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Supplemental Information

Spatio-temporal Dynamics of Intratumoral Immune Cells Reveal the Immune Landscape in Human Cancer

Gabriela Bindea, Bernhard Mlecnik, Marie Tosolini, Amos Kirilovsky, Maximilian Waldner, Anna C. Obenauf, Helen Angell, Tessa Fredriksen, Lucie Lafontaine, Anne Berger, Patrick Bruneval, Wolf Herman Fridman, Christoph Becker, Franck Pagès, Michael R. Speicher, Zlatko Trajanoski, and Jérôme Galon

EXPERIMENTAL PROCEDURES

The Immunome profile selection from public available data

Gene transcription profiles for the major leukocyte types in humans were downloaded

http://linkage.garvan.unsw.edu.au/public/microarrays/Arthritis_Inflammation/index.html.

This dataset (Immunome, Chtanova 2005) allowed to establish which genes were expressed in each leukocyte type, but also which genes were expressed in each immune subpopulation after activation. The Immunome was completed with DNA microarray data from CD8 T cells and NK cells and integrated with normal colon mucosa and cancer cell lines based on the same Affymetrix platform (HG-U133A). Five CD8 T cell samples from healthy donors (GSE6740, Hyrcza 2007) and three colon cancer cell line (sw480) samples derived from a primary tumor (GSE1323, Provenzani 2006) were downloaded from Gene Expression Omnibus (Barrett 2005). Four NK cell samples (E-MEXP-380, Wendt 2006) and 22 normal human colon mucosa samples (E-MTAB-57, Ancona 2006), were downloaded from ArrayExpress (Parkinson 2007).

The raw data from immune cells transcriptome as well as the normal mucosa and colon cancer raw data were normalized together with R software and packages from the Bioconductor project, using the GCRMA algorithm (Wu 2004). Finally, the log₂ intensities of the gene expression data were used for further analysis. Normalized data are available upon request.

A variety of cell types and subtypes was analyzed: B cells, DC, iDC, aDC, Eosinophils, Macrophages, Mast cells, Neutrophils, NK cells, NK CD56dim cells, NK CD56bright cells, T cell, Cytotoxic cells, CD8 T cells, T $\gamma\delta$, T helper cells, Tcm, Tem, Th1, Th2, Tf γ . The groups: DC, NK cells, T cells, T helper cells are represented by genes highly expressed on all corresponding subpopulations (e.g. on all T cell subsets for the group T cells). Based on common highly expressed genes in NK cells, CD8 T cells and Tgd, the Cytotoxic cells group was defined.

Replicates for each cell type were pooled into groups for selecting genes preferentially high expressed. The expression level of each gene was compared

between the groups and specific genes for each cell type were selected using the R software. The minimum expression of a gene in cell type specific replicates was compared to the highest mean expression of the gene in all other groups. In case of only one replicate per cell type, the expression value itself was considered. The difference between the minimum expression in the analyzed group and maximum mean value of all other groups was calculated. The same selection method was subsequently applied on all cell types.

The most expressed DNA microarray probes (Affymetrix) were selected as representative for a cell type. The groups evolutionary related have a smaller number of genes preferentially expressed. Known markers for particular cell types were found in the immune selected genes, such as CD19 (B cells), CD209 (DC), LAMP3 (aDC), CD3E (T cells), CD8A (CD8 T cells), TRD (Tgd), IFNG (Th1), providing a robust validation for the selection method used. The selection was completed by adding cell type specific genes for the cell subpopulations not included in the Immunome: plasmacytoid DC (pDC) (IL3RA or CD123), T helper 17 (Th17) (IL-17, RORC), regulatory T cells (Treg) (FOXP3), Blood vessels (CDH5), and Lymphatic vessels (PDPN, VEGFD, VEGFC). In total, 577 genes (681 Affymetrix probes, Table S1) were selected. The expression of the selected genes after normalization in Genesis (Sturn 2002) can be seen in Fig. 1. Batch effects were estimated with the TCGA Batch Effects Tool. The R package was downloaded from <http://bioinformatics.mdanderson.org/tcgabatcheffects>. The Dispersion Separability Criterion (DSC) was used to quantify the amount of batch effect in the data (MBatch R script, 1000 permutations). No batch effects were affecting the analysis: DSC = 0.279 and pValue = 0.089. (Batch effects would be expected to be present if the p-value were significant (less than 0.05) and the DSC value was high (greater than 0.5)).

The cohorts of patients and the type of analysis performed

The immune reaction was tested by different techniques in three randomly selected cohorts of colorectal cancer (CRC) patients. Table S7 summarizes the clinical characteristics of the patients. The cohorts used had similar clinical

characteristics and no statistical difference between them could be identified. The tissue sample material was collected at the Laennec-HEGP Hospitals (Hopital European Georges Pompidou). The 686 Affy probes (577 genes) expression was investigated in 105 CRC patients (cohort1) using a DNA microarray Affymetrix platform. Out of the 577 genes, 81 representative genes (Table S3) were investigated by Low Density Array (LDA) Real-Time Taqman PCR (qPCR) in 153 CRC patients (cohort2). A good correlation was obtained between the Affymetrix and the qPCR data (e.g. CXCL13, $r = 0.77$ [0.64-0.86]; GNLY, $r = 0.92$ [0.8-0.97]; all $pValue < 0.001$). A restricted number of markers (15) were tested by Tissue Microarray (TMA) in 107 CRC patients (cohort3). A secure Web-based database, TME.db was built for the management of the patient data. Ethical, Legal and Social Implications were approved by ethical review board. The observation time in the cohorts was the interval between diagnosis and last contact (death or last follow-up). Data were censored at the last follow-up for patients without relapse, or death. Time to recurrence or disease-free time was defined as the interval from the date of surgery to confirmed tumor relapse date for relapsed patients, and from the date of surgery to the date of last follow-up for disease-free patients.

Affymetrix gene chip analysis

The tissue sample material was collected at the Laennec-HEGP Hospitals (Hopital European Georges Pompidou) which was snap-frozen within 15 minutes after surgery and stored in liquid nitrogen. 105 frozen tumor specimens and 5 normal specimens from distant tissue were randomly selected for RNA extraction. The total RNA was isolated by homogenization with the RNeasy isolation kit (Qiagen, Valencia, CA). A bioanalyzer (Agilent Technologies, Palo Alto, CA) was used to evaluate the integrity and the quantity of the RNA. From this RNA, 110 Affymetrix gene chips were done on the same platform (HG-U133A plus) than the Immunome using the HG-U133A GeneChip 3' IVT Express Kit. The raw data was normalized using the GCRMA algorithm. Finally, the log2 intensities of the gene expression data were used for further analysis. For correlation analysis the spots which were not significant with MAS5Calls and had a log2 intensity lower than 3 were excluded from the analysis due to insufficient sensitivity. The expression of the 681 probes was

normalized and hierarchical clustered in Genesis (Pearson Uncentered algorithm, Average Linkage).

Low density array (LDA) Real-Time Taqman qPCR analysis

This study was based on tissue sample material collected at the Laennec-HEGP Hospitals (Hopital Europeen Georges Pompidou) which was snap-frozen within 15 minutes after surgery and stored in liquid nitrogen. From this material 153 frozen tumor specimens were randomly selected for RNA extraction. The total RNA was isolated by homogenization with the RNeasy isolation kit (Qiagen, Valencia, CA). A bioanalyzer (Agilent Technologies, Palo Alto, CA) was used to evaluate the integrity and the quantity of the RNA. The 153 analyzed RNA samples were all from different patients. 81 genes were selected for real-time TaqMan analysis. These gene selection covers the representative cell subpopulations according to the Immunome selection. The RT qPCR experiments were all performed according to the manufacturer's instructions (Applied-Biosystems, Foster City, CA). The quantitative real-time TaqMan qPCR analysis was performed using Low Density Arrays and the 7900 robotic real-time PCR-system (Applied Biosystems). As internal control 18S ribosomal RNA primers and probes were used. The data was analyzed using the SDS Software v2.2 (Applied Biosystems) and TME.db statistical module.

Tissue Microarray (TMA) immunohistochemistry analysis

Permanent section H&E-stained slides were reviewed without knowledge of clinical characteristics or outcome. Each section H&E-stained slide was evaluated for the presence of the center of the tumor (CT) and the invasive margin (IM). For each tumor specimen one or two H&E-stained slides containing CT and IM regions with the strongest immune infiltration were selected. Then, two tumor areas from the CT and two tumor areas from the IM were encircled on the H&E sections. These circles were localized in regions the most infiltrated by immune cells. Tissue cylinders (diameter of 0.6 mm for the center of the tumor and 1 mm for the invasive margin) were then punched from the targeted tumor areas of each donor tissue block and deposited into a recipient block using a tissue-arraying instrument (Beecher

Instruments, Alphelys France). After construction of the array block, the recipient block was subsequently cut into 5 micro m sections on silanized glass slides. One such section was placed on a microscopic slide and H&E-stained for histological verification of the adequacy of the arrayed tumor tissues.

Tissue microarray (TMA) sections were incubated (60 min. at room temperature) with monoclonal antibodies against CD3 (SP7), CD8 (4B11), CD45RO (OPD4), CD57 (NK1), ENG (CD105), Tryptase (AA1), CD1A (Ab-5), Granulocytes (BM-2), PDPN (D2-40), cytokeratin (AE1AE3), cytokeratin-8 (Neomarkers, Fremont, CA), FOXP3 (ab20034; AbCam, Cambridge, United Kingdom) CD68 (PGM-1), CD20 (L26; DAKO, Carpinteria, CA), IL3RA (IL3RA; ATLAS Antibodies, Stockholm, Sweden) and IL-17 (H-132; Santa Cruz Biotechnology, Santa Cruz, CA). Envision+ system (enzyme-conjugated polymer backbone coupled to secondary antibodies) and DAB-chromogen were applied (Dako, Copenhagen, Denmark). Double stainings were revealed with phosphate-conjugated secondary antibodies and FastBlue-chromogen. For single stainings, tissue sections were counterstained with Harris hematoxylin. Isotype-matched mouse monoclonal antibodies were used as negative controls. Slides were analyzed using an image analysis workstation (Spot Browser, ALPHELYS). Polychromatic high-resolution spot-images (740x540 pixel, 1.181 µm/pixel resolution) were obtained (x200 fold magnification). The density was recorded as the number of positive cells per unit tissue surface area. For each duplicate, the mean density was used for statistical analysis. For each tumor, the duplicate of spots showed a good level of homogeneity of stained cell densities in each tumor region (CT and IM) (Galon 2006).

Array Comparative Genomic Hybridization (aCGH)

Samples were homogenized (ceramic beads and FastPrep-24, MP biomedical) in 430 ul of a lysis buffer (Tris 1M – EDTA 0,5M pH8; SDS 20%; proteinase K), and incubated overnight at 37°C. Genomic DNA was extracted by phenol–chloroform extraction and ethanol precipitation. Genomic DNA was re-suspended in 200 ul of highly pure water. Concentrations were evaluated by Optic Density measurement. Samples were labeled using a Bioprime Array CGH Genomic Labeling Kit according to the manufacturer's instructions (Invitrogen, Carlsberg, CA). 500 ng test DNA and

reference DNA (Promega, Madison, WI) were differentially labeled with dCTP-Cy5 and dCTP-Cy3, respectively (GE Healthcare, Piscataway, NJ). Array CGH was carried out using a whole genome oligonucleotide microarray platform (Human Genome CGH 44B Microarray Kit; Agilent Technologies, Santa Clara, CA, USA). This array consists of approximately 43 000 60-mer oligonucleotide probes with a spatial resolution of 43 kb. Samples were labelled with the Bioprime Array CGH Genomic Labeling System (Invitrogen, Carlsberg, California, USA) according to the manufacturer's instructions. Further steps were performed according to the manufacturer's protocol (version 6.0). Slides were scanned using a microarray scanner (G2505B) and images were analysed using CGH Analytics software 3.4.40 (both from Agilent Technologies) with the statistical algorithm ADM-2, sensitivity threshold was 6.0. Along the chromosomes, the frequency in the cohort and the mean amplitude of the gain of each gene were used to calculate an amplification score (SCORE = frequency * amplitude). In the same way, a deletion score was calculated.

The Tumoral Microenvironment Database (TME.db)

TME.db is a Web based application built on a 3-tier architecture which is implemented using the Java2 Enterprise Edition (J2EE) technology and is accessible via a standard Web browser. The underlying relational database model is designed as a cancer patient oriented database which takes all the patients anamnesis and clinical and medical history information into account whereby all patients are linked to a specific hospital. The patient information additionally includes personal problems, surgery and detailed cancer information.

Additionally the model allows to store a variety of different high-throughput experiments: Flow Cytometric (FACS) phenotyping, proliferation analysis data, Real Time TaqMan qPCR gene expression assay data and Immunohistochemical Tissue Micro Array (TMA) data, Microsatelite Instability (MSI), Single Nucleotide Polymorphism (SNP). Most of these experiments were performed on the available dissected cancer patient tissue samples. TME.db joins and integrates all different types of data analyses and stores them in a common place where all the determined analysis parameters are linked in a clear way dependent on the sample material and

the experiment type. The web interface to TME.db also provides a statistical module that connects to customized R services which allows for the automatic testing of normality, calculation of logrank tests and Cox-Regression hazard ratios by using R and Bioconductor packages. Hypergeometric test is used for oversignificance calculations. If multiple hypothesis are tested, P-value correction methods are applied. The analysis is fast, reliable and transparent.

Network and Landscape Visualization

Gene-gene/protein-protein interrelations inferred from different experimental data using CluePedia were visualized in Cytoscape/ClueGO. The Organic algorithm that determines the node positions based on their connectivity was used for laying out the networks. The color of the nodes and their size was based on different node attributes available for the analyzed dataset. For example, the nodes were colored depending on the cell type (Fig S3A and Fig. S6), the fold increase/decrease of the cell density (Fig S4) and the size of the nodes showed the log₂ Hazard Ratio (Fig S3A). To investigate the biological role of the genes we used ClueGO and CluePedia, Cytoscape plugins we have developed. Compared to other enrichment tools, ClueGO provides networks of functions interconnected based on kappa score. The size of the nodes shows the term significance after Bonferroni correction. Fig S1B shows a comparison of the biological role of the genes upregulated in patient Cluster1 and of the genes upregulated in patient Cluster2 (Fig 1B). The ontologies used were: Gene Ontology, KEGG and BioCarta. Biological functions were visualized together with their associated genes (CluePedia). Gene-gene interrelations were STRING (*Search Tool for the Retrieval of Interacting Genes/Proteins*) scores. Correlations between genes/proteins were calculated using CluePedia (Fig S2 and Fig S6). Further, interrelations between different immune cell infiltrating tumors were integrated into a network. Based on this network, a 3D visualization of the immune landscape was created using java. In the 3D visualization, the x and y position of the genes was extracted from the Cytoscape network and for the third dimension, the cell density (Fig 5a) and the Hazard ratio values (Fig 5b) were used.

Migration assays

Tumour cells and tumour infiltrating lymphocytes (TILs) were isolated as previously described. TILs were seeded at 5×10^5 cells/well into the upper inserts of a 6.5 mm, 5 mm pore permeable support Transwells (Costar). The lower transwell chamber contained patient matched tumour cells (1×10^6 cells/well), patient matched 3-day tumour supernatants, or soluble recombinant human CXCL13 (500 ng/ml, R&D Systems). An anti-CXCL13 neutralising antibody (10 mg/ml, R&D Systems) was pre-incubated in the lower transwell chamber for 1 hour prior to addition of TILs. The co-culture was incubated for 24 hours at 37°C. Cells in the lower chamber were collected and analysed using flow cytometry for CD45, CD3, CD4, CD8, (BioLegend), NKP46 and CD68 (BD Pharmingen). Tumour cells were excluded from the analysis using CD45+ gating. A pre-transwell tumour cell control sample was also analysed to determine the residual TILs, post isolation, remaining in the lower chamber.

In vivo experiments – anti-tumor immune response

Mice

2-4 month old C57Bl/6, CXCR5-/ and RAG1-/ mice were held and bred in microisolator cages and all experiments were performed according to committee-approved protocols.

Cell lines

The murine C57Bl/6 CRC tumor cell line was kindly provided by Michael Neumaier (Institute of Clinical Chemistry, Medical Faculty Mannheim of the University of Heidelberg; Mannheim, Germany). Cells were cultured at 37°C and 5% CO₂ in DMEM medium (DMEM + GlutaMAX -I, Invitrogen) supplemented with Glucose, Pyruvat, 10% heat-inactivated FCS and penicillin/streptomycin.

Mouse endoscopy and orthotopic tumor injection model

Mice were anesthetized using Isoflurane and endoscopy was performed as previously described (Becker et al. 2006). Endoscopic injection of tumor cells was previously described (Zigmond et al. 2011). For endoscopic injection of tumor cells, a polythene tube (outer diameter 0.96 mm, inner diameter 0.58 mm, Smiths Medical

International Ltd.) was equipped with a 20G needle (Becton Dickinson). The tube with the needle was inserted into the working channel of the endoscope. Before insertion of the endoscope into the colon of mice, the needle was positioned inside the working channel in order to avoid damage of the colonic mucosa. After insertion of the endoscope, the needle was pushed out of the working channel under endoscopic control. The tip of the needle was then carefully inserted through the mucosa into the submucosa and a total volume of 50 µl cell suspension (number of cells as detailed in the respective figure legends) was injected slowly into the submucosa. Anti-CXCL13 antibodies were injected similarly into the submucosa. During subsequent weeks, tumor growth was analyzed at indicated time points using a previously described endoscopic scoring system (Becker et al. 2006).

Histology

At indicated time points, mice were sacrificed, tumor tissue was isolated and frozen tissue specimens were prepared. Tissue sections were subsequently fixed with 4% paraformaldehyde and stained with hematoxylin and eosin or further processed for immunohistochemistry as previously described (Waldner et al. 2010). In short, paraformaldehyde fixed sections were incubated with methanol, avidin/biotin blocking reagent (Vector Laboratories) and protein blocking reagent (Dako). Subsequently, primary antibodies dissolved in TBST/0.5% BSA were administered on the sections over night at 4°C. Afterwards, slides were incubated with biotinylated secondary antibodies, streptavidin-HRP and Tyramide (Cy3 and FITC, Perkin Elmer) respectively. Cell nuclei were counterstained with DAPI (Invitrogen). Imaging was performed with a widefield or confocal fluorescence microscope (Leica).

Quantitative analysis of gene expression

Total RNA was isolated from frozen tissue specimens with RNeasy columns (Qiagen), including DNase I digestion. cDNA was subsequently generated using the iScript cDNA Synthesis kit (Bio-Rad Laboratories). Quantitative real-time PCR analysis was performed with specific primers (Qiagen) and QuantiTect Sybr Green (Qiagen). Gene expression was calculated relative to the expression of a house-keeping gene (HPRT) using the $\Delta\Delta Ct$ algorithm.

