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Received: March 29, 2024.

Accepted: August 23, 2024.

Citation: Valeria Tosello, Ludovica Di Martino, Adonia E. Papathanassiou, Silvia Dalla Santa, Marco Pizzi, Lara Mussolin, Jingjing Liu, Pieter Van Vlierberghe, and Erich Piovan.

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Haematologica. 2024 Sept 5. doi: 10.3324/haematol.2024.285552 [Epub ahead of print]

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

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Running title: BCAT1 sustains the oncogenic function of NOTCH1 and represents a therapeutic target

CONFLICT OF INTEREST

There are no financial conflicts of interest to declare.

ACKNOWLEDGEMENTS

We thank Sonia Minuzzo for providing T-ALL xenografts and Laura Bonaldi for help with epifluorescence microscopy. We are grateful to Ilaria Talli for technical assistance in setting up methylation specific assays. Special thanks to Jiyang, Yu and Angela Grassi for doing preliminary gene expression profiling analysis and help with bioinformatics analyses concerning the various datasets used in the present study. We are especially grateful to our co-author, Pieter van Vlierberghe, who recently passed away, for his enthusiastic contribution, warmth and friendship.

FUNDING

This work was supported by the Italian Foundation for Cancer Research (Fondazione AIRC) grants to E.P. (IG2018#22233); Ex 60% to E.P (University of Padova). There are no conflicts of interest to declare.

AUTHOR CONTRIBUTIONS

L.D.M. performed ChIP analyses, performed some in vitro experiments with inhibitors, performed qRT-PCR experiments and helped in writing the first draft of the manuscript; V.T. generated NOTCH1-dependent mouse T-ALLs, performed in vitro and in vivo therapeutic experiments and helped in writing the first draft of the manuscript; A.E.P. provided the BCAT inhibitor, helped in designing in vivo therapeutic experiments and helped in writing the manuscript; L.D.M. and S.D.S. helped in setting up the protocol for performing the immunophenotypic characterization of the leukemia in *Bcat1* WT and KO mice and performed some analyses; L.M. performed patient selection and provided clinical data; M.P. performed and helped in

interpreting IHC results; J.L. helped in bioinformatical analyses. P.V.V. helped in analyzing ChIP-seq data and provided reagents; E.P. designed and performed some experiments, directed research, analyzed data and wrote the paper. All the authors read and edited the manuscript.

DATA AVAILABILITY STATEMENT: The study utilized, in part, publicly available datasets (Gene Expression Omnibus, Chinese Leukemia Genotype-Phenotype Archive). Raw data for this study were generated at HMT (Tokyo, Japan) and Active Motif (Waterloo, Belgium). Derived data supporting the findings of this study are available from the corresponding author upon reasonable request.

Word count: Abstract: 168; Main text: 6079

ABSTRACT

High levels of branched-chain amino acid (BCAA) transaminase 1 (BCAT1) have been associated with tumor aggressiveness and drug resistance in several cancer types. Nevertheless, the mechanistic role of BCAT1 in T-cell acute lymphoblastic leukemia (T-ALL) remains uncertain. We provide evidence that *Bcat1* was over-expressed following NOTCH1-induced transformation of leukemic progenitors and that NOTCH1 directly controlled BCAT1 expression by binding to a BCAT1 promoter. Further, using a NOTCH1 gain-of-function retroviral model of T-ALL, mouse cells genetically deficient for *Bcat1* showed defects in developing leukemia. In murine T-ALL cells, *Bcat1* depletion or inhibition redirected leucine metabolism towards production of 3-hydroxy butyrate (3-HB), an endogenous histone deacetylase inhibitor. Consistently, BCAT1 depleted cells showed altered protein acetylation levels which correlated with a pronounced sensitivity to DNA damaging agents. In human NOTCH1-dependent leukemias, high expression levels of BCAT1 may predispose to worse prognosis. Therapeutically, BCAT1 inhibition specifically synergized with etoposide to eliminate tumors in patient-derived xenograft models suggesting that BCAT1 inhibitors may have a part to play in salvage protocols for refractory T-ALL.

INTRODUCTION

T-ALL is an aggressive hematological cancer accounting for $\approx 15\%$ of pediatric and $\approx 25\%$ of adult ALL cases, requiring intensive chemotherapy regimens^{1, 2}. Notwithstanding improved cure rates, especially in pediatric cases, a significant fraction of patients ($\sim 15\%$) relapse. Children and adults with relapsed T-ALL face poor prognosis due to low remission rates and increased morbidity and mortality with salvage therapy. There is no doubt that more effective treatment strategies are needed, especially for refractory T-ALL. It is generally accepted that T-ALL is a heterogeneous disease, the result of a wide spectrum of genetic lesions and environmental cues that cooperate to promote leukemogenesis^{3, 4} leading to the aberrant growth of immature T-cell progenitors. Gain-of function mutations in NOTCH1 are amongst the most common genetic alterations found in T-ALL⁵. NOTCH1 plays an important physiological role in promoting T-cell lineage and cell growth during thymic development. Its activation following ligand binding requires proteolytic cleavage by γ -secretase-containing protease complexes as well as translocation of the cleaved NOTCH1 intracellular domain (NICD) to the nucleus to facilitate the transcription of numerous downstream targets⁶. NOTCH1 gain-of function mutations (mutNOTCH1) in T-ALL determine the activation of NOTCH1 in the absence of a ligand and/or prevent termination of NOTCH1 signaling in the nucleus. Constitutive NOTCH1 signaling in T-ALL is linked to the transcriptional activation of numerous anabolic pathways involved in cell growth such as ribosome biosynthesis, protein translation and nucleotide and amino acid metabolism^{7, 8}. In addition to its transcriptional activities, NOTCH1 is a direct, negative regulator of DNA damage response (DDR) through binding and inhibiting of the ATM (Ataxia-Telangiectasia Mutated) Ser/Thr kinase⁹. This links

NOTCH1 activation to the high number of genetic alterations found in T-ALL, which are thought to be driven by errant DNA repair.

The present study reports that, in addition to its direct effect on the HR pathway, mutNOTCH1 indirectly regulates DDR by upregulating BCAT1. Specifically, we found that BCAT1 was a transcriptional target of mutNOTCH1, which was expressed early in the process of leukemogenesis and shown to regulate not only branched chain amino acid (BCAA) levels but also ketone body synthesis (3-hydroxybutyrate, 3-HB). 3-HB accumulation in BCAT1 deficient cells modified protein acetylation levels and altered DDR resulting in accentuated DNA damage and cell death, especially when combined with a genotoxic insult. The increased chemosensitivity to double strand break (DSB)-inducing agents, observed in T-ALL models following BCAT1 inhibition, suggests that BCAT1 is a novel therapeutic target in T-ALL.

METHODS

Western blotting

Total cell lysates were prepared using RIPA lysis buffer supplemented with phosphatase inhibitor cocktail set I and II (Sigma-Aldrich, Merck, Darmstadt, Germany) and protease inhibitor cocktail tablets (Roche, Burgess Hill, UK) and normalized for protein concentration using the BCA method (Pierce, Pero, Italy). For Western blotting, protein samples were separated on 4-12% gradient Tris-Glycine or 3-8% Tris-Acetate SDS-PAGE Gels (Invitrogen) and transferred to PVDF membrane (Millipore). Antibodies against tubulin (TU-02), MYC and p53 (DO-1) were from Santa Cruz Biotechnology (Dallas, TX, USA); antibodies recognizing Cleaved NOTCH-1 (ICN1; Val 1744), β -actin, p21, BCAT2, BCAT1, Ku-80, Ku-70, Histone H3, cleaved PARP-1, cleaved caspase 3, phosphorylated H2AX (pS139), phosphorylated DNA-PKcs (pS2056), total DNA-PKcs, phosphorylated ATM (pS1981), total ATM, phosphorylated CHK2 (pT68), total CHK2, phosphorylated TP53 (pS15), acetylated p53 (K382) and GADPH were from Cell Signaling Technology (Danvers, MA, USA). Acetyl-Histone H3 Antibody Sampler Kit (#9927) was also from Cell Signaling Technology. Mouse anti-BCAT1 (BD Pharmingen, Oxford, U.K) was also used. The BioRad ChemiDoc XRS Imager was used to capture the signals from the blots.

Chromatin Immunoprecipitation (ChIP) qPCR

ChIP assays were performed using the SimpleChIP plus Enzymatic Chromatin IP kit (Cell Signaling Technology, #9005) following the manufacturer's protocol. Briefly, 4×10^6 cells were fixed with formaldehyde in a final concentration of 1% for 10 minutes at room temperature. The crosslinking reaction was quenched with a 5M glycine solution, and the cells were then centrifuged, washed twice with ice-cold PBS and lysed. Cell nuclei were prepared and chromatin was digested with micrococcal nuclease, then sonicated. The sheared chromatin was immunoprecipitated with human Notch-1 intracellular domain antibody (R&D Systems, Minneapolis, MN; Cat#AF3647). Normal sheep IgG (Cat#5-001-A, R&D Systems) was used as a non-specific antibody control for immunoprecipitation. Following an overnight incubation with antibodies, 30 μ l of Protein G Magnetic Beads was added at 4°C for 2 h. Beads were washed, and chromatin was eluted. Crosslinks were reverted according to kit instructions. The DNA was purified using DNA Purification Buffers and Spin Columns (Cell Signaling Technology #14209) following kit instructions. The immunoprecipitated DNA was subjected to real-time PCR reaction using ChIP primer sets (listed in *Online Supplementary Table S1*), which were designed to include the promoter and negative regions for BCAT1 gene. HES1 promoter region was used as positive control. Fold enrichment was calculated as a ratio of amplification efficiency of ChIP sample over that of the IgG. More specifically, the amplification efficiency (AE) of each primer set was used to determine the amplification efficiency of the ChIP sample and the IgG

sample as follows: % ChIP = AE(Input Ct – ChIP Ct) x (dilution factor; Fd)(100); % IgG = AE(Input Ct – IgG Ct) x(Fd)(100); Fold Enrichment = % ChIP / % IgG.

Statistical Analyses

Results were expressed as mean value \pm Standard Deviation (SD). Student's *t*-test and nonparametric *t*-test (Mann-Whitney) were used where appropriate. A non-parametric test (Fisher's exact test) was used to compare qualitative data. The Kaplan–Meier method was used to estimate the distributions of overall survival (OS). OS was considered as the time from diagnosis to date of death. The log-rank test was used to compare survival distributions. All statistical tests were two sided, unpaired and $P < 0.05$ was considered statistically significant (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$). Analysis of drugs' interaction was performed using Combenefit software¹⁰. The sample size for animal xenograft experiments was determined on the basis of prior studies that yielded a two-tailed statistical test with ~80% power to detect a twofold change in tumour burden ($\alpha=0.05$). All attempts at replication were consistent for all animal and cell culture experiments.

Mouse experiments

The study was approved by the Institutional Review Board (OPBA) of the University of Padova (protocol code 238591; 25 June 2019) and the Italian Ministry of Health (DGSAF 0006112; 177/2020-PR; 10/03/2020).

Information on cell lines and primary leukemia samples, mouse transplantation experiments and studies, flow cytometry and analysis of T-cell distribution, quantitative real-time PCR, total histone extraction, immunohistochemistry, immunoprecipitation of acetylated proteins, neutral comet assay, analysis of publicly available datasets, RNA-sequencing and gene-set enrichment analysis, steady state metabolite profiling, stable-isotope tracing experiments, analysis of ChIP-seq databases, cell viability assays and flow cytometry, plasmids, lentiviral constructs and viral production, luciferase reporter experiments, methylation specific PCR (MSP) methods are detailed in the *Online Supplementary Materials and methods section*.

RESULTS

NOTCH1 upregulates BCAT1 expression in NOTCH1 mutated human T-ALL by binding to a BCAT1 promoter. To understand the role that BCAT1 plays in T-ALL development, we analyzed gene expression data from a NOTCH1-induced murine T-ALL (NIC) model. In that model, overexpression of an activated, intracellular form of Notch1 (*ICN1*) in transplanted Lin-negative murine hematopoietic cells leads to the development of an abnormal CD4⁺CD8⁺ double positive (DP) T cell subset at 2 weeks of transplantation followed by the rise of a highly tumorigenic DP leukemic population at 6-8 weeks of transplantation^{11, 12}. In the gene set of Figure 1A, *Bcat1* was highly upregulated in leukemic DP cells compared to normal DP cells. The increase in *Bcat1* expression occurred early in T-ALL development as evident from the heat map of *Online Supplementary Figure S1A*, and was unique among other enzymes involved in BCAA metabolism (eg, *Bcat2*, *Bckdha*, and *Bckdhb*), whose expression did not exhibit a specific pattern (*Online Supplementary Figure S1A*). To confirm the above observations, we compared transcript and protein levels of *Bcat1* and *Bcat2* in thymocytes isolated from normal C57/BL6 mice and leukemic cells obtained from spleens of mice bearing T-ALL tumors. The tumors were induced through overexpression of an activated form of NOTCH1 lacking a major portion of the extracellular domain (ΔE -NOTCH1). As in the case of the NIC model, the development of leukemia in the ΔE -NOTCH1 model (NOTCH1-T tumors) was associated with increased *Bcat1* levels (Figure 1B). On the other hand, the gene expression of *Bcat2*, the mitochondrial isoform of

BCAT, was not consistently altered with the development of leukemia, although a decrease was observed in the protein levels in NOTCH1-T tumors (*Online Supplementary Figure S1B, C*). The results suggest that the expression of Bcat1 and Bcat2 in NOTCH1-T tumors may be anti-correlated. Since Bcat1 and Bcat2 are metabolic enzymes, we attempted to identify a leukemia-specific metabolic signature by extracting metabolites from NOTCH1-T tumors (N=3) and murine thymic tissue (N=3). We quantified 112 metabolites by using a highly sensitive capillary electrophoresis-time-of-flight mass spectrometry (CE-TOFMS) and capillary electrophoresis-tandem mass spectrometry (CE-MS/MS) (*Online Supplementary Figure S1D*). While thymic tissue preferentially expressed metabolites associated with lipid oxidation (e.g., carnitine and citric acid) as well as purine and pyrimidine metabolism, metabolites found elevated in NOTCH1-T tumors were linked to glycolysis (lactic acid) and TCA cycle replenishment (succinic, fumaric, and malic acids) indicating a significant metabolic shift with development of leukemia (*Online Supplementary Figure S1E*). This metabolic feature was maintained when heavily infiltrated thymuses were used as a source of leukemia (*Online Supplementary Figure S2A*). NOTCH1-T tumors were also characterized by increased concentrations of BCAAs (*Online Supplementary Figures S1F, S2B*). While BCAA biosynthesis was identified as a significantly enriched pathway in NOTCH1-T tumors by metabolite set enrichment analysis (*Online Supplementary Figure S1E*), active uptake could not be excluded as the tumors showed increased expression of the neutral amino acid transporter *slc7a5* (LAT1) compared to normal thymic tissues (*Online Supplementary Figure S1G*).

To determine if BCAT1 overexpression is also a characteristic of human T-ALL, we utilized a publicly available dataset, which profiled both normal human thymocyte populations and bone marrow samples of childhood T-ALL patients at the time of diagnosis¹³. We found that BCAT1 was highly expressed in numerous T-ALL samples (*Online Supplementary Figure S1H*). To confirm that human T-ALL is indeed linked to increased BCAT1 expression, we used a comprehensive microarray data set^{14, 15} consisting of T-ALL patients (N=57) and thymocyte subsets (7 thymocyte and mature T-cell subsets derived from 3 independent donors). BCAT1 expression was again found to be significantly upregulated in a fraction of T-ALL specimens compared to thymocyte subsets (Figure 1C). T-ALL can be subclassified into three differentiation stages based on cluster of differentiation (CD) surface markers, such as early/precortical, cortical, and mature/postcortical. To identify patient groups with upregulated BCAT1 expression, we utilized a well-characterized T-ALL gene dataset (TARGET cohort), obtained from 264 pediatric T-ALL patients¹⁶. We found BCAT1 to be preferentially expressed in the cortical (CD1a positive) T-ALL immunophenotypical subgroup (*Online Supplementary Figure S1I*). Since *NOTCH1* activating mutations are highly prevalent in the cortical subgroup³, we hypothesized that *NOTCH1* regulates BCAT1 expression. Sub-dividing the TARGET cohort of patients into *NOTCH1/FBXW7*-mutated and *NOTCH1/FBXW7* wild-type disclosed that the former had higher BCAT1 levels compared to *NOTCH1* wild-type patients (*Online Supplementary Figure S1J*). This observation was confirmed in two independent T-ALL cohorts composed of 37 diagnostic pediatric samples included in the Children's Oncology Group P9404 study¹⁷ and 130 pediatric and adult samples from the Shanghai Institute of Hematology project with known *NOTCH1* mutational status (*Online Supplementary Figure S1K, L*)¹⁸. We then analyzed BCAT1 expression in a comprehensive panel of T-ALL cell lines. *Online Supplementary Figure S1M* discloses a heterogeneous pattern of BCAT1 protein expression, which was not evidently correlated with the mutational status of *NOTCH1*, as detected by the presence of ICN1, although BCAT1 transcript expression did correlate with *HES1* expression (*Online Supplementary Figure S1N*). *HES1* gene is a well-known *NOTCH1*-target gene. We also evaluated the methylation status of *BCAT1* promoter in a cell line panel and determined that gene methylation status controlled BCAT1 expression in a particular cell line (*Online Supplementary Figure S1O, P*). We also analyzed the transcript and protein levels (Figure 1D) of BCAT1 in previously generated patient derived xenografts (PDX)^{19, 20}. PDX samples possessing activated *NOTCH1* (*NOTCH1/FBXW7* mutant/*NICD1*-positive cases) showed higher BCAT1 levels compared to *NICD1*-negative cases (Figure 1D). Finally, we evaluated BCAT1 and *HES1* expression levels using immunohistochemistry in primary T-cell lymphoblastic leukemia/lymphoma (T-ALL/T-LBL; N=10), PDX samples (N=10) and normal human thymuses (N=3). We found weak expression of all three markers in normal thymus (*Online Supplementary Figure S3A*). The staining pattern for BCAT1 and *HES1* was rather heterogeneous in leukemia samples (*Online Supplementary*

Figure S3B, C), however we found a statistically significant association between BCAT1 expression and HES1 staining (Fisher's exact test $P < 0.05$; *Online Supplementary Figure S3C*). We used HES1 staining as a surrogate for NOTCH1 activation status as Sanger based sequencing of *NOTCH1* and *FBXW7* genes from FFPE material failed in most patient cases. On the other hand, we found no association between BCAT2 and HES1 staining (*Online Supplementary Figure S3D*). These results further suggest that NOTCH1-activated leukemia cases express higher levels of BCAT1. Based on the above evidence, we hypothesized that NOTCH1 activation leads to BCAT1 overexpression.

