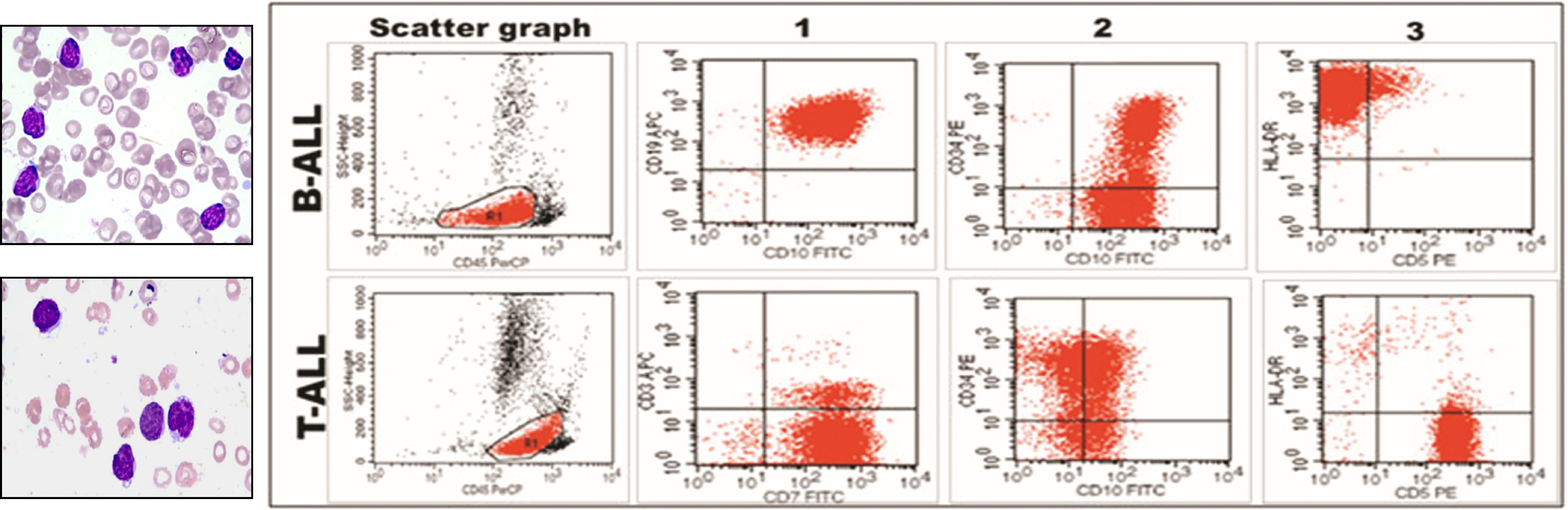
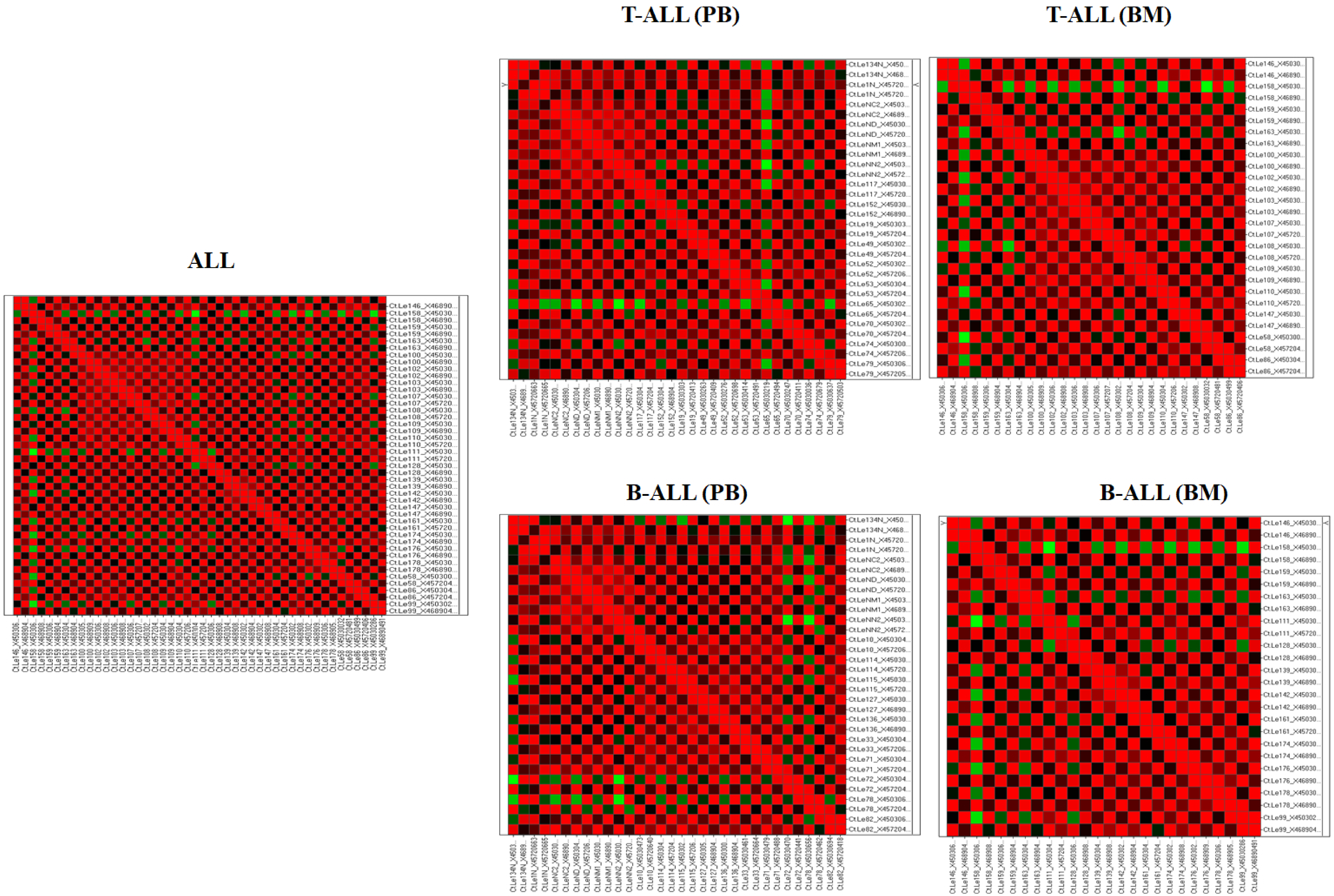
Figure S1.



