



Myelopoiesis GSE42519

Cutoff: 4.5

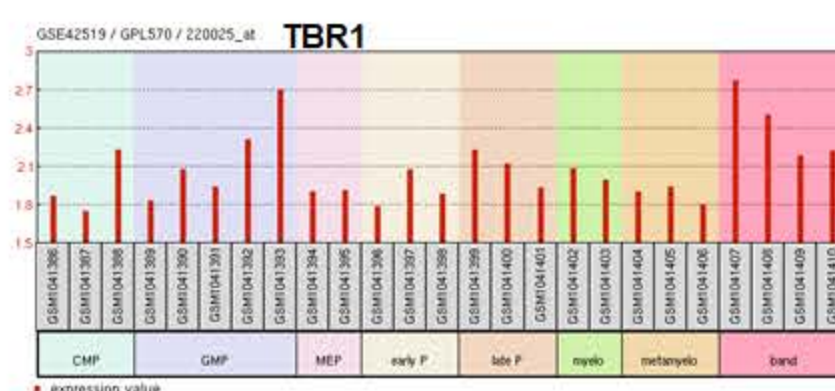
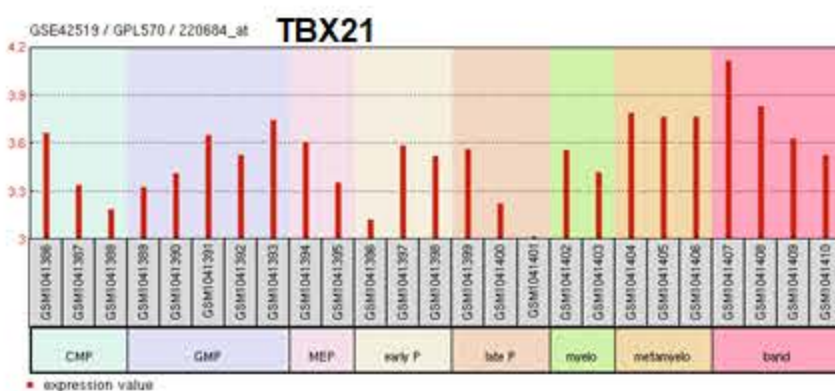
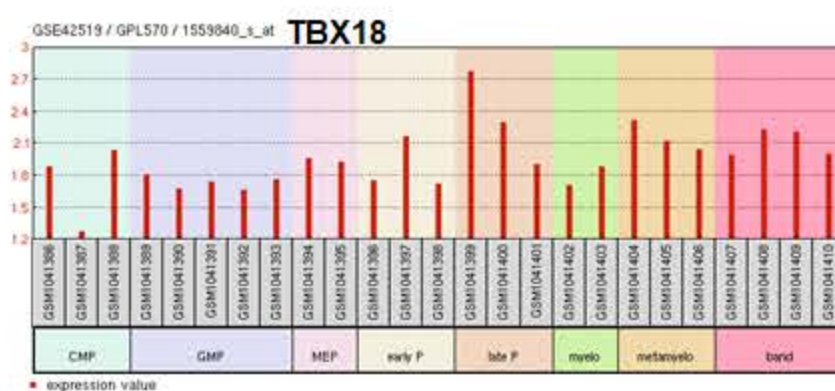
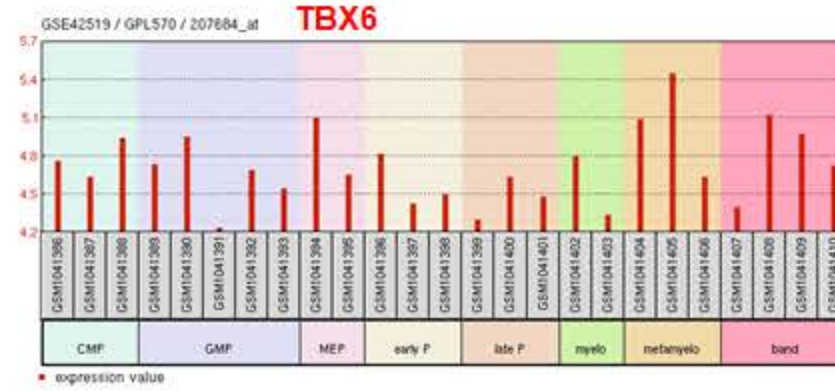
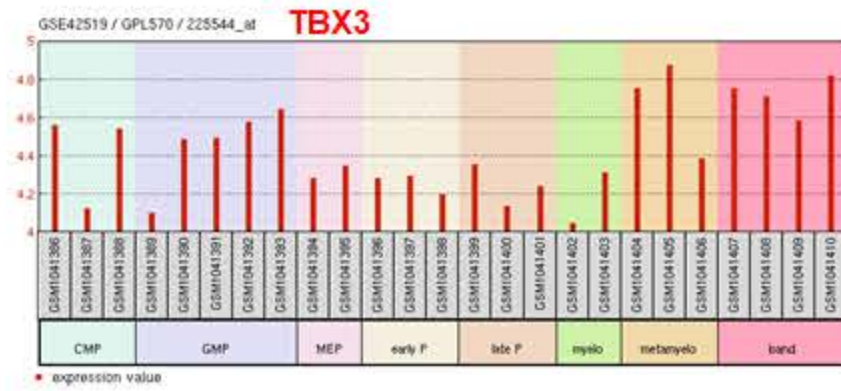
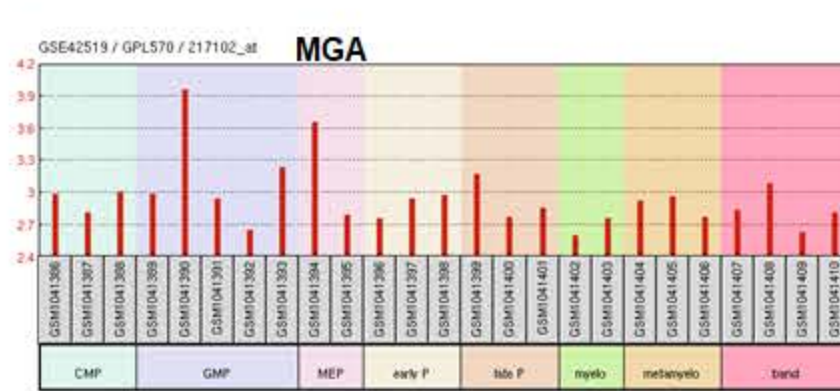
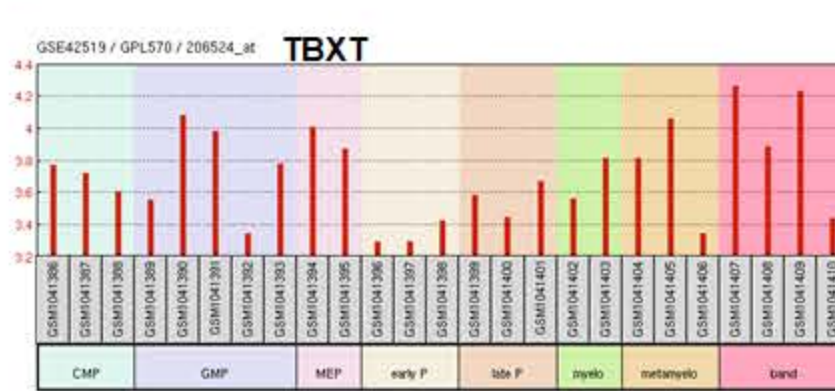
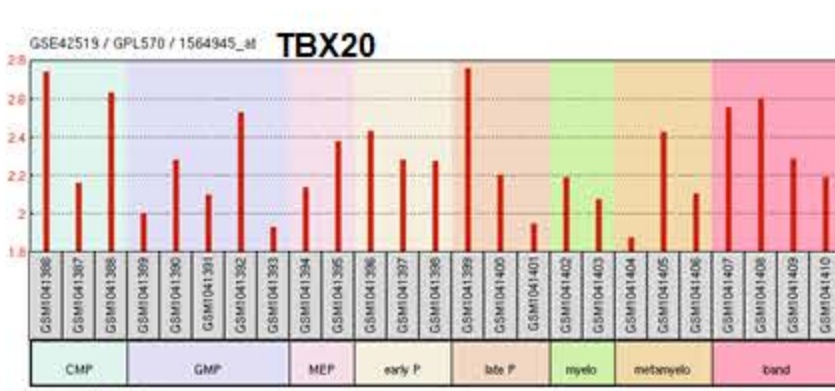