To additionally evaluate whether BCAT1 represents a novel NOTCH1 downstream target gene, we treated NOTCH1-T tumor-bearing mice (5 independent tumors) with the gamma secretase inhibitor dibenzazepine (DBZ) and subjected vehicle-control (DMSO) and treated (DBZ) tumors to transcriptomic analysis. We found that *Bcat1* gene expression was highly downregulated following in vivo NOTCH1 inhibition (*Online Supplementary Figure S4A*). Downregulation of *Bcat1* was also observed following similar analysis of *HDΔPEST NOTCH1* (*NOTCH1* mutant allele harboring both HD and PEST domain mutations) leukemias treated ex-vivo with DBZ²¹ (data not shown). Further, treatment of human *NOTCH1* mutant T-ALL cell lines (in vitro) and PDX samples (in vivo) with DBZ markedly reduced BCAT1 transcript and protein levels (Figure 1E and *Online Supplementary Figure S4B, C*). To determine whether NOTCH1 directly regulates BCAT1 expression in T-ALL, we analyzed deposited chromatin immunoprecipitation followed by next-generation sequencing (ChIP-seq) data of NOTCH1 chromatin binding sites in HPB-ALL cells, which are NOTCH1-mutant and MYC expressing T-ALL cells²². We found numerous NOTCH1 peaks in the BCAT1 locus; particularly prominent was a peak of ≈ 0.5 kb near the BCAT1 transcription start site (TSS) (Figure 1F). In the vicinity of this peak region, a RBPJ site was found upstream of the TSS. To functionally characterize the potential role of this NOTCH1 binding region in BCAT1 gene regulation, we inspected Encyclopedia of DNA Elements (ENCODE) data for epigenetic histone marks in this region in T-ALL cells. These analyses revealed bona fide promoter features associated with this region, including occupancy and high levels of DNA polymerase II (Pol II) and high levels of histone H3 Lys4 trimethylation (H3K4me3) (*Online Supplementary Figure S5*). Transposase-accessible chromatin with sequencing (ATAC-Seq) data also support an open chromatin state in this region (*Online Supplementary Figure S5*). Local ChIP experiments using specific primers centered around this region were performed in PF382 cells, which are NOTCH1 mutant and present modest levels of MYC protein expression (*Online Supplementary Figure S4C*). This analysis confirmed NOTCH1 binding in this area of the BCAT1 promoter region (Figure 1F). Based on these results, we proposed that this NOTCH1 bound region could function as an important regulatory element driving BCAT1 expression in T-ALL cells. Consistent with that hypothesis, luciferase reporter assays in ICN1 transfected HEK 293T cells showed a dose dependent activation of a reporter construct containing this ~ 0.5 kb region of the BCAT1 promoter (including the upstream RBPJ binding site) (*Online Supplementary Figure S4D*). Reporter activity was severely reduced following mutation of the RBPJ binding site (*Online Supplementary Figure S4D*). Further, ICN1 induced reporter activity was progressively reduced using CB103, a highly selective and potent inhibitor of the CSL-NICD gene transcription complex²³ (*Online Supplementary Figure S4E*). On the other hand, knockdown of MYC or the use of JQ1²⁴ only modestly affected ICN1 induced reporter activity (*Online Supplementary Figure S4F, G*), strongly suggesting that MYC does not play a major role in regulating the activity of this region. Coherently, in HPB T-ALL cells (*Online Supplementary Figure S4H*), luciferase reporter assays showed strong activation of this BCAT1 promoter reporter construct. Further, in HPB T-ALL cells reporter activity could progressively be reduced using CB103 (*Online Supplementary Figure S4I*) or following inactivation (deletion or mutation) of the RBPJ binding site, suggesting a prominent role for NOTCH1 in regulating reporter activity in T-ALL cells (*Online Supplementary Figure S4J*). This notion was further strengthened by the observation that forced increased expression of ICN1 in HPB T-ALL cells augmented BCAT1 promoter reporter activity but had very modest effects on the transcriptional activity of the BCAT1 promoter construct having the RBPJ binding site mutated (*Online Supplementary Figure S4K*).

Canonical functions of BCAT1 in T-ALL. To examine the role of Bcat1 in T-ALL development, we used a NOTCH1-dependent T-ALL mouse model (ΔE -NOTCH1). Transduced BM progenitor cells (GFP+Lineage-cKit+Sca1+) from *Bcat1 KO* and *Bcat1 WT* were transplanted into lethally irradiated C57BL/6J hosts (*Online Supplementary Figure S6A*). Despite no evidence of engraftment defects three weeks post-transplant, mice receiving *Bcat1 KO* ΔE -NOTCH1 GFP+ cells showed a significant delay in succumbing to leukemia respect to mice receiving *Bcat1 WT* ΔE -NOTCH1 GFP+ cells (Figure 2A). The immunophenotype of established leukemias was similar amongst genotypes (*Online Supplementary Figure S6B*). We thus hypothesized that Bcat1 may be implicated in cell cycle progression or apoptosis of T-ALL cells. To examine this, we evaluated Edu incorporation and Annexin V staining in leukemic cells obtained from diseased animals. *Bcat1 KO* T-ALL cells showed a decrease in the proportion of cells in the S-phase of the cell cycle (Figure 2B) and a modest increase in apoptotic cells (*Online Supplementary Figure S6C*). These results suggest that Bcat1 promotes survival and proliferation of NOTCH1-mutant T-ALL. We thus examined the in vitro and in vivo effects of BCAT1 gene depletion by short-hairpin RNA (shRNA) in human leukemia cell lines expressing high levels of the protein. Bcat1 silencing was associated with cell cycle arrest at the G1 phase (Figure 2C and *Online Supplementary Figure S7A*), inhibition of proliferation (Figure 2D), and induction of apoptosis (*Online Supplementary Figure S7B*) in vitro and decreased tumor growth in vivo (Figure 2E, F, *Online Supplementary Figure S7C*). Different cell lines exhibited differential sensitivity to the effects of BCAT1 depletion, which was also dependent on the type of assay used. Whereas BCAT1 silenced MOLT4 cells were far more apoptotic than CCRF-CEM cells in vitro (*Online Supplementary Figure S7B*), the opposite was true for tumor growth in vivo. Indeed, BCAT1 silencing in CCRF-CEM cells strongly affected their growth in vivo (Figure 2E), whereas, in MOLT4 cells, it yielded only a modest reduction in tumor burden and a moderate increase in survival (Figure 2F, *Online Supplementary Figure S7C*). BCAT1 silenced DND41 cells also recorded a high degree of apoptosis (*Online Supplementary Figure S7B*). We speculate that loss of BCAT1 in human T-ALL is associated with cell cycle arrest, apoptosis, and delayed tumor growth in vivo.

To determine the putative mechanism behind the functional dependence of NOTCH1-mutant T-ALL cells on Bcat1, gene expression analysis was performed by RNA-seq on leukemic cells isolated from spleens of diseased mice at the moment of sacrifice. Comparison of gene expression profiles of *Bcat1 WT* and *Bcat1 KO* ΔE -NOTCH1 tumors identified 470 differentially expressed genes (≥ 2 Fold change, $P < 0.05$, $FDR \leq 0.1$; Figure 3A and *Online Supplementary Table S2*). The majority of these genes showed decreased expression in *Bcat1 KO* ΔE -NOTCH1 tumors (data not shown). Gene set enrichment analysis (GSEA) identified four significantly different pathways: “G2M checkpoint”, “mitotic spindle”, “epithelial mesenchymal transition”, and “E2F targets”, all downregulated in *Bcat1 KO* ΔE -NOTCH1 cells (*Online Supplementary Table S3*; Figure 3B). On the other hand, GSEA analysis identified 18 significantly different pathways upregulated in *Bcat1 KO* ΔE -NOTCH1 cells, including “DNA repair”, “apoptosis”, and “p53 pathway” (*Online Supplementary Table S3*; Figure 3C). These results are consistent with our functional data and suggest that Bcat1 may be implicated in regulating the DNA damage response (DDR). To follow-up on this possibility, we evaluated the levels of γ H2AX, a surrogate marker of DNA damage and double strand breaks (DSB) abundance in Bcat1 depleted cells. We found that Bcat1 KO or BCAT1 depleted cells had higher basal levels of γ H2AX compared to Bcat1 expressing cells (Figure 3D).

Subsequently, we examined the metabolic impact of Bcat1 depletion on ΔE -NOTCH1 leukemias. Briefly, we extracted metabolites from *Bcat1 WT* and *Bcat1 KO* ΔE -NOTCH1 tumors, and quantified 56 metabolites by mass spectrometry to examine the metabolic impact of *Bcat1* loss on ΔE -NOTCH1 leukemias (Figure 3E). We found N=19 differentially expressed metabolites between the pairs of compared *Bcat1 WT* and *Bcat1 KO* ΔE -NOTCH1 tumors (Figure 3E). Of these, four metabolites (leucine, glutamine, 3-hydroxybutyrate (3-HB) and lactic acid) were consistently modulated in other compared tumors (data not shown). Further, we performed $^{13}\text{C}_6$ -Leu stable-isotope tracing experiments to track the metabolic fate of BCAA in ΔE NOTCH1 leukemias. The results, which are shown in *Online Supplementary Figure S8*, indicated that $^{13}\text{C}_6$ -Leu was readily taken up by *Bcat1 WT* tumors and that *Bcat1 KO* tumors had increased levels of (m+6)

Leu compared to *WT* tumors, presumably due to lack of Bcat1. Again, a relevant amount of labeled leucine was incorporated in 3-HB in both groups, with *Bcat1 KO* tumors showing increased levels of (m+2 and m+3) 3-HB compared to *WT* tumors (*Online Supplementary Figure S8*). On the other hand, major TCA metabolites (with the exception of citrate) exhibited very low isotopic labeling indicating that ΔE -*NOTCH1* leukemias probably do not utilize BCAAs for the replenishment of the TCA cycle. This result may however be influenced by our experimental approach using $^{13}\text{C}_6$ -Leu bolus injection rather than constant infusion.

The BCAT1 inhibitor, ERG245, recapitulates the functional consequences of Bcat1 depletion.

Given our observations that BCAT1 could be a therapeutic target in T-ALL, we evaluated the effects of a novel BCAT1-specific inhibitor, ERG245²⁵. Treatment of ΔE *NOTCH1 Bcat1 WT* leukemias with ERG245 was highly apoptotic and induced a potent cell cycle arrest (Figure 4A, B and *Online Supplementary Figure S9A, B*). Interestingly, ΔE *NOTCH1 Bcat1 KO* leukemias were almost refractory to this drug, even at high concentrations (Figure 4C). On the other hand, human T-ALL cell lines and PDX samples were less sensitive to the effects of ERG245, with only high doses determining effects on viability or cell cycle (Figure 4D, E; *Online Supplementary Figures S9C, D and S10A, B*). We further performed $^{13}\text{C}_6$ -Leu stable-isotope tracing experiments to examine the metabolic impact of BCAT1 inhibition on ΔE -*NOTCH1* leukemias. Briefly, *NOTCH1-T*-tumor bearing mice were treated in vivo with vehicle control or ERG245²⁵, and perfused with $^{13}\text{C}_6$ -Leu just prior sacrifice. Cellular metabolites from snap-frozen spleens were then extracted and quantified. The results, which are shown in *Online Supplementary Figure S11*, indicated that $^{13}\text{C}_6$ -Leu was readily uptaken by the tumors and that tumors treated with ERG245 had increased levels of (m+6) Leu compared to tumors treated with vehicle-control, presumably due to inhibition of Bcat1 (*Online Supplementary Figure S11*). Two major metabolic events were observed with BCAT1 inhibition: a) a partial break in the TCA cycle between citrate and succinate, and b) increased synthesis of 3-HB. In *Online Supplementary Figure S11*, accumulation of citrate and isocitrate are noted with a concomitant decrease in the levels of succinate and fumarate. A similar TCA cycle break was reported by Ko et al. in LPS-stimulated macrophages treated with a different but structurally related BCAT1 inhibitor²⁶. Considering that accumulation of TCA components previously noted in *NOTCH1-T* tumors (*Online Supplementary Figure S1D*), the break in the TCA cycle with BCAT1 inhibition constitutes a significant metabolic shift. Again, with the exception of citrate, major TCA metabolites exhibited limited isotopic labeling indicating that *NOTCH1-T* tumors may not utilize BCAAs for the replenishment of the TCA cycle, at least under our experimental conditions of bolus injection. ERG245-driven inhibition of BCAT1 induced a modest decrease in the levels of isoleucine and valine (data not shown) in tandem with an increase in the isotopic labeling of citrate and 3-HB. Acetyl-CoA or succinyl-CoA (and propionyl-CoA) are the main end-products of BCAA metabolism, with acetyl-CoA that can be used to synthesize citrate and/or ketone bodies such as acetoacetate and 3-HB. These findings are similar to the metabolic effects obtained in *Bcat1 KO* ΔE -*NOTCH1* tumors (*Online Supplementary Figure S8*). We speculate that, following BCAT1 inhibition or depletion, there is a shift towards leucine and 3-HB synthesis. 3-HB is known to act as an energy source in the absence of sufficient glucose and to inhibit class I histone deacetylases (HDACs)²⁷, thus influencing the acetylation state of proteins and/or the epigenetic regulation of genes.

BCAT1 depletion increases chemosensitivity of T-ALL cells and is dependent on its enzymatic activity. Given that our results implicate BCAT1 in regulating DDR, we examined if the cytotoxicity of DSB-inducing agents increases in the absence of BCAT1. The data suggest that BCAT1-depletion significantly enhances the sensitivity of murine and human T-ALL cells to etoposide (Figure 5A-C and *Online Supplementary Figure S10C, D*). ΔE -*NOTCH1 Bcat1 KO* leukemias were particularly sensitive to etoposide (Figure 5A). In Figure 5B, early apoptotic CCRF-CEM cells (Annexin⁺ Sytox Red⁻) and late apoptotic or necrotic CCRF-CEM cells (Annexin⁺ Sytox Red⁺) were evident at 48h of etoposide treatment; both populations increased significantly when etoposide was combined with BCAT1 depletion (Figure 5B). Similar results were obtained with DND41 (*Online Supplementary Figure S10C*) and MOLT4 cells (*Online*

Supplementary Figure S10D). Increased chemosensitivity in BCAT1-depleted cells was also observed when cells were exposed to other drugs such as doxorubicin (*Online Supplementary Figure S10E-F*). To understand the effect of BCAT1 silencing on etoposide-induced DNA damage, we examined the presence of DNA DSBs in CCRF-CEM cells transduced with shBCAT1 after treatment with etoposide for different time periods by determining the levels of γ H2AX, a surrogate marker of DSB abundance (Figure 5C and *Online Supplementary Figure S12A*). Additionally, we performed a neutral comet assay to determine the extent of DNA damage (DSB). In this assay, the % tail DNA can be used to quantitate DNA damage. We found that BCAT1-depleted cells exposed to etoposide presented considerably more tail DNA compared to control cells, especially at the 6h timepoint (Figure 5D). We also examined the phosphorylation status of key proteins that control activation of different DNA DSB repair pathways (DNA-PK for c-NHEJ pathway and ATM for HR pathway) or cell cycle arrest (CHK2 and p53). *Online Supplementary Figure S12B* indicates that both c-NHEJ and HR pathways were involved in repairing etoposide-induced DNA damage. Whereas control and BCAT1-depleted CCRF-CEM cells exhibited similar rates of ATM phosphorylation, DNA-PK was subject to an accentuated phosphorylation in BCAT1-depleted cells (*Online Supplementary Figure S12B*). Interestingly, increased DNA sensing was not associated with DNA DSB repair but with further DNA damage, as intimated by the dramatic increase in the levels of γ H2AX in BCAT1-depleted cells compared to control cells (Figure 5C and *Online Supplementary Figure S12A, B*). The combination of BCAT1 silencing and etoposide treatment was also associated with increased levels of phosphorylated CHK2 and p53 (*Online Supplementary Figure S12B*). Cleaved PARP-1 was observed only at 24h of etoposide treatment suggesting that the failure of the cells with depleted BCAT1 to repair DNA DSBs leads to extensive DNA damage and eventually apoptosis (*Online Supplementary Figure S12A*).

We next determined whether the metabolic function of BCAT1 contributes in modulating the sensitivity to DNA damaging agents. To this end we constructed a BCAT1 catalytic-inactive mutant where we abolished transaminase activity through mutation of lysine 222 to alanine (BCAT1^{K222A})²⁸. Next, we analyzed the phenotypic impact of expressing wild-type BCAT1 (BCAT1^{WT}) and BCAT1^{K222A} in BCAT1 depleted CCRF-CEM cells treated with etoposide. We found that overexpression of BCAT1^{WT} was able to partially rescue the phenotype of BCAT1 depleted cells (*Online Supplementary Figures S13A and S12C*), while BCAT1^{K222A} overexpressing cells maintain sensitivity to etoposide much like parental BCAT1 depleted cells (*Online Supplementary Figure S13A and S12C*). These data suggest that BCAT1 catalytic activity is required for maintaining resistance to DNA damaging agents such as etoposide. Since we found 3-HB (a putative HDAC inhibitor) to accumulate in *Bcat1 KO* and ERG245 treated murine T-ALL, we evaluated whether this metabolite could be implicated in modulating sensitivity to etoposide. CCRF-CEM cells treated with increasing doses of 3-HB showed sensitization to the cytotoxic effects of etoposide (*Online Supplementary Figure S13B*). Similar results were obtained in a human T-ALL PDX model (PDX#47; *Online Supplementary Figure S12D-F*). Interestingly, the well-known HDAC inhibitor, NaB, was also highly effective in sensitizing cells to the cytotoxic effects of etoposide (*Online Supplementary Figures S13B and S12D-F*), further suggesting a common mode of action between 3-HB and NaB. Following up on these observations, we initially determined whether *Bcat1*/BCAT1 depletion or inhibition could modulate the epigenetic state (acetylation) of histones. We found H3K27 acetylation to be consistently increased in *Bcat1 KO* and BCAT1 depleted cells (*Online Supplementary Figure S12G, H*), similarly to 3-HB treated cells (*Online Supplementary Figure S12I*). Interestingly, increased acetylation of proteins implicated in DDR response (p53, Ku-70, Ku-80) was also found in BCAT1 depleted cells, especially after etoposide treatment (*Online Supplementary Figure S12J*). These results suggest that altered acetylation of signaling proteins may contribute to the chemo-sensitizing effect of BCAT1 depletion/inhibition.

BCAT1 overexpression correlates with poor survival and its pharmacological inhibition synergizes with DNA-damaging chemotherapy in T-ALL cells. To investigate the putative clinical relevance of high BCAT1 expression, we used the TARGET T-ALL cohort composed of over 260 T-ALL patients¹⁶. Using the mean BCAT1 expression level as the cut-off for subdividing high and low BCAT1 expression, we found that BCAT1 levels had a prognostic significance (*Online Supplementary Figure S14A*).

Another disease characterized by frequent constitutive activation of the NOTCH1 signaling cascade (by mutational and non-mutational mechanisms) is chronic lymphocytic leukemia (CLL)^{29, 30}. We also evaluated the prognostic significance in a profiled CLL cohort (N=107) with known clinical response (survival)³¹. Using the mean BCAT1 expression level as the cut-off for subdividing high and low BCAT1 expression, BCAT1 levels were also found to have a prognostic significance (*Online Supplementary Figure S14A*). These results suggest that BCAT1 may have a prognostic significance in these two NOTCH1-dependent leukemias and may further represent a valid therapeutic target.

Following-up on our observation that knock-down of BCAT1 increased the sensitivity of T-ALL cells to DNA damaging agents, we investigated whether pharmacological inhibition of BCAT1 using ERG245 could also improve the antitumor efficacy of DNA damaging agents. We found that ERG245 potentiated the effects of DNA damaging drugs such as etoposide (Figure 6A, B; *Online Supplementary Figures S14B, C and S15A-C*), cytarabine (*Online Supplementary Figure S15C*) and doxorubicin (*Online Supplementary Figure S15C*) in T-ALL cell lines (MOLT4, CCRF-CEM, and DND41) and PDX cells (Figure 6C, D and *Online Supplementary Figures S14D-J, S15D, E and S16A-C*). The combinatory effect of ERG245 and a DNA-damaging agent was synergistic in most cases and most pronounced for etoposide (*Online Supplementary Figure S15C*). Levels of γ H2AX increased dramatically following addition of ERG245 to T-ALL cells treated with etoposide (Figure 6B and *Online Supplementary Figures S14F, S16A*). That increase was accompanied by induction of apoptosis as indicated by the presence of cleaved PARP-1. Next, we used a xenograft-based approach to test the effects of combining BCAT1 inhibition with etoposide in in vivo models of T-ALL. We injected luciferase expressing PDX#27 (PDX#27-luc) cells into NSG mice and treated them with vehicle, ERG245 (30mg/kg, three times a week), etoposide (15mg/kg, twice a week) or the combination of the two drugs for 14 days. Tumor burden was evaluated using bioluminescence, hCD45⁺ staining, and spleen weight as human T-ALL is characterized by elevated levels of CD45⁺ blasts and splenomegaly. Whereas etoposide treatment decreased tumor burden by almost one-log unit of bioluminescence compared to vehicle, the combination of etoposide and ERG245 decreased it by almost two-log units (Figure 6D). The efficacy of the combination treatment was additionally reflected in the other markers used to assess tumor growth: mice treated with etoposide and ERG245 exhibited lower levels of human CD45⁺ blasts in the peripheral blood (PB; *Online Supplementary Figure S16B*), spleen and bone marrow (not shown). Further, these mice did not show splenomegaly (*Online Supplementary Figure S16C*). Actually, our results suggest that mice in the combination group experienced almost complete elimination of tumor cells (N=5; blasts <1%) in PB, and all mice had experienced partial remission (>90% reduction of blasts compared to vehicle treated mice at day 28) in target organs (bone marrow, spleen). In contrast, mice that received etoposide monotherapy exhibited much smaller tumor burden decreases, while almost complete elimination of tumor cells (blasts <1% in any compartment) were absent in that group. Impact on overall survival was not evaluated. Similar results were obtained in another highly aggressive PDX model, PDX#19. Here, luciferase expressing PDX#19 (PDX#19-luc) cells were injected into NSG mice and treated with vehicle, ERG245 (30mg/kg, three times a week), etoposide (10mg/kg, twice a week) or the combination for 10 days before evaluating tumor burden (*Online Supplementary Figure S14G-J*). The data again highlight that BCAT1 inhibition greatly potentiates the antitumor activity of etoposide in vivo.