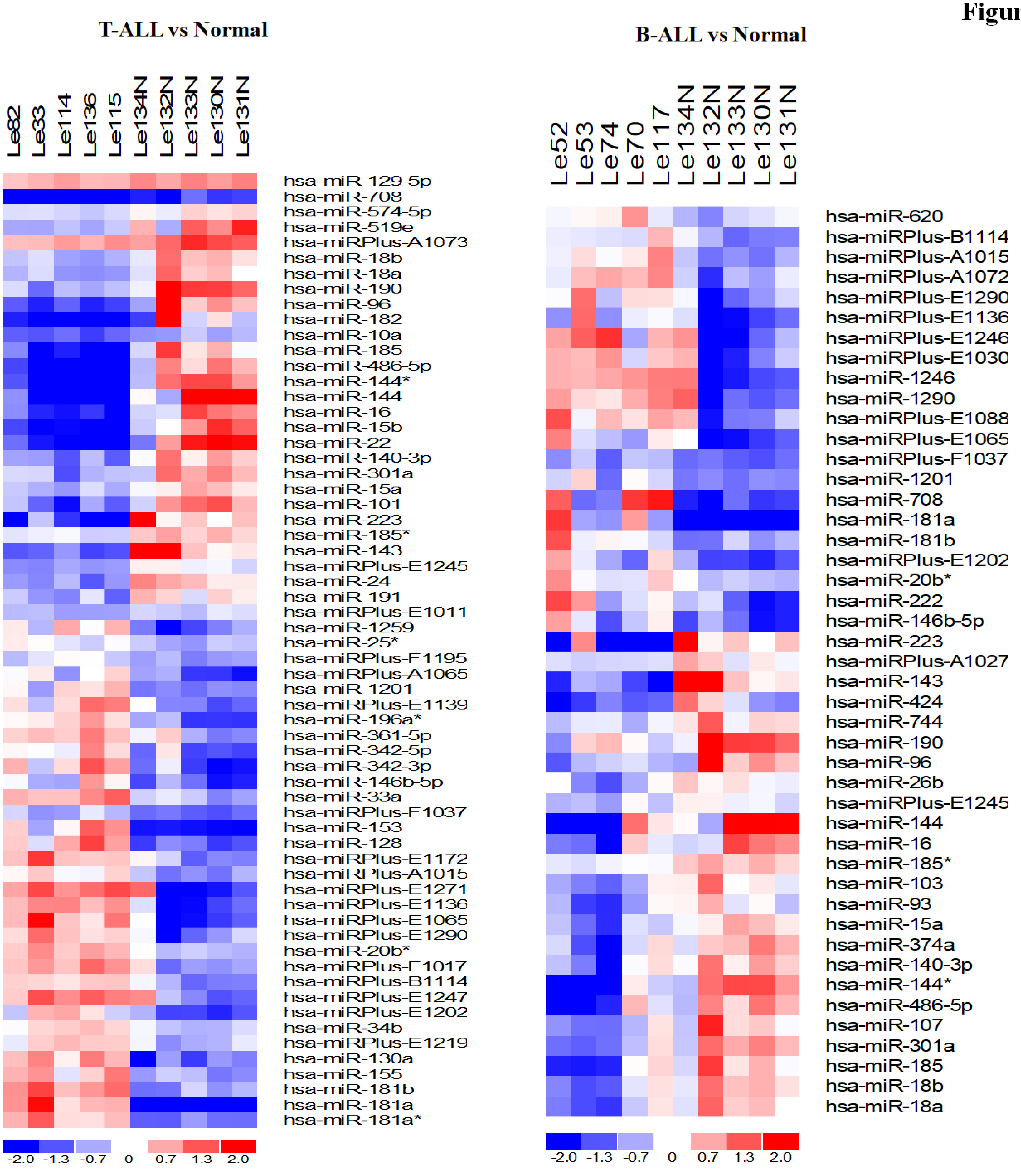
Supplementary Figure 1: **Flow cytometric analysis of T-ALL and B-ALL** (A) Flow cytometry of leukemic samples by CD45 gating shows B-ALL expressing CD 19, CD10, CD34 and HLA-DR. (B) shows T-ALL expressing CD7, CD5 CD10 and CD34. The panel of directly conjugated antibodies with different fluorochromes comprised of CD13 (PE- L138), CD14 (APC- MOP9), CD33 (FITC-P67.6), CD117 (APC104D2), MPO (FITC-5B8), CD10 (FITCHI10a), CD2 (PE-S5.2), CD3 (APC-SK7), CD3 (FITC-UCHT1), CD4 (PESK3), CD5 (PEL17F12), CD7 (FITC-4H9), CD23 (APC-EBVCS-5), CD8 (FITC-SKI), CD19 (PERCPr-4G7), CD25 (APC-2A3), CD20 (APC-L27), CD34 (PE-8G12), CD61 (FITC-RUU-PL7F12), CD22 (PE-S-HCL-1), CD38 (FITCHB7), CD64 (F-10.1), CD19 (APC-SJ25C1), CD45 (PERCP-2D1), CD79a (PE-2ST8.5H7), HLA-DR (APC-L243).

Figure S2.



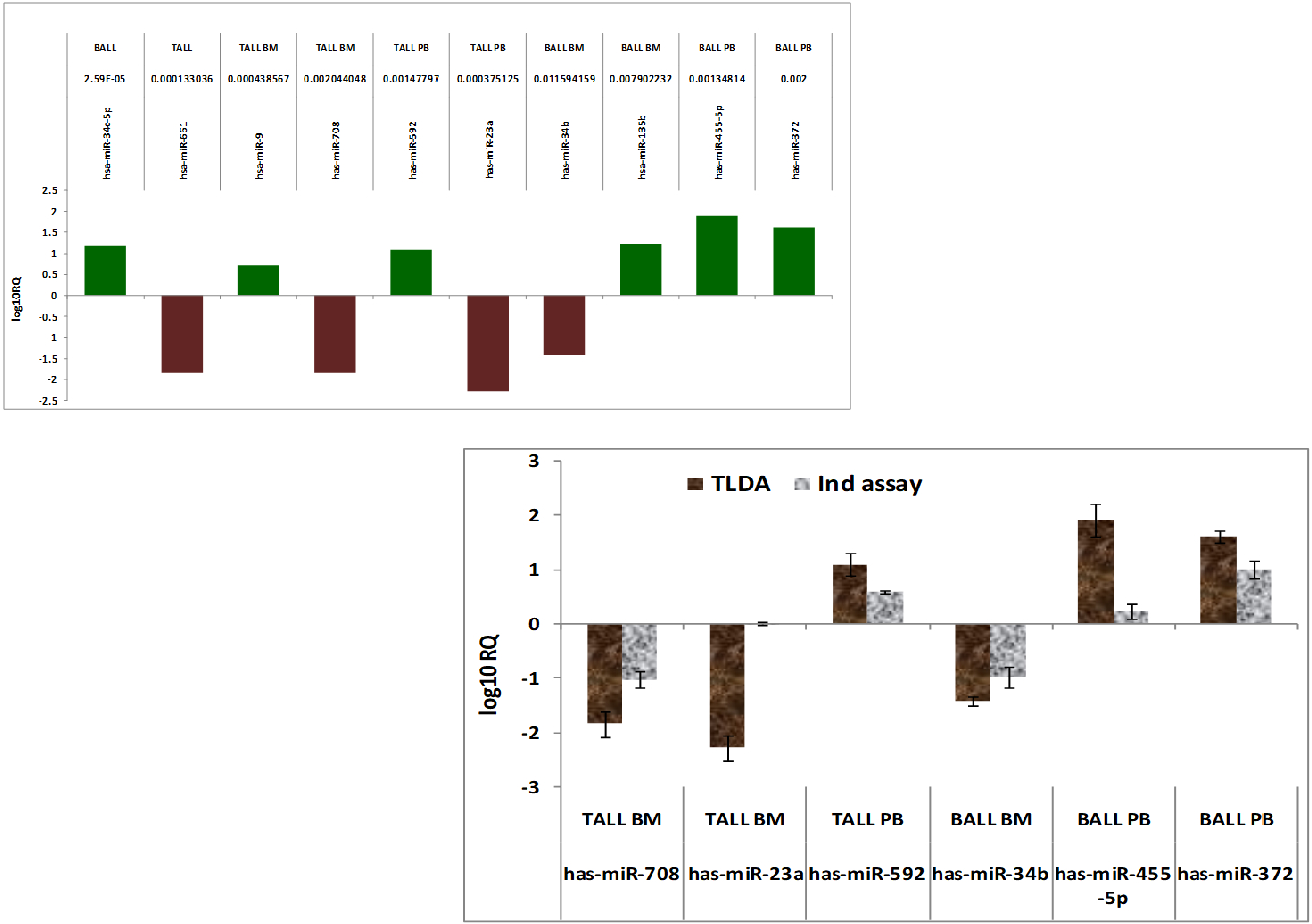
Supplementary Figure 2: Heat map of microRNA expression profiles in A-LL. TLDA heatmap depicting gene expression profiles of microRNAs. Green colour in the heatmap depicts downregulated microRNAs and red colour represents up-regulated microRNAs.

Figure S3.



