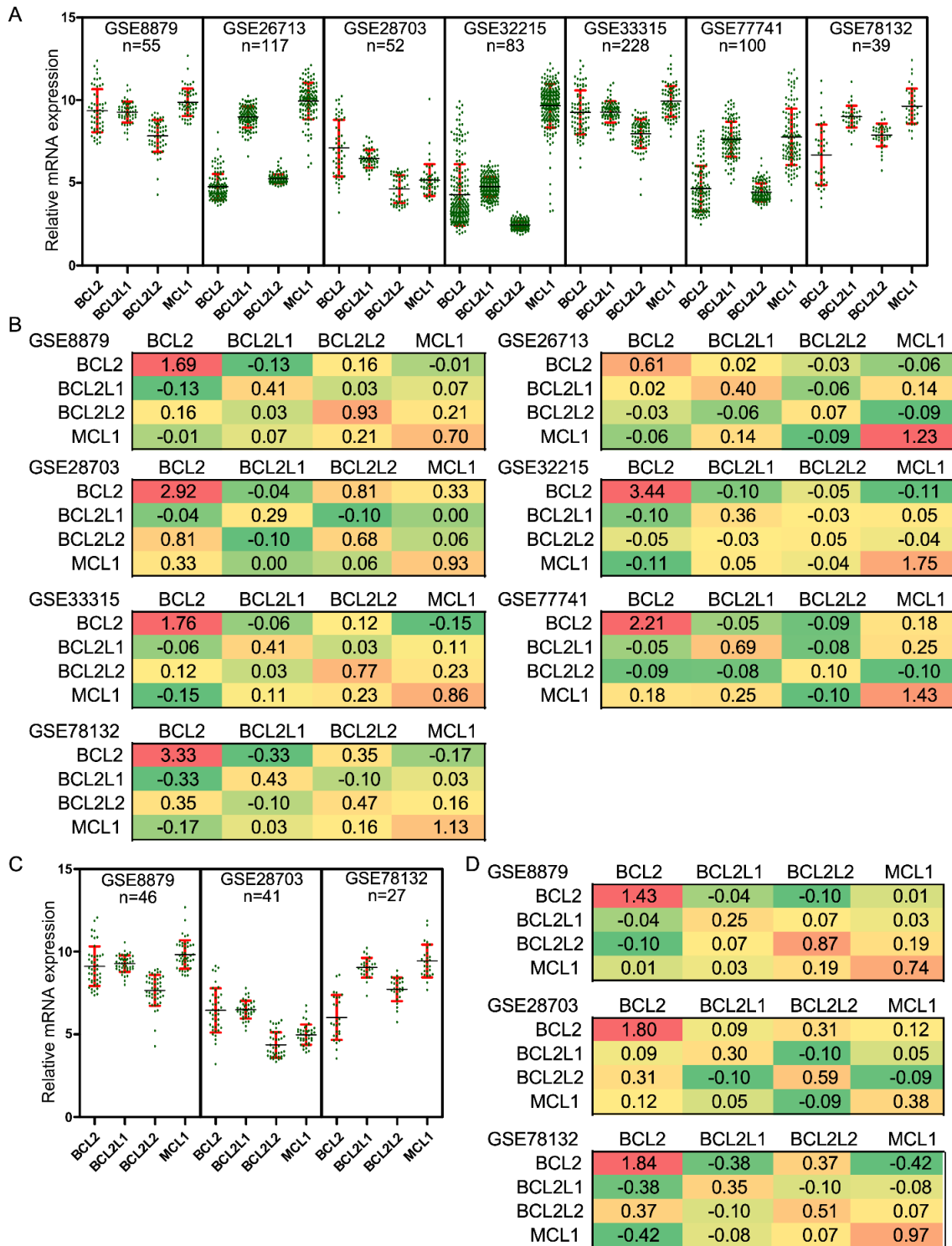
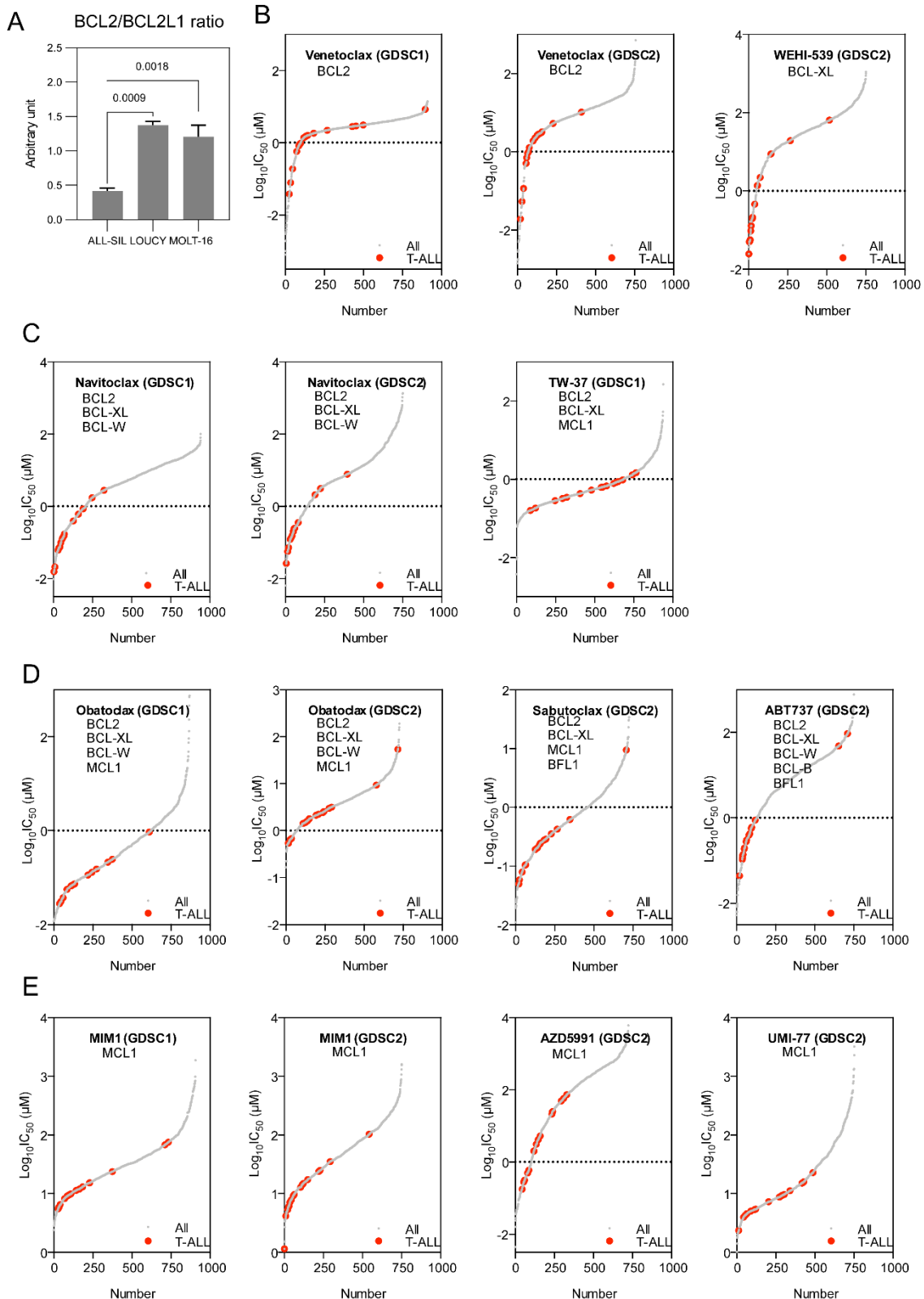