DISCUSSION

The present study elucidates the unique role that BCAT1 plays in T-ALL. BCAT1 is the cytosolic enzyme commonly responsible for the reversible transfer of an amino group from leucine, isoleucine, and valine to alpha-ketoglutarate (α -KG) to form glutamate and the corresponding α -ketoacid³². Here, we report that BCAT1 is a downstream target of mutated NOTCH1. Mutations that activate NOTCH1 signaling are found in more than 65% of all T-ALL cases and considered a hallmark of the disease. Our experiments revealed that Notch1 binds to Bcat1 promoter and increases Bcat1 gene transcription early in the process of

leukemogenesis in experimental models of T-ALL, as well as in clinical samples of patients suffering from the disease. Such an increase confers metabolic and other advantages to the leukemic cells. Compared to thymic tissues, we show that NOTCH1-T tumors exhibit elevated levels of TCA cycle metabolites. For the same tumors, we report a break in the TCA cycle with BCAT1 inhibition and impaired metabolic activity as determined by the downregulation of many essential metabolites. At the same time, BCAT1 inhibition or Bcat1 depletion appears to redirect leucine metabolism towards synthesis of leucine and 3-HB, an HDAC inhibitor, suggesting that BCAT1 may also regulate protein acetylation. Indeed, we find increased acetylation of histones (H3K27) and repair proteins (Ku70/Ku80) in Bcat1/BCAT1 depleted cells. Another interesting finding was that BCAT1 depletion or inhibition resulted in increased levels of γ H2AX, a marker of increased DNA damage. Although we do not provide any direct experimental evidence, this may be linked to an anti-oxidant role for the BCAT1 CXXC motif, normally buffering intracellular reactive oxygen species (ROS)³³.

Deletion of Bcat1 seems associated with faulty DDR and induction of apoptosis, especially following exposure to DNA damaging agents. Collectively, our study indicates that NOTCH1 upregulates BCAT1 to metabolically reprogram the cells and to ensure cell survival upon DNA damage possibly through altered 3-HB synthesis and protein acetylation (see Figure 7). This is in line with numerous studies suggesting that NOTCH1 controls oncogenic pathways that promote cell proliferation and survival, metabolic reprogramming, and resistance to chemotherapy through transcriptional activation of downstream target genes. Although non-canonical functions have previously been assigned to BCAT1 and linked to its redox state^{25, 28, 34}, increased sensitivity to etoposide in BCAT1 depleted cells seems to be dependent on its transaminase activity. We speculate that following BCAT1 depletion/inhibition, cells adapt increasing ketone body synthesis (3-HB) which initially has growth-promoting effects (through its anti-oxidant effect at low concentrations), but as it accumulates, it paradoxically promotes cell death through its capacity to inhibit HDACs^{35, 36} and promote protein acetylation. This accumulation of 3-HB seems to potentiate the cytotoxic effects of DNA damaging agents such as etoposide. We hypothesize that NOTCH1 directly⁹ and indirectly (through BCAT1 upregulation) represses DDR in order to promote cell survival in the presence of a genotoxic insult. The same mechanism might be at play during leukemogenesis, which allows for the accumulation of genetic lesions, the survival of the cells, and ultimately the onset of T-ALL.

The role of BCAT1 in leukemia and other cancers is currently an active area of research. Numerous reports have indicated that BCAT1 is a risk-factor in multiple cancers: its expression is associated with tumor progression, increased chemoresistance, and poor prognosis^{37, 38}. In agreement, our experiments suggest that high BCAT1 expression correlates with poor survival in NOTCH1-driven malignancies (T-ALL, B-CLL) and that inhibition of BCAT1 increases the chemosensitivity of T-ALL cells towards cytotoxic drugs, known to induce DSBs, such as the topoisomerase II inhibitor etoposide. In two aggressive PDX models, the combination of ERG245 and etoposide markedly reduced tumor burden, almost completely cleared CD45⁺ blasts from the blood, and abolished splenomegaly in the majority of the treated animals indicating that BCAT1 could be a novel therapeutic target in T-ALL particularly in salvage protocols.

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Figure legends

Figure 1. BCAT1 is upregulated during NOTCH1-dependent transformation. (A) Heat map showing the top 50 most down-regulated and up-regulated genes between normal double positive (DP) cells and *ICN1*-induced DP leukemic cells (NIC Tumors). (B) Expression levels (qRT-PCR; left) of *Bcat1* 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. $**P < 0.01$. Western blot (right) showing protein expression levels of ICN1 and Bcat1. β -actin and tubulin are shown as loading controls. Graphical representation of Bcat1/ β -actin ratios (extreme right). Bars represent mean values. ICN1: intracellular NOTCH1. (C) Box plot showing the expression of BCAT1 mRNA in T-ALL patients (N=57) and thymocyte subsets (7 thymocyte and mature T-cell subsets derived from (N=3) independent donors; quantile-normalized microarray results downloaded from GSE33469 and GSE33470. CD3⁺ and CD3⁻ DP cells were grouped together. CD1⁺ and CD1⁻ CD34⁺ cells were grouped together. Boxes represent first and third quartiles and line represents the median. Statistical analysis between groups was performed using unpaired two-sided t-test. (D) BCAT1 transcript (top) and protein levels (bottom) in total human thymus, *NOTCH1* wild-type and *NOTCH1* activated/mutated patient derived T-ALL xenografts (PDX). Significance was calculated using a nonparametric t-test (Mann-Whitney). $**P < 0.01$. ICN1, MYC and PTEN protein levels are also shown. β -actin is shown as loading control. (E) PDX samples were treated in vivo with DBZ (10 μ g/kg every 8 hours for a total of 3 injections) or vehicle (DMSO) for 24h before analysis of BCAT1 transcript levels. For statistical analysis, an unpaired t-test was used. $**P < 0.01$, $***P < 0.001$. (F) NOTCH1 ChIP-seq binding (left) in the BCAT1 locus in HPB T-ALL cells. Inset shows the location of ChIP-qPCR amplicons near NOTCH-1 peak region (P1-P2) and in a negative control region (NL). Chromatin from PF382 cells was subjected to ChIP using a NOTCH1 antibody (right). The indicated regions (P1, P2 and NL) were PCR amplified from the precipitated and input DNA. Fold enrichment was calculated as a ratio of amplification efficiency of ChIP sample over that of the IgG control. Shown are means \pm SD (N \geq 3). For statistical analysis, an unpaired t-test was used. $***P < 0.001$.

Figure 2. Functional effects of BCAT1 depletion. (A) Kaplan-Meier survival curves of overall survival in lethally irradiated C57BL/6J hosts transplanted with BM cells (WT or KO for *Bcat1*) transduced with ΔE -*NOTCH1* allele. Data from two independent transplantation experiments were pooled together. Log-rank Mantel-Cox test was performed to calculate *P* value. $***P < 0.001$. Shaded area represents 95% CI. (B) Representative plots (left) and bar graph representation (S-phase fraction; right) of ex vivo EdU incorporation in ΔE -*NOTCH1* leukemias WT and null for *Bcat1*. Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. $***P < 0.001$. (C) Representative plots (left) and bar graph representation (S-phase fraction; right) of MOLT4 cells transduced with shCTRL, shBCAT1 #1 or shBCAT1 #2 seven 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. $***P < 0.001$. (D) T-ALL cells were transduced with control vector (shCTRL) or vector containing shRNA sequences against BCAT1 (shBCAT1 #1, shBCAT1 #2). Expression of BCAT1 and tubulin was analyzed by immunoblotting seven days post transduction (left panels) in DND41 and MOLT4. Starting from seven days post-puromycin selection, cell proliferation was evaluated by determining cell number (DND41) or ATP levels by bioluminescence (MOLT4). Significance was calculated using an unpaired two-tailed t-test. $*P < 0.05$, $**P < 0.01$. (E) Representative images of bioluminescence (top) and quantitative analysis of tumor burden (bottom) in NSG mice xenografted with CCRF-CEM cells expressing luciferase and transduced with shCTRL or shBCAT1 (#1 and #2). Analysis after 15 days post-transplant is shown. Significance was calculated using an unpaired two-tailed t-test. $**P < 0.01$. (F) Representative images of bioluminescence (top) and quantitative analysis of tumor burden (bottom) in NSG mice xenografted with MOLT4 cells expressing luciferase and transduced with shCTRL or shBCAT1 (#1 and #2). Analysis after 15 days post-transplant is shown. Significance was calculated using an unpaired two-tailed t-test. $*P < 0.05$, $**P < 0.01$.

Figure 3. Canonical functions of Bcat1. (A) Heat map representation of the top down- and up-regulated genes between ΔE -NOTCH1 tumors WT or KO for *Bcat1*. Two independent WT and KO tumors were analyzed. *Bcat1* gene is highlighted in red. (B) Gene set enrichment analysis (GSEA) identified three significantly enriched gene sets involved in cell cycle regulation downregulated in *Bcat1* KO T-ALL cells. The normalized enrichment score (NES) and the nominal *P* value are illustrated. (C) Gene set enrichment analysis (GSEA) identified three significantly enriched gene sets involved in DNA damage response upregulated in *Bcat1* KO T-ALL cells. The normalized enrichment score (NES) and the nominal *P* value are illustrated. (D) Immunoblots of γ H2AX, p21 and *Bcat1* in tumors WT or KO for *Bcat1* (top). α -Tubulin is shown as loading control. T-ALL cells (CCRF-CEM, DND41, MOLT4) transduced with shCTRL/CAS9 or shBCAT1 (#1 and #2)/sgBCAT1 were analyzed by immunoblotting for γ H2AX and BCAT1 (bottom). β -actin is shown as loading control. (E) Heatmap representation (left) of the top 50 differentially expressed metabolites identified by capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS) between ΔE -NOTCH1 leukemias wild-type and KO for *Bcat1*. Metabolites that are significantly and consistently differentially expressed in multiple comparisons are highlighted in red. Volcano plot (right) showing differentially expressed metabolites (≥ 1.5 fold change, $P < 0.05$; in red and blue) identified by capillary electrophoresis time-of-flight mass spectrometry (CE-TOFMS) between ΔE -NOTCH1 leukemias wild-type and KO for *Bcat1*. Metabolites that are significantly and consistently differentially expressed in multiple comparisons are encircled.

Figure 4. ERG245, a BCAT1 specific inhibitor mimics the functional consequences of Bcat1 depletion.

(A) Representative plots of apoptosis in ΔE -NOTCH1 leukemia wild-type for *Bcat1* (WT#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μ M- 1 mM). (B) Representative plots of ΔE NOTCH1 leukemia wild-type for *Bcat1* (WT#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μ M-500 μ M). Cells were then assessed for EdU incorporation by fluorescence-activated cell sorting (FACS) analysis. (C) Representative cell viability analysis in ΔE -NOTCH1 tumors WT (WT#3) or KO (KO#3, #1) for *Bcat1*. Murine T-ALL cells were treated *in vitro* for 48h with PBS (vehicle) or increasing doses of ERG245 (100 μ M- 1 mM). Data is shown as mean \pm SD. (D) Representative plots of T-ALL cell lines (CCRF-CEM, DND41) treated in vitro for 72h with PBS (vehicle) or ERG245 (300 μ M). Cells were then assessed for EdU incorporation by fluorescence-activated cell sorting (FACS) analysis. (E) Representative plots of PDX#27 treated in vitro for 72h with PBS (vehicle) or increasing doses of ERG245 (300 μ M- 1 mM). Cells were then assessed for EdU incorporation by fluorescence-activated cell sorting (FACS) analysis.

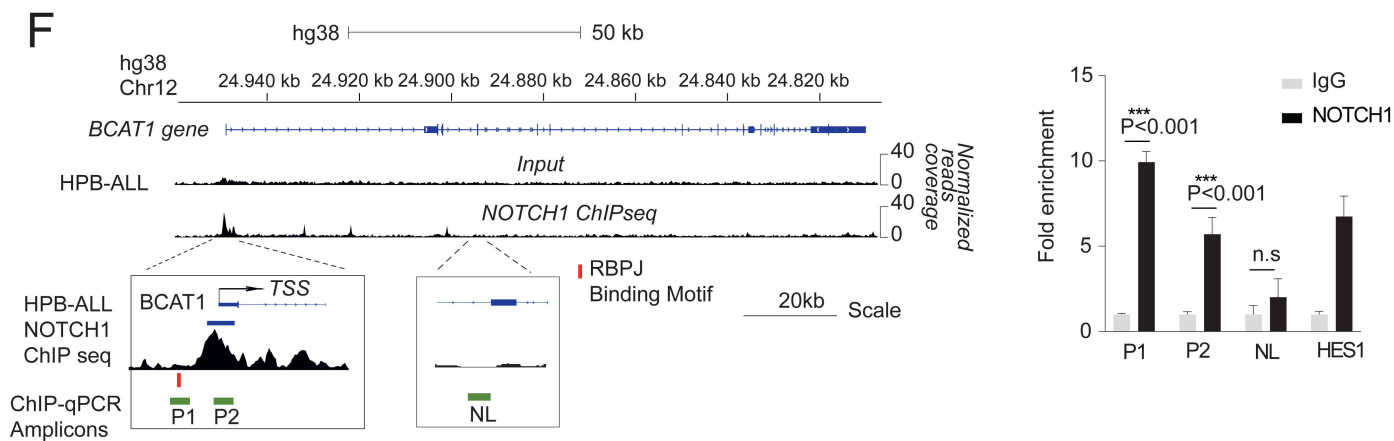
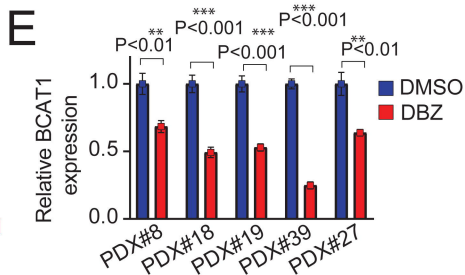
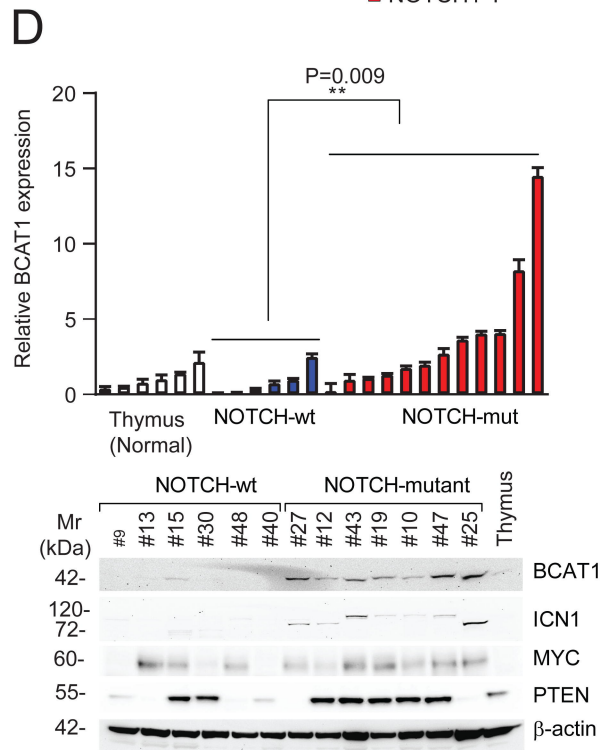
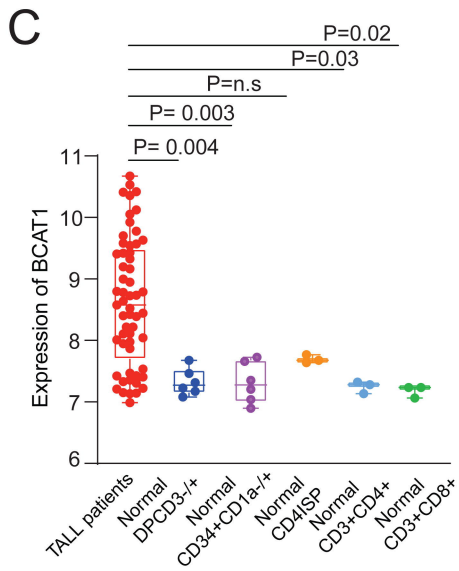
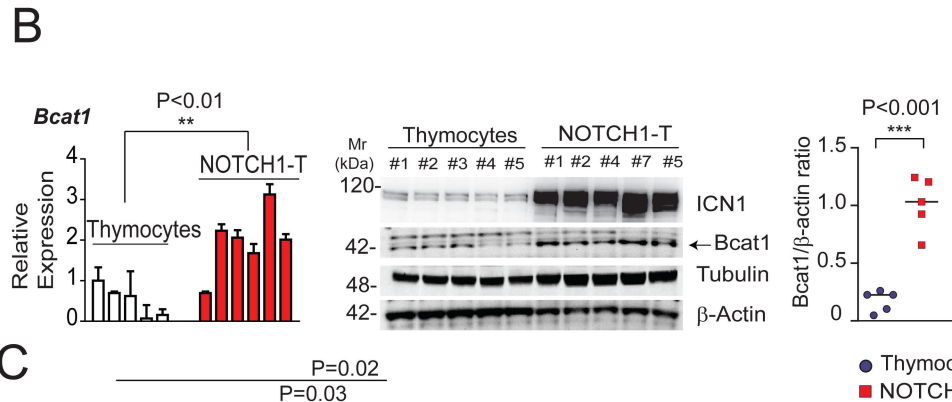
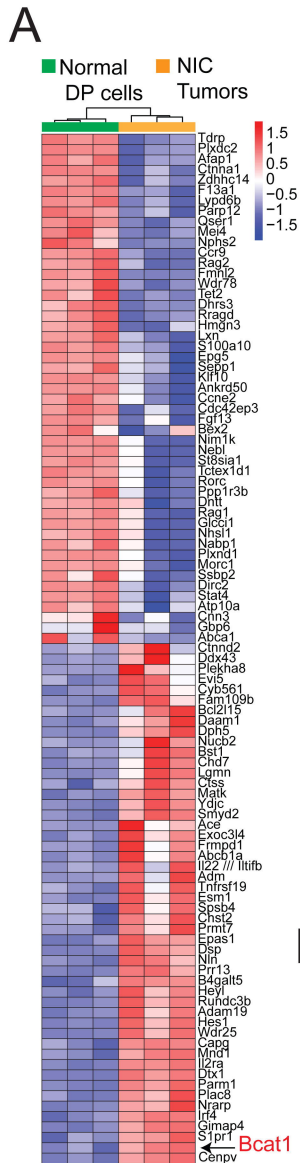
Figure 5. BCAT1 loss induces a dysfunctional DNA damage response following etoposide treatment.