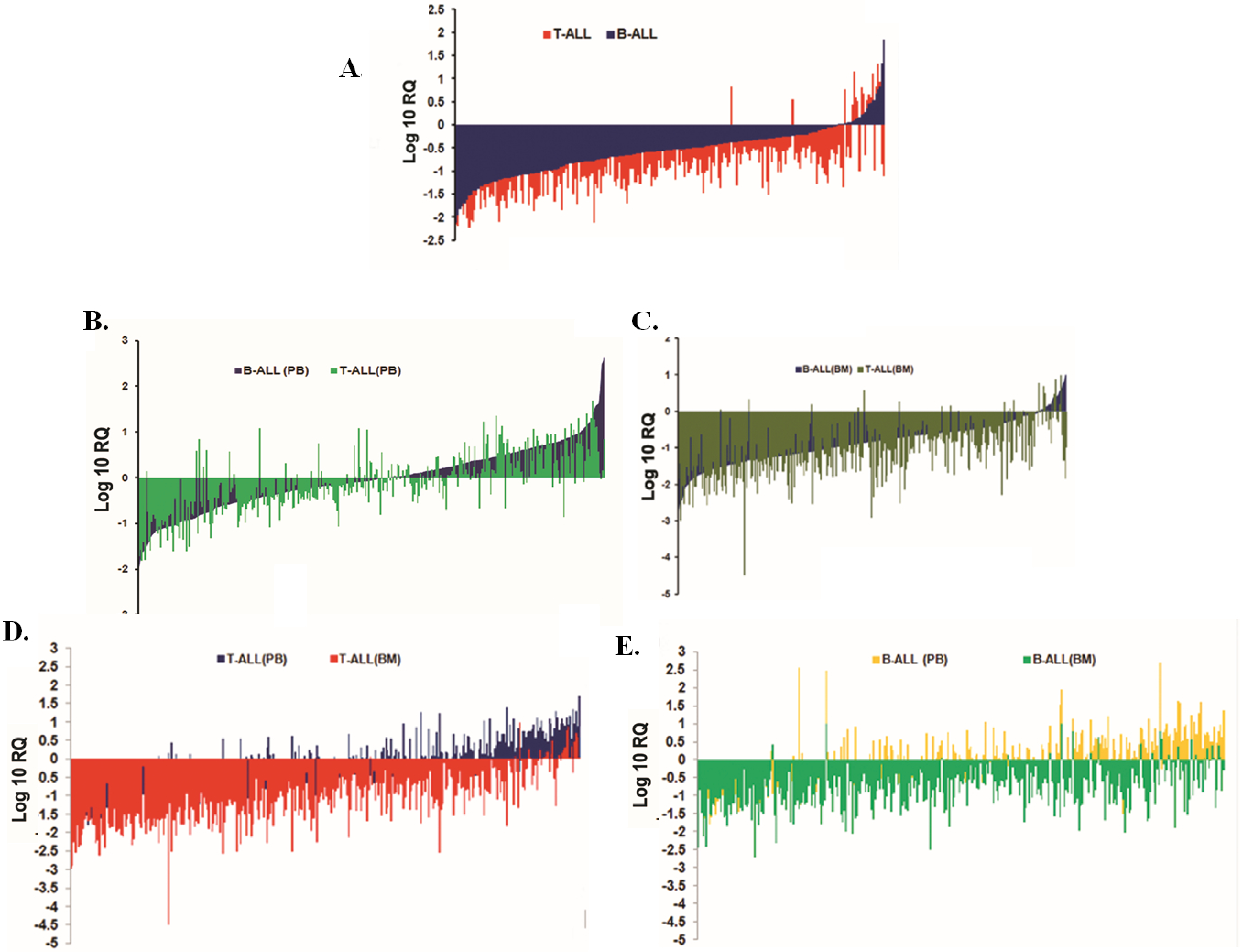
Supplementary Figure 3: Map of microRNA expression profiles in A-LL. Heat map depicting unsupervised hierarchical clustering of microRNA expression using LNA arrays.

Figure S4.



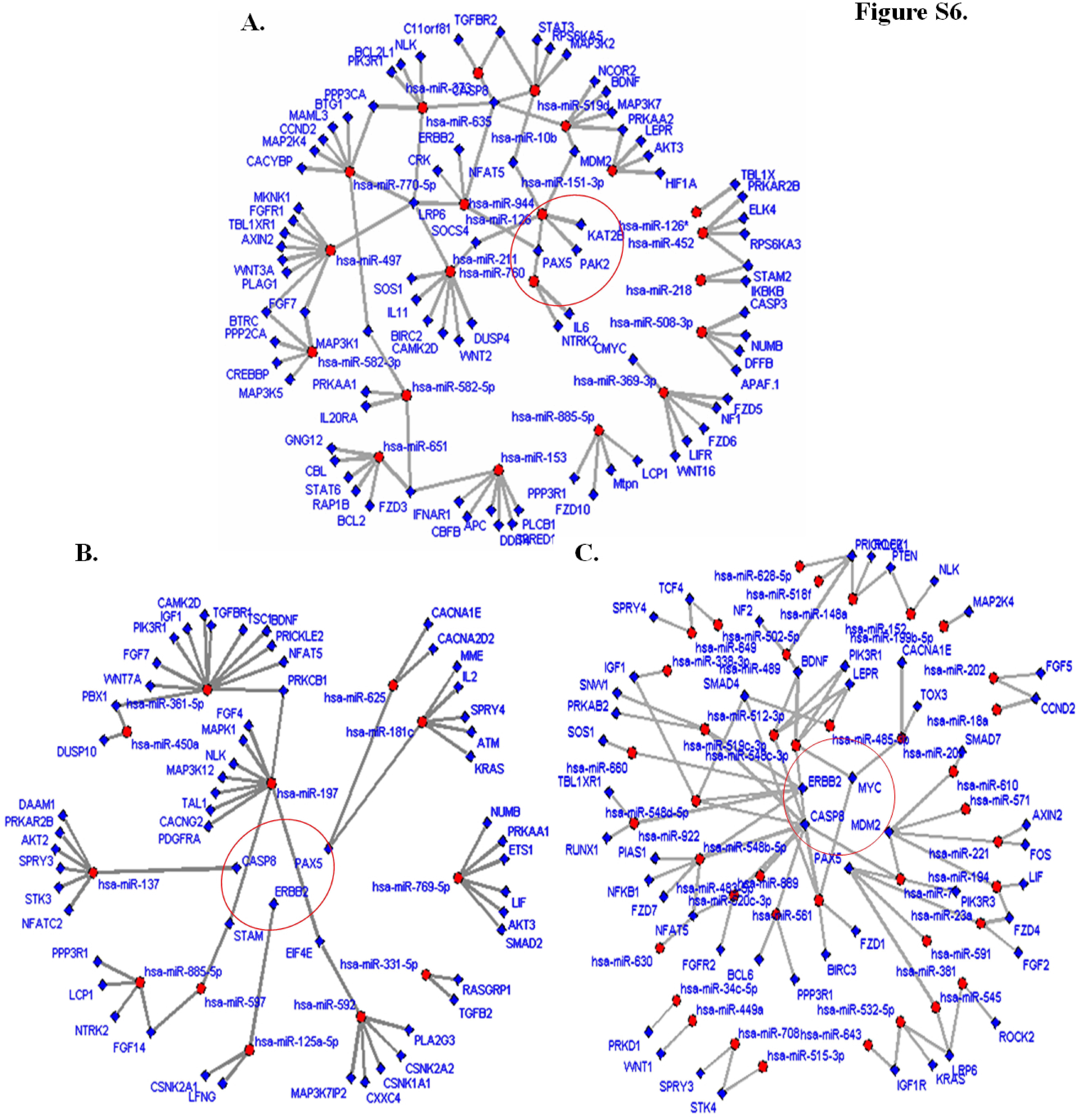
Supplementary Figure 4: microRNAs selected for individual assay validation. Common microRNAs that showed significant up/down regulation from TLDA and LNA arrays were subjected to double blind validation assays.

Figure S5.



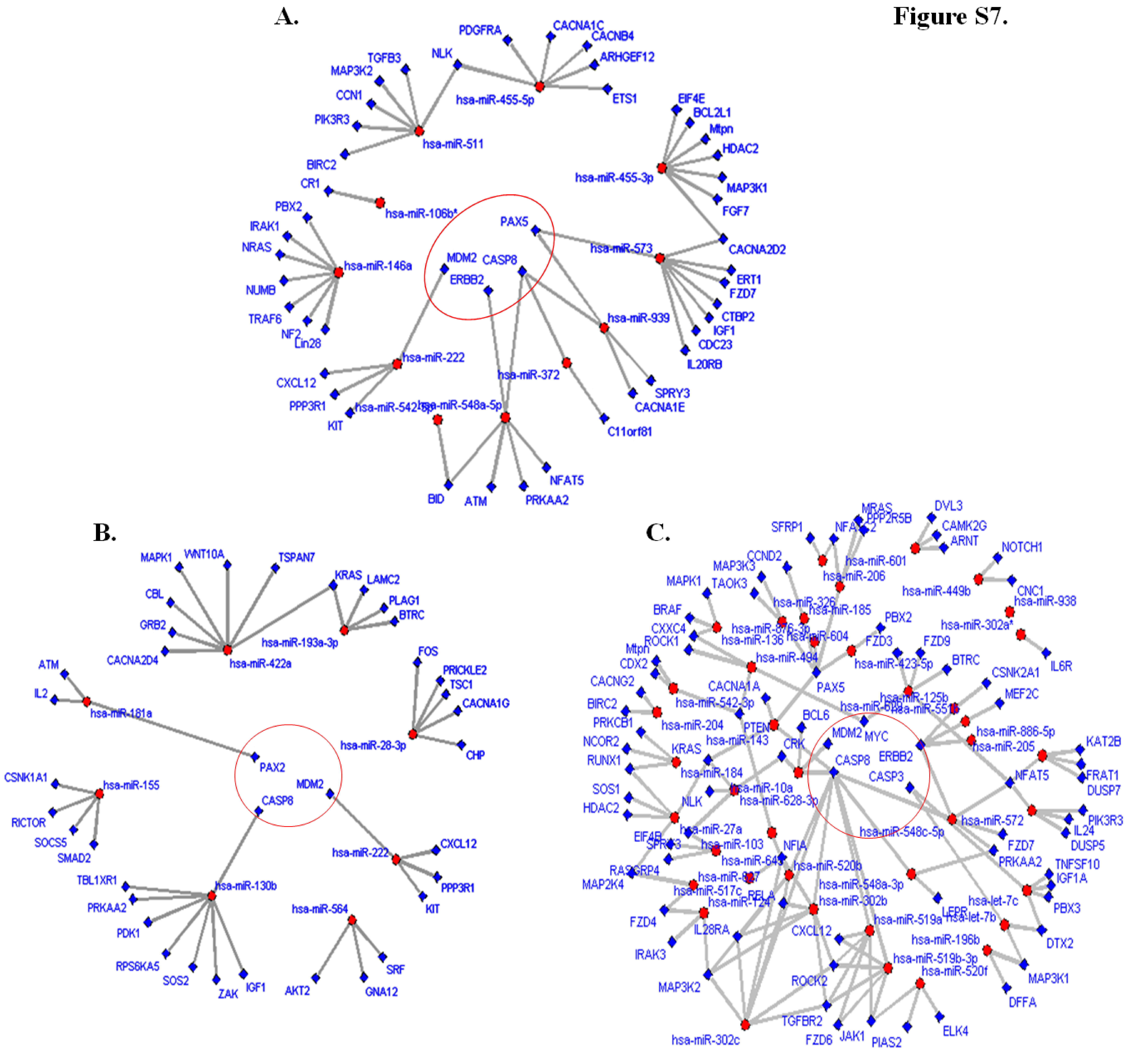
Supplementary Figure 5: microRNA expression trend of T-ALL vs B-ALL (A) between TALL and B-ALL (B) between Peripheral Blood (PB) of T-ALL and B-ALL and (C) bone marrow (BM) of T-ALL and B-ALL (D & E) endogenous differences between PB and BM of TALL and B-ALL respectively.

