

BCAT1 is a NOTCH1 target and sustains the oncogenic function of NOTCH1

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MATERIALS AND METHODS

Cell lines and primary leukemia samples. Human embryonic kidney (HEK) 293T cells were maintained in DMEM containing 10% fetal bovine serum (FBS) and 0.05 mg/ml penicillin/streptomycin. All T-ALL cell lines were maintained in RPMI-1640 media supplemented with 10% FBS and 0.05 mg/ml penicillin/streptomycin. We tested cell lines regularly for mycoplasma contamination. Primary T-ALL cells were expanded *in vivo* via i.v. injection in 6–8 weeks old female NOD SCID IL2R^{γnull} (NSG) immunodeficient mice. T-ALL cells from spleens of xenografted mice were cultured *in vitro* in MEM-alpha media supplemented with 10% human serum and cytokines for the duration of functional assays (48–72h). Patient derived xenograft (PDX) and cell line authentication was determined by analyzing several loci of short tandem repeats (STRs) using a commercial kit (PowerPlex 16 HS System, Madison, WI, USA). NOTCH1-induced T-ALL murine models were previously generated by transduction of bone marrow progenitors with activated forms of NOTCH1 oncogene (*NOTCH1 L1601P ΔPEST* or *ΔE-NOTCH1*)¹. Spleens of diseased mice were used as a source of murine T-ALL cells for further studies. Thymuses from 6 weeks old normal C57/BL6 mice were obtained. Procedures involving animals and their care conformed with institutional guidelines and were authorized by local (OPBA) and national (Italian Ministry of Health) animal ethical committees.

Mouse transplantation experiments. *Bcat1* knockout (^{-/-}; KO) mice on a C57BL/6J background were generated using the CRISPR/Cas9 technology by Cyagen, (CA, USA). NOTCH1-induced T-ALL tumors were generated in mice as previously described ². Briefly, bone marrow (BM) cells were collected from 6- to 12-week-old WT and *Bcat1* KO C57BL/6 mice and BM progenitors (Lin-) were purified by negative selection using magnetic sorting (Miltenyi Biotec, Bergisch Gladbach, Germany). The cells were cultured overnight in the presence of the following cytokines (all from Peprotech, London, U.K.): mIL-3 (10 ng/mL), mIL-6 (10 ng/mL), mFLT3L (50 ng/mL), mIL7 (100 ng/mL) and mSCF (50 ng/mL). The cells were then washed, resuspended in retroviral supernatant (ΔE -NOTCH1), placed in the same cytokine cocktail containing polybrene (4 μ g/mL), and centrifuged at 1,290g for 90 minutes. A second round of spinoculation was performed the following day. After flow cytometric analysis of transduced progenitors, approximately 50×10^4 Lin⁻/Sca1⁺/GFP⁺ cells of each genotype were injected i.v. into lethally irradiated (9 Gy) recipients (6–8-week-old C57BL/6 female mice). Mice were bled after 2–3 weeks to monitor engraftment and evaluate the presence of circulating immature T cell progenitors by flow cytometry. Tumour bearing mice were euthanized and primary tumour cells were extracted from their spleens. For *in vitro* studies, ΔE -NOTCH1 tumors were cultured in RPMI-1640 supplemented with 20% FBS, mIL-7 (10 ng/mL), mIL-2 (5ng/mL) and β -mercaptoethanol. Procedures involving animals and their care conformed with institutional guidelines and were authorized by local (OPBA) and national (Italian Ministry of Health) animal ethical committees.

Flow cytometry and analysis of T-cell distribution. Peripheral Blood (PB) and spleens were harvested from WT and KO mice. Red blood cell (RBC) lysis was performed using a hypotonic solution containing ammonium chloride for all samples. Briefly, the cells were blocked for 10 minutes with CD16/CD32 (mouse BD FC Block, BD Pharmingen, Oxford, U.K.) diluted 1:100 in PBS at 4°C and subsequently stained for 30 minutes with a combination of following panel of antibodies: Cd3e-BV421/BV510 (Biolegend, London., U.K.), Cd8-BV605/PE, Cd4-FITC/APC (all from BD Pharmingen). The fixable viability stain dye (FVS780; BD) was used to analyze only viable cells. Cells were analyzed on a BD LSR II flow cytometer and acquired data was analyzed with FlowJo (Tree Star Inc., Ashland, OR).

Quantitative real-time PCR. Total RNA from human and mouse samples were extracted using Trizol reagent (Invitrogen, Thermo Fisher Scientific, Waltham, MA, USA). RNA from thymic samples were from a previous study³. These samples were obtained as surgical tissue discards from pediatric patients, ranging in age from 2 days to 5 years, undergoing cardiac surgery at the University Hospital of Padova, after informed consent. cDNA was generated with the Super Script First Strand Synthesis System for RT-PCR (Invitrogen) and analyzed by quantitative real-time PCR using SYBR Green PCR Master Mix (Applied Biosystems, Paisley, UK) and the HT 7900 Real-Time PCR System (Applied Biosystems). All primers were KICqStart™ Primers from Sigma-Aldrich. Primer sequences are available upon request. Every sample was analyzed in triplicate and relative expression levels were normalized to RPL19 or β2-microglobulin expression using the ΔΔCT method.

Total histone extraction. Total histones were obtained using the EpiQuik total histone extraction kit (Epigentek, Farmingdale, NY. USA), according to the manufacturer's recommendations. Histone extracts were normalized for protein concentration using the Bradford method (Pierce).

Immunohistochemistry. All primary T-ALL (and T-cell lymphoblastic lymphoma; T-LBL) cases were retrieved from the archives of the Pathology Unit of Padua University Hospital (Padua-Italy). Patient derived xenograft (PDX) samples were previously generated^{4,5}. Immunohistochemical (IHC) analysis was performed on 4 µm-thick formalin-fixed paraffin-embedded (FFPE) tissue sections with the Bond Polymer Refine Detection kit in an automated immunostainer (BOND-MAX system; Leica Biosystems–Newcastle upon Tyne, UK), as previously described⁶. IHC analyses were run using the following primary antibodies: anti-BCAT1 (clone 51/ECA39, BD Pharmingen), anti-HES1 (clone D6P2U, Cell Signaling Technology), anti-BCAT2 (clone D8K3O, Cell Signaling Technology). Immunostains were performed on whole tissue sections. Appropriate positive and negative controls were also included. Thymic tissue (N=3) was run in parallel to assess BCAT1, BCAT2 and HES1 expression in normal T cell precursors. The following two-tiered scoring system was used to assess the expression of these markers: (i) low expressor: no staining (0) or weak positivity (+1) in <10% of tumor cells; (ii) high expressor: moderate to strong positivity (2+ to 3+) in ≥10% of tumor cells. The scoring system was based on cytoplasmic (BCAT1/BCAT2) or nuclear expression (HES1) of each marker and intensity scores were defined by comparison with positive controls (i.e. NOTCH1 mutated PDX samples with high BCAT1 and HES1 expression documented in western blot). Specifically, strong (score 3+) positivity was attributed to cases with protein expression comparable to that of the positive controls, moderate (score 2+) positivity to cases with protein expression slightly fainter than controls, and weak (score 1+) positivity to cases with barely detectable protein expression.

Immunoprecipitation of acetylated proteins. Immunoprecipitation of acetylated proteins was performed using the Signal-seeker Acetyl-Lysine detection kit (Cytoskeleton, Inc., Denver, CO, USA) according to the manufacturer's recommendations. Briefly, cells were lysed in diluted BlastR lysis buffer containing class I and II HDAC inhibitor (Trichostatin A; TSA) and class III HDAC inhibitor (Nicotinamide). Approximately 2 mg of protein was pre-cleared with Protein G–agarose (Santa Cruz Biotechnology) at 4°C for 30 min before being incubated with Acetyl-lysine Affinity beads or Acetyl-lysine IP control beads overnight at 4°C. Beads were washed three times with BlastR-2 wash buffer and bound proteins eluted with bead elution buffer. Immune complexes were analyzed by SDS-PAGE and immunoblot.

Neutral comet assay. T-ALL cells were treated with vehicle (DMSO) or etoposide (1 µM) for 0 to 6h. The neutral comet assay was performed using the CometAssay Silver Kit (R&D Systems; #4251-050-K). Briefly, cells were

mixed with CometAssay LMAgarose (R&D Systems; 1:10[v/v]). Once the agarose had solidified, the cells were lysed with lysis solution (R&D Systems) overnight. The following day, we placed the slides briefly in neutral electrophoresis buffer (R&D Systems) before being placing them in an electrophoresis chamber containing neutral electrophoresis buffer. The slides were subjected to electrophoresis at 1V/cm for 1h at 4°C. We washed the slides in 70% ethanol. After drying the slides at room temperature, we stained the comets with SYBR-gold (ThermoFisher Scientific, #S11494). We viewed the comets by epifluorescence microscopy. For comet analysis we used the Open Comet software⁷ to quantify the percentage of DNA in the tail in at least 50 comets per condition.

Analysis of publicly available datasets. Expression data for BCAA metabolic genes in primary T-ALL patients and thymic subpopulations were obtained from GSE46170⁸. Microarray data were also obtained from GSE12948⁹, GSE14959¹⁰, E-MTAB-9279¹, CGAS00000000002¹¹, GSE33469¹², GSE33470¹³. RNA sequencing (RNA-seq) data of 264 pediatric T-ALL patients from St. Jude¹⁴ was used. Gene expression data of B-cell chronic lymphocytic leukemia (B-CLL) patients analyzed with HGU133+2.0 Affymetrix GeneChip arrays (N = 107) was obtained from Gene Expression Omnibus (GSE22762)¹⁵. BCAT1 expression levels were extracted and used to generate Kaplan–Meier survival plots. The mean BCAT1 expression level was used as cut-off to define high and low BCAT1 expression.

RNA-sequencing and gene-set enrichment analysis. Total RNA from the spleens of ΔE -NOTCH1 leukemia-bearing WT and *Bcat1* KO C57BL/6 mice was extracted using the RNAeasy Mini Kit (Qiagen, Hilden Germany), according to the manufacturer's instructions. Library preparation and paired-end RNA sequencing using Illumina NextSeq 500, as well as downstream data analysis, were performed by Active Motif (Waterloo, Belgium). Sequenced reads were mapped to the genome using the STAR aligner with default settings and uniquely mapped reads were counted. Normalized counts per million and differential gene expression were determined with DESeq2. Hierarchical clustering of Z score and log fold-change expression values used in heatmaps was carried out using GenePattern software¹⁶. RNAseq data was also analyzed using iDEP¹⁷. Gene set enrichment analysis (GSEA) analysis was performed using gene sets from the Molecular Signature Database at the Broad Institute (<https://www.gsea-msigdb.org/gsea/msigdb/index.jsp>) as previously described¹⁸ using GenePattern software. Primary data has been deposited in GEO (GSE267966) and will be released September 1 2024.

Steady state metabolite profiling. Spleens (N=3) and thymuses (N=2) from ΔE -NOTCH1 leukemia bearing mice and thymic tissue from 6 weeks old normal C57/BL6 mice (N=3-5) were obtained. Flash-frozen tissue (spleen or thymus) was subsequently analyzed by Capillary Electrophoresis Time-of-Flight Mass Spectrometry (CE-TOFMS; Ω -scan analysis, HMT, Tokyo, Japan). For in vivo experiments, we analyzed flash-frozen tissue (spleen) from ΔE -NOTCH1 leukemia bearing mice with WT (N=3) and *Bcat1* KO genotype (N=3) by CE-TOFMS (C-scope analysis, HMT, Tokyo, Japan). Further, ΔE -NOTCH1 leukemia bearing mice (N=3 each) were injected intraperitoneally (i.p.) with three doses of ERG245 (30mg/kg), which is a potent BCAT1 inhibitor, at 8 h intervals or vehicle (PBS). Identification of known chemical entities was based on comparison to metabolomics library entries of purified standards and was performed by HMT. Heatmap representation of metabolites identified by CE-TOFMS in NOTCH1-induced (ΔE -NOTCH1) leukemia cells treated with vehicle (PBS) or ERG245, ΔE -NOTCH1 tumors versus normal thymic tissue or ΔE -NOTCH1 tumors WT versus KO for *Bcat1* was performed using MetaboAnalyst¹⁹.

Stable-isotope tracing experiments. For the stable isotope-tracing experiments using primary cells, *ΔE-NOTCH1* leukemia bearing mice were injected i.p. with three doses of ERG245 (30mg/kg) at 8 h intervals or vehicle (PBS). Ten minutes before sacrifice mice were injected i.v. with ¹³C₆ Leu (Cambridge Isotope laboratories, Tewksbury, MA, USA) and spleens were flash-frozen. In another set of experiments, *ΔE-NOTCH1* leukemia bearing mice (WT and *Bcat1* KO) were injected i.v. with ¹³C₆ Leu (Cambridge Isotope laboratories) and spleens flash-frozen. Flash-frozen splenic tissue was subsequently analyzed by F-scope CE-TOFMS (HMT, Tokyo, Japan).

Analysis of ChIP-seq databases. The ChIP-seq data presented in this study were obtained from NCBI GEO under the following accession IDs: GSM959056 (HPB-ALL-NOTCH1)²⁰, GSM2521494 (MOLT4-PolII)²¹, GSM4271227 (MOLT4-H3K4me3)²² and GSM3693104 (ATACseq MOLT4)²³. Fastq files from these public ChIPSeq and ATACseq datasets were downloaded and mapped to human reference genome (GRCH38/hg38) using Bowtie2 (version 2.5.0)²⁴ with default parameters. MACS2 (version 2.2.7.1)²⁵ was used to call peaks. Next, Bedgraphs generated by MACS2 were converted to BigWig files with UCSC – wigtoBigWig tool (version 357) and displayed using pyGenomeTracks (version 3.7)²⁶.

Cell viability assays and flow cytometry. We analyzed cell viability/proliferation in T-ALL cell lines via the bioluminescent method Vialight plus (Lonza, Basel, Switzerland) or by counting live cells after trypan blue staining. For assays evaluating the effects of drugs on T-ALL cell lines, viability was evaluated after 72h. In detail, human T-ALL cells (3×10^5) or mouse T-ALL cells (0.5×10^5) were seeded in 24-well flat-bottom plates and treated with increasing doses of the various compounds: Etoposide (50-500 nM), Cytarabine/Ara-C (25-100 nM), Doxorubicin hydrochloride (25-100 nM) all from Selleck (Selleck Chemicals LLC, Houston, TX), ERG245 (200-1000 μM; Ergon Pharmaceuticals, Washington DC, NW, USA). Dibenzazepine (DBZ; Syncom, Groningen, the Netherlands) was used in selected experiments. DL-β-hydroxybutyrate (3-HB; sodium salt) and sodium butyrate (NaB) were from Sigma-Aldrich. We analyzed apoptosis after 48-72h by flow cytometry (FACS) after staining with Annexin V-FITC (Roche) or Annexin V-PE (BD Biosciences, Milan, Italy) and SYTOX Red dead cell stain (Invitrogen). Apoptosis was defined as the sum of the percentage of Annexin V⁺ and Annexin V⁺/SYTOX Red⁺ cells. Analysis of proliferation combined with cell cycle profile was performed using the Click-iT™ EdU Flow Cytometry Assay Kit (Life Technologies) according to the manufacturer's instructions. The samples were collected on a FACSCalibur (BD Biosciences) using Cell Quest software (BD Biosciences), and analysed with FlowJo (Tree Star Inc., Ashland, OR).

Plasmids, lentiviral constructs and viral production. For BCAT1 silencing experiments, HEK293T were transfected with pGipz non-silencing shRNA control, shBCAT1#1 (V3LH5-337223), shBCAT1#2 (V2LH5-64329) and appropriate packaging plasmids using JetPEI transfection reagent (Polyplus, Illkirch, France). Inactivation of human BCAT1 in T-ALL cells using the CRISPR-Cas9 technology was achieved using the guide sequence for BCAT1 (TATTAGGTCTTAGCCTG; sgBCAT1)²⁷ which was cloned into LentiCRISPRV2 puro vector (Addgene #98290). BCAT1 over-expression was done using pLenti-BCAT1-Myc-DDK-P2A-Puro (RC219229L3; Origene, Rockville, MD, USA). Plasmids carrying the catalytic inactive mutant of BCAT1 (K222A) was synthesized and cloned in pLenti-Myc-DDK-P2A-Puro vector by Genewiz (ALENTA Life Sciences, Chelmsford, MA, USA). For viral production, viral supernatant from transfected cells was collected 48h after transfection, filtered and used to infect target cells. All infections of T-ALL cells were performed by spinoculation. After infection, T-ALL cells were selected for 3-7 days in puromycin before functional assays.

Luciferase reporter experiments. To perform reporter assays, BCAT1 promoter (-1407 to +195 relative to the TSS) was cloned into the pGL4.23[luc2/minP] vector (E841A, Promega, Madison, WI, USA) using Bgl II and Hind III restriction sites by Genewiz (ALENTA Life Sciences, Chelmsford, MA, USA). Constructs having the RBP-J binding site (TGGGAA) mutated or deleted were also generated. To measure the capacity of ICN1 transcription factor to induce BCAT1 expression, HEK293T cells were co-transfected with pGL4.23[luc2/minP] vector containing the above mentioned BCAT1 promoter (pGL4-BCAT1 promoter) and increasing amounts of pcDNA3-ICN1 (kind gift of A. Weng; Terry Fox Laboratory, BC Cancer Agency, Vancouver, Canada) and Renilla luciferase vector (Promega). In some experiments using HEK293T cells, pGL4-BCAT1 promoter construct with the RBP-J binding site (TGGGAA) mutated was used. To determine the effects of NOTCH1-inhibition on reporter activity, pcDNA3-ICN1 transfected cells were treated for 48h with increasing amounts of CB103 (Selleck). To evaluate the contribution of MYC to reporter activity, pcDNA3-ICN1 transfected cells were either transfected with MYC targeting hairpins (pLKO-shMYC#1 (TRCN0000039640), pLKO-shMYC#2 (TRCN0000174055)) or increasing amounts of the BRD4 inhibitor, JQ1 (Selleck). Experiments were repeated at least twice and performed at least in quadruplicate. Luciferase activity was measured 72h post-transfection by Dual-Glo Luciferase Reporter assay kit (Promega) according to the manufacturer's guidelines. For reporter assays in T-ALL cells, we resuspended 1.5×10^6 HPB-ALL cells in 20 μ L of SF Nucleofector Solution (Lonza) with the addition of 700 ng of pGL4.23 vectors (BCAT1 promoter or control constructs) and 300 ng of pGL4.74 [hRluc/TK] Renilla luciferase reporter plasmid (Promega). Cells were electroporated (Amaxa Nucleofector; Lonza) using program CM130 and resuspended in 1 ml of RPMI / 20%FCS and incubated at 37°C/ 5% CO₂ for 48 hrs. In some experiments HPB-ALL cells were co-transfected with pcDNA3-ICN1 or treated with CB103. Experiments were repeated three times and performed at least in quadruplicate. Luciferase activity was measured 48-72h post-transfection by Dual-Luciferase Reporter assay kit (Promega). Relative luciferase activity was calculated as Firefly luciferase activity normalized against Renilla luciferase activity.