CEL files included in the immunome analysis

Garvan Institute

http://linkage.garvan.unsw.edu.au/public/microarrays/Arthritis_Inflammation/index.html

A_TS_RN_CD19+_U133A_130104.CEL
A_TS_2CD19+_U133A_180204.CEL
A_LW_imDC_U133A_200503.CEL
A_SZ_imDC2_U133A_250603.CEL
A_LW_DC6hLPS_U133A_200503.CEL
A_SZ_6hLPSDC2_U133A_250603.CEL
A_SZ_6hLPS_HCDC2_U133A.CEL
A_LW_DC6hLPS_HC_U133A.CEL
A_LW_DC48hLPS_U133A_200503.CEL
A_SZ_48hLPSDC2_U133A_250603.CEL
A_LW_DC48hLPS_HC_U133A.CEL
A_SZ_48hLPS_HCDC2_U133A.CEL
A_MF_ControlEosinophil.CEL
A_MF_2hrEosinophils.CEL
A_LW_macroctrl_U133A_130503.CEL
A_SZ_mac2cont_U133A_240603.CEL
A_LW_macro_LPS_U133A_130503.CEL
A_SZ_mac2LPS_U133A_240603.CEL
A_LW_macro_LPS_HC_U133A.CEL
A_SZ_mac2LPS_HC_U133A.CEL
A_MF_ControlMASTCELL_U133A.CEL
A_LW_mastcellctrl_U133A.CEL
A_MF_IgEMASTCELL_U133A.CEL
A_LW_mastcellIgE_U133A.CEL
A_LW_neutrophil_U133A.CEL
A_MF_neutrophils_U133A.CEL

A_TS_MSNeutroLPS_U133A.CEL
A_TS_RN_gdTcells_U133A.CEL
A_TS_RN_gdTcellsREP_A.CEL
A_MF_CCR7+_U133A_190202.CEL
A_MF_CCR7-_U133A_190202.CEL
A_MF_TH1human_U133A_290502.CEL
A_TS_TC_Th1_U133A_141003.CEL
A_MF_TH2human_U133A_290502.CEL
A_TS_TC_Th2_U133A_141003.CEL
A_LW_CD57+_U133A_030603.CEL
A_LW_CD57+_U133A_121102.CEL
A_MF_CD57+_U133A_010502.CEL

E-MEXP-380

E-MEXP-380-raw-cel-494753931.cel
E-MEXP-380-raw-cel-494753975.cel
E-MEXP-380-raw-cel-494754019.cel
E-MEXP-380-raw-cel-494754063.cel

GSE1323

GSM21712.CEL
GSM21713.CEL
GSM21714.CEL

GSE6740

GSM155229.CEL
GSM155232.CEL
GSM155234.CEL
GSM155236.CEL
GSM155238.CEL

E-MTAB-57

CSS_COLON_N_2.CEL
CSS_COLON_N_1.CEL
CSS_COLON_N_3.CEL
CSS_COLON_N_4.CEL
CSS_COLON_N_5.CEL
CSS_COLON_N_6.CEL
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Fig S1A. Disease-Free Survival Kaplan Meier curves for the two patient groups
Patient Cluster 1 (red) and Cluster 2 (black) have different risk to relapse (logrank P-value = 2.46e-02, HR = 1.996 [1.07–3.74]).

Fig S1B. Biological role of the genes upregulated in patient Cluster1 and patient Cluster2

Functions of the upregulated genes in each of the patient clusters was investigated using ClueGO and CluePedia, Cytoscape plugins that visualize networks of functions interconnected based on kappa score. The size of the nodes shows the term significance after Bonferroni correction. Functions representative for cluster1 and cluster2 are shown in red and green, respectively. The color gradient shows the gene proportion of each cluster associated with the term. Equal proportions of the two clusters is shown in white. In the present visualization we integrated the functions with the corresponding genes. Genes upregulated in Cluster1 and Cluster2 are shown in red and green, respectively and are interconnected based on STRING (Search Tool for the Retrieval of Interacting Genes/Proteins) scores. Activation, binding and expression scores are shown in green, blue and yellow, respectively.

Figure S1, related to Figure 1.

Fig S2. Correlations between different approaches

(A) Cell type specific markers are significantly over-expressed, regardless of the activation status. Fig S1A shows two examples, CD209 and MSR1, markers of dendritic cells and macrophages, respectively. Different conditions of activation within the tumor could modify the gene expression level. However, in the immunome compendium, the selected genes were highly expressed on a specific cell type. The expression data was also measured in purified immune cells found in different activation status. For example, immature dendritic cells (DC), as well as immature DCs activated either in the presence of 100 ng/ml lipopolysaccharide (LPS) alone or 100 ng/ml LPS + 10 mM hydrocortisone (HC) were investigated. Activated DCs were harvested after 6h stimulation and mature DCs were harvested after 48 stimulation. Similarly, for macrophages, the expression was measured in controls and after activation for 4 h either in the presence of 100 ng/ml LPS alone or 100 ng/ml LPS +

10 mM hydrocortisone (HC). CD209 was over-expressed in all activation conditions of dendritic cells compared to macrophages. MSR1 was over-expressed in all activation conditions of macrophages compared to dendritic cells.

(B) Characterization of immune cell type specific genes and correlations between these genes. The immunome selection includes genes with high expression that are preferentially expressed on a particular cell type. Expression data from purified immune cells was investigated. Subsets of T cells in different conditions (Tcm, Tem, Th1, Th2, Treg, Th17, Tf_h) were used to define specific genes at different T cell differentiation levels. Using these selection criteria, known markers of immune cells were found: CD19 (B cells), CD209 (DC), LAMP3 (aDC), CD3E (T cells), TRD (Tgd), IFNG (Th1), GNLY, GZMK, PRF1 (Cytotoxic cells). The presence of those markers, between the selected genes, constitutes a robust validation of the selection method used. Furthermore, immune subpopulations like dendritic cells, macrophages, mast cells and neutrophils, were investigated in different activation status and the most representative genes were kept (those over-expressed regardless of the activation status). Four examples are illustrated. All T cell subsets (all blue dots corresponding to 16 experiments) express CD2 and CD3G (left upper panel). All T cell subsets express CD3G, in contrast to PDCD1, a Tf_h marker expressed only in the Tf_h subset (3 experiments corresponding to 3 purple dots) (right upper panel). CXCR1 and CXCR2 are both preferentially expressed by Neutrophils (3 experiments corresponding to 3 brown dots) (left lower panel). Similarly, CD19 and MS4A1 (CD20) are expressed specifically by B cells (2 orange dots corresponding to two experiments) (right lower panel).

(C) Shows expression data from colorectal tumors measured with DNA microarray (Affymetrix). CD2 and CD3G, markers of T cell subsets, correlate (left panel). CD8 T cell and Cytotoxic cell markers correlate: CD8A - GZMA (right panel). All r values > 0.6, all P-value <0.0001. In contrast, markers from different cell types did not correlate (data not shown).

(D) Shows gene expression correlation between markers using qPCR Low Density Array (LDA). Correlation plot examples are illustrated for T cell-related genes, CD3G – CD28 (left) and ZAP70– CD3G (right). All r values > 0.6, all P-value <0.0001.

(E) Shows gene expression correlation between markers measured with DNA

microarray (Affymetrix) and qPCR Low Density Array (LDA). Correlation analyses were performed for genes with detectable expression (Affymetrix, expression higher than a log₂ intensity of 3). Correlation plot examples are illustrated for CD8A (CD8 Cytotoxic cells) (left) and GNLY (Cytotoxic cells) (right). All P-value <0.0001.

(F) Shows correlation between gene expression (qPCR Low Density Array) and in situ cell density quantification using Tissue microarray (TMA). CD8-CT and CD8A (left) and CD8-CT and GZMA (right). R values > 0.26, P-values <0.03. Not surprisingly, correlations were weaker when comparing qPCR and TMA, in comparison to two techniques investigating gene expression levels. First, different biological parameters (proteins and mRNA) were evaluated, and gene expression variations do not always translate into similar changes in protein expression. Second, different tumor tissue specimens were used between the two techniques, a frozen piece of tumor for qPCR (good RNA quality), and another piece of tumor for IHC (FFPE tumor block). Third, different regions of the tumor were evaluated between the two techniques, whole tumor for qPCR, versus immune cell density in different tumor regions, CT and IM, for IHC.

(G) Protein expression by flow cytometry (FACS). In order to test cell subset variation and marker expression, it is needed to quantify the expression of the marker on isolated cell populations. Flow cytometry (FACS) analyses were performed on fresh colon tumor samples and blood from 40 patients. Markers specific for cell subpopulations were tested. The mean fluorescence intensity (MFI) level of CD28 (T cell marker), CD8 (Cytotoxic T cells), ICOS (Tfh) and CD152 (Th1 cells) in blood and tumors in the corresponding CD3+ T cell subpopulation and in the negative control subpopulation (CD3-) are illustrated. The MFI level is higher in specific cells compared to non-specific cells (P<0.0001). These findings were valid in both in blood and within tumors. Importantly, negative control subpopulation (CD3-) expressed very low levels of each T cell subpopulation marker. This supports the specificity of these markers for T cell subpopulations within the tumor microenvironment.

Figure S2, related to Figure 2.

Fig S3. Interrelations between cell types revealed by a qPCR network

(A) Pearson correlation network of qPCR data from 153 CRC patients visualized in Cytoscape. The nodes represent cell type specific genes and the color of the nodes corresponds to different cell types. The connecting lines (edges) represent the level of correlation (r) between two genes. The proximity of genes illustrate the degree of correlation. A Cytoscape filtering of the edges with $r < 0.6$ and $r > -0.6$ was performed. Only positive correlation remained after filtering. Nodes represented by circles show a positive impact ($HR < 1$) on the DFS of patients, whereas triangles show a negative impact ($HR > 1$). The size of the nodes shows the logrank significance of the genes. Three levels of the significance were defined: large nodes ($P\text{-value} < 0.05$), median nodes ($P\text{-value} \geq 0.05$ and $P\text{-value} < 0.1$) and small nodes ($P\text{-value} > 0.1$). The Network layout was done using the organic algorithm. Groups of T cells (blue), B cells (orange) and macrophages (red) are presented.

(B) Correlation matrix of the 577 genes initially selected based on their DNA microarray (Affymetrix) measured expression. Genes having the expression level higher than 3 in more than 66% of the patients (expression values lower 3 (undetectable) were set to NaN) are shown.

(C) Correlation matrix of the 81 genes based on their DNA microarray (Affymetrix) measured expression. Genes having the expression level higher than 3 in more than 66% of the patients (expression values lower 3 (undetectable) were set to NaN) are shown.

Figure S3, related to Figure 2.

Fig S4. In situ immunostainings of immune subpopulations, and analysis of immune cell densities at the center (CT) and invasive margin (IM) of the tumor relative to the tumor stage

Representative examples of CD3, Tumor, CD8, CD57, CD45RO, FoxP3, CXCR5, Tryptase, CD20, CD68, CD1A, IL3RA, Granulocytes, PDPN, and ENG immunostaining of colorectal cancer tissue microarray (left). Tum stands for Tumor and CS stands for counter staining. Tissue sections are counterstained with methylene blue. Slides are analyzed using the image analysis workstation SpotBrowser. Polychromatic high-resolution spot-images (740x540 pixel, 1.181 $\mu\text{m}/\text{pixel}$ resolution) are obtained (x200 fold magnification). Measurements are

recorded as the number of positive cells per tissue surface unit (mm^2).

The evolution of the immune cell densities during tumor progression in 107 CRC patients revealed by TMA (right). The mean cell density for each tumor stage (T1, T2, T3, T4) was calculated as number of positive cells per tissue surface unit (mm^2) in the center of the tumor (CT) represented by a circle and in the invasive margin (IM) represented by a hexagon. The stage transition is indicated as node label (e.g. T1->T2). The color of the node represents the fold change increase (red) or decrease (green) in the stage transition.

Over time the CD3 density decreased more in CT than in IM. In the IM the most important decrease of CD3 cells was in advanced cancer, at the T3-T4 transition ($P < 0.05$). The CD8 cell density decreased mainly in the intratumoral tissue, in IM (T3 and T4 vs. T1, both $P < 0.001$). CD45RO cells presented a behavior similar to CD3, with a marked decrease in CT over time especially in late stages T3 ($P < 0.001$) and T4 ($P < 0.01$) compared to T1. From the T cell subpopulations, only the Tfh cells showed a more important increase of their density in the IM, at the T1-T2 transition. An increased density of B cells in late cancer stages (T1-T3 transition, $P < 0.05$) could be shown in CT. Compared to the adaptive immune cells, the densities of the Neutrophils, iDCs, pDCs, macrophages increased in CT and slightly in IM during tumor development. Significantly more Neutrophils and pDCs were present at later tumor stages (T1 vs T3, $P < 0.001$ and $P < 0.05$, respectively). Mast cells could not be evaluated in stage T1. Th17 data is not shown.

Figure S4, related to Figure 4.

Fig S5. The impact on patient DFS of B cell and Tfh markers

Kaplan Meier curves for Disease Free Survival (DFS) for CD20, B cell specific gene, the B cell chemoattractant (CXCL13) and CD8 (Cytotoxic T cells) showed significant difference between the group of high (red) vs. low (black) immune infiltrates at the minimum P-value cutoff. **(A)** CD8-CT (Cytotoxic T cells). **(B)** MS4A1/CD20 (B cells). **(C)** CXCL13 (Tfh). The combined effect of those markers on DFS is presented. In red, high densities of both markers (HiHi), heterogeneous densities (HiLo/LoHi) in green and in black low densities (LoLo). **(D)** CD8-CT/CD20-IM, **(E)**. CD8-CT/CXCL13, **(F)** CD20-IM/CXCL13.

Figure S5, related to Figure 5.

Fig S6. Interrelations between CXCL13, IL21 and immune cell subsets

CXCL13, IL21 and IL21R expression were measured (qPCR) in 153 CRC patients. Correlations between CXCL13, IL21 and IL21R and cell markers were calculated using CluePedia Cytoscape plugin and visualized in a network together with immune cell subtypes. Markers associated to a cell type share the color of the node. The edges represent Spearman's rank correlation values ($r>0.5$) and are colored in green (CXCL13), pink (IL21) and blue (IL21R), respectively. Example of CluePedia correlation plots are shown for CXCL13 with TBX21 and CD8A (left side).

Figure S6, related to Figure 6.

Table S1. Table with the Immunome selection

577 genes (681 DNA microarray probes, Affymetrix) preferentially expressed in cell types present in the tumor microenvironment.

Table S1, related to Figure 1.

Table S2. Cell type overrepresentation in patient clusters

Cell type overrepresentation in patient clusters presented in Fig. S2. High expressed genes (DNA microarray, normalized expression >1) were counted for each cell type in Cluster 1 and Cluster 2. The overrepresentation was calculated with Fisher Exact Test as reported to the total high expressed genes in both patient clusters.

Table S2, related to Figure 1.

Table S3. qPCR genes

81 cell type specific genes tested with LDA. Genes logrank significant for DFS with a Hazard Ratio (HR) < 1 (good impact on patient outcome) are marked with red and with HR > 1 (bad outcome) with black respectively.

Table S3, related to Figure 2.

Table S4. Cell type overrepresentation in functional clusters (qPCR)

Fisher Exact Test was used.

Table S4, related to Figure 4.

Table S5. Correlation of B cells with other cell types

Examples of correlation between B-cell genes and genes specific for other cell types.

Table S5, related to Figure 5.

Table S6. Combined prognostic of B and T cells in colorectal cancer patients.

We investigated the combined prognostic impact of B and T cells in our CRC cohort. A strong highly significant ($P < 0.0001$) positive DFS impact of high densities of B cells in the invasive margin of tumor ($HR = 4.04$) and a weaker effect ($HR = 1.4$) in the center of the tumor respectively. When comparing B and T cells we could see that the impact of the B cell densities lies between the HR values of CD8 ($HR = 2.25$) and CD45RO ($HR = 6.20$). When combining the densities of B cells from the invasive margin with the densities of T cell subsets from both tumor regions we can see the beneficial effect of B cells increasing the hazard ratio of CD8 from $HR = 9.14$ ($CD8_{CT+IM}$) to $HR = 12.49$ ($CD20_{IM}+CD8_{CT+IM}$) between the high and low groups. Similar results we can see with CD45RO with an increase of $HR = 8.79$ ($CD45RO_{CT+IM}$) to $HR = 11.29$ ($CD20_{IM}+CD45RO_{CT+IM}$) between the high and low groups. Thus, there exists an additional beneficial effect of B cells from the invasive margin when combined with T cells densities from both tumor regions.

Table S6, related to Figure 5-6.

Table S7. Comparison of cohorts according to clinical parameters

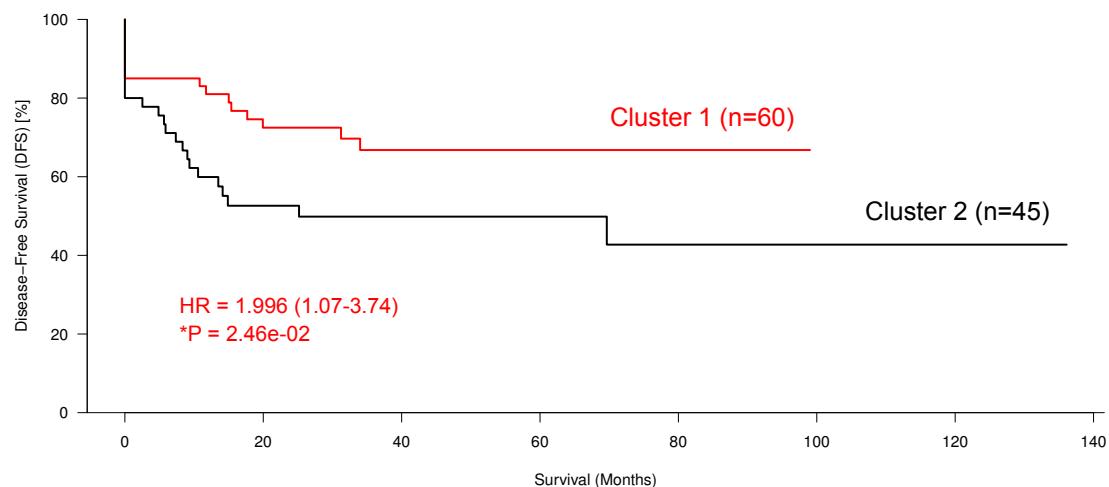
Comparison of the clinical parameters of the three cohorts of patients used for the analysis.

Table S7, related to methods.