Figure S6.



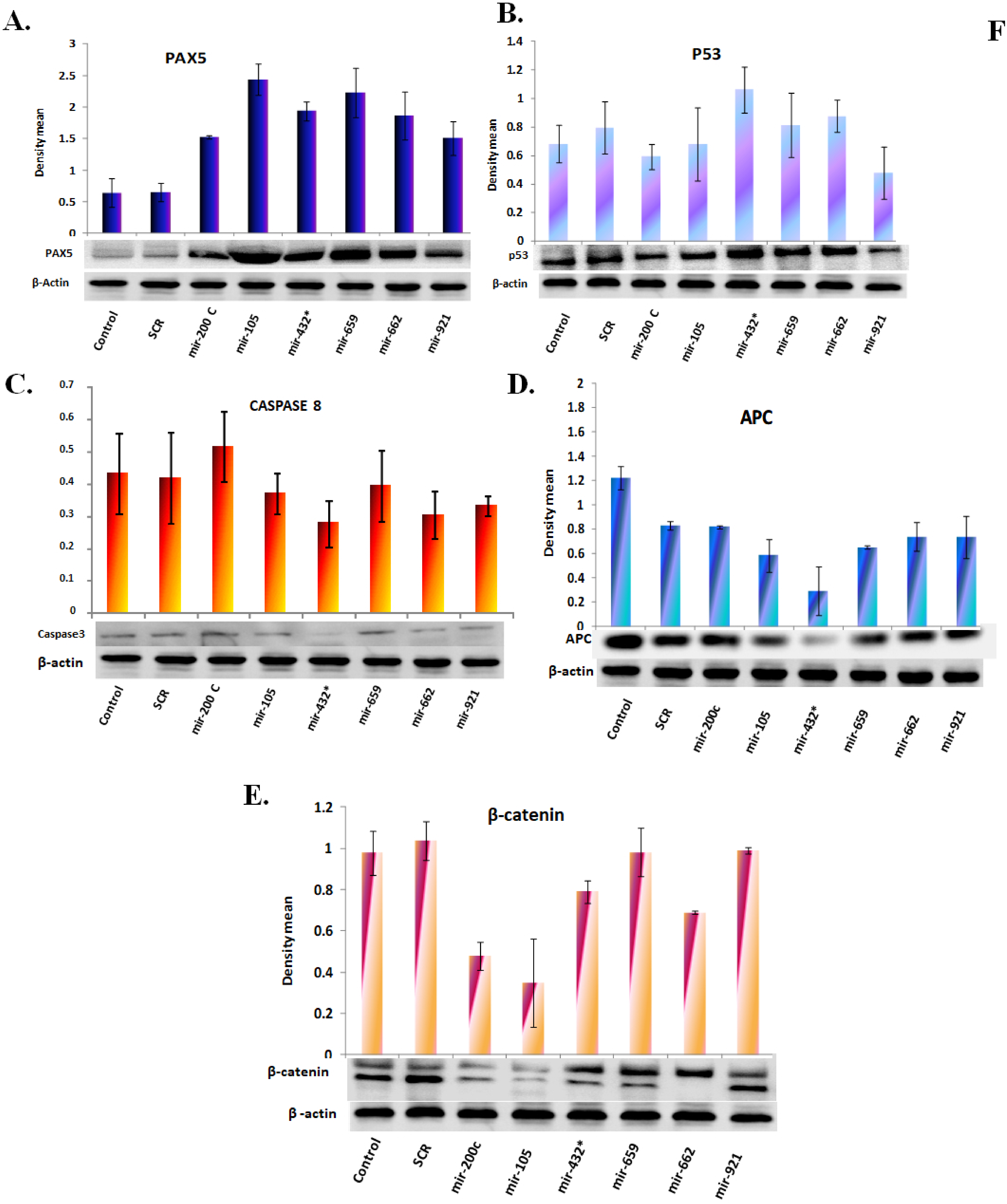
Supplementary Figure 6: MicroRNAs-target interaction network (A) Significant microRNA and their target interaction in T-ALL ,(B) T-ALL (PB) and (C) T-ALL (BM). microRNAs are represented as red circle and their target genes are represented as blue rectangle.

Figure S7.



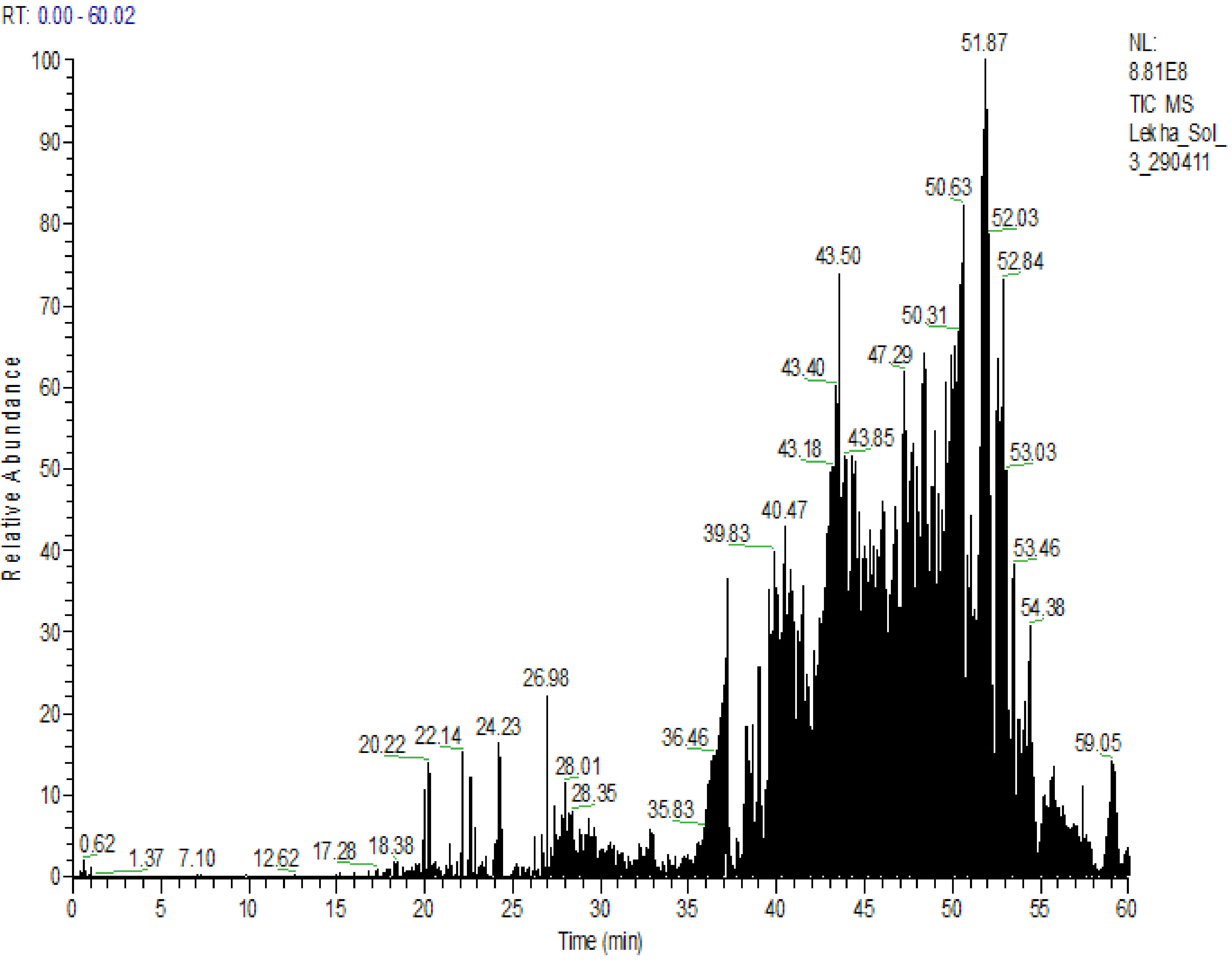
Supplementary Figure 7: MicroRNAs-target interaction network (A) Significant microRNA and their target interaction in B-ALL ,(B) B-ALL (PB) and (C) B-ALL (BM). microRNAs are represented as red circle and their target genes are represented as blue rectangle.

