SUPPLEMENTARY APPENDIX

Autophagy inhibition as a potential future targeted therapy for ETV6-RUNX1-driven B-cell precursor acute lymphoblastic leukemia

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SUPPLEMENTARY DATA

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SUPPLEMENTARY METHODS

Cell lines

B-cell precursor acute lymphoblastic leukemia (BCP-ALL) cell lines NALM6 (B-Other; IGH-DUX4), REH (ETV6-RUNX1), and 697 (TCF3-PBX1), T-ALL cell lines JURKAT (hypotetraploid) and LOUCY (del(5); t(16;20)) and human embryonic kidney cell line HEK293T were obtained from DSMZ (Braunschweig, Germany) and used only at low passages. REHS1 (REH subclone #1; ETV6-RUNX1) is a ETV6-RUNX1 positive cell line with identical genetic background as REH, but with different phenotypic characteristics (proliferation and drug resistance profiles). DNA fingerprinting was performed routinely on these cell lines to verify their genetic status. ALL cell lines were cultured in RPMI-1640 medium (Gibco, Life Technologies, Bleiswijk, the Netherlands) supplemented with 10% fetal calf serum (FCS) and 1% penicillin-streptomycin at 37 °C and 5% CO_2. HEK293T cells were cultured in high glucose Dulbecco's Modified Eagle's Medium with Glutamax (Gibco) supplemented with 10% FCS and 1% penicillin-streptomycin at 37 °C and 5% CO_2.

Isolation of CD34-positive hematopoietic cells from cord blood

Mononuclear cells were isolated from umbilical cord blood (UCB) using Lymphoprep sucrose-gradient centrifugation (1.077 g/ml, Nycomed Pharma, Oslo, Norway). Immunomagnetic cell separation, using magnetic beads coated with CD34 antibodies (Miltenyi Biotec, Gladbach, Germany), was performed to isolate CD34-positive hematopoietic progenitor cells (CB-$CD34^+$ cells). Cells were cultured in Iscove's Modified Dulbecco's Medium (Gibco) supplemented with 10% FCS, 50μM β-mercaptoethanol, 1% penicillin-streptomycin, 2mM glutamine, stem cell factor (SCF; 50ng/mL; Peprotech) and fms-like tyrosine kinase-3 ligand (Flt3L; 50 ng/mL; Peprotech) at 37°C and 5% CO2. UCB was obtained after informed consent was provided according to the Declaration of Helsinki.

Protocols were approved by the ethics committee of the Erasmus University Medical Centre in Rotterdam.

Isolation of primary BCP-ALL leukemic blasts from patients

Bone marrow aspirates were obtained from children with newly diagnosed BCP-ALL prior to treatment. Immunophenotype and genetic subtype were determined by local hospital procedures and monitored by the central diagnostic laboratory of the Dutch Childhood Oncology Group (DCOG) in The Hague. Primary BCP-ALL cells were subsequently isolated as previously described (1). We included 654 ALL patients including 172 ETV6-RUNX1 positive BCP-ALL patients and 401 ETV6-RUNX1 negative BCP-ALL patients. In short, mononuclear cells were collected using Lymphoprep sucrose-gradient centrifugation (1.077 g/ml, Nycomed Pharma, Oslo, Norway). To determine the percentage of leukemic cells in the mononuclear cell fraction, May-Grünwald-Giemsa staining was performed on cytospin preparations. If necessary, the samples were further enriched, to obtain at least 95% leukemic blasts, by depletion of normal hematopoietic cells using anti-CD lineage marker coated magnetic beads (Dynal, Oslo, Norway). Cells were cultured in RPMI Dutch-modified medium (Gibco) supplemented with 20% FCS, Insulin transferrin sodium selenite (ITS), glutamin and gentamycin at 37 °C and 5% CO_2. Bone marrow aspirates were obtained after informed consent was provided according to the Declaration of Helsinki. Protocols were approved by the ethics committee of the Erasmus University Medical Centre in Rotterdam.

Isolation and characterization of primary MSCs

Mesenchymal stromal cells (MSCs) were isolated, as previously described (2), from bone marrow aspirates collected during diagnostic procedures. In short, colony-forming MSCs were selected by culturing bone marrow aspirates in low glucose DMEM (Gibco)

supplemented with 15% FCS, 1% penicillin-streptomycin, vitamin C, and fibroblast growth factor (FGF) at 37°C and 5% CO_2. A panel of positive (CD44/ CD90/ CD105/ CD54/ CD73/ CD146/ CD166/ STRO-1) and negative surface markers (CD19/ CD45/ CD34) was used to characterize primary MSCs. Flow cytometric analysis was performed using the human mesenchymal stem cell marker antibody panel (R&D Systems, Minneapolis, MN, USA) and the monoclonal antibodies CD54-PE, CD73-PE, CD34-PE, and IgG1-PE (BD Biosciences, San Jose, CA, USA). The multilineage potential of the selected MSCs was confirmed by allowing the cells to differentiate towards adipocytes (Oil Red O staining), osteocytes (*Alizarin Red* S staining), and chondrocytes (Col2a/Thionine/Alcian Blue staining).

Production of bicistronic retrovirus and retroviral transduction of CB-CD34+ cells

To generate retrovirus, bicistronic retroviral DNA constructs were used expressing the *ETV6-RUNX1* fusion gene and enhanced Green Fluorescent Protein (eGFP). As a control, a construct expressing only eGFP was used. Both vectors consisted of a pMSCV promoter region, an internal ribosomal entry site and an ampicillin resistance cassette. HEK293T cells were co-transfected with these constructs and second-generation retroviral packaging vectors using XtremeGENE 9 tranfection reagents (Roche, Basel, Switzerland). Viral particles were collected in IMDM 48 hours after transfection. $CD34^+$ hematopoietic progenitors were pre-cultured overnight as described above, upon which cells were divided in two fractions. One fraction was transduced with ETV6-RUNX1-IRES-eGFP, while the other fraction was transduced with control EV-IRES-eGFP. Transductions were performed with fresh retrovirus in retronectin (Takara, Otsu, Japan) coated wells.

Fluorescence activated cell sorting of transduced CB-$CD34^+$ cells

Transduced CB-$CD34^+$ cells were sorted using a BD ARIA II sorter (BD Biosciences) after

staining with DAPI (Sigma) and PeCy7-conjugated CD34 antibody (BD Biosciences). The DAPI negative, CD34 positive and GFP positive population (see Fig. S8C for gating strategy) was used for further experiments. The purity of the sorts, as determined by flowcytometric analysis of the sorted cells, was in all cases at least 95% (see Fig. S4B for a representative post-sort analysis of purity).

Linear RNA amplification and gene expression profiling of CB-CD34$^+$ cells

After sorting, DAPI$^-$ CD34$^+$ GFP$^+$ CB-CD34$^+$ cells were lysed and RNA was extracted using Nucleospin RNA XS extraction columns according to manufacturer's protocol (Macherey-Nagel, Düren, Germany). Quality of RNA was determined by on-chip-electrophoresis using a RNA Pico Chip according to manufacturer's protocol (Agilent Technologies, Santa Clara, CA, USA). RNA Integrity scores (RIN) were higher than 8 for all samples. RNA was subsequently linearly amplified using the Nugen WT-Amplification™ pico system (Nugen, San Carlos, CA, USA). This system is based on RNA-dependent DNA polymerase activity and was previously reported to be most suitable for amplification and gene expression of picograms of input RNA (3). Samples were run on Affymetrix GeneChip Human Genome U133 Plus 2.0 microarrays (Santa Clara, CA, USA). Data were normalized using vsnRMA and analyzed using a linear mixed model (4). The model was fitted to ETV6-RUNX1, RUNX1-RUNX1T1 and EV data derived for each respective umbilical cord blood donor. Data derived from the RUNX1-RUNX1T1 transduced umbilical cord blood donors were omitted for further analyses in this manuscript and singularly used for estimating the within umbilical cord blood variance. Genes were considered differentially expressed when $p \leq 0.05$ after multiple testing correction using false discovery rate (FDR). Differential gene expression was visualized using TIBCO Spotfire software (Perkin Elmer, Waltham, MA, USA).

Microarray data are available in the ArrayExpress database (http://www.ebi.ac.uk/arrayexpress) under accession number E-MTAB-3466.

Gene expression profiling of primary BCP-ALL leukemic blasts from patients

Sample preparation and gene expression profiling of leukemic blasts derived from bone marrow aspirates was performed as earlier described (5). In short, DNA and total RNA were isolated using TRIzol reagents (Invitrogen Life Technologies, Breda, the Netherlands) or using the QIAamp DNA Blood mini kit (Qiagen, Venlo, the Netherlands) in accordance with the manufacturer's protocol and subsequently RNA quality was determined using a Bioanalyzer 2100 (Agilent, Amstelveen, the Netherlands). Only samples with an RNA integrity value >7 were processed further. cDNA and cRNA were synthesized using an in vitro transcription one-cycle kit (Affymetrix, Santa Clara, CA). Affymetrix U133 plus 2.0 gene-expression microarrays were processed, and data were extracted, as described previously (1). Microarray data are available in the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo/).

Ingenuity Pathway Analysis

Gene networks were generated and functional analysis of differential gene expression was performed using QIAGEN's Ingenuity Pathway Analysis (IPA, QIAGEN, Redwood City, USA). The expected increase or decrease of biological functions, based on the observed change in gene expression, was defined as a regulation Z score and was considered significant when larger than 2 or smaller than -2. P-values represent results of a right-tailed Fisher's Exact Test after Benjamini-Hochberg multiple testing correction.

Western blot

For protein analysis, cells were lysed using a cold lysis buffer containing 25 mM Tris pH 7.4, 150 mM NaCl, 5mM EDTA pH 8.0, 1% Triton X-100, 10% Glycerol, 10 mM Sodium-pyrophosphate, 1 mM Sodium-orthovanadate, 10 mM Glycerolphosphate, Dithiothreitol, Phenylmethylsulfonyl Fluoride, Aprotinin and Sodium-Fluoride. Equal amounts of protein were separated on a 10% acrylamide gel and subsequently blotted on a nitrocellulose membrane using the Trans-Blot Turbo Transfer System (Bio-rad, Hercules, CA, USA). Primary antibodies used were: β-actin (ab6276, Abcam, Cambridge, UK), LC3B (#2775, Cell Signaling, Danvers, MA, USA), SQSTM1/p62 (#8025, Cell Signaling), Vps34 (#3358, Cell Signaling) and Vps34 (#4263, Cell Signaling). Fluorescently labeled secondary IRDye antibodies were purchased from LI-COR Biosciences (Lincoln, NE, USA) and blots were scanned using an Odyssey Infrared Imaging System (LI-COR Biosciences).

Reverse Phase Protein Array

Reverse phase protein arrays were performed in collaboration with prof. dr. E. Petricoin (George Mason University, Manassas, VA, USA) as previously described (6). In short, normal bone-marrow samples and pediatric BCP-ALL patient cells were lysed in Tissue Protein extraction reagent (T-PER; Pierce, Thermo Scientific, Waltham, MA, USA), containing 300mM NaCl, 1 mM orthovanadate and protease inhibitors. Lysates were spotted twice in triplicate on glass-backed nitrocellulose-coated array slides. Reverse-phase protein arrays were performed according to manufacturer's protocol. Data were normalized for total protein levels and was corrected for background staining. Primary antibodies used were: Vps34 (#3358 and #4263, Cell Signaling), and SQSTM1/p62 (#8025, Cell Signaling).

siRNA knockdown

Silencing of ETV6-RUNX1 and Vps34 in REH cells or ETV6-RUNX1 transduced CB-

$CD34^+$ cells was achieved by transfection of siRNAs with Dharmafect 4 (Thermo Scientific). 72 hours after transfection, cells were transfected again. Twenty-four hours after the second hit, cells were analyzed. The following siRNAs were used to silence ETV6-RUNX1: siETV6-RUNX1 #1: CCAUUGGGAGAAUAGC**AGA**AUGCAU; siETV6-RUNX1 #5: UGGGAGAAUAGC**AGA**AUGCAUACUU (7). Vps34 targeting siRNAs were purchased from Origene (Rockville, MD, USA).

Real-time PCR

RNA was extracted using Nucleospin RNA XS extraction columns according to manufacturer's protocol (Macherey-Nagel, Düren, Germany), upon which cDNA was synthesized. mRNA levels were quantified by incorporation of SYBR green (Thermo Scientific) during quantitative real-time PCR (Applied Biosystems 7900HT). Primers are described in supplementary methods.

Luciferase reporter assays

To study Vps34 promoter activity, a pEZX reporter construct consisting of a 1.4 kB region (-1383 to +58) of the Vps34 promoter upstream of the Gaussia luciferase gene (Genecopoeia, Rockville, MD, USA; HPRM12127) was used. The reporter construct was transfected in HEK293T cells together with the constructs of interest. In all experimental conditions, the amount of transfected DNA was equalized per backbone. At the end of the experiment, GFP expression was quantified in each sample by flow cytometric analysis and used to normalize luciferase activity. Constructs are described in supplementary methods.

MTT cytotoxicity assay

The sensitivity of ALL cell lines to hydroxychloroquine was analyzed using 3-(4,5-

dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay as described before (8). Cell survival was determined after 4 days of hydroxychloroquine exposure. Background signal was subtracted and experimental conditions are depicted as the percentage of signal compared to the untreated control.

Lentiviral knockdown of Vps34

Lentivirus was produced by transfecting HEK293T cells with second generation lentiviral helper vectors pPax2 (Addgene plasmid 12260) and VSV-G envelope (pMD2G; Addgene plasmid 12259) together with pLKO.1 Mission vector (Sigma) targeting *PIK3C3* (Vps34). Transfection was performed using XtremeGENE transfection reagent according to manufacturer's protocol (Promega, Madison, WI, USA). Target sequences used to silence PIK3C3 were: GCTGCACAACAGACATTTGTA (shVps34#1; TRCN0000037798); GAGGCAAATATCCAGTTATAT (shVps34#2; TRCN0000196290); CCACGAGAGATCAGTTAAATA (shVps34#3; TRCN0000037794); GAGATGTACTTGAACGTAATG (shVps34#4; TRCN0000196840). Target sequence for used non-mammalian shRNA control vector was CAACAAGATGAAGAGCACCAA (NSC; SHC002). Virus was collected and concentrated by ultracentrifugation. For every experiment and every cell line, virus was titrated to obtain a transduction efficiency of 90%. This condition was equal to an MOI of 2.5. Cell lines were transduced using a spin-infection protocol. Cells were subsequently selected using the puromycin selection marker. A MACSQuant Analyzer (Miltenyi Biotec, Germany) was used to determine the number of viable, Propidium Iodide negative, cells.

Confocal laser scanning microscopy

Autophagy levels were visualized by the number and volume of LC3B positive vesicles. To quantify autophagy levels, confocal scanning microscopy was performed. REH cells were allowed to attach to a glass slide coated with 10 µg/mL fibronectin (Sigma) for 30 minutes. Cells were subsequently fixated using 3% formaldehyde in PBS for 10 minutes at room temperature. After fixation, slides were blocked with 10% FCS and 0.2% goat serum in PBS and subsequently incubated overnight at 4°C with LC3B antibody (#2775, Cell Signaling). Slides were subsequently washed twice with PBS and stained with goat-anti-rabbit-Alexa 488 secondary antibody for 1 hour. After three PBS washes, slides were stained with DAPI (Sigma) for 5 minutes and mounted with ProLong Gold antifade reagent (Life Technologies). Images were acquired using a confocal laser scanning microscope (Leica SP5). Sequential scanning of different channels was performed at a resolution of 1024 x 1024 pixels in the *x y* plane and 0.15 µm steps in *z*-direction.

The system was equipped with a 63× plan-apochromat oil 1.4 NA DIC objective. The pinhole diameter was set to 1 airy unit (95.5 µm). DAPI and LC3B-anti-rabbit-Alexa 488 were excited with a 488-nm Argon laser and a 405-nm Diode-Pumped Solid-State laser, respectively. Fiji software was used for imaging processing. Brightness and contrast were optimized and applied to the entire image. Z-project using all slides and maximum intensity projection was used to show the number of LC3B-positive vesicles in Figure 4. For quantification of LC3B-positive vesicles, Z-stacks of images were deconvolved and processed using Huygens Professional software. Both the number and the average volume of vesicles were analyzed. For the quantification of number and volume of LC3B-positive vesicles, we excluded cells with atypical nuclei. For each experiment, LC3B-positive vesicles were quantified in at least 6 cells. 3D-deconvolved images shown in Fig. 3 were created using the same software.

Cell viability assays

Primary patient cells (1 x 10^6 cells) were co-cultured with or without primary mesenchymal stromal cells (5 x 10^4) for five days in a 24-well plate at 37 °C and 5% CO_2. Stromal cells were allowed to attach prior to the start of the experiment. Before the start of each experiment, leukemic cells were screened for CD19 positivity (Brilliant Violet 421 anti-human CD19 antibody). After five days of culture the percentage of viable leukemic cells was determined by flow cytometic analysis after staining with Brilliant Violet 421 anti-human CD19 antibody (Biolegend), FITC Annexin V (Biolegend), and Propidium Iodide (PI; Sigma) Primary leukemic cells were exposed to L-Asparaginase, Prednisolone or 6-Mercaptopurine in a concentration that was lethal to 50% of the patient derived leukemic cells (IC_{50}) as determined upfront by a 4-day MTT assay (1).

Primers used for real-time PCR

Primers for *ETV6-RUNX1* were 5'-TCGGGAAGACCTGGCTTACA-3' (forward) and 5'-TGGCATCGTGGACGTCTCTA-3' (reverse). Primers for *PIK3C3* (Vps34) were 5'-CCTGGAAGACCCAATGTTGAAG-3' (forward) and 5'-CGGGACCATACACATCCCAT-3' (reverse) or 5'-AGTTCCCGGTGTAGGTGGTA-3' (forward) and 5'-ACATTGGGTCTTCCAGGACA-3' (reverse). To normalize data, *HPRT* or *RPS20* were used as reference genes. Primers used were: *HPRT* 5'-TGACACTGGCAAAACAATGCA-3' (forward) and 5'-GGTCCTTTTCACCAGCAAGCT (reverse); *RPS20*: 5′-AAGGGCTGAGGATTTTTG-3′ (forward) and 5′-CGTTGCGGCTTGTTAG-3′ (reverse).

Constructs used for luciferase reporter assays

Constructs used were: pCMV5-RUNX1 (Addgene; plasmid 12426(9)); pCMV5-CBFβ

(Addgene; plasmid 12427(9)), pMSCV-ETV6-RUNX1 (a kind gift from Dr. Owen Williams, London, UK) , pCMV6-XL5-HEY1 (Origene; plasmid SC115467), pcDNA3-EGR1 (Addgene; plasmid 11729(10)), pMT2-GATA1 (Addgene; plasmid 13626(11)), pFLAG-CMV2-GATA2 (Addgene; plasmid 1418(12)).

Statistical analysis

Statistical analysis of microarray data of paired (EV-eGFP$^+$ versus ETV6-RUNX1-eGFP$^+$) CB-CD34$^+$ was performed using a linear mixed model in which multiple testing correction was applied by FDR (see also Material and Methods section on linear RNA amplification and gene expression profiling of CB-CD34$^+$ cells). Microarray data of primary cells from ALL patients was normalized using vsnrma, batch effects were removed using the empirical Bayes method, and data were analyzed using LIMMA and FDR multiple testing correction.
Both the Student's t-test and the Student's paired t-test were used as statistical test when applicable. Bar graphs represent the mean of biological replicates. Error bars represent standard error of the mean (S.E.M.).

