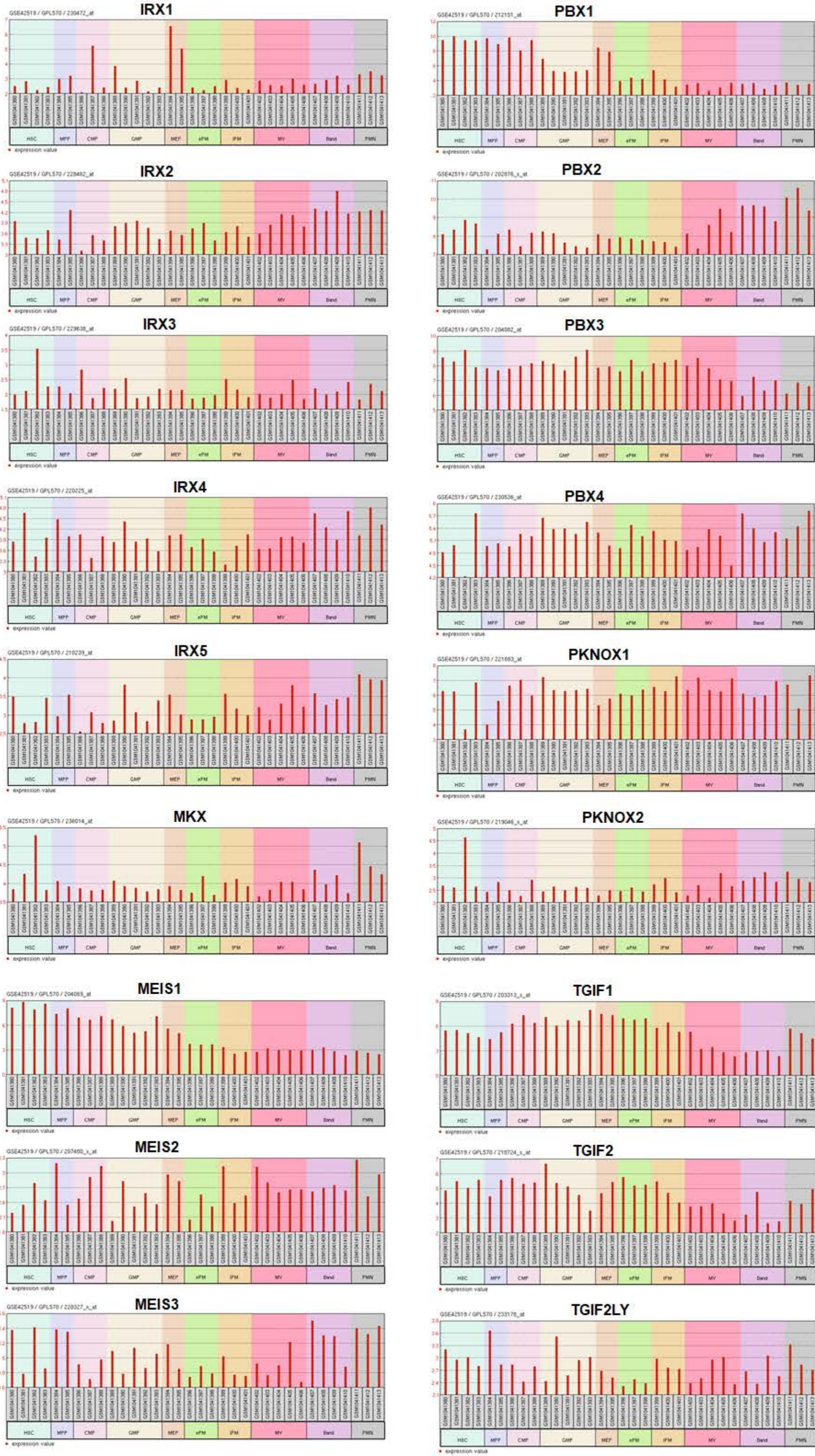


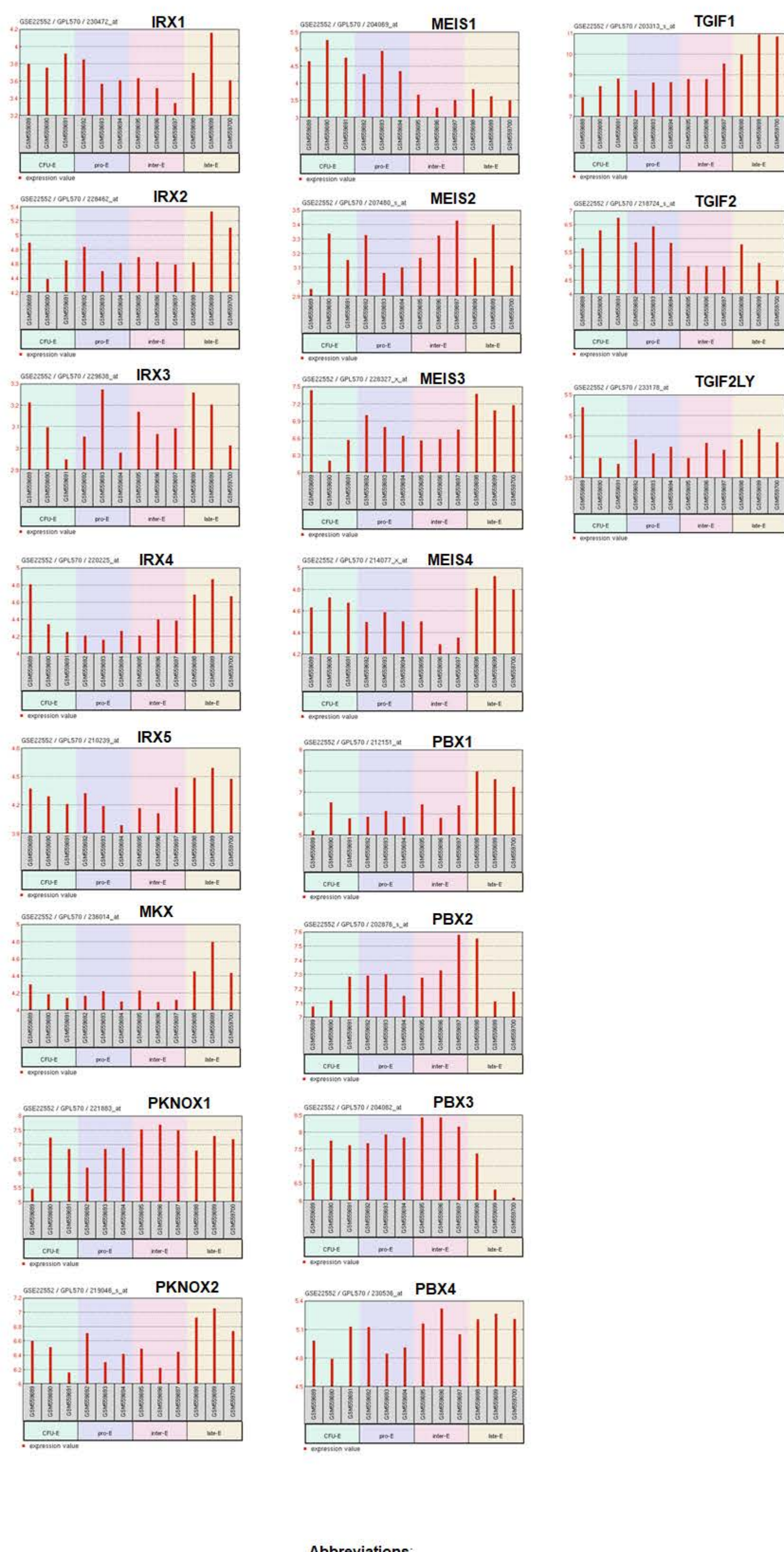
Myelopoiesis dataset GSE42519 (cutoff: 5)



**Abbreviations:**

HSC: hematopoietic stem cell  
MPP: myeloid primed progenitor  
CMP: common myeloid progenitor  
GMP: granulo-myeloid progenitor  
MEP: megakaryocytic-erythroid progenitor  
e PM: early promyelocyte  
IPM: late promyelocyte  
MY: myelocyte  
Band: band cells  
PMN: polymorphonuclear cells