Figure S8.

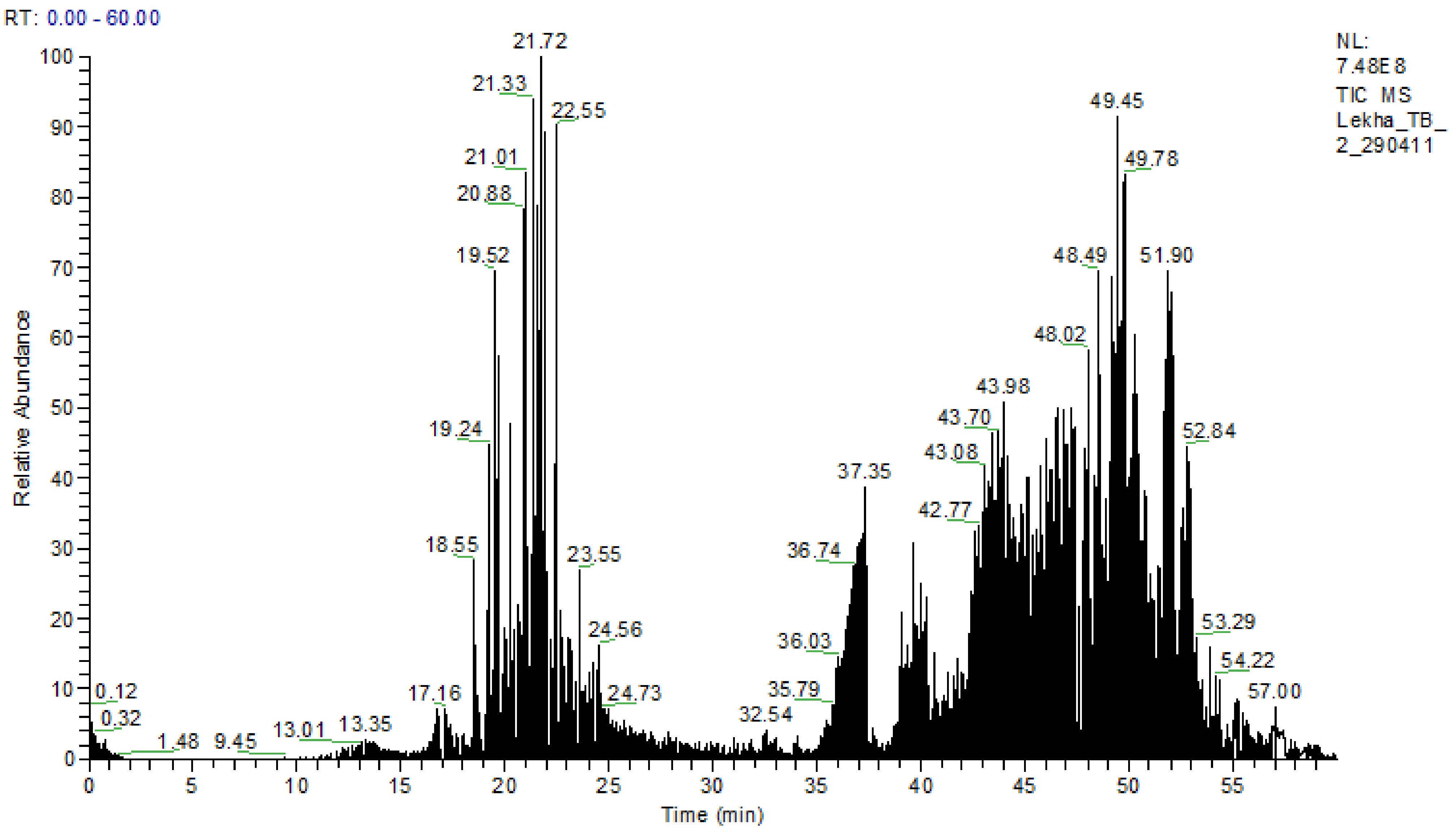


Supplementary Figure 8: Densitometric analysis. microRNAs probes transfected in Jurkat cell lines showing the respective target shutdown (A) PAX5, (B) P53, (C) caspase8, (D) APC, (E) ß-catenin.

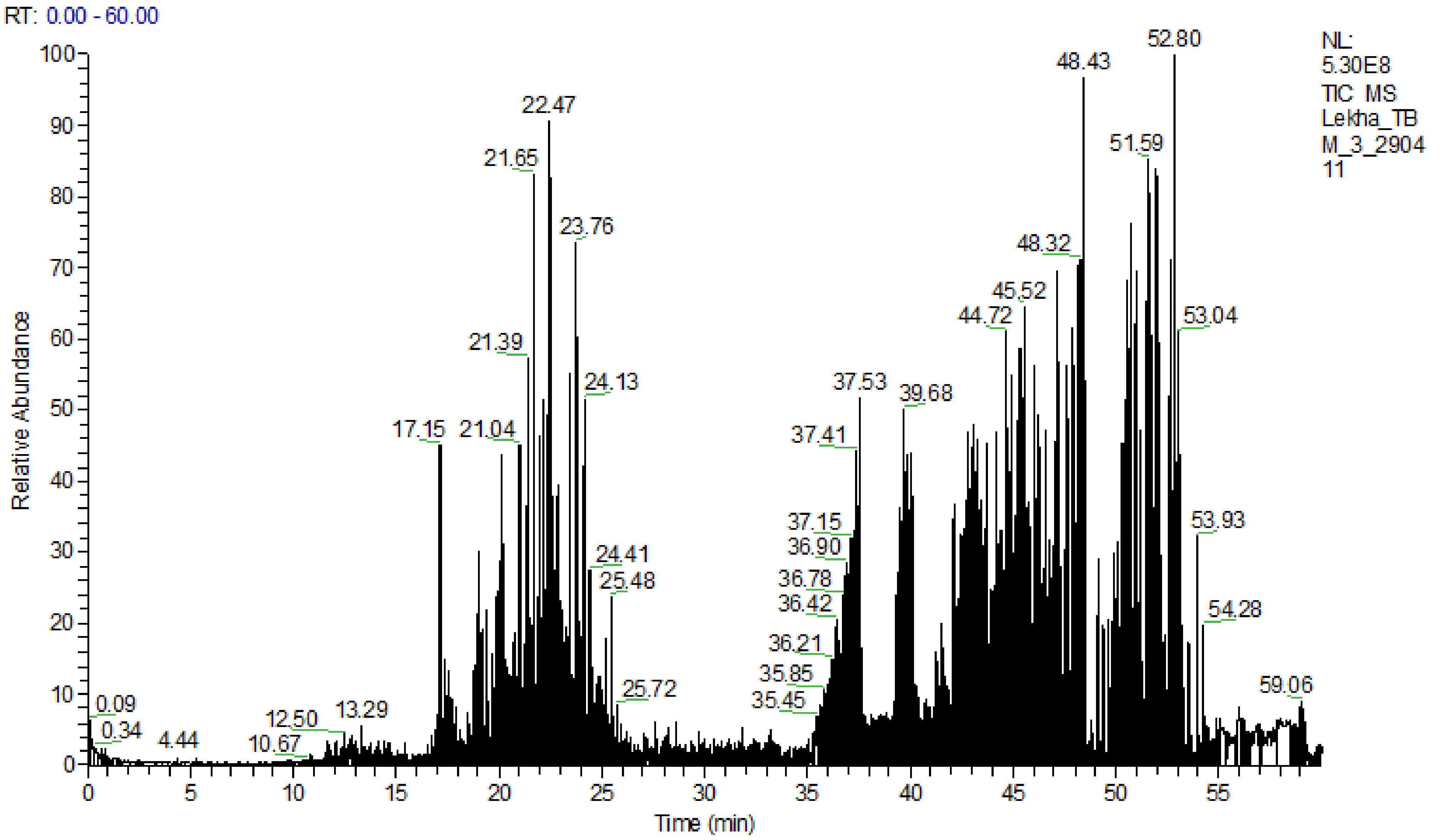
Figure S9.