Video S1

The evolution of the immune cell subpopulations with the tumor progression

A



B

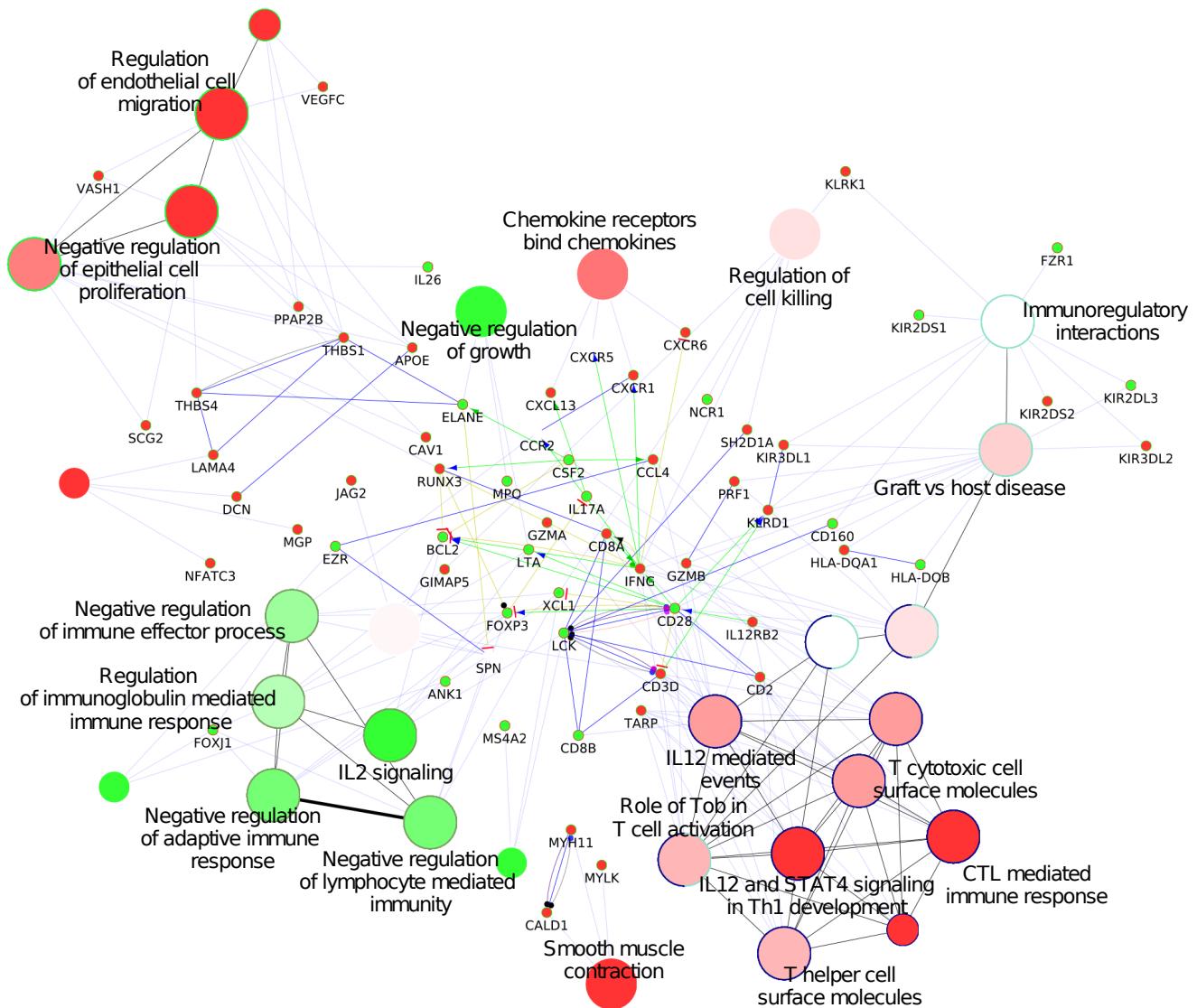
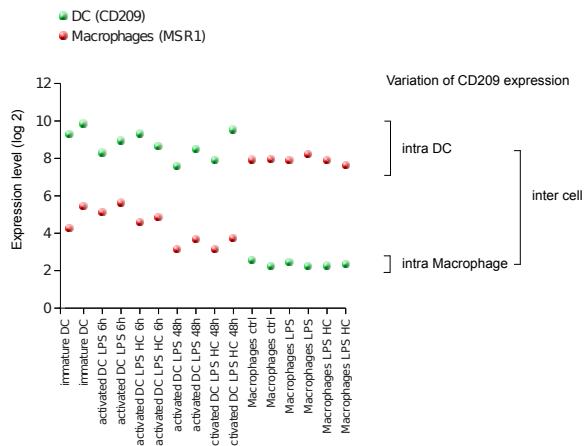


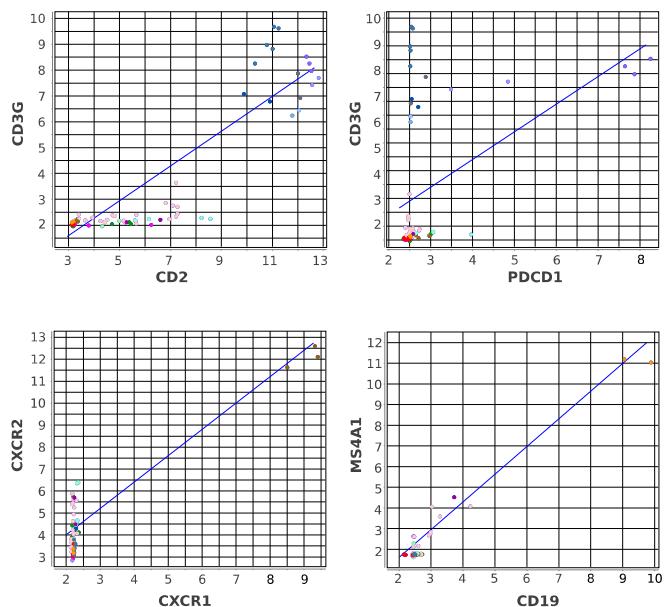
Figure S1

A

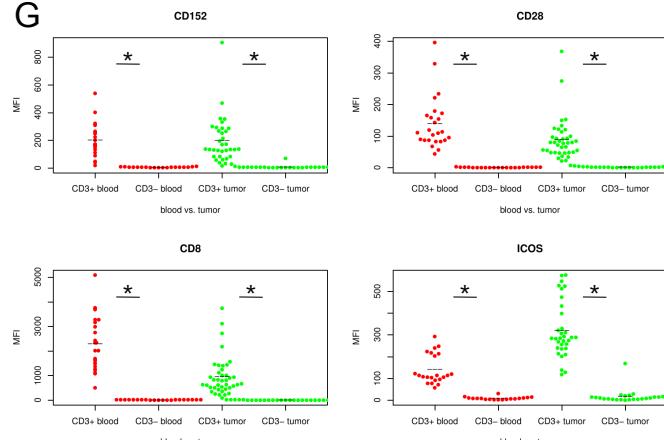


B

**Gene expression level in the immunome dataset
(purified immune cells)**

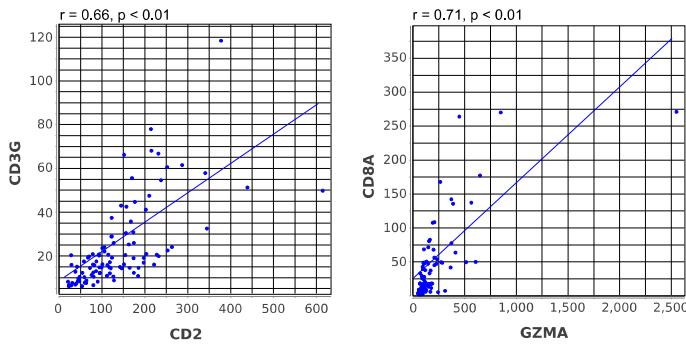


G



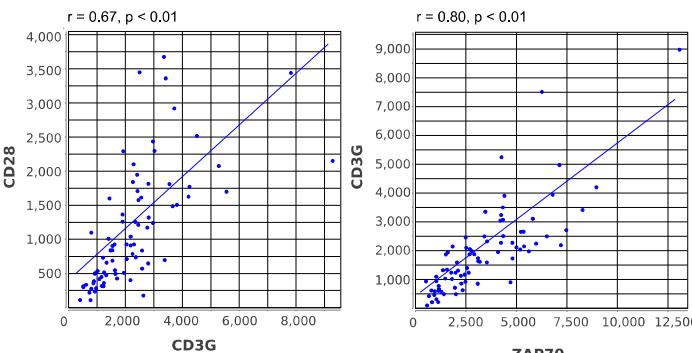
C

**Gene expression correlation within colorectal tumors
(Affymetrix vs Affymetrix)**



D

**Gene expression correlation within colorectal tumors
(qPCR LDA vs qPCR LDA)**



E

**Gene expression correlation within colorectal tumors
(Affymetrix vs qPCR LDA)**



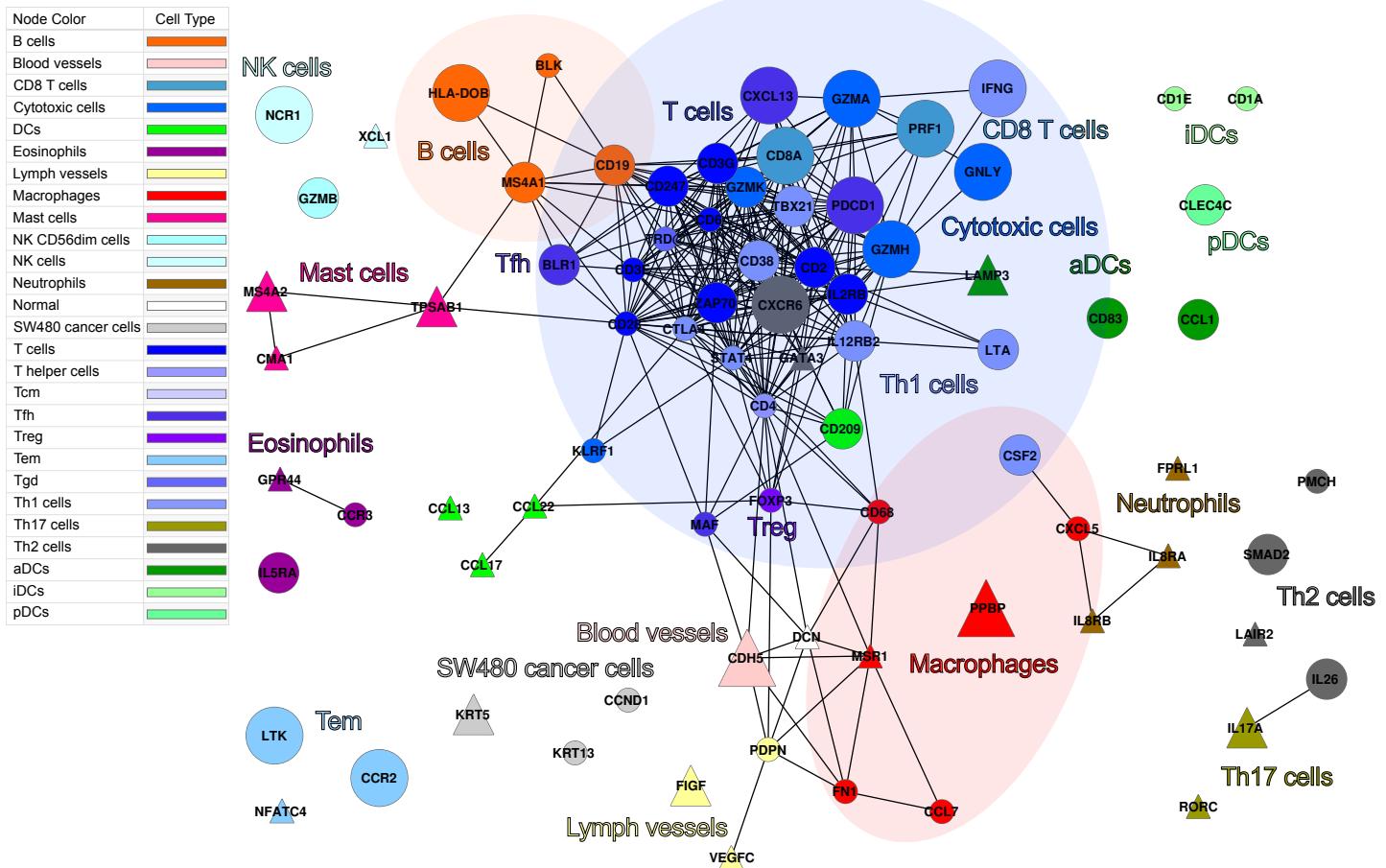
F

**Correlation between gene expression level and immune cell density
(qPCR LDA vs Tissue microarray)**



Figure S2

A



B

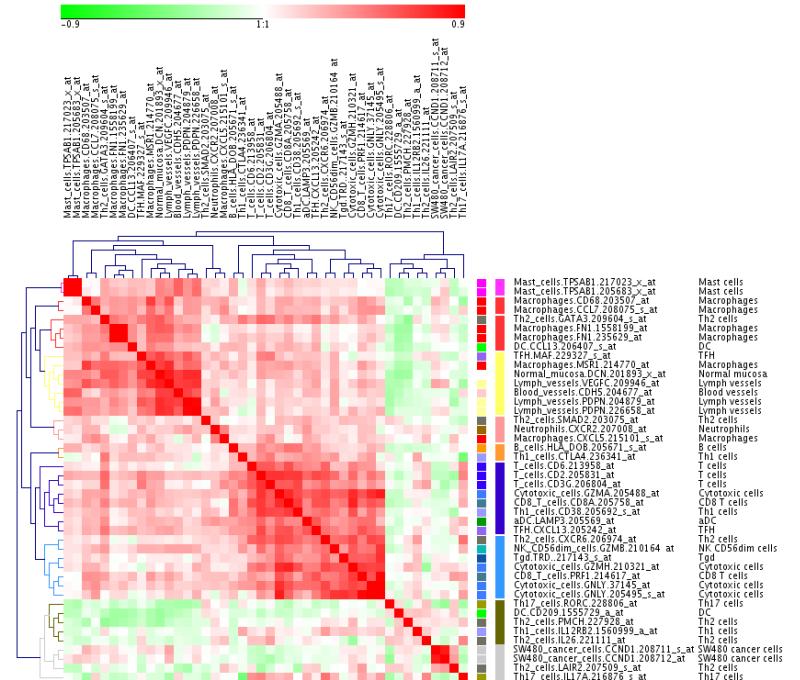
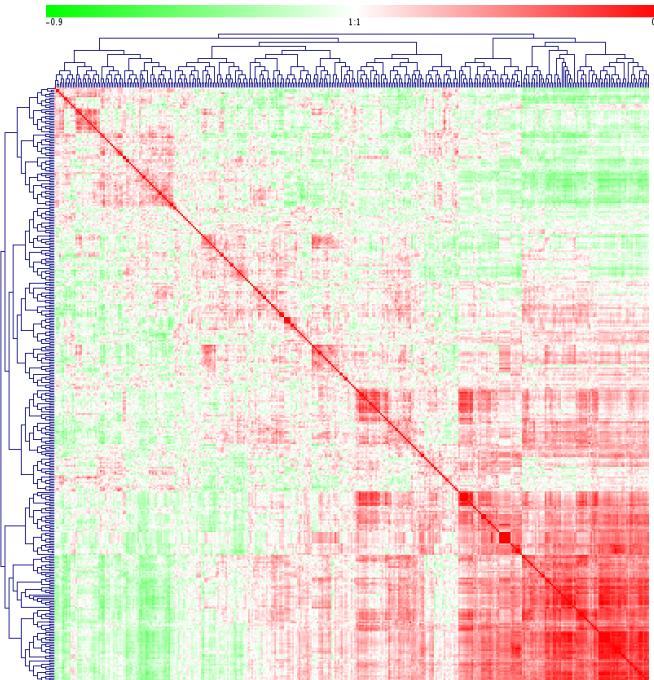