Mouse studies. NOTCH1-induced T-ALL tumors (generated using both *HD-ΔPEST* and *ΔE* alleles¹) were secondarily transplanted intravenous (i.v.) into sub-lethally irradiated recipients (C57BL/6 females of 6-8 weeks). Tumor bearing mice were euthanized and primary tumor cells extracted from the spleens of leukemic mice. T-ALL PDX samples⁴ were expanded in vivo via i.v. injection into female 6-8 weeks old NOD Rag1null IL2R γ null immunodeficient mice (NSG mice; Charles River, Wilmington, MA, USA). Tumor bearing mice were euthanized and tumor cells extracted from the spleens of leukemic mice and used in functional assays. For the evaluation of BCAT1 function in vivo, we infected MOLT4 or CCRF-CEM control (shCTRL) or BCAT1 deficient (shBCAT1#1/ shBCAT1#2) leukemic cells with lentiviral particles expressing luciferase (FUW-Cherry-LUC) and injected them i.v. into NSG mice (5×10^6 cells/mouse; N=5 per experimental group). We evaluated disease progression by in vivo bioimaging with the In Vivo Imaging System (IVIS, Xenogen, Grantham, UK). In therapy related experiments, PDX leukemic cells (T-ALL#19 or T-ALL#27) were infected with lentiviral particles expressing luciferase (FUW-Cherry-LUC) and injected i.v. into 6-8-week-old female NSG mice. After tumor engraftment (human CD45+ blasts $\geq 1\%$ in peripheral blood), we treated homogeneous groups of animals (N=5) with vehicle (DMSO/PBS), Etoposide (10 mg/kg or 15 mg/kg twice a week; intraperitoneal), ERG245 (30 mg/kg three times a week; intraperitoneal) or the combination Etoposide (10 mg/kg or 15 mg/kg twice a week; intraperitoneal) + ERG245 (30 mg/kg three times a week; intraperitoneal) for 10-15 days. We evaluated disease progression and therapy response by in vivo bioimaging with the In Vivo Imaging System IVIS Spectrum (Xenogen), spleen weight and human CD45 analysis by flow cytometry. Xenografted mice were age- and sex-matched and randomly assigned to groups. No blinding methods were used. Procedures involving animals and their care conformed with institutional guidelines and were authorized by local (OPBA) and national animal ethical committees (Italian Ministry of Health; DGSAF 0006112; 177/2020-PR).

BCAT1 promoter methylation testing by Methylation specific PCR (MSP). Genomic DNA was extracted from T-ALL cell lines (DNeasy kit, Qiagen) according to the manufacturer's instructions. A total of 500 ng of genomic DNA was bisulfite modified using EZ DNA Methylation™ Kit (Zymo Research, Irvine, CA, USA). Bisulfite modified DNA (20ng) was amplified with BCAT1 promoter specific primers (listed in *Online Supplementary Table S4*). A bisulphite-conversion specific actin beta (ACTB) PCR was performed (primers listed in *Online Supplementary Table S4*) to determine total amount of analyzed DNA. PCR conditions used are available upon request. PCR products were loaded on 2% agarose, stained with SYBR safe DNA gel stain (Thermo Fisher Scientific), and visualized under UV illumination.

Table S1: Primer sequences for amplification of BCAT1 promoter following ChIP

TARGET LOCI	DIRECTION	SEQUENCE (5' to 3')
BCAT1 <i>P1</i>	FORWARD	CTCTGGGAAAGAGAGATCGGCA
BCAT1 <i>P1</i>	REVERSE	CTGCATGCTGAGAGGACCAC
BCAT1 <i>P2</i>	FORWARD	AATCTTCGGGCTGGGAGAGA
BCAT1 <i>P2</i>	REVERSE	GCAGATCCCAAGGGTCGTAG
HES1 <i>P1</i>	FORWARD	AAGTTCACACGAGCCGTTTC
HES1 <i>P1</i>	REVERSE	GCTGTTATCAGCACCAAGCTC
BCAT1 <i>NL</i>	FORWARD	GTATCGCTCTGCTGTGAGGG
BCAT1 <i>NL</i>	REVERSE	GTCAACACCGTGACCCGTTA

Table S2_Differentially expressed genes between Bcat1KO and Bcat1WT NOTCH1-dependent leukemias

Ensemble ID	Symbol	DETUMOR_KO- log2FoldChange	DETUMOR_KO- WT_padj	DETUMOR_WT#_1	DETUMOR_WT#_2	DETUMOR_WT#_3	DETUMOR_WT#_1	DETUMOR_WT#_2	DETUMOR_WT#_3	DETUMOR_KO#_1	DETUMOR_KO#_2	DETUMOR_KO#_3	
ENSMUSG00000045010	Gm4779	10.64676018	6.46E-21	2.80947046	2.32265191	2.32279427	2	2.320152159	2	7.84426317	7.8406322	7.9512576	
ENSMUSG00000090015	Gm15446	7.2171665549	1.55E-14	2	2.58616865	2	2	2	2	5.45829491	5.8780348	5.9514022	
ENSMUSG00000046774	8030474K03Rik	6.937006211	1.12E-10	4.17376203	4.25078255	4.39582017	2	2.3198067	2.320152159	2.32024072	7.17869317	7.2143575	
ENSMUSG00000031125	3830403N18Rik	6.836535449	1.38E-08	2.58660819	2	2	4.51477944	4.314811199	3.80131951	7.41663134	7.6533656	7.3008695	
ENSMUSG00000095574	Trbv12-1	6.774001762	1.21E-15	3.32488999	3.32409844	2.58640584	2	2.3198067	2.320152159	2.32024072	5.99882775	6.0397503	5.9279464
ENSMUSG00000076468	Trbv5	6.574131398	6.64E-08	4.646413927	5.67331939	6.72308315	4.23953364	4.452152566	4.45251622	12.3866952	13.400864	13.28948	7.2655037
ENSMUSG00000076873	Trdv5	6.308259504	6.57E-17	3.70385595	3.70294367	3.46218583	3.15554545	3.900368117	3.57933023	6.6992374	6.6817489	6.2639549	10.216645
ENSMUSG00000018849	Wwc1	6.038304381	0.012449	2.58660819	2	2	2.32279427	2.3198067	2.320152159	2	6.7669798	6.7896504	6.9159751
ENSMUSG00000076472	Trbv15	6.12351585	5.55E-17	2.80947046	2.58640584	2	2	2	2	2.39906228	2.3209407	2.9985073	4.3912513
ENSMUSG00000093954	Gm16867	4.994981262	1.78E-11	3.32488999	3.00180885	3.17232976	2.3198067	2.582001393	2.32024072	7.56863151	7.2173083	7.4889326	5.2842203
ENSMUSG00000102361	Ighv8-5	4.679381378	0.000424	2.32291573	2.32265191	2.32279427	5.41661938	5.606353695	5.34992256	6.3876093	6.5517291	10.012709	9.9287142
ENSMUSG00000069308	H4c17	4.567884131	0.001886	2	2	2	2	2	2	2.58214219	2.32117796	3.805222	2.8067906
ENSMUSG00000039058	Ak5	4.565594451	0.0118454	2	2	2.58640584	2.3198067	2	2.8037367	5.55444488	5.6958765	5.7251591	2.3216648
ENSMUSG00000084997	Gm15471	4.065396929	9.55E-05	2.58660819	2.8089055	2.58640584	3.15554545	3.45377331	3.16529327	7.10731028	7.08563638	3.1691935	3.5826201
ENSMUSG00000022156	Gzme	4.029909245	0.0002217	2	2.32265191	2.58640584	2	2.320152159	2.58214912	2.80681915	3.1671805	3.5829719	5.2842203
ENSMUSG00000036242	Armh4	3.932010222	0.0087328	3.2046783	2.32265191	2.32279427	2.80280525	2	2.58214912	4.6320195	5.8533786	5.6976827	2.3216648
ENSMUSG00000078161	Erich3	3.786469008	0.0037746	2	2.32265191	2.58640584	2.3198067	2.320152159	2	3.16923045	2.3209407	2.5839675	4.9057492
ENSMUSG000000340457	Myrl	3.757288127	9.04E-06	3.24288999	2.8089055	2.32279427	2.3198067	2	2.41689524	4.0536837	3.805222	5.3563635	5.2882481
ENSMUSG00000031137	Fgf11	3.681374957	7.68E-05	2.80947046	2.58616865	2.58640584	2.58142511	2.582001393	2.32024072	3.45636601	3.9962936	5.2839756	5.7801385
ENSMUSG00000016722	Marvd3	3.650379111	0.0385308	2	2	2.3198067	2.320152159	2	2.99937492	3.4562874	3.9977603	5.4230771	5.5528283
ENSMUSG00000070732	Rbbm4	3.519759705	2.29E-05	2	3.17119349	3.46218583	2.80280525	3.694282913	3.31686005	6.30259635	6.7316343	5.4521973	2.3215434
ENSMUSG00000015437	Gzmb	3.391219953	5.42E-35	3.24288999	4.0902884	3.91006404	4.79824119	4.575547338	4.385475338	7.75366023	7.0464333	7.1686446	6.939114
ENSMUSG00000020182	Ddc	3.373616911	1.67E-05	3.24288999	3.24288994	3.46218583	3.45377331	3.31686005	3.698747365	6.8025878	6.5970492	4.1671919	4.1684284
ENSMUSG00000040170	Fmo2	3.228087338	0.0058496	3.24288999	3.4617334	3.58784774	2.99469065	3.316593717	3.31686005	7.03221076	7.6775959	6.7520113	3.4585936
ENSMUSG00000023963	Cyp39a	3.107736897	2.19E-05	3.24288999	2.8089055	2.32279427	2.3198067	2	2.41689524	4.0536837	3.805222	5.3563635	5.2882481
ENSMUSG00000035688	Thrsp	3.094750268	0.0021854	3.24288999	3.00180885	2.32279427	2.3198067	2.582001393	2.32024072	3.45636601	3.9962936	5.2839756	5.7801385
ENSMUSG00000060014	Prg4	3.053068811	0.0042042	3.17050864	2.31719349	3.46218583	2.80280525	3.694282913	3.31686005	6.30259635	6.9159751	3.9059249	4.5820339
ENSMUSG00000076492	Trib2-1	3.045468074	0.0057546	2.80722252	8.09631967	3.05945318	5.4476368	5.576980748	4.6932871	7.72669362	7.1624941	7.7358091	11.192211
ENSMUSG00000019124	Scrn1	3.020547911	0.001713	3.15050864	2.58616865	3.58784774	2.80280525	2.803546666	2.99577786	5.62356951	6.4215511	5.9791999	3.3211383
ENSMUSG00000020182	Lrmida	2.932944581	1.53E-06	3.24288999	2.8089055	2.32279427	2.3198067	2.58020525	3.16498644	3.56945903	4.39130526	5.2456599	6.3910631
ENSMUSG00000040170	Fmo2	3.228087338	0.0058496	3.24288999	3.4617334	3.58784774	2.99469065	3.316593717	3.31686005	7.03221076	7.6775959	6.7520113	3.4585936
ENSMUSG00000023963	Gypc1	3.107736897	2.19E-05	3.24288999	2.8089055	2.32279427	2.3198067	2	2.41689524	4.0536837	3.805222	5.3563635	5.2882481
ENSMUSG00000035688	Thrsp	3.094750268	0.0021854	3.24288999	3.00180885	2.32279427	2.3198067	2.582001393	2.32024072	3.45636601	3.9962936	5.2839756	5.7801385
ENSMUSG00000060014	Prg4	3.053068811	0.0042042	3.17050864	2.31719349	3.46218583	2.80280525	3.694282913	3.31686005	6.30259635	6.9159751	3.9059249	4.5820339
ENSMUSG00000021747	Cfap20dc	3.045468074	0.0057546	2.80722252	8.09631967	3.05945318	5.4476368	5.576980748	4.6932871	7.72669362	7.1624941	7.7358091	11.192211
ENSMUSG00000019124	Kcn1	3.020547911	0.001713	3.15050864	2.58616865	3.58784774	2.80280525	2.803546666	2.99577786	5.62356951	6.4215511	5.9791999	3.3211383
ENSMUSG00000020182	Lrmida	2.932944581	1.53E-06	3.24288999	2.8089055	2.32279427	2.3198067	2.58020525	3.16498644	3.56945903	4.39130526	5.2456599	6.3910631
ENSMUSG00000038233	Gask1a	2.874848371	1.46E-07	2.80947046	2.58616865	3.00216447	2.80280525	3.45377331	2.58214912	4.24155126	4.51859743	5.6135004	5.1682145
ENSMUSG00000023963	Cyp39a	3.107736897	2.19E-05	3.24288999	2.8089055	2.32279427	2.3198067	2	2.41689524	4.0536837	3.805222	5.3563635	5.2882481
ENSMUSG00000022000	Gucy2	2.763132983	6.70E-19	3.58784822	3.5877338	3.90128038	3.29210525	3.69459039	3.68529867	5.6498556	6.4565805	6.5065355	6.371694
ENSMUSG00000045790	Cddc149	2.754692052	0.0003375	4.03700144	3.4617334	3.43252507	2.3198067	2.5802001393	2.32024072	3.4562874	3.99582776	4.0581792	2.3215434
ENSMUSG00000021747	Trib2-1	2.700104024	0.022972	4.39631085	4.3952444	5.1313511	5.28215421	5.282001393	2.32024072	3.4562874	3.99582776	4.0581792	2.3215434
ENSMUSG00000057408	Kcn1	2.667415749	0.0403233	3.24288999	2.32265191	3.17232297	2.3198067	2.803546666	2.99577786	5.62356951	6.4215511	5.9791999	3.3211383
ENSMUSG00000061451	Tmem151a	2.666946075	0.0199102	3.24288999	2.58616865	3.00216447	2.80280525	3.45377331	2.58214912	4.24155126	4.51859371	5.6120058	5.1620058
ENSMUSG00000095130	Ighv1-39	2.652023111	0.0385283	5.00431594	4.52654927	5.1313511	4.8652001393	2.32024072	3.4562874	3.99582776	4.0581792	7.2371257	9.7012357
ENSMUSG00000012518	Pck1	2.623350500	0.0001202	3.24288999	2.8089055	2.32279427	2.3198067	2.5802001393	2.32024072	3.4562874	3.99582776	4.0581792	2.3215434
ENSMUSG00000066677	Fif208	2.346690953	0.05E-05	3.24288999	2.8089055	2.32279427	2.3198067	2.5802001393	2.32024072	3.4562874	3.99582776	4.0581792	2.3215434
ENSMUSG00000022200	Npr3	2.325598348	0.0017351	3.91050864	4.09027144	4.09077189	4.35267087	4.9090667	5.00368667	5.92956893	6.4203606	6.40860667	6.46046146
ENSMUSG00000076525	Gk1-99	2.306716522	0.08507303	4.86122324	4.86109829	5.32973324	5.32538969	6.78733888	7.68733898	8.6023006	8.6200906	8.64064114	8.6226996
ENSMUSG000000109998	T30208E13	2.221289309	0.0127299	3.17266678	2.58616865	3.58640584	3.58640584	5.282001393	2.32024072	3.4562874	3.99582776	4.0581792	2.3215434
ENSMUSG00000032952	Mid1	2.2212534186	1.04E-14	4.79058943	4.72717737	5.34377332	5.34577331	6.53063595	6.53063595	7.56202277	7.56202277	8.7889571	8.7202227
ENSMUSG00000020681	Ace	1.982498272	1.47E-12	4.09027144	3.91006404	3.24279427	3.2198067	2.8037367	2.8037367	6.5802006	6.5802006	7.52064	8.1019899
ENSMUSG00000008845	Cd163	1.978349202	0.0006192	8.04377556	7.93429357	7.63359055	8.35143528</td						