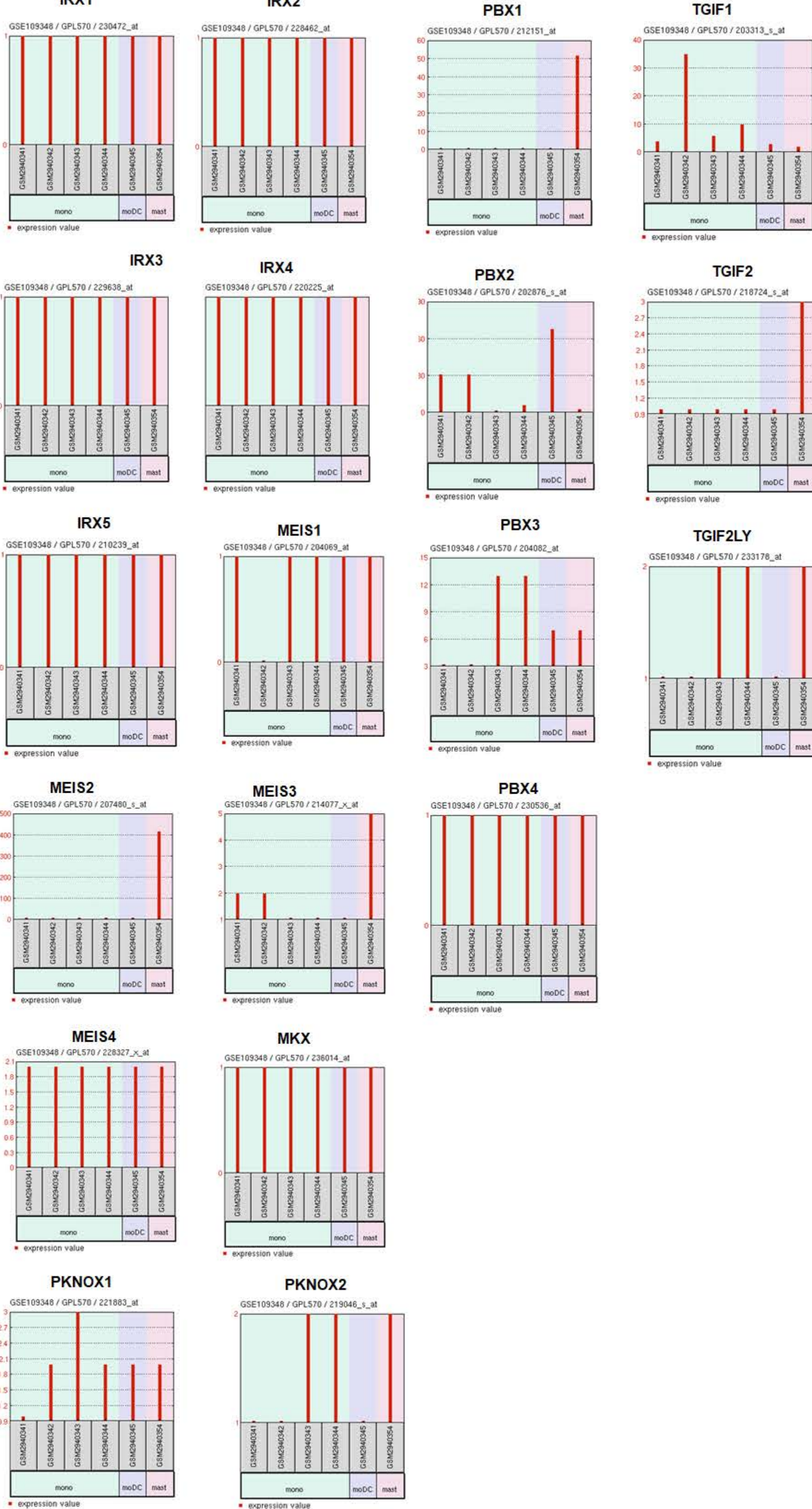
Myelopoiesis dataset GSE22552 (cutoff: 7)



**Abbreviations:**

CFU-E: colony-forming unit erythroblasts  
Pro-E: pro-erythroblast  
inter-E: intermediate erythroblast  
late-E: late erythroblast