Figure S3

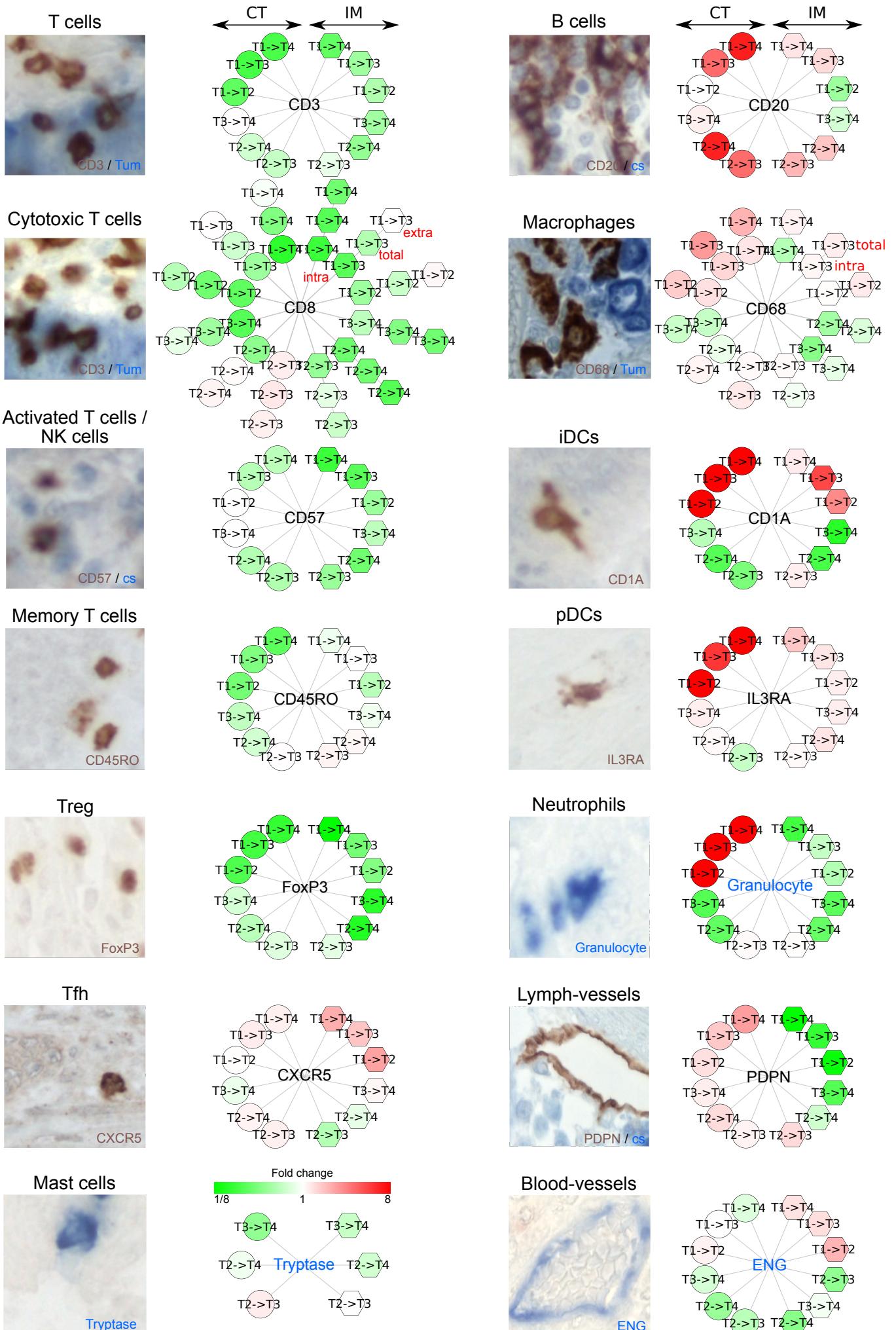


Figure S4

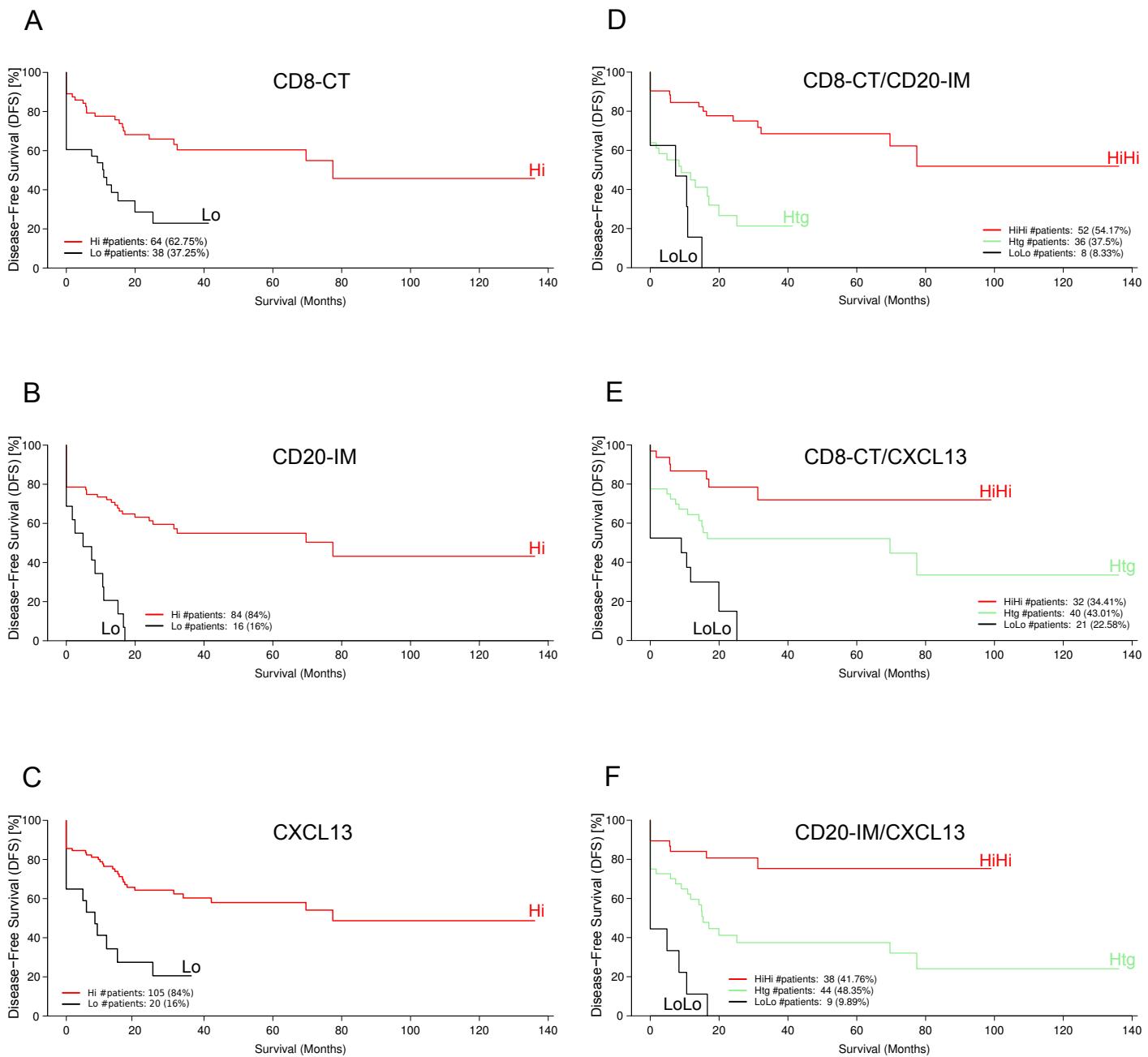


Figure S5

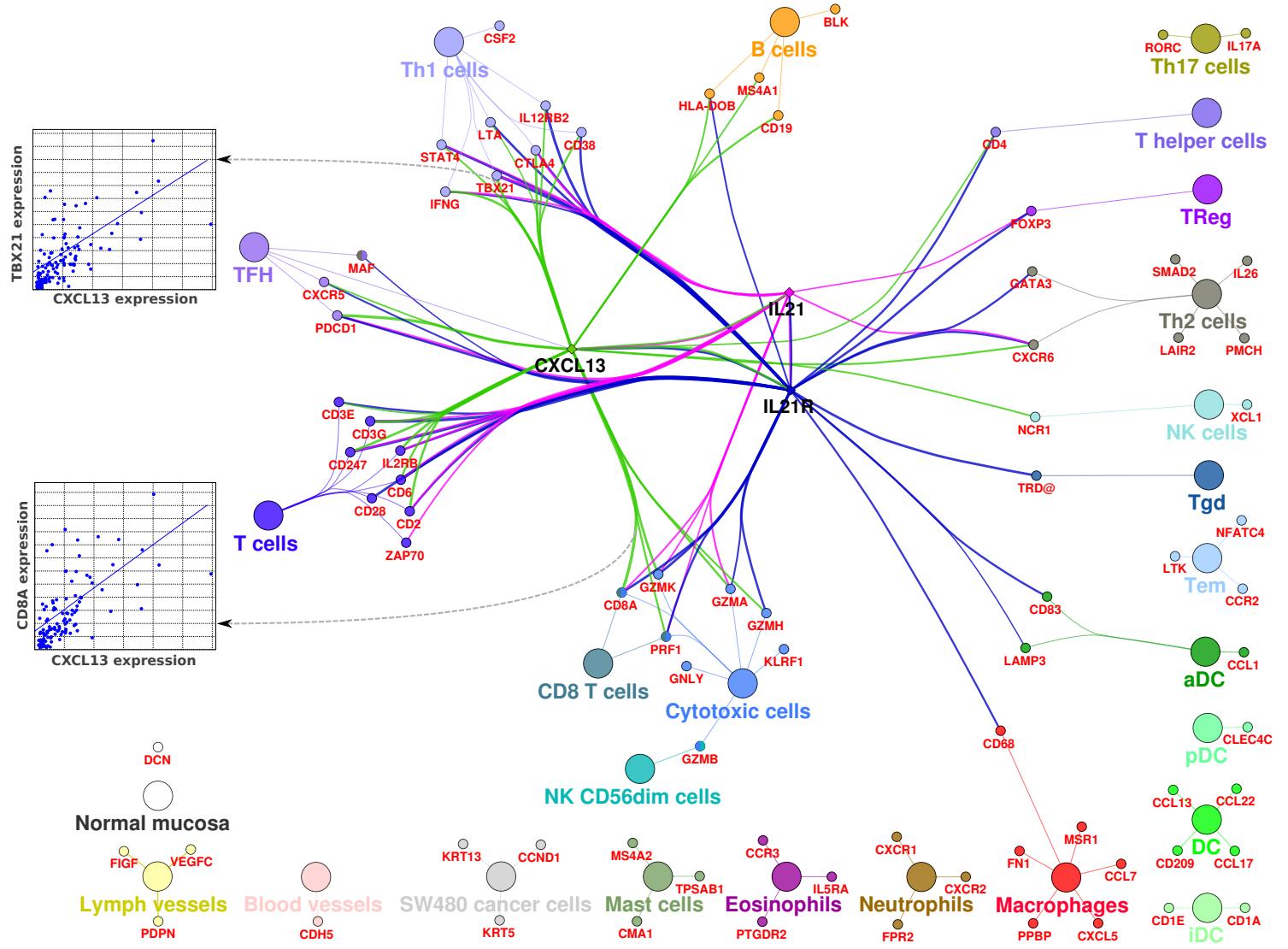


Figure S6

CellType	Symbol	AffymetrixID	UGCluster	EntrezGene Name
B cells	MS4A1	217418_x_at	Hs.438040	931 membrane-spanning 4-domains, subfamily A, member 1
B cells	TCL1A	209959_s_at	Hs.2484	8115 T-cell leukemia/lymphoma 1A
B cells	MS4A1	210356_x_at	Hs.438040	931 membrane-spanning 4-domains, subfamily A, member 1
B cells	TCL1A	39318_at	Hs.2484	8115 T-cell leukemia/lymphoma 1A
B cells	HLA-DOB	205671_s_at	Hs.1802	3112 major histocompatibility complex, class II, DO beta
B cells	PNOC	205901_at	Hs.88218	5368 prepronociceptin
B cells	KIAA0125	206478_at	Hs.632338, Hs.64925	9834 KIAA0125
B cells	CD19	206398_s_at	Hs.652262	930 CD19 molecule
B cells	CR2	205544_s_at	Hs.445757	1380 complement component (3d/Epstein Barr virus) receptor 2
B cells	IGHG1	213674_x_at	Hs.510635	3500 immunoglobulin heavy constant gamma 1 (G1m marker)
B cells	FCRL2	221239_s_at	Hs.437393	79368 Fc receptor-like 2
B cells	BLK	206255_at	Hs.146591	640 B lymphoid tyrosine kinase
B cells	IGHG1	222285_at	Hs.510635	3500 immunoglobulin heavy constant gamma 1 (G1m marker)
B cells	COCH	205229_s_at	Hs.21016	1690 coagulation factor C homolog, cochlin (Limulus polyphemus)
B cells	OSBP10	219073_s_at	Hs.150122	114884 oxysterol binding protein-like 10
B cells	IGHA1	215118_s_at	Hs.648398	3493 immunoglobulin heavy constant alpha 1
B cells	TNFRSF17	206641_at	Hs.2556	608 tumor necrosis factor receptor superfamily, member 17
B cells	ABC4B	207819_s_at	Hs.654403	5244 ATP-binding cassette, sub-family B (MDR/TAP), member 4
B cells	BLNK	207655_s_at	Hs.665244	29760 B-cell linker
B cells	GLDC	204836_at	Hs.584238	2731 glycine dehydrogenase (decarboxylating)
B cells	MEF2C	209200_at	Hs.654474	4208 myocyte enhancer factor 2C
B cells	MEF2C	209199_s_at	Hs.654474	4208 myocyte enhancer factor 2C
B cells	IGHM	209374_s_at	Hs.510635	3507 immunoglobulin heavy constant mu
B cells	FAM30A	220377_at	Hs.649259	29064 family with sequence similarity 30, member A
B cells	SPIB	205861_at	Hs.437905	6689 Spi-B transcription factor (Spi-1/PU.1 related)
B cells	BCL11A	219497_s_at	Hs.370549	53335 B-cell CLL/lymphoma 11A (zinc finger protein)
B cells	GNG7	206896_s_at	Hs.515544	2788 guanine nucleotide binding protein (G protein), gamma 7
B cells	IGKC	215217_at	Hs.449621	3514 immunoglobulin kappa constant
B cells	CD72	215925_s_at	Hs.116481	971 CD72 molecule
B cells	MICAL3	212715_s_at	Hs.528024, Hs.64643	57553 microtubule associated monooxygenase, calponin and LIM domain containing 3
B cells	BCL11A	210347_s_at	Hs.370549	53335 B-cell CLL/lymphoma 11A (zinc finger protein)
B cells	BACH2	221234_s_at	Hs.269764	60468 BTB and CNC homology 1, basic leucine zipper transcription factor 2
B cells	IGL@	217138_x_at	Hs.449585	3535 immunoglobulin lambda locus
B cells	CCR9	207445_s_at	Hs.225946	10803 chemokine (C-C motif) receptor 9
B cells	QRS1	218948_at	Hs.406917	55278 glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
B cells	DTNB	215565_at	Hs.307720	1838 dystrofelin, beta
B cells	HLA-DQA1	212671_s_at	Hs.387679	3117 major histocompatibility complex, class II, DQ alpha 1
B cells	SCN3A	210432_s_at	Hs.435274, Hs.67109	6328 sodium channel, voltage-gated, type III, alpha subunit
B cells	QRS1	218949_s_at	Hs.406917	55278 glutaminyl-tRNA synthase (glutamine-hydrolyzing)-like 1
B cells	SLC15A2	205316_at	Hs.518089	6565 solute carrier family 15 (H+/peptide transporter), member 2
T cells	PRKQ	210038_at	Hs.498570	5588 protein kinase C, theta
T cells	CD3D	213539_at	Hs.504048	915 CD3d molecule, delta (CD3-TCR complex)
T cells	CD3G	206804_at	Hs.2259	917 CD3g molecule, gamma (CD3-TCR complex)
T cells	CD28	206545_at	Hs.591629	940 CD28 molecule
T cells	LCK	204891_s_at	Hs.470627	3932 lymphocyte-specific protein tyrosine kinase
T cells	TRAT1	217147_s_at	Hs.138701	50852 T cell receptor associated transmembrane adaptor 1
T cells	PRKQ	210039_s_at	Hs.498570	5588 protein kinase C, theta
T cells	BCL11B	219528_s_at	Hs.510396	64919 B-cell CLL/lymphoma 11B (zinc finger protein)
T cells	CD2	205831_at	Hs.523500	914 CD2 molecule
T cells	LCK	204890_s_at	Hs.470627	3932 lymphocyte-specific protein tyrosine kinase
T cells	TRBC1	213193_x_at	Hs.654496	28639 T cell receptor beta constant 1
T cells	TRBC1	210915_x_at	Hs.654496	28639 T cell receptor beta constant 1
T cells	TRA@	209670_at	Hs.74647	28755 T cell receptor alpha constant
T cells	ITM2A	202747_s_at	Hs.17109	9452 integral membrane protein 2A
T cells	SH2D1A	210116_at	Hs.349094	4068 SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)
T cells	CD6	213958_s_at	Hs.643167	923 CD6 molecule
T cells	CD96	206761_at	Hs.142023	10225 CD96 molecule
T cells	NCALD	211685_s_at	Hs.492427, Hs.68013	83988 neurocalcin delta
T cells	GIMAP5	218805_at	Hs.647079	55340 GTPase, IMAP family member 5
T cells	TRA@	209671_x_at	Hs.74647	6955 T cell receptor alpha locus
T cells	CD3E	205456_s_at	Hs.3003	916 CD3d molecule, epsilon (CD3-TCR complex)
T cells	SKAP1	205790_at	Hs.316931	8631 src kinase associated phosphoprotein 1
T cells	TRA@	213830_at	Hs.74647	6955 T cell receptor alpha locus
T cells	TRA@	216191_s_at	Hs.74647	6955 T cell receptor alpha locus
T helper cells	ICOS	210439_at	Hs.56247	29851 inducible T-cell co-stimulator
T helper cells	LRBA	214109_at	Hs.480938	987 LPS-responsive vesicle trafficking, beach and anchor containing
T helper cells	ITM2A	202746_at	Hs.17109	9452 integral membrane protein 2A
T helper cells	FAM111A	218248_at	Hs.150651	63901 family with sequence similarity 111, member A
T helper cells	PHF10	219126_at	Hs.435933	55274 PHD finger protein 10
T helper cells	NUP107	218768_at	Hs.524574	57122 nucleoporin 107kDa
T helper cells	SEC24C	202361_at	Hs.654429	9632 SEC24 related gene family, member C (S. cerevisiae)
T helper cells	NAP1L4	201414_s_at	Hs.501684	4676 nucleosome assembly protein 1-like 4
T helper cells	BATF	205965_at	Hs.509664	10538 basic leucine zipper transcription factor, ATF-like
T helper cells	ASF1A	203428_s_at	Hs.292316	25842 ASF1 anti-silencing function 1 homolog A (S. cerevisiae)
T helper cells	FRYL	212546_s_at	Hs.631525, Hs.64632	285527 FRY-like
T helper cells	FUSIP1	213594_x_at	Hs.3530, Hs.652334	10772 FUS interacting protein (serine/arginine-rich) 1
T helper cells	TRA@	215524_x_at	Hs.74647, Hs.499145	10730 YME1-like 1 (S. cerevisiae)
T helper cells	TRA@	217412_at	6955	
T helper cells	RPA1	201528_at	Hs.461925, Hs.59556	6117 replication protein A1, 70kDa
T helper cells	UBE2L3	200683_s_at	Hs.108104, Hs.69370	7332 ubiquitin-conjugating enzyme E2L 3
T helper cells	ANP32B	201306_s_at	Hs.494604	10541 acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
T helper cells	DDX50	221699_s_at	Hs.522984	79009 DEAD (Asp-Glu-Ala-Asp) box polypeptide 50
T helper cells	C13orf34	219544_at	Hs.653132	79866 chromosome 13 open reading frame 34
T helper cells	PPP2R5C	213305_s_at	Hs.368264	5527 protein phosphatase 2, regulatory subunit B', gamma isoform
T helper cells	SLC25A12	203340_s_at	Hs.470608	8604 solute carrier family 25 (mitochondrial carrier, Aralar), member 12
T helper cells	ATF2	205446_s_at	Hs.694722	1386 activating transcription factor 2
T helper cells	CD28	211856_x_at	Hs.591629	940 CD28 molecule
T helper cells	GOLGA8A	208798_x_at	Hs.182982	23015 golgi autoantigen, golgin subfamily a, 8A
Tcm	CDC14A	210441_at	Hs.127411	8556 CDC14 cell division cycle 14 homolog A (S. cerevisiae)
Tcm	ATM	208442_s_at	Hs.367437	472 ataxia telangiectasia mutated
Tcm	USP9Y	206624_s_at	Hs.655309	8287 ubiquitin specific peptidase 9, Y-linked (fat facets-like, Drosophila)
Tcm	PCNX	215175_at	Hs.446559	22990 pecanex homolog (Drosophila)
Tcm	ATM	210858_x_at	Hs.367437	472 ataxia telangiectasia mutated
Tcm	FOXP1	215221_at	Hs.431498	27086 forkhead box P1
Tcm	KLF12	206965_at	Hs.373857, Hs.59250	11278 Kruppel-like factor 12
Tcm	ST3GAL1	215874_at	Hs.584803	6482 ST3 beta-galactoside alpha-2,3-sialyltransferase 1
Tcm	INPP4B	215864_at	Hs.658245	8821 inositol polyphosphate-4-phosphatase, type II, 105kDa
Tcm	CASP8	207686_s_at	Hs.655983	841 caspase 8, apoptosis-related cysteine peptidase
Tcm	MLL	216624_s_at	Hs.258855, Hs.66447	4297 myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)
Tcm	PCM1	209997_x_at	Hs.491148	5108 pericentriolar material 1
Tcm	RP11-74E24.2	205787_x_at	Hs.546686	441155 zinc finger CCCH-type domain-containing pseudogene
Tcm	PHC3	215521_at	Hs.529592, Hs.69446	80012 polyhomeotic homolog 3 (Drosophila)
Tcm	NFATC3	210556_at	Hs.632209	4775 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 3
Tcm	LOC202134	215133_s_at	Hs.646912, Hs.65568	202134 hypothetical protein LOC202134
Tcm	TIMM8A	210800_at	Hs.447877	1678 translocase of inner mitochondrial membrane 8 homolog A (yeast)
Tcm	ATF7IP	216197_at	Hs.591151	55729 activating transcription factor 7 interacting protein
Tcm	REPS1	215201_at	Hs.334603	85021 RALBP1 associated Eps domain containing 1
Tcm	PSPC1	215083_at	Hs.213198	55269 parapsenile component 1
Tcm	RPP38	215743_at	Hs.60339	9397 N-myristoyltransferase 2
Tcm	HNRPH1	213472_at	Hs.604001	3187 heterogeneous nuclear ribonucleoprotein H1 (H)
Tcm	STX16	221638_s_at	Hs.307913	8675 syntaxin 16

Table S1 (1/6)