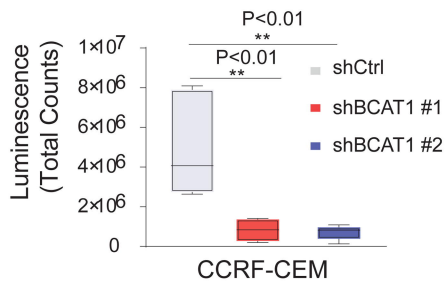
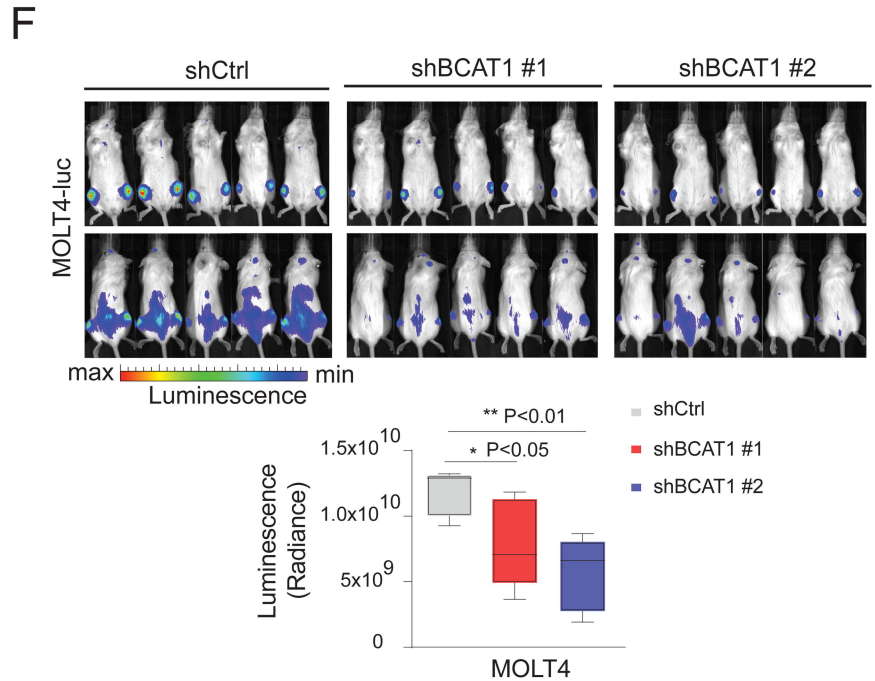
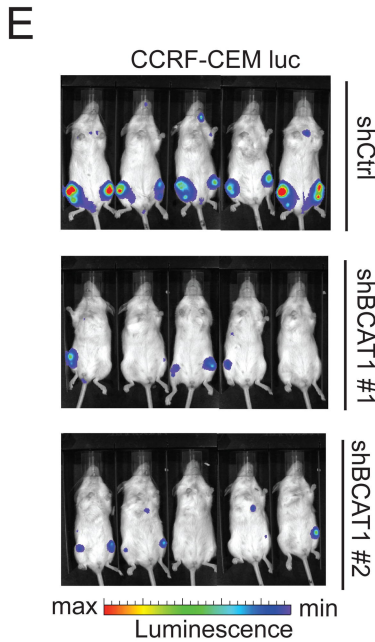
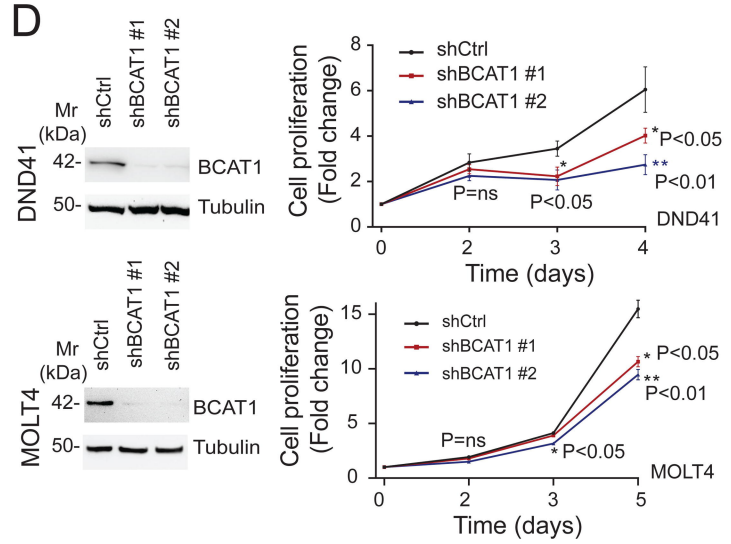
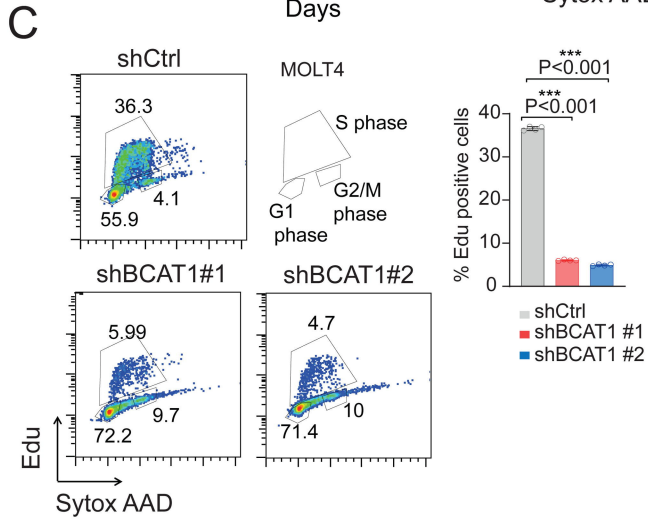
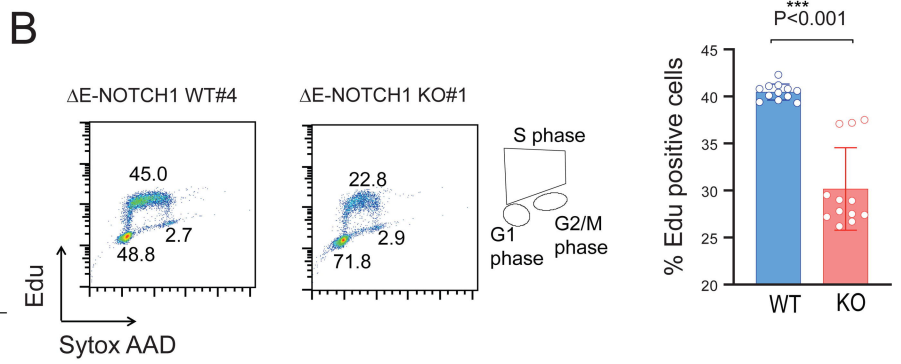
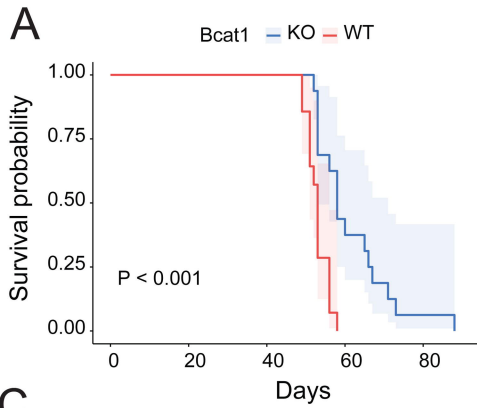
(A) Representative cell viability analysis (left) in ΔE -NOTCH1 tumors WT (WT#1) or KO (KO#6) for *Bcat1*. Murine T-ALL cells were treated *in vitro* for 48h with DMSO (vehicle) or increasing concentrations of etoposide (25-100 nM). Data is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$. Quantification of apoptosis (right) in ΔE -NOTCH1 tumors WT (WT#1) or KO (KO#6) for *Bcat1* treated in vitro for 48h with DMSO (vehicle) or increasing concentrations of etoposide (25-100 nM). Data is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. * $P < 0.05$, ** $P < 0.01$. (B) Representative plots of apoptosis (top) in CCRF-CEM T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) and treated in vitro for 48h with DMSO (vehicle) or etoposide (100 nM or 1 μ M). Quantification of apoptosis (bottom) in CCRF-CEM T-ALL cells transduced with shCTRL or shBCAT1 (#1 and #2) and treated in vitro for 48h with DMSO (vehicle) or etoposide (100 nM- 2 μ M). Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. (C) Expression of cleaved PARP-1 and phosphorylated γ H2AX was analyzed by immunoblotting in CCRF-CEM 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). β -actin and GADPH are shown as loading controls. (D) Representative neutral comet images (left) performed in CCRF-CEM cells infected with a control shRNA (shCTRL) or BCAT1-targeting

shRNAs (shBCAT1#1, shBCAT1#2) either untreated or after etoposide treatment (1 μ M) for 2 or 6 hours. Dot plot (right) showing individual percentages of comet tail DNA. The median value of 50-80 nuclei per experimental condition is indicated. Statistical analysis was conducted by using the Mann-Whitney test. Data are representative of 2 independent experiments.

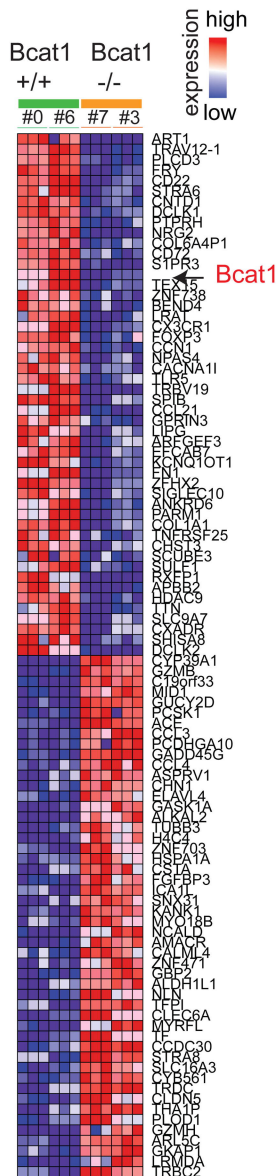
Figure 6. BCAT1 specific inhibition increases response to DNA-damaging agents, especially etoposide, in vitro and in vivo. (A) Representative plots of apoptosis in MOLT4 T-ALL cells treated with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop; 50-75 nM) or the combination (ERG245 + Etop) for 48h. (B) Representative plots of annexin V staining (left panels) in DND41 T-ALL cells treated with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop) or the combination (ERG245 + Etop) for 48h. Western blot analysis (right panels) of PARP-1 (total or cleaved PARP-1), and phosphorylated γ H2AX in DND41 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. (C) Representative plots (left) and bar graph representation (right) of apoptosis (Annexin V positive) in ex vivo obtained PDX#39 cells treated with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop; 50-250 nM) or the combination (ERG245 + Etop) for 48h. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. (D) Representative images of bioluminescence (left) in NSG mice xenografted with PDX#27 cells expressing luciferase (PDX#27-luc) and treated with vehicle (DMSO), BCAT1 inhibitor (ERG245; 30 mg/kg three times a week), etoposide (Etop; 15 mg/kg twice a week) or the combination (ERG245 + Etop). Analysis before (day 13 post-transplantation) and 15 days after start of treatment (day 28 post-transplantation) is shown. Quantitative analysis of tumor load (right) via in vivo bioluminescence imaging of NSG mice xenografted with PDX#27-luc after treatment (day 28 post-transplantation) with vehicle (DMSO), BCAT1 inhibitor (ERG245), etoposide (Etop) or the combination (ERG245 + Etop). Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$, *** $P < 0.001$. n.s.=not significant.

Figure 7. Schematic illustration of the proposed role of BCAT1 in regulating T-ALL response to DNA damaging agents in BCAT1 high and BCAT1 silenced/functionally inhibited T-ALL cells. BCAT1 inhibition induces a partial break in the TCA cycle between citrate and succinate leading to citrate accumulation and directing leucine metabolism towards 3-HB synthesis. 3-HB is known to act as an energy source in the absence of sufficient glucose and as it builds-up it inhibits class I histone deacetylases (HDACs), leading to increased acetylation of proteins such as histones and DNA damage response proteins (including KU70 and KU80) modifying their activity^{39,40} and possibly priming cells to the deleterious effects of DNA damaging agents. Following the exposure to DNA damaging agents (etoposide) this leads to accentuated DNA damage leading to cell death.



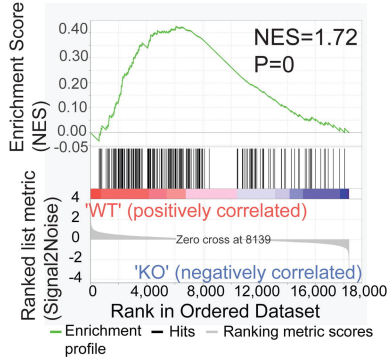


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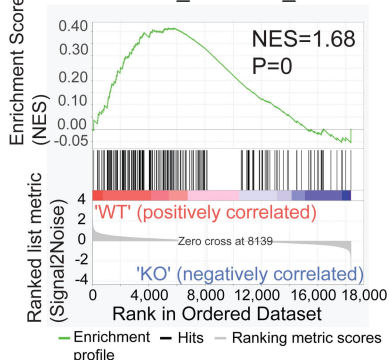


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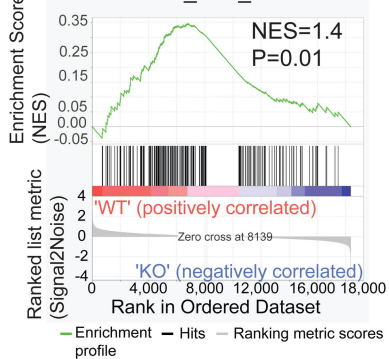
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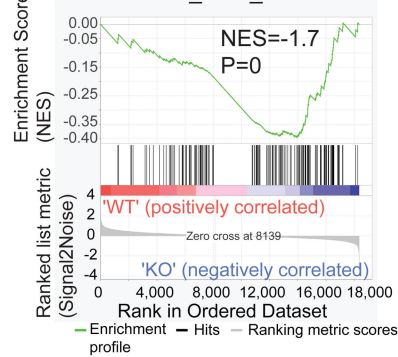


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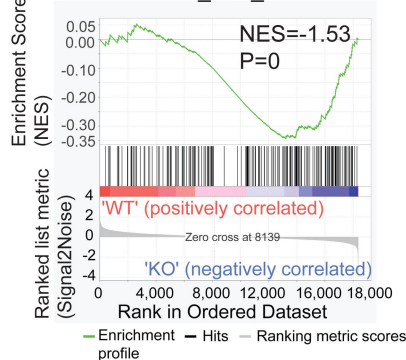


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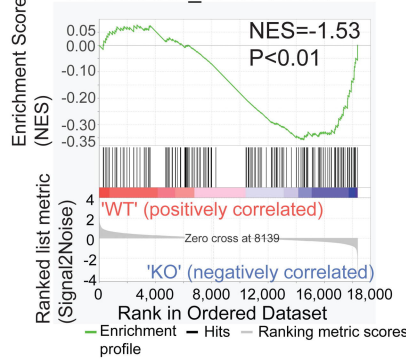
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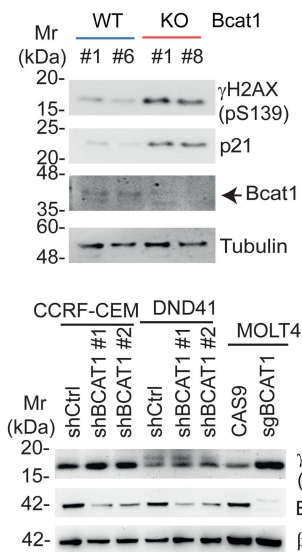
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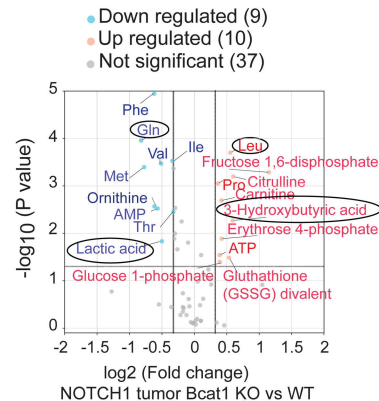
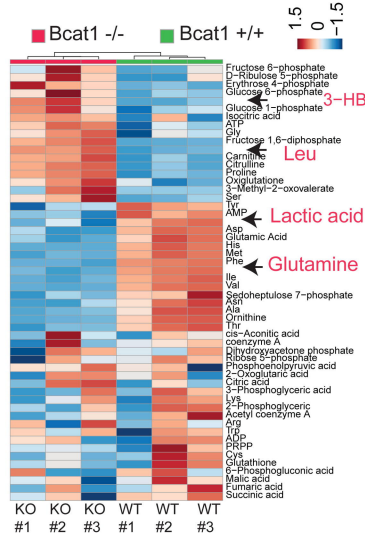
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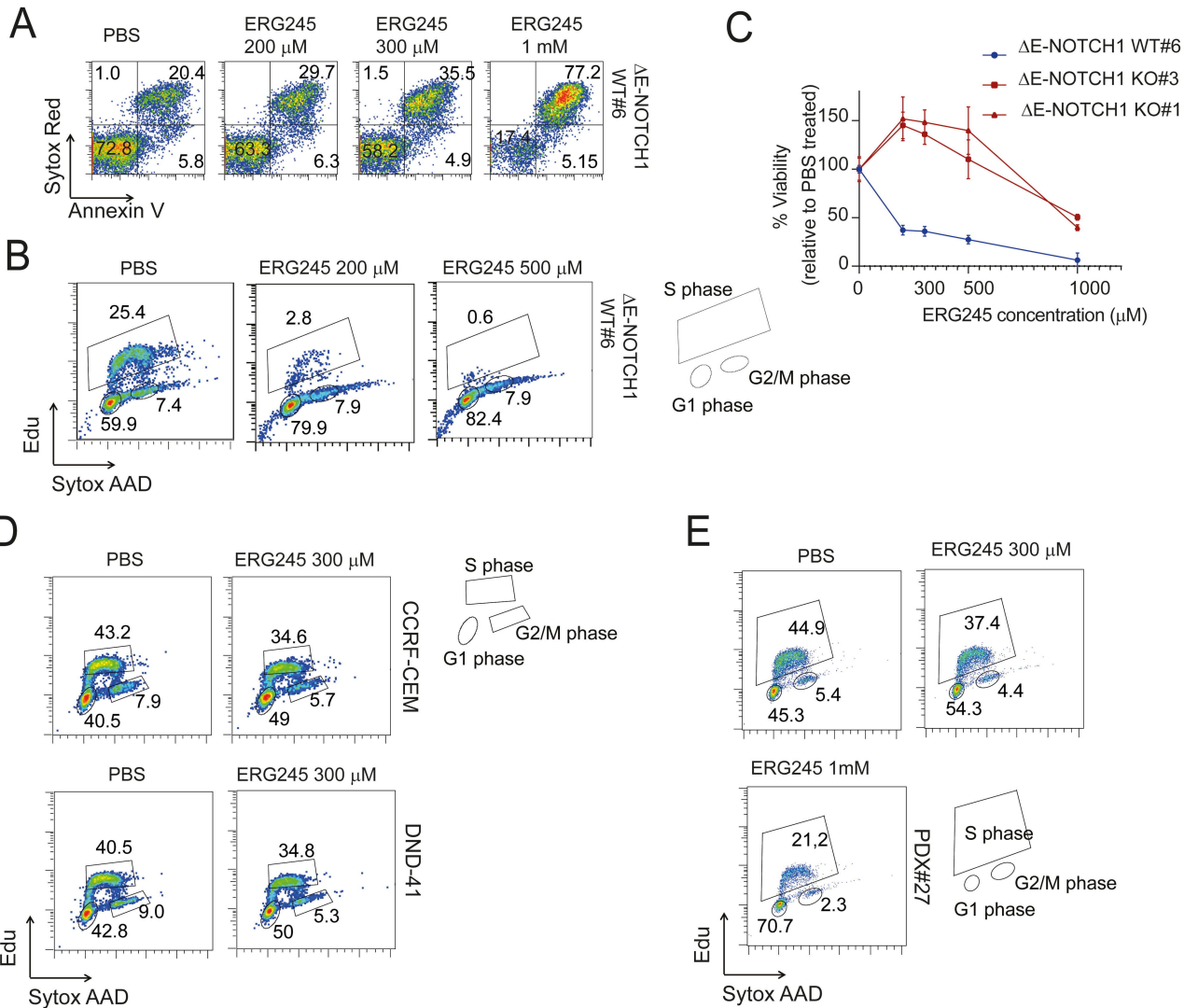