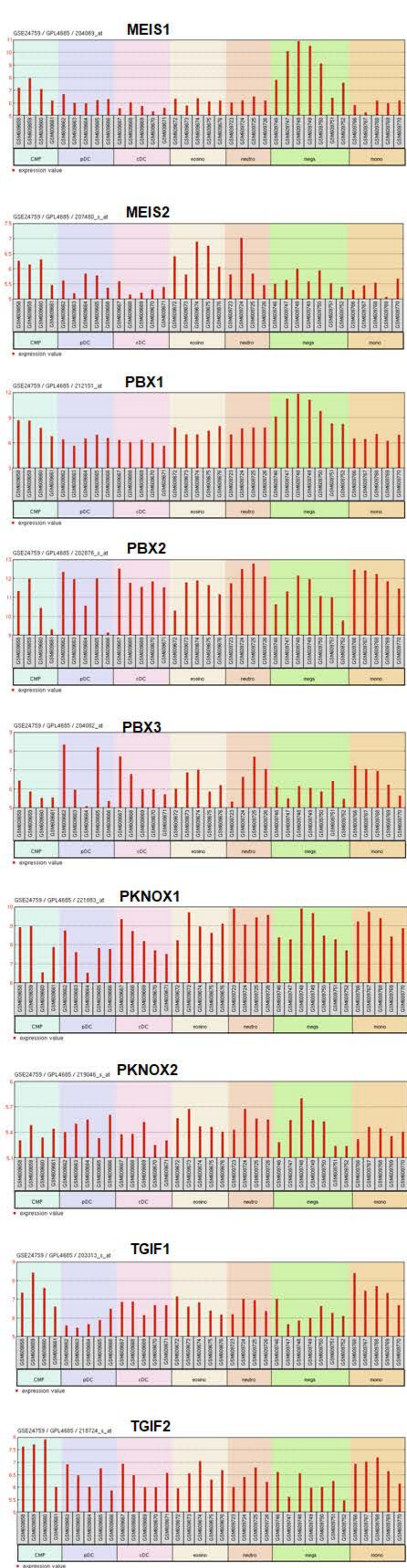
Myelopoiesis dataset GSE109348 (cutoff: 7)



**Abbreviations:**

mono: monocyte  
moDC: monocyte-derived dendritic cell  
mast: mast cell

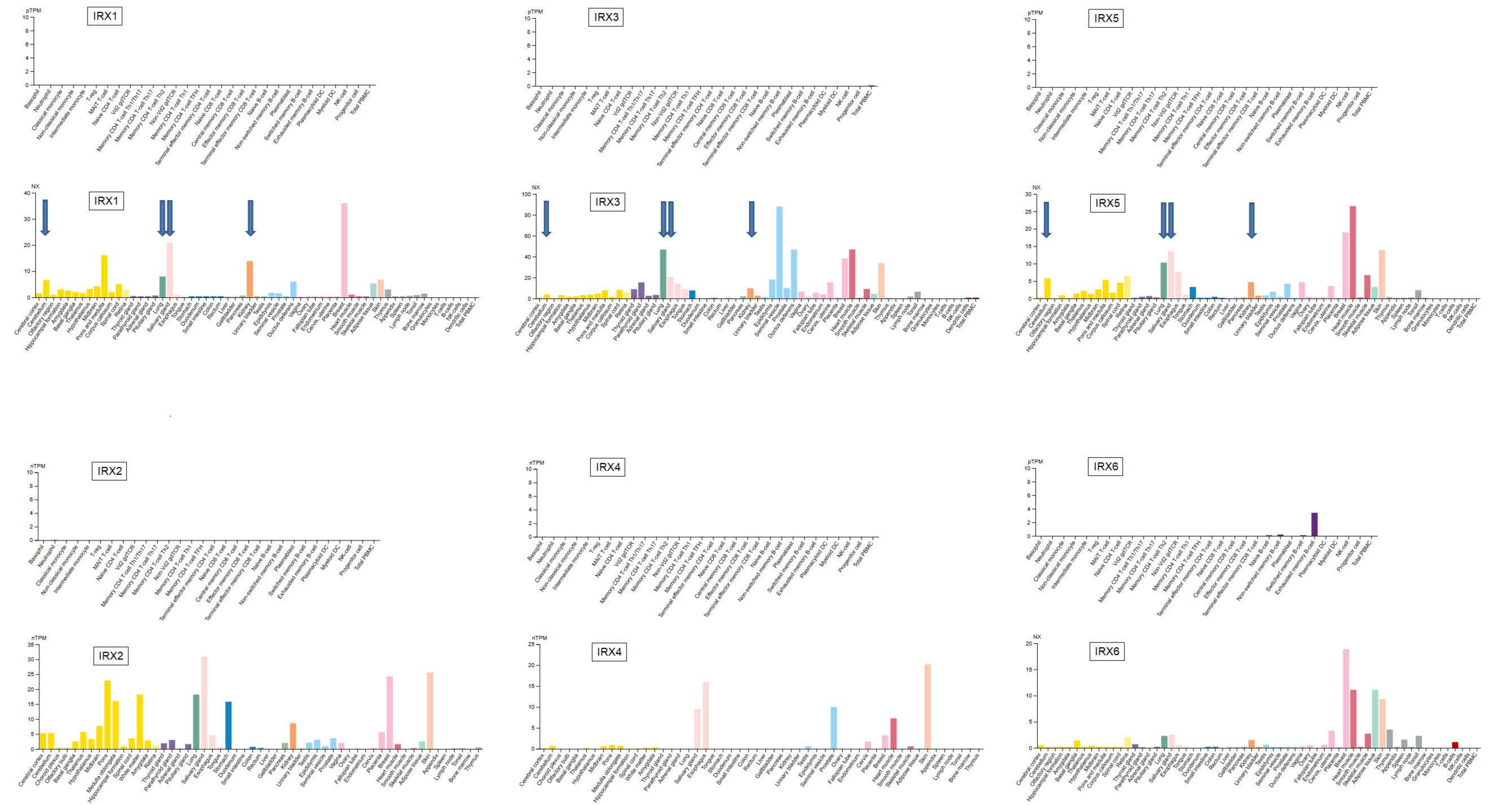
Myelopoiesis dataset GSE24759 (cutoff: 7)