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SUPPLEMENTARY FIGURE LEGENDS

Supplementary Figure S1. Ectopic expression of ETV6-RUNX1 in healthy CD34$^+$ progenitors activates pro-proliferative and pro-survival transcriptional networks

To generate retrovirus, bicistronic retroviral DNA constructs were used co-expressing ETV6-RUNX1 and eGFP. CD34-positive hematopoietic progenitors (CB-CD34$^+$ cells) were isolated from cord blood, upon which cells were divided in two fractions. One fraction was transduced with ETV6-RUNX1-IRES-eGFP, while the other fraction was transduced with control EV-IRES-eGFP (n = 5 biological replicates). Forty hours after transduction, CD34$^+$ DAPI$^-$ eGFP$^+$ hematopoietic progenitors were sorted (for gating strategy see supplementary Figure 1). After sorting, RNA was extracted, checked for quality and linearly amplified. Gene expression analysis was subsequently performed using Affymetrix Genechip microarrays.

(**A**) Flowchart of the experimental approach.

(**B**) Heat map displaying gene probe sets that were either over-expressed (in red) or under-expressed (in blue) in comparison to the mean expression of all probe sets. Forty hours after transduction, 196 gene probe sets were significantly ($p \leq 0.05$; FDR-adjusted) over-expressed or under-expressed in ETV6-RUNX1 positive CB-CD34$^+$ cells in comparison to control CB-CD34$^+$ cells. Data were analyzed using a linear mixed model. Genes were considered differentially expressed when $p \leq 0.05$ after multiple testing correction using false discovery rate (FDR).

(**C**) Ingenuity pathway analysis of the differentially expressed genes was performed to elucidate the interconnected transcriptional network present within this gene set. The level of up- (red) and down-regulation (blue) of genes was visualized by the intensity of the colors. Direct relationships were marked with undotted arrows. Indirect relationships were marked with dotted arrows.

(**D**-**E**) Ingenuity pathway analysis was used to analyze gene ontology (GO) functional categories and activation of disease/function annotation based on current literature. Functional categories inducing a pro-survival or a pro-proliferative state in ETV6-RUNX1-positive HPCs and the differentially regulated genes responsible for this prediction are shown.

Supplementary Figure S2. Pathway analysis of ETV6-RUNX1 positive CD34+ hematopoietic progenitors.

(**A**) Ingenuity pathway analysis was used to analyze gene ontology (GO) functional categories and activation of disease/ function annotation based on current literature. Significantly regulated functional categories are listed with their p-value (right-tailed Fisher Exact Test after Benjamini-Hochberg multiple testing correction) and regulation Z-score. This analysis reflect the pathways induced in CB-CD34+ cells by ETV6-RUNX1 40 hours after transduction

(**B**) Schematic representation of differentially regulated genes predicted to induce cellular homeostasis.

(**C**) Ingenuity pathway analysis was used to analyze gene ontology (GO) functional categories and activation of disease/function annotation based on current literature. Table shows annotations that were similarly activated in ETV6-RUNX1 positive BCP-ALL patients and ETV6-RUNX1 positive CB-$CD34^{+}$ cells (40 hours after transduction). The top 500 differentially expressed genes between ETV6-RUNX1 positive and EVT6-RUNX1 negative patients in the Erasmus MC cohort were used for this analysis.

Supplementary Figure S3. Vps34 is recurrently up-regulated in ETV6-RUNX1 positive BCP-ALL.

We compared gene expression levels in ETV6-RUNX1 positive ALL cells with gene expression levels in ETV6-RUNX1 negative ALL cells. We used 5 cohorts in which ETV6-RUNX1 positive BCP-ALL patients were included and gene expression data were publically available. In addition, we analyzed differential gene expression in an ETV6-RUNX1 knockdown study performed in an ETV6-RUNX1 positive leukemic cell line. “Yes” represents the differential expression of the gene in the particular study. “No” represents no differential expression of the gene in the study. “?” represents unavailable data.

Supplementary Figure S4. Early effects of ETV6-RUNX1 expression in CB-CD34+ cells

(**A**) Flow chart used to study the early effects of ETV6-RUNX1 fusion protein expression in cord blood-derived CD34-positive hematopoietic progenitors (CB-CD34+ cells). CB-CD34+ cells were isolated from cord blood. Per cord blood donor, cells were divided in two fractions of which one was transduced with ETV6-RUNX1-IRES-GFP and the other fraction with control EV-IRES-GFP. Viable transduced HPCs were sorted after 20 hours based on DAPI negativity and CD34 and GFP positivity. RNA was extracted from sorted CB-CD34+ cells, controlled for quality and linearly amplified after which gene expression analysis was performed with Affymetrix GeneChip Human Genome U133 Plus 2.0 microarrays.

(**B**) Graphs showing the gating strategy used to sort alive, CD34-positive, transduced cord blood cells. First living cells were gated based on FSC, SSC and the absence of DAPI incorporation. CD34-positive cells were selected based on the positive expression compared to an isotype control. Finally, CD34-positive transduced cells were sorted based on eGFP expression. Post-sort purity was more than 95%.

(**C**) Graph showing gene expression levels of *ETV6-RUNX1* relative to housekeeping gene RPS20 quantified with Q-PCR (n = 5). EV represents levels in CB-CD34+ cells transduced

with the empty vector control. ETV6-RUNX1 represents levels in CB-CD34+ cells transduced with the ETV6-RUNX1 vector. Data are means ± SEM; *** $p \leq 0.001$.

(**D**) Heat map showing which gene probe sets are relatively over-expressed (in red) and which gene probe sets are relatively under-expressed (in blue) compared to the mean expression of all differentially regulated gene probe sets. 203 gene probe sets were significantly ($p \leq 0.05$; FDR-adjusted) over-expressed or under-expressed when ETV6-RUNX1 positive HPCs were compared to control HPCs 20 hours after transduction.

Supplementary Figure S5. Vps34 expression in ETV6-RUNX1 positive cells

(**A**) Graph showing the 2log expression (at initial diagnosis) of the gene probe set mapped to Vps34 in a cohort of 98 pediatric ALL patients that eventually relapsed after treatment (relapsed patients in the Erasmus MC cohort). Grey dashed line represents mean expression of all patients. Gene expression of ETV6-RUNX1 positive patients was compared to gene expression of all other B-ALL patients (excluding T-ALL): *** FDR-adjusted $p = 5.11*10^{-6}$.

(**B**) Graph showing gene expression of ETV6-RUNX1 after knockdown of the ETV6-RUNX1 fusion protein. mRNA levels were determined in REH (n=2) and ETV6-RUNX1 transduced CB-CD34+ cells (n=1) by Q-PCR, normalized to HPRT, and compared to the average expression of cells transfected with scrambled control siRNAs ($n = 3$, $p \leq 0.05$).

Supplementary Figure S6. Autophagy levels are high in ETV6-RUNX1 positive BCP-ALL cells

(**A**) Western blot analysis of proteins important in the autophagy pathway, namely Vps34, p62 (sequestosome 1), and LC3B in primary patient BCP-ALL cells (n=5 for ETV6-RUNX1 positive BCP-ALL patients; n=6 for ETV6-RUNX1 negative BCP-ALL patients).

(**B**) Quantification of experiment performed in (**A**). Protein expression of Vps34 and p62 is relative to actin expression.

(**C**) Quantification of protein levels of Vps34 measured by reverse phase protein array (RPPA) in 10 normal bone marrow samples (nBM), 30 ETV6-RUNX1 positive primary BCP-ALL patient samples (ETV6-RUNX1+), and 29 B-Other primary BCP-ALL patient samples (BO). Data are means ± S.E.M.; * $p \leq 0.05$, *** $p \leq 0.001$.

(**D**) Representative confocal images of REH cells after permeabilization and staining with DAPI and LC3B antibody. Z-stacks were deconvolved using Huygens Professional software, after which number and volume of LC3B-positive vesicles could be quantified.

Supplementary Figure S7. Vps34 is essential for the survival of ETV6-RUNX1 positive leukemic cells

(**A**) ETV6-RUNX1-positive (REH and REHS1) and ETV6-RUNX1-negative (NALM6) BCP-ALL cells were lentivirally transduced with scrambled shRNA control (NSC) or two distinct Vps34 shRNA constructs. NI represents non-infected cells. Cells were cultured for 18 days. To determine the effect on proliferation, cell counts were performed every 2-3 days. The average increase in cell numbers per day. T-test was performed to compare control conditions (NSC) with Vps34 knockdown conditions (n = 3, ** $p \leq 0.01$, *** $p \leq 0.001$). Error bars represent S.E.M.

(**B**) ETV6-RUNX1-positive (REH) BCP-ALL cells were lentivirally transduced with scrambled shRNA control (NSC) or two distinct shRNA constructs to silence Vps34 expression. After 7 days of culture, flow cytometrical analysis was performed to determine the effect of Vps34 knockdown on survival and cell cycle progression. Representative FACS plots are shown (n = 3).

(**C**) Schematic representation of the different transcript variants of Vps34, based on currently available literature (Ensembl Genome Browser; ENSG00000078142) and the binding locations of shVps34#1-shVps34#4.

(**D**) Representative western blot showing the knockdown of Vps34 in REH cells.

(**E-F**) ETV6-RUNX1-positive (REH and REHS1) and ETV6-RUNX1-negative (NALM6) BCP-ALL cells were lentivirally transduced with scrambled shRNA control (NSC, black) or two distinct Vps34 shRNA constructs (grey; shVps34 #3 and shVps34#4). NI represents non-infected cells. Cells were cultured for 18 days. To determine the effect on proliferation, cell counts were performed every 2-3 days. Representative graphs are shown (**E**). The average increase in cell numbers per day is shown in **(F)**. T-test was performed to compare control conditions (NSC) with Vps34 knockdown conditions (n = 3, ** $p \leq 0.01$, *** $p \leq 0.001$). Error bars represent S.E.M.

(**G-H**) ETV6-RUNX1-positive (REH) BCP-ALL cells were lentivirally transduced with scrambled shRNA control (NSC) or two distinct shRNA constructs to silence Vps34 expression. After 7 days of culture, flow cytometrical analysis was performed to determine the effect of Vps34 knockdown on survival and cell cycle progression. The percentage of viable (AnnexinV positive, Propidium Iodide negative), actively cycling cells was determined using DyeCycle. Data were depicted as the percentage of cells in active cell cycle (S, G2, M stage) at day 7 after transduction (n = 2, * $p \leq 0.05$) (**G**). The percentages of early apoptotic (AnnexinV positive, Propidium Iodide negative) and late apoptotic (Propidium Iodide positive) cells were determined 7 days after transduction (n = 2, * $p \leq 0.05$, *** $p \leq 0.001$) (**H**). Error bars represent S.E.M.

Supplementary Figure S8. ETV6-RUNX1 positive ALL cells are relatively sensitive to treatment with hydroxychloroquine

(**A**) Bar graph showing the cell viability of HCQ-treated conditions (10 µg/ml) compared to HCQ-untreated conditions after 4 days (MTT). Green bars represent ETV6-RUNX1 positive

BCP-ALL cell lines. Black bars represent ETV6-RUNX1 negative BCP-ALL cell lines. Dark grey bars represent T-ALL cell lines.

(**B**) Calculation of IC_{50} concentrations of two ETV6-RUNX1-positive ALL cell lines (green), and two ETV6-RUNX1-negative ALL cell lines (black and gray). n = 4, *** $p \leq 0.001$. IC_{50} values for Jurkat cells were not reached during treatment with 40 µg/ml HCQ (the highest concentration used in this assay).

(**C**) Flow cytometrical gating strategy used to analyze survival after HCQ treatment of primary BCP-ALL patient samples in co-culture. First, forward and sideward scatter were used to gate living and apoptotic events. Second, primary mesenchymal stromal cells (MSCs) were gated out based on CD19-expression and autofluorescence in the Amcyan channel (events in red gate were excluded from analysis). Then, viable cells were gated based on Annexin-V and Propidium Iodide staining and subsequently based on CD19-expression. Percentage of living cells was calculated by dividing the number of AnnexinV negative, PI negative, CD19 positive events by the number of events after gating out the MSCs.

(**D**) Graph showing relative survival of primary ETV6-RUNX1 negative BCP-ALL cells after treatment with increasing concentrations of HCQ compared to untreated controls. Light grey bars represent treatment with 5 µg/ml HCQ. Grey bars represent treatment with 10 µg/ml HCQ. Experiment was performed in absence and presence of primary MSCs (n=3 for conditions in absence of MSCs, n = 5 for conditions in presence of MSCs).

Supplementary Figure S9. Autophagy inhibition sensitizes ETV6-RUNX1 positive BCP-ALL

(**A**) Primary ETV6-RUNX1-positive BCP-ALL cells were cultured in absence or presence of IC-50 concentrations of L-Asparaginase and increasing concentrations of HCQ. Flow cytometric analysis was performed to determine the percentage of non-apoptotic (Annexin V negative, Propidium Iodide negative, CD19 positive) cells (for gating strategy see

supplementary Figure 6d). First, the survival of primary leukemic blasts in presence of L-Asparaginase was compared to their survival in absence of L-Asparaginase (see supplementary Figure 7a for the effect of asparaginase in the absence of treatment with other effectors). Next, data was depicted as fold reduction compared to HCQ-untreated controls.

(**B**) Primary ETV6-RUNX1-positive BCP-ALL cells were co-cultured with primary MSCs in absence or presence of IC-50 concentrations of L-Asparaginase and increasing concentrations of HCQ. Flow cytometric analysis was performed to determine the percentage of non-apoptotic cells. The survival of primary leukemic blasts in presence of L-Asparaginase was compared to their survival in absence of L-Asparaginase. Next, data from individual patients was depicted as fold reduction compared to HCQ-untreated controls. Light grey bars represent treatment with 5 µg/ml HCQ. Grey bars represent treatment with 10 µg/ml HCQ. Dark grey bars represent treatment with 20 µg/ml HCQ. Experiment was performed twice with cells of patients #1 and #2.

(**C**) Co-culture experiments were performed with primary ETV6-RUNX1 positive BCP-ALL cells and MSCs. Cells were cultured in presence or absence of L-Asparaginase and increasing concentrations of HCQ. Flow cytometric analysis was performed to determine the percentage of non-apoptotic cells. The survival of primary leukemic blasts in presence of L-Asparaginase was compared to their survival in absence of L-Asparaginase. Next, data from individual patients was depicted as fold reduction compared to HCQ-untreated controls. Data were depicted as fold reduction compared to HCQ-untreated controls (n=4 for HCQ 2.5 µg/ml; n = 5 for HCQ 5 µg/ml and 10 µg/ml; n=3 for HCQ 20 µg/ml).

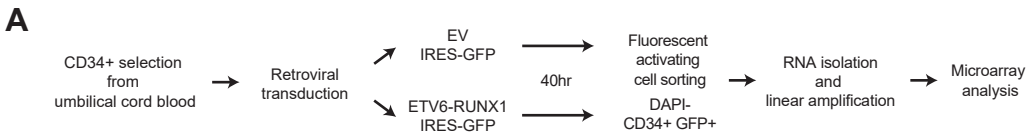
(**D**) Co-culture experiments were performed with primary ETV6-RUNX1 negative BCP-ALL cells and MSCs. Cells were cultured in presence or absence of L-Asparaginase and increasing concentrations of HCQ. Flow cytometric analysis was performed to determine the percentage of non-apoptotic cells. The survival of primary leukemic blasts in presence of L-Asparaginase

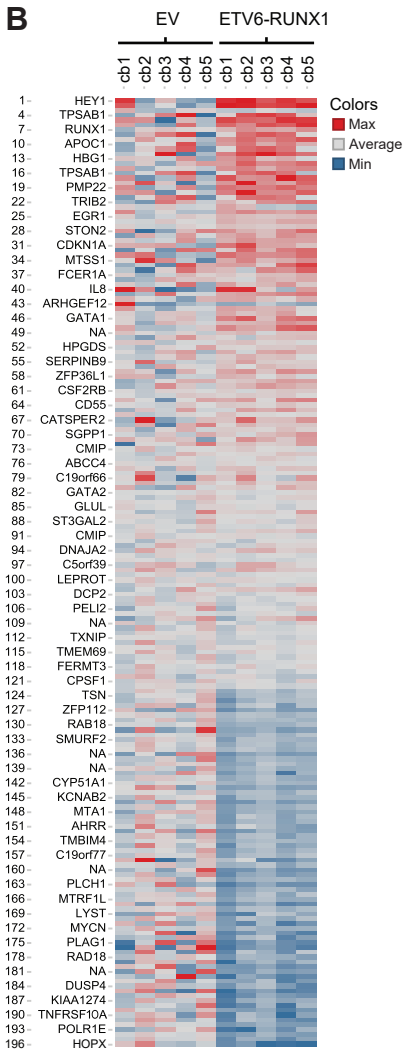
was compared to their survival in absence of L-Asparaginase. Next, data was depicted as fold reduction compared to HCQ-untreated controls (n = 3 for conditions in absence of MSCs, n = 5 for conditions in presence of MSCs).

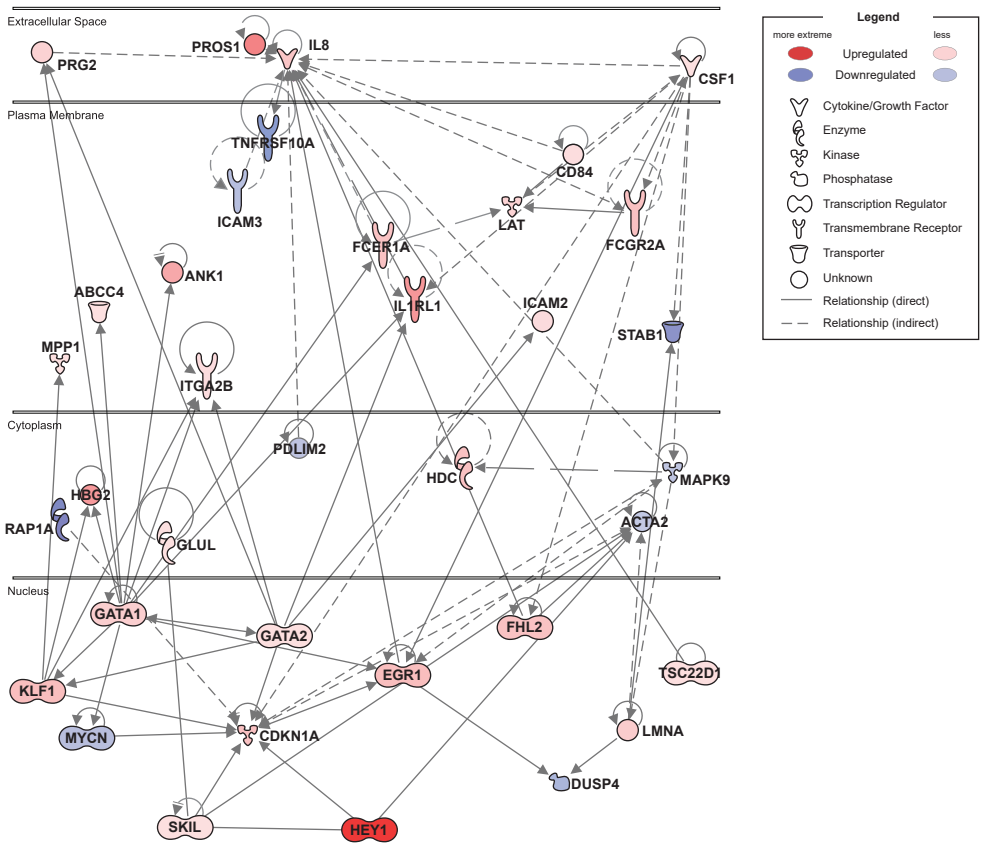
(**E/F**) Co-culture experiments were performed with primary ETV6-RUNX1 positive BCP-ALL cells and MSCs. Cells were cultured in presence or absence of Prednisolone (**E**) or 6-Mercaptopurine (**F**) and increasing concentrations of HCQ. Flow cytometric analysis was performed to determine the percentage of non-apoptotic (Annexin V negative, Propidium Iodide negative, CD19 positive) cells. The survival of primary leukemic blasts in presence of Prednisolone (**E**) of 6-Mercaptopurine (**F**) was compared to their survival in absence of these drugs. Next, data was depicted as fold reduction compared to HCQ-untreated controls (n = 5 for conditions in absence of MSCs, n = 7 for conditions in presence of MSCs for (**E**), n = 4 for conditions in absence of MSCs, n = 4 for conditions in presence of MSCs for (**F**)).