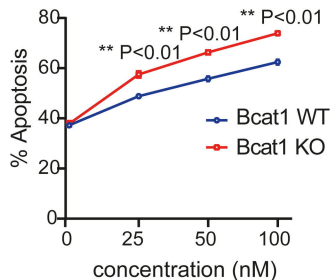
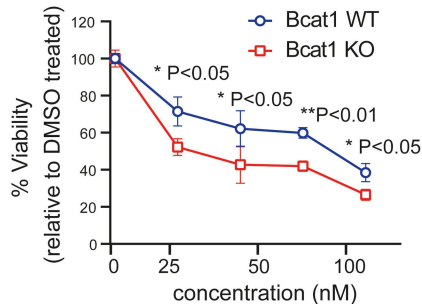
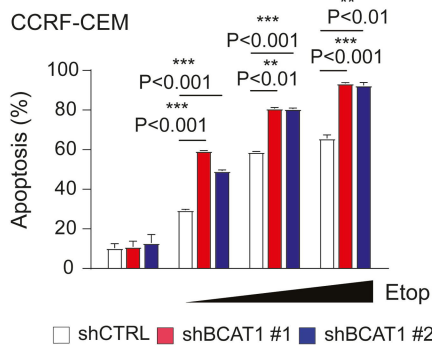
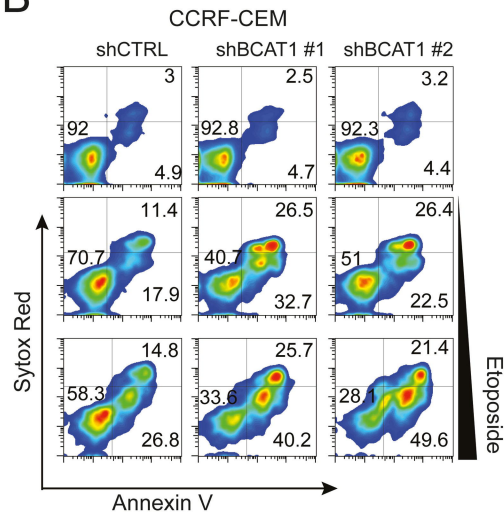
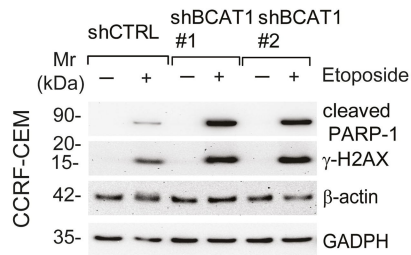
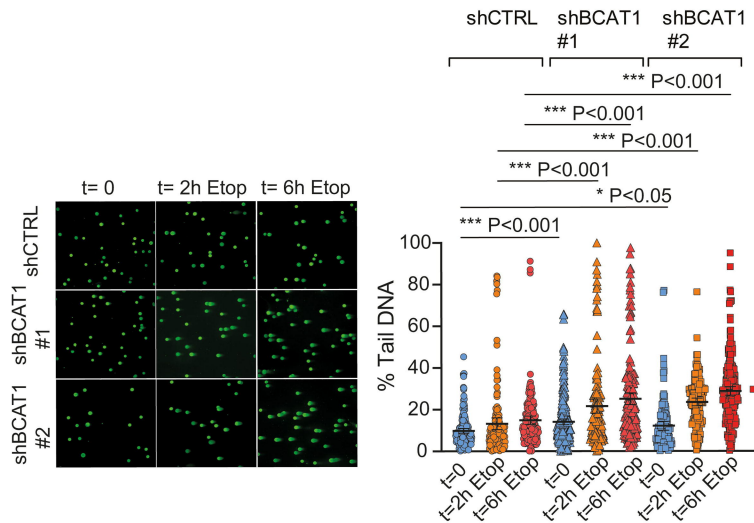
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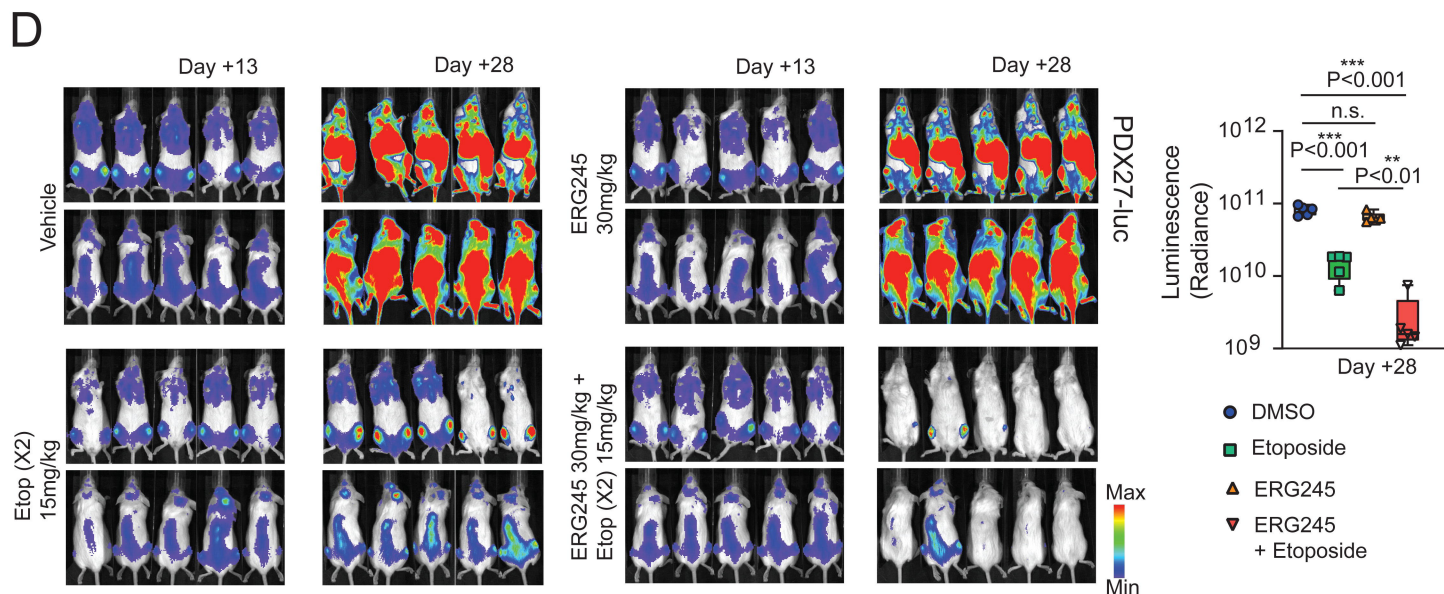
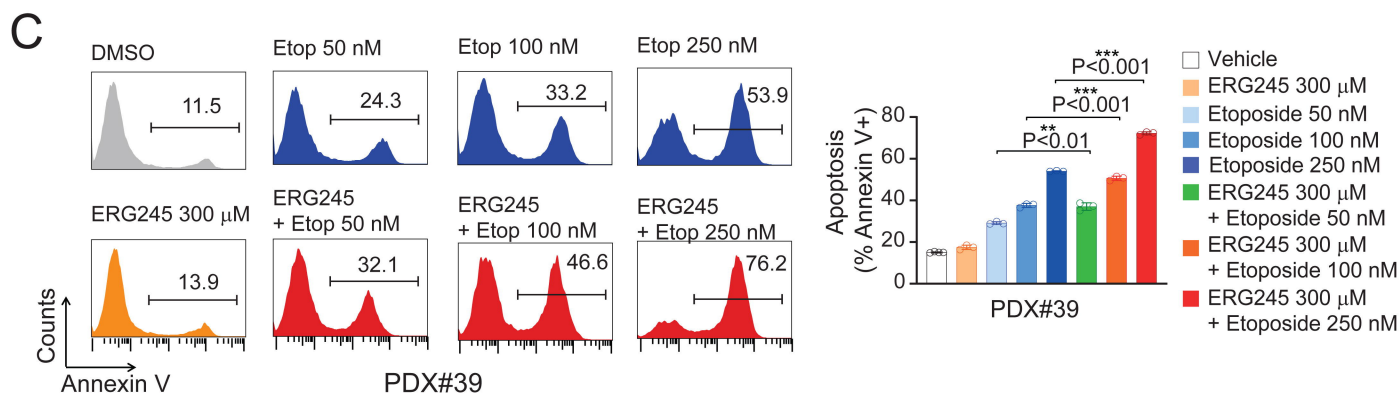
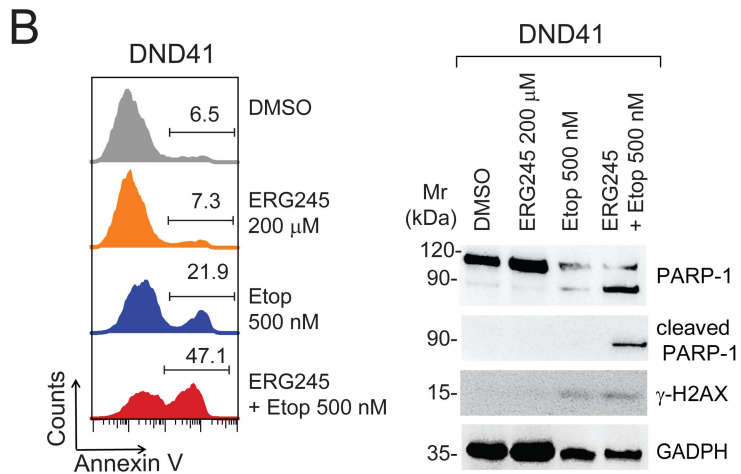
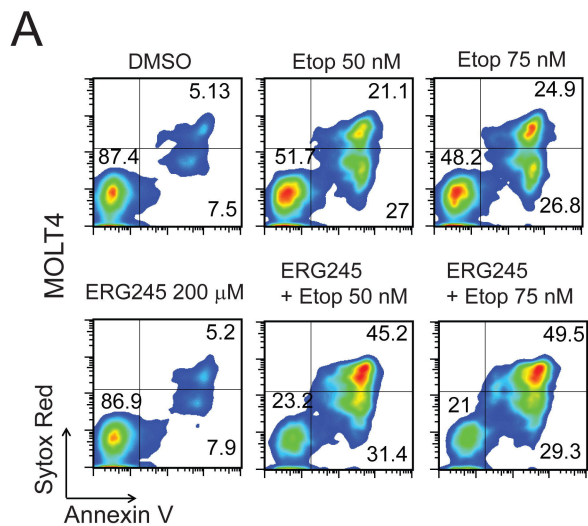


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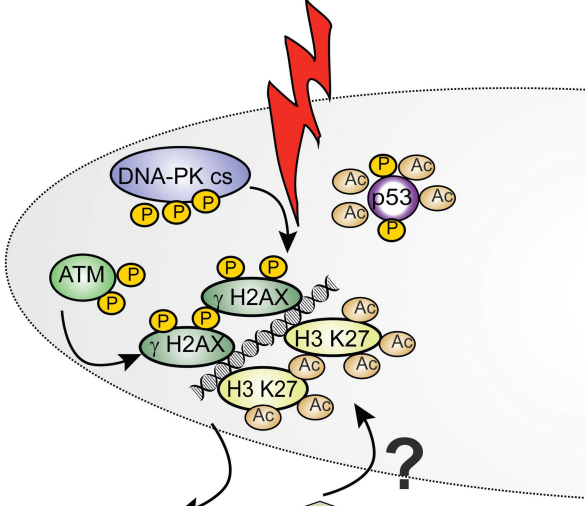


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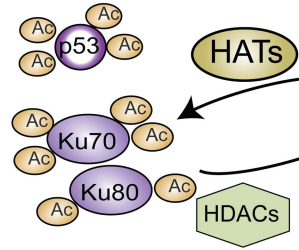


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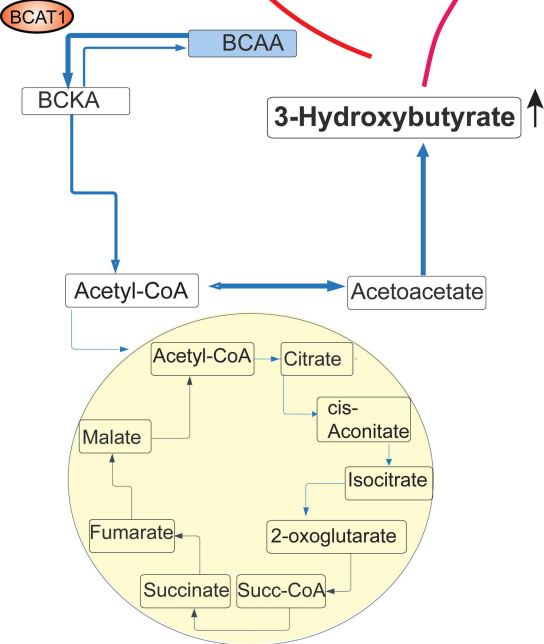
DNA DAMAGE



APOPTOSIS

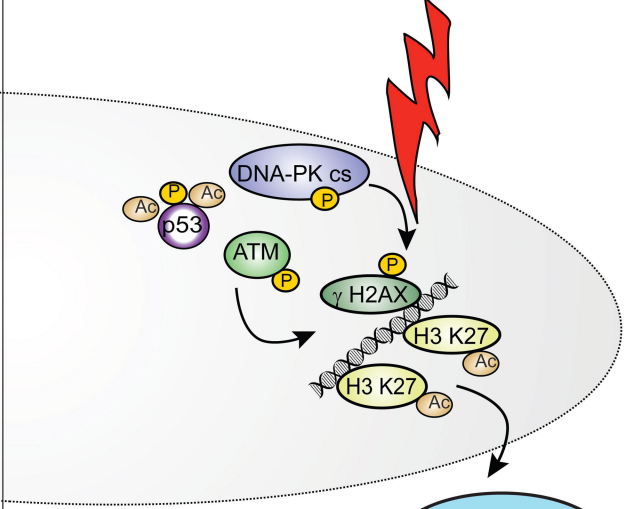


3-Hydroxybutyrate ↑

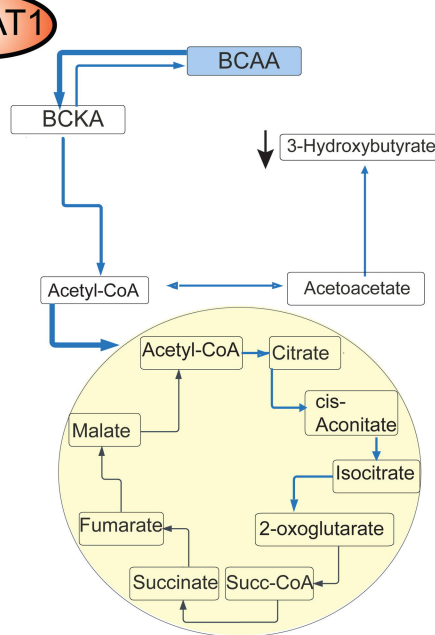
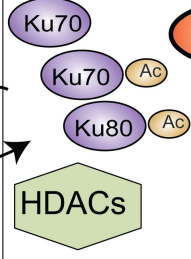


BCAT1 HIGH

DNA DAMAGE



REPAIR/
SURVIVAL



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

Valeria Tosello*, Ludovica Di Martino*, Adonia E. Papathanassiu, Silvia Dalla Santa, Marco Pizzi, Lara Mussolin, Jingjing Liu, Pieter van Vlierberghe†, Erich Piovan

†Deceased.

*these two authors contributed equally to the work

SUPPLEMENTARY DATA:

-Supplementary Materials and Methods

-Supplementary Tables

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

Table S2: Differentially expressed genes between *Bcat1* KO and *Bcat1* WT NOTCH1-dependent leukemias

Table S3. Hallmark pathways enriched in *Bcat1* WT and KO leukemias

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

-Supplementary Figures

Figure S1. BCAT1 is highly expressed in NOTCH1 mutant T-cell acute lymphoblastic leukemia (T-ALL)

Figure S2. ΔE -NOTCH1 tumors derived from infiltrated spleen and thymus have a similar metabolic profile

Figure S3. BCAT1 expression associates with NOTCH1 activation in human T-ALL

Figure S4. BCAT1 is modulated upon NOTCH1 inhibition

Figure S5. The NOTCH1 binding region in the BCAT1 locus is associated with promoter features in T-ALL cells

Figure S6. *Bcat1* promotes NOTCH1-dependent leukemia onset

Figure S7. Functional effects of BCAT1 depletion

Figure S8. Metabolic impact of *Bcat1* depletion on ΔE -NOTCH1 leukemias

Figure S9. Functional effects of a BCAT1 specific inhibitor, ERG245

Figure S10. BCAT1 specific inhibition has modest cytotoxic effects on human T-ALL, while BCAT1 depletion increases sensitivity to DNA damaging agents

Figure S11. Metabolic impact of BCAT1 inhibition on ΔE -NOTCH1 leukemias

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 function

Figure S13. Metabolic function of BCAT1 contributes in modulating the sensitivity to DNA damaging agents

Figure S14. BCAT1 expression correlates with prognosis in NOTCH1-dependent leukemias and represents a therapeutic target in T-ALL

Figure S15. BCAT inhibition synergizes with numerous chemotherapeutic drugs to reduce cell viability

Figure S16. BCAT1 inhibition synergizes with etoposide to reduce viability

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 γ null (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 Δ PEST* or *Δ E-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 described². 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 (Δ E-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, Δ E-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 β 2-microglobulin expression using the $\Delta\Delta$ CT 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 μ m-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 \geq 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 μ M) 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 RNeasy 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-PolIII)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. Di-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 (TATTAGGTCTTTAGCCTG; 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-APEST* 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 Rag1 null 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	CTCTGGGAAAGAGATCGGCA
BCAT1 <i>P1</i>	REVERSE	CTGCATGCTGAGAGGACCAC
BCAT1 <i>P2</i>	FORWARD	AATCTTCGGGCTGGGAGAGA
BCAT1 <i>P2</i>	REVERSE	GCAGATCCCAAGGGTCGTAG
HES1 <i>P1</i>	FORWARD	AAGTTTCACACGAGCCGTTT
HES1 <i>P1</i>	REVERSE	GCTGTTATCAGCACCAGCTC
BCAT1 <i>NL</i>	FORWARD	GTATCGCTCTGCTGTGAGGG
BCAT1 <i>NL</i>	REVERSE	GTCAACACCGTGACCCGTTA

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
HALLMARK_ADIPOGENESIS	-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	-0.5775	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	GAGAGATTTTATTATTTGGGGGC
BCAT1-prom-T1-M	REVERSE	CTAACCGTATAAACCGAATCTACGA
BCAT1-prom-T1-U	FORWARD	GAGAGATTTTATTATTTGGGGGTG
BCAT1-prom-T1-U	REVERSE	TAACCATATAAACCAAATCTACAAC
BCAT1-prom-T1-WT*	FORWARD	GTGTCTTCCTGCTGATGCAA
BCAT1-prom-T1-WT	REVERSE	AGATCCCAAGGGTCGTAGC
ACTB	FORWARD	GTGATGGAGGAGGTTTAGTAAGTT
ACTB	REVERSE	AATTACAAAAACCACAACCTAATAAA

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

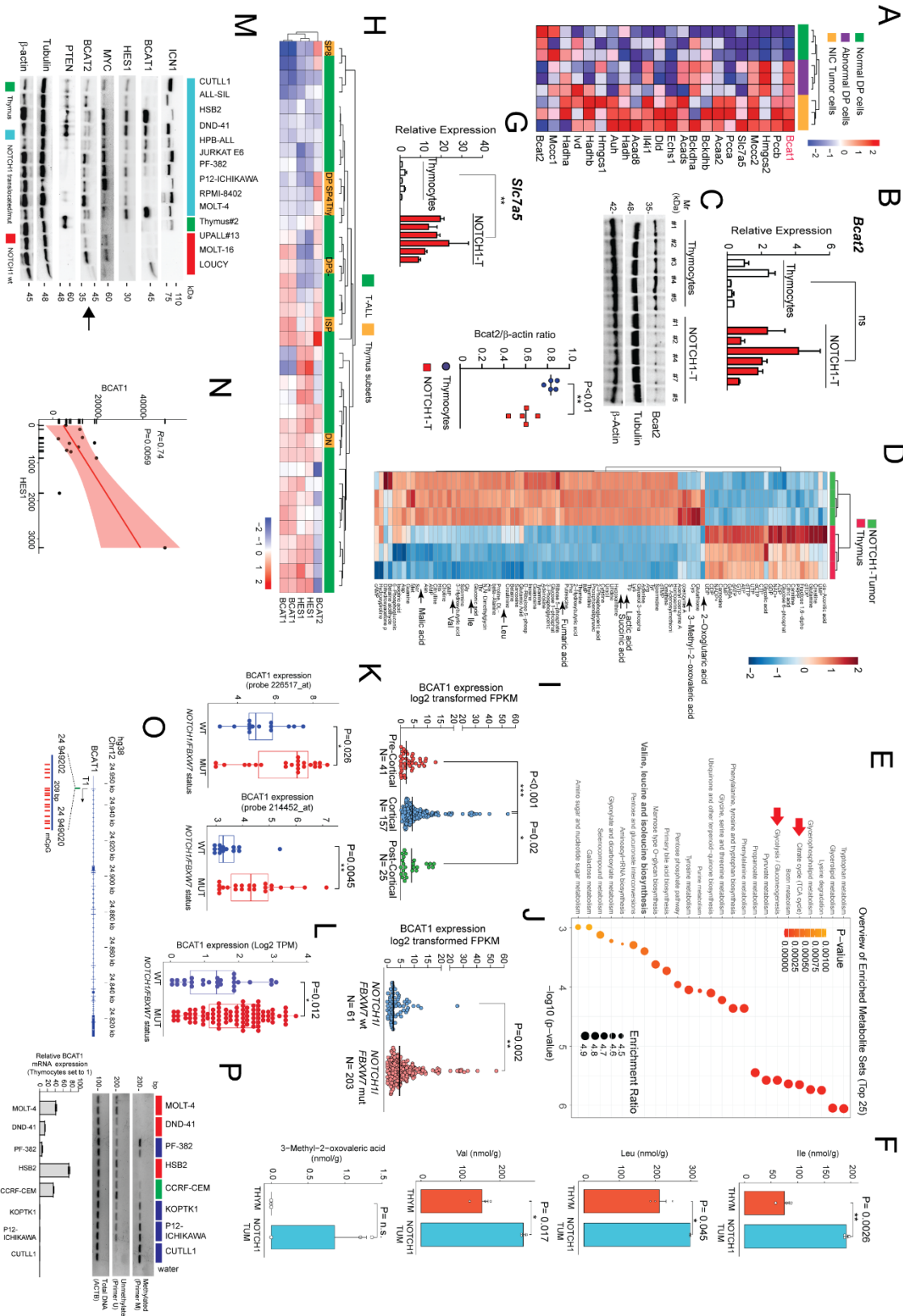


Figure S1. BCAT1 is highly expressed in NOTCH1 mutant T-cell acute lymphoblastic leukemia (T-ALL). (A) Heat map showing the expression levels of BCAA metabolic genes (N=22) between normal, abnormal (pre-

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) (CGAS00000000002)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 T1²⁹,³⁰ was 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).