ENSMUSG000000015854	Cd5l	1.372277129	0.0112117	11.0547707	11.0690248	11.0575647	10.2771082	10.28689573	10.2987709	12.7625851	12.749111	12.771802	10.834736	10.819064	10.810257	
ENSMUSG000000054072	lglp1	1.35608973	9.06E-30	8.04925097	8.3478669	8.4921176	8.19407762	8.120508951	8.0195793	9.73515736	9.6586386	9.6957321	9.2933121	9.4311336	9.4819021	
ENSMUSG000000078190	Dnm3os	1.351121881	0.031713	4.25182216	4.0902284	3.81044603	4.9494351	4.850310455	4.747686861	6.20827055	6.4958656	6.0846517	4.4583541	4.9038484	4.583359	
ENSMUSG000000062380	Tubb3	1.347486732	4.97E-08	6.83764871	6.91038566	6.7456312	7.18932456	7.598611844	7.36678712	7.36678712	7.365364865	8.898973	8.6336677	8.0967343	7.9390567	8.1925857
ENSMUSG000000025355	Mmp19	1.346021271	0.007989	5.75945423	6.13269523	6.86200878	6.61919647	6.450935812	6.5154742	8.1228881	8.5153735	8.1107984	8.608058	6.6831226	8.810331	
ENSMUSG000000035042	Ccl5	1.319536213	0.004292	5.17430934	5.36081511	5.91029831	6.23785108	6.483348273	6.38426458	7.72669362	7.6245127	7.6117839	6.7536193	6.8545874	6.6275099	
ENSMUSG000000015947	Fcg1r	1.313112517	0.0007776	6.61940434	6.64732718	6.67658164	6.95548763	7.024794002	7.16170391	8.68175632	8.591297	8.7519282	7.2178869	7.4228316	7.2460537	
ENSMUSG000000030087	Klf15	1.308463239	0.0238154	5.32636716	5.55789694	4.70410076	5.16047261	5.349521258	5.03696515	7.22760162	6.9838967	6.962893	5.3563635	5.2822481	5.1275786	
ENSMUSG000000102748	Pcdhg2	1.298948604	0.031344	3.70385559	2.8089055	2.58640584	3.15555453	4.080606087	2.99577786	4.39130525	3.9962936	4.0851792	3.9990123	4.8043426	4.0859914	
ENSMUSG000000063415	Cyp26b1	1.279944905	0.0041252	5.7324803	5.46271875	5.86200878	6.0774525	5.96894512	6.079505	7.76695684	7.6317802	7.5669316	6.0648508	6.1644304	6.320099	
ENSMUSG000000027954	Efnaf1	1.267903381	0.0437339	5.75945423	5.36825203	5.73192013	5.07808018	4.946446378	3.99366215	5.23235052	5.2827219	7.1983912	7.0409858	7.110772		
ENSMUSG000000071716	Apo7e	1.265367583	4.31E-07	6.95896984	6.73139962	6.60460401	5.71807878	5.96894512	6.2208143	7.9116597	8.7186573	7.4808956	7.3824188	7.5664174	7.6491655	
ENSMUSG000000095028	Sirpb1p	1.25418795	0.023827	4.25182216	4.58797597	4.52713369	4.69144319	4.922214091	5.24036336	4.62462429	4.63894728	5.3207428	4.5205689	4.9525203		
ENSMUSG000000078922	Tqtp1	1.247814368	0.0002397	7.03802412	7.13279528	7.08101331	6.75793778	7.68538592	7.67826481	4.74663839	7.38721245	8.6097212	8.6149063	8.6985338		
ENSMUSG000000079018	Ly6c1	1.246490667	3.57E-05	7.94148901	7.8364421	7.86223222	7.59691102	7.506993378	7.44294829	9.40176898	9.4108268	9.3257065	8.3296162	8.1863578	8.3947032	
ENSMUSG000000045502	Hcar2	1.233419498	0.0097398	6.86274267	7.10154208	7.26160001	6.84771084	7.16355745	6.99108035	7.68636286	8.6208151	8.7009453	7.3824188	7.0034474	7.1410633	
ENSMUSG000000054513	Hmox1	1.226379242	0.0071959	11.6839656	11.7148479	11.7060601	11.70747941	11.7588972	11.7455915	11.5385951	11.578172	11.508854	11.796175	11.831363		
ENSMUSG000000078780	Gm1510	1.223238221	0.003422	5.9114938	5.75823544	5.95824332	5.87272847	6.59922422	5.72010376	7.5986882	7.378878	7.5745045	0.0431569	6.6027843	6.2649621	
ENSMUSG000000069792	Wfcd17	1.206534765	7.84E-05	7.81219846	7.83646421	7.79867633	8.8032378	8.66361126	9.84581235	9.7911198	9.9240303	9.1124347	9.1411681	9.103773		
ENSMUSG000000062661	Ncs1	1.20551236	0.0303741	4.52736397	4.81045442	4.32538969	4.94493511	4.575748304	4.24125532	4.45480862	4.85372	4.804795	6.0862233	6.0841549	6.4575947	
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ENSMUSG000000106438	Gm32051	1.19244001	0.0313241	7.94667514	7.6473994	5.71993112	6.97838265	7.181167553	6.96909248	9.16868325	9.1849145	9.113785	7.2081719	7.3094565	7.2075809	
ENSMUSG000000028987	Erf1f	1.188126433	0.002018	6.71659366	6.3957609	6.47684999	7.05576935	7.09988163	6.89871662	5.84660354	6.4171768	8.2778222	7.2933373	7.4641701	7.2742496	
ENSMUSG000000030088	Adhl11	1.177837161	0.00011262	5.58948364	5.64718627	5.4633646	5.59566882	7.463316554	6.45136042	7.8086832	7.1347479	7.9453124	7.2633633	7.6054453		
ENSMUSG000000073555	Gm4951	1.174891247	1.54E-05	6.02699627	6.91341597	6.66233611	6.48168924	6.450935812	6.60580968	7.88751393	7.94305325	11.0853605	10.953619	11.087793	9.3385411	
ENSMUSG000000043585	Spic	1.170911007	0.0113104	9.46842793	9.63477427	9.50417742	9.64941038	9.557199357	9.62452816	11.3974951	11.357555	11.325132	9.5986026	9.7090988	9.5924101	
ENSMUSG000000027489	Snta1	1.162500152	0.006175	5.7324803	5.38411597	5.71932013	6.23785108	6.89660817	6.64963648	6.98971662	7.5245125	7.5284591	6.1686812	6.2820677	6.1479311	
ENSMUSG000000021453	Gad445g	1.16029276	1.82E-30	5.82355009	8.61090871	7.80125159	6.33378902	8.417466959	5.97618494	5.9686347	5.9537617	9.6180905	9.6812507	9.6288335		
ENSMUSG000000047798	Cd300lf	1.156608499	0.0014401	7.52052367	7.70398571	7.6473994	7.57778902	7.682415038	7.61376735	9.26554423	9.301149	9.3212122	7.9412189	8.0733527	8.00373	
ENSMUSG000000057378	Ryr3	1.154887553	0.022938	4.95842939	4.32482117	4.86171081	4.7458302	5.467553804	6.436755992	6.10734854	5.8780348	5.6118449	5.0864827	5.4838651	5.6242398	
ENSMUSG000000056486	Chn1	1.15453962	0.0008282	5.3858252	5.387738	5.31046103	4.23955353	3.900368117	3.81031951	5.64271863	5.6463374	5.64270583	6.7393084	7.2633633	7.6054453	
ENSMUSG000000023913	Pla2g	1.154129381	0.0207404	8.90273562	8.88831602	8.8899855	9.650511597	9.605853781	9.4591968	11.0835603	10.953619	11.087793	9.3385411	9.3995178	9.3109706	
ENSMUSG000000066363	Serpina3t	1.151086701	0.0001003	7.161466507	6.886160307	7.98382266	7.957205224	7.652272272	7.80536485	7.613486953	7.64638308	8.6341714	8.7232093	8.7514051	8.7021469	
ENSMUSG000000022257	Laptm4b	1.14433724	0.026227	7.51621788	7.19582363	7.47996206	8.69660817	8.40496483	8.48991114	8.63178329	8.6875107	9.6282052	10.4804866	10.4196111	10.501907	
ENSMUSG000000024529	Lox	1.140649138	0.0056506	5.95881011	6.2128736	6.17401724	6.46557494	7.65961043	6.4676575	7.8379751	8.0878858	8.026841	6.5837004	6.7101664	6.7057654	
ENSMUSG000000072720	Myo18b	1.136985479	0.0001606	4.32558746	5.25267388	5.1737707	4.78421419	4.31481199	4.80010939	6.10734654	5.8533786	5.8567548	5.46252635	5.4245194		
ENSMUSG000000052957	Gas1	1.134132543	0.0391598	4.03070016	4.70304995	4.32482117	4.86171081	4.8976572	4.850310455	5.03696515	5.95302658	6.3876093	5.6517291	5.7357657	5.1275786	
ENSMUSG000000035873	Pawr	1.133034895	0.0131976	3.91050864	3.42482117	3.80983383	3.62520288	3.62520288	3.62520288	3.62520288	3.62520288	3.62520288	3.62520288	3.62520288		
ENSMUSG0000000505150	Zip7p	1.10959322	0.0050953	5.38825252	5.07793455	5.17702935	5.35778902	5.300636117	5.37933023	5.37933023	5.37933023	5.37933023	5.37933023	5.37933023		
ENSMUSG0000000502270	Fpr2	1.094051639	0.0301596	5.04827871	5.04757181	5.05215202	5.47451758	5.47451758	5.47451758	5.47451758	5.47451758	5.47451758	5.47451758	5.47451758		
ENSMUSG000000070369	Acer2	1.049537535	0.0057338	6.662294795	6.58849374	6.55182281	6.55882921	6.51198645	6.51198645	6.51198645	6.51198645	6.51198645	6.51198645	6.51198645	6.5124057	
ENSMUSG000000030807	Tvcam1	1.06322666	0.0092361	12.6237726	12.6127919	12.61749793	13.3637893	13.3637893	13.3637893	13.3637893	13.3637893	13.3637893	13.3637893	13.3637893		
ENSMUSG000000021567	Nkd2	1.060530853	0.0103659	5.52038625	5.12458745	5.00375869	5.38269568	5.1241051	5.00803065	5.84428313	5.84428313	5.84428313	5.84428313	5.84428313	5.84428313	
ENSMUSG000000038702	Dsel	1.057716783	0.0107457	5.04827871	5.24954522	5.00092322	5.38633777	5.38633777	5.38633777	5.38633777	5.38633777	5.38633777	5.38633777	5.38633777		
ENSMUSG000000050105	Grrp1	1.056746936	0.0029387	4.86223234	5.003164	4.52713629	5.07808018	5.64622387	5.64622387	5.64622387	5.64622387	5.64622387	5.64622387	5.64622387		
ENSMUSG000000036689	Ago 2	1.01701368	0.0117118	5.81193468	6.13362563	6.13362563	6.13362563	6.133625								

ENSMUSG000000073821	8030451A03Rik EN	-2.034526497	0.0015178	4.17376203	4.32482117	4.00324548	5.77149776	5.664223877	5.82502842	2.80681915	3.5816684	3.3201366	4.1689007	3.6980072	3.4582072
ENSMUSG000000031289	II13ra2	-2.058257339	0.00657229	5.64839374	5.39558892	5.00378569	7.57757194	7.568714194	7.58417614	4.69938173	4.2440258	4.3575315	5.4906532	5.2822458	5.6986634
ENSMUSG000000025905	Oprk1	-2.074340283	0.036233	5.09181499	4.81045442	4.7401076	5.82686532	5.82984884	8.52301676	6.20827055	6.40468	5.6119669	4.8568457	5.3891376	4.4578572
ENSMUSG000000074689	Ighv1-81	-2.078084829	0.0143003	6.8874076	6.49530804	7.11272495	10.3937047	10.34757759	10.3380831	6.48422893	6.7082664	7.0951324	7.7866094	7.7312607	7.7395785
ENSMUSG000000034731	Dgkh	-2.078894396	0.020105	6.82493613	6.77166724	9.77235151	9.55166062	9.576107386	9.44280291	6.47453922	6.7082664	6.4065447	6.67116	6.9154646	6.7376815
ENSMUSG000000048001	Hes5	-2.088807711	0.0428446	4.91116549	4.95734574	5.04819618	9.20860188	9.306304012	9.32475128	6.71304274	6.3703341	6.59704932	6.2082076	5.9509084	5.8808491
ENSMUSG000000039691	Tspan10	-2.100528015	0.0003984	5.09181499	5.13248572	4.91064028	6.31182357	6.276958431	6.40133334	2.99937492	3.1389638	3.3201366	4.6993254	4.5206589	4.3907597
ENSMUSG000000087670	9530036M11Rik	-2.114066048	0.0201062	3.3248899	2.58616865	3.17232976	3.79976415	3.579034195	3.57933023	2.58454581	2.3209407	2	2.8067906	2.3212258	2.5843213
ENSMUSG000000076880	Ighv6-6	-2.114257759	0.0200546	5.46391545	5.67575754	5.86200878	9.3795943	9.355282733	9.42830383	6.10734654	5.9022768	5.9279464	6.8690927	6.7108684	6.7396145
ENSMUSG000000067242	Lgl1	-2.200640717	0.0064262	4.52763697	4.3952449	4.32538969	7.14953168	7.295105165	7.20122591	5.08635957	5.4194791	4.6413475	3.9990123	3.9973646	3.9985569
ENSMUSG0000000114204	Gm35279	-2.217445901	1.85E-05	4.00370016	4.26564927	4.39582017	4.8767527	4.575584204	4.08100044	5.46863601	3.1389638	3.4562874	3.1682663	5.8814153	5.7781007
ENSMUSG000000048903	Bnip5	-2.229472198	0.0404492	7.95321895	8.05349049	7.89970876	4.9449351	4.899179037	4.6932873	3.45683601	3.1682663	5.8814153	5.7781007	5.27216413	
ENSMUSG000000040536	Necab1	-2.231610422	0.0404492	7.36233637	7.2323378	7.37926114	10.6241862	11.5374844	11.8859126	8.146802097	8.3349672	8.1468022	8.6533321	8.7171676	8.5905525
ENSMUSG000000058246	Gm10037	-2.270456851	0.0003526	4.52763697	4.0902284	3.81044063	4.23953532	4.694282913	4.31561673	2.80681915	5.5283164	3.4575315	2.3216648	2.9982436	2
ENSMUSG000000091679	Vmn2r96	-2.275034215	0.000118	4.39631085	4.3282117	3.46218583	4.38371152	4.314811199	4.51657988	2.99937492	2	4.5375315	2.8067906	2.5837918	2.8065305
ENSMUSG000000015599	Ttkb1	-2.282287469	0.0480931	3.17266678	3.0018088	2.3227942	3.15535543	3.99332894	3.9069388	2.80681915	2.3209407	2.3213112	2.8067906	2	
ENSMUSG000000096638	Ighv2-9	-2.31394373	0.0120474	4.46346759	3.8099388	3.45982017	7.49739094	7.58427375	7.58417614	8.30641687	3.9962936	3.4562874	3.1682663	5.8814153	5.7781007
ENSMUSG000000103749	Pcdhg5	-2.32085305	0.0062016	3.32488989	3.17119346	3.00432545	4.07934524	4.0937493	3.99332894	3.232167809	3.52080275	3.4575315	2.5845236	2	2.3215434
ENSMUSG000000034634	Ly6d	-2.323074219	0.0074472	10.1912088	10.1016343	9.0309819	13.29557	13.24981526	13.4378543	10.810127	10.892912	10.8101081	9.8175571	8.6295157	8.9406057
ENSMUSG0000000108187	4930511E03Rik	-2.326450410	0.0294094	4.64799974	5.64817827	4.81106345	3.31555453	3.202152566	3.45405584	2.3209407	2.5839675	2.30867906	3.4571958	3.3207737	
ENSMUSG000000086638	4930405A21Rik	-2.349510243	0.0294962	3.17266678	3.8099388	3.17232976	4.1615675	3.54537331	3.80131951	2.80681915	2.5389675	2.3216648	2.5837918	2.8065305	
ENSMUSG000000077431	Gm22591	-2.349610144	0.0018982	4.00370016	3.8099388	3.45238969	3.15555453	3.16593717	3.31686005	2.80681915	2.3209407	2	4.5375315	2.8067906	2.5837918
ENSMUSG000000031297	Scl7c3	-2.35364877	0.0070118	4.0370016	4.3952449	4.52713626	6.55966862	6.606172633	6.54649305	4.3836150	3.9901213	4.4565564	3.9985569		
ENSMUSG000000096461	Igkv14-130	-2.354985026	0.0111291	4.70461338	4.70394952	4.17390555	7.8097293	7.58427375	7.58417614	8.30641687	3.99632936	3.4562874	3.1682663	5.8814153	5.7781007
ENSMUSG000000094686	Cd12a1	-2.373678825	7.02E-05	6.9705819	6.74479473	6.77235151	8.15943499	8.068046255	8.16156813	5.52080275	5.75301304	5.520835	5.2467492	4.85208223	5.979884
ENSMUSG000000040907	Alp1a3	-2.3733074219	0.0074472	10.1912088	10.1016343	9.0309819	13.29557	13.24981526	13.4378543	10.810127	10.892912	10.8101081	9.8175571	8.6295157	8.9406057
ENSMUSG000000049100	Pcdh1	-2.373222738	0.0024843	3.81044063	3.8099088	3.90771789	3.79976415	3.74957718	3.740410817	3.70831756	3.80364167	3.4562874	3.9047007	5.0863008	5.7781007
ENSMUSG0000000112797	Gm30034	-2.413884508	0.0260061	2.80947046	2.85816865	3.17232976	5.19968894	5.546446959	5.34992256	5.28545481	3.3189638	3.2311312	3.1691935	3.8058495	3.3207737
ENSMUSG000000012350	Ehf	-2.423718249	0.0057917	4.17376203	4.46239037	4.7041076	7.07713855	7.37051529	7.17168638	3.16923045	3.9776703	4.3912513	4.9511354	4.8563221	
ENSMUSG000000095889	Ighv1-58	-2.435715155	0.0184221	4.58907321	4.32482117	3.58784774	7.82875198	7.939610206	8.00290208	3.584129	3.9047007	5.4906532	5.1261702	5.2077371	
ENSMUSG000000076577	Ighv8-30	-2.4403939	0.0002292	4.84532692	8.54680683	5.041861059	11.4676407	11.44077569	11.4504746	8.0540581	4.8478918	8.3677366	8.1244422	8.1206568	8.0315279
ENSMUSG000000099478	Ighv1-54	-2.454515336	0.0162546	4.86223324	3.0031646	4.3952449	8.58524464	8.27951696	8.60265489	5.16863057	5.52083597	5.1672072	4.5224741	4.5820339	4.1684284
ENSMUSG000000040351	Sorsc1	-2.457804767	0.0042414	2.58660819	3.0018088	3.9106044	3.79976415	4.24004848	4.24004848	4.08100044	2.32167809	3.5833164	3.5839675	2.5845236	3.1215434
ENSMUSG000000094491	Igkv1-133	-2.496119535	0.0148364	4.70461358	4.26564927	4.17320955	7.94373022	7.30871789	7.3810783	8.07381756	3.80364172	3.4562874	3.9047007	5.0863008	5.7781007
ENSMUSG000000096670	Ighv2-6	-2.517592735	0.0307395	3.00246783	2.85816865	3.17232976	5.19968894	5.546446959	5.34992256	5.28545481	3.3189638	3.2311312	3.1691935	3.8058495	3.3207737
ENSMUSG0000000940451	Ighv1-36	-2.525450440	0.0049439	4.46346769	4.25078255	4.00324548	4.82081908	4.782875198	7.904153197	7.69214615	4.80628319	4.3801138	4.6413475	4.6993254	4.2464084
ENSMUSG000000030268	Bcat1	-2.545263577	3.80E-08	6.80479354	8.4589018	8.5892422	9.4972157	9.502577265	9.52808079	5.3831631	5.9022768	5.1263377	7.1983912	7.3017373	
ENSMUSG000000095981	Ighv10-1	-2.561629689	0.0042839	4.95894299	5.13248679	5.481961059	8.444646959	8.594816351	8.602645499	8.62654949	5.32080275	5.9962396	6.5692242	6.0190694	5.9050945
ENSMUSG000000095705	Ighv10-3	-2.565463433	0.0100645	4.75908943	5.46215452	5.5855649	9.306890624	9.295556056	9.28125062	9.29937492	5.49058095	5.16202783	6.0209243	6.3019538	6.3019538
ENSMUSG000000026616	Ct2	-2.69202042	0.0140466	5.55910126	4.24954255	5.21579488	6.9278512	7.02209472	7.38233748	8.3690584	3.6399556056	2.58214912	2.99937492	3.1697733	2.9990381
ENSMUSG000000034486	Gbx2	-2.727323324	0.0044927	3.70385599	3.17119346	3.81044063	3.99220264	3.295556056	3.295556056	2.805160044	2	2	2.8067906	2.3212258	2.9990381
ENSMUSG000000094345	Igkv14-126	-2.733466338	0.019965	5.21352852	5.25161228	5.1313511	9.095347293	9.204320984	9.34950901	9.316923045	3.183968793	2.4268879	4.6409042	4.3203887	
ENSMUSG000000035429	Ptprh	-2.772718258	0.0027258	3.17266678	3.2409844	3.46218583	3.79976415	3.316593717	3.450455084	2.32167809	3.2321312	2.8067906	2.3212258	2.9990381	
ENSMUSG000000038086	Hspb2	-2.805994146	0.0105016	4.72612616	3.42521626	3.2428117	3.58784774	7.22804926	7.161271392	7.29553879	2.9975301	3.5836561	5.1275786		
ENSMUSG0000000969489	Ighv2-5	-2.814570406	0.01212	3.70385599	4.0902284	3.24254078	5.05133774	5.11371934	5.102002323	5.23024072	3.20867906	3.1671805	4.2402556	4.805914	4.0595705
ENSMUSG0000000994166	Srca3l	-2.822115619	0.0081977	3.24889899	3.17119346	3.0715									

