | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91236082 | 0,97853811 |
| 7 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92853919 | 0,97843967 |
| 1 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,75681903 | 0,97830641 |
| 5 | CD3D | TRAT1 | SIRPG | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,92050868 | 0,97818705 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91548771 | 0,9781817 |
| 4 | CD3D | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90577063 | 0,97814869 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,92304723 | 0,97800406 |
| 3 | TRAT1 | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89950978 | 0,97798174 |
| 2 | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85122584 | 0,97794878 |
| 6 | CD3D | TRAT1 | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91515526 | 0,97782743 |
| 6 | CD3D | CD3G | CD6 | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92370532 | 0,9778208 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | 0,91858137 | 0,97769068 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,9170705 | 0,97768732 |
| 5 | SIRPG | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90813742 | 0,97756704 |
| 5 | CD3D | CD3G | ICOS | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90809651 | 0,97749405 |
| 5 | CD3D | SIRPG | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90303719 | 0,97720862 |
| 4 | TRAT1 | SIRPG | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90977627 | 0,97709096 |
| 4 | CD3D | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89374118 | 0,97706635 |
| 2 | CD3D | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88090848 | 0,97705724 |
| 3 | SIRPG | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88339036 | 0,97691126 |

| | | | | | | | | | | | | | | |
|---|-------|--------|--------|--------|-------|-------|------|----|----|-----|----|----|------------|------------|
| 4 | CD3D | TRAT1 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91425693 | 0,97690079 |
| 6 | CD3D | SIRPG | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,9241663 | 0,97689721 |
| 5 | SIRPG | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91506719 | 0,97687138 |
| 4 | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89700036 | 0,97680085 |
| 5 | CD3D | SIRPG | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91206798 | 0,97668323 |
| 3 | CD3D | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90195313 | 0,97666871 |
| 5 | SIRPG | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,910972 | 0,97657961 |
| 1 | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77842579 | 0,97656786 |
| 5 | CD3D | SIRPG | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,91397249 | 0,97649855 |
| 6 | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,92709427 | 0,97620776 |
| 4 | CD3D | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89684342 | 0,97617726 |
| 4 | CD3D | CD3G | CD6 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,8995606 | 0,97598877 |
| 4 | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89741299 | 0,97591675 |
| 7 | CD3D | SIRPG | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | CD5 | NA | NA | 0,91903077 | 0,97583954 |
| 5 | CD3D | SIRPG | CD3G | ICOS | CD6 | NA | NA | NA | NA | NA | NA | NA | 0,90490536 | 0,97580667 |
| 5 | CD3D | CD3G | THEMIS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91813897 | 0,9757138 |
| 7 | CD3D | SIRPG | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92670887 | 0,97568243 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | 0,91409528 | 0,97556058 |
| 5 | TRAT1 | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9217647 | 0,97546789 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91762933 | 0,97546761 |
| 6 | CD3D | CD3G | ICOS | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,91398175 | 0,97527146 |

| | | | | | | | | | | | | | | | |
|---|-------|--------|--------|-------|-------|------|----|----|----|----|----|----|----|------------|------------|
| 5 | CD3D | TRAT1 | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91024164 | 0,97514725 |
| 4 | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89745258 | 0,974929 |
| 4 | SIRPG | CD3G | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91160704 | 0,97479281 |
| 4 | SIRPG | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90605281 | 0,97476192 |
| 4 | CD3D | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90084186 | 0,97474268 |
| 2 | ICOS | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85398393 | 0,97457428 |
| 6 | CD3D | CD3G | CD6 | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,92004659 | 0,97454845 |
| 5 | CD3D | TRAT1 | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91002577 | 0,97433709 |
| 4 | CD3D | SIRPG | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,897642 | 0,97378551 |
| 3 | CD3G | CD6 | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89543335 | 0,97374496 |
| 3 | TRAT1 | SIRPG | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89651721 | 0,97373076 |
| 5 | CD3D | TRAT1 | SIRPG | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91308088 | 0,97360671 |
| 4 | SIRPG | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90294602 | 0,97358932 |
| 3 | TRAT1 | SIRPG | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8900353 | 0,97357123 |
| 4 | CD3D | SIRPG | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89541186 | 0,97351618 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9139157 | 0,97351236 |
| 3 | CD3D | CD3G | ICOS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88466977 | 0,97351098 |
| 4 | CD3D | SIRPG | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90115481 | 0,97327939 |
| 5 | TRAT1 | SIRPG | CD3G | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91906219 | 0,97313201 |
| 2 | TRAT1 | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86880124 | 0,97309253 |
| 2 | SIRPG | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86311727 | 0,97285672 |