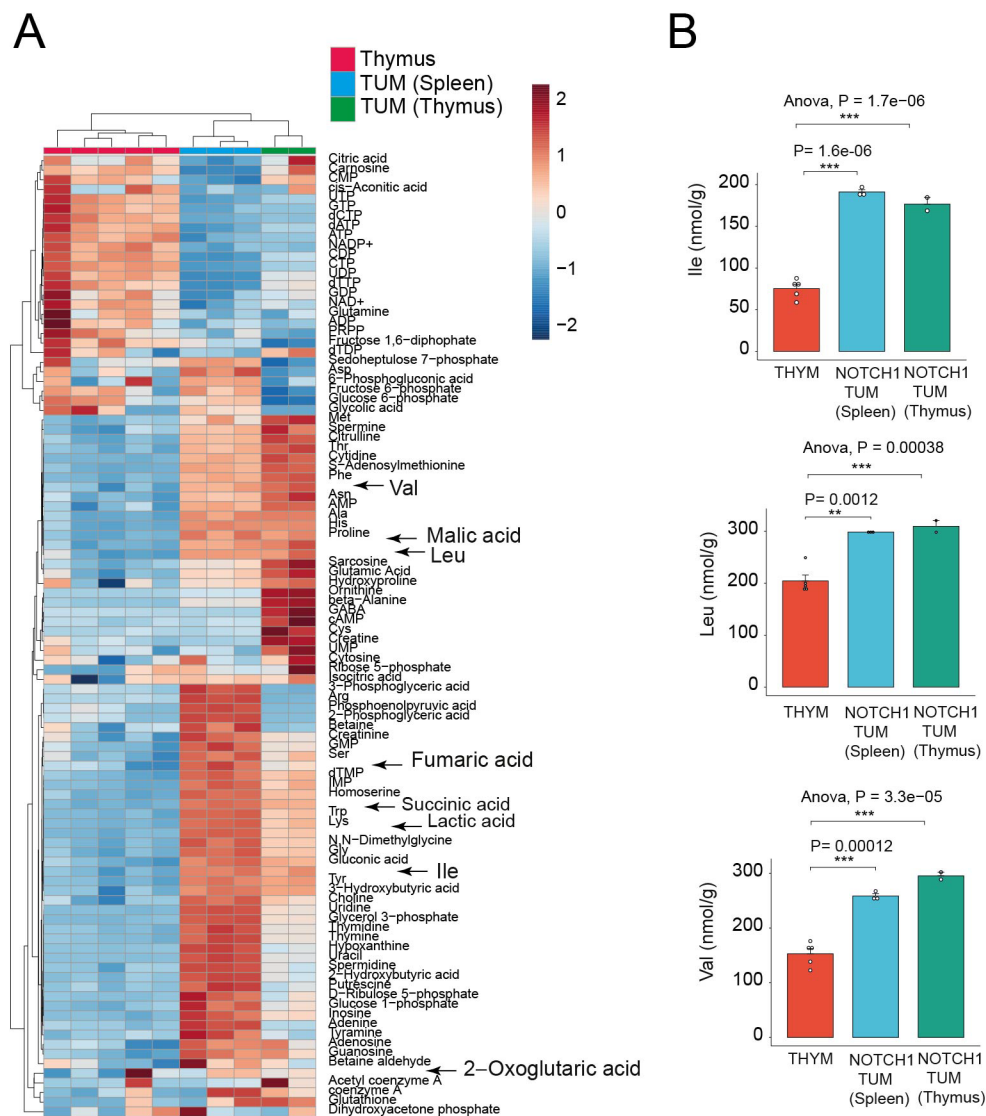


Figure S2. ΔE -NOTCH1 tumors derived from infiltrated spleen and thymus have a similar metabolic profile.

(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). ** $P < 0.01$, *** $P < 0.001$.

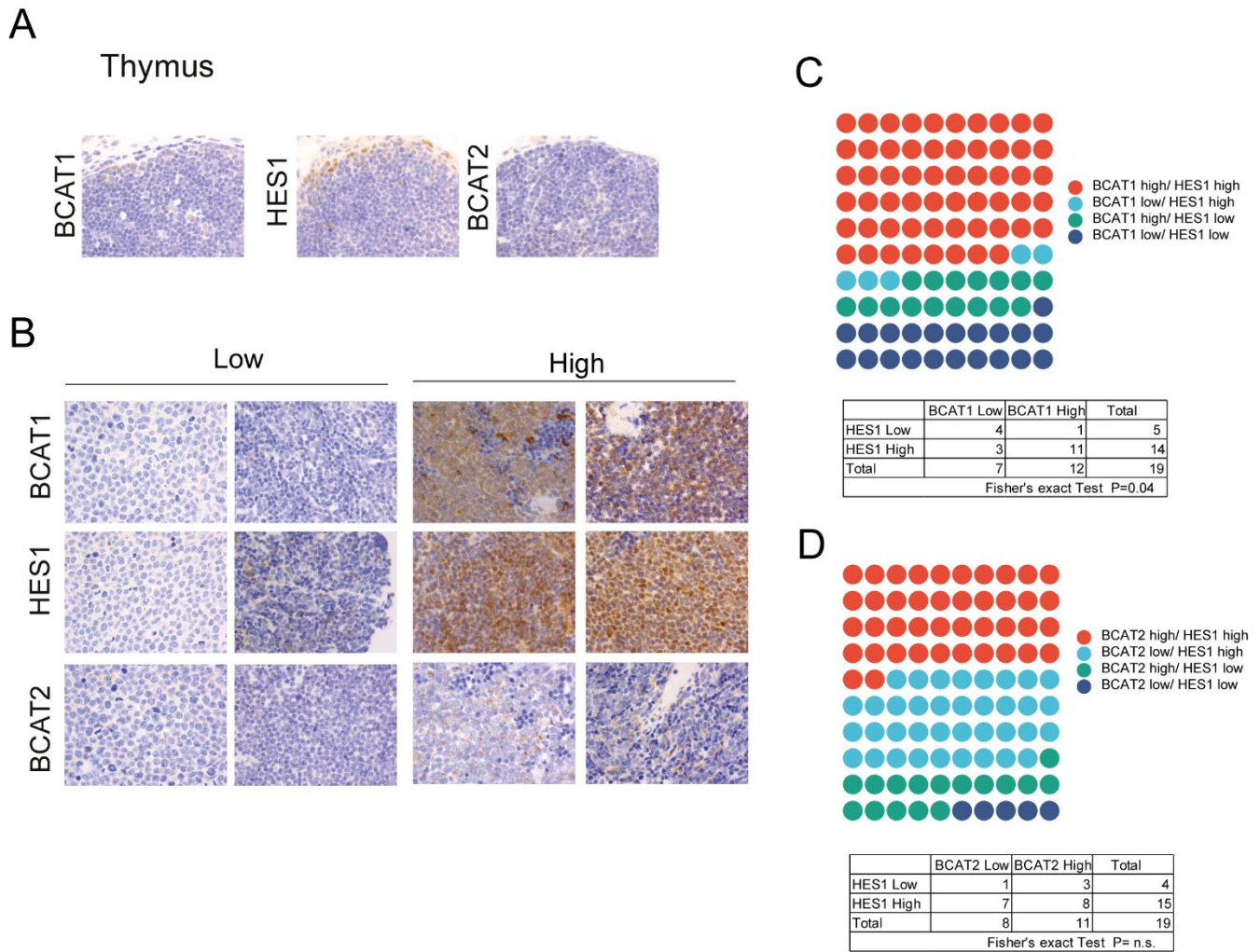


Figure S3. BCAT1 expression associates with NOTCH1 activation in human T-ALL. (A) BCAT1 (left), HES1 (middle) and BCAT2 (right) immunohistochemical staining of human thymus (top): original magnification 400 \times . (B) Immunohistochemical staining for BCAT1 (top), HES1 (middle), and BCAT2 (bottom) in representative cases of T-ALL showing low (0, +1) and high (+2, +3) expression levels. Original magnification \times 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).

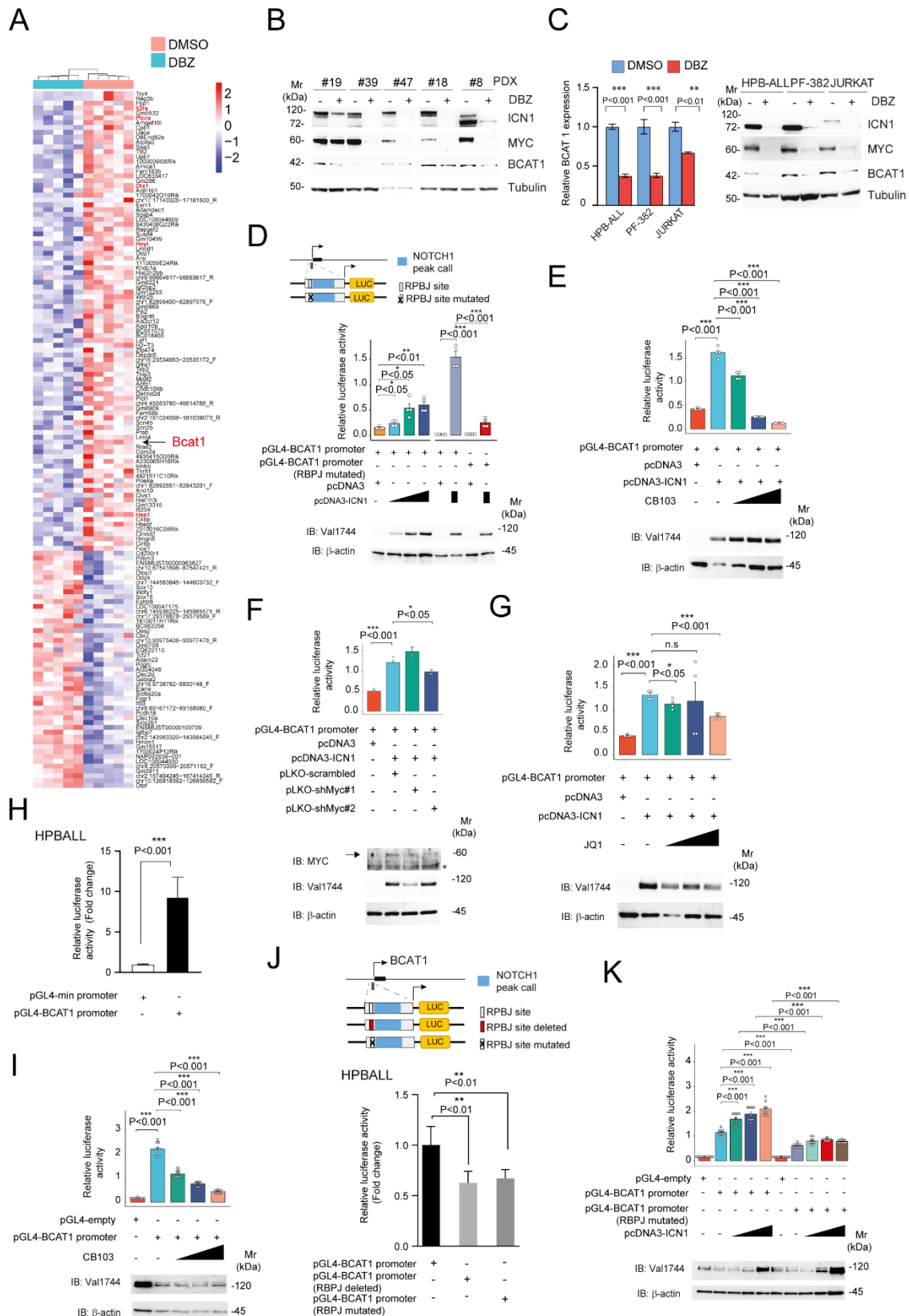


Figure S4. BCAT1 is modulated upon NOTCH1 inhibition. (A) Heat map representation of the top down-regulated genes following in vivo DBZ treatment of five ΔE -NOTCH1 tumors. BCAT1 and selected known

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 \pm 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 \pm 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 \pm 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 \pm 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 \pm 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 \pm 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.

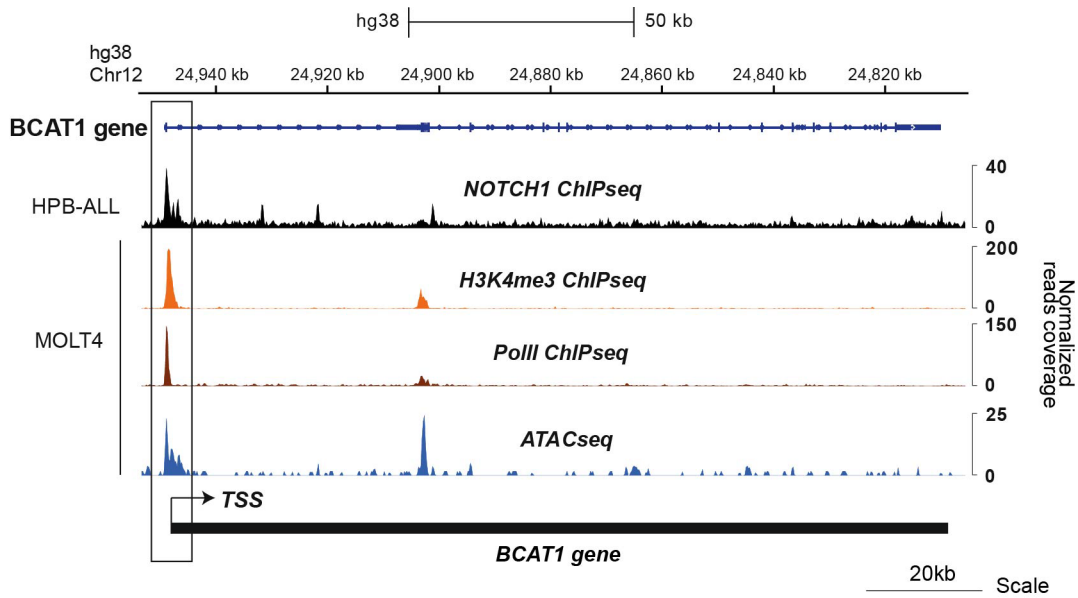


Figure S5. The NOTCH1 binding region in the BCAT1 locus is associated with promoter features in T-ALL cells. Profiles of H3K4me3, Pol II and NOTCH1 ChIP-seq binding in the BCAT1 locus in T-ALL cells. ATAC-seq data for the same region is also shown.

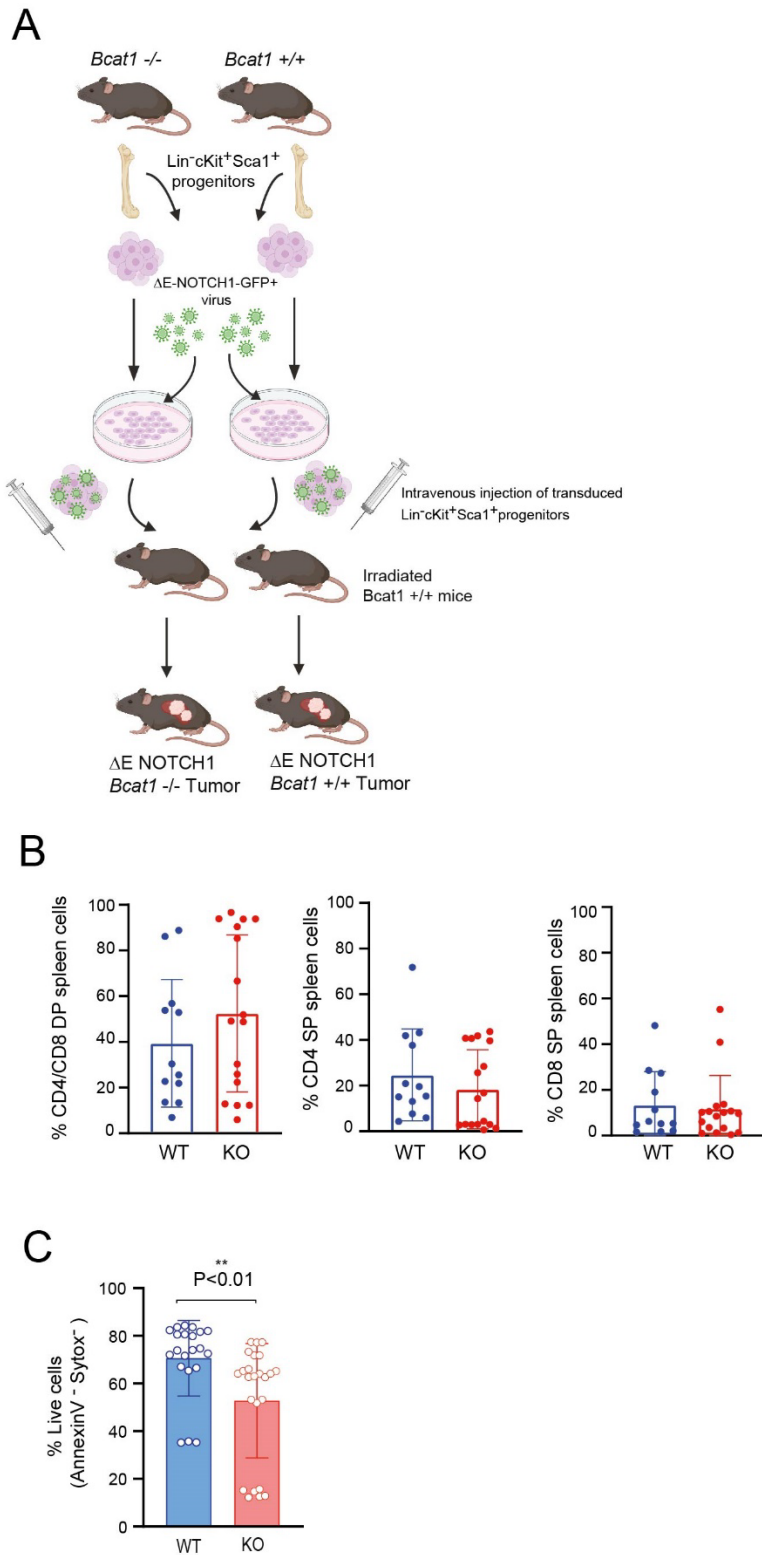


Figure S6. *Bcat1* promotes NOTCH1-dependent leukemia onset. (A) Schematic representation of the experimental procedure for the generation of ΔE -NOTCH1 leukemias wild-type (WT; +/+) and null (KO; -/-) for *Bcat1*. Image was generated with BioRender software. (B) Immunophenotype distribution showing 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 \pm SD. Significance was calculated using an unpaired two-tailed t-test. ** $P < 0.01$.