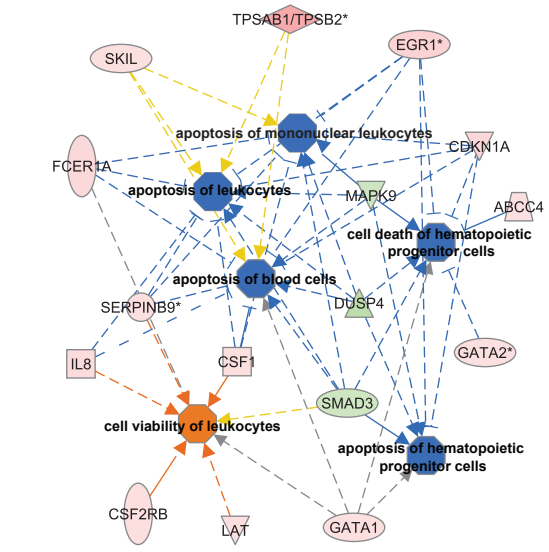
Error bars represent S.E.M.

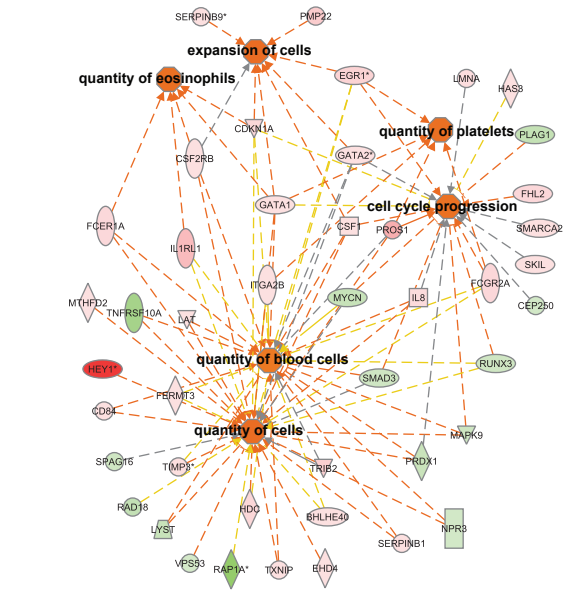
Supplementary Figure S1. Ectopic expression of ETV6-RUNX1 in healthy CD34+ progenitors activates pro-proliferative and pro-survival transcriptional networks











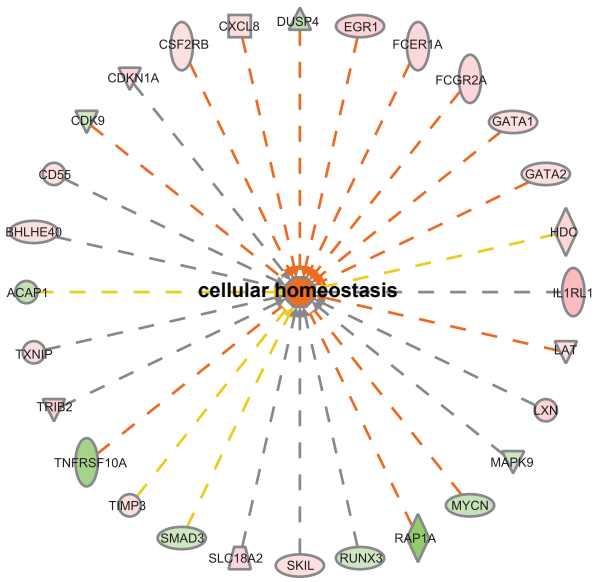
Supplementary Figure S2. Pathway analysis of ETV6-RUNX1 positive CD34+ hematopoietic progenitors

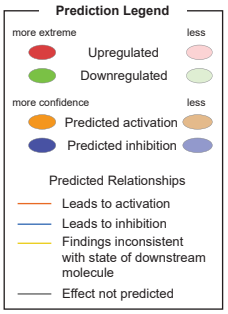
A

Diseases or Functions Annotation	p-Value	Activation z-score
survival of organism	3,93E-02	3,221
production of reactive oxygen species	4,49E-02	2,979
organization of cytoplasm	4,49E-02	2,612
expansion of cells	4,49E-02	2,578
quantity of cells	2,19E-03	2,554
differentiation of bone marrow cells	2,56E-02	2,412
degranulation of phagocytes	3,05E-03	2,355
cellular homeostasis	1,43E-02	2,297
aggregation of cells	1,51E-02	2,206
differentiation of HPCs	2,42E-02	2,187
quantity of blood platelets	4,49E-02	2,169
quantity of eosinophils	2,92E-02	2,125
binding of cells	9,47E-03	2,118
cell cycle progression	3,73E-02	2,042
engulfment of cells	2,19E-02	2,024
recruitment of leukocytes	2,44E-03	2,021
response of granulocytes	2,19E-02	2,000
fibrosis	4,49E-02	-2,126
apoptosis of hematopoietic progenitor cells	4,49E-02	-2,183
cell death of hematopoietic progenitor cells	1,70E-02	-2,211
inflammation of liver	1,51E-02	-2,236
apoptosis of blood cells	3,69E-02	-2,349
apoptosis of leukocytes	4,49E-02	-2,369
apoptosis of mononuclear leukocytes	4,49E-02	-2,401
hypertrophy of heart	4,49E-02	-2,425
organismal death	1,63E-03	-2,601

Activation Z-score
Colors
3,22
0.00
-2,60

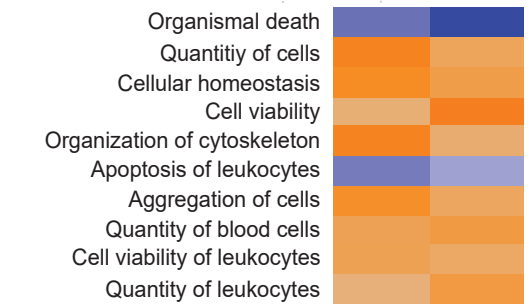
B





C

Pathway analysis of ETV6-RUNX1 positive CB-CD34+ and patients



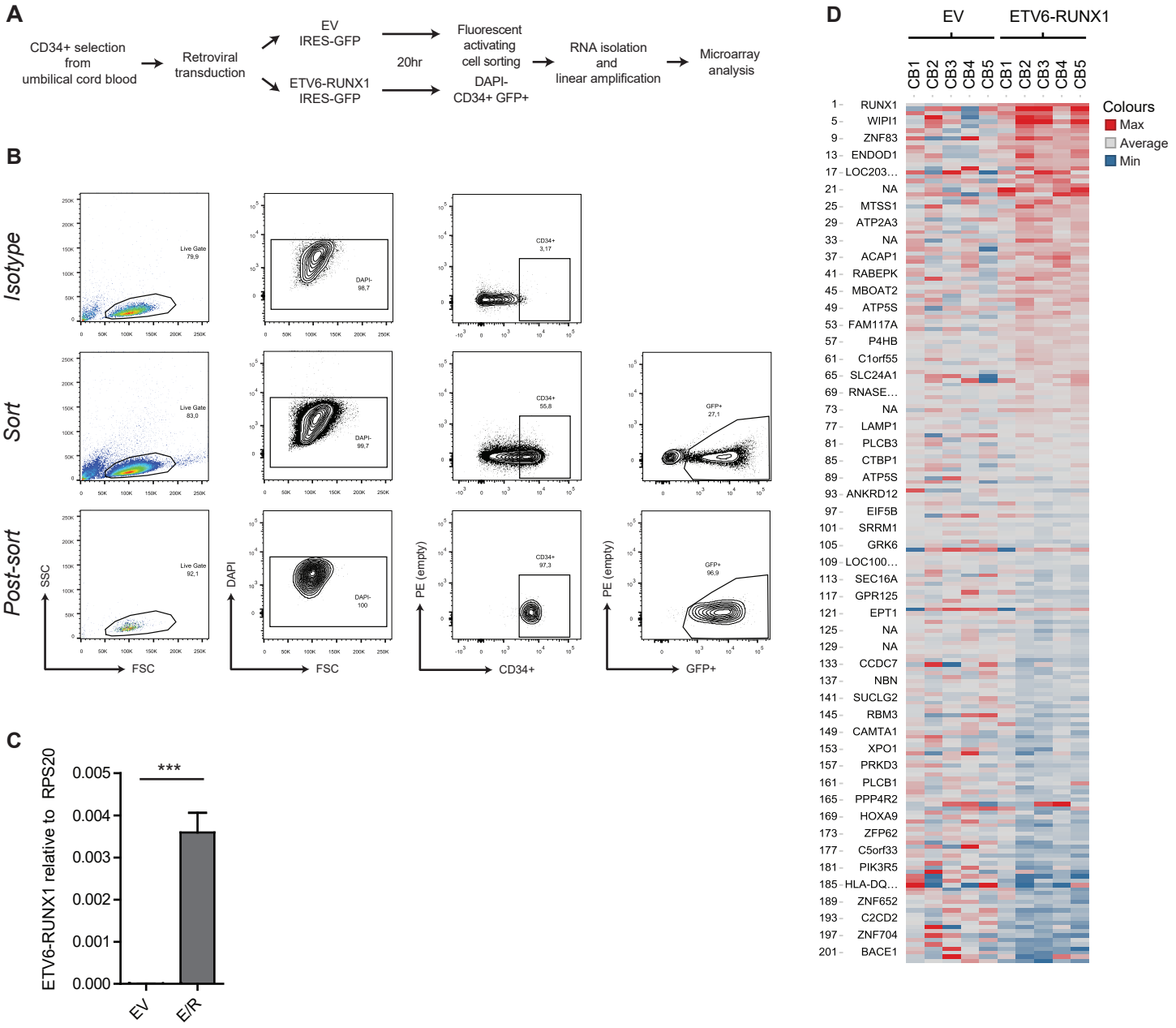
Activation Z-score
Colours
2.75
0.00
-5.16

	CB-CD34	Top500
Organismal death	p = 0.00163	p = 0.00553
Quantitiy of cells	p = 0.00219	p = 0.0522
Cellular homeostasis	p = 0.0143	p = 0.0946
Cell viability	p = 0.0135	p = 0.00816
Organization of cytoskeleton	p = 0.0449	p = 0.0214
Apoptosis of leukocytes	p = 0.0449	p = 0.150
Aggregation of cells	p = 0.0151	p = 0.150
Quantity of blood cells	p = 0.000202	p = 0.0404
Cell viability of leukocytes	p = 0.0308	p = 0.150
Quantity of leukocytes	p = 0.000930	p = 0.0517

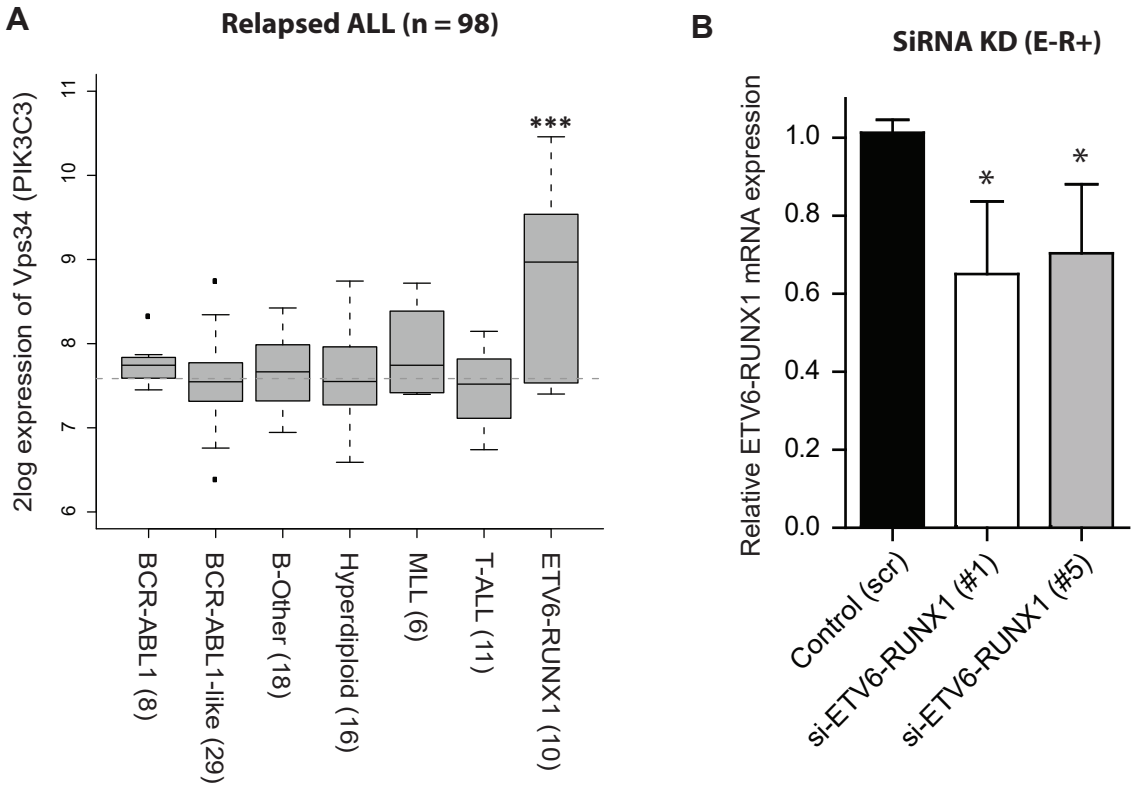
Supplementary Figure S3. Vps34 is recurrently up-regulated in ETV6-RUNX1 positive BCP-ALL.

	Patient cohorts					shRNA-KD E-R
	Yeoh	Den Boer	Gandemer	Andersson	Fine	Fuka
Gene Symbol	Cancer Cell 2002	Lancet Onc 2009	BMC Gen 2007	PNAS 2005	Blood 2004	PLoS One, 2011
PIK3C3 (Vps34)	yes	yes	yes	yes	?	yes
TCFL5	yes	yes	yes	no	yes	no
EPOR	yes	yes	no	no	yes	no
TUSC3	yes	yes	no	yes	?	no
ARHGEF4	yes	yes	yes	no	?	yes
TNFRSF21	yes	yes	no	yes	?	yes
ABHD3	yes	yes	no	yes	?	no
FCHSD2	yes	yes	no	yes	?	no
NOVA1	yes	yes	no	yes	?	no
IDI1	yes	yes	no	yes	?	no
KCNN1	yes	yes	no	no	?	no
CLIC5	yes	yes	no	no	?	no
TNS1	yes	yes	no	no	?	no
BIRC7	yes	yes	no	no	?	no

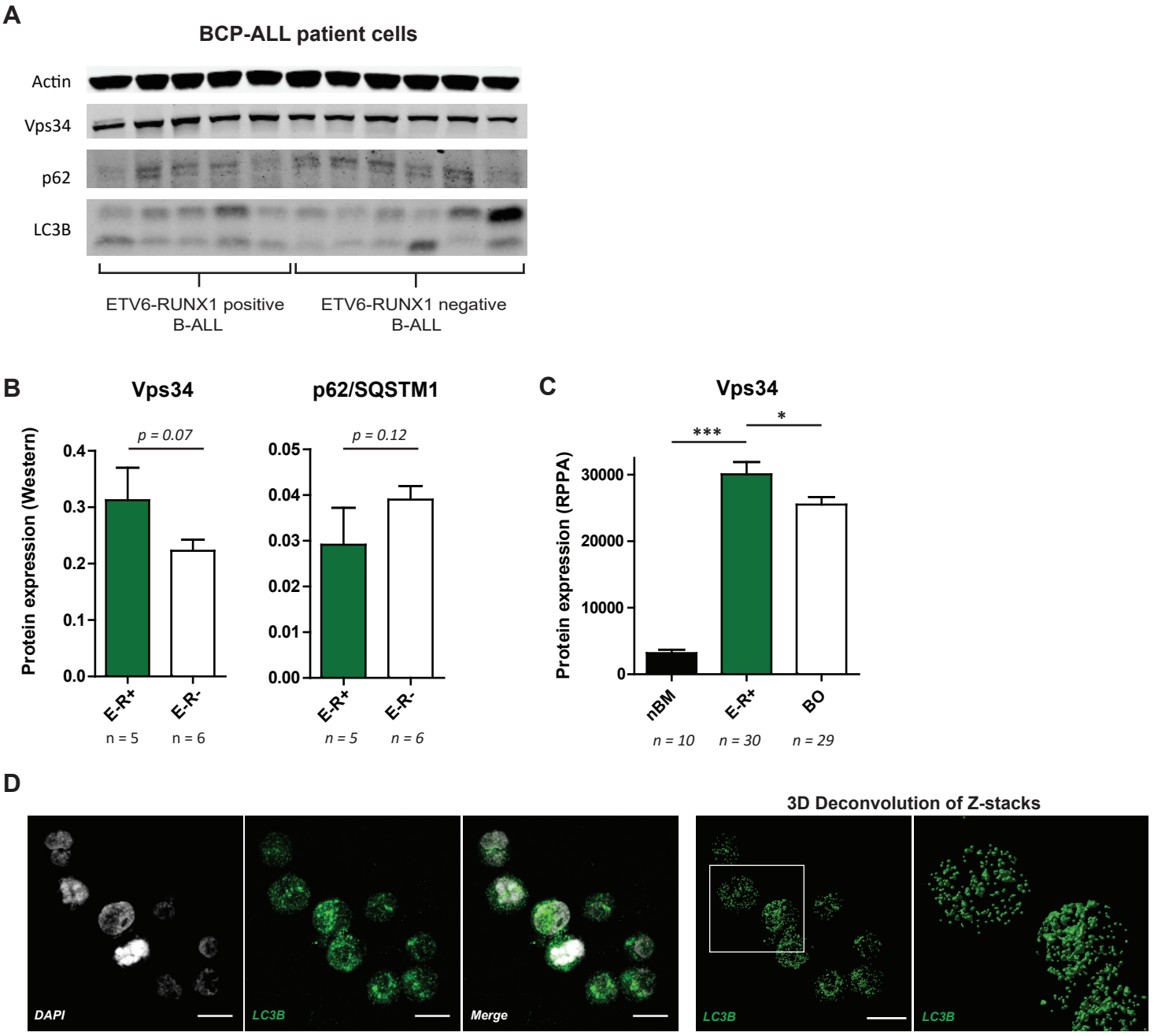
Suplementary Figure S4. Early effects of ETV6-RUNX1 expression in cord blood-derived CD34+ progenitors