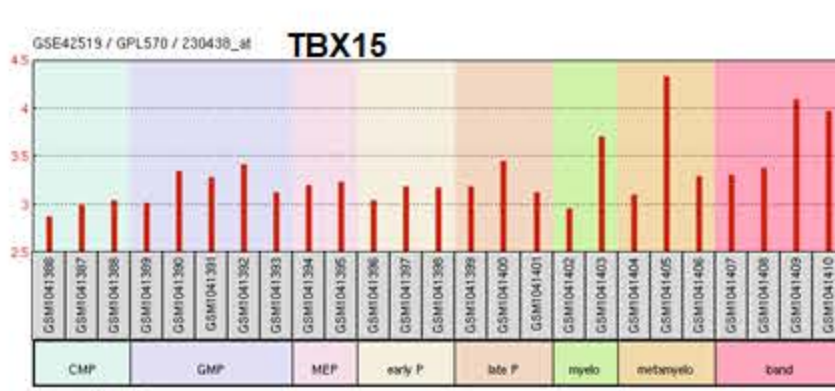
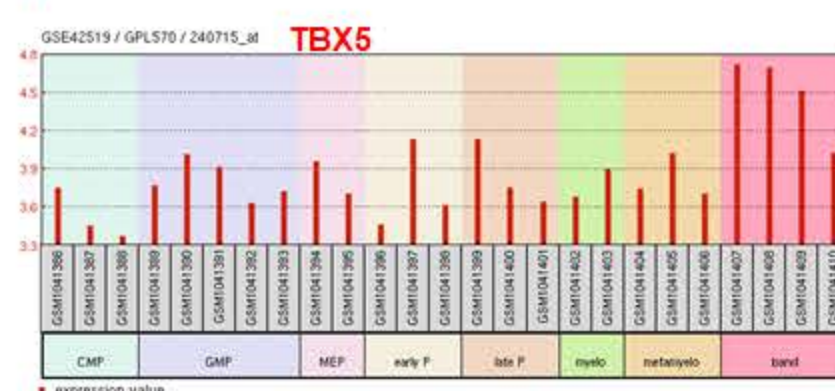
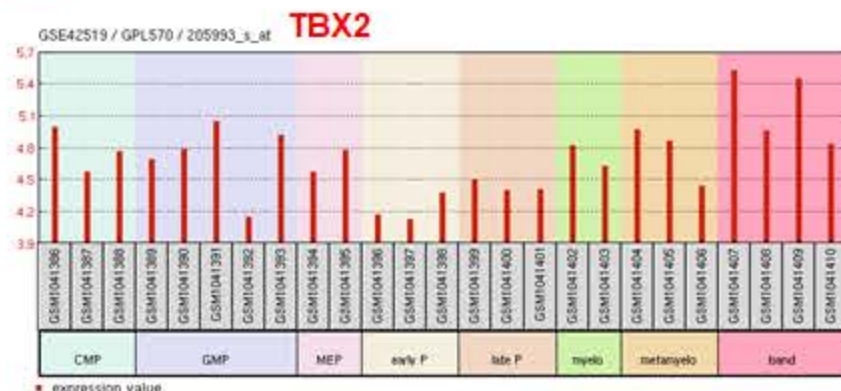
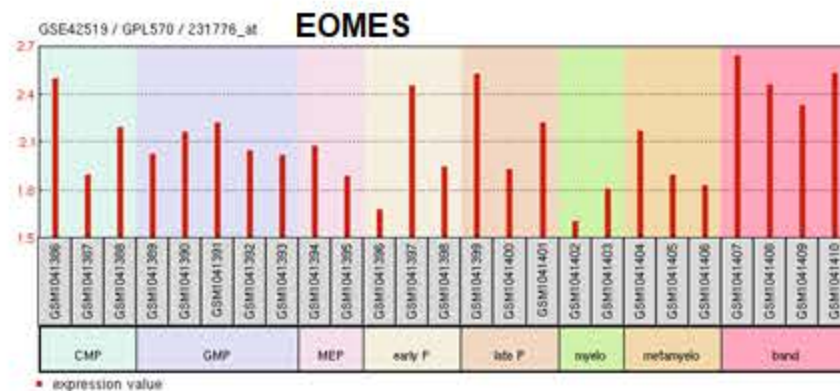
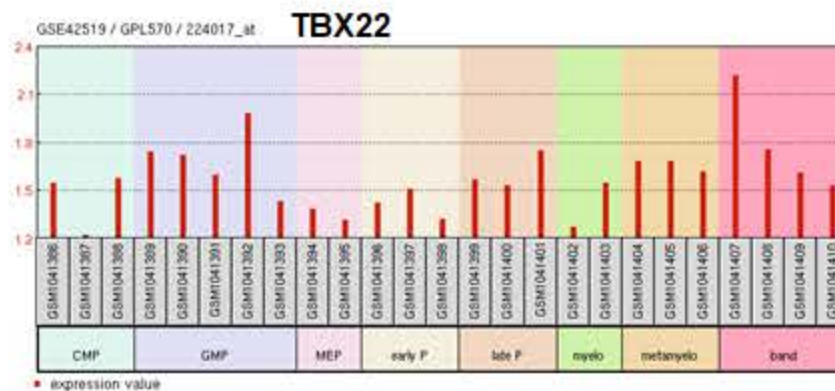
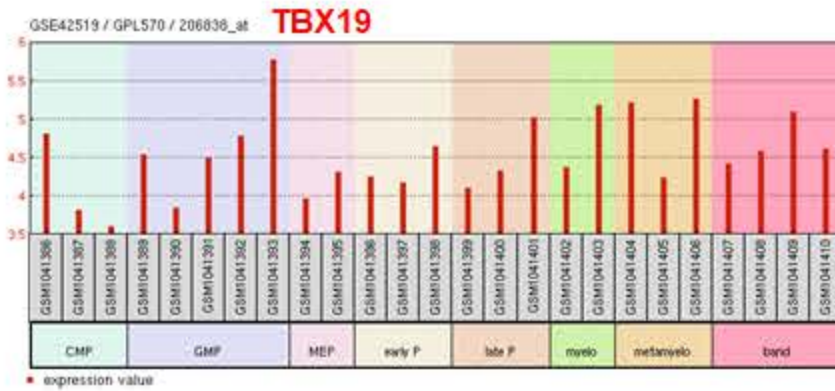
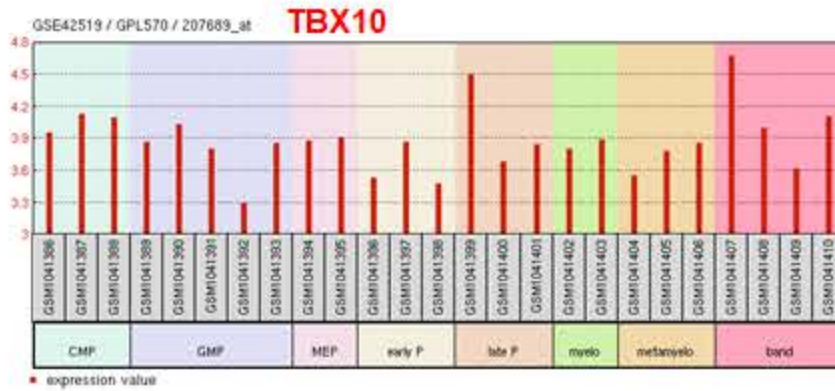
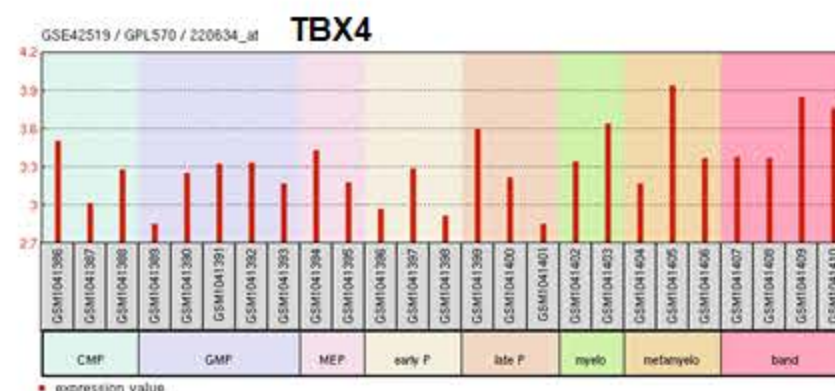
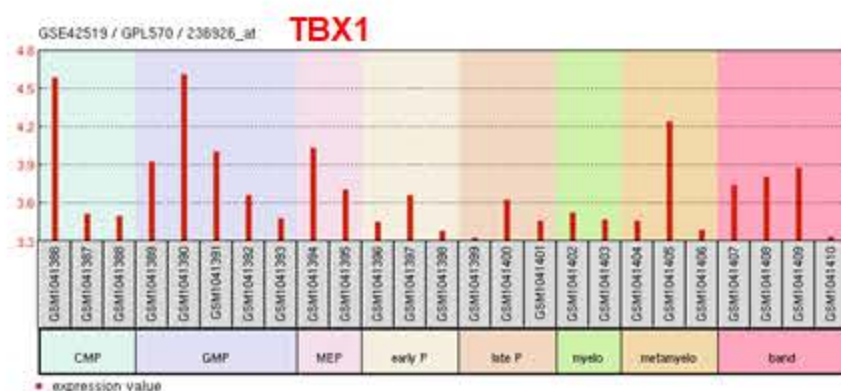