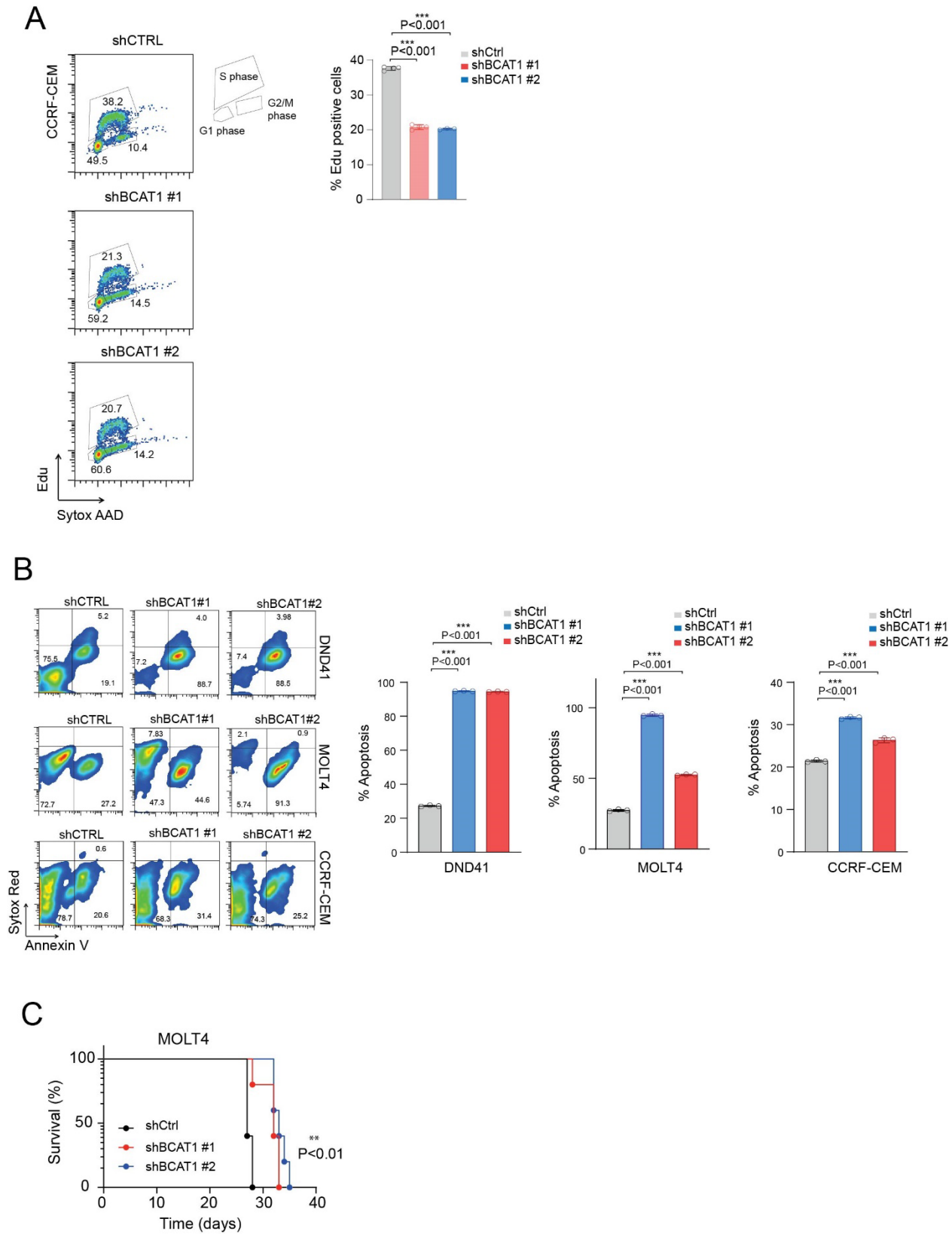


Figure S7. Functional effects of BCAT1 depletion. (A) Representative plots (left) and bar graph representation (right) of CCRF-CEM cells transduced with shCTRL, shBCAT1#1 or shBCAT1#2 twelve days post-puromycin

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. ** $P < 0.01$.

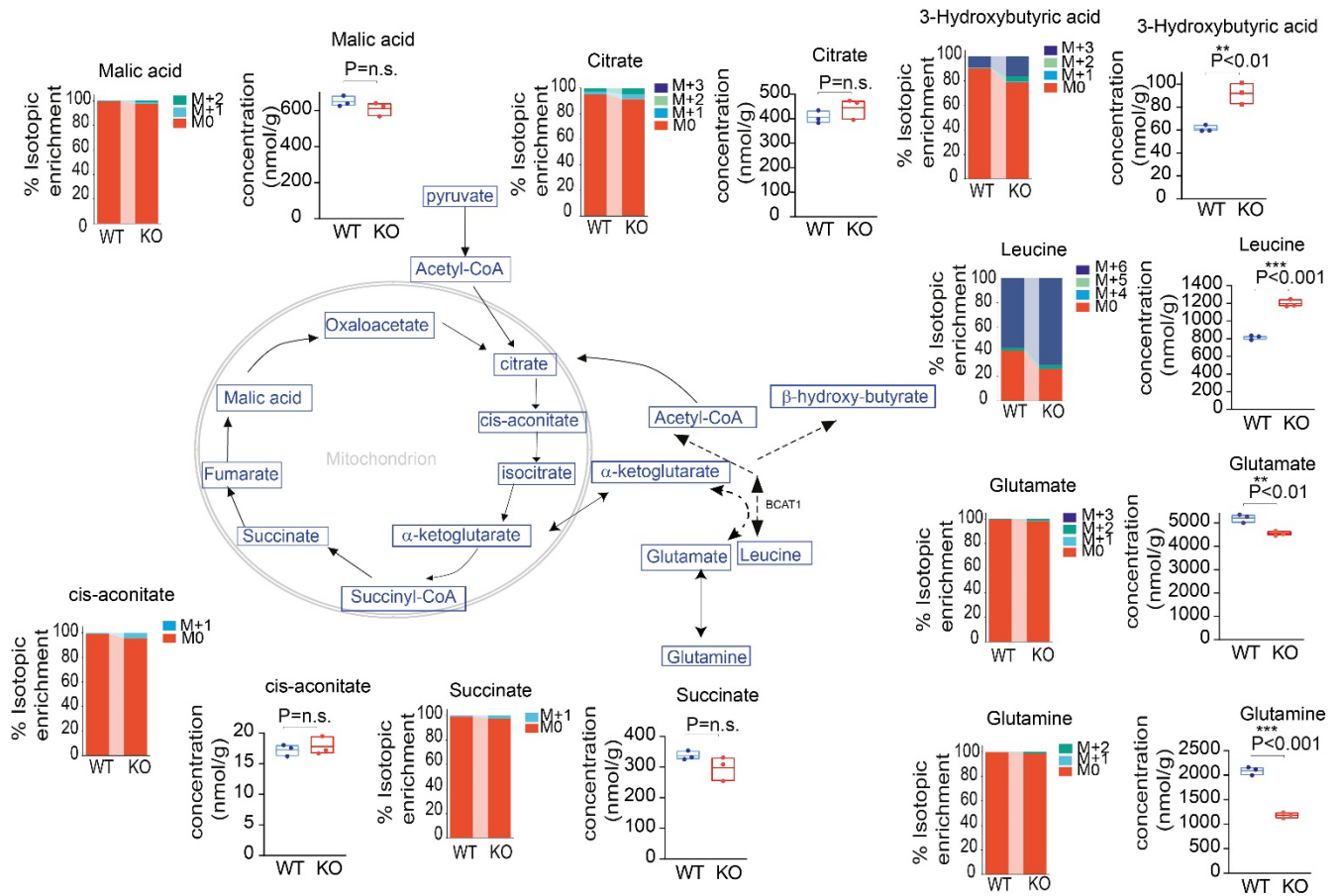


Figure S8. Metabolic impact of Bcat1 depletion on ΔE -NOTCH1 leukemias. Results for *in vivo* isotope-tracing experiments following i.v. administration of $^{13}\text{C}_6$ Leu in ΔE -NOTCH1 leukemias WT and KO for *Bcat1*. Mean percentages (from N=3 determinations) of $^{13}\text{C}_6$ Leu derived: (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.

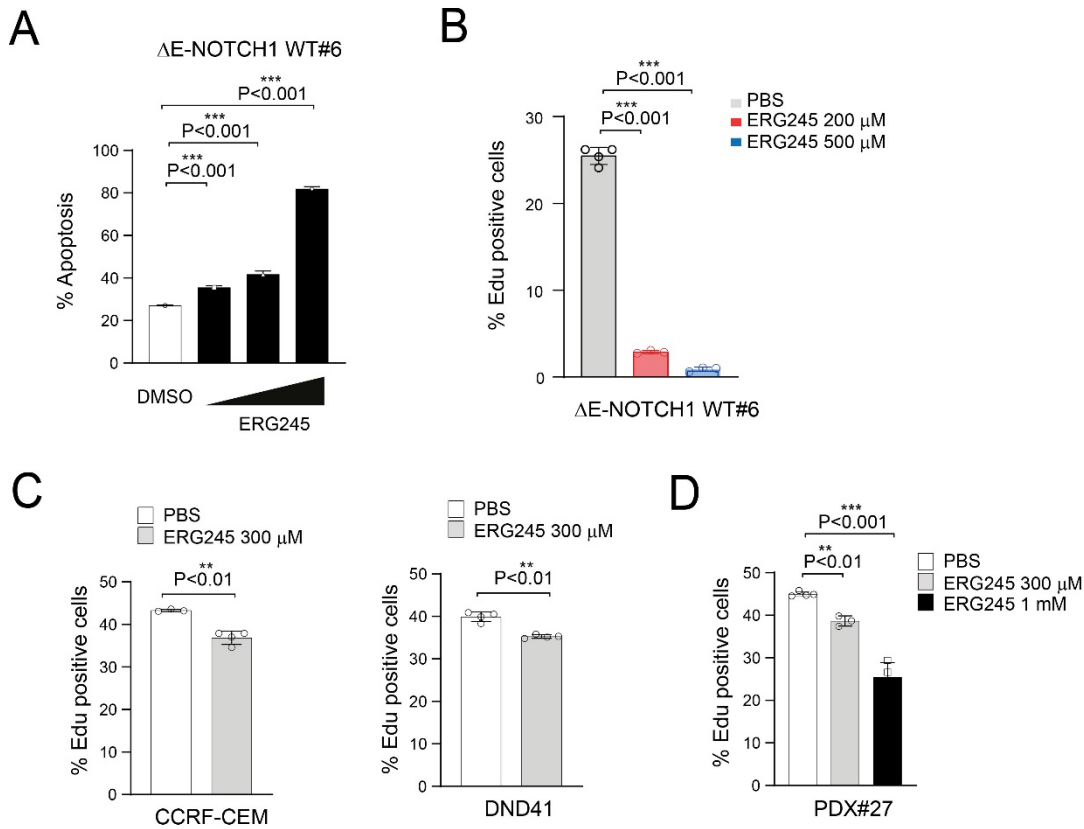


Figure S9. Functional effects of a BCAT1 specific inhibitor, ERG245. (A) Quantification of apoptosis in ΔE -*NOTCH1* leukemia wild-type for *Bcat1* (WT#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μ M-1 mM). Data for bar graph is shown as mean \pm SD. Significance was calculated using an unpaired two-tailed t-test. *** P < 0.001. (B) Quantification of EdU incorporation (S-phase cells) in ΔE *NOTCH1* leukemia wild-type for *Bcat1* (WT#6) treated in vitro for 48h with PBS (vehicle) or increasing doses of ERG245 (200 μ M- 500 μ M). 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 μ M). 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 μ M-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.

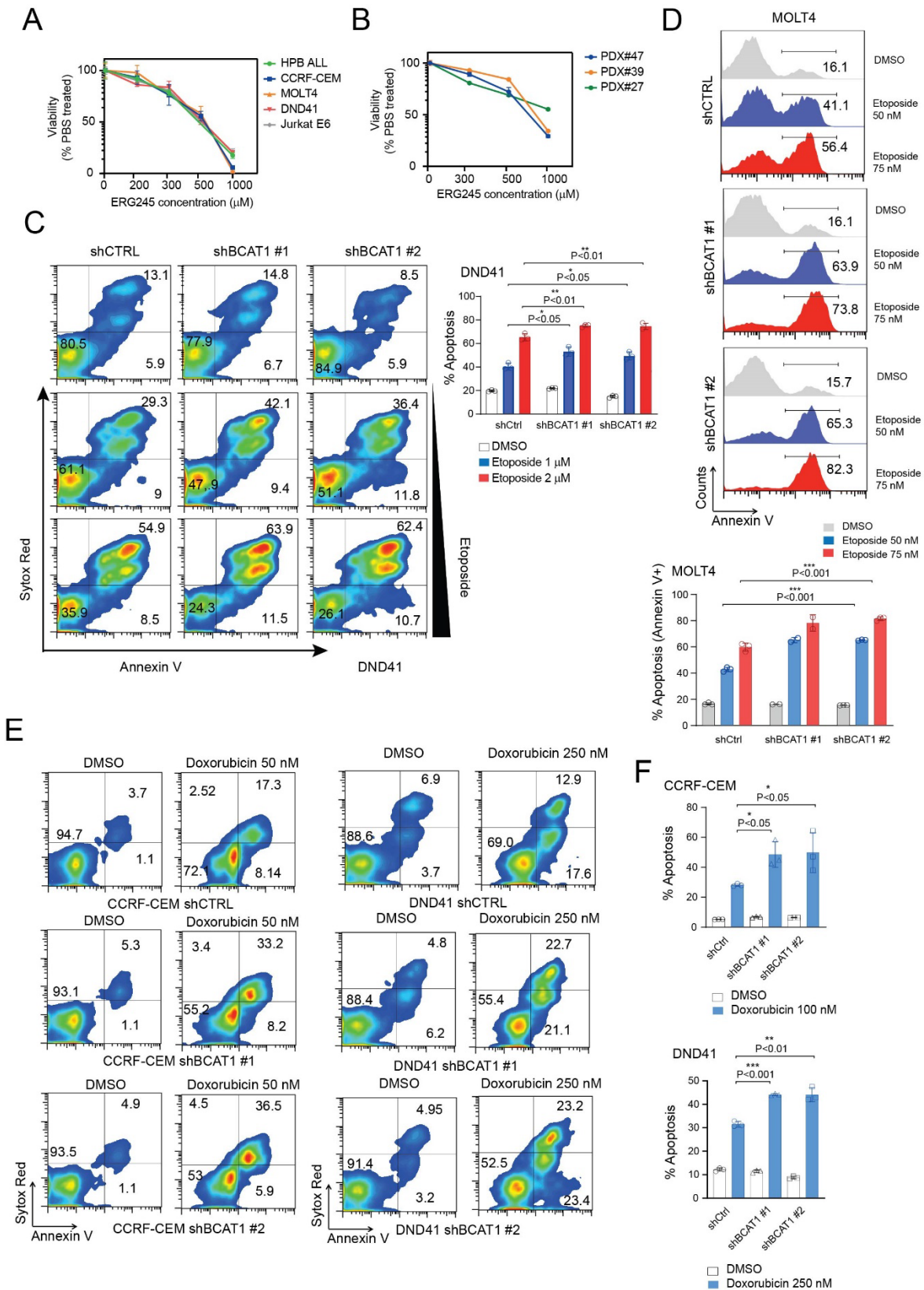


Figure S10. BCAT1 specific inhibition has modest cytotoxic effects on human T-ALL, while BCAT1 depletion increases sensitivity to DNA damaging agents. (A) Cell viability analysis in T-ALL cell lines (HPB-

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. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$.

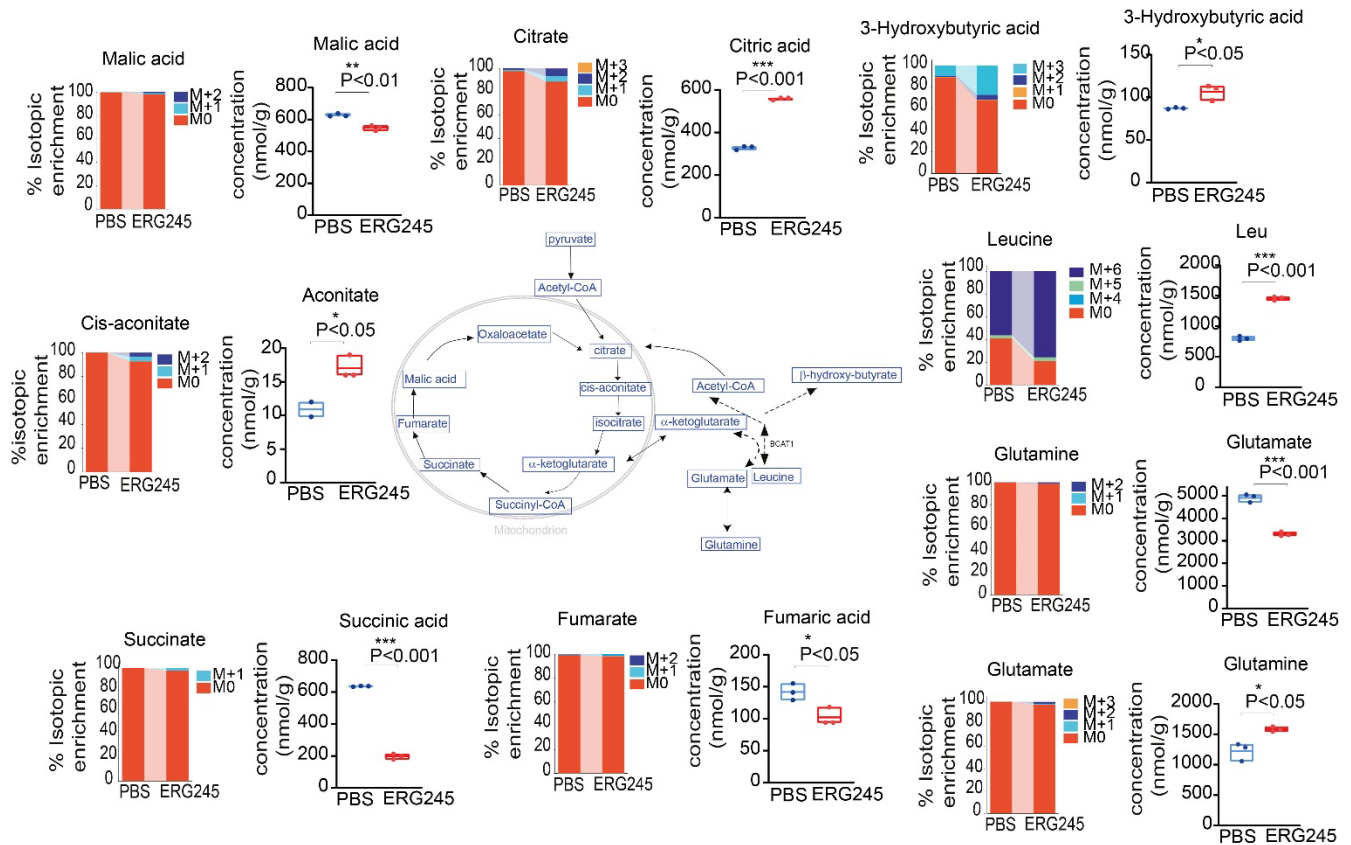


Figure S11. Metabolic impact of BCAT1 inhibition on ΔE -NOTCH1 leukemias. Results for *in vivo* isotope-tracing experiments following i.v. administration of $^{13}\text{C}_6$ Leu in primary ΔE -NOTCH1 leukemic tissue (N=3) treated with vehicle (PBS) or BCAT1-specific inhibitor, ERG245 (30 mg/kg every 8 hours for 24h). Percentages of $^{13}\text{C}_6$ Leu derived: (i) TCA intermediates: citrate (M0, M+1, M+2, M3), 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, M3), glutamine (M0, M+1, M+2) and beta-hydroxybutyrate (M0, M+1, M+2, M3) 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