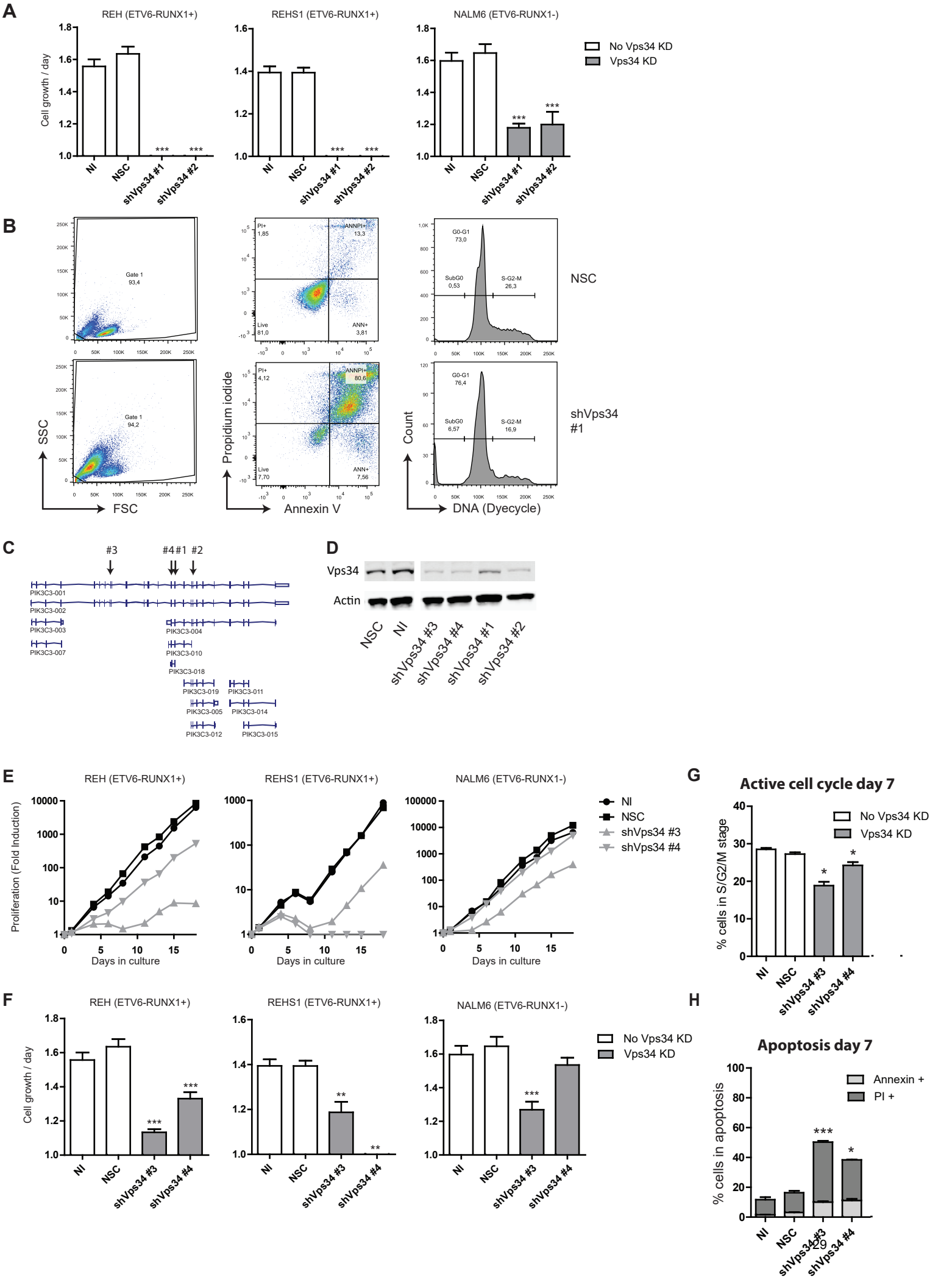
Supplementary Figure S5. Vps34 expression in ETV6-RUNX1 positive cells



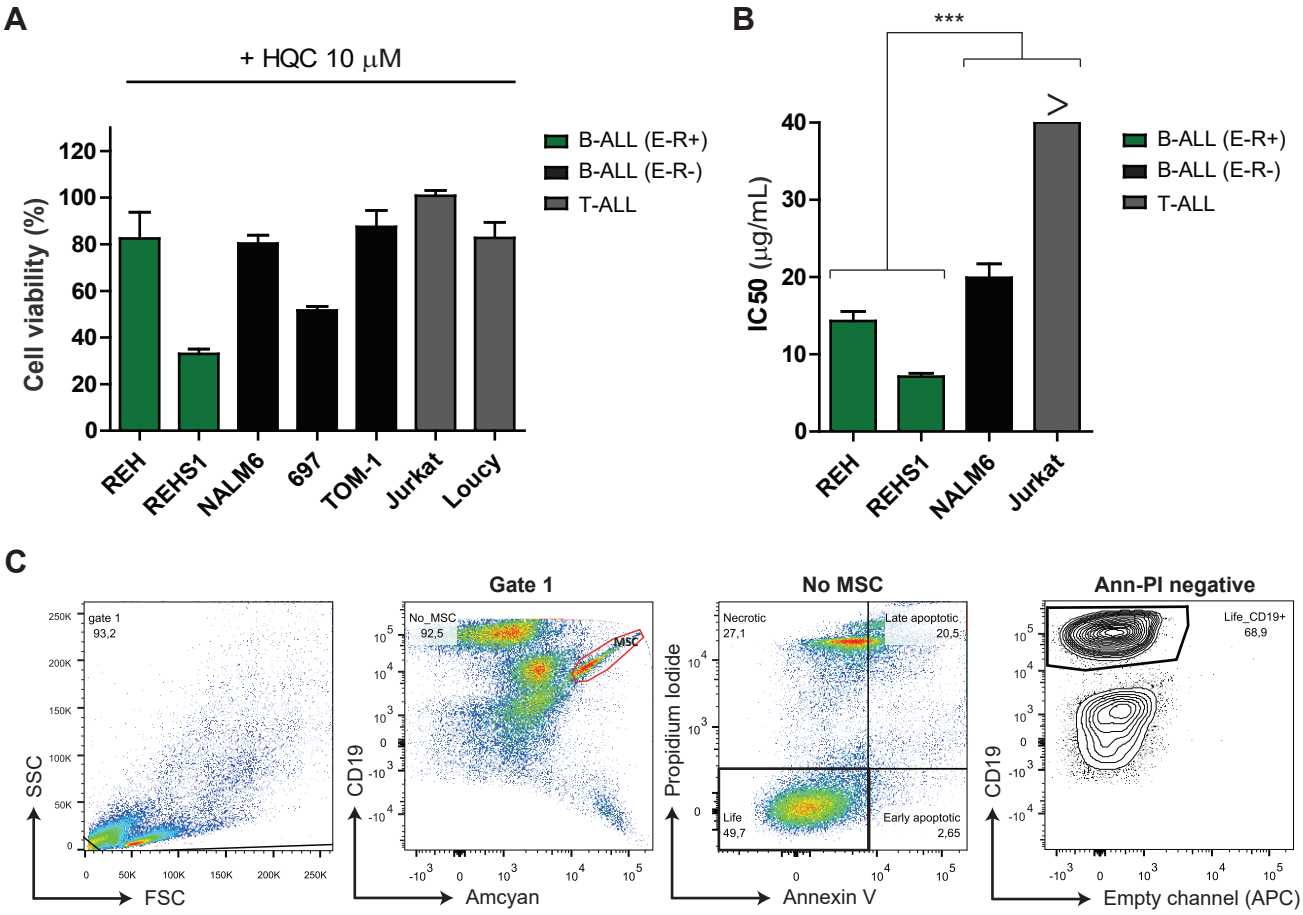
Supplementary Figure S6. Autophagy levels are high in ETV6-RUNX1 positive BCP-ALL cells

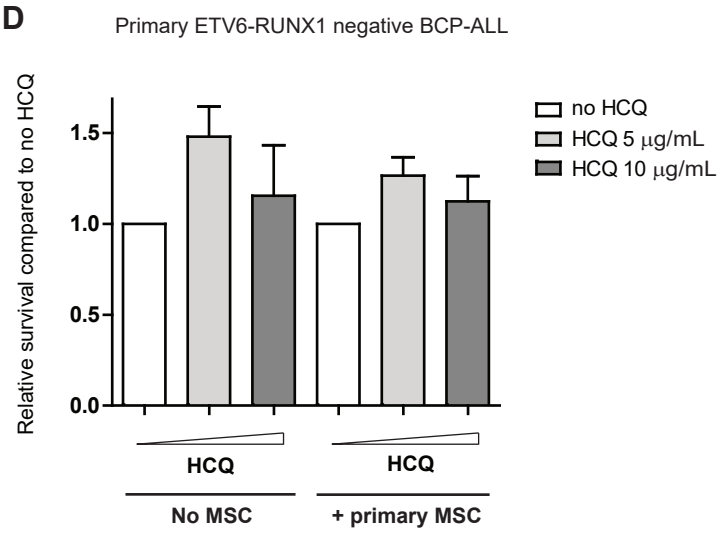


Supplementary Figure S7. Vps34 is essential for the survival of ETV6-RUNX1 positive leukemic cells

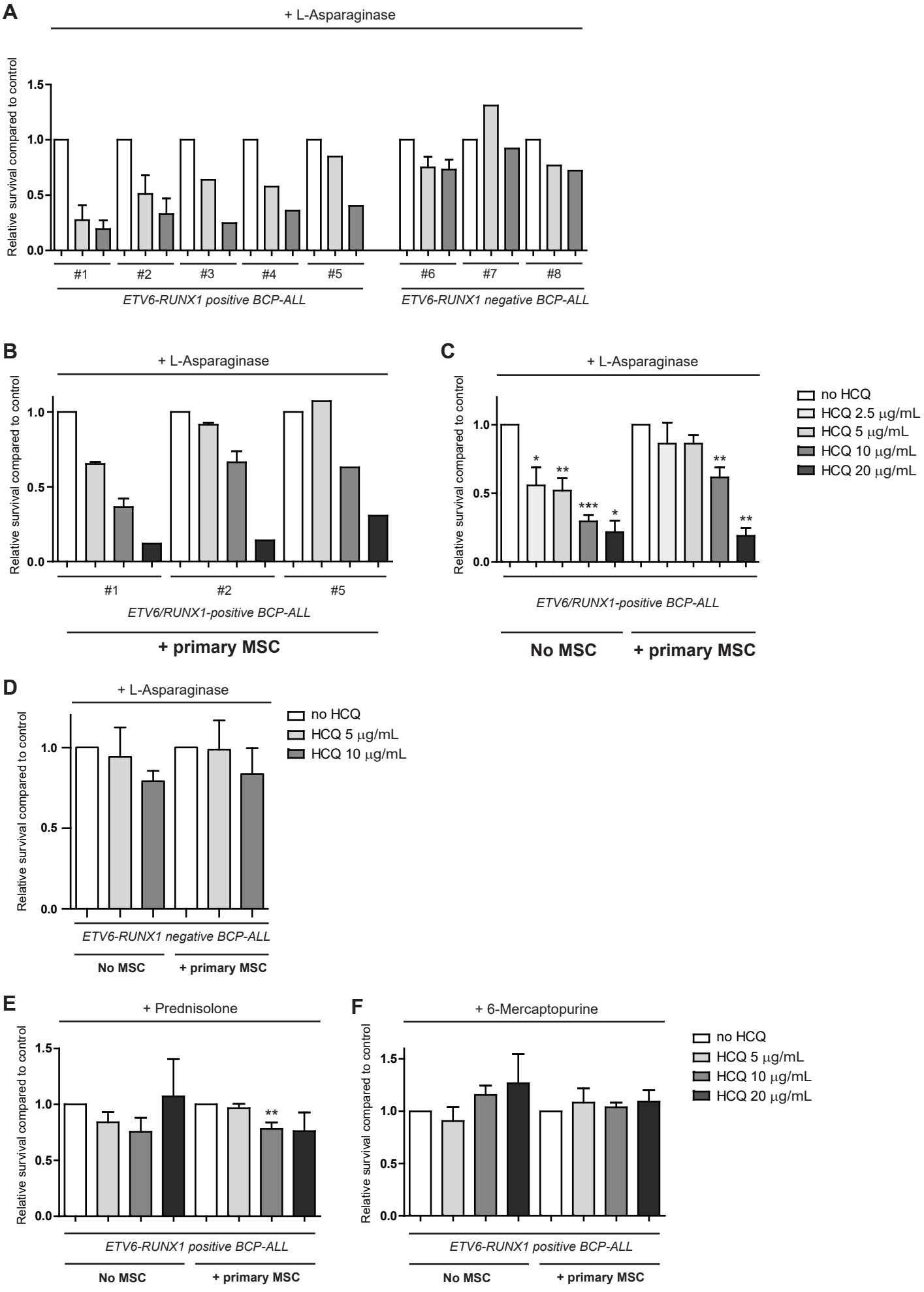


Supplementary Figure S8. ETV6-RUNX1 negative ALL cells are not sensitive to treatment with hydroxychloroquine





Supplementary Figure S9. Autophagy inhibition sensitizes ETV6-RUNX1 positive BCP-ALL to L-Asparaginase



Supplementary Table 1. Differentially regulated genes in ETV6-RUNX1 positive primary leukemic cells

Probe.ID	Chr	Chr.band	Gene.Symbol	Gene.Name	logFC	AveExpr	t	P.Value	adj.P.Val
206231_at	19	19p13.1	**KCNN1**	potassium intermediate/small conductance calcium-activated ch	2,77	7,49	43,45	1,08E-183	5,92E-179
227377_at	17	17q21.32	**IGF2BP1**	insulin-like growth factor 2 mRNA binding protein 1	2,11	6,74	36,96	5,87E-154	1,61E-149
213317_at	6	6p21.1-p12.1	**CLIC5**	chloride intracellular channel 5	4,23	5,38	35,93	5,11E-149	9,30E-145
210683_at	19	19p13.3	**NRTN**	neurturin	3,05	6,15	35,45	1,01E-146	1,38E-142
226817_at	18	18q12.1	**DSC2**	desmocollin 2	1,95	6,77	33,23	6,96E-136	7,61E-132
213423_x_at	8	8p22	**TUSC3**	tumor suppressor candidate 3	2,37	5,75	33,02	8,18E-135	7,45E-131
237206_at	17	17p11.2	**MYOCD**	myocardin	2,60	5,91	32,86	4,74E-134	3,71E-130
206032_at	18	18q12.1	**DSC3**	desmocollin 3	2,55	5,92	32,69	3,28E-133	2,24E-129
209962_at	19	19p13.3-p13.2	**EPOR**	erythropoietin receptor	1,64	6,32	32,68	3,78E-133	2,30E-129
206033_s_at	18	18q12.1	**DSC3**	desmocollin 3	2,44	5,43	32,60	9,81E-133	5,36E-129
220451_s_at	20	20q13.3	**BIRC7**	baculoviral IAP repeat-containing 7	1,12	7,10	32,43	6,40E-132	3,18E-128
37986_at	19	19p13.3-p13.2	**EPOR**	erythropoietin receptor	1,03	5,91	32,02	7,42E-130	3,38E-126
219866_at	6	6p21.1-p12.1	**CLIC5**	chloride intracellular channel 5	1,89	6,74	31,85	5,05E-129	2,12E-125
215054_at	19	19p13.3-p13.2	**EPOR**	erythropoietin receptor	1,58	6,77	31,01	8,28E-125	3,24E-121
238532_at	14	14q24.3-q31.1	**DPF3**	D4, zinc and double PHD fingers, family 3	2,19	6,10	30,79	1,07E-123	3,89E-120
1552519_at	2	2q24.1	**ACVR1C**	activin A receptor, type IC	1,93	6,09	30,47	4,52E-122	1,54E-118
205109_s_at	2	2q22	**ARHGEF4**	Rho guanine nucleotide exchange factor (GEF) 4	2,34	6,51	30,19	1,21E-120	3,88E-117
209228_x_at	8	8p22	**TUSC3**	tumor suppressor candidate 3	1,55	6,02	30,11	2,99E-120	9,09E-117
221747_at	2	2q35-q36	**TNS1**	tensin 1	1,25	6,75	29,71	3,46E-118	9,95E-115
203464_s_at	17	17p11.2	**EPN2**	epsin 2	0,60	6,81	29,60	1,26E-117	3,43E-114
1556511_a_at	NA	NA	**---**	---	2,19	6,08	28,74	3,17E-113	8,26E-110
236442_at	14	14q24.3-q31.1	**DPF3**	D4, zinc and double PHD fingers, family 3	1,58	5,95	28,30	5,25E-111	1,31E-107
238727_at	2	2q36.1	**---**	---	1,38	4,67	28,22	1,36E-110	3,24E-107
218864_at	2	2q35-q36	**TNS1**	tensin 1	1,13	6,38	27,95	3,55E-109	8,10E-106
209963_s_at	19	19p13.3-p13.2	**EPOR**	erythropoietin receptor	0,73	6,37	27,93	4,26E-109	9,32E-106
243917_at	6	6p21.1-p12.1	**CLIC5**	chloride intracellular channel 5	1,19	6,34	27,90	6,18E-109	1,30E-105
221748_s_at	2	2q35-q36	**TNS1**	tensin 1	2,64	7,47	27,85	1,17E-108	2,37E-105
205862_at	2	2p25.1	**GREB1**	growth regulation by estrogen in breast cancer 1	2,05	4,40	27,51	6,52E-107	1,27E-103
223552_at	7	7q31.3	**LRRC4**	leucine rich repeat containing 4	0,80	6,83	27,39	2,63E-106	4,96E-103
232750_at	2	2q35-q36	**TNS1**	Tensin 1	1,44	5,75	27,33	5,30E-106	9,66E-103
207437_at	14	14q	**NOVA1**	neuro-oncological ventral antigen 1	1,12	4,07	27,19	3,00E-105	5,29E-102
241505_at	NA	NA	**---**	---	2,21	7,66	27,07	1,20E-104	2,06E-101
227862_at	1	1p36.11	**TRNP1**	TMF1-regulated nuclear protein 1	2,05	6,66	26,98	3,63E-104	6,02E-101
238275_at	17	17q21.2-q21.3	**HAP1**	huntingtin-associated protein 1	1,01	5,92	26,67	1,48E-102	2,39E-99
229339_at	NA	NA	**MYOCD**	myocardin	1,48	5,86	26,63	2,32E-102	3,63E-99
223689_at	17	17q21.32	**IGF2BP1**	insulin-like growth factor 2 mRNA binding protein 1	0,60	5,98	26,54	6,82E-102	1,04E-98
235501_at	NA	NA	**---**	---	1,43	6,56	26,47	1,47E-101	2,17E-98
1553734_at	14	14q32.2	**AK7**	adenylate kinase 7	1,63	5,48	26,41	3,32E-101	4,77E-98
206460_at	1	1p36.32	**AJAP1**	adherens junctions associated protein 1	1,35	5,50	26,37	5,04E-101	7,06E-98
231455_at	2	2p25.2	**FLJ42418**	FLJ42418 protein	2,13	5,46	26,12	1,01E-99	1,38E-96
203324_s_at	7	7q31.1	**CAV2**	caveolin 2	1,60	4,77	25,60	5,39E-97	7,18E-94
241239_at	17	17p11.2	**---**	---	0,94	5,54	25,59	5,98E-97	7,78E-94
214110_s_at	2	2p11.1	**---**	---	1,35	6,54	25,58	6,25E-97	7,95E-94
205794_s_at	14	14q	**NOVA1**	neuro-oncological ventral antigen 1	1,10	5,26	25,48	2,10E-96	2,60E-93
1564149_at	NA	NA	**---**	---	1,53	6,35	25,30	1,96E-95	2,38E-92
204160_s_at	6	6p12.3	**ENPP4**	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	1,80	5,86	25,21	5,41E-95	6,43E-92
215790_at	1	1p36.32	**AJAP1**	adherens junctions associated protein 1	0,94	5,13	25,16	1,02E-94	1,18E-91
1563182_at	2	2q24.1	**ACVR1C**	activin A receptor, type IC	1,51	5,02	25,15	1,07E-94	1,21E-91
239246_at	13	13q32.2	**FARP1**	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chonc	1,66	5,58	25,12	1,53E-94	1,71E-91
235694_at	20	20q13.3-qter	**TCFL5**	transcription factor-like 5 (basic helix-loop-helix)	2,42	7,44	24,95	1,23E-93	1,35E-90
222943_at	4	4p15.31	**GBA3**	glucosidase, beta, acid 3 (cytosolic)	1,90	5,73	24,92	1,79E-93	1,92E-90
203184_at	5	5q23-q31	**FBN2**	fibrillin 2	1,91	5,49	24,88	2,80E-93	2,94E-90
202382_s_at	5	5q21	**GNPDA1**	glucosamine-6-phosphate deaminase 1	1,01	6,06	24,87	3,13E-93	3,23E-90
202517_at	4	4p16.1-p15	**CRMP1**	collapsin response mediator protein 1	1,97	8,19	24,74	1,49E-92	1,51E-89
238617_at	NA	NA	**---**	---	1,19	5,84	24,43	6,29E-91	6,25E-88
1569348_at	22	22q11.2	**psiTPTE22**	TPTE pseudogene	1,62	5,36	24,40	9,29E-91	9,07E-88
210058_at	6	6p21.31	**MAPK13**	mitogen-activated protein kinase 13	0,86	6,33	24,24	5,93E-90	5,68E-87
201976_s_at	5	5p15.1-p14.3	**MYO10**	myosin X	2,35	6,66	24,15	1,73E-89	1,63E-86
229230_at	3	3q29	**OSTalpha**	organic solute transporter alpha	1,52	5,36	24,07	4,90E-89	4,54E-86
223468_s_at	15	15q26.1	**RGMA**	RGM domain family, member A	1,74	7,45	24,06	5,50E-89	5,02E-86
211222_s_at	17	17q21.2-q21.3	**HAP1**	huntingtin-associated protein 1	0,78	6,82	23,97	1,66E-88	1,49E-85
224725_at	18	18q11.2	**MIB1**	mindbomb homolog 1 (Drosophila)	1,92	7,28	23,90	3,81E-88	3,36E-85
229638_at	16	16q12.2	**IRX3**	iroquois homeobox 3	2,57	5,57	23,88	4,70E-88	4,08E-85
213558_at	7	7q11.23-q21.3	**PCLO**	piccolo (presynaptic cytomatrix protein)	2,49	6,23	23,86	5,85E-88	4,99E-85
219954_s_at	4	4p15.31	**GBA3**	glucosidase, beta, acid 3 (cytosolic)	1,47	5,90	23,78	1,47E-87	1,23E-84
218804_at	11	11q13.3	**ANO1**	anoctamin 1, calcium activated chloride channel	2,10	5,23	23,73	2,90E-87	2,40E-84
213122_at	8	8q22.1	**TSPYL5**	TSPY-like 5	2,61	6,28	23,53	3,11E-86	2,54E-83
244218_at	NA	NA	**---**	---	0,78	5,71	23,51	3,99E-86	3,21E-83
201911_s_at	13	13q32.2	**FARP1**	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chonc	1,35	6,34	23,49	5,25E-86	4,16E-83
204914_s_at	2	2p25	**SOX11**	SRY (sex determining region Y)-box 11	3,84	7,10	23,44	8,88E-86	6,94E-83
217628_at	6	6p21.1-p12.1	**CLIC5**	chloride intracellular channel 5	0,87	5,99	23,30	4,77E-85	3,67E-82
204161_s_at	6	6p12.3	**ENPP4**	ectonucleotide pyrophosphatase/phosphodiesterase 4 (putative)	1,22	5,02	23,16	2,75E-84	2,09E-81
242133_s_at	NA	NA	**---**	---	0,93	6,06	23,09	6,04E-84	4,53E-81
226548_at	16	16p11.2	**SBK1**	SH3-binding domain kinase 1	1,14	7,27	23,09	6,22E-84	4,59E-81
230923_at	3	3p14.1	**FAM19A1**	family with sequence similarity 19 (chemokine (C-C motif)-like),	1,74	5,45	22,93	3,95E-83	2,88E-80
211891_s_at	2	2q22	**ARHGEF4**	Rho guanine nucleotide exchange factor (GEF) 4	0,70	6,14	22,92	4,49E-83	3,23E-80
204751_x_at	18	18q12.1	**DSC2**	desmocollin 2	0,92	4,60	22,89	6,87E-83	4,88E-80
218625_at	6	6p25.1	**NRN1**	neuritin 1	3,49	7,84	22,80	1,88E-82	1,31E-79
228158_at	1	1q21.1	**LOC645166 ///**	lymphocyte-specific protein 1 pseudogene /// lymphocyte-specif	1,23	6,56	22,78	2,66E-82	1,84E-79
238133_at	NA	NA	**---**	---	1,30	6,25	22,42	1,96E-80	1,34E-77
210650_s_at	7	7q11.23-q21.3	**PCLO**	piccolo (presynaptic cytomatrix protein)	2,31	5,46	22,41	2,12E-80	1,43E-77
204849_at	20	20q13.3-qter	**TCFL5**	transcription factor-like 5 (basic helix-loop-helix)	2,50	9,19	22,41	2,17E-80	1,44E-77
215149_at	NA	NA	**---**	---	1,07	5,88	22,37	3,37E-80	2,22E-77
204913_s_at	2	2p25	**SOX11**	SRY (sex determining region Y)-box 11	3,59	6,41	22,35	4,37E-80	2,84E-77
218078_s_at	3	3p21.31	**ZDHHC3**	zinc finger, DHHC-type containing 3	0,81	7,59	22,27	1,11E-79	7,14E-77
227996_at	13	13q32.2	**FARP1**	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chonc	0,64	5,57	22,24	1,54E-79	9,76E-77