Normal



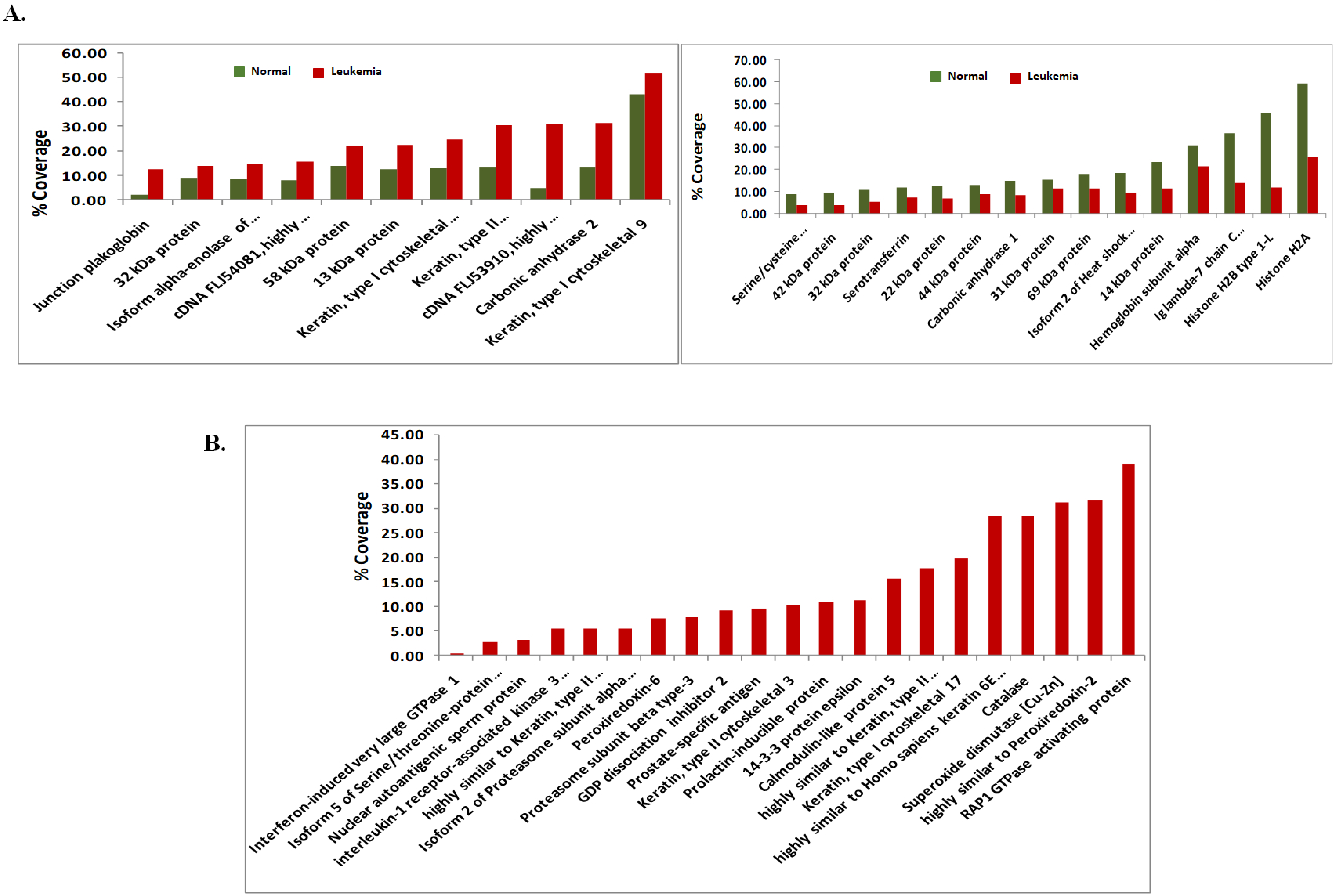
T-ALL PB



T-ALL BM

Supplementary Figure 9: Total ion current (TIC) chromatogram profile of the LC–MS/MS analysis performed using ALL samples. T-ALL samples showed endogenous differences in their peak patterns as compared to the normal samples.

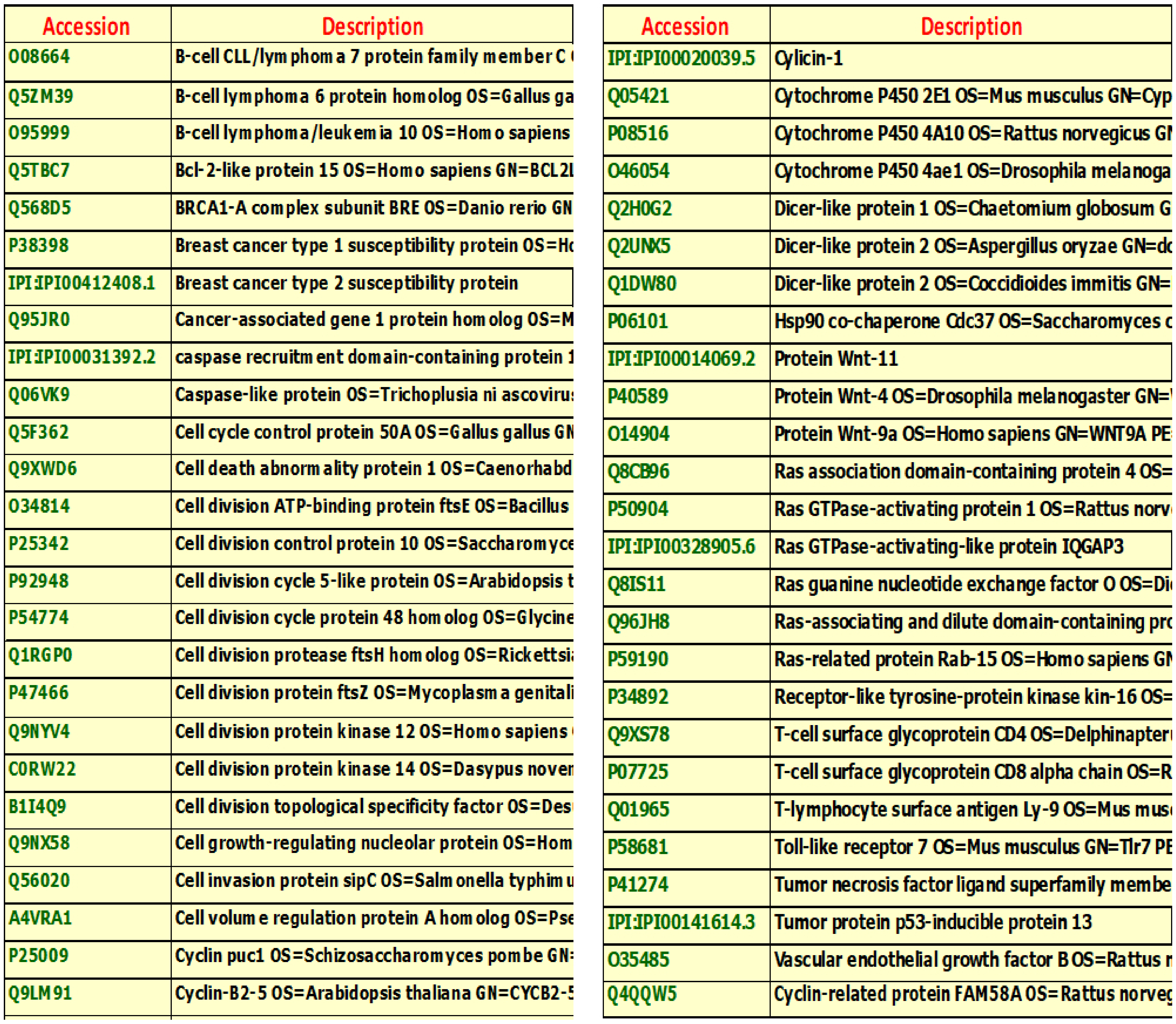
Figure S10.



Supplementary Figure 10: Protein profiling in ALL samples. (A) Protein expression profile of leukemic and normal samples reveals differential expression of proteins. (B) Proteins expressed only in Leukemia samples.