Figure S2: T-box gene activities using dataset GSE42519 for particular stages of myelopoiesis. A cutoff was set at 4.5.

Erythropoiesis GSE22552

Cutoff: 6.0

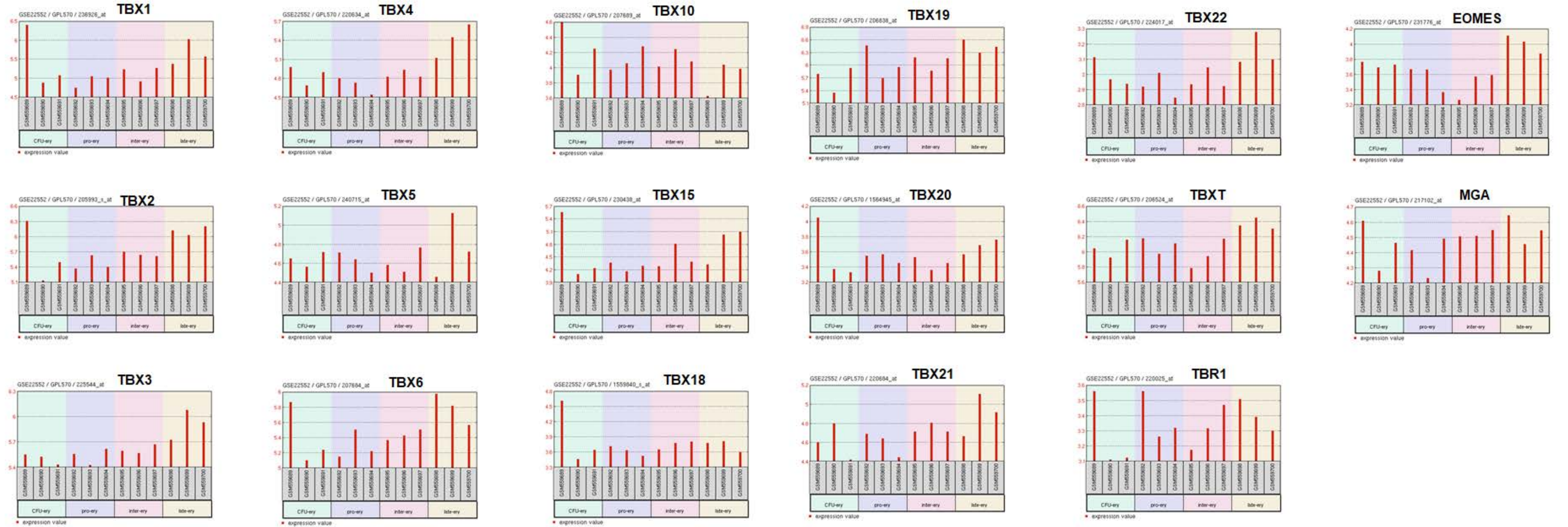


Figure S3: T-box gene activities using dataset GSE22552 for particular stages of erythropoiesis. A cutoff was set at 6.0.

Megakaryocytes GSE40831

Cutoff: 50

Group	Accession	Title	Source name	Cell type
-	GSM1002641	megakaryocytes at day0, biological rep A	umbilical cord blood	CD34-CD41+CD61+CD45- megakaryocytes
-	GSM1002642	megakaryocytes at day0, biological rep B	umbilical cord blood	CD34-CD41+CD61+CD45- megakaryocytes
-	GSM1002643	megakaryocytes at day4, biological rep A	Lin- cell culture derived samples, day4	CD34-CD41+CD61+CD45- megakaryocytes
-	GSM1002644	megakaryocytes at day4, biological rep B	Lin- cell culture derived samples, day4	CD34-CD41+CD61+CD45- megakaryocytes
-	GSM1002645	CFU-M at day0, biological rep A	umbilical cord blood	CD34-CD33+CD13+ colony forming unit-monocytes
-	GSM1002646	CFU-M at day0, biological rep B	umbilical cord blood	CD34-CD33+CD13+ colony forming unit-monocytes
-	GSM1002647	CFU-M at day4, biological rep A	Lin- cell culture derived samples, day4	CD34-CD33+CD13+ colony forming unit-monocytes
-	GSM1002648	CFU-M at day4, biological rep B	Lin- cell culture derived samples, day4	CD34-CD33+CD13+ colony forming unit-monocytes