Tcm	CYLD	214272_at	Hs.578973	1540 cylindromatosis (turban tumor syndrome)
Tcm	SNRPN	216850_at	Hs.564847, Hs.63216	6638 small nuclear ribonucleoprotein polypeptide N
Tcm	TRAF3IP3	215275_at	Hs.147434	80342 TRAF3 interacting protein 3
Tcm	NEFL	221805_at	Hs.521461	4747 neurofibril light polypeptide 68kDa
Tcm	POLR2J2	217610_at	Hs.654726, Hs.69363	246721 DNA directed RNA polymerase II polypeptide J-related
Tcm	AQP3	203747_at	Hs.234642	360 aquaporin 3 (Gill blood group)
Tcm	CG030	215105_at	Hs.658751	116828 hypothetical gene CG030
Tcm	PDXDC2	215920_s_at	Hs.513695	283970 pyridoxal-dependent decarboxylase domain containing 2
Tcm	CLUAP1	204576_s_at	Hs.155995	23059 clusterin associated protein 1
Tcm	DOCK9	215041_s_at	Hs.654825	23348 dedicator of cytokinesis 9
Tcm	CYorf15B	214131_at	Hs.592254	84663 chromosome Y open reading frame 15B
Tcm	CREBFZ	213584_s_at	Hs.535319, Hs.65701	58487 CREB/ATF bZIP transcription factor
Tcm	CEP68	207971_s_at	Hs.693614	23177 centrosomal protein 68kDa
Tcm	TXK	206828_at	Hs.479669	7294 TXK tyrosine kinase
Tcm	SLC7A6	203578_s_at	Hs.653193	9057 solute carrier family 7 (cationic amino acid transporter, y+ system), member 6
Tcm	FYB	205285_s_at	Hs.370503	2533 FYN binding protein (FYB-120/130)
Tcm	MAP3K1	214786_at	Hs.657756	4214 mitogen-activated protein kinase kinase kinase 1
Tem	TRA@	217397_at	Hs.74647	6955 T cell receptor alpha locus
Tem	PRKY	206279_at	Hs.632287	5616 protein kinase, Y-linked
Tem	VIL2	217230_at	Hs.693594	7430 villin 2 (ezrin)
Tem	GDPD5	32502_at	Hs.503297, Hs.67186	81544 glycerophosphodiester phosphodiesterase domain containing 5
Tem	CCR2	206978_at	Hs.644637	1231 chemokine (C-C motif) receptor 2
Tem	MEFV	208262_x_at	Hs.632221	4210 Mediterranean fever
Tem	C7orf54	210109_at	Hs.657377	27099 chromosome 7 open reading frame 54
Tem	FL11	210786_s_at	Hs.504281	2313 Friend leukemia virus integration 1
Tem	TBC1D5	201815_s_at	Hs.475629	9779 TBC1 domain family, member 5
Tem	DDX17	208719_s_at	Hs.528305, Hs.66542	10521 DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
Tem	AKT3	212609_s_at	Hs.498292	10000 v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)
Tem	EWSR1	211825_s_at	Hs.374477	2130 Ewing sarcoma breakpoint region 1
Tem	TBCD	201759_at	Hs.464391	6904 tubulin folding cofactor D
Tem	CCR2	207994_at	Hs.644637	1231 chemokine (C-C motif) receptor 2
Tem	NFATC4	205897_at	Hs.77810	4776 nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
Tem	LTK	207106_s_at	Hs.434481	4058 leukocyte tyrosine kinase
Th1 cells	IFNG	210354_at	Hs.856	3458 interferon, gamma
Th1 cells	LTA	206975_at	Hs.36	4049 lymphotxin alpha (TNF superfamily, member 1)
Th1 cells	APBB2	213419_at	Hs.479602	323 amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
Th1 cells	DOK5	214844_s_at	Hs.656582	55816 docking protein 5
Th1 cells	IL12RB2	206999_at	Hs.479347	3595 interleukin 12 receptor, beta 2
Th1 cells	APBB2	40148_at	Hs.479602	323 amyloid beta (A4) precursor protein-binding, family B, member 2 (Fe65-like)
Th1 cells	APOD	201525_at	Hs.522555	347 apolipoprotein D
Th1 cells	ZBTB32	220118_at	Hs.99430	27033 zinc finger and BTB domain containing 32
Th1 cells	CD38	205692_s_at	Hs.479214	952 CD38 molecule
Th1 cells	CSF2	210229_s_at	Hs.1349	1437 colony stimulating factor 2 (granulocyte-macrophage)
Th1 cells	CTLA4	221331_x_at	Hs.247824	1493 cytotoxic T-lymphocyte-associated protein 4
Th1 cells	CD70	206508_at	Hs.501497	970 CD70 molecule
Th1 cells	DPP4	211478_s_at	Hs.368912	1803 dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)
Th1 cells	EGFL6	219454_at	Hs.12844	25975 EGFL-like-domain, multiple 6
Th1 cells	BST2	201641_at	Hs.118110	684 bone marrow stromal cell antigen 2
Th1 cells	DUSP5	209457_at	Hs.2128	1847 dual specificity phosphatase 5
Th1 cells	LRP8	205282_at	Hs.576154	7804 low density lipoprotein receptor-related protein 8, apolipoprotein e receptor
Th1 cells	IL22	221165_s_at	Hs.287369	50616 interleukin 22
Th1 cells	DGKI	206806_at	Hs.242947	9162 diacylglycerol kinase, iota
Th1 cells	CCL4	204103_at	Hs.75703	6351 chemokine (C-C motif) ligand 4
Th1 cells	DPP4	203716_s_at	Hs.368912	1803 dipeptidyl-peptidase 4 (CD26, adenosine deaminase complexing protein 2)
Th1 cells	GGT1	211417_x_at	Hs.595809, Hs.64553	2678 gamma-glutamyltransferase 1
Th1 cells	LRRN3	209840_s_at	Hs.3781	54674 leucine rich repeat neuronal 3
Th1 cells	SYNGR3	205691_at	Hs.435277	9143 synaptogyrin 3
Th1 cells	ATP9A	212062_at	Hs.592144	10079 ATPase, Class II, type 9A
Th1 cells	BTG3	205548_s_at	Hs.473420	10950 BTG family, member 3
Th1 cells	CMAH	210571_s_at	Hs.484918	8418 cytidine monophosphate-N-acetylneuraminate acetyltransferase (CMP-N-acetylneuraminate monooxygenase)
Th1 cells	HBEGF	38037_at	Hs.799	1839 heparin-binding EGF-like growth factor
Th1 cells	SGCB	205120_s_at	Hs.438953	6443 sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
Th2 cells	PMCH	206942_s_at	Hs.694729	5367 pro-melanin-concentrating hormone
Th2 cells	AH1	220841_s_at	Hs.386684	54806 Abelson helper integration site 1
Th2 cells	PTGIS	208131_s_at	Hs.302085	5740 prostaglandin I2 (prostacyclin) synthase
Th2 cells	AH1	220842_at	Hs.386684	54806 Abelson helper integration site 1
Th2 cells	CXCR6	211469_s_at	Hs.34526	10663 chemokine (C-X-C motif) receptor 6
Th2 cells	EV15	209717_at	Hs.656836	7813 ectopic viral integration site 5
Th2 cells	AH1	221569_at	Hs.386684	54806 Abelson helper integration site 1
Th2 cells	IL26	221111_at	Hs.272350	55801 interleukin 26
Th2 cells	MB	204179_at	Hs.517586	4151 myoglobin
Th2 cells	NEIL3	219502_at	Hs.405467	55247 neil endonuclease VIII-like 3 (E. coli)
Th2 cells	GSTA4	202967_at	Hs.485557	2941 glutathione S-transferase A4
Th2 cells	PHEX	210617_at	Hs.495834	5251 phosphate regulating endopeptidase homolog, X-linked (hypophosphatemia, vitamin D resistant rickets)
Th2 cells	SMAD2	203076_s_at	Hs.12253, Hs.598146	4087 SMAD family member 2
Th2 cells	CENPF	209172_s_at	Hs.497741	1063 centromere protein F, 350/400ka (mitosin)
Th2 cells	ANK1	208353_x_at	Hs.654438, Hs.66737	286 ankyrin 1, erythrocytic
Th2 cells	ADCY1	213245_at	Hs.192215	107 adenylate cyclase 1 (brain)
Th2 cells	AI582773	214373_at	Hs.655175	728210 hypothetical protein LOC728210
Th2 cells	LAIR2	207509_s_at	Hs.43803	3904 leukocyte-associated immunoglobulin-like receptor 2
Th2 cells	SNRPD1	202691_at	Hs.464734	6632 small nuclear ribonucleoprotein D1 polypeptide 16kDa
Th2 cells	CXCR6	206974_at	Hs.34526	10663 chemokine (C-X-C motif) receptor 6
Th2 cells	MICAL2	212472_at	Hs.501928	9645 microtubule associated monooxygenase, calponin and LIM domain containing 2
Th2 cells	DHFR	202534_x_at	Hs.648635, Hs.65455	1719 dihydrofolate reductase
Th2 cells	SMAD2	203077_s_at	Hs.12253, Hs.598146	4087 SMAD family member 2
Th2 cells	WDHD1	204728_s_at	Hs.385998	11169 WD repeat and HMG-box DNA binding protein 1
Th2 cells	BIRC5	210334_x_at	Hs.514527	332 baculovirus IAP repeat-containing 5 (survivin)
Th2 cells	DHFR	48808_at	Hs.648635, Hs.65455	1719 dihydrofolate reductase
Th2 cells	SLC39A14	212110_at	Hs.491232	23516 solute carrier family 39 (zinc transporter), member 14
Th2 cells	HELLS	220085_at	Hs.655830	3070 helicase, lymphoid-specific
Th2 cells	LIMA1	217892_s_at	Hs.525419	51474 LIM domain and actin binding 1
Th2 cells	CDC25C	205167_s_at	Hs.656	995 cell division cycle 25 homolog C (S. pombe)
Th2 cells	CDC7	204510_at	Hs.533573	8317 cell division cycle 7 homolog (S. cerevisiae)
Th2 cells	GATA3	209602_s_at	Hs.524134	2625 GATA binding protein 3
TFH	CHI3L2	213060_s_at	Hs.514840	1117 chitinase 3-like 2
TFH	CXCL13	205242_at	Hs.100431	10563 chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)
TFH	MYO7A	33197_at	Hs.370421	4647 myosin VIIA
TFH	CHGB	204260_at	Hs.516874	1114 chromogranin B (secretogranin 1)
TFH	MYO7A	208189_s_at	Hs.370421	4647 myosin VIIA
TFH	ICA1	210547_x_at	Hs.487561	3382 islet cell autoantigen 1, 69kDa
TFH	HEY1	218839_at	Hs.234434	23462 hairy/enhancer-of-split related with YRPW motif 1
TFH	CDK5R1	204995_at	Hs.500015	8851 cyclin-dependent kinase 5, regulatory subunit 1 (p35)
TFH	ST8SIA1	210073_at	Hs.408614	6489 ST8 alpha-N-acetyl-neuraminate alpha-2,6-sialyltransferase 1
TFH	PDCD1	207634_at	Hs.158297	5133 programmed cell death 1
TFH	BLR1	216734_s_at	Hs.113916	643 Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)
TFH	KIAA1324	221874_at	Hs.642705	57535 KIAA1324
TFH	PVALB	205336_at	Hs.295449	5816 parvalbumin
TFH	ICA1	207949_s_at	Hs.487561	3382 islet cell autoantigen 1, 69kDa
TFH	TSHR	210055_at	Hs.160411	7253 thyroid stimulating hormone receptor
TFH	C18orf11	209574_s_at	Hs.149363	753 chromosome 18 open reading frame 1
TFH	HEY1	44783_s_at	Hs.234434	23462 hairy/enhancer-of-split related with YRPW motif 1
TFH	TOX	204529_s_at	Hs.491805, Hs.63485	9760 thymocyte selection-associated high mobility group box

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TFH	BLR1	206126_at	Hs.113916	643 Burkitt lymphoma receptor 1, GTP binding protein (chemokine (C-X-C motif) receptor 5)
TFH	SLC7A10	220868_s_at	Hs.58679	56301 solute carrier family 7, (neutral amino acid transporter, y+ system) member 10
TFH	SMAD1	210993_s_at	Hs.656534	4086 SMAD family member 1
TFH	POMT1	218476_at	Hs.522449	10585 protein-O-mannosyltransferase 1
TFH	PASK	216945_x_at	Hs.694813	23178 PAS domain containing serine/threonine kinase
TFH	MKL2	218259_at	Hs.592047	57496 MKL/myocardin-like 2
TFH	PTPN13	204201_s_at	Hs.436142	5783 protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)
TFH	PASK	213534_s_at	Hs.694813	23178 PAS domain containing serine/threonine kinase
TFH	KCNK5	219615_s_at	Hs.444448	8645 potassium channel, subfamily K, member 5
TFH	C18orf11	207996_s_at	Hs.149363	753 chromosome 18 open reading frame 1
TFH	ZNF764	57516_at	Hs.132227	92959 zinc finger protein 764
TFH	MAF	206363_at	Hs.134859	4094 v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
TFH	MYO6	210480_s_at	Hs.149387	4646 myosin VI
TFH	SIRPG	220485_s_at	Hs.590883	55423 signal-regulatory protein gamma
TFH	THADA	54632_at	Hs.369592	63892 thyroid adenoma associated
TFH	THADA	220212_s_at	Hs.369592	63892 thyroid adenoma associated
TFH	MAGEH1	218573_at	Hs.279819	28986 melanoma antigen family H, 1
TFH	B3GAT1	219521_at	Hs.381050	27087 beta-1,3-glycuronidyltransferase 1 (glucuronosyltransferase P)
TFH	MAF	209348_s_at	Hs.134859	4094 v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)
TFH	SH3TC1	219256_s_at	Hs.479116	54436 SH3 domain and tetraricopeptide repeats 1
TFH	HIST1H4K	214463_x_at	Hs.528055	8362 histone cluster 1, H4k
TFH	STK39	202786_at	Hs.276271	27347 serine threonine kinase 39 (STE20/SPS1 homolog, yeast)
Th17 cells	IL17A	208402_at	Hs.41724	3605 interleukin 17A
Th17 cells	IL17A	216876_s_at	Hs.41724	3605 interleukin 17A
Th17 cells	IL17RA	205707_at	Hs.129751	23765 interleukin 17 receptor A
Th17 cells	RORC	206419_at	Hs.256022, Hs.60799	6097 RAR-related orphan receptor C
TReg	FOXP3	221333_at	Hs.247700	50943 forkhead box P3
TReg	FOXP3	221334_s_at	Hs.247700	50943 forkhead box P3
CD8 T cells	CD8B	207979_s_at	Hs.405667	926 CD8b molecule
CD8 T cells	CD8A	205758_at	Hs.86258	925 CD8a molecule
CD8 T cells	CD8B	215332_s_at	Hs.405667	926 CD8b molecule
CD8 T cells	PF4	206390_x_at	Hs.81564	5196 platelet factor 4 (chemokine (C-X-C motif) ligand 4)
CD8 T cells	PRR5	47069_at	Hs.102336	55615 proline rich 5 (renal)
CD8 T cells	SF1	210172_at	Hs.502829	7536 splicing factor 1
CD8 T cells	LIME1	219541_at	Hs.233220	54923 Lck interacting transmembrane adaptor 1
CD8 T cells	DNAJB1	200684_s_at	Hs.515210	3337 DnaJ (Hsp40) homolog, subfamily B, member 1
CD8 T cells	ARHGAP8	219168_s_at	Hs.102336	55615 proline rich 5 (renal)
CD8 T cells	GZMM	207460_at	Hs.465511	3004 granzyme M (lymphocyte met-ase 1)
CD8 T cells	SLC16A7	207057_at	Hs.439643	9194 solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
CD8 T cells	SFRS7	213649_at	Hs.309090	6432 splicing factor, arginine/serine-rich 7, 35kDa
CD8 T cells	APBA2	209871_s_at	Hs.618112	321 amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
CD8 T cells	C4orf15	210054_at	Hs.368454	79441 chromosome 4 open reading frame 15
CD8 T cells	LEPROTL1	202595_s_at	Hs.146585	23484 leptin receptor overlapping transcript-like 1
CD8 T cells	ZFP36L2	201367_s_at	Hs.503093, Hs.64506	678 zinc finger protein 36, C3H type-like 2
CD8 T cells	GADD45A	203725_at	Hs.80409	1647 growth arrest and DNA-damage-inducible, alpha
CD8 T cells	ZFP36L2	201369_s_at	Hs.503093, Hs.64506	678 zinc finger protein 36, C3H type-like 2
CD8 T cells	MYST3	216361_s_at	Hs.591848	7994 MYST histone acetyltransferase (monocytic leukemia) 3
CD8 T cells	ZEB1	208078_s_at	Hs.124503	6935 zinc finger E-box binding homeobox 1
CD8 T cells	ZNF609	212620_at	Hs.595451, Hs.68343	23060 zinc finger protein 609
CD8 T cells	C12orf47	64432_at	Hs.333120	51275 chromosome 12 open reading frame 47
CD8 T cells	THUMPD1	206555_s_at	Hs.460232	55623 THUMP domain containing 1
CD8 T cells	VAMP2	201557_at	Hs.25348	6844 vesicle-associated membrane protein 2 (synaptobrevin 2)
CD8 T cells	ZNF91	206059_at	Hs.654471	7644 zinc finger protein 91
CD8 T cells	ZNF22	218006_s_at	Hs.462693, Hs.65512	7570 zinc finger protein 22 (KOX 15)
CD8 T cells	TMCF6	214958_s_at	Hs.632227	11322 transmembrane channel-like 6
CD8 T cells	DNAJB1	200666_s_at	Hs.515210	3337 DnaJ (Hsp40) homolog, subfamily B, member 1
CD8 T cells	FLT3LG	210607_at	Hs.428	2323 fms-related tyrosine kinase 3 ligand
CD8 T cells	CDKN2AIP	218929_at	Hs.644077	55862 CDKN2A interacting protein
CD8 T cells	TSC22D3	207001_x_at	Hs.522074	1831 TSC22 domain family, member 3
CD8 T cells	TBCC	202495_at	Hs.75064	6903 tubulin folding cofactor C
CD8 T cells	RBM3	208319_s_at	Hs.301404	5935 RNA binding motif (RNP1, RRM) protein 3
CD8 T cells	ABT1	218405_at	Hs.254406	29777 activator of basal transcription 1
CD8 T cells	C19orf6	212574_x_at	Hs.515003	91304 chromosome 19 open reading frame 6
CD8 T cells	CAMLG	203538_at	Hs.529846	819 calcium modulating ligand
CD8 T cells	PPP1R2	202165_at	Hs.535731	5504 protein phosphatase 1, regulatory (inhibitor) subunit 2
CD8 T cells	AES	217729_s_at	Hs.515053	166 amino-terminal enhancer of split
CD8 T cells	KLF9	203543_s_at	Hs.150557, Hs.60226	687 Kruppel-like factor 9
CD8 T cells	PRF1	214617_at	Hs.2200	5551 perforin 1 (pore forming protein)
Tgd	TRD@	217143_s_at	Hs.74647	6964 T cell receptor delta locus
Tgd	TARP	211144_x_at	Hs.534032	445347 TCR gamma alternate reading frame protein
Tgd	C10rf61	205103_at	Hs.380027	10485 chromosome 1 open reading frame 61
Tgd	TRGV9	209813_x_at	Hs.534032	6983 T cell receptor gamma variable 9
Tgd	CD160	207840_at	Hs.488237	11126 CD160 molecule
Tgd	TARP	216920_s_at	Hs.534032	445347 TCR gamma alternate reading frame protein
Tgd	FEZ1	203562_at	Hs.224008	9638 fasciculation and elongation protein zeta 1 (zygin 1)
Cytotoxic cells	KLRD1	210606_x_at	Hs.5562457	3824 killer cell lectin-like receptor subfamily D, member 1
Cytotoxic cells	KLRF1	220646_s_at	Hs.183125	51348 killer cell lectin-like receptor subfamily F, member 1
Cytotoxic cells	GNLY	37145_at	Hs.105806	10578 granlysins
Cytotoxic cells	GNLY	205495_s_at	Hs.105806	10578 granlysins
Cytotoxic cells	CTSW	214450_at	Hs.416848	1521 cathepsin W
Cytotoxic cells	KLRB1	214470_at	Hs.169824	3820 killer cell lectin-like receptor subfamily B, member 1
Cytotoxic cells	KLRD1	207795_s_at	Hs.5562457	3824 killer cell lectin-like receptor subfamily D, member 1
Cytotoxic cells	KLRK1	205821_at	Hs.387787	22914 killer cell lectin-like receptor subfamily K, member 1
Cytotoxic cells	NKG7	213915_at	Hs.10306	4818 natural killer cell group 7 sequence
Cytotoxic cells	GZMH	210321_at	Hs.348264	2999 granzyme H (cathepsin G-like 2, protein h-CCP)
Cytotoxic cells	KLRD1	207796_x_at	Hs.5562457	3824 killer cell lectin-like receptor subfamily D, member 1
Cytotoxic cells	SIGIRR	218921_at	Hs.501624	59307 single immunoglobulin and toll-interleukin 1 receptor (TIR) domain
Cytotoxic cells	ZBTB16	205883_at	Hs.591945, Hs.68214	7704 zinc finger and BTB domain containing 16
Cytotoxic cells	RUNX3	204198_s_at	Hs.170019	864 runt-related transcription factor 3
Cytotoxic cells	APOL3	221087_s_at	Hs.474737	80833 apolipoprotein L, 3
Cytotoxic cells	RORA	210426_x_at	Hs.654353	6095 RAR-related orphan receptor A
Cytotoxic cells	APBA2	209870_s_at	Hs.618112	321 amyloid beta (A4) precursor protein-binding, family A, member 2 (X11-like)
Cytotoxic cells	SIGIRR	52940_at	Hs.501624	59307 single immunoglobulin and toll-interleukin 1 receptor (TIR) domain
Cytotoxic cells	WHDC1L1	213908_at	Hs.212670, Hs.65530	339005 WAS protein homology region 2 domain containing 1-like 1
Cytotoxic cells	DUSP2	204794_at	Hs.1183	1844 dual specificity phosphatase 2
Cytotoxic cells	GZMA	205488_at	Hs.90708	3001 granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)
NK cells	LOC643313	211050_x_at	Hs.676949	643313 similar to hypothetical protein LOC284701
NK cells	GAGE2	207739_s_at	Hs.658117	2574 G antigen 2
NK cells	ZNF747	206180_x_at	Hs.592032	65988 zinc finger protein 747
NK cells	XCL1	206366_x_at	Hs.546295	6375 chemokine (C motif) ligand 1
NK cells	XCL2	214567_s_at	Hs.458346	6846 chemokine (C motif) ligand 2
NK cells	AF107846	217058_at	Hs.125898	2778 GNAS complex locus
NK cells	SLC30A5	220181_x_at	Hs.631975	64924 solute carrier family 30 (zinc transporter), member 5
NK cells	NM_014114	220691_at	Hs.654698	259230 sphingomyelin synthase 1
NK cells	MCM3AP	215582_x_at	Hs.389037	8888 minichromosome maintenance complex component 3 associated protein
NK cells	TBXA2R	207555_s_at	Hs.442530	6915 thromboxane A2 receptor
NK cells	CDC5L	209057_x_at	Hs.485471	988 CDC5 cell division cycle 5-like (S. pombe)
NK cells	LOC730096	215182_x_at	Hs.572908	730096 hypothetical protein LOC730096
NK cells	FUT5	211225_at	Hs.631843	2527 fucosyltransferase 5 (alpha (1,3)fucosyltransferase)
NK cells	FGF18	206986_at	Hs.87191	8817 fibroblast growth factor 18
NK cells	MRC2	209280_at	Hs.7835	9902 mannose receptor, C type 2
NK cells	RP5-886K2.1	208014_x_at	Hs.485471	27308 neuronal thread protein AD7c-NTF
NK cells	SPN	216981_x_at	Hs.632188	6693 sialophorin (leukosialin, CD43)
NK cells	PSM5	210459_at	Hs.505059	5710 proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
NK cells	PRX	220024_s_at	Hs.205457	57716 periaxin
NK cells	FZR1	209415_at	Hs.413133	51343 fizzy/cell division cycle 20 related 1 (Drosophila)