Figure S11.

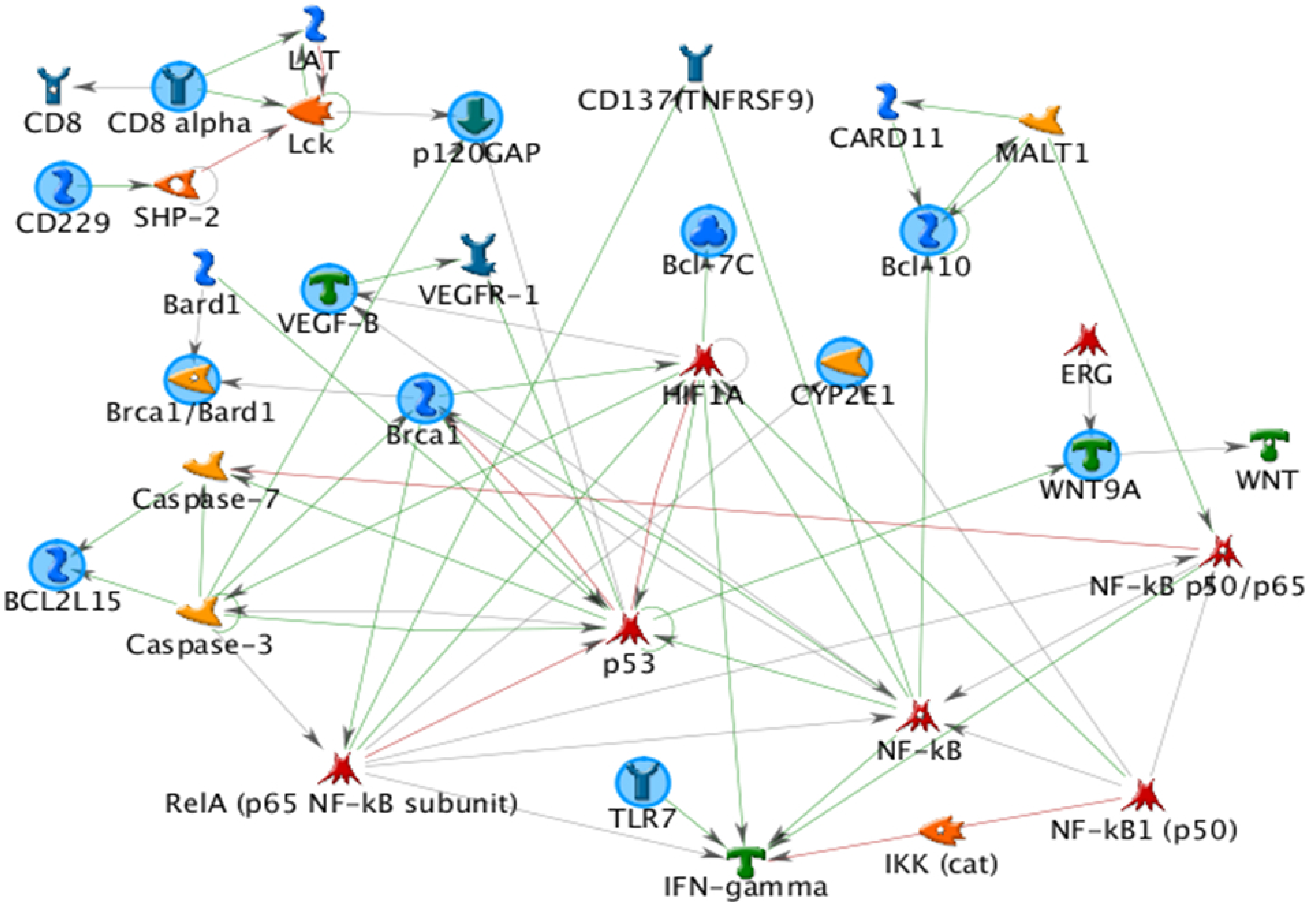
A.



Accession	Description
O08664	B-cell CLL/lymphoma 7 protein family member C
Q5ZM39	B-cell lymphoma 6 protein homolog OS=Gallus ga
O95999	B-cell lymphoma/leukemia 10 OS=Homo sapiens
Q5TBC7	Bcl-2-like protein 15 OS=Homo sapiens GN=BCL2L
Q568D5	BRCA1-A complex subunit BRE OS=Danio rerio GN
P38398	Breast cancer type 1 susceptibility protein OS=H
IPI:IPI00412408.1	Breast cancer type 2 susceptibility protein
Q95JR0	Cancer-associated gene 1 protein homolog OS=M
IPI:IPI00031392.2	caspase recruitment domain-containing protein
Q06VK9	Caspase-like protein OS=Trichoplusia ni ascoviru
Q5F362	Cell cycle control protein 50A OS=Gallus gallus G
Q9XWD6	Cell death abnormality protein 1 OS=Caenorhabd
O34814	Cell division ATP-binding protein ftsE OS=Bacillus
P25342	Cell division control protein 10 OS=Saccharomyce
P92948	Cell division cycle 5-like protein OS=Arabidopsis t
P54774	Cell division cycle protein 48 homolog OS=Glycine
Q1RGP0	Cell division protease ftsH homolog OS=Rickettsi
P47466	Cell division protein ftsZ OS=Mycoplasma genitali
Q9NYV4	Cell division protein kinase 12 OS=Homo sapiens
C0RW22	Cell division protein kinase 14 OS=Dasypus nover
B1I4Q9	Cell division topological specificity factor OS=Des
Q9NX58	Cell growth-regulating nucleolar protein OS=Hom
Q56020	Cell invasion protein sipC OS=Salmonella typhimu
A4VRA1	Cell volume regulation protein A homolog OS=Pse
P25009	Cyclin puc1 OS=Schizosaccharomyces pombe GN
Q9LM91	Cyclin-B2-5 OS=Arabidopsis thaliana GN=CYCB2-

Accession	Description
IPI:IPI00020039.5	Cylicin-1
Q05421	Cytochrome P450 2E1 OS=Mus musculus GN=Cyp
P08516	Cytochrome P450 4A10 OS=Rattus norvegicus G
O46054	Cytochrome P450 4ae1 OS=Drosophila melanoga
Q2H0G2	Dicer-like protein 1 OS=Chaetomium globosum G
Q2UNX5	Dicer-like protein 2 OS=Aspergillus oryzae GN=d
Q1DW80	Dicer-like protein 2 OS=Coccidioides immitis GN=
P06101	Hsp90 co-chaperone Cdc37 OS=Saccharomyces
IPI:IPI00014069.2	Protein Wnt-11
P40589	Protein Wnt-4 OS=Drosophila melanogaster GN=
O14904	Protein Wnt-9a OS=Homo sapiens GN=WNT9A PE
Q8CB96	Ras association domain-containing protein 4 OS=
P50904	Ras GTPase-activating protein 1 OS=Rattus norv
IPI:IPI00328905.6	Ras GTPase-activating-like protein IQGAP3
Q8IS11	Ras guanine nucleotide exchange factor O OS=Di
Q96JH8	Ras-associating and dilute domain-containing pro
P59190	Ras-related protein Rab-15 OS=Homo sapiens G
P34892	Receptor-like tyrosine-protein kinase kin-16 OS=
Q9XS78	T-cell surface glycoprotein CD4 OS=Delphinapter
P07725	T-cell surface glycoprotein CD8 alpha chain OS=R
Q01965	T-lymphocyte surface antigen Ly-9 OS=Mus mus
P58681	Toll-like receptor 7 OS=Mus musculus GN=Tlr7 PE
P41274	Tumor necrosis factor ligand superfamily membe
IPI:IPI00141614.3	Tumor protein p53-inducible protein 13
O35485	Vascular endothelial growth factor B OS=Rattus
Q4QQW5	Cyclin-related protein FAM58A OS=Rattus norveg