242881_x_at	NA	NA	**---**	---	2,80	5,23	22,17	3,86E-79	2,43E-76
205952_at	2	2p23	**KCNK3**	potassium channel, subfamily K, member 3	2,05	5,72	22,15	4,72E-79	2,93E-76
208056_s_at	16	16q24	**CBFA2T3**	core-binding factor, runt domain, alpha subunit 2; translocated t	1,53	8,57	22,15	4,83E-79	2,97E-76
235492_at	6	6q22.31	**RNF217**	ring finger protein 217	0,83	5,11	22,06	1,35E-78	8,18E-76
240950_s_at	19	19q13.33	**CCDC155**	coiled-coil domain containing 155	1,40	6,04	21,96	4,64E-78	2,79E-75
203463_s_at	17	17p11.2	**EPN2**	epsin 2	0,38	6,38	21,83	2,19E-77	1,30E-74
218077_s_at	3	3p21.31	**ZDHHC3**	zinc finger, DHHC-type containing 3	0,65	6,77	21,73	7,07E-77	4,16E-74
215717_s_at	5	5q23-q31	**FBN2**	fibrillin 2	1,10	4,54	21,71	9,67E-77	5,62E-74
1562713_a_at	18	18q22-q23	**NETO1**	neuropilin (NRP) and tolloid (TLL)-like 1	1,50	6,24	21,68	1,36E-76	7,85E-74
204915_s_at	2	2p25	**SOX11**	SRY (sex determining region Y)-box 11	2,59	6,54	21,63	2,29E-76	1,30E-73
236236_at	NA	NA	**WNK3**	WNK lysine deficient protein kinase 3	0,54	5,15	21,48	1,49E-75	8,39E-73
1552736_a_at	18	18q22-q23	**NETO1**	neuropilin (NRP) and tolloid (TLL)-like 1	1,65	5,86	21,46	1,86E-75	1,04E-72
218813_s_at	9	9q34	**SH3GLB2**	SH3-domain GRB2-like endophilin B2	1,51	7,24	21,37	5,15E-75	2,84E-72
210059_s_at	6	6p21.31	**MAPK13**	mitogen-activated protein kinase 13	0,64	6,11	21,29	1,42E-74	7,74E-72
208690_s_at	10	10q22-q26.3	**PDLIM1**	PDZ and LIM domain 1	-1,92	11,14	-21,28	1,61E-74	8,74E-72
201910_at	13	13q32.2	**FARP1**	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chonc	0,93	6,72	21,16	6,21E-74	3,33E-71
239942_at	NA	NA	**---**	---	1,83	5,44	21,00	4,22E-73	2,24E-70
239118_at	1	1p13	**KCNA2**	potassium voltage-gated channel, shaker-related subfamily, mer	0,96	5,38	20,97	6,62E-73	3,48E-70
203038_at	6	6q22.2-q22.3	**PTPRK**	protein tyrosine phosphatase, receptor type, K	2,67	6,20	20,94	9,25E-73	4,82E-70
244107_at	NA	NA	**---**	---	1,13	4,90	20,90	1,45E-72	7,48E-70
224726_at	18	18q11.2	**MIB1**	mindbomb homolog 1 (Drosophila)	1,65	7,29	20,89	1,56E-72	7,99E-70
204750_s_at	18	18q12.1	**DSC2**	desmocollin 2	0,55	5,03	20,86	2,46E-72	1,25E-69
231015_at	3	3q13-q21	**KLF15**	Kruppel-like factor 15	0,51	6,26	20,85	2,50E-72	1,25E-69
224720_at	18	18q11.2	**MIB1**	mindbomb homolog 1 (Drosophila)	2,02	7,68	20,84	2,97E-72	1,48E-69
1555168_a_at	7	7q11	**CALN1**	calneuron 1	1,22	6,46	20,77	6,50E-72	3,20E-69
243159_x_at	NA	NA	**---**	---	1,79	4,77	20,73	1,14E-71	5,59E-69
202789_at	20	20q12-q13.1	**PLCG1**	phospholipase C, gamma 1	0,74	7,39	20,71	1,40E-71	6,75E-69
224907_s_at	9	9q34	**SH3GLB2**	SH3-domain GRB2-like endophilin B2	0,98	7,25	20,69	1,68E-71	8,04E-69
242563_at	NA	NA	**---**	---	1,41	6,57	20,67	2,30E-71	1,09E-68
239673_at	NA	NA	**---**	---	2,34	6,88	20,64	3,32E-71	1,56E-68
209227_at	8	8p22	**TUSC3**	tumor suppressor candidate 3	0,69	4,73	20,61	4,72E-71	2,21E-68
215789_s_at	1	1p36.32	**AJAP1**	adherens junctions associated protein 1	0,73	6,12	20,52	1,27E-70	5,86E-68
203910_at	1	1p22.1	**ARHGAP29**	Rho GTPase activating protein 29	2,62	7,03	20,42	4,30E-70	1,97E-67
226473_at	17	17q25.3	**CBX2**	chromobox homolog 2	0,89	7,04	20,41	4,92E-70	2,24E-67
223885_at	7	7q11	**CALN1**	calneuron 1	1,90	6,64	20,20	5,55E-69	2,51E-66
221246_x_at	2	2q35-q36	**TNS1**	tensin 1	0,60	6,63	20,17	8,88E-69	3,98E-66
235500_at	14	14q11.2	**HNRNPC**	heterogeneous nuclear ribonucleoprotein C (C1/C2)	1,02	6,95	20,14	1,18E-68	5,25E-66
213017_at	18	18q11.2	**ABHD3**	abhydrolase domain containing 3	1,65	8,61	20,12	1,50E-68	6,61E-66
237398_at	NA	NA	**---**	---	0,85	6,22	20,07	2,63E-68	1,15E-65
1559910_at	NA	NA	**---**	---	1,71	6,39	20,05	3,27E-68	1,42E-65
230698_at	7	7q11	**CALN1**	calneuron 1	2,30	5,84	20,05	3,54E-68	1,52E-65
1554140_at	1	1p31.3	**WDR78**	WD repeat domain 78	1,62	5,35	20,00	6,53E-68	2,79E-65
233850_s_at	20	20p13	**EBF4**	early B-cell factor 4	0,57	6,89	19,98	7,97E-68	3,38E-65
233609_at	6	6q22.2-q22.3	**PTPRK**	Protein tyrosine phosphatase, receptor type, K	1,67	5,02	19,94	1,32E-67	5,56E-65
215006_at	NA	NA	**---**	---	1,47	9,49	19,89	2,20E-67	9,18E-65
236430_at	16	16q22.1	**TMED6**	transmembrane emp24 protein transport domain containing 6	2,63	7,91	19,82	4,96E-67	2,06E-64
1557103_a_at	19	19q13.32	**LMTK3**	lemur tyrosine kinase 3	0,65	5,12	19,81	5,93E-67	2,44E-64
204743_at	3	3q13.2	**TAGLN3**	transgelin 3	0,55	6,35	19,79	7,52E-67	3,07E-64
220276_at	12	12p12.3	**RERGL**	RERG/RAS-like	1,30	5,05	19,78	7,97E-67	3,23E-64
244350_at	5	5p15.1-p14.3	**MYO10**	myosin X	0,68	4,61	19,77	9,71E-67	3,90E-64
203925_at	1	1p22.1	**GCLM**	glutamate-cysteine ligase, modifier subunit	1,29	6,86	19,76	1,02E-66	4,06E-64
203431_s_at	11	11q24-q25	**ARHGAP32**	Rho GTPase activating protein 32	1,17	5,95	19,74	1,38E-66	5,46E-64
227634_at	10	10q26.3	**STK32C**	serine/threonine kinase 32C	0,65	6,70	19,65	4,09E-66	1,61E-63
219360_s_at	19	19q13.33	**TRPM4**	transient receptor potential cation channel, subfamily M, membe	2,08	6,50	19,61	6,10E-66	2,38E-63
232549_at	21	21q11	**RBM11**	RNA binding motif protein 11	1,01	4,58	19,59	7,65E-66	2,97E-63
220002_at	1	1q44	**KIF26B**	kinesin family member 26B	0,50	5,49	19,59	7,81E-66	3,01E-63
218608_at	1	1p36	**ATP13A2**	ATPase type 13A2	-0,73	6,92	-19,54	1,40E-65	5,35E-63
226549_at	16	16p11.2	**SBK1**	SH3-binding domain kinase 1	0,59	6,56	19,49	2,47E-65	9,36E-63
211548_s_at	4	4q34-q35	**HPGD**	hydroxyprostaglandin dehydrogenase 15-(NAD)	0,94	4,92	19,33	1,65E-64	6,22E-62
201334_s_at	11	11q23.3	**ARHGEF12**	Rho guanine nucleotide exchange factor (GEF) 12	1,75	7,50	19,29	2,73E-64	1,02E-61
212158_at	8	8q22-q23	**SDC2**	syndecan 2	2,42	7,42	19,26	3,94E-64	1,47E-61
203914_x_at	4	4q34-q35	**HPGD**	hydroxyprostaglandin dehydrogenase 15-(NAD)	0,93	5,14	19,25	4,17E-64	1,54E-61
226885_at	NA	NA	**---**	---	0,96	4,94	19,21	6,56E-64	2,41E-61
1554026_a_at	5	5p15.1-p14.3	**MYO10**	myosin X	2,88	8,04	19,19	8,75E-64	3,19E-61
242196_at	NA	NA	**ARHGAP32**	Rho GTPase activating protein 32	0,90	4,96	19,19	8,93E-64	3,23E-61
229912_at	7	7p22.2	**SDK1**	sidekick homolog 1, cell adhesion molecule (chicken)	0,85	5,49	19,18	9,69E-64	3,49E-61
211795_s_at	5	5p13.1	**FYB**	FYN binding protein	1,75	6,74	19,18	9,83E-64	3,51E-61
232282_at	X	Xp11.23-p11.21	**WNK3**	WNK lysine deficient protein kinase 3	0,63	4,99	19,16	1,25E-63	4,42E-61
243742_at	NA	NA	**LOC100505797**	hypothetical LOC100505797	1,15	5,46	19,13	1,80E-63	6,36E-61
212399_s_at	3	3p25.2	**VGLL4**	vestigial like 4 (Drosophila)	0,92	8,45	19,04	5,19E-63	1,82E-60
220227_at	20	20q13.3	**CDH4**	cadherin 4, type 1, R-cadherin (retinal)	1,26	6,26	19,03	5,87E-63	2,04E-60
226171_at	3	3p21.31	**ZDHHC3**	zinc finger, DHHC-type containing 3	0,56	6,57	19,00	8,13E-63	2,81E-60
212063_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,82	9,65	-18,98	9,95E-63	3,42E-60
227266_s_at	5	5p13.1	**FYB**	FYN binding protein	1,95	6,94	18,91	2,19E-62	7,47E-60
203913_s_at	4	4q34-q35	**HPGD**	hydroxyprostaglandin dehydrogenase 15-(NAD)	1,61	4,86	18,91	2,27E-62	7,70E-60
220692_at	7	7q22.1	**---**	---	0,78	7,23	18,91	2,39E-62	8,06E-60
243952_at	22	22q11.2	**---**	---	0,81	5,55	18,90	2,59E-62	8,68E-60
206866_at	20	20q13.3	**CDH4**	cadherin 4, type 1, R-cadherin (retinal)	1,11	6,56	18,89	2,79E-62	9,32E-60
219471_at	13	13q14.12	**C13orf18**	chromosome 13 open reading frame 18	1,74	8,62	18,85	4,55E-62	1,51E-59
235801_at	NA	NA	**TUSC3**	tumor suppressor candidate 3	0,60	4,22	18,82	6,52E-62	2,15E-59
233518_at	NA	NA	**---**	---	0,73	4,99	18,78	9,93E-62	3,25E-59
221042_s_at	14	14q32.13	**CLMN**	calmin (calponin-like, transmembrane)	0,85	6,19	18,69	3,00E-61	9,76E-59
215516_at	7	7q22-q31.2	**LAMB4**	laminin, beta 4	0,78	4,37	18,65	4,58E-61	1,48E-58
212154_at	8	8q22-q23	**SDC2**	syndecan 2	2,02	7,45	18,64	5,57E-61	1,79E-58
219093_at	2	2q36.3	**PID1**	phosphotyrosine interaction domain containing 1	1,04	5,04	18,62	6,93E-61	2,21E-58
232235_at	18	18q22.1	**DSEL**	dermatan sulfate epimerase-like	1,29	4,60	18,59	9,61E-61	3,05E-58
209695_at	8	8q24.3	**PTP4A3**	protein tyrosine phosphatase type IVA, member 3	1,69	8,56	18,58	1,03E-60	3,27E-58
215843_s_at	10	10q23-q24	**TLL2**	tolloid-like 2	0,52	5,84	18,51	2,38E-60	7,49E-58
204115_at	7	7q21	**GNG11**	guanine nucleotide binding protein (G protein), gamma 11	3,03	8,88	18,48	3,34E-60	1,04E-57