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NK cells	ZNF205	206416_s_at	Hs.592088	7755 zinc finger protein 205
NK cells	AL080130	212972_x_at		323
NK cells	ZNF528	215019_x_at	Hs.662043	84436 zinc finger protein 528
NK cells	MAPRE3	203842_s_at	Hs.515860	22924 microtubule-associated protein, RP/EB family, member 3
NK cells	BCL2	207004_at	Hs.150749	596 B-cell CLL/lymphoma 2
NK cells	NM_017616	221068_at	Hs.284208	25959 ankyrin repeat domain 25
NK cells	ARL6IP2	217580_x_at	Hs.190440	64225 ADP-ribosylation factor-like 6 interacting protein 2
NK cells	SPN	206057_x_at	Hs.632188	6693 sialophosphatase (leukosialin, CD43)
NK cells	FZR1	211865_s_at	Hs.413133	51343 fizzy/cell division cycle 20 related 1 (Drosophila)
NK cells	PDLIM4	214174_s_at	Hs.424312	8572 PDZ and LIM domain 4
NK cells	NM_014274	206827_s_at	Hs.302740, Hs.63896	55503 transient receptor potential cation channel, subfamily V, member 6
NK cells	LDR3	216888_at	Hs.657271	11155 LIM domain binding 3
NK cells	ADARB1	209979_at	Hs.474018	104 adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
NK cells	SMEK1	215607_x_at	Hs.533887	55671 SMEK homolog 1, suppressor ofmek1 (Dictyostelium)
NK cells	TCTN2	206438_x_at	Hs.167165	79867 tectonic family member 2
NK cells	TINAGL1	219058_x_at	Hs.199368	64129 tubulointerstitial nephritis antigen-like 1
NK cells	IGFBP5	203426_s_at	Hs.635441	3488 insulin-like growth factor binding protein 5
NK cells	ALDH1B1	209646_x_at	Hs.436219	219 aldehyde dehydrogenase 1 family, member B1
NK cells	NCR1	217095_x_at	Hs.97084	9437 natural cytotoxicity triggering receptor 1
NK cells	NCR1	217088_s_at	Hs.97084	9437 natural cytotoxicity triggering receptor 1
NK cells	NCR1	207860_at	Hs.97084	9437 natural cytotoxicity triggering receptor 1
NK CD56dim cells	KIR3DL2	207314_x_at	Hs.645228, Hs.64553	3812 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
NK CD56dim cells	KIR3DL2	216907_x_at	Hs.645228, Hs.64553	3812 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
NK CD56dim cells	SPON2	218638_s_at	Hs.302963	10417 spondin 2, extracellular matrix protein
NK CD56dim cells	KIR2DL3	208179_x_at	Hs.654605, Hs.65460	3804 killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 3
NK CD56dim cells	GZMB	210164_at	Hs.1051	3002 granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)
NK CD56dim cells	KIR3DS1	211389_x_at	Hs.659860, Hs.66110	3813 killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1
NK CD56dim cells	KIR3DL1	211687_x_at	Hs.645228	3811 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1
NK CD56dim cells	FLJ20699	216434_at	Hs.435832	55020 hypothetical protein FLJ20699
NK CD56dim cells	TMEPAI	217875_s_at	Hs.517155	56937 transmembrane, prostate androgen induced RNA
NK CD56dim cells	KIR3DL2	211688_x_at	Hs.645228, Hs.64553	3812 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
NK CD56dim cells	IL2R1	221658_s_at	Hs.210546	50615 interleukin 21 receptor
NK CD56dim cells	KIR3DL2	207313_x_at	Hs.645228, Hs.64553	3812 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 2
NK CD56dim cells	KIR3DL3	216676_x_at	Hs.645224	115653 killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 3
NK CD56dim cells	KIR2DS5	208203_x_at	Hs.659860	3810 killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 5
NK CD56dim cells	KIR2DS2	211532_x_at	Hs.512572, Hs.65460	3807 killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2
NK CD56dim cells	GTF3C1	202320_at	Hs.371718	2975 general transcription factor IIIC, polypeptide 1, alpha 220kDa
NK CD56dim cells	KIR2DS1	216552_x_at	Hs.661101	3806 killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1
NK CD56dim cells	EDG8	221417_x_at	Hs.501561	53637 endothelial differentiation, sphingolipid G-protein-coupled receptor, 8
NK CD56bright cells	DUSP4	204014_at	Hs.417962	1846 dual specificity phosphatase 4
NK CD56bright cells	RRAD	204803_s_at	Hs.1027	6236 Ras-related associated with diabetes
NK CD56bright cells	XCL1	206365_at	Hs.546295	6375 chemokine (C-motif) ligand 1
NK CD56bright cells	PLA2G6	215938_s_at	Hs.170479	8398 phospholipase A2, group VI (cytosolic, calcium-independent)
NK CD56bright cells	PLA2G6	204691_at	Hs.170479	8398 phospholipase A2, group VI (cytosolic, calcium-independent)
NK CD56bright cells	NIBP	221672_s_at	Hs.654911	83696 NIK and IKK(beta) binding protein
NK CD56bright cells	FOXJ1	205906_at	Hs.651204	2302 forkhead box J1
NK CD56bright cells	03/06/09	215908_at	Hs.432862	10299 membrane-associated ring finger (C3HC4) 6
NK CD56bright cells	DUSP4	204015_s_at	Hs.417962	1846 dual specificity phosphatase 4
NK CD56bright cells	PLA2G6	210647_at	Hs.170479	8398 phospholipase A2, group VI (cytosolic, calcium-independent)
NK CD56bright cells	MADD	38398_at	Hs.82548	8567 MAP-kinase activating death domain
NK CD56bright cells	BG255923	215409_at	Hs.352614	254531 1-acetylcerol-3-phosphate O-acyltransferase 7 (lysophosphatidic acid acyltransferase, etc)
NK CD56bright cells	MPPED1	206436_at	Hs.592198	758 metallophosphoesterase domain containing 1
NK CD56bright cells	MUC3B	214676_x_at	Hs.489354	57876 mucin 3B, cell surface associated
DC	CD209	207277_at	Hs.278694	30835 CD209 molecule
DC	CCL17	207900_at	Hs.546294	6361 chemokine (C-C motif) ligand 17
DC	HSD11B1	205404_at	Hs.195040	3290 hydroxysteroid (11-beta) dehydrogenase 1
DC	CCL13	206407_s_at	Hs.414629	6357 chemokine (C-C motif) ligand 13
DC	CCL22	207861_at	Hs.534347	6367 chemokine (C-C motif) ligand 22
DC	PPF1BP2	212841_s_at	Hs.655714	8495 PTPRF interacting protein, binding protein 2 (liprin beta 2)
DC	NPR1	32625_at	Hs.490330	4881 natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)
DC	CD1B	206749_at	Hs.1310	910 CD1b molecule
DC	VASH1	203940_s_at	Hs.525479	22846 Vaspinin 1
DC	F13A1	203305_at	Hs.335513	2162 coagulation factor XIII, A1 polypeptide
DC	CD1E	215784_at	Hs.249217	913 CD1e molecule
DC	MMP12	204580_at	Hs.1695	4321 matrix metalloproteinase 12 (macrophage elastase)
DC	FABP4	203980_at	Hs.391561	2167 fatty acid binding protein 4, adipocyte
DC	CLEC10A	206682_at	Hs.54403	10462 C-type lectin domain family 10, member A
DC	SYT17	205613_at	Hs.258326	51760 synaptotagmin XVII
DC	MS4A6A	219666_at	Hs.523702	64231 membrane-spanning 4-domains, subfamily A, member 6A
DC	CTNS	204925_at	Hs.187667	1497 cystinosine, nephropathic
DC	CARD9	220162_s_at	Hs.694071	64170 caspase recruitment domain family, member 9
DC	CD1E	208592_s_at	Hs.249217	913 CD1e molecule
DC	ABC62	209735_at	Hs.480218	9429 ATP-binding cassette, sub-family G (WHITE), member 2
DC	CD1A	210325_at	Hs.1309	909 CD1a molecule
DC	PPARG	208510_s_at	Hs.162646	5468 peroxisome proliferator-activated receptor gamma
DC	RAP1GAP	203911_at	Hs.148178	5909 RAP1 GTPase activating protein
DC	SLC7A8	216604_s_at	Hs.632348	23428 solute carrier family 7 (cystic amino acid transporter, y+ system), member 8
DC	GSTT1	203815_at	Hs.268573, Hs.56802	2952 glutathione S-transferase theta 1
DC	NM_021941	218019_s_at	Hs.284491	8566 pyridoxal (pyridoxine, vitamin B6) kinase
DC	FZD2	210220_at	Hs.142912	2535 frizzled homolog 2 (Drosophila)
DC	CSF1R	203104_at	Hs.654394	1438 colony stimulating factor 1 receptor, formerly McDonough feline sarcoma viral (v-fms) oncogene homolog
DC	HS3ST2	219697_at	Hs.115830, Hs.62253	9956 heparan sulfate (glucosamine) 3-O-sulfotransferase 2
DC	CH25H	206932_at	Hs.47357	9023 cholesterol 25-hydroxylase
DC	LMAN2L	221274_s_at	Hs.655743	81562 lectin, mannose-binding 2-like
DC	SLC26A6	221572_s_at	Hs.631925, Hs.66320	65010 sulfotransferrin 26, member 6
DC	BLVRB	202201_at	Hs.515785	645 biliverdin reductase B (flavin reductase (NADPH))
DC	NUDT9	218375_at	Hs.149500	53343 nudix (nucleoside diphosphate linked moiety X)-type motif 9
DC	PREP	204117_at	Hs.436564	5550 prolyl endopeptidase
DC	TM7SF4	221266_s_at	Hs.652230	81501 transmembrane 7 superfamily member 4
DC	TACSTD2	202286_s_at	Hs.23582	4070 tumor-associated calcium signal transducer 2
DC	CD1C	205987_at	Hs.132448	911 CD1c molecule
aDC	CCL1	207533_at	Hs.72918	6346 chemokine (C-C motif) ligand 1
aDC	EB13	219424_at	Hs.501452	10148 Epstein-Barr virus induced gene 3
aDC	INDO	210029_at	Hs.840	3620 indoleamine-pyrole 2,3 dioxygenase
aDC	LAMP3	205569_at	Hs.518448	27074 lysosomal-associated membrane protein 3
aDC	OAS3	218400_at	Hs.528634	4940 2'-5'-oligoadenylate synthetase 3, 100kDa
pDC	IL3RA	206148_at	Hs.632790	3563 interleukin 3 receptor, alpha (low affinity)
Eosinophils	IL5RA	211517_s_at	Hs.68876	3568 interleukin 5 receptor, alpha
Eosinophils	KCNH2	210036_s_at	Hs.647099	3575 potassium voltage-gated channel, subfamily H (eag-related), member 2
Eosinophils	CCR3	208304_at	Hs.506190	1232 chemokine (C-C motif) receptor 3
Eosinophils	ACACB	49452_at	Hs.234898	32 acetyl-Coenzyme A carboxylase beta
Eosinophils	THBS1	201108_s_at	Hs.164226	7057 thrombospondin 1
Eosinophils	GALC	211810_s_at	Hs.513439	2581 galactosylceramidase
Eosinophils	TKTL1	214183_s_at	Hs.102866	8277 transketolase-like 1
Eosinophils	RNU2	210230_at	Hs.676605	728965 hypothetical protein LOC728965
Eosinophils	CLC	206207_at	Hs.889	1178 Charcot-Leyden crystal protein
Eosinophils	THBS1	201109_s_at	Hs.164226	7057 thrombospondin 1
Eosinophils	HIST1H1C	209398_at	Hs.7644	3006 histone cluster 1, H1c
Eosinophils	CYSLTR2	220813_at	Hs.253706, Hs.61431	57105 cysteinyl leukotriene receptor 2
Eosinophils	HRH4	221170_at	Hs.287388	59340 histamine receptor H4
Eosinophils	RNASE2	206111_at	Hs.728	6036 ribonuclease, RNase A family, 2 (Iver, eosinophil-derived neurotoxin)
Eosinophils	CAT	211922_s_at	Hs.502302	847 catalase

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Eosinophils	LRP5L	214873_at	Hs.634058	91355 low density lipoprotein receptor-related protein 5-like
Eosinophils	SYNJ1	207594_s_at	Hs.473632	8867 synaptosomal 1
Eosinophils	SYNJ1	212990_at	Hs.473632	8867 synaptosomal 1
Eosinophils	THBS4	204776_at	Hs.211426	7060 thrombospondin 4
Eosinophils	GPR44	206361_at	Hs.299567	11251 G protein-coupled receptor 44
Eosinophils	KBTBD11	204301_at	Hs.5333	9920 kelch repeat and BTB (POZ) domain containing 11
Eosinophils	HES1	203394_s_at	Hs.250666	3280 hairy and enhancer of split 1, (Drosophila)
Eosinophils	ABHD2	205566_at	Hs.122337, Hs.66646	11057 abhydrolase domain containing 2
Eosinophils	TIPARP	212665_at	Hs.12813, Hs.547611	25976 TCDD-inducible poly(ADP-ribose) polymerase
Eosinophils	SMPD3	219695_at	Hs.368421	55512 sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
Eosinophils	MYO15B	59375_at	Hs.390817	80022 myosin XVB pseudogene
Eosinophils	TGIF1	203313_s_at	Hs.373550	7050 TGFB-induced factor homeobox 1
Eosinophils	RRP12	216360_X_at	Hs.434251	23223 ribosomal RNA processing 12 homolog (S. cerevisiae)
Eosinophils	ACACB	43427_at	Hs.234898	32 acetyl-Coenzyme A carboxylase beta
Eosinophils	IGSF2	207167_at	Hs.654598	9398 immunoglobulin superfamily, member 2
Eosinophils	HES1	203395_s_at	Hs.250666	3280 hairy and enhancer of split 1, (Drosophila)
Eosinophils	RCOR3	218344_s_at	Hs.356399	55785 REST corepressor 3
Eosinophils	EPN2	203463_s_at	Hs.655086	22905 epsin 2
Eosinophils	C9orf156	222195_s_at	Hs.9196	51531 chromosome 9 open reading frame 156
Eosinophils	SIAH1	202981_X_at	Hs.295923	6477 seven in absenta homolog 1 (Drosophila)
Eosinophils	ACACB	221928_at	Hs.234898	32 acetyl-Coenzyme A carboxylase beta
Macrophages	MARCO	205819_at	Hs.67726	8685 macrophage receptor with collagenous structure
Macrophages	CXCL5	214974_X_at	Hs.89714	6374 chemokine (C-X-C motif) ligand 5
Macrophages	SCG5	203889_at	Hs.156540	6447 secretogranin V (T72 protein)
Macrophages	SULT1C2	205342_s_at	Hs.436123	6819 sulfotransferase family, cytosolic, 1C, member 2
Macrophages	SULT1C2	211470_s_at	Hs.436123	6819 sulfotransferase family, cytosolic, 1C, member 2
Macrophages	MSR1	214770_at	Hs.147635	4481 macrophage scavenger receptor 1
Macrophages	CTSK	202450_s_at	Hs.632466	1513 cathepsin K
Macrophages	PTGDS	221287_X_at	Hs.446429	5730 prostaglandin D2 synthase 21kDa (brain)
Macrophages	COLEC12	221019_s_at	Hs.464422	81035 collectin sub-family member 12
Macrophages	GPC4	204984_at	Hs.58367	2239 glycan 4
Macrophages	MSR1	208423_s_at	Hs.147635	4481 macrophage scavenger receptor 1
Macrophages	PCOLCE2	219295_s_at	Hs.8944	26577 procollagen C-endopeptidase enhancer 2
Macrophages	CHIT1	208168_s_at	Hs.201688	1118 chitinase 1 (chitotriosidase)
Macrophages	PTGDS	211748_X_at	Hs.446429	5730 prostaglandin D2 synthase 21kDa (brain)
Macrophages	KAL1	205206_at	Hs.521869	3730 Kallmann syndrome 1 sequence
Macrophages	CLEC5A	219890_at	Hs.446235	23601 C-type lectin domain family 5, member A
Macrophages	GPC4	204983_s_at	Hs.58367	2239 glycan 4
Macrophages	ME1	204058_at	Hs.21160	4199 malic enzyme 1, NADP(+)-dependent, cytosolic
Macrophages	DNASE2B	220380_at	Hs.129142	58511 deoxyribonuclease II beta
Macrophages	CCL7	208075_s_at	Hs.251526	6354 chemokine (C-C motif) ligand 7
Macrophages	FN1	214701_s_at	Hs.203717	2335 fibronectin 1
Macrophages	CD163	203645_s_at	Hs.504641	9332 CD163 molecule
Macrophages	GM2A	215891_s_at	Hs.483873	2760 GM2 ganglioside activator
Macrophages	SCARB2	201647_s_at	Hs.349656	950 scavenger receptor class B, member 2
Macrophages	BCAT1	214452_at	Hs.438993	586 branched chain aminotransferase 1, cytosolic
Macrophages	BCAT1	214390_s_at	Hs.438993	586 branched chain aminotransferase 1, cytosolic
Macrophages	RA14	202052_s_at	Hs.431400	28064 retinoic acid induced 14
Macrophages	MSR1	211887_X_at	Hs.147635	4481 macrophage scavenger receptor 1
Macrophages	COL8A2	52651_at	Hs.353001	1296 collagen, type VIII, alpha 2
Macrophages	CD163	215049_at	Hs.504641	9332 CD163 molecule
Macrophages	APOE	203381_s_at	Hs.654439	348 apolipoprotein E
Macrophages	CHI3L1	203936_s_at	Hs.382202	1116 chitinase 3-like 1 (cartilage glycoprotein-39)
Macrophages	ATG7	218673_s_at	Hs.38032	10533 ATG7 autophagy related 7 homolog (S. cerevisiae)
Macrophages	CD84	211190_X_at	Hs.398093	8832 CD84 molecule
Macrophages	FDX1	203646_at	Hs.744	2230 ferredoxin 1
Macrophages	MS4A4A	219607_s_at	Hs.325960	51338 membrane-spanning 4-domains, subfamily A, member 4
Macrophages	SGMS1	212989_at	Hs.654698	25923 sphingomyelin synthase 1
Macrophages	EMP1	201324_at	Hs.436298	2012 epithelial membrane protein 1
Macrophages	CYBB	203922_s_at	Hs.292356	1536 cytochrome b-245, beta polypeptide (chronic granulomatous disease)
Macrophages	CD68	203507_at	Hs.647419	968 CD68 molecule
Mast cells	PRG2	211743_s_at	Hs.512633	5553 proteoglycan 2, bone marrow (natural killer cell activator, eosinophil granule major basic protein)
Mast cells	CTSG	205653_at	Hs.421724	1511 cathepsin G
Mast cells	TPSAB1	215382_X_at	Hs.405479	7177 tryptase alpha/beta 1
Mast cells	SLC18A2	205857_at	Hs.654476	6571 solute carrier family 18 (vesicular monoamine), member 2
Mast cells	TPSAB1	205683_at	Hs.405479	7177 tryptase alpha/beta 1
Mast cells	MS4A2	207497_s_at	Hs.386748	2206 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for, beta polypeptide)
Mast cells	CPA3	205624_at	Hs.646	1359 carboxypeptidase A3 (mast cell)
Mast cells	TPSB2	207134_X_at	Hs.405479, Hs.59298	64499 tryptase beta 2
Mast cells	TPSAB1	216474_X_at	Hs.405479	7177 tryptase alpha/beta 1
Mast cells	NM_003293	207741_X_at	Hs.405479, Hs.59298	64499 tryptase beta 2
Mast cells	TPSAB1	210084_at	Hs.405479	7177 tryptase alpha/beta 1
Mast cells	MS4A2	207496_at	Hs.386748	2206 membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for, beta polypeptide)
Mast cells	TPSAB1	217023_X_at	Hs.405479	7177 tryptase alpha/beta 1
Mast cells	GATA2	209710_at	Hs.367725	2624 GATA binding protein 2
Mast cells	HDC	207067_s_at	Hs.1481	3067 histidine decarboxylase
Mast cells	LOH11CR2A	210102_at	Hs.152944	4013 loss of heterozygosity, 11, chromosomal region 2, gene A
Mast cells	SIGLE6	210796_X_at	Hs.397255	946 sialic acid binding Ig-like lectin 6
Mast cells	ELA2	206871_at	Hs.99863	1991 elastase 2, neutrophil
Mast cells	LOH11CR2A	205011_at	Hs.152944	4013 loss of heterozygosity, 11, chromosomal region 2, gene A
Mast cells	CMA1	214533_at	Hs.135626	1215 chymase 1, mast cell
Mast cells	SIGLE6	206520_X_at	Hs.397255	946 sialic acid binding Ig-like lectin 6
Mast cells	PGDS	206726_at	Hs.128433	27306 prostaglandin D2 synthase, hematopoietic
Mast cells	MLPH	182111_s_at	Hs.102406	79083 melanophilin
Mast cells	ADCYAP1	206281_at	Hs.592343	116 adenylate cyclase activating polypeptide 1 (pituitary)
Mast cells	SIGLE6	206519_X_at	Hs.397255	946 sialic acid binding Ig-like lectin 6
Mast cells	SLC24A3	57588_at	Hs.654790	57419 solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
Mast cells	CALB2	205428_s_at	Hs.106857	794 calbindin 2, 29kDa (calretinin)
Mast cells	SLC24A3	219050_at	Hs.654790	57419 solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
Mast cells	KIT	205051_s_at	Hs.479754	3815 v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
Mast cells	TAL1	206283_s_at	Hs.525198	6886 T-cell acute lymphocytic leukemia 1
Mast cells	ABCC4	203196_at	Hs.508423	10257 ATP-binding cassette, sub-family C (CFTR/MRP), member 4
Mast cells	PPM1H	212868_at	Hs.435479	57460 protein phosphatase 1H (PP2C domain containing)
Mast cells	MAOB	204041_at	Hs.654473	4129 monoamine oxidase B
Mast cells	HPGD	211549_s_at	Hs.655491	3248 hydroxyprostaglandin dehydrogenase 15-(NAD)
Mast cells	SCG2	204035_at	Hs.516726	7857 secretogranin II (chromogranin C)
Mast cells	PTGS1	205127_at	Hs.201978	5742 prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
Mast cells	CEACAM8	206676_at	Hs.41	1088 carcinoembryonic antigen-related cell adhesion molecule 8
Mast cells	MPO	203949_at	Hs.458272	4353 myeloperoxidase
Mast cells	NR0B1	206645_s_at	Hs.268490	190 nuclear receptor subfamily 0, group B, member 1
Mast cells	LOC339524	215039_at	Hs.306423, Hs.61529	339524 hypothetical protein LOC339524
Neutrophils	CSF3R	203591_s_at	Hs.524517	1441 colony stimulating factor 3 receptor (granulocyte)
Neutrophils	CYP4F3	206515_at	Hs.106242	4051 cytochrome P450, family 4, subfamily F, polypeptide 3
Neutrophils	VNN3	220528_at	Hs.183656	55350 vanin 3
Neutrophils	FPR1	210773_s_at	Hs.99855	2358 formyl peptide receptor-like 1
Neutrophils	KCNJ15	216782_at	Hs.411299	3772 potassium inwardly-rectifying channel, subfamily J, member 15
Neutrophils	MME	203434_s_at	Hs.307734	4311 membrane metallo-endopeptidase
Neutrophils	IL8RA	207094_at	Hs.194778	3577 interleukin 8 receptor, alpha
Neutrophils	IL8RB	207008_at	Hs.846	3579 interleukin 8 receptor, beta
Neutrophils	MME	203435_s_at	Hs.307734	4311 membrane metallo-endopeptidase
Neutrophils	FCGR3B	204007_at	Hs.372679	2215 Fc fragment of IgG, low affinity IIb, receptor (CD16b)
Neutrophils	DYSF	218660_at	Hs.252180	8291 dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)
Neutrophils	KCNJ15	211806_s_at	Hs.411299	3772 potassium inwardly-rectifying channel, subfamily J, member 15
Neutrophils	FCAR	211816_X_at	Hs.659872	2204 Fc fragment of IgA, receptor for
Neutrophils	FCAR	211307_s_at	Hs.659872	2204 Fc fragment of IgA, receptor for
Neutrophils	CEACAM3	210789_X_at	Hs.11	1084 carcinoembryonic antigen-related cell adhesion molecule 3
Neutrophils	FPRL1	210772_at	Hs.99855	2358 formyl peptide receptor-like 1