Table S3_Hallmark pathways enriched in Bcat1 WT and KO leukemias

Pathways enriched in Bcat1 WT leukemias	ES	NES	NOM p-val	FDR q-val
HALLMARK_G2M_CHECKPOINT	0.42567	1.71925	0	0.006739
HALLMARK_MITOTIC_SPINDLE	0.41392	1.68235	0	0.006137
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.34885	1.423	0.004451	0.097323
HALLMARK_E2F_TARGETS	0.34738	1.40488	0.0118871	0.087318
HALLMARK_IL2_STAT5_SIGNALING	0.29979	1.21522	0.0751105	0.416291
HALLMARK_UV_RESPONSE_DN	0.31143	1.21287	0.1036496	0.353612
HALLMARK_COAGULATION	0.28995	1.13833	0.1869301	0.530567
HALLMARK_ESTROGEN_RESPONSE_EARLY	0.27199	1.10751	0.2315341	0.573327
HALLMARK_INFLAMMATORY_RESPONSE	0.2671	1.07843	0.2759104	0.6134
HALLMARK_HEDGEHOG_SIGNALING	0.34868	1.06397	0.3468697	0.604395
HALLMARK_TGF_BETA_SIGNALING	0.31186	1.04334	0.3811802	0.620579
HALLMARK_MYOGENESIS	0.25379	1.03423	0.3644444	0.600102
HALLMARK_TNFA_SIGNALING_VIA_NFKB	0.23717	0.97192	0.5369318	0.76375
HALLMARK_SPERMATOGENESIS	0.25016	0.96383	0.5342262	0.735256
HALLMARK_KRAS_SIGNALING_DN	0.23191	0.94643	0.6017442	0.739215
HALLMARK_ESTROGEN_RESPONSE_LATE	0.2323	0.94442	0.6143057	0.69889
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	0.24033	0.91822	0.6308943	0.73008
HALLMARK_ANGIOGENESIS	0.26646	0.83742	0.744186	0.88554
HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.21143	0.66439	0.9622642	0.992732

Pathways enriched in Bcat1 KO leukemias	ES	NES	NOM p-val	FDR q-val
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-0.55955	-2.41774	0	0
HALLMARKADIPOGENESIS	-0.44633	-1.96541	0	0
HALLMARK_PEROXISOME	-0.42111	-1.68117	0.0026667	0.016598
HALLMARK_DNA_REPAIR	-0.39622	-1.6771	0	0.01317
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-0.48062	-1.62967	0.0025063	0.014993
HALLMARK_XENOBIOTIC_METABOLISM	-0.36976	-1.60909	0	0.014463
HALLMARK_INTERFERON_ALPHA_RESPONSE	-0.40215	-1.58082	0.005102	0.016218
HALLMARK_APOPTOSIS	-0.35749	-1.53048	0	0.023055
HALLMARK_P53_PATHWAY	-0.34366	-1.52925	0.0030211	0.020832
HALLMARK_BILE_ACID_METABOLISM	-0.37796	-1.51214	0.0058651	0.021403
HALLMARK_IL6_JAK_STAT3_SIGNALING	-0.39037	-1.4898	0.0086207	0.023926
HALLMARK_FATTY_ACID_METABOLISM	-0.34599	-1.47731	0.0031847	0.02465
HALLMARK_HYPOXIA	-0.3309	-1.44721	0.006079	0.029479
HALLMARK_INTERFERON_GAMMA_RESPONSE	-0.3166	-1.39444	0.012945	0.045257
HALLMARK_PI3K_AKT_MTOR_SIGNALING	-0.3471	-1.38569	0.0258621	0.046325
HALLMARK_COMPLEMENT	-0.31305	-1.35672	0.0186916	0.056331
HALLMARK_ALLOGRAFT_REJECTION	-0.29664	-1.30317	0.020339	0.081336
HALLMARK_PANCREAS_BETA_CELLS	-0.37285	-1.26095	0.1234867	0.110291
HALLMARK_KRAS_SIGNALING_UP	-0.27289	-1.20407	0.070946	0.166313
HALLMARK_MTORC1_SIGNALING	-0.27663	-1.20235	0.0758621	0.160013
HALLMARK_APICAL_JUNCTION	-0.26799	-1.18999	0.0664452	0.170627
HALLMARK_GLYCOLYSIS	-0.26816	-1.18638	0.0827815	0.167523
HALLMARK_MYC_TARGETS_V1	-0.25788	-1.13489	0.1456954	0.234451
HALLMARK_HEME_METABOLISM	-0.25118	-1.09828	0.2024169	0.292568
HALLMARK_UV_RESPONSE_UP	-0.25492	-1.08273	0.2739274	0.316627
HALLMARK_PROTEIN_SECRETION	-0.26803	-1.05734	0.3164894	0.359791
HALLMARK_NOTCH_SIGNALING	-0.31323	-0.98176	0.4774347	0.565478
HALLMARK_CHOLESTEROL_HOMEOSTASIS	-0.249	-0.94304	0.5605263	0.671222
HALLMARK_ANDROGEN_RESPONSE	-0.22428	-0.88852	0.7147059	0.817348
HALLMARK_APICAL_SURFACE	-0.23808	-0.81848	0.8004751	0.938566
HALLMARK_MYC_TARGETS_V2	-0.16052	-0.57775	0.9976247	0.999054

Table S4: Primer sequences for amplification of BCAT1 promoter using Methylation Specific PCR (MSP)

TARGET LOCI	DIRECTION	SEQUENCE (5' to 3')
BCAT1-prom-T1-M	FORWARD	GAGAGATTTATTATTGGGGGC
BCAT1-prom-T1-M	REVERSE	CTAACCGTATAAACCGAATCTACGA
BCAT1-prom-T1-U	FORWARD	GAGAGATTTATTATTGGGGGTG
BCAT1-prom-T1-U	REVERSE	TAACCATAAACCAAATCTACAAC
BCAT1-prom-T1-WT*	FORWARD	GTGTCTTCCTGCTGATGCAA
BCAT1-prom-T1-WT	REVERSE	AGATCCAAGGGTCGTAGC
ACTB	FORWARD	GTGATGGAGGAGGTTAGTAAGTT
ACTB	REVERSE	AATTACAAAAACCAACCTAATAAA

*WT, represents unmodified or wild-type primers. M, methylation-specific primers; and U, unmethylated-specific primers.

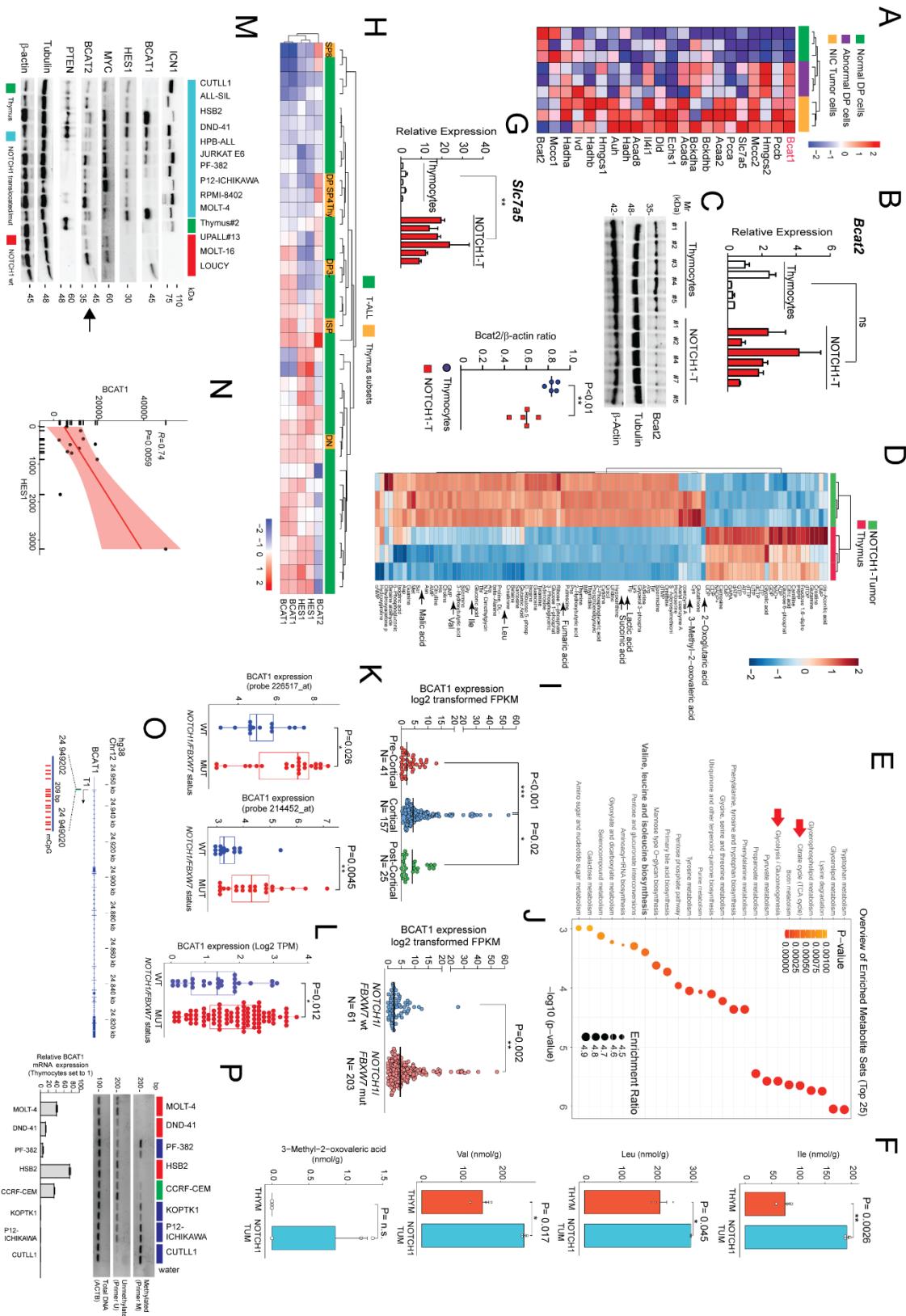
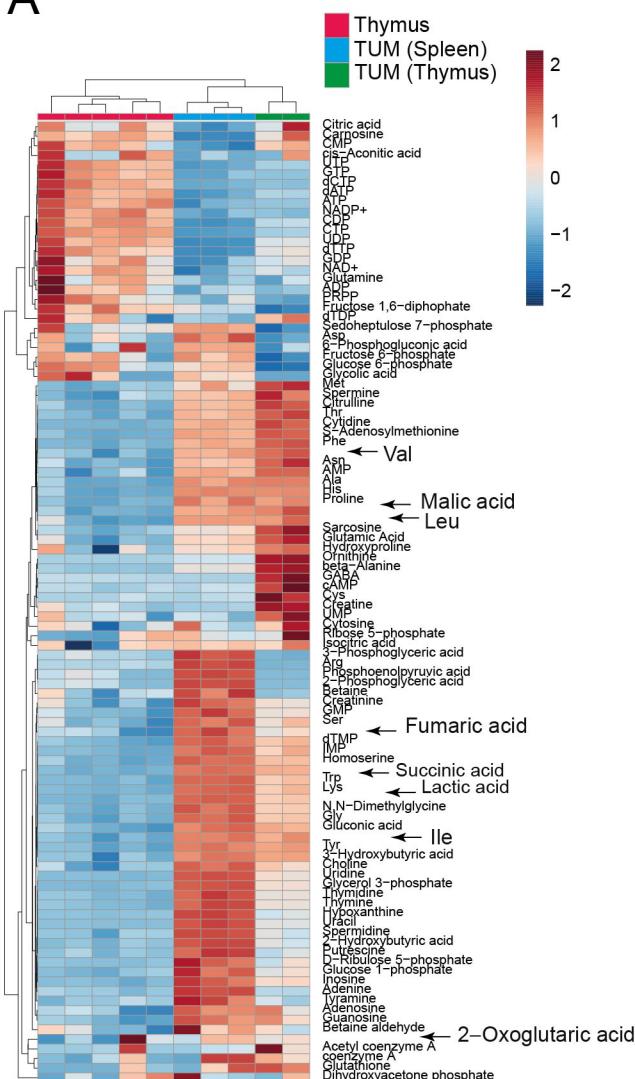


Figure S1. BCAT1 is highly expressed in NOTCH1 mutant T-cell acute lymphoblastic leukemia (T-ALL). (A) Heat map showing the expression levels of BCAA metabolic genes (N=22) between normal, abnormal (pre-

leukemic) DP cells and *ICN1*-induced DP leukemic cells (NIC Tumors). (B) Expression levels (qRT-PCR) of *Bcat2* in thymocytes obtained from 6-8 weeks old C57/Bl6 mice and leukemic cells from six *ΔE-NOTCH1* T-ALL tumors (NOTCH1-T). Significance was calculated using an unpaired two-tailed t-test. ns= not significant. (C) Western blot (top) showing protein expression levels of Bcat2. β-actin and tubulin are shown as loading controls. Graphical representation of Bcat2/β-actin ratios (bottom). Bars represent mean values. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$. (D) Heatmap representation of metabolites identified by capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS) of thymic tissue (N=3) obtained from 6 weeks old C57/Bl6 mice and NOTCH1-induced *ΔE-NOTCH1* tumor tissue (spleen; N=3). (E) Metabolite Set Enrichment Analysis (MSEA) was used to determine differentially enriched metabolite sets between normal thymic tissue and *ΔE-NOTCH1* tumors. The top 25 enriched pathways are shown. (F) Quantification of tissue BCAA (isoleucine, leucine and valine) and BCKA (3-methyl-2-oxovaleric acid, KMV) in thymic tissue (N=3) obtained from 6 weeks old C57/Bl6 mice and NOTCH1-induced *ΔE-NOTCH1* tumor tissue (spleen; N=3). Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$. (G) Expression levels (qRT-PCR) of *Lat1* (*slc7a5*) in thymocytes obtained from 6-8 weeks old C57/Bl6 mice and leukemic cells from six *ΔE-NOTCH1* T-ALL tumors (NOTCH1-T). Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$. (H) Heat map showing the expression levels of BCAT1 (two probes), BCAT2 and HES1 (surrogate of activated NOTCH1) between healthy human thymic subpopulations and total thymus and diagnostic pediatric T-ALL samples (N=32). SP8=CD8 single positive, DP= CD3 negative CD4 and CD8 double positive, SP4= CD4 single positive, Thy=total thymus, DP3= CD3 positive CD4 and CD8 double positive, ISP=intermediate single positive, DN= CD4 and CD8 double negative. (I) BCAT1 expression levels in immunophenotypically distinct T-ALL subtypes (pre-cortical, cortical and post-cortical). Significance was calculated using a nonparametric t-test (Mann-Whitney). * $P < 0.05$, *** $P < 0.001$. (J) BCAT1 expression levels in *NOTCH1/FBXW7* wild-type (wt) and *NOTCH1/FBXW7* mutated (mut) T-ALL in COG ALL TARGET cohort¹⁴. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$. (K) BCAT1 expression levels in *NOTCH1/FBXW7* wt (wt) and *NOTCH1/FBXW7* mutated (mut) T-ALL in GSE14959 cohort (N=37)¹⁰. Two different probes are shown. Significance was calculated using a nonparametric t-test (Mann-Whitney). * $P < 0.05$, ** $P < 0.01$. (L) BCAT1 expression levels in NOTCH1 wild-type (wt) and NOTCH1 activated (*NOTCH1/FBXW7* mutated) T-ALL (adult and pediatric) (CGAS000000000002)¹¹. Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$. (M) Western blot analysis of ICN1, BCAT1, HES1, MYC, BCAT2, PTEN in T-ALL cell lines. Tubulin and β-actin are shown as loading controls. Cell lines with un-mutated NOTCH1 (wt) or activated NOTCH1 signaling (mutated/translocated) are shown. Arrow indicates specific band. (N) Correlation analysis between expression levels of BCAT1 and HES1 in T-ALL cell lines (ALL-SIL, CCRF-HSB2, DND41, HPB-ALL, Jurkat, PF-382, P12-Ichikawa, RPMI8402, MOLT4, CCRF-CEM, MOLT-3, MOLT-16; N=12) from GSE168386²⁸. (O) Schematic drawing of BCAT1 gene structure (left) with amplicon coordinates indicated (UCSC Genome browser GRCh38/hg38 version). Methylated cytosines residing in CpG sites are depicted as red lines. (P) Methylation specific PCR (MSP) of BCAT1 promoter T1²⁹, ³⁰was set-up and used to evaluate methylation status of BCAT1 in T-ALL cell lines. Primer sets used for amplification are designated as unmethylated (U) and methylated (M). A bisulphite-conversion specific beta-actin gene (*ACTB*) PCR assay was performed as control assay to evaluate total amount of analyzed DNA. All DNA samples were bisulfite-treated. Relative BCAT1 transcript levels of the analyzed T-ALL cell lines are also shown (lower panel). BCAT1 expression is relative to a human thymocyte sample (#1).