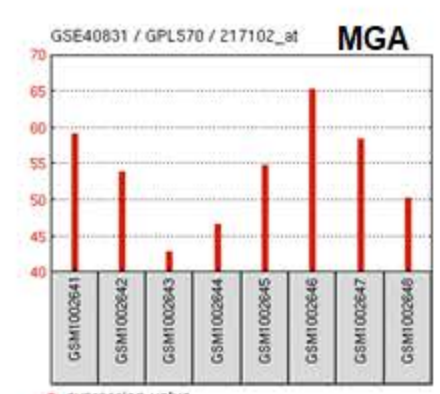
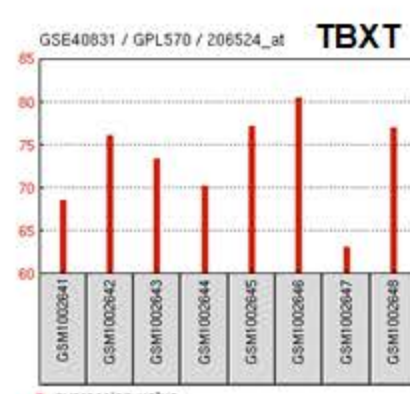
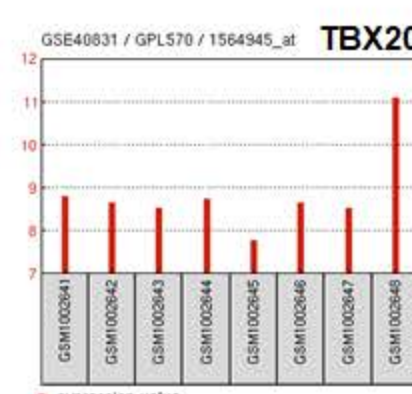
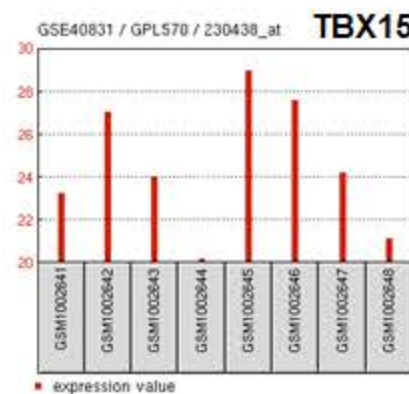
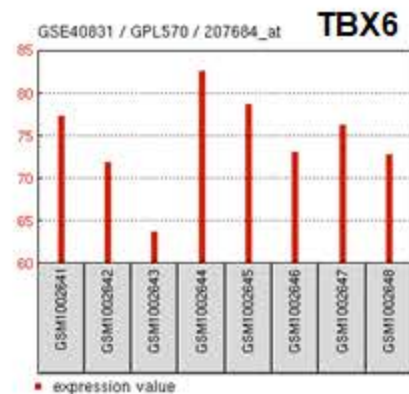
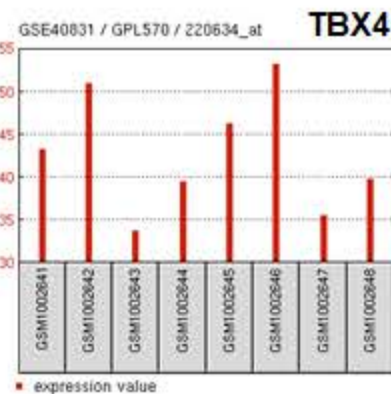
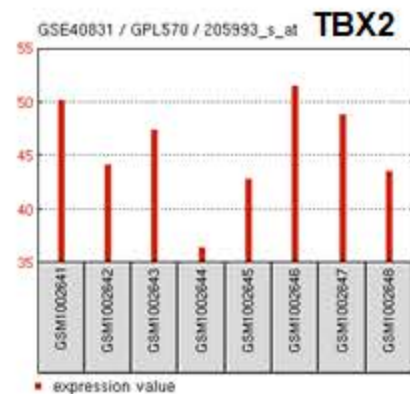
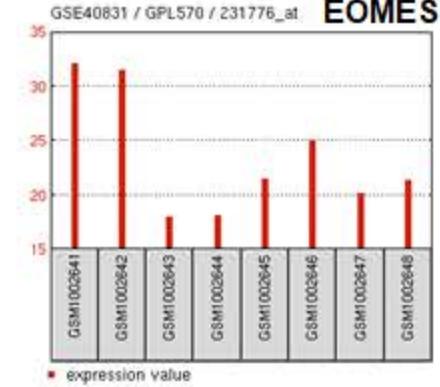
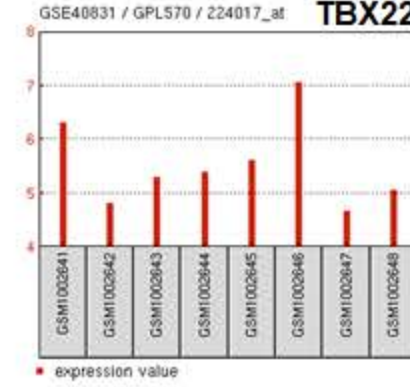
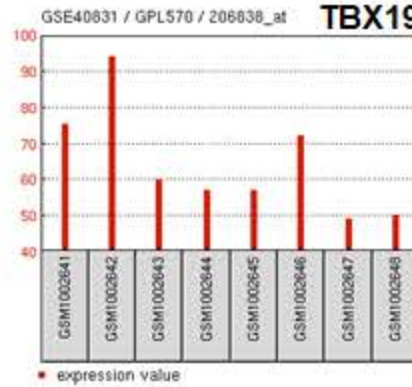
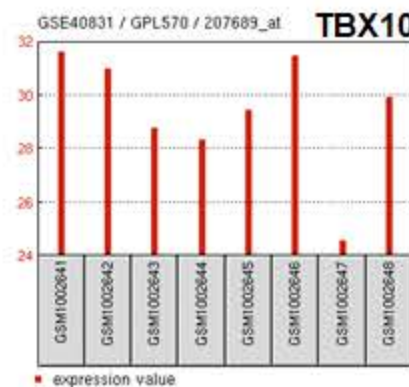
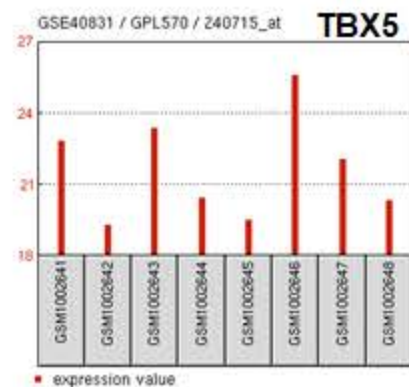
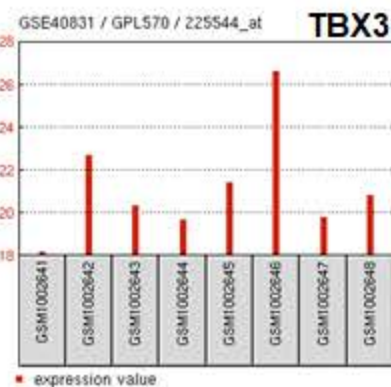
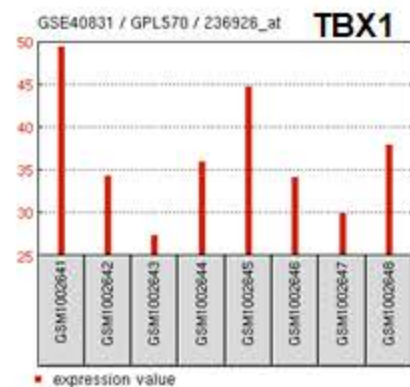


Figure S4: T-box gene activities using dataset GSE40831 for megakaryocytes. A cutoff was set at 50.