206574_s_at	8	8q24.3	**PTP4A3**	protein tyrosine phosphatase type IVA, member 3	1,64	8,38	18,47	3,99E-60	1,24E-57
201590_x_at	15	15q21-q22	**ANXA2**	annexin A2	-1,72	9,27	-18,47	4,01E-60	1,24E-57
203611_at	16	16q22.1	**TERF2**	telomeric repeat binding factor 2	2,08	9,48	18,39	1,04E-59	3,19E-57
228116_at	14	14q11.1	**DUXAP10**	Double homeobox A pseudogene 10	0,81	6,46	18,38	1,13E-59	3,44E-57
205259_at	4	4q31.1	**NR3C2**	nuclear receptor subfamily 3, group C, member 2	1,31	5,99	18,30	2,64E-59	8,03E-57
219753_at	7	7q22.1	**STAG3**	stromal antigen 3	1,72	9,13	18,28	3,55E-59	1,07E-56
210427_x_at	15	15q21-q22	**ANXA2**	annexin A2	-1,72	9,22	-18,28	3,58E-59	1,08E-56
201005_at	12	12p13.3	**CD9**	CD9 molecule	-2,40	10,44	-18,25	5,08E-59	1,52E-56
213503_x_at	15	15q21-q22	**ANXA2**	annexin A2	-1,66	9,23	-18,23	6,49E-59	1,93E-56
209198_s_at	1	1q21.2	**SYT11**	synaptotagmin XI	-1,14	6,00	-18,17	1,20E-58	3,54E-56
212157_at	8	8q22-q23	**SDC2**	syndecan 2	0,74	6,17	18,17	1,27E-58	3,72E-56
231487_at	14	14q32.13	**COX8C**	cytochrome c oxidase subunit 8C	1,17	5,09	18,16	1,34E-58	3,90E-56
210791_s_at	11	11q24-q25	**ARHGAP32**	Rho GTPase activating protein 32	0,69	6,07	18,14	1,84E-58	5,36E-56
1559689_a_at	17	17p11.2	**GRAPL**	GRB2-related adaptor protein-like	0,52	5,04	18,13	1,94E-58	5,61E-56
224432_at	9	9q34	**SH3GLB2**	SH3-domain GRB2-like endophilin B2	0,35	7,50	18,08	3,38E-58	9,72E-56
1564109_at	22	22q11.21	**LOC284865**	hypothetical LOC284865	0,52	6,60	18,05	4,93E-58	1,41E-55
243367_at	NA	NA	**---**	---	0,56	5,22	18,04	5,40E-58	1,54E-55
224520_s_at	12	12q14.2-q15	**BEST3**	bestrophin 3	1,74	5,44	18,02	6,93E-58	1,96E-55
226612_at	5	5p15.31	**UBE2QL1**	ubiquitin-conjugating enzyme E2Q family-like 1	0,95	4,76	17,98	1,08E-57	3,03E-55
203323_at	7	7q31.1	**CAV2**	caveolin 2	0,78	4,67	17,98	1,13E-57	3,17E-55
1554076_s_at	11	11q23.3	**TMEM136**	transmembrane protein 136	0,65	6,37	17,97	1,32E-57	3,68E-55
208862_s_at	11	11q11	**CTNND1**	catenin (cadherin-associated protein), delta 1	-0,77	6,33	-17,89	3,11E-57	8,63E-55
203401_at	X	Xp22.3-p22.2	**PRPS2**	phosphoribosyl pyrophosphate synthetase 2	-1,24	7,48	-17,89	3,16E-57	8,72E-55
242977_at	1	1q25.2	**LOC10050612**	hypothetical LOC100506128 /// hypothetical LOC100509355	0,80	4,55	17,84	5,93E-57	1,63E-54
210239_at	16	16q11.2-q13	**IRX5**	iroquois homeobox 5	1,01	6,08	17,81	8,23E-57	2,25E-54
235379_at	NA	NA	**LOC10050611**	hypothetical LOC100506114	0,37	5,81	17,80	8,87E-57	2,41E-54
224722_at	18	18q11.2	**MIB1**	mindbomb homolog 1 (Drosophila)	1,66	5,93	17,80	9,51E-57	2,57E-54
232227_at	NA	NA	**LOC10050597**	hypothetical LOC100505976	1,54	7,01	17,79	9,68E-57	2,61E-54
209197_at	1	1q21.2	**SYT11**	synaptotagmin XI	-1,33	7,00	-17,79	1,04E-56	2,79E-54
201335_s_at	11	11q23.3	**ARHGEF12**	Rho guanine nucleotide exchange factor (GEF) 12	0,47	4,70	17,76	1,37E-56	3,67E-54
226038_at	8	8p23.1	**LONRF1**	LON peptidase N-terminal domain and ring finger 1	1,40	7,85	17,76	1,41E-56	3,74E-54
223393_s_at	19	19q12	**TSHZ3**	teashirt zinc finger homeobox 3	0,64	5,68	17,75	1,57E-56	4,14E-54
239975_at	6	6p21.3	**HLA-DPB2**	major histocompatibility complex, class II, DP beta 2 (pseudogen	0,85	4,98	17,73	1,97E-56	5,19E-54
204489_s_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,62	8,85	-17,71	2,42E-56	6,32E-54
219746_at	14	14q24.3-q31.1	**DPF3**	D4, zinc and double PHD fingers, family 3	0,37	5,96	17,71	2,58E-56	6,73E-54
209866_s_at	4	4q13.1	**LPHN3**	latrophilin 3	1,12	5,10	17,66	4,28E-56	1,11E-53
230186_at	11	11q23.3	**TMEM136**	transmembrane protein 136	0,47	6,29	17,66	4,72E-56	1,22E-53
225129_at	16	16q13	**CPNE2**	copine II	1,37	9,51	17,64	5,43E-56	1,39E-53
211240_x_at	11	11q11	**CTNND1**	catenin (cadherin-associated protein), delta 1	-0,77	6,99	-17,64	5,95E-56	1,52E-53
210664_s_at	2	2q32	**TFPI**	tissue factor pathway inhibitor (lipoprotein-associated coagulatic	1,95	5,92	17,60	8,74E-56	2,22E-53
206190_at	2	2q21	**GPR17**	G protein-coupled receptor 17	0,87	5,52	17,48	3,50E-55	8,86E-53
217848_s_at	10	10q11.1-q24	**PPA1**	pyrophosphatase (inorganic) 1	-1,24	9,60	-17,46	4,70E-55	1,18E-52
209035_at	11	11p11.2	**MDK**	midkine (neurite growth-promoting factor 2)	1,47	9,01	17,44	5,48E-55	1,37E-52
232436_at	19	19qter	**ZNF274**	zinc finger protein 274	0,77	8,21	17,41	8,29E-55	2,07E-52
240084_at	17	17q25.3	**---**	---	0,98	7,16	17,33	1,89E-54	4,69E-52
237899_at	19	19q13.43	**LOC10050792**	hypothetical LOC100507928	0,42	6,36	17,32	2,10E-54	5,21E-52
205671_s_at	6	6p21.3	**HLA-DOB**	major histocompatibility complex, class II, DO beta	1,00	6,64	17,27	3,84E-54	9,46E-52
228910_at	NA	NA	**---**	---	-0,70	7,10	-17,26	4,23E-54	1,04E-51
214004_s_at	3	3p25.2	**VGLL4**	vestigial like 4 (Drosophila)	0,76	8,52	17,24	5,37E-54	1,31E-51
213258_at	2	2q32	**TFPI**	tissue factor pathway inhibitor (lipoprotein-associated coagulatic	1,93	5,26	17,23	6,17E-54	1,50E-51
225757_s_at	14	14q32.13	**CLMN**	calmin (calponin-like, transmembrane)	0,67	6,70	17,20	8,70E-54	2,11E-51
44790_s_at	13	13q14.12	**C13orf18**	chromosome 13 open reading frame 18	1,95	8,76	17,20	8,75E-54	2,11E-51
225548_at	4	4q21.1	**SHROOM3**	shroom family member 3	1,47	6,44	17,12	2,06E-53	4,94E-51
235108_at	NA	NA	**KCNK3**	potassium channel, subfamily K, member 3	0,57	5,78	17,11	2,50E-53	5,96E-51
203904_x_at	11	11p11.2	**CD82**	CD82 molecule	-0,82	8,54	-17,07	3,76E-53	8,94E-51
215322_at	NA	NA	**---**	---	1,24	8,07	17,04	5,27E-53	1,25E-50
202838_at	1	1p34	**FUCA1**	fucosidase, alpha-L- 1, tissue	1,14	7,87	17,04	5,35E-53	1,26E-50
1552904_at	18	18q22-q23	**NETO1**	neuropilin (NRP) and tolloid (TLL)-like 1	0,67	4,14	17,00	8,24E-53	1,93E-50
209835_x_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,56	8,19	-17,00	8,90E-53	2,08E-50
227684_at	19	19p13.2	**S1PR2**	sphingosine-1-phosphate receptor 2	0,49	7,01	16,99	8,96E-53	2,09E-50
237003_at	12	12q14.2-q15	**BEST3**	bestrophin 3	1,08	6,25	16,99	9,03E-53	2,09E-50
231726_at	5	5q31	**PCDHB14**	protocadherin beta 14	1,39	4,82	16,99	9,47E-53	2,18E-50
201563_at	15	15q15.3	**SORD**	sorbitol dehydrogenase	-1,27	6,73	-16,94	1,59E-52	3,66E-50
242546_at	14	14q11.1	**FLJ39632**	hypothetical LOC642477	0,74	4,98	16,90	2,55E-52	5,84E-50
210665_at	2	2q32	**TFPI**	tissue factor pathway inhibitor (lipoprotein-associated coagulatic	1,88	5,25	16,88	3,36E-52	7,65E-50
213714_at	10	10p12	**CACNB2**	calcium channel, voltage-dependent, beta 2 subunit	1,23	5,65	16,86	3,99E-52	9,04E-50
203474_at	5	5q13.3	**IQGAP2**	IQ motif containing GTPase activating protein 2	-1,21	7,37	-16,85	4,62E-52	1,04E-49
1554141_s_at	1	1p31.3	**WDR78**	WD repeat domain 78	0,70	5,30	16,85	4,73E-52	1,06E-49
240178_at	NA	NA	**---**	---	0,88	6,12	16,85	4,78E-52	1,07E-49
212014_x_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,52	8,16	-16,84	5,01E-52	1,12E-49
210916_s_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,32	8,11	-16,84	5,04E-52	1,12E-49
204490_s_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,51	8,05	-16,82	6,22E-52	1,38E-49
236679_x_at	NA	NA	**---**	---	0,27	7,05	16,81	7,38E-52	1,63E-49
203335_at	10	10p13	**PHYH**	phytanoyl-CoA 2-hydroxylase	1,61	8,42	16,79	9,17E-52	2,01E-49
223471_at	12	12q14.3	**RAB3IP**	RAB3A interacting protein (rabin3)	1,22	6,60	16,79	9,60E-52	2,10E-49
1568619_s_at	16	16p12.3	**ITPRIPL2**	inositol 1,4,5-triphosphate receptor interacting protein-like 2	-1,02	5,77	-16,77	1,19E-51	2,60E-49
1559114_a_at	2	2q37.3	**CXCR7**	Chemokine (C-X-C motif) receptor 7	0,38	5,47	16,75	1,50E-51	3,26E-49
207069_s_at	15	15q21-q22	**SMAD6**	SMAD family member 6	0,56	5,50	16,73	1,84E-51	3,97E-49
1557403_s_at	NA	NA	**---**	---	1,26	4,85	16,73	1,85E-51	3,98E-49
212912_at	6	6q27	**RPS6KA2**	ribosomal protein S6 kinase, 90kDa, polypeptide 2	1,25	6,09	16,73	1,88E-51	4,04E-49
201287_s_at	2	2p24.1	**SDC1**	syndecan 1	0,70	6,67	16,72	1,90E-51	4,05E-49
229407_at	7	7p22.2	**SDK1**	sidekick homolog 1, cell adhesion molecule (chicken)	0,63	5,77	16,69	2,70E-51	5,73E-49
205538_at	9	9q22.3	**CORO2A**	coronin, actin binding protein, 2A	0,37	5,23	16,67	3,33E-51	7,06E-49
1563509_at	NA	NA	**---**	---	0,41	6,39	16,67	3,61E-51	7,61E-49
233217_at	NA	NA	**---**	---	1,26	7,15	16,66	3,90E-51	8,21E-49
233317_at	12	12p13.3	**CD9**	CD9 molecule	-1,23	6,97	-16,66	4,03E-51	8,44E-49
225530_at	19	19p13.3	**MOBKL2A**	MOB1, Mps One Binder kinase activator-like 2A (yeast)	-1,55	9,57	-16,65	4,19E-51	8,75E-49
211368_s_at	11	11q23	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, b	-1,46	6,60	-16,64	4,70E-51	9,77E-49
1555978_s_at	NA	NA	**---**	---	-1,20	6,87	-16,64	4,88E-51	1,01E-48

232825_s_at	18	18q22.1	**DSEL**	dermatan sulfate epimerase-like	0,72	5,30	16,60	8,14E-51	1,68E-48
231882_at	ˌ \\"Ur	NA	**FLJ39632**	hypothetical LOC642477	0,61	6,60	16,59	9,06E-51	1,86E-48
234250_at	NA	NA	**---**	---	1,80	6,21	16,56	1,22E-50	2,49E-48
205122_at	9	9q31	**TMEFF1**	transmembrane protein with EGF-like and two follistatin-like dor	1,25	5,29	16,56	1,27E-50	2,59E-48
1557905_s_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,35	8,75	-16,56	1,27E-50	2,59E-48
205466_s_at	4	4p16	**HS3ST1**	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	1,16	5,41	16,55	1,38E-50	2,80E-48
223392_s_at	19	19q12	**TSHZ3**	teashirt zinc finger homeobox 3	0,37	5,91	16,54	1,44E-50	2,90E-48
229622_at	2	2q37.3	**FAM132B**	family with sequence similarity 132, member B	1,10	6,50	16,54	1,55E-50	3,12E-48
204494_s_at	15	15q24.2	**C15orf39**	chromosome 15 open reading frame 39	-1,17	7,83	-16,52	1,83E-50	3,67E-48
1557919_a_at	6	NA	**---**	---	1,76	8,09	16,52	1,90E-50	3,79E-48
236140_at	1	1p22.1	**GCLM**	glutamate-cysteine ligase, modifier subunit	1,23	5,58	16,47	3,41E-50	6,77E-48
213174_at	14	14q24.2	**TTC9**	tetratricopeptide repeat domain 9	0,47	6,33	16,45	4,27E-50	8,45E-48
228906_at	10	10q21	**TET1**	tet oncogene 1	0,53	5,24	16,38	8,83E-50	1,74E-47
213994_s_at	11	11p15.2	**SPON1**	spondin 1, extracellular matrix protein	1,55	5,58	16,38	9,14E-50	1,80E-47
212706_at	7	7q22	**RASA4**	RAS p21 protein activator 4	1,09	7,97	16,35	1,29E-49	2,52E-47
208939_at	10	10p14	**SEPHS1**	selenophosphate synthetase 1	0,91	8,06	16,34	1,45E-49	2,84E-47
243618_s_at	4	4q31.22	**ZNF827**	Zinc finger protein 827	1,18	7,42	16,34	1,49E-49	2,90E-47
228329_at	1	1p32-p31	**DAB1**	disabled homolog 1 (Drosophila)	0,85	5,03	16,34	1,52E-49	2,94E-47
228127_at	NA	NA	**KCNK3**	potassium channel, subfamily K, member 3	0,51	7,28	16,33	1,62E-49	3,13E-47
217523_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,73	8,72	-16,33	1,69E-49	3,25E-47
213394_at	15	15q15.1	**MAPKBP1**	mitogen-activated protein kinase binding protein 1	-1,18	7,48	-16,28	2,67E-49	5,12E-47
218017_s_at	8	8p11.1	**HGSNAT**	heparan-alpha-glucosaminide N-acetyltransferase	0,97	7,13	16,26	3,34E-49	6,38E-47
227792_at	16	16p12.3	**ITPRIPL2**	inositol 1,4,5-triphosphate receptor interacting protein-like 2	-1,64	6,21	-16,23	5,18E-49	9,83E-47
203620_s_at	11	11q13.4	**FCHSD2**	FCH and double SH3 domains 2	1,16	8,43	16,23	5,18E-49	9,83E-47
202192_s_at	17	17p13.1	**GAS7**	growth arrest-specific 7	-1,01	8,98	-16,21	6,21E-49	1,18E-46
213989_x_at	21	21q22.13	**SETD4**	SET domain containing 4	0,62	6,92	16,19	7,39E-49	1,39E-46
226733_at	1	1q31	**PFKFB2**	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	2,04	6,52	16,18	8,44E-49	1,59E-46
222496_s_at	4	4p13-p12	**RBM47**	RNA binding motif protein 47	-1,52	6,66	-16,16	1,12E-48	2,10E-46
219855_at	X	Xp11.22	**NUDT11**	nudix (nucleoside diphosphate linked moiety X)-type motif 11	1,28	6,60	16,15	1,24E-48	2,32E-46
239930_at	1	1q41-q42	**GALNT2**	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalact	-1,30	7,95	-16,11	1,96E-48	3,64E-46
211367_s_at	11	11q23	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, b	-1,17	6,04	-16,08	2,69E-48	4,98E-46
1560577_at	NA	NA	**---**	---	0,43	6,54	16,07	2,82E-48	5,20E-46
1558128_at	14	14q32.2	**LOC730202**	hypothetical protein LOC730202	0,79	6,11	16,07	3,04E-48	5,60E-46
220197_at	7	7q33-q34	**ATP6V0A4**	ATPase, H+ transporting, lysosomal V0 subunit a4	0,92	5,57	16,05	3,77E-48	6,91E-46
208407_s_at	11	11q11	**CTNND1**	catenin (cadherin-associated protein), delta 1	-0,77	6,22	-16,05	3,78E-48	6,91E-46
206686_at	2	2q31.1	**PDK1**	pyruvate dehydrogenase kinase, isozyme 1	0,45	6,83	16,03	4,78E-48	8,72E-46
240446_at	NA	NA	**---**	---	0,72	6,17	15,98	8,12E-48	1,47E-45
210993_s_at	4	4q31	**SMAD1**	SMAD family member 1	2,35	9,33	15,96	9,48E-48	1,72E-45
229648_at	NA	NA	**ARHGAP32**	Rho GTPase activating protein 32	0,65	5,37	15,96	9,59E-48	1,73E-45
223032_x_at	5	5q35.3	**PRELID1**	PRELI domain containing 1	-0,94	8,80	-15,96	9,73E-48	1,75E-45
233770_at	NA	NA	**---**	---	0,78	4,92	15,95	1,09E-47	1,95E-45
208940_at	10	10p14	**SEPHS1**	selenophosphate synthetase 1	0,90	7,31	15,95	1,13E-47	2,01E-45
235334_at	1	1p31.1	**ST6GALNAC3**	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acety	0,51	4,92	15,90	1,84E-47	3,27E-45
230844_at	2	2q36.1	**LOC440934**	Hypothetical LOC440934	0,38	5,33	15,87	2,77E-47	4,91E-45
233469_at	22	22q11.2	**psiTPTE22**	TPTE pseudogene	0,43	5,68	15,86	3,11E-47	5,50E-45
211549_s_at	4	4q34-q35	**HPGD**	hydroxyprostaglandin dehydrogenase 15-(NAD)	0,54	5,51	15,84	3,93E-47	6,93E-45
230352_at	X	Xp22.3-p22.2	**PRPS2**	Phosphoribosyl pyrophosphate synthetase 2	-0,93	6,82	-15,77	7,93E-47	1,39E-44
203467_at	22	22q13.2	**PMM1**	phosphomannomutase 1	0,36	6,67	15,75	1,02E-46	1,78E-44
1554168_a_at	X	Xp22.1-p21.3	**SH3KBP1**	SH3-domain kinase binding protein 1	-0,94	8,98	-15,71	1,58E-46	2,76E-44
225525_at	22	22q11.23	**KIAA1671**	KIAA1671	1,11	6,50	15,68	2,18E-46	3,80E-44
211366_x_at	11	11q23	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, b	-0,97	7,24	-15,66	2,79E-46	4,84E-44
238755_at	NA	NA	**RASSF10**	Ras association (RalGDS/AF-6) domain family (N-terminal) memb	0,93	5,28	15,63	3,81E-46	6,59E-44
205006_s_at	10	10p13	**NMT2**	N-myristoyltransferase 2	1,07	7,17	15,62	4,06E-46	7,00E-44
218024_at	6	6q27	**BRP44L**	brain protein 44-like	-0,71	8,29	-15,62	4,08E-46	7,02E-44
203370_s_at	5	5q35.3	**PDLIM7**	PDZ and LIM domain 7 (enigma)	0,69	6,83	15,62	4,30E-46	7,36E-44
233133_at	NA	NA	**---**	---	0,53	4,08	15,60	5,05E-46	8,64E-44
212438_at	2	2p14	**SNRNP27**	small nuclear ribonucleoprotein 27kDa (U4/U6.U5)	0,68	8,47	15,60	5,57E-46	9,49E-44
227177_at	9	9q22.3	**CORO2A**	coronin, actin binding protein, 2A	0,50	5,31	15,58	6,46E-46	1,10E-43
203748_x_at	2	2q24.2	**RBMS1**	RNA binding motif, single stranded interacting protein 1	0,83	8,43	15,57	7,42E-46	1,26E-43
1564236_at	NA	NA	**---**	---	0,95	4,96	15,57	7,78E-46	1,31E-43
204396_s_at	10	10q24-qter	**GRK5**	G protein-coupled receptor kinase 5	1,64	7,38	15,56	8,09E-46	1,36E-43
211794_at	5	5p13.1	**FYB**	FYN binding protein	0,62	6,53	15,56	8,11E-46	1,36E-43
201286_at	2	2p24.1	**SDC1**	syndecan 1	0,67	6,08	15,56	8,11E-46	1,36E-43
202084_s_at	17	17q25.1-q25.2	**SEC14L1**	SEC14-like 1 (S. cerevisiae)	-1,00	8,45	-15,55	9,53E-46	1,59E-43
206498_at	15	15q11.2-q12	**OCA2**	oculocutaneous albinism II	0,40	6,36	15,54	9,75E-46	1,62E-43
205285_s_at	5	5p13.1	**FYB**	FYN binding protein	0,76	6,38	15,52	1,21E-45	2,01E-43
233035_at	NA	NA	**---**	---	0,48	4,23	15,50	1,51E-45	2,49E-43
208816_x_at	9	9p13	**ANXA2P2**	annexin A2 pseudogene 2	-0,93	8,63	-15,50	1,58E-45	2,60E-43
224562_at	1	1p36.11-p34.3	**WASF2**	WAS protein family, member 2	0,83	10,17	15,49	1,68E-45	2,76E-43
206306_at	15	15q14-q15	**RYR3**	ryanodine receptor 3	0,79	4,65	15,49	1,87E-45	3,06E-43
242637_at	NA	NA	**---**	---	0,56	5,82	15,48	2,06E-45	3,37E-43
239935_at	14	14q21.3	**MDGA2**	MAM domain containing glycosylphosphatidylinositol anchor 2	0,64	3,99	15,47	2,16E-45	3,51E-43
223398_at	9	9q22.31	**C9orf89**	chromosome 9 open reading frame 89	-0,76	7,94	-15,47	2,20E-45	3,57E-43
204487_s_at	11	11p15.5	**KCNQ1**	potassium voltage-gated channel, KQT-like subfamily, member 1	0,68	7,46	15,46	2,35E-45	3,80E-43
207266_x_at	2	2q24.2	**RBMS1**	RNA binding motif, single stranded interacting protein 1	0,81	8,23	15,44	3,08E-45	4,96E-43
223228_at	22	22q13.31	**LDOC1L**	leucine zipper, down-regulated in cancer 1-like	1,11	7,04	15,44	3,13E-45	5,03E-43
230720_at	6	6p23	**RNF182**	ring finger protein 182	0,86	5,49	15,43	3,25E-45	5,22E-43
214378_at	2	2q32	**TFPI**	tissue factor pathway inhibitor (lipoprotein-associated coagulatic	0,78	5,20	15,41	4,21E-45	6,73E-43
200636_s_at	1	1p34	**PTPRF**	protein tyrosine phosphatase, receptor type, F	0,69	6,19	15,40	4,91E-45	7,82E-43
1552703_s_at	11	NA	**CARD16 /// CA**	caspase recruitment domain family, member 16 /// caspase 1, a	-1,45	7,28	-15,37	6,29E-45	9,99E-43
222235_s_at	10	10q11.21	**CSGALNACT2**	chondroitin sulfate N-acetylgalactosaminyltransferase 2	-1,14	8,94	-15,37	6,30E-45	9,99E-43
223991_s_at	18	18q12.2	**GALNT2**	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalact	-0,95	7,25	-15,37	6,91E-45	1,09E-42
234986_at	NA	NA	**GCLM**	glutamate-cysteine ligase, modifier subunit	0,94	4,47	15,35	7,95E-45	1,25E-42
209970_x_at	11	11q23	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, b	-1,10	7,16	-15,35	8,10E-45	1,27E-42
1556474_a_at	2	2q37.3	**FLJ38379**	hypothetical FLJ38379	1,48	6,36	15,34	8,77E-45	1,37E-42
202732_at	20	20q12-q13.1	**PKIG**	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	-1,58	7,49	-15,34	9,60E-45	1,50E-42
1558139_at	14	14q11.1	**FLJ39632**	hypothetical LOC642477	0,57	5,50	15,33	1,03E-44	1,60E-42
208015_at	4	4q31	**SMAD1**	SMAD family member 1	1,52	6,34	15,32	1,17E-44	1,81E-42
216873_s_at	1	1q21.3	**ATP8B2**	ATPase, class I, type 8B, member 2	0,30	7,34	15,31	1,22E-44	1,89E-42