A



B

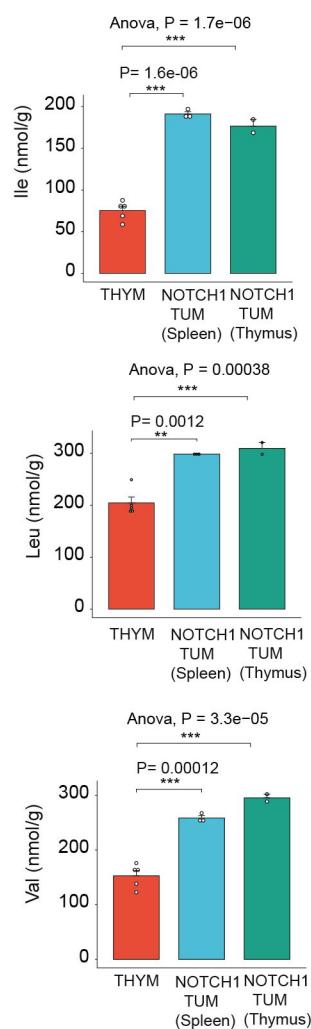


Figure S2. ΔE -NOTCH1 tumors derived from infiltrated spleen and thymus have a similar metabolic profile.
 (A) Heatmap representation of metabolites identified by capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS) of thymic tissue (N=5) obtained from 6 weeks old C57/Bl6 mice and NOTCH1-induced ΔE -NOTCH1 tumor tissue (spleen; N=3 or thymus; N=2). Selected metabolites differentially expressed between normal and leukemic tissue are remarked. (B) Quantification of tissue BCAA (isoleucine, leucine and valine) in thymic tissue (N=5) obtained from 6 weeks old C57/Bl6 mice and NOTCH1-induced ΔE -NOTCH1 tumor tissue (spleen; N=3 or thymus; N=2). Significance was calculated using an unpaired two-tailed t-test or ANOVA test (normal versus leukemia). **P< 0.01, ***P< 0.001.

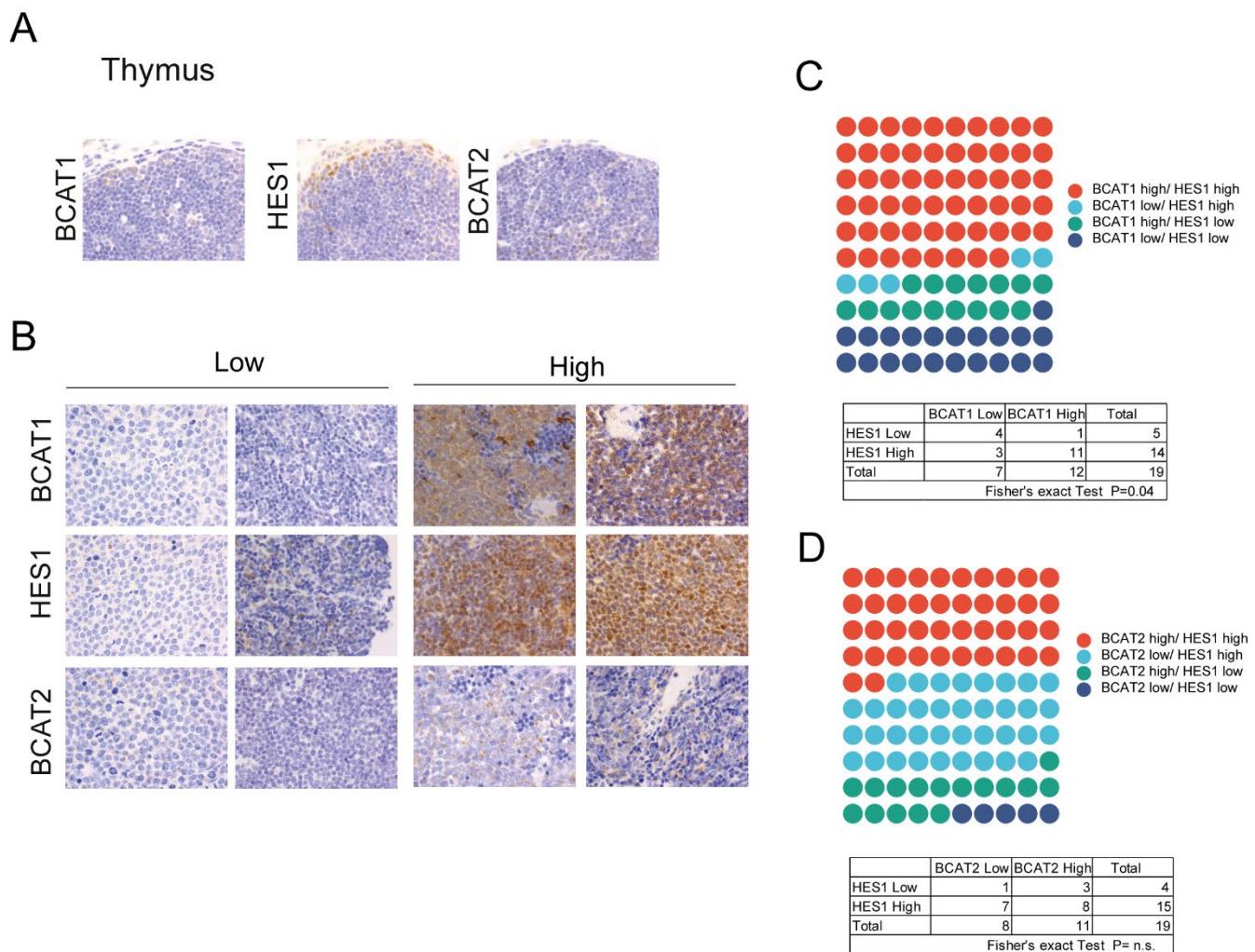


Figure S3. BCAT1 expression associates with NOTCH1 activation in human T-ALL. (A) BCAT1 (left), HES1 (middle) and BCAT2 (right) immunohistochemical staining of human thymus (top): original magnification 400×. (B) Immunohistochemical staining for BCAT1 (top), HES1 (middle), and BCAT2 (bottom) in representative cases of T-ALL showing low (0, +1) and high (+2, +3) expression levels. Original magnification ×400. (c) Circle waffle representation of BCAT1 immunohistochemical staining results obtained in T-ALL/T-LBL/PDX samples analysed (top) and correlation table for Fisher's exact test (bottom). (D) Circle waffle representation of BCAT2 immunohistochemical staining results obtained in T-ALL/T-LBL/PDX samples analysed (top) and correlation table for Fisher's exact test (bottom).

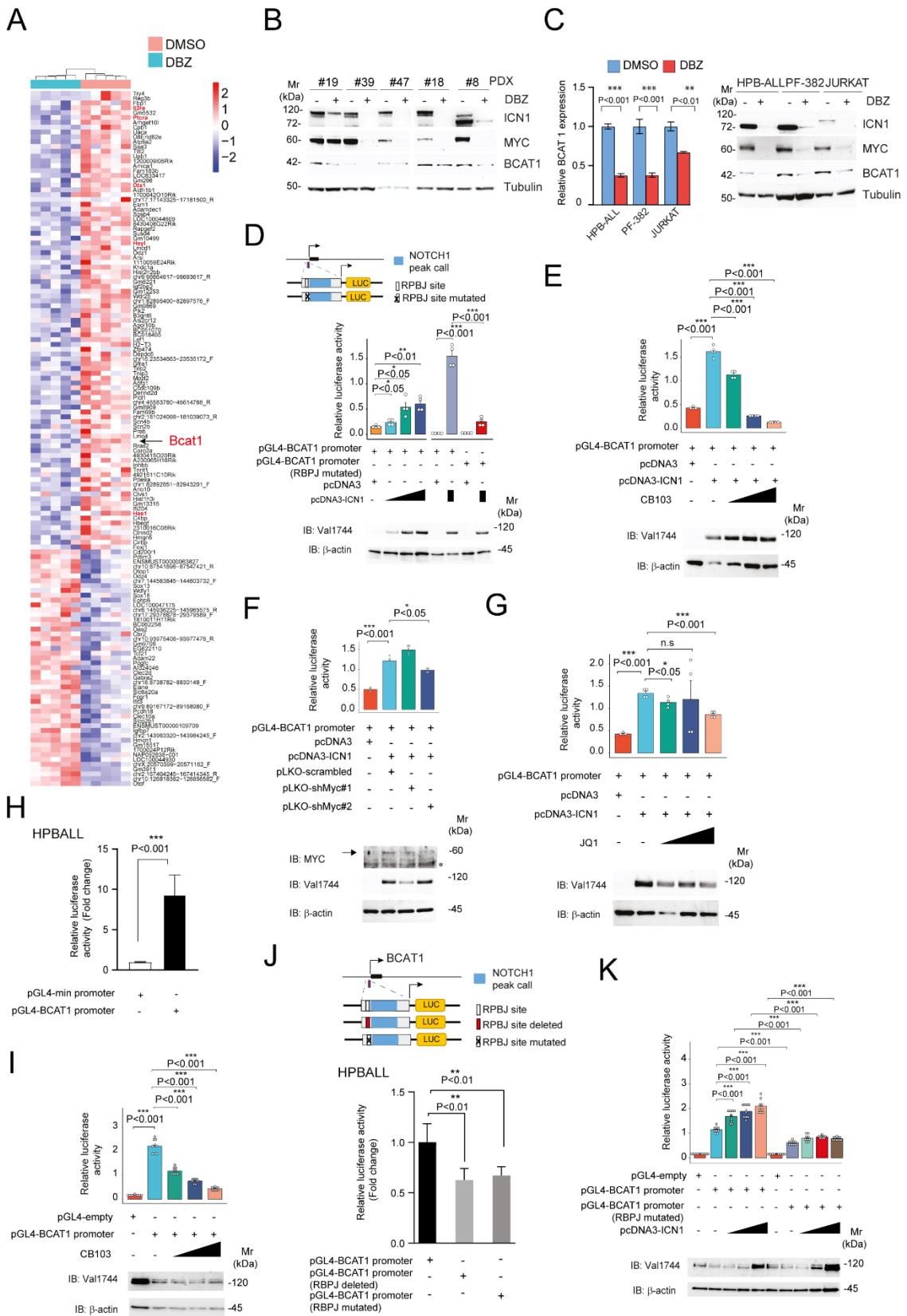


Figure S4. BCAT1 is modulated upon NOTCH1 inhibition. (A) Heat map representation of the top down-regulated genes following in vivo DBZ treatment of five ΔE -NOTCH1 tumors. BCAT1 and selected known

NOTCH1 target genes are shown¹. (B) PDX samples were treated in vivo with DBZ (10 µg/kg every 8 hours for a total of 3 injections) or vehicle (DMSO) for 24h before analysis of BCAT1 protein levels. ICN1 and MYC proteins are also shown. Tubulin is shown as loading control. (C) T-ALL cell lines were treated with DBZ (250 nM) or vehicle for 72h before analysis of BCAT1 transcript (left) or BCAT1 protein levels (right). ICN1 and MYC proteins are also shown. Tubulin is shown as loading control. Mean value and SD are shown. For statistical analysis, an unpaired t-test was used. **P< 0.01. ***P< 0.001. (D) Schematic representation (top) of *BCAT1* promoter construct (BCAT1-Luc) containing the region -1407 to +195 from the transcription start site (TSS) including the proximal RBPJ binding site. The location of the NOTCH1 ChIP peak is also depicted on the reporter construct. HEK 293T cells were co-transfected with pGL4 luciferase reporter construct (BCAT1-Luc) and different amounts of pcDNA3-ICN1 or control plasmid. In some experiments, HEK 293T cells were also co-transfected with BCAT1-Luc having the RBPJ site mutated and ICN1 plasmid. Immunoblot shows expression levels of ICN1 in transfected cells. β-actin is shown as loading control. Error bars indicate ± SD. Results from one of two independent experiments performed in quadruplicate are shown. Significance was calculated using an unpaired two-tailed t-test. * P< 0.05, **P< 0.01, ***P< 0.001. (E) HEK 293T cells were co-transfected with pGL4 luciferase reporter construct (BCAT1-Luc) and ICN1 or control plasmid. After 24h, ICN1 transfected cells were treated with increasing concentration of CB103 (10 nM-1 µM) or vehicle for 48h. Immunoblot shows expression levels of ICN1 in transfected cells. β-actin is shown as loading control. Error bars indicate ± SD. Results from one of two independent experiments performed in quadruplicate are shown. Significance was calculated using an unpaired two-tailed t-test. ***P< 0.001. (F) HEK 293T cells were co-transfected with pGL4 luciferase reporter construct (BCAT1-Luc) and ICN1 or control plasmid. After 24h, ICN1 transfected cells were transfected with plasmids silencing MYC (pLKO-shMYC#1, pLKO-shMYC#2) or non-silencing control (pLKO-shscrambled). Cells were harvested 48h later. Immunoblot shows expression levels of MYC and ICN1 in transfected cells. β-actin is shown as loading control. Arrow indicates specific band. Asterisc (*) indicates non-specific band. Error bars indicate ± SD. Results from one of two independent experiments performed in quadruplicate are shown. Significance was calculated using an unpaired two-tailed t-test. * P< 0.05, ***P< 0.001. (G) HEK 293T cells were co-transfected with pGL4 luciferase reporter construct (BCAT1-Luc) and ICN1 or control plasmid. After 24h, ICN1 transfected cells were treated with increasing concentrations of JQ1 (10 nM-1 µM) or vehicle for 48h. Immunoblot shows expression levels of ICN1 in transfected cells. β-actin is shown as loading control. Error bars indicate ± SD. Results from one of two independent experiments performed in quadruplicate are shown. Significance was calculated using an unpaired two-tailed t-test. * P< 0.05, *** P< 0.001. n.s=not significant. (H) Relative luciferase reporter activity in HPB T-ALL cells transfected with a BCAT1 promoter construct (BCAT1-Luc) or empty pGL4minP plasmid. Mean value and SD are shown (N =6). For statistical analysis, an unpaired t-test was used. ***P< 0.001. The experiment was repeated three times with similar results. (I) Relative luciferase reporter activity in HPB T-ALL cells transfected with pGL4 luciferase reporter construct (BCAT1-Luc) or control plasmid. After 24h, transfected cells were treated with increasing concentration of CB103 (0.5 µM-5 µM) or vehicle for 48h. Immunoblot shows expression levels of ICN1 in transfected cells. β-actin is shown as loading control. Error bars indicate ± SD. Results from one of two independent experiments performed is shown. Significance was calculated using an unpaired two-tailed t-test. ***P< 0.001. (J) Relative luciferase reporter activity in HPB T-ALL cells transfected with BCAT1-Luc wt construct, BCAT1-Luc having the RBPJ site deleted or mutated. Mean value and SD are shown (N=6). For statistical analysis, an unpaired t-test was used. **P< 0.01. The experiment was repeated three times with similar results. (K) Relative luciferase reporter activity in HPB T-ALL cells transfected with BCAT1-Luc wt construct, BCAT1-Luc having the RBPJ site mutated or control vector. These cells were co-transfected with increasing concentrations of pcDNA3-ICN1 or control plasmid (100-500 ng). Error bars indicate ± SD. For statistical analysis, an unpaired t-test was used. ***P< 0.001. Immunoblot shows expression levels of ICN1 in transfected cells. β-actin is shown as loading control.

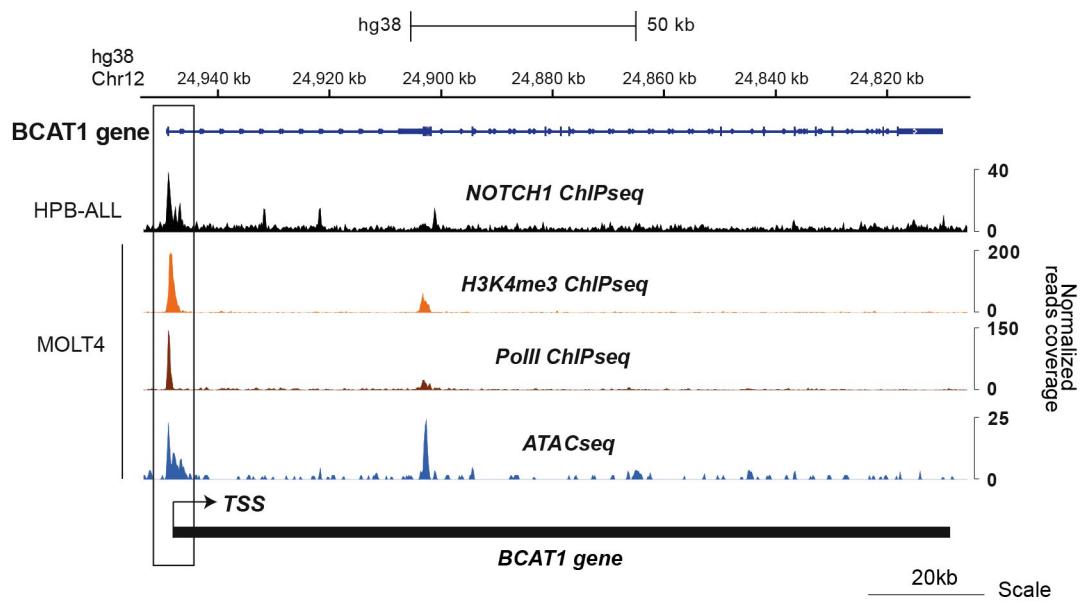
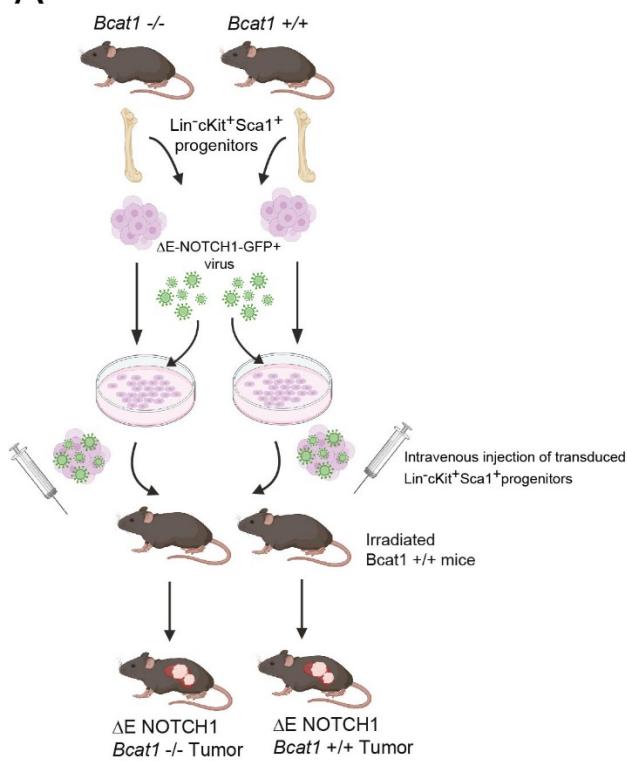
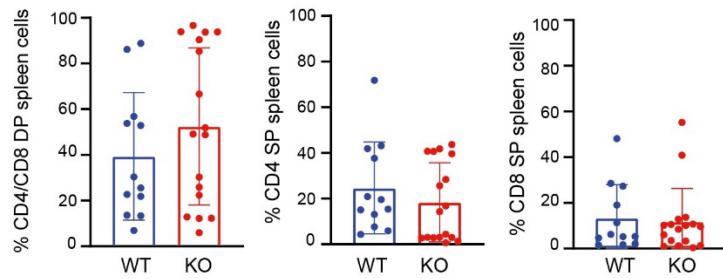


Figure S5. The NOTCH1 binding region in the BCAT1 locus is associated with promoter features in T-ALL cells. Profiles of H3K4me3, Pol II and NOTCH1 ChIP-seq binding in the BCAT1 locus in T-ALL cells. ATAC-seq data for the same region is also shown.