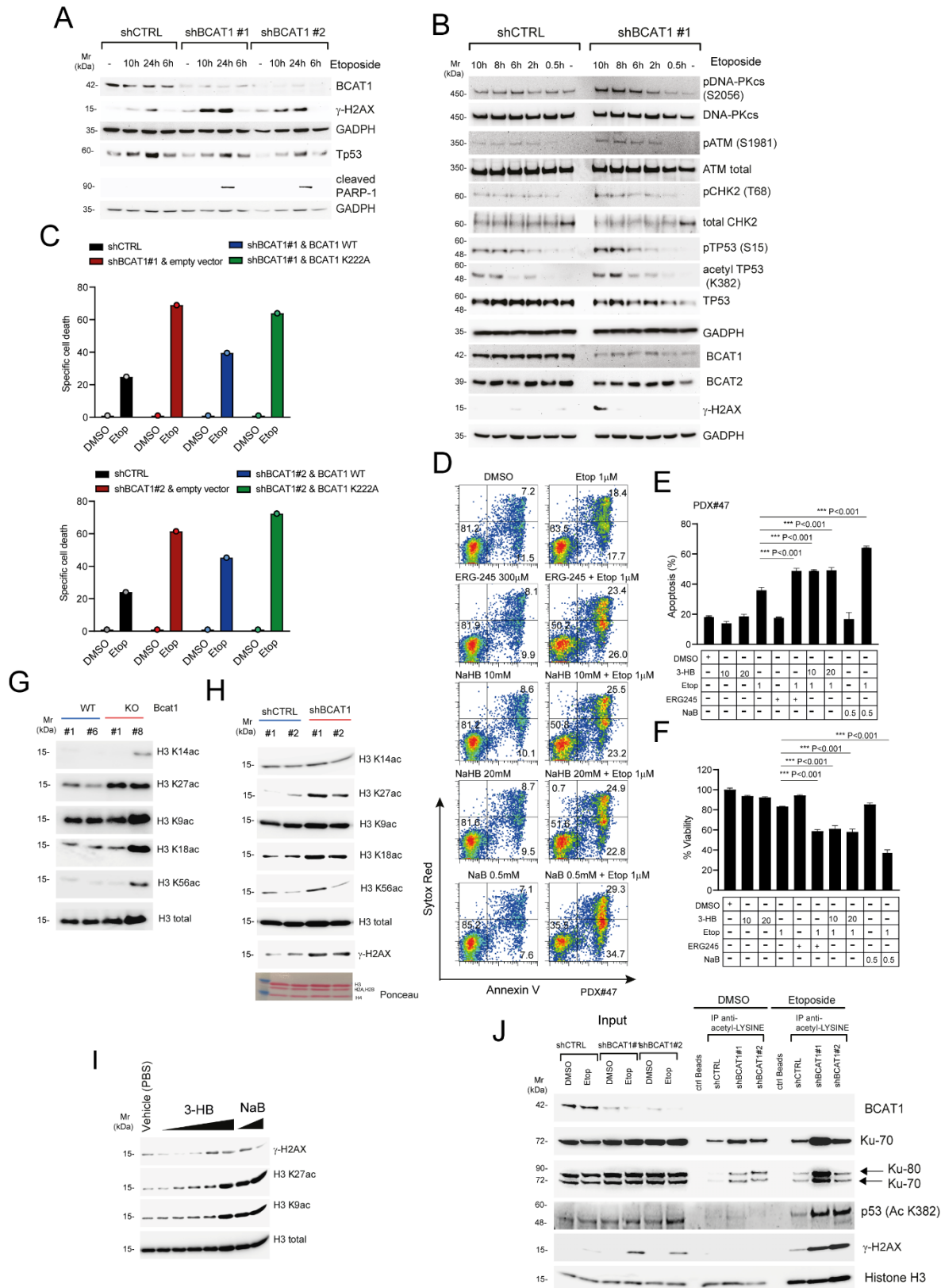
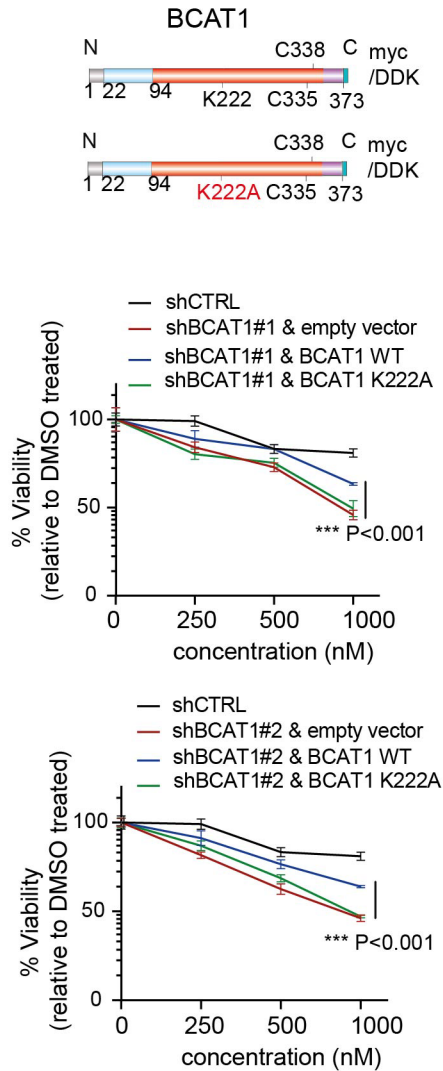


Figure S12. Increased responsiveness to DNA damaging agents in BCAT1 depleted cells is associated with an altered DNA damage response and dependent on its catalytic activity. (A) CCRF-CEM T-ALL cells

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 TALL 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).

A



B

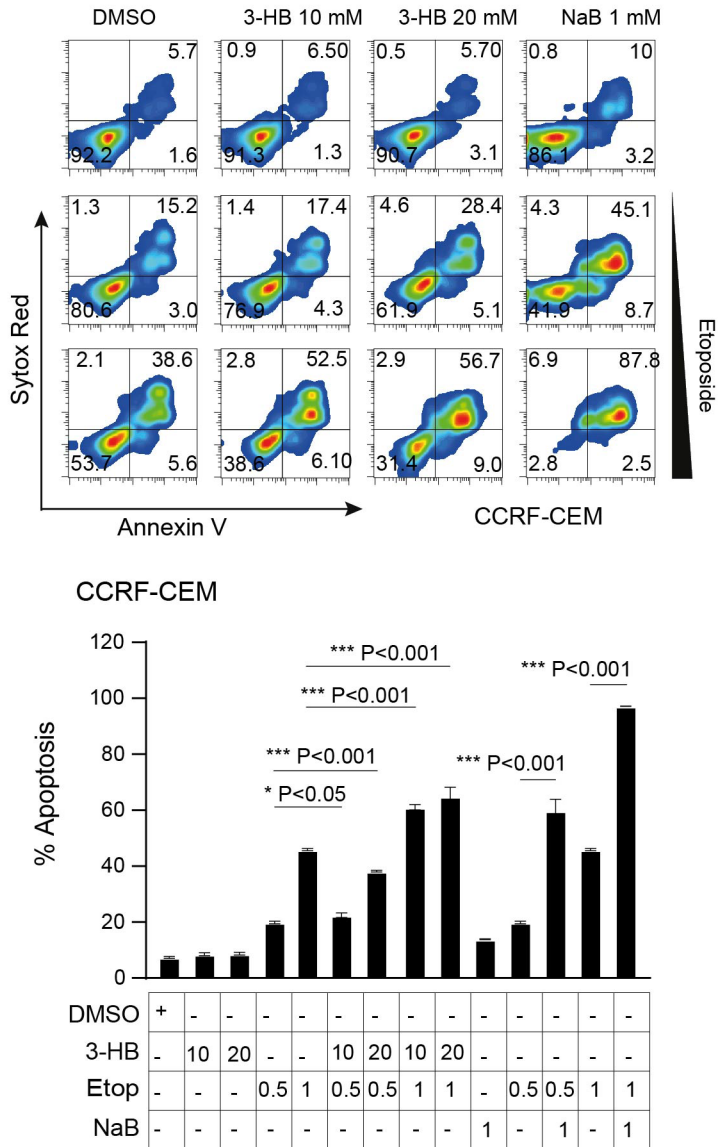


Figure S13. Metabolic function of BCAT1 contributes in modulating the sensitivity to DNA damaging agents. (A) Schematic representations (top) of the constructs encoding full-length (WT) and catalytic inactive mutant of BCAT1 (K222A). Cell viability analysis (lower panels) in BCAT1 depleted CCRF-CEM T-ALL 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. * $P < 0.05$, *** $P < 0.001$.

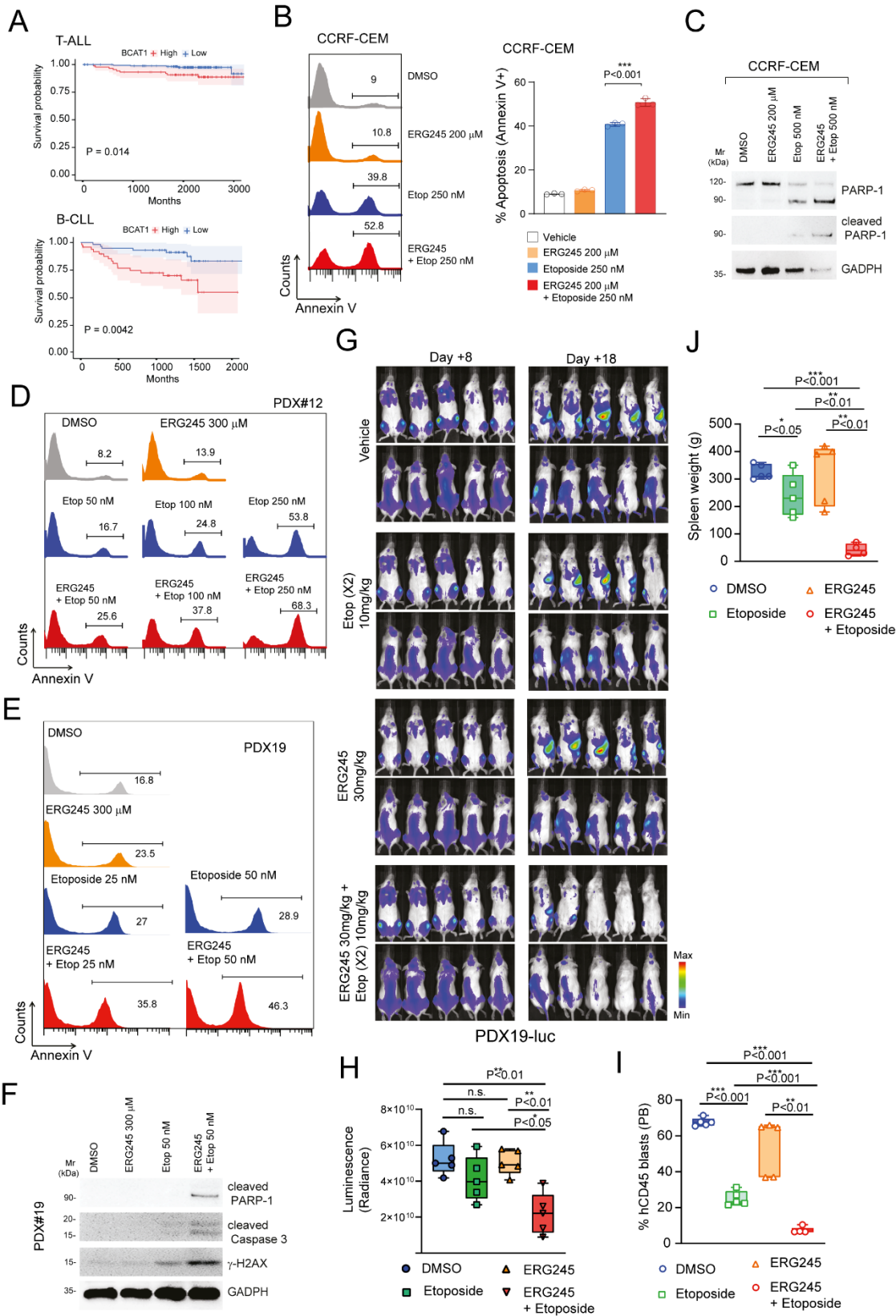


Figure S14. BCAT1 expression correlates with prognosis in NOTCH1-dependent leukemias and represents a therapeutic target in T-ALL. (A) Kaplan–Meier survival curves (top) of the entire series of 261 T-ALL patients

(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. $*P < 0.05$, $**P < 0.01$, $***P < 0.001$.

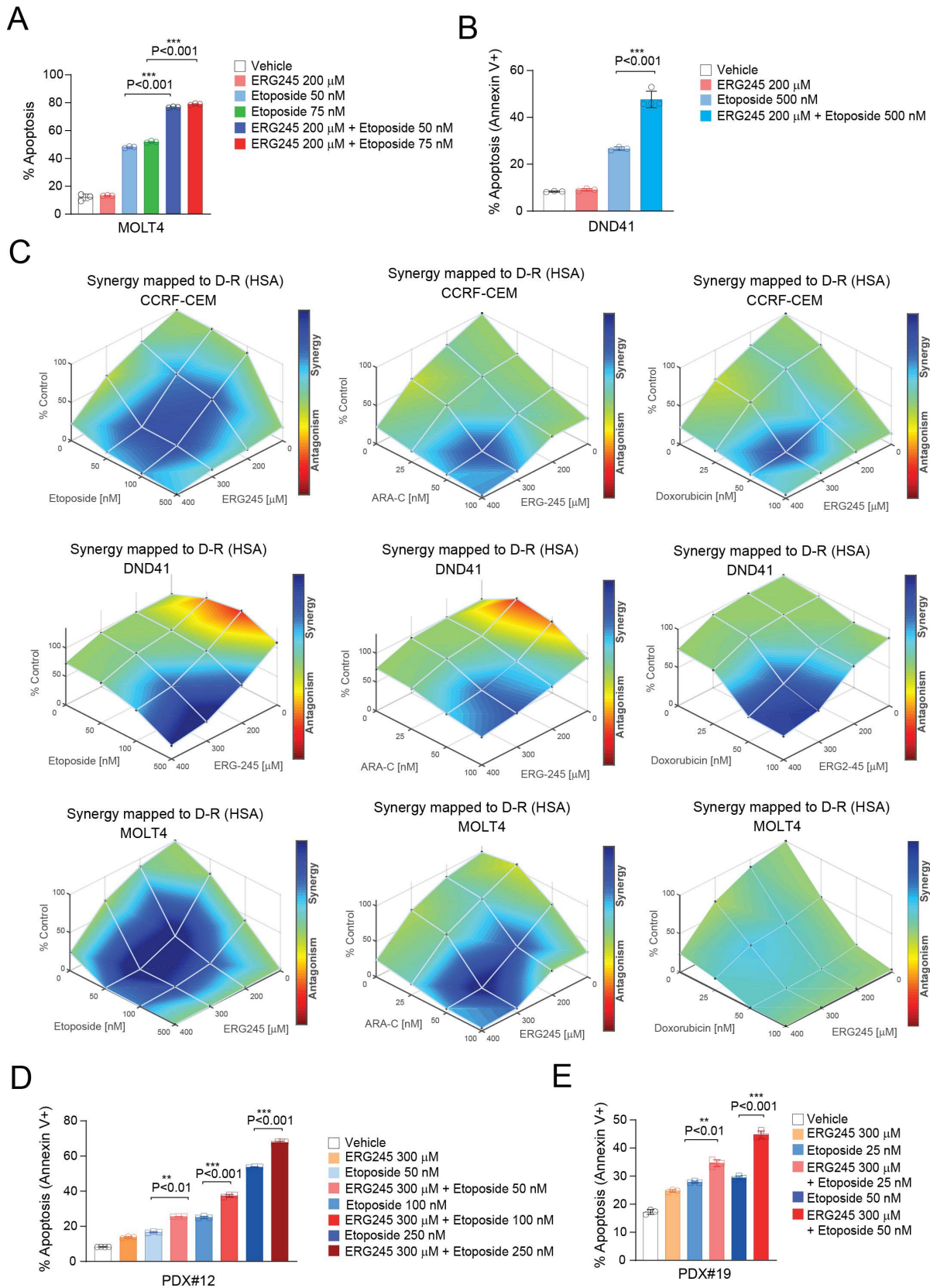


Figure S15. BCAT1 inhibition synergizes with numerous chemotherapeutic drugs to reduce cell viability. (A) Quantification of apoptosis in MOLT4 T-ALL cells treated with vehicle (DMSO), BCAT inhibitor (ERG245),

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 Combenefit 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. ** $P < 0.01$, *** $P < 0.001$.

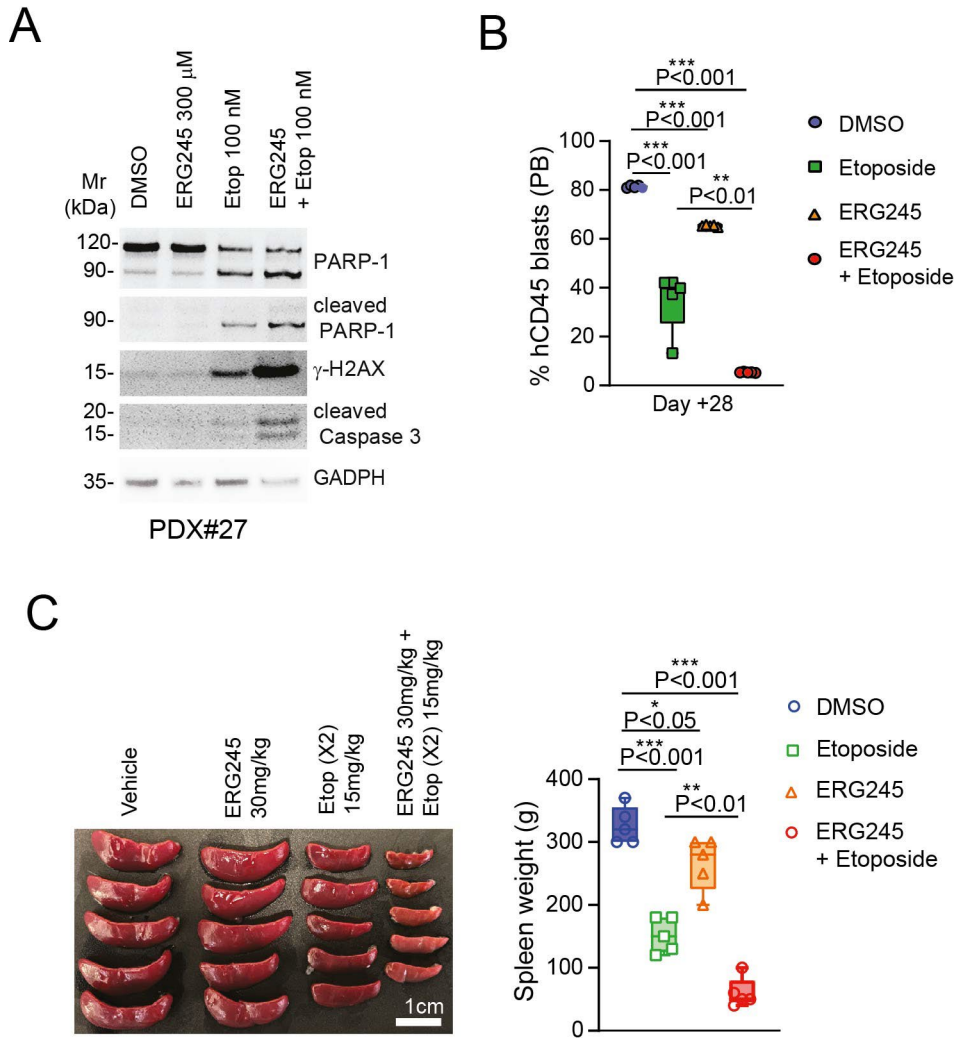


Figure S16. BCAT1 inhibition synergizes with etoposide to reduce viability. (A) Western blot analysis of PARP-1 (total or cleaved PARP-1), phosphorylated γ H2AX and cleaved caspase 3 in PDX#27 cells treated for 48h with DMSO (vehicle), ERG245 (300 μ M), etoposide (Etop; 100 nM) or ERG245 + Etop. GADPH 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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