205565_s_at	9	9q13-q21.1	**FXN**	frataxin	-0,92	6,36	-15,30	1,36E-44	2,10E-42
203957_at	2	2p25.1	**E2F6**	E2F transcription factor 6	0,81	6,69	15,30	1,50E-44	2,31E-42
227593_at	1	1p36.21	**FLJ37453**	hypothetical LOC729614	0,74	8,04	15,29	1,56E-44	2,39E-42
243462_s_at	NA	NA	**---**	---	1,01	6,56	15,24	2,65E-44	4,06E-42
219314_s_at	14	14q11	**ZNF219**	zinc finger protein 219	0,40	7,10	15,23	3,17E-44	4,85E-42
243617_at	4	4q31.22	**ZNF827**	Zinc finger protein 827	0,43	6,20	15,21	3,96E-44	6,03E-42
206324_s_at	15	15q22.31	**DAPK2**	death-associated protein kinase 2	0,37	6,11	15,20	4,18E-44	6,34E-42
204495_s_at	15	15q24.2	**C15orf39**	chromosome 15 open reading frame 39	-0,74	7,47	-15,19	4,73E-44	7,17E-42
206034_at	18	18q21.3	**SERPINB8**	serpin peptidase inhibitor, clade B (ovalbumin), member 8	-0,89	6,92	-15,18	5,02E-44	7,58E-42
1552623_at	19	19p13.11	**HSH2D**	hematopoietic SH2 domain containing	-1,06	7,20	-15,18	5,27E-44	7,93E-42
208613_s_at	3	3p14.3	**FLNB**	filamin B, beta	-0,69	7,14	-15,18	5,28E-44	7,93E-42
1560318_at	1	1p22.1	**ARHGAP29**	Rho GTPase activating protein 29	0,90	4,82	15,17	5,75E-44	8,61E-42
244852_at	18	18q22.1	**DSEL**	dermatan sulfate epimerase-like	0,56	4,26	15,14	7,78E-44	1,16E-41
227827_at	NA	NA	**---**	---	0,43	4,09	15,14	7,95E-44	1,19E-41
206150_at	12	12p13	**CD27**	CD27 molecule	1,48	7,89	15,13	9,06E-44	1,35E-41
218152_at	15	15q24	**HMG20A**	high-mobility group 20A	1,18	7,33	15,12	1,04E-43	1,54E-41
225522_at	2	2p14	**AAK1**	AP2 associated kinase 1	-0,78	8,06	-15,11	1,07E-43	1,59E-41
223082_at	X	Xp22.1-p21.3	**SH3KBP1**	SH3-domain kinase binding protein 1	-0,86	9,90	-15,11	1,11E-43	1,64E-41
205434_s_at	2	2p14	**AAK1**	AP2 associated kinase 1	-0,74	9,53	-15,10	1,21E-43	1,78E-41
205640_at	11	11q13	**ALDH3B1**	aldehyde dehydrogenase 3 family, member B1	-0,76	6,84	-15,10	1,24E-43	1,82E-41
213172_at	14	14q24.2	**TTC9**	tetratricopeptide repeat domain 9	0,75	4,90	15,10	1,31E-43	1,91E-41
209868_s_at	2	2q24.2	**RBMS1**	RNA binding motif, single stranded interacting protein 1	0,89	8,15	15,10	1,32E-43	1,92E-41
222108_at	12	12q13.11	**AMIGO2**	adhesion molecule with Ig-like domain 2	1,26	6,35	15,09	1,40E-43	2,04E-41
238081_at	4	4q21.3	**NCRNA00247**	non-protein coding RNA 247	0,77	4,31	15,05	2,25E-43	3,26E-41
223195_s_at	1	1p35.3	**SESN2**	sestrin 2	1,06	8,47	15,04	2,52E-43	3,64E-41
218871_x_at	10	10q11.21	**CSGALNACT2**	chondroitin sulfate N-acetylgalactosaminyltransferase 2	-1,05	9,28	-15,00	3,57E-43	5,14E-41
227352_at	19	19p13.2	**C19orf39**	chromosome 19 open reading frame 39	0,39	6,40	14,98	4,79E-43	6,89E-41
210024_s_at	2	2q32.1	**UBE2E3**	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)	1,73	8,91	14,95	6,25E-43	8,97E-41
209167_at	X	Xp22.2	**GPM6B**	glycoprotein M6B	-1,79	6,69	-14,95	6,45E-43	9,23E-41
223420_at	12	12q13.2	**DNAJC14**	DnaJ (Hsp40) homolog, subfamily C, member 14	0,62	8,10	14,93	7,61E-43	1,09E-40
235618_at	19	19q13.11	**ZNF507**	zinc finger protein 507	0,61	6,58	14,92	8,48E-43	1,21E-40
1555977_at	NA	NA	**---**	---	-0,78	7,04	-14,92	8,71E-43	1,24E-40
209436_at	11	11p15.2	**SPON1**	spondin 1, extracellular matrix protein	1,29	6,37	14,91	1,01E-42	1,42E-40
236440_at	NA	NA	**NETO1**	neuropilin (NRP) and tolloid (TLL)-like 1	0,42	5,69	14,91	1,02E-42	1,44E-40
201319_at	18	18p11.31	**MYL12A**	myosin, light chain 12A, regulatory, non-sarcomeric	-0,82	9,86	-14,91	1,03E-42	1,46E-40
219250_s_at	20	20p11	**FLRT3**	fibronectin leucine rich transmembrane protein 3	0,48	5,11	14,90	1,15E-42	1,62E-40
227405_s_at	10	10p11.21	**FZD8**	frizzled homolog 8 (Drosophila)	1,27	7,85	14,89	1,20E-42	1,69E-40
202808_at	10	10q24.32	**C10orf26**	chromosome 10 open reading frame 26	1,06	7,61	14,89	1,22E-42	1,71E-40
1556473_at	2	2q37.3	**FLJ38379**	hypothetical FLJ38379	1,24	5,97	14,88	1,35E-42	1,88E-40
239348_at	NA	NA	**---**	---	1,31	6,82	14,88	1,35E-42	1,88E-40
218035_s_at	4	4p13-p12	**RBM47**	RNA binding motif protein 47	-1,10	5,92	-14,87	1,43E-42	1,99E-40
219597_s_at	15	15q15.3	**DUOX1**	dual oxidase 1	0,39	6,22	14,87	1,56E-42	2,15E-40
202191_s_at	17	17p13.1	**GAS7**	growth arrest-specific 7	-1,07	8,24	-14,86	1,74E-42	2,41E-40
227798_at	4	4q31	**SMAD1**	SMAD family member 1	2,32	8,35	14,85	1,94E-42	2,67E-40
1568827_at	8	8p23.3	**LOC401442**	hypothetical LOC401442	0,52	5,31	14,84	2,15E-42	2,95E-40
1570114_at	14	14q21.3	**MDGA2**	MAM domain containing glycosylphosphatidylinositol anchor 2	0,37	4,33	14,83	2,44E-42	3,34E-40
241574_s_at	17	17q21.32	**IGF2BP1**	Insulin-like growth factor 2 mRNA binding protein 1	0,31	5,29	14,80	3,16E-42	4,32E-40
1565868_at	11	11p13	**CD44**	CD44 molecule (Indian blood group)	-1,21	7,01	-14,79	3,67E-42	5,01E-40
226018_at	7	7p15.1	**C7orf41**	chromosome 7 open reading frame 41	-0,97	5,79	-14,79	3,73E-42	5,07E-40
209867_s_at	4	4q13.1	**LPHN3**	latrophilin 3	0,58	5,62	14,78	3,81E-42	5,16E-40
202669_s_at	13	13q33	**EFNB2**	ephrin-B2	1,36	7,13	14,78	3,96E-42	5,35E-40
233000_x_at	20	20q13.33	**DPH3P1**	DPH3, KTI11 homolog (S. cerevisiae) pseudogene 1	0,29	6,28	14,77	4,43E-42	5,98E-40
1558280_s_at	1	1p22.1	**ARHGAP29**	Rho GTPase activating protein 29	0,68	4,94	14,73	7,02E-42	9,45E-40
203543_s_at	9	9q13	**KLF9**	Kruppel-like factor 9	-2,12	7,30	-14,73	7,11E-42	9,56E-40
1559419_at	10	10p12	**CACNB2**	calcium channel, voltage-dependent, beta 2 subunit	1,02	4,96	14,72	7,31E-42	9,79E-40
204897_at	5	5p13.1	**PTGER4**	prostaglandin E receptor 4 (subtype EP4)	-1,62	10,44	-14,69	1,01E-41	1,35E-39
208109_s_at	15	15q23-q24	**C15orf5**	chromosome 15 open reading frame 5	1,27	5,96	14,69	1,09E-41	1,45E-39
219438_at	1	1p35.2	**NKAIN1**	Na+/K+ transporting ATPase interacting 1	0,45	6,26	14,68	1,18E-41	1,58E-39
1556768_at	NA	NA	**LOC100144604**	hypothetical LOC100144604	0,39	6,21	14,67	1,29E-41	1,71E-39
219154_at	12	12q24.31	**TMEM120B**	transmembrane protein 120B	0,44	6,55	14,67	1,34E-41	1,77E-39
213993_at	11	11p15.2	**SPON1**	spondin 1, extracellular matrix protein	1,00	4,70	14,63	1,95E-41	2,58E-39
206626_x_at	X	Xp11.23-p11.22	**SSX1**	synovial sarcoma, X breakpoint 1	0,39	5,61	14,63	1,97E-41	2,59E-39
206591_at	11	11p13	**RAG1**	recombination activating gene 1	1,71	6,95	14,62	2,10E-41	2,76E-39
1555269_a_at	11	11q13.3	**ANO1**	anoctamin 1, calcium activated chloride channel	0,34	6,40	14,62	2,27E-41	2,98E-39
232903_at	NA	NA	**---**	---	0,53	5,00	14,61	2,53E-41	3,31E-39
218856_at	6	6p21.1-p12.2	**TNFRSF21**	tumor necrosis factor receptor superfamily, member 21	1,53	9,22	14,60	2,78E-41	3,63E-39
217901_at	18	18q12.1	**DSG2**	desmoglein 2	1,24	6,21	14,59	3,19E-41	4,16E-39
209170_s_at	X	Xp22.2	**GPM6B**	glycoprotein M6B	-1,77	7,00	-14,57	3,61E-41	4,69E-39
227998_at	1	1q21	**S100A16**	S100 calcium binding protein A16	-2,46	9,94	-14,56	4,14E-41	5,36E-39
226288_s_at	17	17p13.1	**NLGN2**	neuroligin 2	0,30	7,26	14,56	4,20E-41	5,43E-39
217787_s_at	1	1q41-q42	**GALNT2**	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalact	-0,86	7,38	-14,56	4,37E-41	5,64E-39
210497_x_at	X	Xp11.23-p11.22	**SSX2 /// SSX2B**	synovial sarcoma, X breakpoint 2 /// synovial sarcoma, X breakpo	0,32	6,09	14,55	4,87E-41	6,27E-39
214581_x_at	6	6p21.1-p12.2	**TNFRSF21**	tumor necrosis factor receptor superfamily, member 21	1,54	7,82	14,54	5,38E-41	6,90E-39
204297_at	18	18q12.3	**PIK3C3**	phosphoinositide-3-kinase, class 3	0,98	7,94	14,53	5,66E-41	7,24E-39
1554827_a_at	16	16q12-q13	**ADCY7**	adenylate cyclase 7	-0,29	6,48	-14,51	7,28E-41	9,30E-39
206400_at	19	19q13.2	**LGALS7 /// LGA**	lectin, galactoside-binding, soluble, 7 /// lectin, galactoside-bindi	0,76	6,13	14,51	7,45E-41	9,50E-39
202887_s_at	10	10pter-q26.12	**DDIT4**	DNA-damage-inducible transcript 4	-1,01	11,36	-14,51	7,54E-41	9,59E-39
207776_s_at	10	10p12	**CACNB2**	calcium channel, voltage-dependent, beta 2 subunit	0,84	5,92	14,50	7,66E-41	9,72E-39
220968_s_at	12	12p13.33-p13.32	**TSPAN9**	tetraspanin 9	0,37	7,13	14,48	9,74E-41	1,23E-38
225912_at	8	8q22	**TP53INP1**	tumor protein p53 inducible nuclear protein 1	1,92	11,15	14,48	1,02E-40	1,29E-38
201136_at	X	Xp11.23	**PLP2**	proteolipid protein 2 (colonic epithelium-enriched)	-1,18	10,71	-14,46	1,17E-40	1,47E-38
228432_at	12	12q14.3	**RAB3IP**	RAB3A interacting protein (rabin3)	0,38	5,16	14,46	1,20E-40	1,51E-38
201188_s_at	6	6p21	**ITPR3**	inositol 1,4,5-triphosphate receptor, type 3	0,68	7,07	14,46	1,25E-40	1,57E-38
220648_at	10	10p15.3	**ADARB2**	adenosine deaminase, RNA-specific, B2	0,46	5,74	14,44	1,49E-40	1,86E-38
224148_at	5	5p13.1	**FYB**	FYN binding protein	0,57	4,45	14,43	1,60E-40	1,99E-38
203741_s_at	16	16q12-q13	**ADCY7**	adenylate cyclase 7	-1,30	6,71	-14,43	1,68E-40	2,09E-38
205622_at	6	6q21	**SMPD2**	sphingomyelin phosphodiesterase 2, neutral membrane (neutral	-0,41	7,08	-14,43	1,77E-40	2,20E-38
221621_at	17	17q25.2	**C17orf86**	chromosome 17 open reading frame 86	-0,82	5,84	-14,42	1,81E-40	2,24E-38
243432_at	3	3p26.3	**LOC642891**	hypothetical protein LOC642891	0,32	6,37	14,42	1,88E-40	2,33E-38