Supplementary figures

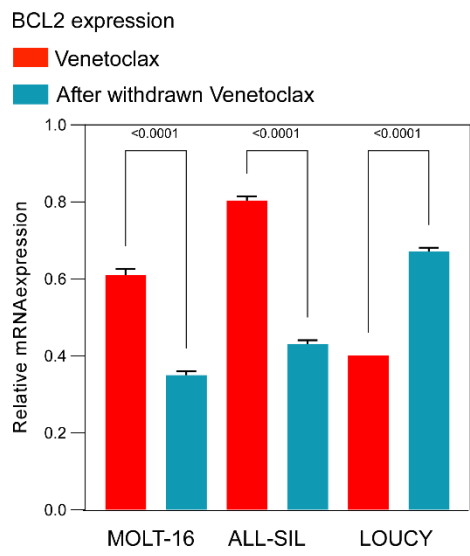
Supplementary figure S1: T-ALL patients with both the ETP and non-ETP groups display differential expression of BCL2 family members. Gene expression data for 7 T-ALL datasets, representing both the ETP and non-ETP groups were downloaded from the NCBI Gene Expression Omnibus. (A) Relative mRNA expression of BCL2, BCL2L1, BCL2L2, and MCL1 of T-ALL patients from the 7 datasets were plotted in dot plots. The red bar represents the SEM. (B) The covariance matrix for the BCL-2 family gene expression was calculated with the cov.wt function in R. (C) Expression values after the removal of ETP-ALL patients are presented. (D) The covariance matrix for the BCL-2 family gene expression after removal of ETP-ALL samples.