A



B



C

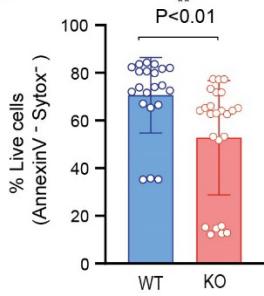


Figure S6. *Bcat1* promotes NOTCH1-dependent leukemia onset. (A) Schematic representation of the experimental procedure for the generation of ΔE -NOTCH1 leukemias wild-type (WT; +/+) and null (KO; -/-) for *Bcat1*. Image was generated with BioRender software. (B) Immunophenotype distribution showing the expression levels of CD4 and CD8 in ΔE -NOTCH1-induced leukemias at the moment of sacrifice. DN, double negative; DP,

double positive; SP, single positive. WT, *Bcat1* wild-type; KO, *Bcat1* null. (C) Quantification of viable cells (Annexin V⁻ Sytox Red⁻) in *ΔE-NOTCH1* leukemias WT and null for *Bcat1* obtained ex vivo (bar graph). Data for bar graph is shown as mean ± SD. Significance was calculated using an unpaired two-tailed t-test. **P<0.01.

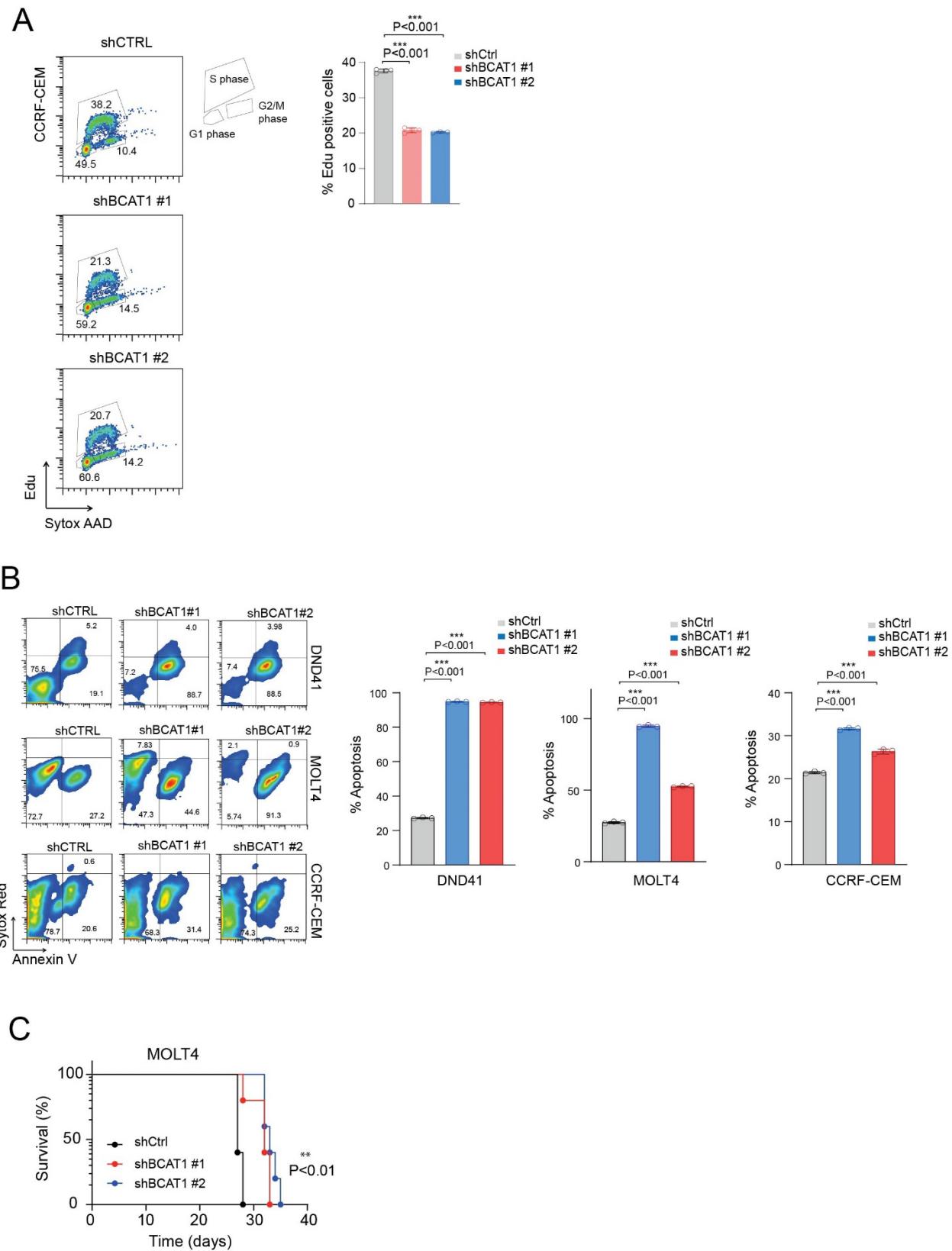


Figure S7. Functional effects of BCAT1 depletion. (A) Representative plots (left) and bar graph representation (right) of CCRF-CEM cells transduced with shCTRL, shBCAT1#1 or shBCAT1#2 twelve days post-puromycin

selection and assessed for EdU incorporation by fluorescence-activated cell sorting (FACS) analysis. Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. *** P < 0.001. (B) Representative plots of apoptosis (left) and quantification of apoptosis (right) in DND41, MOLT4 and CCRF-CEM T-ALL cells transduced with shCTRL, shBCAT1 #1 and shBCAT1 #2 constructs 3-5 days post-puromycin selection. Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. *** P < 0.001. (C) Kaplan-Meier survival curves of overall survival in NSG mice xenografted with MOLT4 cells expressing luciferase and transduced with shCTRL or shBCAT1 (#1 and #2). Log-rank test was performed to calculate P value. ** P < 0.01.

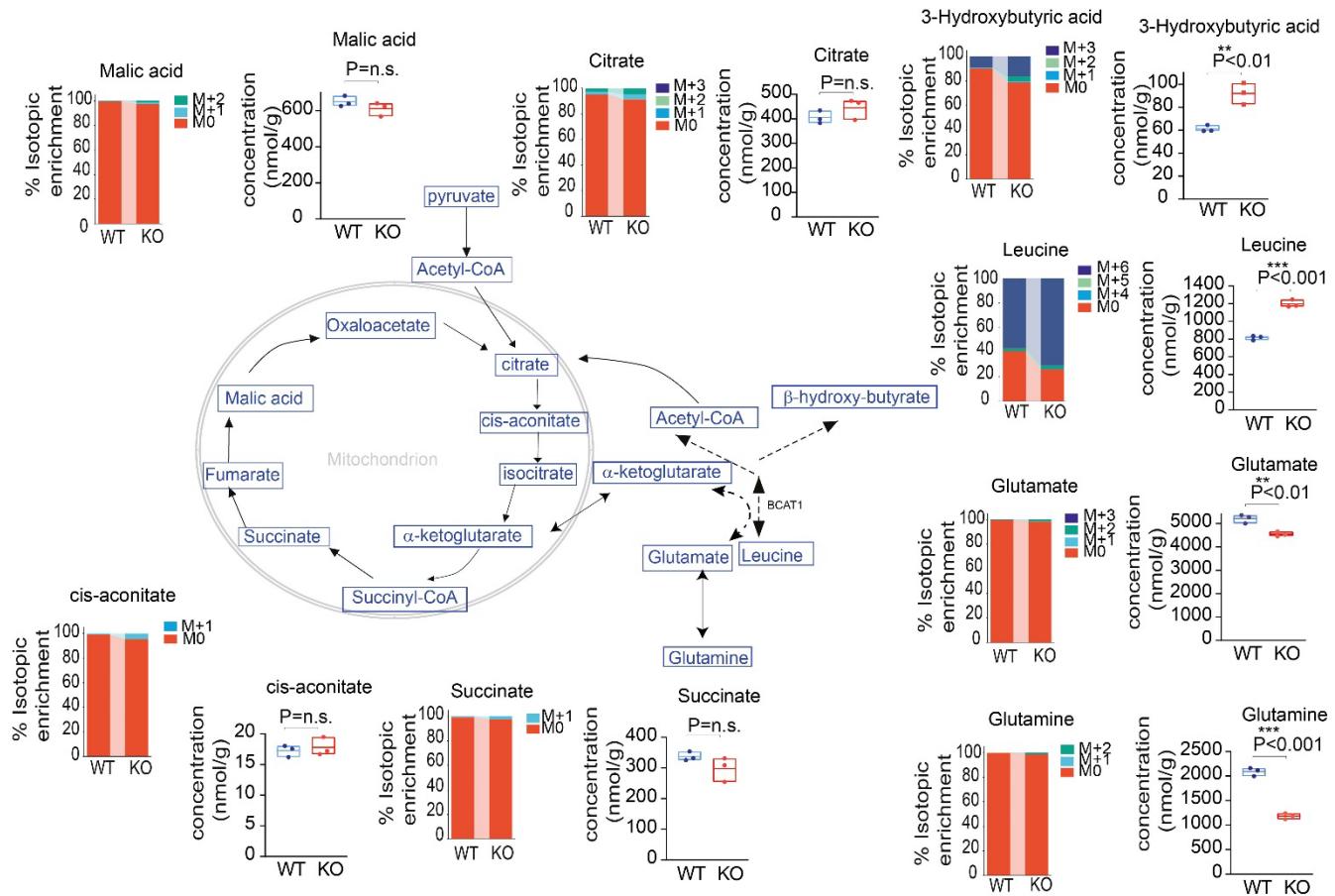


Figure S8. Metabolic impact of Bcat1 depletion on ΔE -NOTCH1 leukemias. Results for *in vivo* isotope-tracing experiments following i.v. administration of $^{13}\text{C}_6$ Leu in ΔE -NOTCH1 leukemias WT and KO for Bcat1. Mean percentages (from N=3 determinations) of $^{13}\text{C}_6$ Leu derived: (i) TCA intermediates: citrate (M0, M+1, M+2, M3), cis-aconitate, (M0, M+1), malic acid (M0, M+1, M+2), succinate (M0, M+1); (ii) BCAA and derivatives: leucine (M0, M+4, M+5, M+6), glutamate (M0, M+1, M+2, M3), glutamine (M0, M+1, M+2) and beta-hydroxybutyrate (M0, M+1, M+2, M+3) are shown. F-scope metabolic quantification for selected metabolites in the same tumors is also shown. Changes in glutaminolysis, TCA cycle intermediates, and BCAA and intermediates are shown as floating bars representing mean \pm SD. Significance was calculated using a nonparametric t-test (Mann-Whitney). *P< 0.05, **P< 0.01, ***P< 0.001. n.s.= not significant.

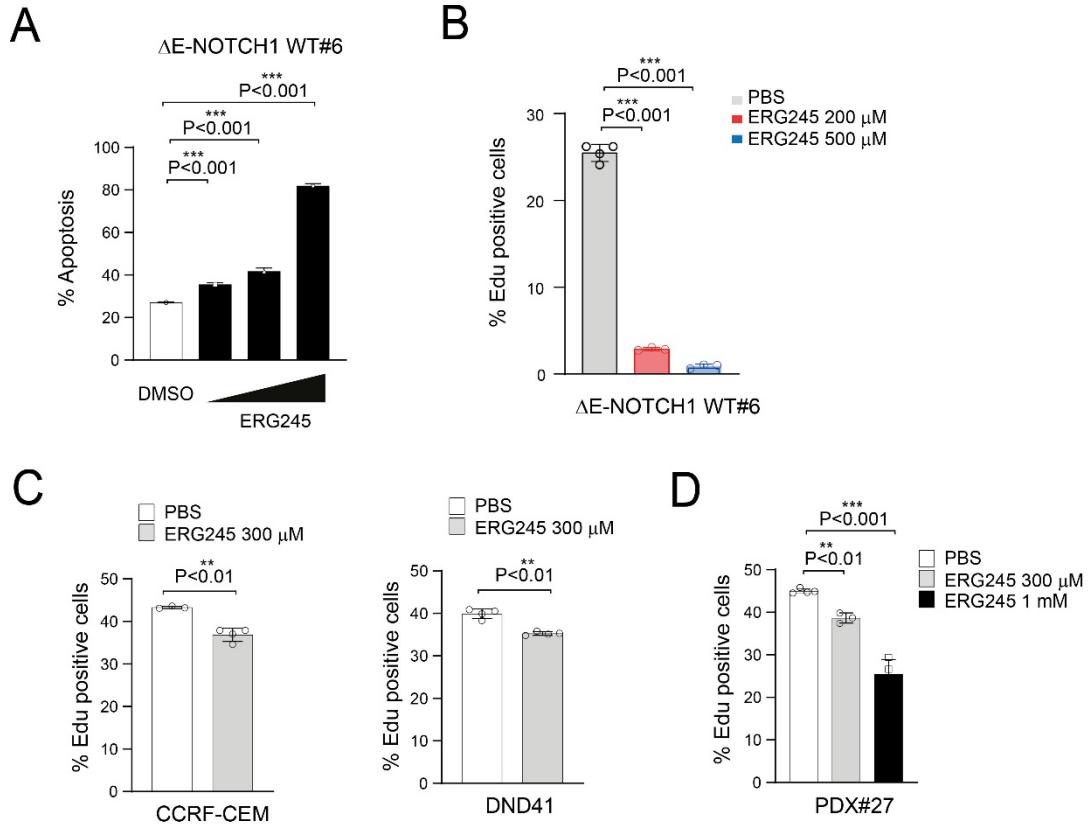


Figure S9. Functional effects of a BCAT1 specific inhibitor, ERG245. (A) Quantification of apoptosis in $\Delta E\text{-NOTCH1}$ leukemia wild-type for *Bcat1* (WT\#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μM -1 mM). Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (B) Quantification of EdU incorporation (S-phase cells) in $\Delta E\text{-NOTCH1}$ leukemia wild-type for *Bcat1* (WT\#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μM - 500 μM). Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (C) Quantification of EdU incorporation (S-phase cells) in T-ALL cell lines (CCRF-CEM, DND41) treated in vitro for 72h with PBS (vehicle) or ERG245 (300 μM). Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$. (D) Quantification of EdU incorporation (S-phase cells) in PDX\#27 treated in vitro for 72h with PBS (vehicle) or increasing doses of ERG245 (300 μM -1 mM). Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$.