| | | | | | | | | | | | | | |
|---|-------|--------|-------|--------|--------|-------|-----|----|----|----|----|------------|------------|
| 6 | CD3D | SIRPG | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | 0,92146024 | 0,97281449 |
| 7 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | 0,92611962 | 0,9727069 |
| 4 | CD3D | TRAT1 | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90631251 | 0,97250376 |
| 6 | CD3D | SIRPG | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | 0,91376148 | 0,97228383 |
| 5 | CD3D | CD3G | ICOS | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | 0,90773874 | 0,97218587 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | NA | NA | NA | NA | NA | NA | 0,91107295 | 0,97210253 |
| 3 | CD3D | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88774442 | 0,97189242 |
| 3 | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88385447 | 0,97188808 |
| 5 | SIRPG | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,90978939 | 0,97176546 |
| 4 | CD3D | SIRPG | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90847876 | 0,97171459 |
| 6 | CD3D | TRAT1 | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | 0,92229188 | 0,97152512 |
| 3 | CD3G | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88459886 | 0,97144336 |
| 4 | CD3D | TRAT1 | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | 0,90394695 | 0,97133123 |
| 5 | SIRPG | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | 0,90195121 | 0,97129987 |
| 3 | SIRPG | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89058071 | 0,97118816 |
| 4 | TRAT1 | CD3G | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,9110829 | 0,97114922 |
| 5 | CD3D | CD3G | CD6 | THEMIS | CD5 | NA | NA | NA | NA | NA | NA | 0,90579188 | 0,97087153 |
| 2 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,81623734 | 0,97086813 |
| 3 | CD3D | CD3G | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,88285975 | 0,97072574 |
| 5 | CD3D | CD3G | CTLA4 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | 0,91289771 | 0,97060534 |
| 2 | TRAT1 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88054338 | 0,97027374 |

| | | | | | | | | | | | | | | | | | |
|---|--------|-------|--------|--------|-------|------|-------|-----|-----|----|----|----|----|----|----|------------|------------|
| 1 | THEMIS | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77177102 | 0,97021521 |
| 4 | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89127754 | 0,97017565 |
| 5 | CD3D | SIRPG | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91540292 | 0,97011629 |
| 5 | CD3D | SIRPG | CD3G | CD6 | CTLA4 | NA | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91490551 | 0,96970042 |
| 4 | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89108042 | 0,96954854 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CTLA4 | CD5 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,92172913 | 0,96949588 |
| 5 | CD3D | SIRPG | CD3G | THEMIS | CD5 | NA | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90982508 | 0,96884322 |
| 1 | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,77633836 | 0,96881319 |
| 3 | SIRPG | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89000013 | 0,96869303 |
| 4 | CD3D | TRAT1 | SIRPG | CD5 | NA | NA | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90884803 | 0,96857532 |
| 4 | CD3D | TRAT1 | SIRPG | CD3G | CD3G | NA | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | 0,90187901 | 0,96788565 |
| 2 | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85868078 | 0,9677618 |
| 4 | CD3D | CD3G | CD6 | CTLA4 | NA | NA | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90625371 | 0,96743877 |
| 6 | CD3D | SIRPG | CD3G | CD6 | CD5 | CD28 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91373703 | 0,96736699 |
| 5 | CD3D | TRAT1 | CD3G | CTLA4 | CD5 | NA | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91705403 | 0,96721815 |
| 6 | CD3D | SIRPG | CD3G | ICOS | CD6 | CD5 | CD6 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | 0,90555349 | 0,9671437 |
| 4 | CD3D | CD6 | CTLA4 | CD5 | NA | NA | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90612359 | 0,96698445 |
| 3 | CD3D | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89172456 | 0,96682286 |
| 3 | CD3D | SIRPG | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89078802 | 0,96667315 |
| 5 | TRAT1 | SIRPG | CD3G | CD6 | CD5 | CD5 | CD6 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | 0,91029422 | 0,9666539 |
| 4 | CD3D | CD3G | THEMIS | CD5 | NA | NA | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,9006474 | 0,96599853 |

| | | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-------|-----|-----|----|----|----|----|----|------------|------------|
| 4 | SIRPG | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89511531 | 0,96578602 |
| 4 | SIRPG | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90040983 | 0,96552241 |
| 3 | CD3D | TRAT1 | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89203842 | 0,965266 |
| 4 | CD3D | SIRPG | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90576546 | 0,96517209 |
| 5 | CD3D | CD3G | ICOS | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,8983304 | 0,96508338 |
| 3 | CD3D | TRAT1 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90203564 | 0,96475898 |
| 5 | CD3D | CD3G | CD6 | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90381097 | 0,96453683 |
| 4 | CD3D | SIRPG | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,91035655 | 0,96427436 |
| 4 | TRAT1 | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90143206 | 0,96396996 |
| 5 | SIRPG | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,91353824 | 0,96392118 |
| 6 | CD3D | TRAT1 | SIRPG | CD3G | CD6 | CD5 | CD5 | NA | NA | NA | NA | NA | 0,91218919 | 0,96299959 |
| 2 | CD3D | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87002645 | 0,96194232 |
| 3 | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8839151 | 0,96178009 |
| 5 | CD3D | SIRPG | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90168085 | 0,96169036 |
| 5 | CD3D | SIRPG | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | 0,90957836 | 0,96139172 |
| 1 | SIRPG | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,79473659 | 0,96053136 |
| 6 | CD3D | SIRPG | CD3G | CD6 | CTLA4 | CD5 | CD5 | NA | NA | NA | NA | NA | 0,91624151 | 0,96040553 |
| 3 | CD3D | CD3G | CTLA4 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89356702 | 0,96034869 |
| 5 | CD3D | TRAT1 | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | 0,90609266 | 0,9598123 |
| 2 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8518487 | 0,95980621 |
| 4 | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,90151529 | 0,95962441 |

| | | | | | | | | | | | | | | | | |
|---|-------|-------|-------|-------|-----|----|----|----|----|----|----|----|----|----|------------|------------|
| 3 | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87321835 | 0,95961487 |
| 4 | TRAT1 | SIRPG | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90362873 | 0,95926986 |
| 3 | CD3D | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89915312 | 0,95725403 |
| 4 | CD3D | CD3G | ICOS | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89413823 | 0,95722047 |
| 3 | SIRPG | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85452039 | 0,95687047 |
| 5 | CD3D | TRAT1 | SIRPG | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90858693 | 0,95621045 |
| 5 | CD3D | CD3G | CD6 | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90917968 | 0,95598993 |
| 4 | SIRPG | CD3G | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90606871 | 0,95597794 |
| 4 | CD3D | CD3G | CD5 | CD28 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89774283 | 0,95573484 |
| 2 | CD3D | SIRPG | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87813176 | 0,95542214 |
| 5 | CD3D | SIRPG | CD3G | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,91271286 | 0,95313334 |
| 4 | CD3D | SIRPG | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88777896 | 0,95284611 |
| 3 | TRAT1 | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89361881 | 0,95246425 |
| 3 | SIRPG | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87758756 | 0,95232602 |
| 4 | CD3D | TRAT1 | CD3G | CD5 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90216191 | 0,94994047 |
| 4 | CD3D | SIRPG | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89178684 | 0,94927 |
| 3 | CD3G | CTLA4 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,89004894 | 0,94665088 |
| 4 | CD3D | CD3G | CTLA4 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,90474098 | 0,94507822 |
| 2 | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,78701543 | 0,94390912 |
| 3 | CD3D | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86840222 | 0,94193218 |
| 4 | SIRPG | CD3G | CD6 | CD5 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87587234 | 0,94060276 |