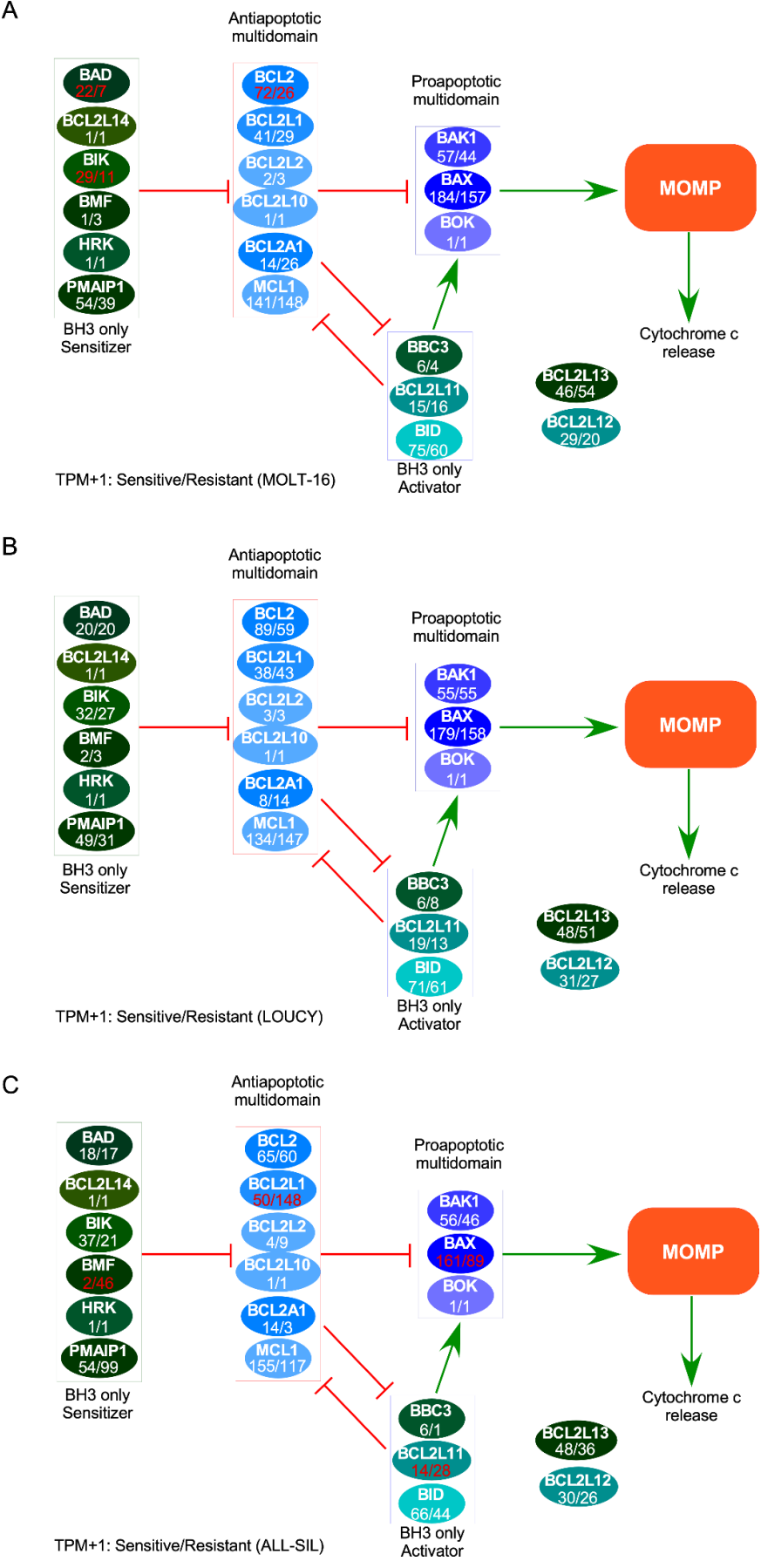
Supplementary figure S2: T-ALL cell lines display a differential response to BCL2 inhibitors. (A) BCL2/BCL2L1 ratios presented in figure 1C were reanalyzed for ALL-SIL, LOUCY, and MOLT-16 cell lines. One-way ANOVA with multiple comparisons was used to determine p values. (B-E) IC₅₀ data for BCL2 family inhibitors were downloaded from the Genomics of Drug Sensitivity in Cancer (GDSC). Red dots represent T-ALL cell lines. IC₅₀ values of (B) BCL-2 and BCL-XL specific inhibitors; (C) BCL-2 inhibitors targeting two BCL-2 family members other than BCL-2; (D) BCL-2 inhibitors targeting three to four other BCL-2 family members other than BCL-2; and (E) MCL-1 specific inhibitors, were plotted for various T-ALL cell lines.