Mono, moDC, mast, granulocytes GSE109348

Cutoff: 4.0

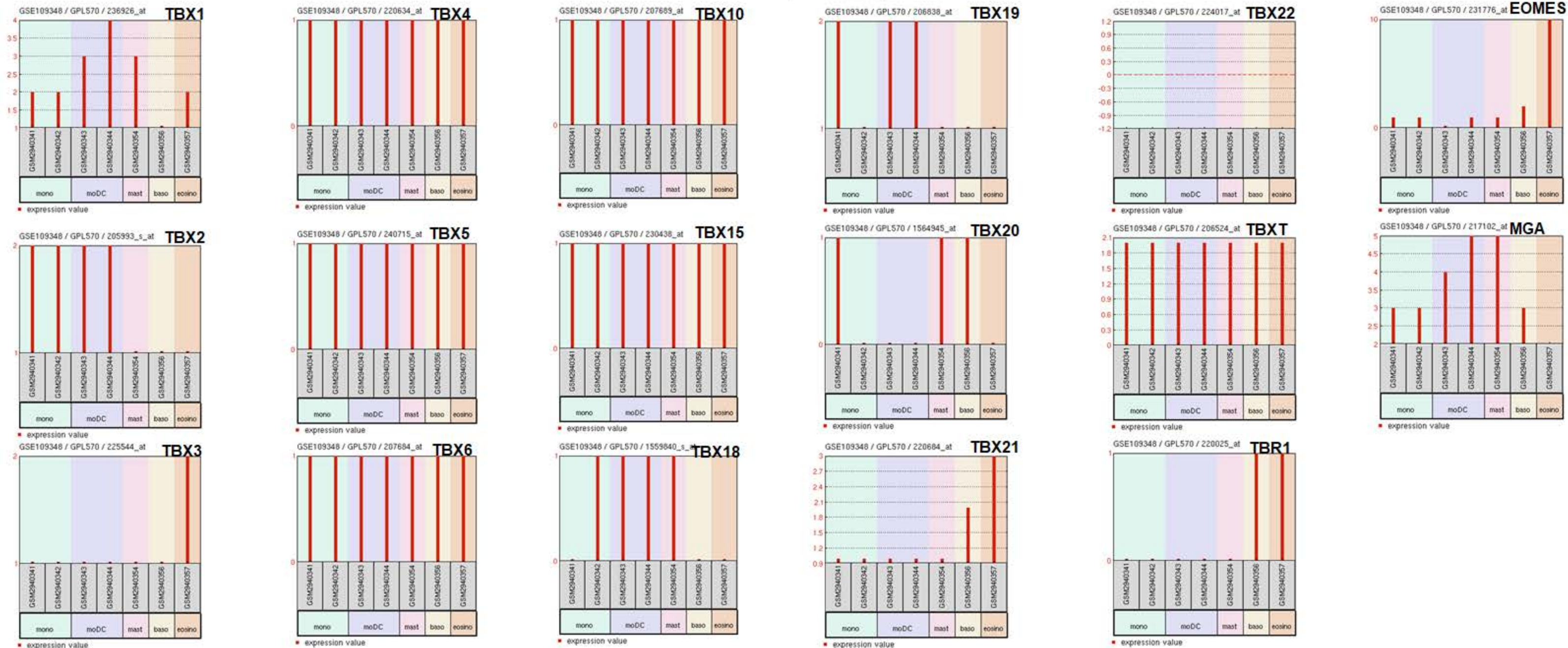


Figure S5: T-box gene activities using dataset GSE109348 for monocytes, monocyte-derived dendritic cells, mast cells and granulocytes. A cutoff was set at 4.0.

AML

Dataset GSE15434 (patients with normal karyotype)

Cutoff: 5.0



Figure S6: T-box gene activities using dataset GSE15434 for AML patients with normal karyotype. A cutoff was set at 5.0. Aberrantly expressed T-box genes are indicated in red.

AML

Dataset GSE14468 (patients diverse aberrations and mutations)