| | | | | | | | | | | | | | | | | |
|---|-------|-------|------|-----|-----|----|----|----|----|----|----|----|----|------------|----|------------|
| 5 | CD3D | SIRPG | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | 0,89178429 | NA | 0,93976728 |
| 2 | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84058253 | NA | 0,93870212 |
| 3 | CD3D | CD3G | CD6 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87584062 | NA | 0,9376678 |
| 3 | CD3D | SIRPG | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,8843147 | NA | 0,93518305 |
| 2 | SIRPG | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,83355431 | NA | 0,93225953 |
| 3 | CD3D | SIRPG | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88195224 | NA | 0,93195229 |
| 1 | CD3D | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85065552 | NA | 0,93094794 |
| 2 | SIRPG | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,85086565 | NA | 0,92872246 |
| 4 | CD3D | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87778458 | NA | 0,92692224 |
| 3 | CD3G | CD6 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,84517943 | NA | 0,92431843 |
| 4 | CD3D | SIRPG | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,88838991 | NA | 0,92184044 |
| 3 | SIRPG | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86705711 | NA | 0,91671721 |
| 2 | CD3D | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86398414 | NA | 0,90429349 |
| 2 | CD3D | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,86133762 | NA | 0,90027373 |
| 3 | CD3D | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,87329721 | NA | 0,89520034 |
| 2 | CD3G | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,82813417 | NA | 0,87347023 |
| 1 | CD5 | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,71218117 | NA | 0,86619448 |
| 1 | CD3G | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | NA | 0,780051 | NA | 0,86156268 |

REFERENCES:

Throughout this application, various references describe the state of the art to which this invention pertains. The disclosures of these references are hereby incorporated by reference
5 into the present disclosure.

CLAIMS:

1. A method for quantifying the population of cells of monocytic origin in a tissue sample obtained from a subject comprising determining the expression level of at least one gene selected from the group consisting of CSF1R, ADAP2, RASSF4, FPR3, TFEC,
5 PLA2G7 and KYN1 where the determined expression level indicates the quantity of the population of cells of monocytic origin in the tissue sample.
2. The method of claim 1 wherein the subject suffers from a cancer.
3. The method of claim 2 wherein the subject suffers from a solid cancer selected from the group consisting of bile duct cancer (e.g. perihilar cancer, distal bile duct cancer,
10 intrahepatic bile duct cancer), bladder cancer, bone cancer (e.g. osteoblastoma, osteochondroma, hemangioma, chondromyxoid fibroma, osteosarcoma, chondrosarcoma, fibrosarcoma, malignant fibrous histiocytoma, giant cell tumor of the bone, chordoma, lymphoma, multiple myeloma), brain and central nervous system cancer (e.g. meningioma, astrocytoma, oligodendrogliomas, ependymoma, gliomas,
15 medulloblastoma, ganglioglioma, Schwannoma, germinoma, craniopharyngioma), breast cancer (e.g. ductal carcinoma in situ, infiltrating ductal carcinoma, infiltrating lobular carcinoma, lobular carcinoma in situ, gynecomastia), Castleman disease (e.g. giant lymph node hyperplasia, angiofollicular lymph node hyperplasia), cervical cancer, colorectal cancer, endometrial cancer (e.g. endometrial adenocarcinoma, adenocarcinoma, papillary serous adenocarcinoma, clear cell), esophagus cancer, gallbladder cancer (mucinous adenocarcinoma, small cell carcinoma), gastrointestinal carcinoid tumors (e.g. choriocarcinoma, chorioadenoma destruens), Hodgkin's disease, non-Hodgkin's lymphoma, Kaposi's sarcoma, kidney cancer (e.g. renal cell cancer), laryngeal and hypopharyngeal cancer, liver cancer (e.g. hemangioma, hepatic adenoma,
20 focal nodular hyperplasia, hepatocellular carcinoma), lung cancer (e.g. small cell lung cancer, non-small cell lung cancer), mesothelioma, plasmacytoma, nasal cavity and paranasal sinus cancer (e.g. esthesioneuroblastoma, midline granuloma), nasopharyngeal cancer, neuroblastoma, oral cavity and oropharyngeal cancer, ovarian cancer, pancreatic cancer, penile cancer, pituitary cancer, prostate cancer,
25 retinoblastoma, rhabdomyosarcoma (e.g. embryonal rhabdomyosarcoma, alveolar rhabdomyosarcoma, pleomorphic rhabdomyosarcoma), salivary gland cancer, skin cancer (e.g. melanoma, nonmelanoma skin cancer), stomach cancer, testicular cancer