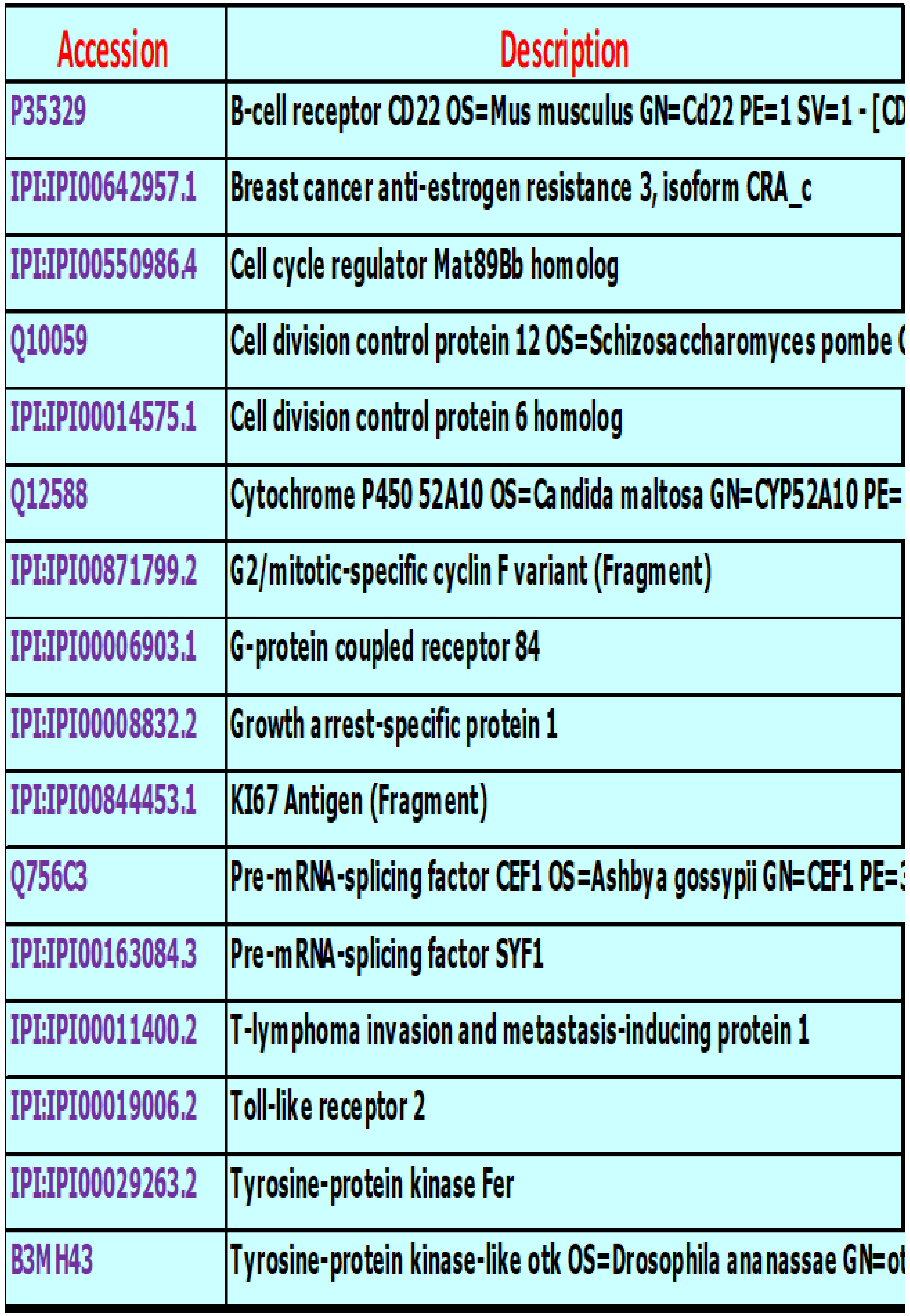
B.



Supplementary Figure 11: Protein profiling in T-ALL(PB) using LTQ Orbitrap (A) Identified proteins with their accession numbers and (B) GeneGo MetaCore pathway analysis revealing various oncogenic targets.

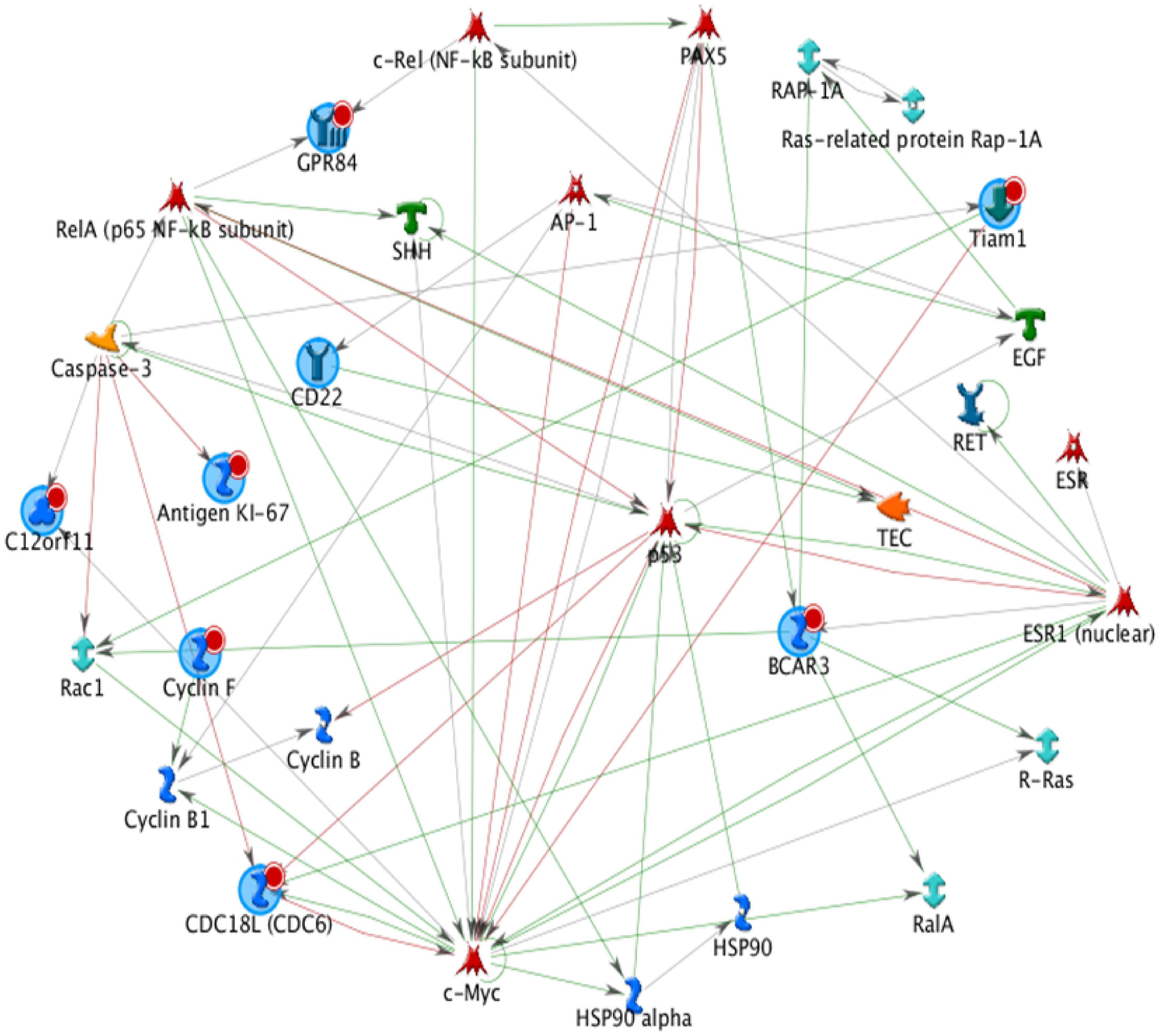
Figure S12.

A.



Accession	Description
P35329	B-cell receptor CD22 OS=Mus musculus GN=Cd22 PE=1 SV=1 - [CD
IPI:IPI00642957.1	Breast cancer anti-estrogen resistance 3, isoform CRA_c
IPI:IPI00550986.4	Cell cycle regulator Mat89Bb homolog
Q10059	Cell division control protein 12 OS=Schizosaccharomyces pombe
IPI:IPI00014575.1	Cell division control protein 6 homolog
Q12588	Cytochrome P450 52A10 OS=Candida maltosa GN=CYP52A10 PE=
IPI:IPI00871799.2	G2/mitotic-specific cyclin F variant (Fragment)
IPI:IPI00006903.1	G-protein coupled receptor 84
IPI:IPI00008832.2	Growth arrest-specific protein 1
IPI:IPI00844453.1	KI67 Antigen (Fragment)
Q756C3	Pre-mRNA-splicing factor CEF1 OS=Ashbya gossypii GN=CEF1 PE=
IPI:IPI00163084.3	Pre-mRNA-splicing factor SYF1
IPI:IPI00011400.2	T-lymphoma invasion and metastasis-inducing protein 1
IPI:IPI00019006.2	Toll-like receptor 2
IPI:IPI00029263.2	Tyrosine-protein kinase Fer
B3MH43	Tyrosine-protein kinase-like otk OS=Drosophila ananassae GN=ot

B.



Supplementary Figure 12: Protein profiling in T-ALL (BM) using LTQ Orbitrap (A) Identified proteins with their accession numbers and (B) GeneGo MetaCore pathway analysis revealing various oncogenic targets.