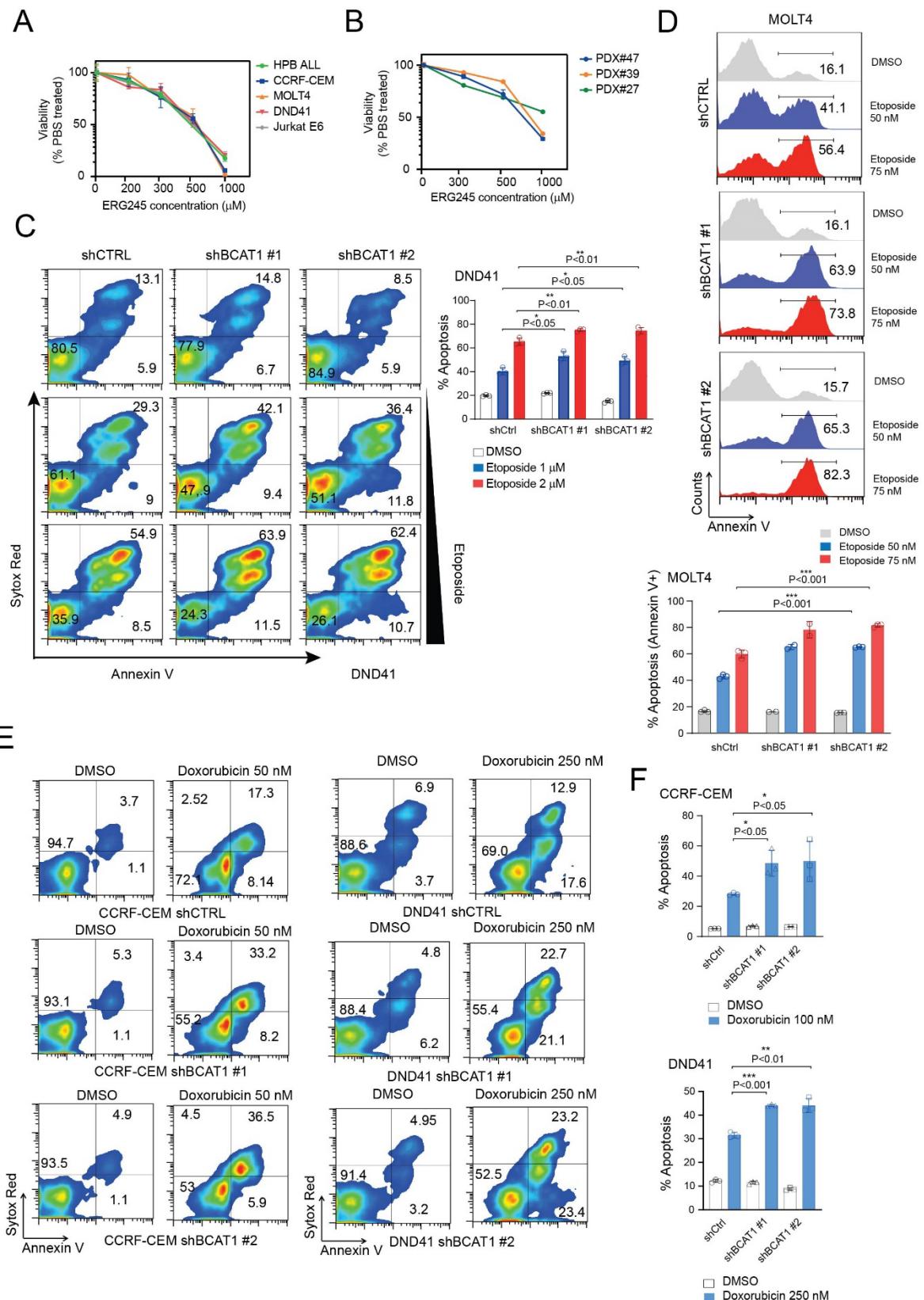


Figure S10. BCAT1 specific inhibition has modest cytotoxic effects on human T-ALL, while BCAT1 depletion increases sensitivity to DNA damaging agents. (A) Cell viability analysis in T-ALL cell lines (HPB-

ALL, CCRF-CEM, MOLT4, DND41, Jurkat E6). T-ALL cells were treated in vitro for 72h with PBS (vehicle) or increasing doses of ERG245 (200 μ M-1 mM). Data is shown as mean \pm SD. (B) Cell viability analysis in PDX samples (PDX#47, PDX#39, PDX#27). T-ALL cells were treated in vitro for 72h with PBS (vehicle) or increasing doses of ERG245 (300 μ M-1 mM). Data is shown as mean \pm SD. (C) Representative plots of apoptosis (left) in DND41 T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) and treated in vitro for 48h with DMSO (vehicle) or etoposide (1 μ M or 2 μ M). Quantification of apoptosis (right) in DND41 T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) and treated in vitro for 48h with DMSO (vehicle) or etoposide (1 μ M or 2 μ M). Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$. (D) Representative plots (top) and bar graph representation (bottom) of annexin V staining in MOLT4 T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) and treated with vehicle (DMSO) or etoposide (Etop; 50-75 nM) for 48h. (E) Representative plots of apoptosis in CCRF-CEM (left) or DND41 (right) T-ALL cells transduced with shCTRL, shBCAT1#1 or shBCAT1#2 and treated with vehicle (DMSO) or doxorubicin (Doxo; 50 or 250 nM, respectively) for 48h. (F) Bar graph representation of apoptosis in CCRF-CEM (top) or DND41 (bottom) T-ALL cells transduced with shCTRL, shBCAT1#1 or shBCAT1#2 and treated with vehicle (DMSO) or doxorubicin (Doxo; 50 or 250 nM, respectively) for 48h. Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

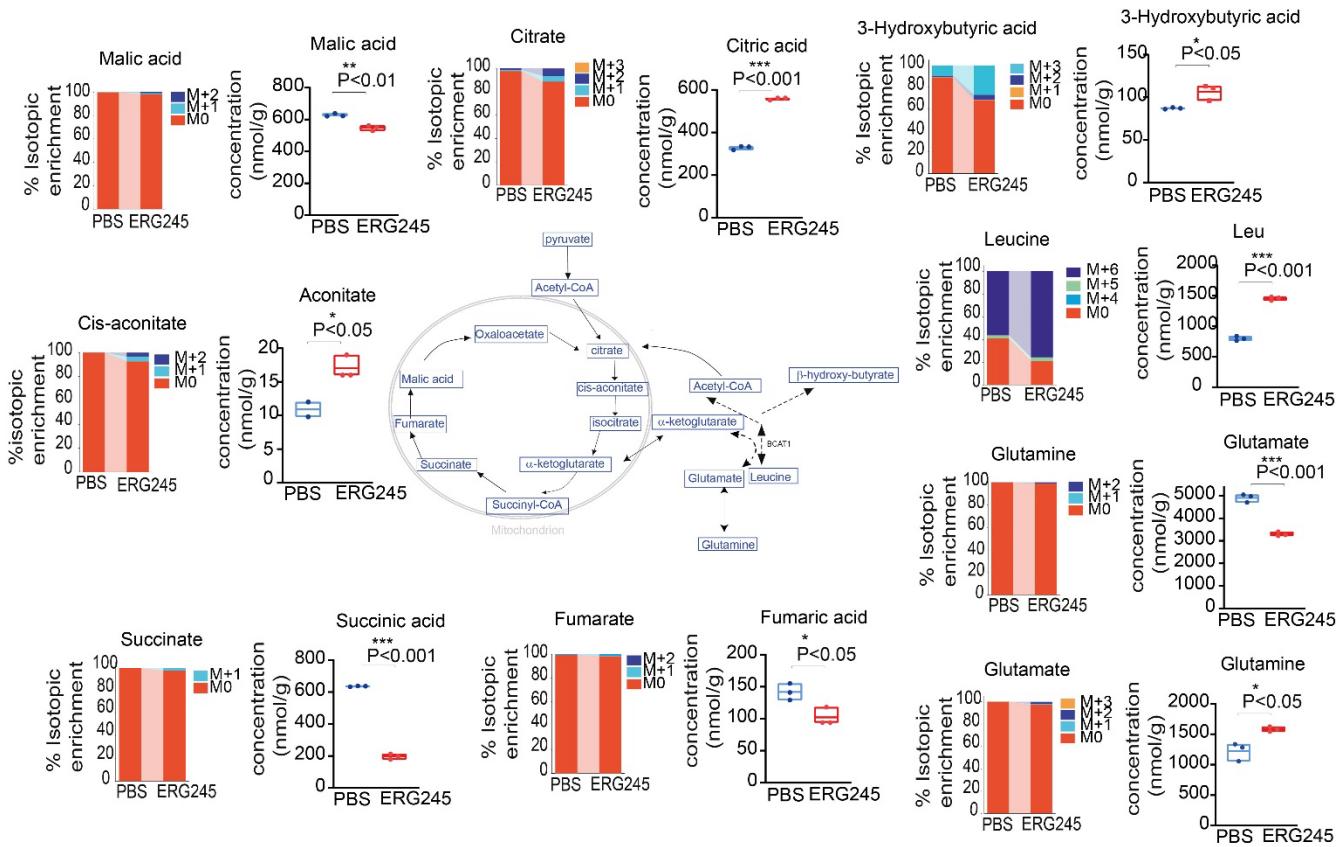


Figure S11. Metabolic impact of BCAT1 inhibition on ΔE -NOTCH1 leukemias. Results for *in vivo* isotope-tracing experiments following i.v. administration of $^{13}\text{C}_6$ Leu in primary ΔE -NOTCH1 leukemic tissue (N=3) treated with vehicle (PBS) or BCAT1-specific inhibitor, ERG245 (30 mg/kg every 8 hours for 24h). Percentages of $^{13}\text{C}_6$ Leu derived: (i) TCA intermediates: citrate (M₀, M₊₁, M₊₂, M₊₃), cis-aconitate, (M₀, M₊₁, M₊₂), fumarate (M₀, M₊₁, M₊₂), malic acid (M₀, M₊₁, M₊₂), succinate (M₀, M₊₁); (ii) BCAA and derivatives: leucine (M₀, M₊₄, M₊₅, M₊₆), glutamate (M₀, M₊₁, M₊₂, M₊₃), glutamine (M₀, M₊₁, M₊₂) and beta-hydroxybutyrate (M₀, M₊₁, M₊₂, M₊₃) are shown. F-scope metabolic quantification for selected metabolites in the same tumors is also shown. Changes in glutaminolysis, TCA cycle intermediates, and BCAA and intermediates are shown as floating bars representing mean \pm SD. Significance was calculated using a nonparametric t-test (Mann-Whitney). *P<0.05, **P<0.01, ***P<0.001. n.s.= not significant

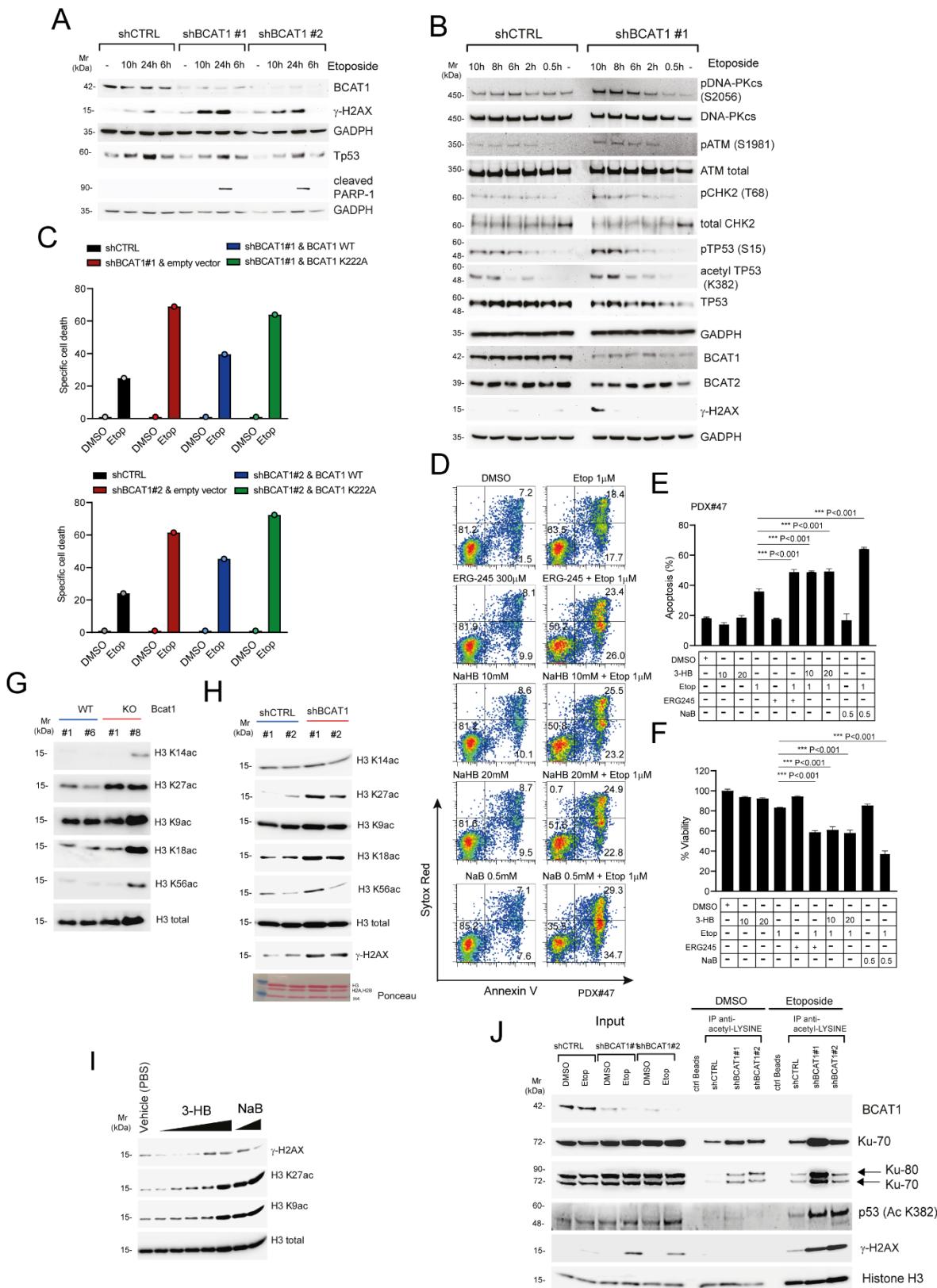


Figure S12. Increased responsiveness to DNA damaging agents in BCAT1 depleted cells is associated with an altered DNA damage response and dependent on its catalytic activity. (A) CCRF-CEM T-ALL cells

transduced with shCTRL or shBCAT1 (#1 and #2) were treated with 1 μ M etoposide for the indicated time. Subsequently, whole cell lysates were collected and analyzed by immunoblotting for proteins implicated in the DNA damage response and apoptosis (γ H2AX, TP53, cleaved PARP-1). GADPH is shown as loading control. (B) CCRF-CEM T-ALL cells transduced with shCTRL or shBCAT1 #1 were treated with 1 μ M etoposide for the indicated time (0-10 hours). Subsequently, whole cell lysates were collected and analyzed by immunoblotting for proteins implicated in the DNA damage response. Total DNA-PKcs, ATM, CHK2 and GADPH are shown as loading controls. (C) Specific apoptosis³¹ analysis in BCAT1 depleted CCRF-CEM T-ALL cells (shBCAT1#1 or shBCAT1#2) engineered to express empty vector, wild-type (WT) or catalytic inactive (K222A) BCAT1 and treated in vitro for 48h with DMSO (vehicle) or etoposide (1 μ M). Specific apoptosis analysis of CCRF-CEM cells infected with a control shRNA (shCTRL) and treated in vitro for 48h with DMSO (vehicle) or etoposide (1 μ M) is also shown. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. (D) Representative plots of apoptosis in PDX#47 cells treated with vehicle (DMSO), 3-HB (10-20 mM), NaB (0.5 mM), ERG245 (300 μ M) etoposide (Etop; 1 μ M) or the combination (ERG245 + Etop or 3-HB + Etop or NaB + Etop) for 48h. (E) Quantification of apoptosis in PDX#47 cells treated in vitro with vehicle (DMSO), 3-HB (10-20 mM), NaB (0.5 mM), ERG245 (300 μ M), etoposide (Etop; 1 μ M) or the combination (3-HB + Etop or ERG245 + Etop or NaB + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (F) Cell viability analysis in PDX#47 cells treated in vitro with vehicle (DMSO), 3-HB (10-20 mM), NaB (0.5 mM), ERG245 (300 μ M), etoposide (Etop; 1 μ M) or the combination (3-HB + Etop or ERG245 + Etop or NaB + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (G) Total histones were extracted from tumors WT or KO for *Bcat1* and immunoblots were performed for acetylated histone H3 variants. Total H3 is shown as loading control. (H) Total histones extracted from CCRF-CEM cells transduced with shCTRL (#1, #2) or shBCAT1 (#1 and #2) were analyzed by immunoblotting for acetylated histone H3 variants and γ H2AX. Total H3 and Ponceau staining are shown as loading controls. (I) CCRF-CEM T-ALL cells were treated for 24h with vehicle or increasing concentrations of 3-HB (1-40 mM) or NaB (0.5-1 mM). Total histones were extracted and analyzed by immunoblotting for selected acetylated histone H3 variants (K27ac, K9ac) and γ H2AX. Total H3 is shown as loading control. (J) CCRF-CEM T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) were treated with vehicle (DMSO) or 1 μ M etoposide for 24h, subsequently whole cell lysates were collected and immunoprecipitated using anti-acetyl-lysine affinity beads or control beads and probed for KU70, KU80, γ H2AX. Total H3 was used as loading control (for input).

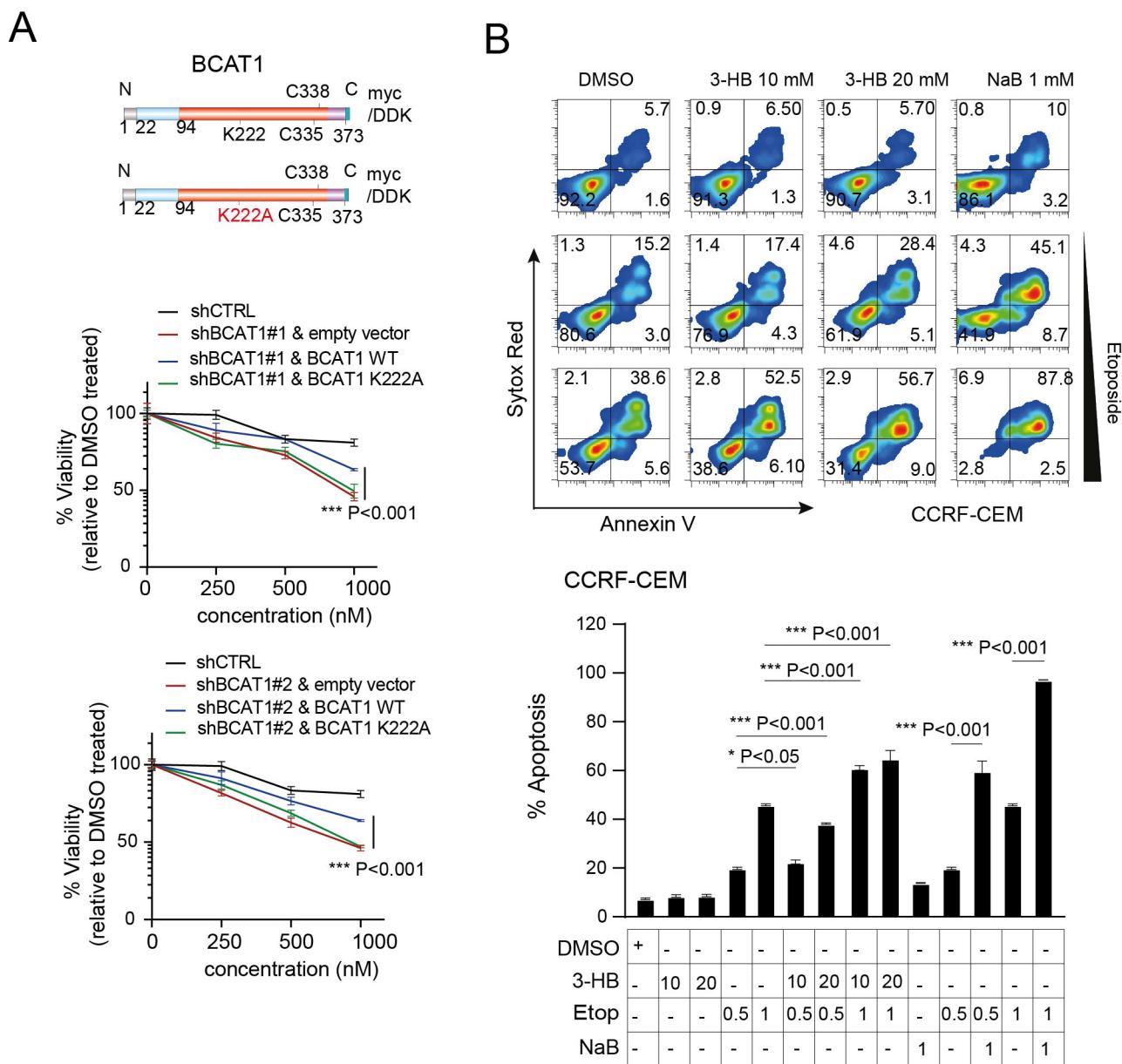


Figure S13. Metabolic function of BCAT1 contributes in modulating the sensitivity to DNA damaging agents. (A) Schematic representations (top) of the constructs encoding full-length (WT) and catalytic inactive mutant of BCAT1 (K222A). Cell viability analysis (lower panels) in BCAT1 depleted CCRF-CEM T-ALL cells (shBCAT1#1 or shBCAT1#2) engineered to express empty vector, wild-type (WT) or catalytic inactive (K222A) BCAT1 and treated in vitro for 48h with DMSO (vehicle) or etoposide (250 nM– 1 μ M). Cell viability analysis of CCRF-CEM cells infected with a control shRNA (shCTRL) and treated in vitro for 48h with DMSO (vehicle) or etoposide (250 nM– 1 μ M) is also shown. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (B) Representative plots of apoptosis (top) or quantification of apoptosis (bottom) in CCRF-CEM T-ALL cells treated with vehicle (DMSO), 3-HB (10-20mM), NaB (1mM), etoposide (Etop; 0.5-1 μ M) or the combination (3-HB + Etop or NaB + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, *** $P < 0.001$.