(e.g. seminoma, nonseminoma germ cell cancer), thymus cancer, thyroid cancer (e.g. follicular carcinoma, anaplastic carcinoma, poorly differentiated carcinoma, medullary thyroid carcinoma, thyroid lymphoma), vaginal cancer, vulvar cancer, and uterine cancer (e.g. uterine leiomyosarcoma).

- 5 4. The method of claim 1 wherein the expression level of 2, 3, 4, 5, 6 or 7 genes is determined at step i).
5. The method of claim 4 wherein the combination of genes is selected from the Table 1.
6. The method of claim 1 which further comprises quantifying at least one further population of cells in the tissue sample.
- 10 7. The method of claim 6 wherein the at least one population of cells is selected from the group consisting of B cells, T cells, NK cells, cytotoxic lymphocytes, neutrophils, myeloid dendritic cells, fibroblasts and endothelial cells (includes lymphatics and blood vessels).
8. The method of claim 1 which further comprises determining the expression level of at
15 least one gene representative of B cells selected from the group consisting of MS4A1, CD19, CD79A, FCRL2, CR2, PAX5, CD22, BANK1 and IGKC.
9. The method of claim 1 which further comprises determining the expression level of at least one gene representative of T cells selected from the group consisting of TRAT1, CD3D, THEMIS, ICOS, SIRPG, CD3G, CTLA4, CD6, CD5 and CD28.
- 20 10. The method of claim 1 which further comprises determining the expression level of at least one gene representative of NK cells selected from the group consisting of KIR2DL1, KIR2DL3, NCR1, KIR3DL1, KIR3DS1, KIR3DL2, SH2D1B, CD160, GENE 2 and KIR2DL4.
11. The method of claim 1 which further comprises determining the expression level of at
25 least one gene representative of cytotoxic lymphocytes selected from the group consisting of KLRC4-KLRK1 /// KLRK1, CD8A, KLRD1, GNLY, EOMES, KLRC3, KLRC4, FGFBP2 and KLRC1 /// KLRC2.

12. The method of claim 1 which further comprises determining the expression level of at least one gene representative of neutrophils selected from the group consisting of CXCR2, VNN3 CYP4F3, HAL, GENE 1, FCGR3B, KCNJ15, CXCR1, STEAP4 and TNFRSF10C.
- 5 13. The method of claim 1 which further comprises determining the expression level of at least one gene representative of myeloid dendritic cells selected from the group consisting of CD1E, CLEC10A, CLIC2, CD1A, WFDC21P and CD1B.
14. The method of claim 1 which further comprises determining the expression level of at least one gene representative of fibroblasts selected from the group consisting of DCN,
10 COL6A2, COL6A1, COL3A1, COL1A1, PAMR1, TAGLN and GREM1.
15. The method of claim 1 which further comprises determining the expression level of at least one gene representative of endothelial cells selected from the group consisting of CDH5, EMCN, MYCT1, ELTD1, ROBO4, CLEC14A, VWF, ESAM, MMRN2 and KDR.