Cutoff: 6.0

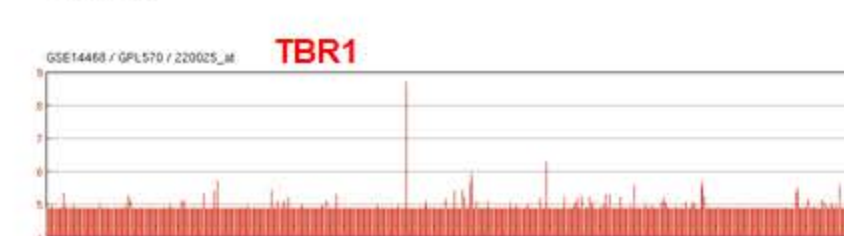
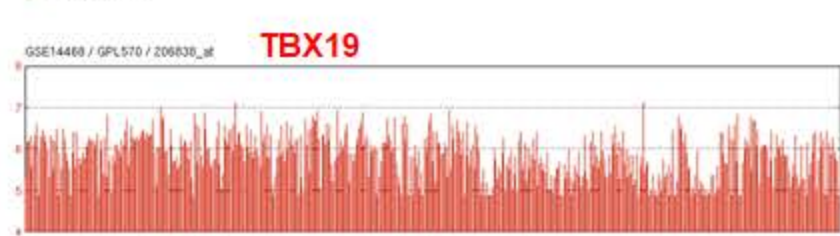
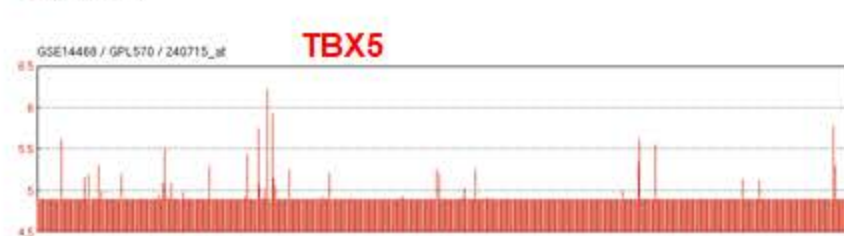
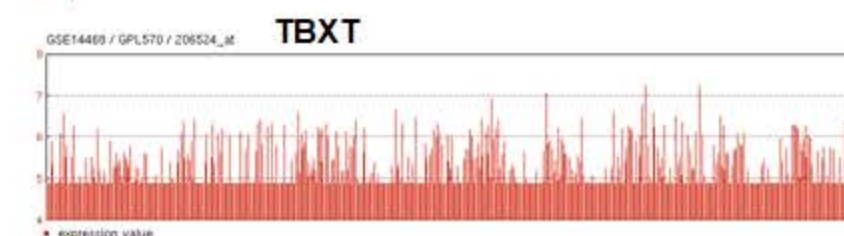
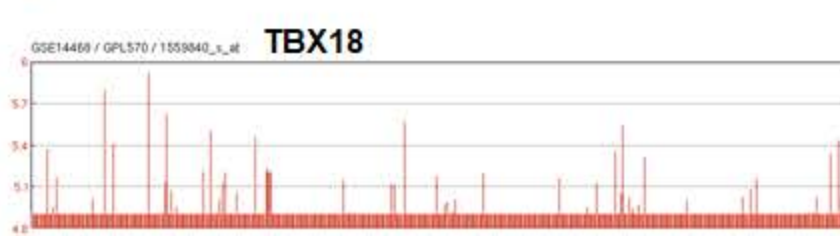
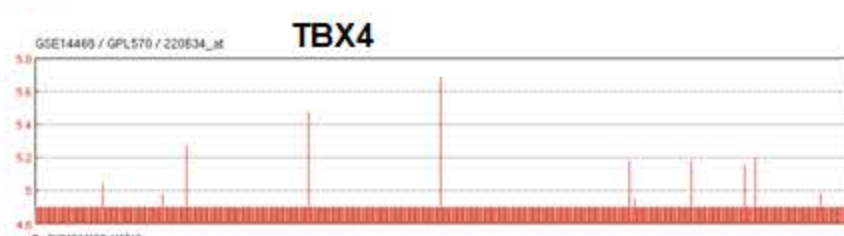
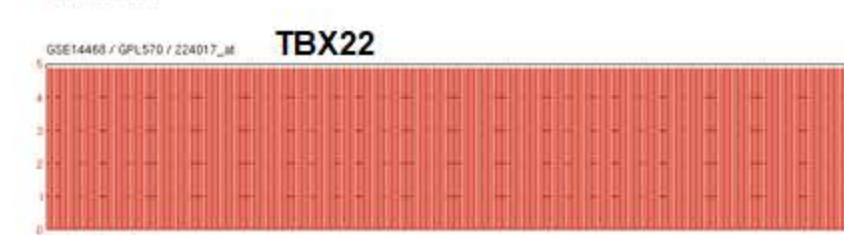
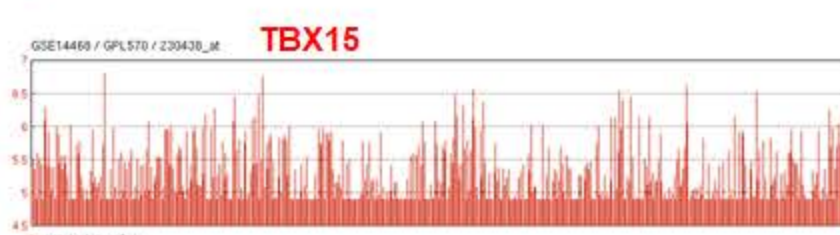
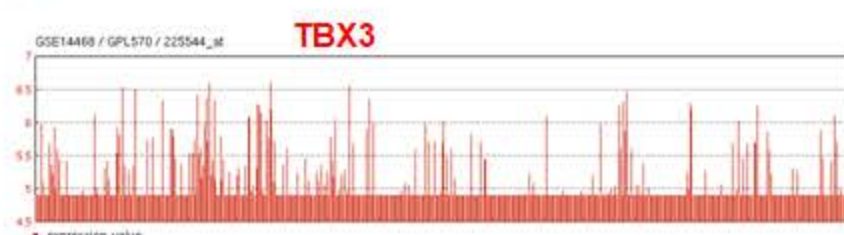