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Neutrophils	HIST1H2BC	214455_at	Hs.658713	8347 histone cluster 1, H2bc
Neutrophils	HPSE	219403_s_at	Hs.44227	10855 heparanase
Neutrophils	FLJ11151	218610_s_at	Hs.460002, Hs.56044	55313 hypothetical protein FLJ11151
Neutrophils	CREB5	205931_s_at	Hs.437075	9586 cAMP responsive element binding protein 5
Neutrophils	S100A12	205863_at	Hs.19413	6283 S100 calcium binding protein A12
Neutrophils	FCGR3B	204006_s_at	Hs.372679	2215 Fc fragment of IgG, low affinity IIIb, receptor (CD16b)
Neutrophils	TNFRSF10C	211163_s_at	Hs.655801	8794 tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
Neutrophils	SLC22A4	205896_at	Hs.310591, Hs.64010	6583 solute carrier family 22 (organic cation transporter), member 4
Neutrophils	KIAA0329	204307_at	Hs.195667	9895 KIAA0329
Neutrophils	SLC25A37	218136_s_at	Hs.122514, Hs.59602	51312 solute carrier family 25, member 37
Neutrophils	BST1	205715_at	Hs.16998	683 bone marrow stromal cell antigen 1
Neutrophils	FCAR	207674_at	Hs.659872	2204 Fc fragment of IgA, receptor for
Neutrophils	CEACAM3	208052_x_at	Hs.11	1084 carcinoembryonic antigen-related cell adhesion molecule 3
Neutrophils	CRISPLD2	221541_at	Hs.513779	83716 cysteine-rich secretory protein LCCL domain containing 2
Neutrophils	TNFRSF10C	206222_at	Hs.655801	8794 tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain
Neutrophils	G0S2	213524_s_at	Hs.432132	50486 G0/G1switch 2
Neutrophils	SIGLECS	220000_at	Hs.310333	8778 sialic acid binding Ig-like lectin 5
Neutrophils	CD93	202878_s_at	Hs.97199	22918 CD93 molecule
Neutrophils	MGM4	206522_at	Hs.122785	8972 maltase-glucamylase (alpha-glucosidase)
Neutrophils	ALPL	215783_s_at	Hs.75431	249 alkaline phosphatase, liver/bone/kidney
Neutrophils	FPR1	205119_s_at	Hs.753	2357 formyl peptide receptor 1
Neutrophils	CD93	202877_s_at	Hs.97199	22918 CD93 molecule
Neutrophils	PDE4B	222326_at	Hs.198072	5142 phosphodiesterase 4B, cAMP-specific (phosphodiesterase E4 duncane homolog, Drosophila)
Neutrophils	LILRB2	210146_x_at	Hs.655652	10288 leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2
SW480 cancer cells	KRT5	201820_at	Hs.433845, Hs.66106	3852 keratin 5 (epidermolytic bullous simplex; Dowling-Meara/Kobner/Weber-Cockayne types)
SW480 cancer cells	RBP1	203423_at	Hs.529571	5947 retinol binding protein 1, cellular
SW480 cancer cells	TRIM29	202504_at	Hs.504115	23650 tripartite motif-containing 29
SW480 cancer cells	DEF65	207529_at	Hs.655233	1670 defensin, alpha 5, Paneth cell-specific
SW480 cancer cells	BMP4	211518_s_at	Hs.68879	652 bone morphogenic protein 4
SW480 cancer cells	EEF1A2	204540_at	Hs.433839	1917 eukaryotic translation elongation factor 1 alpha 2
SW480 cancer cells	VSNL1	203797_at	Hs.444212	7447 visinin-like 1
SW480 cancer cells	ASPPCR1	218908_at	Hs.298351	79058 alveolar soft part sarcoma chromosome region, candidate 1
SW480 cancer cells	IGF2	202409_at	Hs.272259, Hs.52341	3481 insulin-like growth factor 2 (somatomedin A)
SW480 cancer cells	MFAP2	203417_at	Hs.389137	4237 microfibrillar-associated protein 2
SW480 cancer cells	FGF3	214571_at	Hs.37092	2248 fibroblast growth factor 3 (murine mammary tumor virus integration site (v-int-2) oncogene homolog)
SW480 cancer cells	S100A2	204268_at	Hs.516484	6273 S100 calcium binding protein A2
SW480 cancer cells	INHBB	205258_at	Hs.1735	3625 inhibin, beta B
SW480 cancer cells	JAG2	209784_s_at	Hs.433445	3714 jagged 2
SW480 cancer cells	LOC89944	213713_s_at	Hs.436178	89944 hypothetical protein BC008326
SW480 cancer cells	BAMBI	203304_at	Hs.533326	25805 BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)
SW480 cancer cells	JAG2	32137_at	Hs.433445	3714 jagged 2
SW480 cancer cells	BMP7	209591_s_at	Hs.473163	655 bone morphogenic protein 7 (osteogenic protein 1)
SW480 cancer cells	RPP25	219143_s_at	Hs.8562	54913 ribonuclease P/MRP 25kDa subunit
SW480 cancer cells	RHOD	209885_at	Hs.15114	29984 ras homolog gene family, member D
SW480 cancer cells	DHRS2	214079_at	Hs.272499	10202 dehydrogenase/reductase (SDR family) member 2
SW480 cancer cells	ITGB4	204989_s_at	Hs.632226	3691 integrin, beta 4
SW480 cancer cells	NTSR1	207360_s_at	Hs.509869	4923 neurotensin receptor 1 (high affinity)
SW480 cancer cells	STR46	221701_s_at	Hs.24553	64220 stimulated by retinoic acid gene 6 homolog (mouse)
SW480 cancer cells	SLC1A5	208916_at	Hs.631582	6510 solute carrier family 1 (neutral amino acid transporter), member 5
SW480 cancer cells	VSNL1	203798_s_at	Hs.444212	7447 visinin-like 1
SW480 cancer cells	FKBP4	200894_at	Hs.524183	2288 FK506 binding protein 4, 59kDa
SW480 cancer cells	S100A3	206027_at	Hs.557609	6274 S100 calcium binding protein A3
SW480 cancer cells	TEAD4	41037_at	Hs.94865	7004 TEA domain family member 4
SW480 cancer cells	KLK6	204733_at	Hs.79361	5653 kallikrein-related peptidase 6
SW480 cancer cells	CCND1	208711_s_at	Hs.523852	595 cyclin D1
SW480 cancer cells	SLC27A5	219733_s_at	Hs.292177	10988 solute carrier family 27 (fatty acid transporter), member 5
SW480 cancer cells	HOXA9	214651_s_at	Hs.659350	3205 homeobox A9
SW480 cancer cells	F12	205774_at	Hs.1321	2161 coagulation factor XII (Hageman factor)
SW480 cancer cells	LRFN4	219491_at	Hs.209797, Hs.68452	78999 leucine rich repeat and fibronectin type III domain containing 4
SW480 cancer cells	NM_024609	218678_at	Hs.527971	10763 nestin
SW480 cancer cells	SLC6A8	210854_x_at	Hs.540696	6535 solute carrier family 6 (neurotransmitter transporter, creatine), member 8
SW480 cancer cells	PCTK1	207239_s_at	Hs.496068	5127 PCTAIRE protein kinase 1
SW480 cancer cells	SLC6A8	213843_x_at	Hs.540696	6535 solute carrier family 6 (neurotransmitter transporter, creatine), member 8
SW480 cancer cells	KRT13	207935_s_at	Hs.654550	3860 keratin 13
Normal mucosa	TSPAN8	203824_at	Hs.170563	7103 tetraspanin 8
Normal mucosa	LGALS4	204272_at	Hs.5302	3960 lectin, galactoside-binding, soluble, 4 (galectin 4)
Normal mucosa	DCN	201893_x_at	Hs.694789	1634 decorin
Normal mucosa	COL3A1	215076_s_at	Hs.443625, Hs.69378	1281 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
Normal mucosa	COL3A1	201852_x_at	Hs.443625, Hs.69378	1281 collagen, type III, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
Normal mucosa	CEACAM5	201884_at	Hs.466814	1048 carcinoembryonic antigen-related cell adhesion molecule 5
Normal mucosa	TAGLN	205547_s_at	Hs.632099	6876 transgelin
Normal mucosa	KRT20	213953_s_at	Hs.84905	54474 keratin 20
Normal mucosa	DCN	211896_s_at	Hs.694789	1634 decorin
Normal mucosa	MYH11	201497_x_at	Hs.460109	4629 myosin, heavy chain 11, smooth muscle
Normal mucosa	FXYD3	202489_s_at	Hs.301350	5349 FXYD domain containing ion transport regulator 3
Normal mucosa	ACTG2	202274_at	Hs.516105	72 actin, gamma 2, smooth muscle, enteric
Normal mucosa	MYLK	202555_s_at	Hs.556600	4638 myosin, light chain kinase
Normal mucosa	TPM1	210987_x_at	Hs.133892	7168 tropomyosin 1 (alpha)
Normal mucosa	CDH17	209847_at	Hs.591853	1015 cadherin 17, L1 cadherin (liver-intestine)
Normal mucosa	NFIB	209289_at	Hs.370359	4781 nuclear factor I/B
Normal mucosa	MGP	202991_s_at	Hs.365706	4256 matrix Gla protein
Normal mucosa	SPARC1	200795_at	Hs.62886	8404 SPARC-like 1 (mast3, hevin)
Normal mucosa	RG55	209071_s_at	Hs.24950	8490 regulator of G-protein signaling 5
Normal mucosa	MYH11	207961_s_at	Hs.460109	4629 myosin, heavy chain 11, smooth muscle
Normal mucosa	PPAP2B	212226_s_at	Hs.405156, Hs.63878	8613 phosphatidic acid phosphatase type 2B
Normal mucosa	COL3A1	211161_s_at	Hs.443625, Hs.69378	1281 collagen, type II, alpha 1 (Ehlers-Danlos syndrome type IV, autosomal dominant)
Normal mucosa	IGFBP7	201162_at	Hs.479088, Hs.65210	3490 insulin-like growth factor binding protein 7
Normal mucosa	PPAP2B	209355_s_at	Hs.405156, Hs.63878	8613 phosphatidic acid phosphatase type 2B
Normal mucosa	CALD1	201616_s_at	Hs.490203	800 caldesmon 1
Normal mucosa	C1R	212067_s_at	Hs.524224	715 complement component 1, r subcomponent
Normal mucosa	CALD1	212077_at	Hs.490203	800 caldesmon 1
Normal mucosa	AGR2	209173_at	Hs.530009	10551 anterior gradient homolog 2 (Xenopus laevis)
Normal mucosa	GNA11	564_at	Hs.278432, Hs.65478	2767 guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
Normal mucosa	HEPH	203903_s_at	Hs.31720	9843 hephaestin
Normal mucosa	GNA11	213944_x_at	Hs.278432, Hs.65478	2767 guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
Normal mucosa	GNG12	212294_at	Hs.431101	55970 guanine nucleotide binding protein (G protein), gamma 12
Normal mucosa	ADH1B	209612_s_at	Hs.4	125 alcohol dehydrogenase 1B (class I), beta polypeptide
Normal mucosa	TPM1	206116_s_at	Hs.133892	7168 tropomyosin 1 (alpha)
Normal mucosa	CRIM1	202551_s_at	Hs.328247	51232 cysteine rich transmembrane BMP regulator 1 (chordin-like)
Normal mucosa	FBLN1	202994_s_at	Hs.24601	2192 fibulin 1
Normal mucosa	IGFBP5	211959_at	Hs.635441	3488 insulin-like growth factor binding protein 5
Normal mucosa	LAMA4	202202_s_at	Hs.654572	3910 laminin, alpha 4
Normal mucosa	CAV1	212097_at	Hs.74034	857 caveolin 1, caveolae protein, 22kDa
Normal mucosa	WASL	205809_s_at	Hs.143728	8976 Wiskott-Aldrich syndrome-like
Blood vessels	CDH5	204677_at	Hs.76206	1003 cadherin 5, type 2, VE-cadherin (vascular epithelium)
Lymph vessels	PDPN	204879_at	Hs.468675	10630 podoplanin
Lymph vessels	VEGFC	209946_at	Hs.435215	7424 vascular endothelial growth factor C
Lymph vessels	FIGF	206742_at	Hs.11392	2277 c-fos induced growth factor (vascular endothelial growth factor D)

Table S1 (6/6)

Cluster 1			Cluster 2		
Cell Type	FisherTest P-value	Benjamini correction	Cell Type	FisherTest P-value	Benjamini correction
T cells	< 0.0001	< 0.0001	Eosinophils	0.0090	0.0151
Tgd	0.0143	0.0214	T helper	< 0.0001	< 0.0001
Cytotoxic cells	< 0.0001	< 0.0001	Th2	< 0.0001	< 0.0001
Th1	0.0129	0.0205	Th17	< 0.0001	< 0.0001
DC	< 0.0001	< 0.0001	TFH	0.0196	0.0277
iDC	< 0.0001	< 0.0001	Treg	0.0024	0.0046
Macrophages	< 0.0001	< 0.0001	Tcm	0.0292	0.0394
Mast cells	0.0062	0.0111	NK cells	< 0.0001	< 0.0001
Normal mucosa	< 0.0001	< 0.0001	NK CD56bright	0.0001	< 0.001
Lymph vessels	0.0005	< 0.001	NK CD56dim	< 0.0001	< 0.0001
			SW480 cancer cells	0.0351	0.0451