Supplementary figure S3: Relative BCL2 expression for MOLT-16, ALL-SIL, and LOUCY cell lines presented in figure 3D was analyzed using one-way ANOVA with multiple comparisons to determine p values.

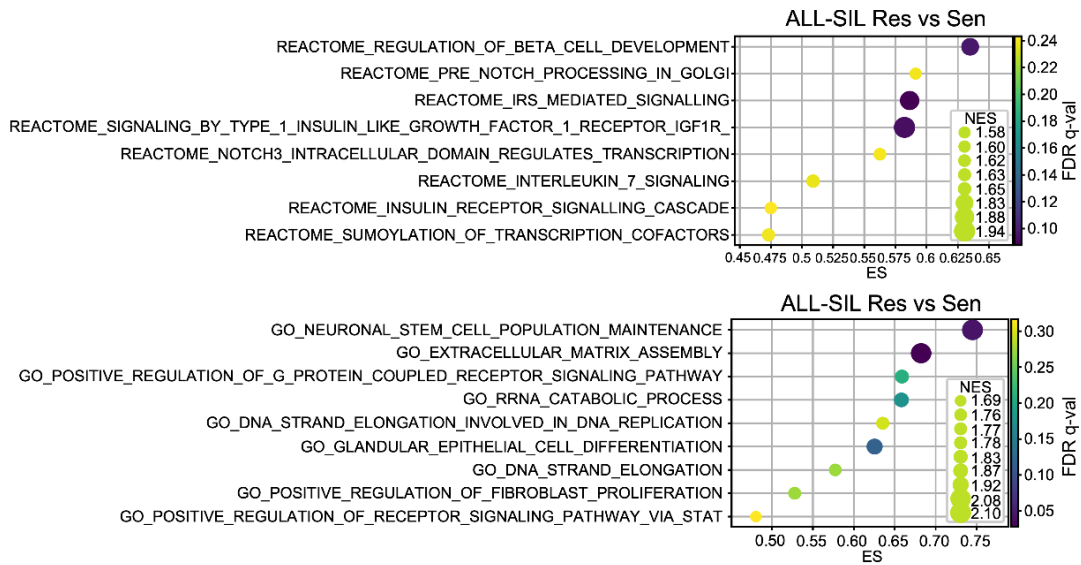


Supplementary figure S4: BCL2 family gene expression in venetoclax-sensitive and -resistant cells.
 (A) MOLT-16, (B) LOUCY, and (C) ALL-SIL cells, both venetoclax-sensitive/resistant were subjected to RNASeq, and the gene expression data of various BCL2 family members are presented here.