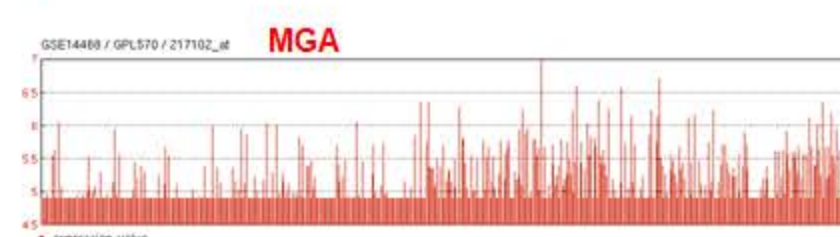
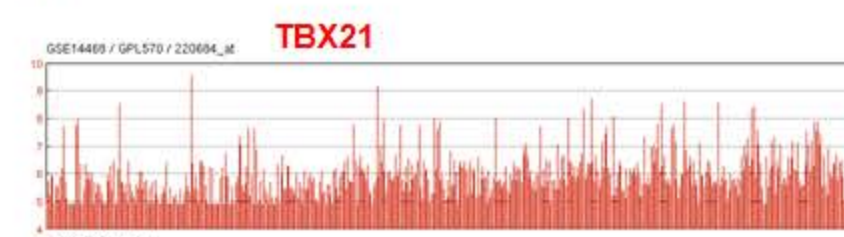
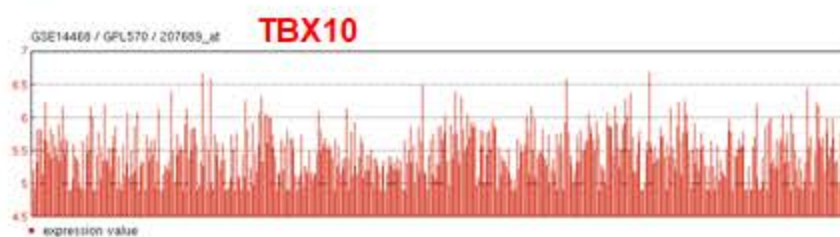
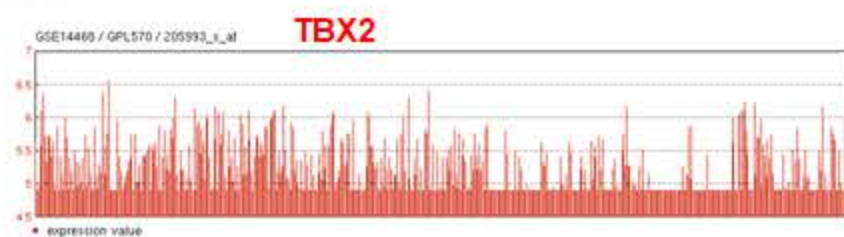
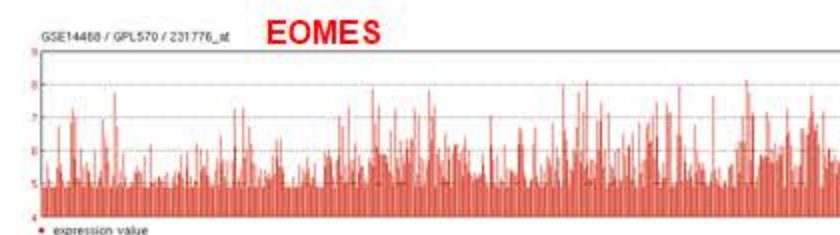
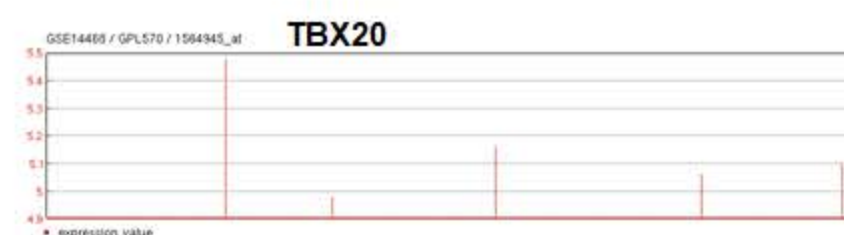
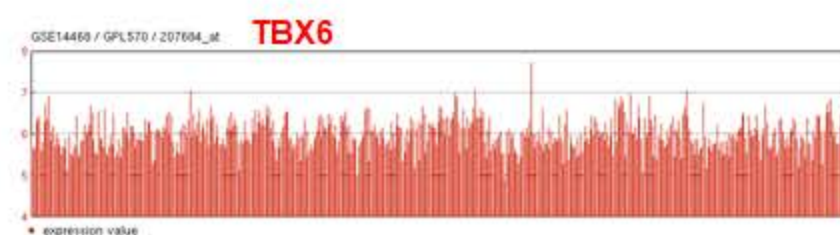
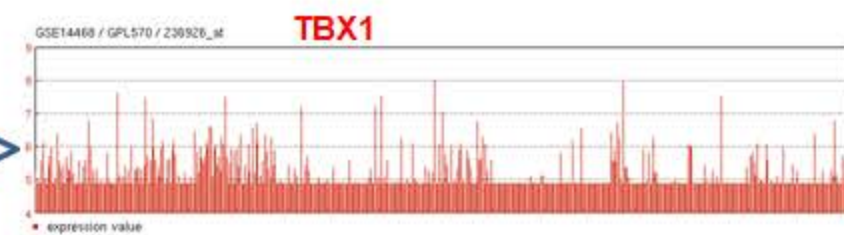
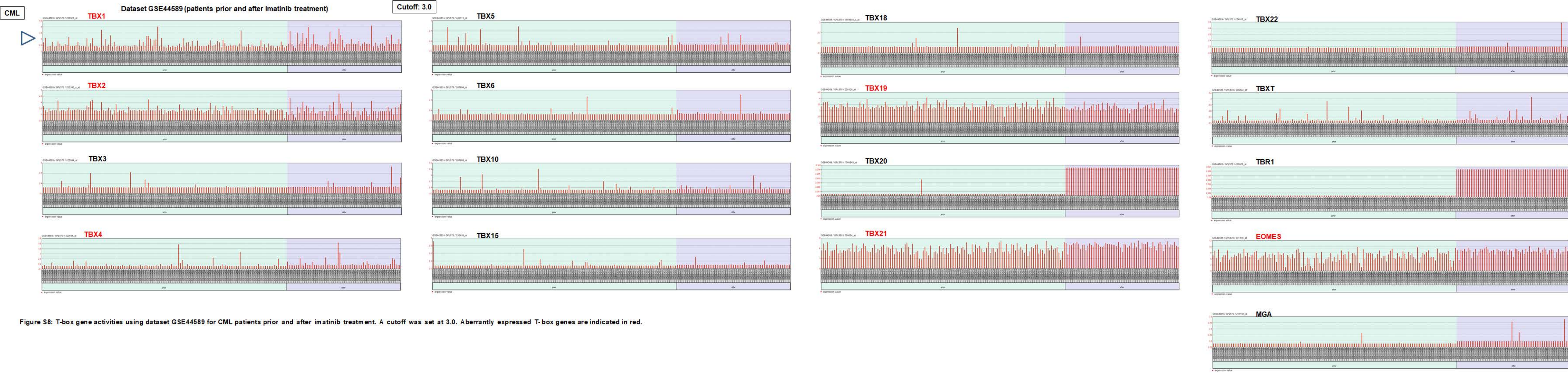
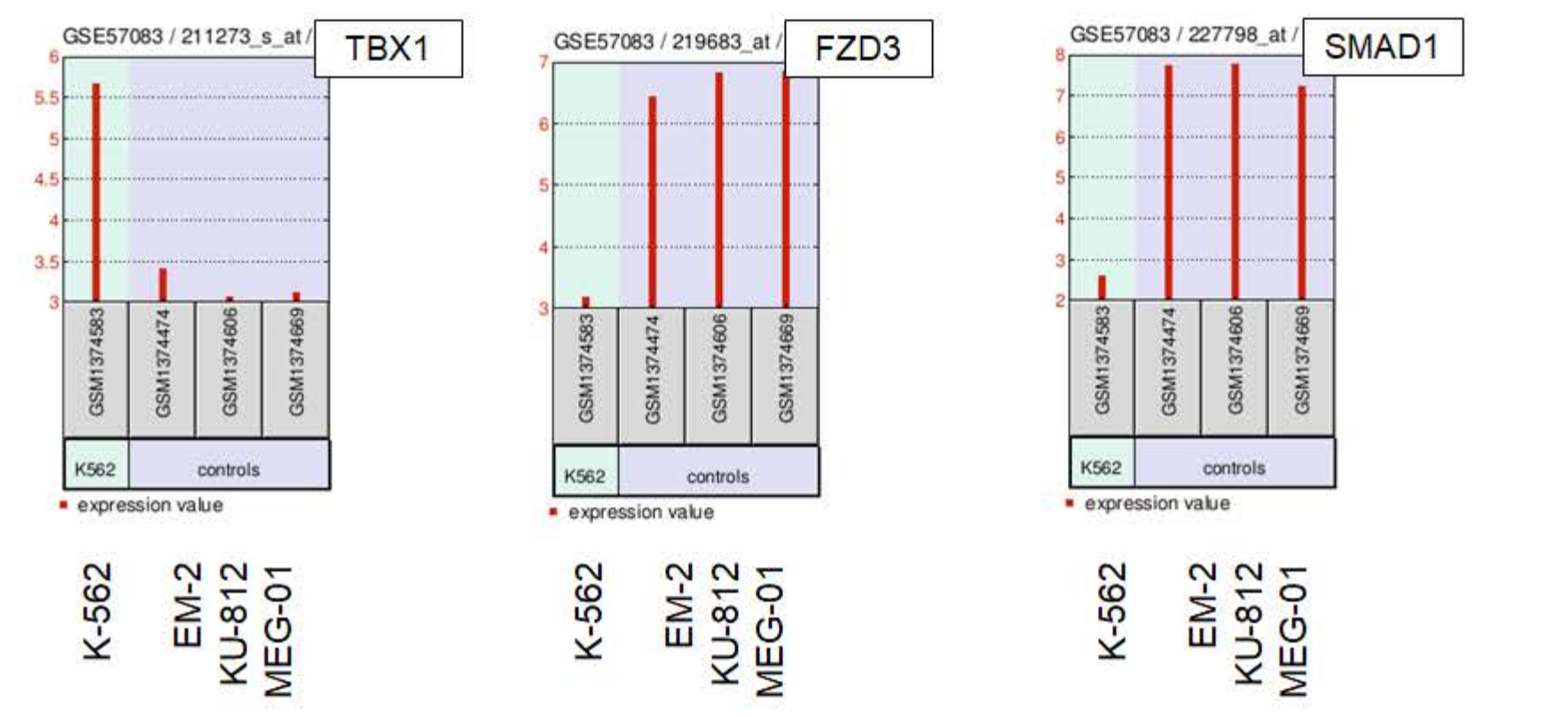