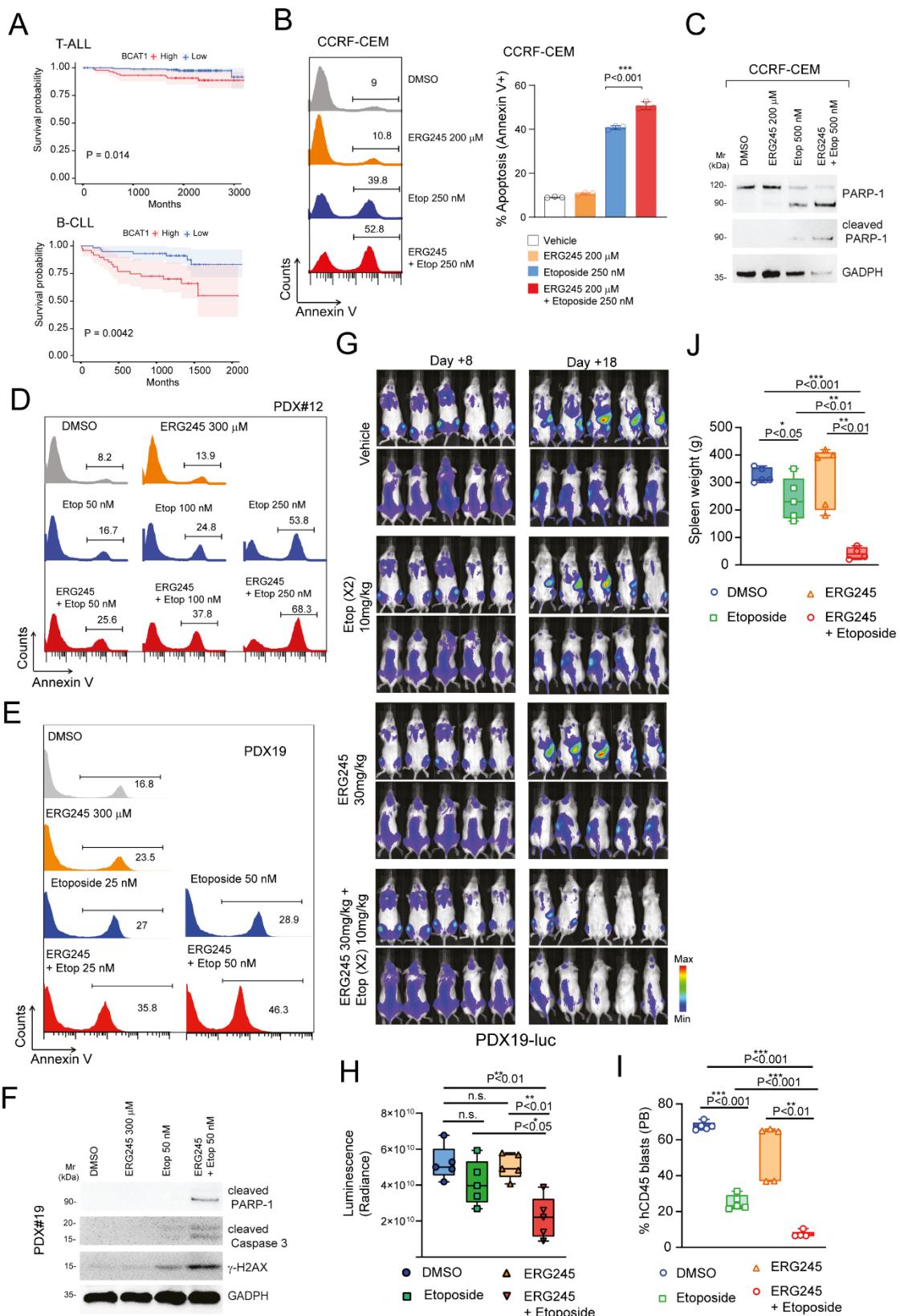


Figure S14. BCAT1 expression correlates with prognosis in NOTCH1-dependent leukemias and represents a therapeutic target in T-ALL. (A) Kaplan–Meier survival curves (top) of the entire series of 261 T-ALL patients

(with reported OS). BCAT1 high cases ($>$ mean expression) or BCAT1 low cases ($<$ mean expression). Log-rank Mantel-Cox test was performed to calculate P value. * $P< 0.05$. Shaded area represents 95% CI. Kaplan-Meier survival curves of a cohort of 107 B-CLL patients (bottom). BCAT1 (probe 22585_at) high cases ($>$ mean expression) or BCAT1 low cases ($<$ mean expression). Log-rank Mantel-Cox test was performed to calculate P value. ** $P< 0.01$. Shaded area represents 95% CI. (B) Representative plots (left) and bar graph representation (right) of annexin V staining in CCRF-CEM T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245), etoposide (Etop) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. *** $P< 0.001$. (C) Western blot analysis of PARP-1 (total or cleaved PARP-1) in CCRF-CEM cells treated for 48h with DMSO (vehicle), ERG245 (200 μ M), etoposide (Etop; 500 nM) or ERG245 + Etop. GADPH was used as protein loading control. (D) Representative plots of annexin V staining in PDX#12 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245; 300 μ M), etoposide (Etop; 50, 100, 250 nM) or the combination (ERG245 + Etop) for 48h. (E) Representative plots of annexin V staining in PDX#19 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245; 300 μ M), etoposide (Etop; 25, 50 nM) or the combination (ERG245 + Etop) for 48h. (F) Western blot analysis of cleaved PARP-1, cleaved caspase 3 and phosphorylated γ H2AX in PDX#19 cells treated for 48h with DMSO (vehicle), ERG245 (300 μ M), etoposide (Etop; 50 nM) or ERG245 + Etop. GADPH was used as protein loading control. (G) Representative images of bioluminescence in NSG mice xenografted with PDX#19 cells expressing luciferase (PDX#19-luc) and treated with vehicle (DMSO), BCAT inhibitor (ERG245; 30 mg/kg three times a week), etoposide (Etop; 10 mg/kg twice a week) or the combination (ERG245 + Etop). Analysis before (day 8 post-transplantation) and 10 days after start of treatment (day 18 post-transplantation) is shown. (H) Quantitative analysis of tumor load via in vivo bioluminescence imaging of NSG mice xenografted with PDX#19-luc 10 days after treatment with vehicle (DMSO), BCAT inhibitor (ERG245), etoposide (Etop) or the combination (ERG245 + Etop). Significance was calculated using an unpaired two-tailed t-test. n.s: not significant. * $P<0.05$, ** $P<0.01$. (I) Quantitative analysis of tumor burden in NSG mice xenografted with PDX#19-luc and treated with vehicle (DMSO), BCAT inhibitor (ERG245), etoposide (Etop) or the combination (ERG245+Etop), estimated by analyzing human CD45 expression in the blood (PB) at sacrifice (t=18 days). Significance was calculated using an unpaired two-tailed t-test. ** $P< 0.01$, *** $P< 0.001$. (J) Analysis of spleen weight in NSG mice xenografted with PDX#19-luc and treated with vehicle (DMSO), BCAT inhibitor (ERG245), etoposide (Etop) or the combination (ERG245+Etop). Significance was calculated using an unpaired two-tailed t-test. * $P< 0.05$, ** $P< 0.01$, *** $P< 0.001$.

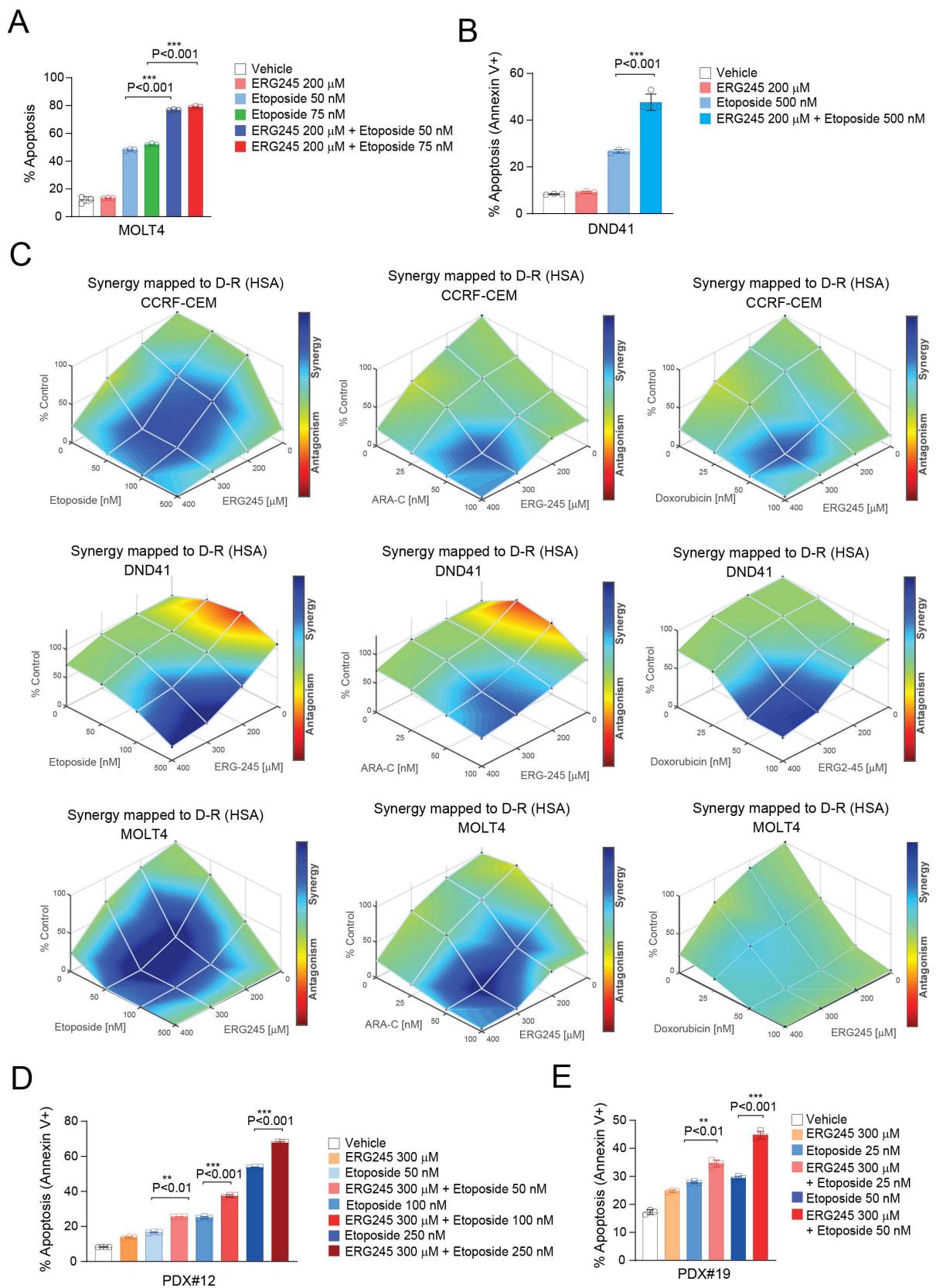


Figure S15. BCAT1 inhibition synergizes with numerous chemotherapeutic drugs to reduce cell viability.
(A) Quantification of apoptosis in MOLT4 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245),

etoposide (Etop; 50-75 nM) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (B) Quantification of apoptosis (Annexin V positive) in DND41 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245), etoposide (Etop) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. *** $P < 0.001$. (C) CCRF-CEM, DND41 and MOLT4 T-ALL cells were incubated with different concentrations of etoposide (0- 500 nM, left panels), cytarabine/ara-C (0- 100 nM, middle panels) or doxorubicin (0- 100 nM, right panels) and ERG245 (0- 400 μ M) for 72h. After treatment, cell viability was assessed using a bioluminescent assay (Vialight plus). Analysis of combination efficacy and synergy for chemotherapeutic drugs (etoposide, ara-C and doxorubicin) and the BCAT inhibitor ERG245 was done using the HSA model with Combefit software. (D) Quantification of apoptosis (Annexin V positive) in PDX#12 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245; 300 μ M), etoposide (Etop: 50, 100, 250 nM) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. (E) Quantification of apoptosis (Annexin V positive) in PDX#19 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245; 300 μ M), etoposide (Etop: 25, 50 nM) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$.

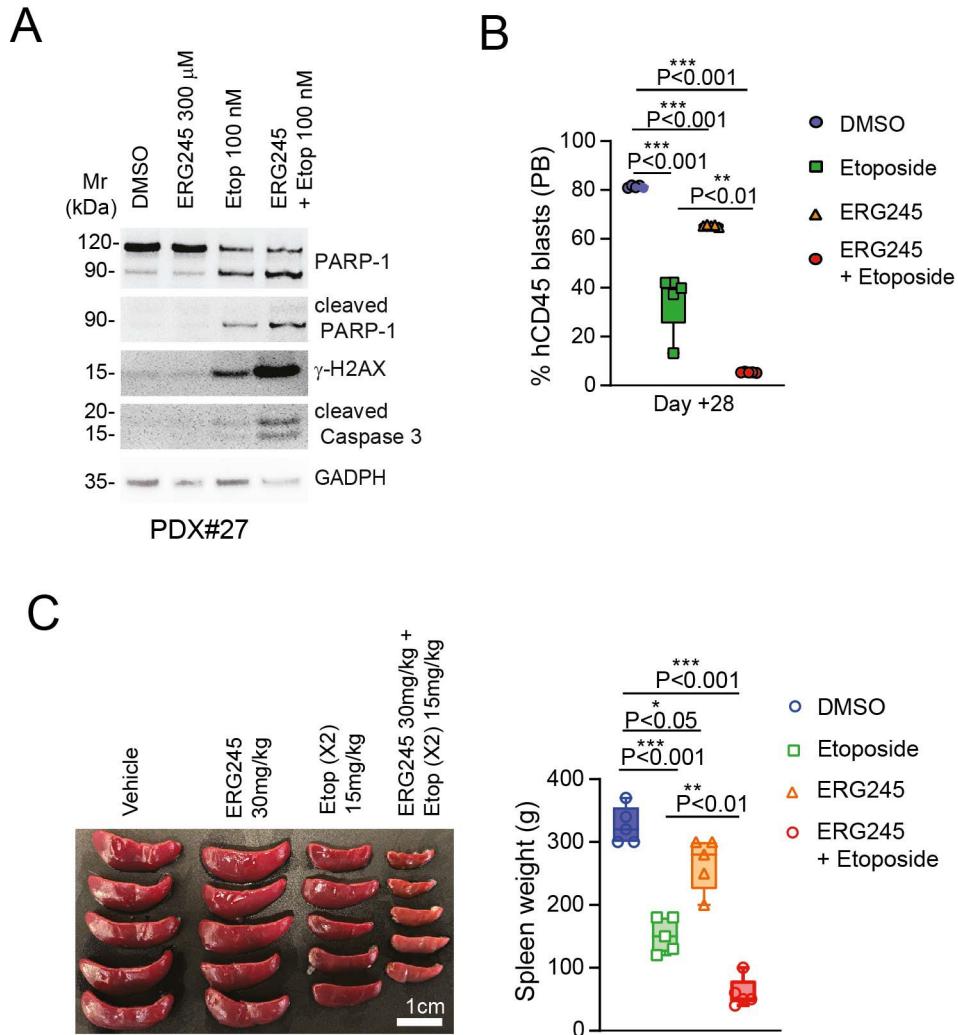


Figure S16. BCAT1 inhibition synergizes with etoposide to reduce viability. (A) Western blot analysis of PARP-1 (total or cleaved PARP-1), phosphorylated γ H2AX and cleaved caspase 3 in PDX#27 cells treated for 48h with DMSO (vehicle), ERG245 (300 μ M), etoposide (Etop; 100 nM) or ERG245 + Etop. GADPH was used as protein loading control. (B) Quantitative analysis of tumor burden in NSG mice xenografted with PDX#27-luc and treated with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop) or the combination (ERG245+Etop), estimated by analyzing human CD45 expression in the blood (PB) at sacrifice. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. (C) Representative images of spleens (left) and analysis of spleen weights (right) in PDX#27-luc xenografted mice at the end of treatment in NSG mice xenografted with PDX#27-luc and treated with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop) or the combination (ERG245+Etop). Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

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