202668_at	13	13q33	**EFNB2**	ephrin-B2	1,85	7,44	14,40	2,24E-40	2,77E-38
1555492_a_at	12	12q14.2-q15	**BEST3**	bestrophin 3	0,63	4,83	14,40	2,27E-40	2,79E-38
212443_at	3	3p21.31	**NBEAL2**	neurobeachin-like 2	-0,69	7,74	-14,39	2,51E-40	3,09E-38
205123_s_at	9	9q31	**TMEFF1**	transmembrane protein with EGF-like and two follistatin-like dor	0,64	4,47	14,37	3,02E-40	3,70E-38
204591_at	3	3p26.1	**CHL1**	cell adhesion molecule with homology to L1CAM (close homolog	0,64	4,47	14,37	3,17E-40	3,87E-38
203860_at	13	13q32	**PCCA**	propionyl CoA carboxylase, alpha polypeptide	1,43	6,43	14,36	3,59E-40	4,38E-38
212956_at	4	4q31.21	**TBC1D9**	TBC1 domain family, member 9 (with GRAM domain)	1,81	7,02	14,35	4,00E-40	4,87E-38
220230_s_at	11	11p15.4	**CYB5R2**	cytochrome b5 reductase 2	1,58	7,33	14,34	4,21E-40	5,11E-38
236718_at	5	5p15.1-p14.3	**MYO10**	myosin X	0,47	4,64	14,31	6,24E-40	7,57E-38
226216_at	19	19p13.3-p13.2	**INSR**	insulin receptor	0,83	7,28	14,30	6,34E-40	7,67E-38
206274_s_at	1	1pter-p36.11	**CROCC**	ciliary rootlet coiled-coil, rootletin	-0,27	6,29	-14,30	6,79E-40	8,20E-38
243461_at	NA	NA	**---**	---	0,65	5,16	14,29	7,61E-40	9,16E-38
228340_at	15	15q22	**TLE3**	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	0,84	7,02	14,26	1,04E-39	1,25E-37
226035_at	16	16p12.1	**USP31**	ubiquitin specific peptidase 31	0,81	6,25	14,24	1,20E-39	1,44E-37
1556354_s_at	19	19p13.2	**RGL3**	ral guanine nucleotide dissociation stimulator-like 3	0,29	4,48	14,23	1,35E-39	1,61E-37
233072_at	9	9q34	**NTNG2**	netrin G2	0,73	6,75	14,23	1,40E-39	1,67E-37
232914_s_at	11	11q14	**SYTL2**	synaptotagmin-like 2	1,36	6,59	14,23	1,48E-39	1,76E-37
226764_at	4	4q31.22	**ZNF827**	zinc finger protein 827	0,84	6,21	14,21	1,65E-39	1,96E-37
203365_s_at	16	16q13-q21	**MMP15**	matrix metallopeptidase 15 (membrane-inserted)	0,39	6,57	14,17	2,63E-39	3,12E-37
214369_s_at	11	11q13	**RASGRP2**	RAS guanyl releasing protein 2 (calcium and DAG-regulated)	-0,76	9,59	-14,16	2,87E-39	3,39E-37
230670_at	3	3q25.1	**IGSF10**	immunoglobulin superfamily, member 10	0,66	6,26	14,16	2,92E-39	3,45E-37
209921_at	4	4q28-q32	**SLC7A11**	solute carrier family 7, (cationic amino acid transporter, y+ syste	0,60	5,32	14,15	3,28E-39	3,86E-37
203895_at	20	20p12	**PLCB4**	phospholipase C, beta 4	1,22	4,82	14,15	3,34E-39	3,93E-37
241506_at	NA	NA	**---**	---	0,59	4,33	14,13	3,90E-39	4,58E-37
202087_s_at	9	9q21-q22	**CTSL1**	cathepsin L1	0,41	6,72	14,12	4,44E-39	5,19E-37
229459_at	22	22q13.32	**FAM19A5**	family with sequence similarity 19 (chemokine (C-C motif)-like),	1,93	5,36	14,12	4,57E-39	5,34E-37
1553102_a_at	5	5q33.1	**CCDC69**	coiled-coil domain containing 69	-1,06	7,72	-14,09	5,84E-39	6,81E-37
1558815_at	4	4q35.1	**SORBS2**	sorbin and SH3 domain containing 2	0,47	4,49	14,09	6,36E-39	7,40E-37
223539_s_at	5	5q12.2-q13.3	**SERF1A /// SEF**	small EDRK-rich factor 1A (telomeric) /// small EDRK-rich factor 1	0,45	7,40	14,08	6,51E-39	7,55E-37
202598_at	1	1q21	**S100A13**	S100 calcium binding protein A13	-0,94	8,90	-14,08	6,90E-39	7,99E-37
202825_at	4	4q35	**SLC25A4**	solute carrier family 25 (mitochondrial carrier; adenine nucleotic	0,42	7,10	14,08	7,02E-39	8,11E-37
235121_at	19	19q13.43	**ZNF542**	zinc finger protein 542	0,66	6,01	14,07	7,63E-39	8,80E-37
204288_s_at	4	4q35.1	**SORBS2**	sorbin and SH3 domain containing 2	0,55	5,90	14,06	8,48E-39	9,76E-37
1554451_s_at	12	12q13.2	**DNAJC14**	DnaJ (Hsp40) homolog, subfamily C, member 14	0,54	6,58	14,06	8,66E-39	9,95E-37
216696_s_at	19	19q13.1	**PRODH2**	proline dehydrogenase (oxidase) 2	0,58	6,62	14,05	9,19E-39	1,05E-36
240532_at	20	20q11.23	**SLC32A1**	solute carrier family 32 (GABA vesicular transporter), member 1	1,08	6,09	14,05	9,65E-39	1,10E-36
231859_at	14	14q32.2	**C14orf132**	chromosome 14 open reading frame 132	0,48	6,37	14,05	9,78E-39	1,12E-36
203523_at	11	11p15.5	**LSP1**	lymphocyte-specific protein 1	-1,22	7,84	-14,03	1,12E-38	1,28E-36
212960_at	4	4q31.21	**TBC1D9**	TBC1 domain family, member 9 (with GRAM domain)	0,56	6,40	14,03	1,16E-38	1,32E-36
204906_at	6	6q27	**RPS6KA2**	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0,37	7,01	14,03	1,19E-38	1,35E-36
212886_at	5	5q33.1	**CCDC69**	coiled-coil domain containing 69	-1,01	7,91	-14,03	1,19E-38	1,35E-36
228570_at	12	12q23.3	**BTBD11**	BTB (POZ) domain containing 11	-1,22	7,05	-14,02	1,24E-38	1,40E-36
240572_s_at	12	12p13.31	**LOC374443**	CLR pseudogene	-1,07	8,19	-14,00	1,64E-38	1,85E-36
241917_at	NA	NA	**---**	---	0,91	5,61	13,99	1,80E-38	2,03E-36
244428_at	2	2p23	**DNMT3A**	DNA (cytosine-5-)-methyltransferase 3 alpha	0,58	7,07	13,99	1,84E-38	2,06E-36
214969_at	14	14q24.3-q31	**MAP3K9**	mitogen-activated protein kinase kinase kinase 9	0,32	6,09	13,97	2,06E-38	2,31E-36
223196_s_at	1	1p35.3	**SESN2**	sestrin 2	0,97	7,78	13,96	2,49E-38	2,78E-36
1553998_at	X	Xq13.1	**DMRTC1 /// DM**	DMRT-like family C1 /// DMRT-like family C1B	0,44	5,45	13,95	2,62E-38	2,93E-36
226698_at	5	5q31.3	**FCHSD1**	FCH and double SH3 domains 1	0,55	6,24	13,94	2,89E-38	3,22E-36
1559420_x_at	10	10p12	**CACNB2**	calcium channel, voltage-dependent, beta 2 subunit	0,85	5,08	13,94	2,93E-38	3,25E-36
205005_s_at	10	10p13	**NMT2**	N-myristoyltransferase 2	0,94	7,04	13,94	3,06E-38	3,40E-36
208405_s_at	6	6q21	**CD164**	CD164 molecule, sialomucin	-0,79	10,63	-13,92	3,55E-38	3,92E-36
227647_at	11	11q13-q14	**KCNE3**	potassium voltage-gated channel, Isk-related family, member 3	1,19	6,91	13,92	3,72E-38	4,11E-36
214743_at	7	7q22.1	**CUX1**	cut-like homeobox 1	0,73	9,98	13,91	4,10E-38	4,52E-36
218557_at	3	3q12.2	**NIT2**	nitrilase family, member 2	-0,73	7,50	-13,90	4,28E-38	4,71E-36
206011_at	11	11q23	**CASP1**	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, be	-1,05	5,79	-13,90	4,50E-38	4,94E-36
215087_at	15	15q24.2	**C15orf39**	chromosome 15 open reading frame 39	-1,02	7,01	-13,89	5,25E-38	5,75E-36
238889_at	2	2p23.3	**AGBL5**	ATP/GTP binding protein-like 5	0,26	5,08	13,87	5,87E-38	6,42E-36

Supplementary Table 2. Differentially regulated genes in ETV6-RUNX1 positive CB-CD34+ cells (40 hours after transduction)

Probeset	p-value	Name	LogFI	FI
44783_s_at	0,02	**HEY1**	3,22	24,92
218839_at	0,00	**HEY1**	2,78	16,10
204537_s_at	0,01	**GABRE**	2,46	11,74
207741_x_at	0,04	**TPSAB1**	2,31	10,04
207808_s_at	0,03	**PROS1**	2,27	9,64
223658_at	0,04	**KCNK6**	2,24	9,42
210805_x_at	0,01	**RUNX1**	2,24	9,36
216474_x_at	0,04	**TPSB2**	2,19	8,96
203661_s_at	0,02	**TMOD1**	2,18	8,81
204416_x_at	0,04	**APOC1**	2,15	8,62
207134_x_at	0,04	**TPSB2**	2,09	8,08
207526_s_at	0,02	**IL1RL1**	2,08	8,02
213515_x_at	0,04	**HBG1**	2,06	7,86
212472_at	0,01	**MICAL2**	1,96	7,12
212771_at	0,01	**FAM171A1**	1,96	7,08
205683_x_at	0,04	**TPSAB1**	1,95	7,04
205389_s_at	0,01	**ANK1**	1,90	6,69
1552378_s_at	0,01	**RDH10**	1,87	6,52
210139_s_at	0,00	**PMP22**	1,80	6,04
226021_at	0,01	**RDH10**	1,78	5,95
215382_x_at	0,02	**TPSAB1**	1,76	5,80
202479_s_at	0,03	**TRIB2**	1,74	5,72
201334_s_at	0,03	**ARHGEF12**	1,68	5,38
227703_s_at	0,03	**SYTL4**	1,67	5,32
201694_s_at	0,02	**EGR1**	1,64	5,14
218729_at	0,04	**LXN**	1,63	5,08
227404_s_at	0,00	**EGR1**	1,62	5,04
227461_at	0,02	**STON2**	1,61	5,02
210504_at	0,04	**KLF1**	1,61	5,02
207067_s_at	0,02	**HDC**	1,56	4,77
202284_s_at	0,04	**CDKN1A**	1,56	4,74
1553328_a_at	0,02	**SLC18A2**	1,56	4,74
202949_s_at	0,04	**FHL2**	1,55	4,69
210360_s_at	0,03	**MTSS1**	1,54	4,67
203561_at	0,02	**FCGR2A**	1,54	4,66
216191_s_at	0,03	**NA**	1,54	4,65
211734_s_at	0,01	**FCER1A**	1,53	4,60
226751_at	0,02	**CNRIP1**	1,50	4,47
210762_s_at	0,04	**DLC1**	1,50	4,46
202859_x_at	0,05	**IL8**	1,48	4,37
202481_at	0,04	**DHRS3**	1,38	3,98
212089_at	0,01	**LMNA**	1,37	3,94
201333_s_at	0,05	**ARHGEF12**	1,36	3,89

201147_s_at	0,04	TIMP3	1,35	3,84
224822_at	0,04	DLC1	1,34	3,83
1555590_a_at	0,05	GATA1	1,33	3,78
226794_at	0,02	STXBP5	1,32	3,76
234541_s_at	0,03	ARHGEF12	1,32	3,74
241615_x_at	0,04	NA	1,29	3,63
211743_s_at	0,04	PRG2	1,22	3,40
211005_at	0,01	LAT	1,22	3,38
206726_at	0,03	HPGDS	1,21	3,36
201150_s_at	0,04	TIMP3	1,21	3,34
1555950_a_at	0,04	CD55	1,20	3,31
209723_at	0,02	SERPINB9	1,18	3,27
204187_at	0,02	GMPR	1,13	3,11
201170_s_at	0,00	BHLHE40	1,12	3,07
211965_at	0,02	ZFP36L1	1,11	3,04
230416_at	0,01	NA	1,10	2,99
227155_at	0,00	LMO4	1,08	2,95
205159_at	0,01	CSF2RB	1,08	2,93
201926_s_at	0,02	CD55	1,07	2,90
209870_s_at	0,02	APBA2	1,04	2,83
201925_s_at	0,00	CD55	1,04	2,82
204683_at	0,02	ICAM2	1,02	2,76
206493_at	0,03	ITGA2B	0,98	2,65
1561405_s_at	0,02	CATSPER2	0,96	2,62
224991_at	0,03	CMIP	0,96	2,61
210358_x_at	0,04	GATA2	0,96	2,61
223391_at	0,05	SGPP1	0,94	2,55
214899_at	0,04	ZNF780B	0,93	2,53
230391_at	0,04	CD84	0,93	2,53
224992_s_at	0,03	CMIP	0,91	2,49
226694_at	0,00	AKAP2	0,90	2,47
209205_s_at	0,00	LMO4	0,88	2,42
203196_at	0,01	ABCC4	0,84	2,32
212335_at	0,00	GNS	0,83	2,30
1563357_at	0,03	NA	0,83	2,30
53720_at	0,02	C19orf66	0,81	2,26
206675_s_at	0,02	SKIL	0,80	2,23
223666_at	0,04	SNX5	0,80	2,22
209710_at	0,02	GATA2	0,79	2,19
202974_at	0,02	MPP1	0,74	2,10
200648_s_at	0,01	GLUL	0,74	2,09
217202_s_at	0,00	GLUL	0,74	2,09
208093_s_at	0,02	NDEL1	0,73	2,07
226921_at	0,02	UBR1	0,72	2,05
229336_at	0,04	ST3GAL2	0,71	2,03
231925_at	0,04	NA	0,70	2,02
224414_s_at	0,04	CARD6	0,67	1,95

231643_s_at	0,04	CMIP	0,66	1,94
230795_at	0,02	NA	0,63	1,88
234985_at	0,03	LDLRAD3	0,62	1,86
226994_at	0,04	DNAJA2	0,60	1,81
204507_s_at	0,03	PPP3R1	0,59	1,81
225799_at	0,04	NA	0,59	1,80
227877_at	0,05	C5orf39	0,58	1,79
210557_x_at	0,01	CSF1	0,58	1,78
215111_s_at	0,04	TSC22D1	0,57	1,76
202377_at	0,04	LEPROT	0,55	1,74
221249_s_at	0,04	FAM117A	0,53	1,70
221778_at	0,04	JHDM1D	0,53	1,69
212919_at	0,05	DCP2	0,51	1,66
223106_at	0,03	TMEM14C	0,50	1,65
221269_s_at	0,02	SH3BGRL3	0,49	1,64
219132_at	0,01	PELI2	0,49	1,64
1556060_a_at	0,01	ZNF451	0,48	1,62
209536_s_at	0,01	EHD4	0,48	1,62
234976_x_at	0,02	NA	0,48	1,61
207157_s_at	0,03	GNG5	0,47	1,59
217416_x_at	0,01	NA	0,46	1,59
201010_s_at	0,02	TXNIP	0,46	1,59
1552980_at	0,03	HAS3	0,46	1,58
212258_s_at	0,02	SMARCA2	0,46	1,58
223335_at	0,04	TMEM69	0,46	1,58
212268_at	0,01	SERPINB1	0,45	1,57
225834_at	0,02	NA	0,44	1,56
223303_at	0,03	FERMT3	0,43	1,53
201720_s_at	0,04	LAPTM5	0,42	1,52
224565_at	0,03	NEAT1	0,42	1,52
33132_at	0,04	CPSF1	0,42	1,52
201844_s_at	0,03	RYBP	0,41	1,51
202599_s_at	0,03	NRIP1	-0,41	1,51
201513_at	0,02	TSN	-0,42	1,52
221707_s_at	0,04	VPS53	-0,42	1,53
218376_s_at	0,04	MICAL1	-0,44	1,55
222237_s_at	0,00	ZFP112	-0,44	1,56
225240_s_at	0,02	MSI2	-0,45	1,57
239314_at	0,02	NHLRC3	-0,45	1,57
224787_s_at	0,04	RAB18	-0,45	1,57
222045_s_at	0,04	PCIF1	-0,47	1,60
219789_at	0,02	NPR3	-0,47	1,60
205596_s_at	0,02	SMURF2	-0,47	1,60
212844_at	0,04	RRP1B	-0,48	1,61
204304_s_at	0,02	PROM1	-0,48	1,61
243002_at	0,00	NA	-0,48	1,61
210894_s_at	0,04	CEP250	-0,48	1,61

224467_s_at	0,01	PDCD2L	-0,49	1,63
237118_at	0,04	NA	-0,49	1,63
225150_s_at	0,03	RTKN	-0,52	1,68
223236_at	0,04	CCDC55	-0,52	1,69
202314_at	0,04	CYP51A1	-0,53	1,70
237518_at	0,03	NA	-0,54	1,71
236023_at	0,04	CDK9	-0,54	1,71
211791_s_at	0,04	KCNAB2	-0,54	1,72
240265_at	0,02	TRAF3IP3	-0,54	1,72
219109_at	0,01	SPAG16	-0,55	1,73
202247_s_at	0,00	MTA1	-0,55	1,74
204197_s_at	0,03	RUNX3	-0,55	1,74
205398_s_at	0,03	SMAD3	-0,55	1,74
229354_at	0,04	AHRR	-0,57	1,77
200974_at	0,04	ACTA2	-0,58	1,78
210570_x_at	0,01	MAPK9	-0,58	1,79
222845_x_at	0,04	TMBIM4	-0,58	1,79
209163_at	0,04	CYB561	-0,58	1,79
219420_s_at	0,04	C1orf163	-0,59	1,80
231982_at	0,04	C19orf77	-0,61	1,83
217611_at	0,01	ERICH1	-0,62	1,85
214452_at	0,05	BCAT1	-0,62	1,86
239016_at	0,01	NA	-0,62	1,86
219165_at	0,04	PDLIM2	-0,62	1,86
217853_at	0,02	TNS3	-0,62	1,87
214745_at	0,00	PLCH1	-0,64	1,89
238239_at	0,04	WDR27	-0,65	1,91
221542_s_at	0,03	ERLIN2	-0,65	1,91
225215_s_at	0,02	MTRF1L	-0,66	1,94
213094_at	0,03	GPR126	-0,67	1,95
208680_at	0,04	PRDX1	-0,68	1,97
215415_s_at	0,04	LYST	-0,70	2,01
204949_at	0,05	ICAM3	-0,70	2,02
229876_at	0,05	PHKA1	-0,71	2,03
209757_s_at	0,04	MYCN	-0,72	2,04
1565544_at	0,03	RNF141	-0,73	2,07
213937_s_at	0,04	FTSJ1	-0,75	2,11
205372_at	0,00	PLAG1	-0,75	2,12
215343_at	0,00	CCDC88C	-0,76	2,13
205213_at	0,04	ACAP1	-0,76	2,15
238670_at	0,02	RAD18	-0,77	2,16
229491_at	0,01	NHEDC2	-0,78	2,18
225828_at	0,04	DAGLB	-0,78	2,18
244000_at	0,03	NA	-0,81	2,25
1552562_at	0,04	ZNF570	-0,85	2,33
235887_at	0,04	NA	-0,86	2,35
226034_at	0,00	DUSP4	-0,87	2,40

231310_at	0,00	**NA**	-0,88	2,42
219207_at	0,03	**EDC3**	-0,93	2,53
231887_s_at	0,03	**KIAA1274**	-1,02	2,77
205196_s_at	0,02	**AP1S1**	-1,05	2,85
212489_at	0,01	**COL5A1**	-1,15	3,17
231775_at	0,04	**TNFRSF10A**	-1,23	3,41
1555320_a_at	0,03	**STAB1**	-1,23	3,42
1555339_at	0,02	**RAP1A**	-1,34	3,83
1568997_at	0,04	**POLR1E**	-1,40	4,07
1555340_x_at	0,00	**RAP1A**	-1,48	4,39
206310_at	0,03	**SPINK2**	-1,51	4,53
211597_s_at	0,05	**HOPX**	-2,00	7,37