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/073055

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12Q1/68
ADD.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED
Minimum documentation searched (classification system followed by classification symbols)
C12Q
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

| C. DOCUMENTS CONSIDERED TO BE RELEVANT | | |
|--|--|-----------------------|
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X | WO 2004/106925 A2 (KOUYAMA YOSHIHISA [JP]) 9 December 2004 (2004-12-09) the whole document | 1-15 |
| A | US 2003/148295 A1 (WAN JACKSON SHEK-LAM [US] ET AL) 7 August 2003 (2003-08-07) the whole document | 1-15 |
| X | WO 03/106706 A2 (MILLENIUM BIOLOG AG [CH]; BRUNNER ANDREAS [CH]; HAGG RUPERT [CH]; TOMM) 24 December 2003 (2003-12-24) the whole document | 1-15 |
| | ----- -/-- | |

Further documents are listed in the continuation of Box C.

See patent family annex.

* Special categories of cited documents :

| | |
|---|---|
| <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier application or patent but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> | <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art</p> <p>"&" document member of the same patent family</p> |
|---|---|

| | |
|--|--|
| Date of the actual completion of the international search 15 November 2016 | Date of mailing of the international search report 25/11/2016 |
| Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016 | Authorized officer Mueller, Frank |

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2016/073055

| C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT | | |
|--|--|-----------------------|
| Category* | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
| X | L. OESPER ET AL: "Quantifying tumor heterogeneity in whole-genome and whole-exome sequencing data", BIOINFORMATICS., vol. 30, no. 24, 8 October 2014 (2014-10-08), pages 3532-3540, XP055249401, GB ISSN: 1367-4803, DOI: 10.1093/bioinformatics/btu651 the whole document ----- | 1-15 |
| X | NEIL A MABBOTT ET AL: "An expression atlas of human primary cells: inference of gene function from coexpression networks", BMC GENOMICS, BIOMED CENTRAL LTD, LONDON, UK, vol. 14, no. 1, 20 September 2013 (2013-09-20), page 632, XP021163126, ISSN: 1471-2164, DOI: 10.1186/1471-2164-14-632 the whole document ----- | 1-15 |
| X | DU X ET AL: "Genomic profiles for human peripheral blood T cells, B cells, natural killer cells, monocytes, and polymorphonuclear cells: Comparisons to ischemic stroke, migraine, and Tourette syndrome", GENOMICS, ACADEMIC PRESS, SAN DIEGO, US, vol. 87, no. 6, 1 June 2006 (2006-06-01), pages 693-703, XP024929515, ISSN: 0888-7543, DOI: 10.1016/J.YGENO.2006.02.003 [retrieved on 2006-06-01] the whole document ----- | 1-15 |

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/EP2016/073055

| Patent document cited in search report | Publication date | Patent family member(s) | Publication date |
|--|------------------|-------------------------|------------------|
| WO 2004106925 A2 | 09-12-2004 | AU 2004243690 A1 | 09-12-2004 |
| | | CA 2518677 A1 | 09-12-2004 |
| | | CN 101044404 A | 26-09-2007 |
| | | EP 1599730 A2 | 30-11-2005 |
| | | JP 2007501407 A | 25-01-2007 |
| | | US 2005032126 A1 | 10-02-2005 |
| | | WO 2004106925 A2 | 09-12-2004 |
| ----- | | | |
| US 2003148295 A1 | 07-08-2003 | AU 2002306768 A1 | 03-10-2002 |
| | | EP 1370696 A2 | 17-12-2003 |
| | | JP 2004519247 A | 02-07-2004 |
| | | US 2003148295 A1 | 07-08-2003 |
| | | WO 02074979 A2 | 26-09-2002 |
| ----- | | | |
| WO 03106706 A2 | 24-12-2003 | AU 2003233743 A1 | 31-12-2003 |
| | | CA 2492504 A1 | 24-12-2003 |
| | | EP 1521844 A2 | 13-04-2005 |
| | | US 2006008803 A1 | 12-01-2006 |
| | | WO 03106706 A2 | 24-12-2003 |
| ----- | | | |