Figure S7: T-box gene activities using dataset GSE14468 for AML patients with diverse aberrations and mutations. A cutoff was set at 6.0. Aberrantly expressed T-box genes are indicated in red.



GEOR analysis of **cell line** dataset GSE57083
comparing K-562 versus CML control cell lines (top-250)



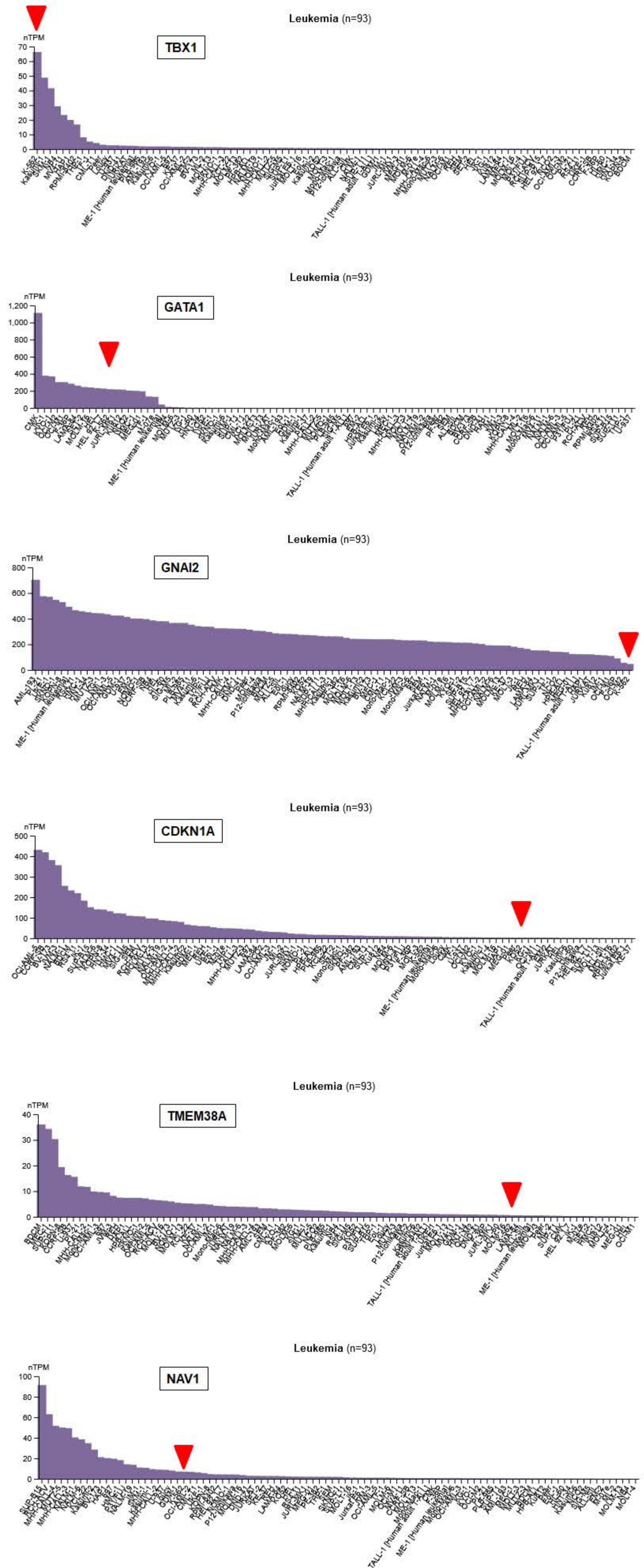


Figure S10: Selected gene activities in 93 leukemia cell lines using RNA-seq data from the Human Protein Atlas for TBX1, GATA1, GNAI2, CDKN1A, TMEM38A and NAV1.

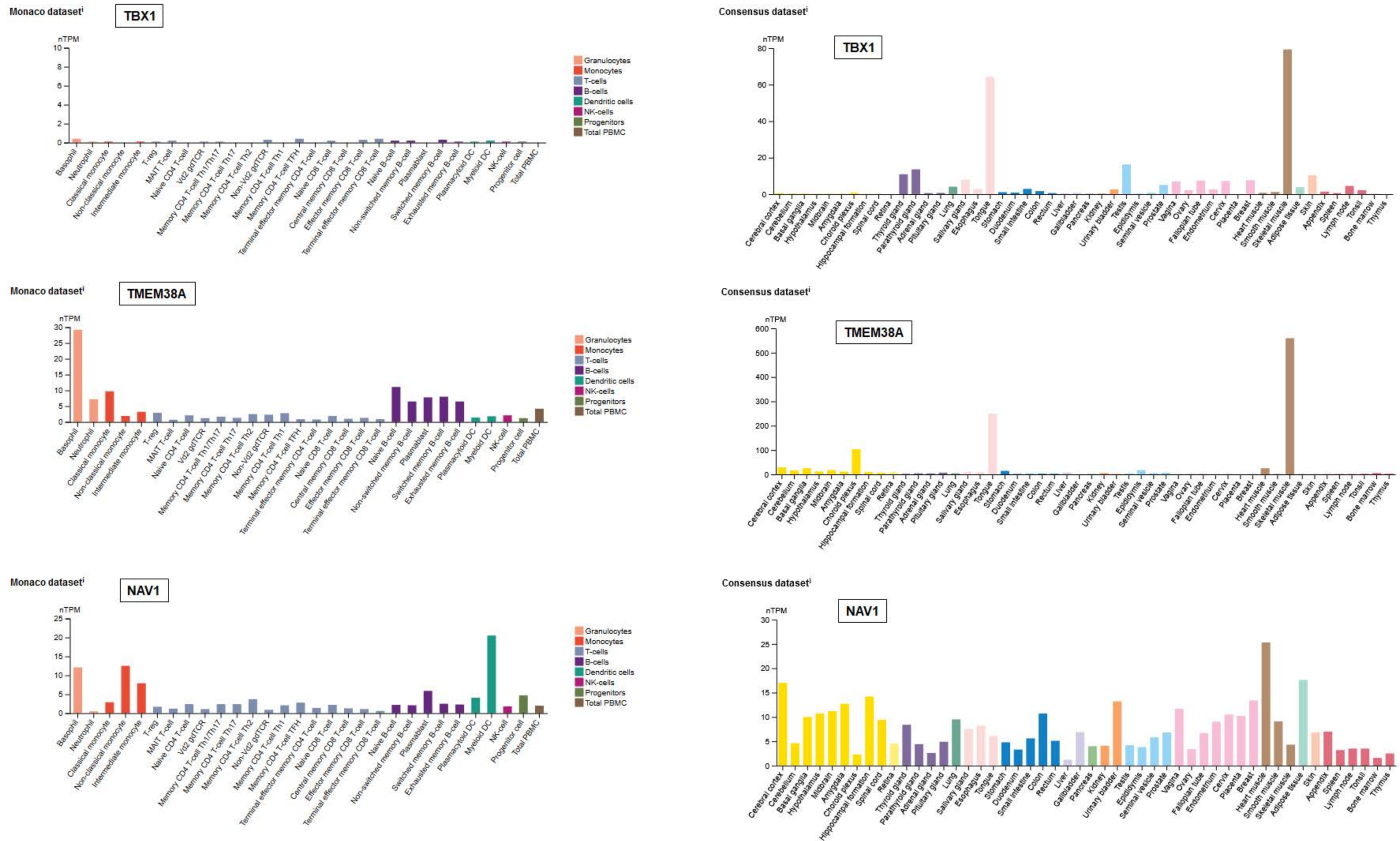


Figure S11: Gene activities for TBX1, TMEM38A and NAV1 using RNA-seq data from the Human Protein Atlas for hematopoietic cell types (Monaco dataset, left) and diverse tissue types (Consensus dataset, right).

external_gene_name	log2FoldChange	padj
AC093525.1	-6.49	9.38E-03
GPR157	-4.17	1.87E-89
AC008763.2	-3.90	9.99E-06
SULT1A4	-2.50	3.40E-05
SPATA17	-1.77	4.71E-02
AP000812.4	-1.74	2.62E-02
ACVR1C	-1.70	3.00E-02
INPP4B	-1.68	4.71E-02
DDX58	-1.28	3.19E-04
SMIM27	-1.13	1.42E-03
TANC2	-0.99	1.38E-02
P2RY11	-0.90	3.88E-02
ESPN	-0.88	2.53E-02
HSPA6	-0.87	4.36E-05
ZNF33B	-0.86	4.32E-02
SAMD11	-0.82	3.87E-03
SYT10	-0.79	3.49E-02
FADS3	-0.79	2.25E-14
LGALS1	-0.75	2.62E-02
HSPE1-MOB4	-0.72	2.57E-02
TBX1	-0.63	2.48E-10
CYRIA	-0.61	2.10E-03
PLAT	0.61	2.65E-02
GGT1	0.62	1.58E-02
GIPC3	0.63	8.99E-03
NAV1	0.68	1.43E-03
AL157935.2	0.92	1.78E-02
FAM114A1	0.97	1.17E-02
HERC3	1.21	5.17E-04
NOTCH3	1.95	3.40E-05
CAPN11	2.04	4.84E-02
TMEM38A	2.62	1.06E-07
DMBT1	3.48	3.72E-03
ZNF385B	5.44	4.71E-02

Table S1: List of potential TBX1 target genes. These genes were statistically significant differentially expressed in K-562 cells treated for TBX1-knockdown (performed in triplicate). Indicated are log2-fold change and the according p-value. The genes TBX1, TMEM38A and NAV1 are highlighted.