Table S2

Cell Type	Symbol	EntrezGene	Name	Hazard Ratio	Logrank P-value	Effect on DFS
aDCs	CCL1	6346	Chemokine (C-C motif) ligand 1	0.49	0.0114	positive
aDCs	CD83	9308	CD83 molecule	0.436	0.0131	positive
aDCs	LAMP3	27074	Lysosomal-associated membrane protein 3	4.562	0.0190	negative
B cells	BLK	640	B lymphoid tyrosine kinase	0.706	0.1740	no effect
B cells	CD19	930	CD19 molecule	0.511	0.0208	positive
B cells	HLA-DOB	3112	Major histocompatibility complex, class II, DO beta	0.26	0.0001	positive
B cells	MS4A1	931	Membrane-spanning 4-domains, subfamily A, member 1	0.362	0.0409	positive
Blood vessels	CDH5	1003	Cadherin 5, type 2, VE-cadherin (vascular epithelium)	2.47	0.0042	negative
DCs	CCL13	6357	Chemokine (C-C motif) ligand 13	1.803	0.1597	no effect
DCs	CCL17	6361	Chemokine (C-C motif) ligand 17	1.59	0.1050	no effect
DCs	CCL22	6367	Chemokine (C-C motif) ligand 22	2.123	0.0723	no effect
DCs	CD209	30835	CD209 molecule	0.163	0.0385	positive
Eosinophils	CCR3	1232	Chemokine (C-C motif) receptor 3, eosinophil eotaxin receptor	0.33	0.0519	no effect
Eosinophils	GPR44	11251	G protein-coupled receptor 44	1.901	0.0529	no effect
Eosinophils	IL5RA	3568	Interleukin 5 receptor, alpha	0.539	0.0176	positive
IDCs	CD1A	909	CD1a molecule, thymocyte antigen	0.481	0.0536	no effect
IDCs	CD1E	913	CD1e molecule, thymocyte antigen	0.698	0.1629	no effect
Lymph vessels	FIGF	2277	C-fos induced growth factor (vascular endothelial growth factor D)	2.666	0.0185	negative
Lymph vessels	PDPN	10630	Podoplanin	0.289	0.0627	no effect
Lymph vessels	VEGFC	7424	Vascular endothelial growth factor C	1.54	0.1461	no effect
Macrophages	CCL7	6354	Chemokine (C-C motif) ligand 7, MONOCYTE CHEMOTACTIC PROTEIN	0.495	0.1639	no effect
Macrophages	CD68	968	CD68 molecule, macrophage antigen (microsialin)	0.58	0.0555	no effect
Macrophages	CXCL5	6374	Chemokine (C-X-C motif) ligand 5	0.784	0.3666	no effect
Macrophages	FN1	2335	Fibronectin 1, migration-stimulating factor	0.69	0.1716	no effect
Macrophages	MSR1	4481	Macrophage scavenger receptor 1	1.457	0.1536	no effect
Macrophages	PPBP	5473	Pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	8.559	0.0003	negative
Mast cells	CMA1	1215	Chymase 1, mast cell	1.92	0.1966	no effect
Mast cells	MS4A2	2206	Membrane-spanning 4-domains, subfamily A, member 2	3.554	0.0202	negative
Mast cells	TPSAB1	7177	Tryptase alpha/beta 1	3.074	0.0104	negative
Neutrophils	FPR1	2358	Formyl peptide receptor 2	1.461	0.2724	no effect
Neutrophils	IL8RA	3577	Interleukin 8 receptor, alpha	1.498	0.1633	no effect
Neutrophils	IL8RB	3579	Interleukin 8 receptor, beta	1.807	0.1716	no effect
NK cells	NCR1	9437	Natural cytotoxicity triggering receptor 1	0.339	0.0002	positive
NK cells	XCL1	6375	Chemokine (C motif) ligand 1	1.582	0.0971	no effect
NK CD56dim cells	GZMB	3002	Granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	0.55	0.0297	positive
Normal	DCN	1634	Decorin	1.81	0.2570	no effect
pDC	CLEC4C	170482	C-type lectin domain family 4, member C, DENDRITIC CELL LECTIN	0.459	0.0151	positive
T cells	CD2	914	CD2 molecule	0.453	0.0181	positive
T cells	CD247	919	CD247 molecule	0.516	0.0265	positive
T cells	CD28	940	CD28 molecule	0.593	0.0941	no effect
T cells	CD3E	916	CD3e molecule, epsilon (CD3-TCR complex)	0.588	0.0618	no effect
T cells	CD3G	917	CD3g molecule, gamma (CD3-TCR complex)	0.534	0.0430	positive
T cells	CD6	923	CD6 molecule	0.635	0.1696	no effect
T cells	IL2RB	3560	Interleukin 2 receptor, beta	0.304	0.0332	positive
T cells	ZAP70	7535	Zeta-chain (TCR) associated protein kinase 70kDa	0.433	0.0194	positive
CD8 T cells	CD8A	925	CD8a molecule	0.427	0.0073	positive
CD8 T cells	PRF1	5551	Perforin 1 (pore forming protein)	0.469	0.0050	positive
Cytotoxic cells	KLRF1	51348	Killer cell lectin-like receptor subfamily F, member 1	0.684	0.2020	no effect
Cytotoxic cells	GNLY	10578	Granulysin	0.303	0.0012	positive
Cytotoxic cells	GZMA	3001	Granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3)	0.376	0.0006	positive
Cytotoxic cells	GZMH	2999	Granzyme H (cathepsin G-like 2, protein h-CCPX)	0.465	0.0045	positive
Cytotoxic cells	GZMK	3003	Granzyme K (granzyme 3; tryptase II)	0.306	0.0168	positive
Tem	CCR2	1231	Chemokine (C-C motif) receptor 2	0.417	0.0031	positive
Tem	LTK	4058	Leukocyte receptor tyrosine kinase	0.209	0.0034	positive
Tem	NFATC4	4776	Nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	1.58	0.1048	no effect
Tgd	TRD@	6964	T-cell antigen receptor, delta polypeptide; T-cell receptor, delta (V,D,J,C)	0.48	0.1015	no effect
SW480 cancer cells	CCND1	595	Cyclin D1	0.668	0.1809	no effect
SW480 cancer cells	KRT13	3860	Keratin 13	0.614	0.2013	no effect
SW480 cancer cells	KRT5	3852	Keratin 5	1.899	0.0492	negative
Th	CD4	920	CD4 molecule	0.7	0.2302	no effect
Th1	CD38	952	CD38 molecule	0.486	0.0176	positive
Th1	CSF2	1437	Colony stimulating factor 2 (granulocyte-macrophage)	0.418	0.0255	positive
Th1	CTLA4	1493	Cytotoxic T-lymphocyte-associated protein 4	0.599	0.0743	no effect
Th1	IFNG	3458	Interferon, gamma	0.326	0.0007	positive
Th1	IL12RB2	3595	Interleukin 12 receptor, beta 2	0.572	0.0461	positive
Th1	LTA	4049	Lymphotoxin alpha (TNF superfamily, member 1)	0.537	0.0325	positive
Th1	STAT4	6775	Signal transducer and activator of transcription 4	0.674	0.1555	no effect
Th1	TBX21	30099	T-box 21	0.474	0.0102	positive
Th17	IL17A	3605	Interleukin 17A	1.778	0.0368	negative
Th17	RORC	6097	RAR-related orphan receptor C	1.921	0.1009	no effect
Th2	CXCR6	10663	Chemokine (C-X-C motif) receptor 6	0.439	0.0094	positive
Th2	GATA3	2625	GATA binding protein 3	2.711	0.0791	no effect
Th2	IL26	55801	Interleukin 26	0.456	0.0422	positive
Th2	LAIR2	3904	Leukocyte-associated immunoglobulin-like receptor 2	1.594	0.1459	no effect
Th2	PMCH	5367	Pro-melanin-concentrating hormone	0.593	0.0564	no effect
Th2	SMAD2	4087	SMAD family member 2	0.525	0.0197	positive
Tfh	BLR1	643	Chemokine (C-X-C motif) receptor 5, monocyte-derived	0.51	0.0219	positive
Tfh	CXCL13	10563	Chemokine (C-X-C motif) ligand 13 (B-cell chemoattractant)	0.312	0.0002	positive
Tfh/Th2	MAF	4094	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	0.664	0.1317	no effect
Tfh	PDCD1	5133	Programmed cell death 1	0.425	0.0062	positive
Treg	FOXP3	50943	Forkhead box P3	0.607	0.0696	no effect

Table S3

	Cell Type	P-value	Significance
Cluster1	SW480 cancer cells	0.0030	**
	Th17 cells	0.0240	*
	Neutrophils	0.0650	.
Cluster4	Mast cells	0.0033	**
	Eosinophils	0.0033	**
Cluster5	iDC	0.0018	**
	DC	0.0011	**
Cluster6	Macrophages	0.0072	**
	Lymph vessels	0.0757	.
Cluster7	Cytotoxic cells	0.0009	**
	CD8 T cells	0.0160	*
Cluster8	B cells	0.0071	**
	T cells	0.0170	*
Cluster9	T cells	0.0006	**
	Th1 cells	0.0570	.

Table S4

B-Cell Marker	Marker Cell Type	Marker Name	pearson correlation, r	Pvalue	Pvalue (Bonferroni)
CD19	B cells	MS4A1 (CD20)	0.905	<0.00001	<0.00001
MS4A1 (CD20)	B cells	CD19	0.905	<0.00001	<0.00001
BLK	B cells	MS4A1 (CD20)	0.812	<0.00001	<0.00001
MS4A1 (CD20)	B cells	BLK	0.812	<0.00001	<0.00001
MS4A1 (CD20)	TFH	BLR1 (CXCR5)	0.811	<0.00001	<0.00001
CD19	B cells	HLA-DOB	0.796	<0.00001	<0.00001
HLA-DOB	B cells	CD19	0.796	<0.00001	<0.00001
CD19	TFH	BLR1 (CXCR5)	0.782	<0.00001	<0.00001
BLK	B cells	CD19	0.773	<0.00001	<0.00001
CD19	B cells	BLK	0.773	<0.00001	<0.00001
HLA-DOB	TFH	BLR1 (CXCR5)	0.722	<0.00001	<0.00001
HLA-DOB	T cells	CD247 (CD3Z)	0.705	<0.00001	<0.00001
HLA-DOB	T cells	CD6	0.702	<0.00001	<0.00001
CD19	T cells	CD6	0.700	<0.00001	<0.00001
HLA-DOB	B cells	MS4A1 (CD20)	0.697	<0.00001	<0.00001
MS4A1 (CD20)	B cells	HLA-DOB	0.697	<0.00001	<0.00001
BLK	TFH	BLR1 (CXCR5)	0.696	<0.00001	<0.00001
CD19	Th1 cells	CD38	0.691	<0.00001	<0.00001
HLA-DOB	T cells	CD2	0.680	<0.00001	<0.00001
CD19	T cells	CD247 (CD3Z)	0.677	<0.00001	<0.00001
HLA-DOB	T cells	CD28	0.677	<0.00001	<0.00001
HLA-DOB	Th1 cells	CTLA4	0.676	<0.00001	<0.00001
HLA-DOB	T cells	CD3G	0.672	<0.00001	<0.00001
CD19	T cells	CD3G	0.647	<0.00001	<0.00001
CD19	CD8 T cells	CD8A	0.645	<0.00001	<0.00001
CD19	TFH	CXCL13	0.643	<0.00001	<0.00001
HLA-DOB	CD8 T cells	CD8A	0.638	<0.00001	<0.00001
HLA-DOB	T cells	ZAP70	0.633	<0.00001	<0.00001
HLA-DOB	Th1 cells	STAT4	0.626	<0.00001	<0.00001
HLA-DOB	DC	CD209	0.624	<0.00001	<0.00001
HLA-DOB	T helper cells	CD4	0.624	<0.00001	<0.00001
HLA-DOB	Cytotoxic cells	GZMK	0.624	<0.00001	<0.00001
BLK	T cells	ZAP70	0.623	<0.00001	<0.00001
MS4A1 (CD20)	Cytotoxic cells	GZMK	0.617	<0.00001	<0.00001
HLA-DOB	Th1 cells	CD38	0.616	<0.00001	<0.00001
HLA-DOB	Tgd	TRD@	0.611	<0.00001	<0.00001
MS4A1 (CD20)	T cells	CD247 (CD3Z)	0.611	<0.00001	<0.00001
HLA-DOB	T cells	CD3E	0.610	<0.00001	<0.00001
BLK	B cells	HLA-DOB	0.610	<0.00001	<0.00001
HLA-DOB	B cells	BLK	0.610	<0.00001	<0.00001
CD19	Cytotoxic cells	GZMK	0.609	<0.00001	<0.00001
MS4A1 (CD20)	T cells	CD6	0.608	<0.00001	<0.00001
CD19	T cells	CD2	0.603	<0.00001	<0.00001
MS4A1 (CD20)	T cells	CD28	0.600	<0.00001	<0.00001
CD19	iDC	CD1A	0.010	0.91	ns
CD19	Cancer cells	CCND1	-0.220	0.02	ns
BLK	Macrophages	CD68	-0.140	0.13	ns
CD19	Macrophages	FN1	0.100	0.27	ns
CD19	Neutrophils	IL8RA	0.060	0.54	ns
HLA-DOB	Eosinophils	GPR44	0.021	0.02	ns

Table S5

Univariate analysis of Disease-free survival (DFS) among patients with UICC-TNM Stage I/II/III/IV colorectal cancer (cohort 107) according to immune parameters						
	Disease-free survival (DFS)			Hazard ratio (95% CI)	P value*	
	Predictive Accuracy (%) c-index	C τ				
According to clinical parameters						
CD20-CT	54.80	56.13	Lo Hi	1.40 (0.96-2.06)*** 1.00 (reference)	ns	
CD20-CT/CXCL13	64.77	66.36	LoLo Het HiHi	4.49 (1.95-10.31)*** 1.95 (1.01-3.75)*** 1.00 (reference)	0.0072** ns	s
CD20-IM	60.33	59.77	Lo Hi	4.04 (2.17-7.56)*** 1.00 (reference)	<0.0001**	s
CD20-IM/CXCL13	69.80	71.03	LoLo Het HiHi	9.56 (3.59-25.44)*** 3.18 (1.55-6.51)*** 1.00 (reference)	<0.0001** 0.0353**	s
CD20-CT/CD20-IM	59.16	61.67	LoLo Het HiHi	3.75 (1.85-7.61)*** 0.82 (1.4-0.48)*** 1.00 (reference)	0.0025** ns	s
CD3-CT	64.11	64.27	Lo Hi	4.05 (2.22-7.39)*** 1.00 (reference)	<0.0001**	s
CD3-CT/CXCL13	69.76	71.05	LoLo Het HiHi	8.37 (3.34-20.97)*** 2.21 (1.13-4.32)*** 1.00 (reference)	<0.0001** ns	s
CD3-IM	61.99	62.04	Lo Hi	2.34 (1.32-4.14)*** 1.00 (reference)	0.0880**	
CD3-IM/CXCL13	66.90	67.96	LoLo Het HiHi	2.67 (1.34-5.35)*** 1.19 (1.02-1.38)*** 1.00 (reference)	0.0090** 0.1872**	s
CD3-CT/CD3-IM	68.75	69.36	LoLo Het HiHi	7.03 (3.06-16.18)*** 1.91 (1.06-3.47)*** 1.00 (reference)	<0.0001** ns	s
CD8-CT	64.64	62.67	Lo Hi	2.87 (1.66-4.96)*** 1.00 (reference)	0.0074**	s
CD3-CT/CXCL13	69.83	69.91	LoLo Het HiHi	7.81 (3.03-20.11)*** 2.16 (1.09-4.28)*** 1.00 (reference)	0.0001** ns	s
CD8-IM	64.11	62.37	Lo Hi	2.52 (1.34-4.74)*** 1.00 (reference)	0.1318**	
CD8-IM/CXCL13	66.44	66.31	LoLo Het HiHi	3.5 (1.39-8.87)*** 0.93 (1.09-0.78)*** 1.00 (reference)	0.1705** ns	
CD8-CT/CD20-IM	70.26	67.90	LoLo Het HiHi	21.5 (2.97-21.5)*** 7.68 (2.14-7.68)*** 1.00 (reference)	<0.0001** 0.0001**	s
CD8-CT/CD8-IM	71.49	70.75	LoLo Het HiHi	9.14 (3.39-24.59)*** 1.24 (0.88-1.73)*** 1.00 (reference)	<0.0001** ns	s
CD20-IM/CD8-CT/CD8-IM	64.01	63.29	LoLoLo Het HiHiHi	12.49 (2.46-63.46)*** 2.83 (1.24-6.47)*** 1.00 (reference)	0.0083** ns	s
CD45RO-CT	65.35	65.95	Lo Hi	3.18 (1.76-5.75)*** 1.00 (reference)	0.0039**	s
CD45RO-CT/CXCL13	69.93	70.97	LoLo Het HiHi	6.27 (2.58-15.23)*** 2.16 (1.04-4.51)*** 1.00 (reference)	0.0004** ns	s
CD45RO-IM	62.07	62.49	Lo Hi	6.20 (1.8-21.32)*** 1.00 (reference)	0.0257**	s
CD45RO-IM/CXCL13	68.36	69.28	LoLo Het HiHi	12.87 (1.99-83.19)*** 6.06 (0.89-41.13)*** 1.00 (reference)	0.0214** ns	s
CD45RO-CT/CD45RO-IM	71.19	72.92		8.79 (2.37-32.68)*** 1.63 (0.83-3.21)*** 1.00 (reference)	0.0031** ns	s
CD20-IM/CD45RO-CT/CD45RO-IM	64.62	65.78	LoLoLo Het HiHiHi	11.29 (2.56-49.78)*** 3.18 (1.08-9.32)*** 1.00 (reference)	0.0047** ns	s

All categorical covariates are transformed into numerical ones before they enter into the cox model. The transformation rule is indicated next to the parameter name. C τ : time-dependent c-index presentation.

*Log-rank P value. **P value correction with Altman et al. *** Corrected by Hollaender et al. s: significant. CI denotes confidence interval.

Table S6

Comparison of cohorts according to clinical parameters

Cohorts	Percentage (total number) of patients			<i>P</i> -value*
	Cohort1 (105pts)	Cohort2 (153pts)	Cohort3 (107pts)	
UICC (TNM) stage				0.1918
I	20 (19)	37 (24.2)	12 (11.2)	
II	34 (32.4)	40 (26.1)	33 (30.8)	
III	29 (27.6)	44 (28.8)	31 (29)	
IV	22 (21)	32 (20.9)	31 (29)	
Tumor (T) stage †				0.0861
pTis-1	6 (5.7)	11 (7.2)	2 (1.9)	
pT2	16 (15.2)	30 (19.6)	13 (12.1)	
pT3	72 (68.6)	85 (55.6)	77 (72)	
pT4	11 (10.5)	27 (17.6)	15 (14)	
N stage				0.562
N0	63 (60)	89 (58.2)	57 (53.3)	
N1	27 (25.7)	36 (23.5)	25 (23.4)	
N2	15 (14.3)	28 (18.3)	25 (23.4)	
M stage				0.2641
M0	83 (79)	121 (79.1)	76 (71)	
M+	22 (21)	32 (20.9)	31 (29)	
Age (yrs)				0.9903
< 65	28 (26.7)	45 (29.4)	32 (29.9)	
65-75	25 (23.8)	36 (23.5)	25 (23.4)	
75-85	36 (34.3)	49 (32)	37 (34.6)	
> 85	16 (15.2)	23 (15)	13 (12.1)	
Gender				0.9816
Male	58 (55.2)	83 (54.2)	59 (55.1)	
Female	47 (44.8)	70 (45.8)	48 (44.9)	
Tumor Location				0.5348
Right colon	37 (35.2)	46 (30.1)	32 (29.9)	
Left colon	17 (16.2)	17 (11.1)	15 (14)	
Transverse colon	8 (7.6)	13 (8.5)	11 (10.3)	
Sigmoid colon	33 (31.4)	46 (30.1)	33 (30.8)	
Rectum	10 (9.5)	31 (20.3)	16 (15)	
Histological grade				0.9498
Well Differentiated	71 (67.6)	103 (67.8)	67 (63.2)	
Moderately Differentiated	31 (29.5)	45 (29.6)	36 (34)	
Poorly Differentiated	3 (2.9)	4 (2.6)	3 (2.8)	
Mucinous Colloid Type				0.7991
No	79 (75.2)	120 (78.4)	84 (78.5)	
Yes	26 (24.8)	33 (21.6)	23 (21.5)	
Neural Invasion				0.6025
No	96 (91.4)	135 (88.2)	93 (86.9)	
Yes	9 (8.6)	18 (11.8)	14 (13.1)	
Peritumoral Embolie				0.4507
No	87 (82.9)	121 (79.1)	81 (75.7)	
Yes	18 (17.1)	32 (20.9)	26 (24.3)	
Carcinomat Lymphangitis				0.9299
No	90 (85.7)	131 (85.6)	90 (84.1)	
Yes	15 (14.3)	22 (14.4)	17 (15.9)	
Occlusion				0.9614
No	90 (85.7)	132 (86.8)	92 (86.8)	
Yes	15 (14.3)	20 (13.2)	14 (13.2)	
Perforation#				0.8879
No	104 (99)	148 (97.4)	104 (98.1)	
Yes	1 (1)	4 (2.6)	2 (1.9)	
Treatment				0.7655
No	65 (61.9)	99 (64.7)	64 (60.4)	
Yes	40 (38.1)	54 (35.3)	42 (39.6)	

† The stage was determined by pathological (p) examination. Tis denotes carcinoma in situ, T1 tumor invading submucosa, T2 tumor invading muscularis propria, T3 tumor penetrating muscularis propria and invading subserosa, and T4 tumor completely through the intestine's wall and invading serosa and nearby tissues. #: Bowel perforation. * Fisher test *P*-value.

Table S7