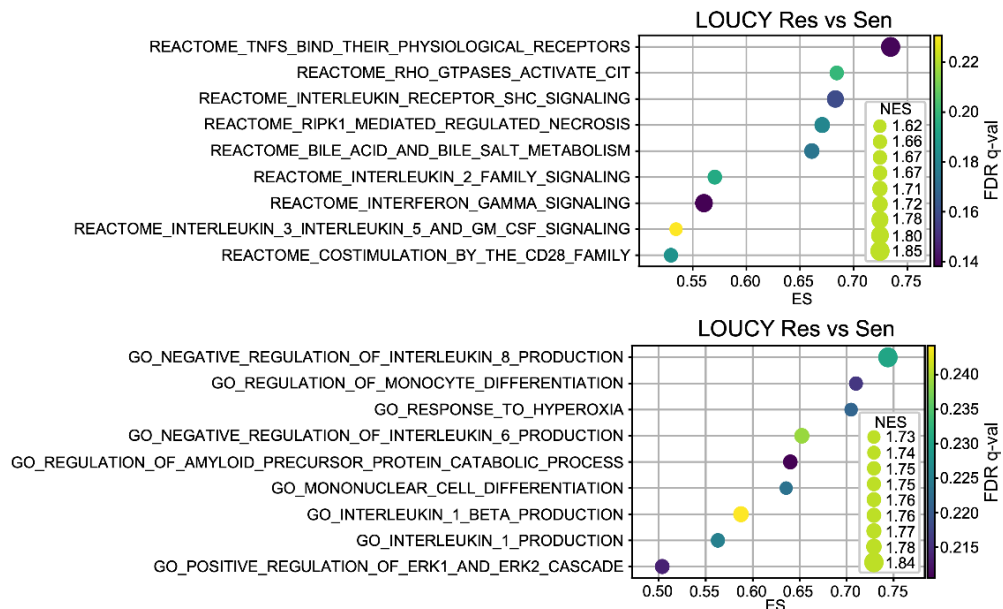


Supplementary figure S5: Gene set enrichment analysis in venetoclax-resistant cells. Gene set enrichment in venetoclax-resistant (A) ALL-SIL, (B) LOUCY and (C) MOLT-16 was determined by GSEA using the Molecular Signatures database MSigDB.

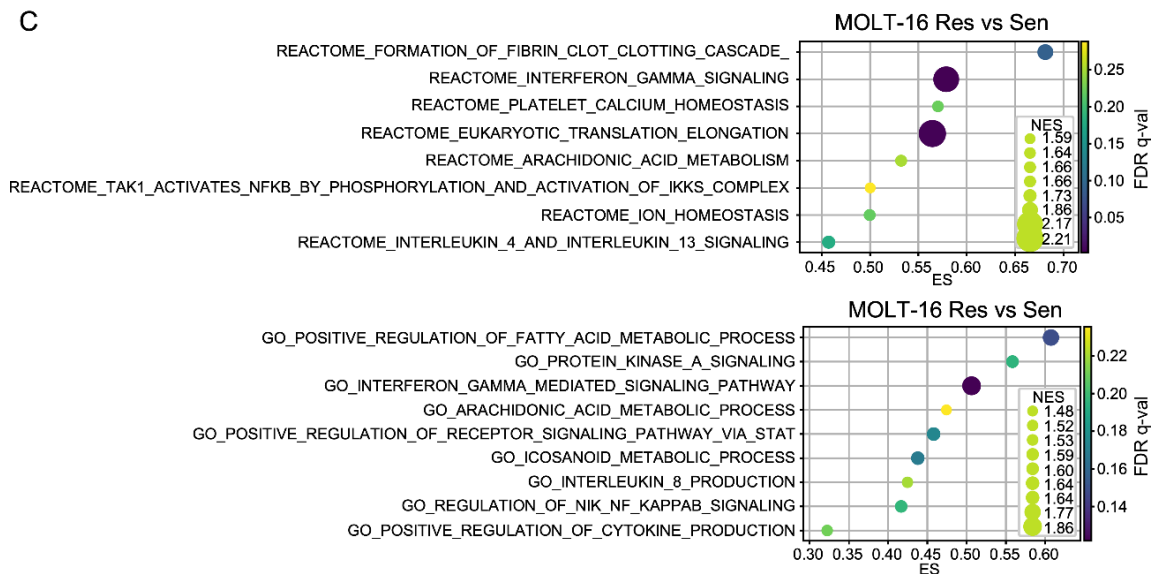
A



B



C



Supplementary Table

Supplementary Table S1: T-ALL cell lines

Cell line	Gender (Age)	Maturity	Mutation	Expression
ALL-SIL	Male (17)	T-ALL relapse	NUP214-ABL1	TLX1
CCRF-CEM	Female (3)	T-ALL relapse		NKX2-5
CML-T1	Female (36)	CML patient	BCR-ABL1	
CTV-1	Man (40)	AML patient	TAL1-TRB	
DND-41	Male (13)	T-ALL; type III cortical	CDKN2A, CDKN2B deletion, p53 mutation	TLX3
JURKAT	Male (14)	ALL relapse		
KE-37	Male (27)	ALL		
LOUCY	Female (38)	T-ALL FAB L2 Chemo-resistant	SET-NUP214	MEF2C
MOLT-4	Male (19)	ALL relapse		
MOLT-16	Female (5)	T-ALL relapse		
P12- ICHIKAWA	Male (7)	ALL		
PF-382	Female (6)	ALL		
RPMI-8402	Female (16)	ALL		
TALL-1	Male (28)	Lymphosarcoma		