**Abbreviations:**

CMP: common myeloid progenitor  
pDC: plasmacytoid dendritic cell  
cDC: conventional dendritic cell  
eosino: eosinophils  
neutro: neutrophils  
mega: megakaryocytes  
mono: monocytes

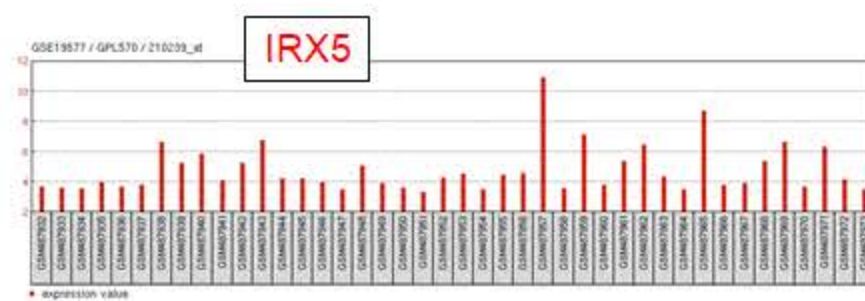
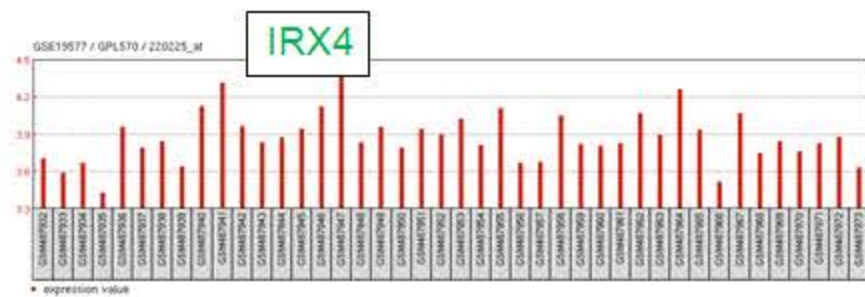
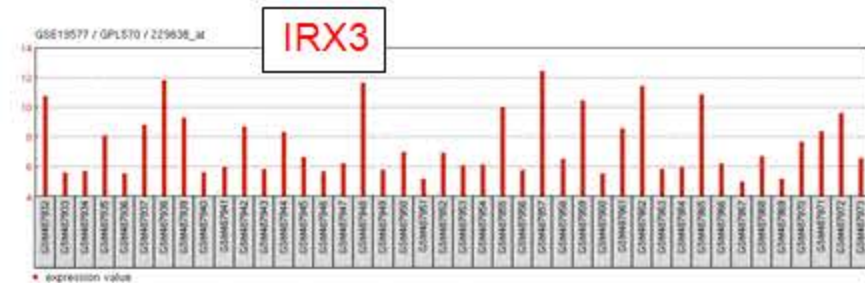
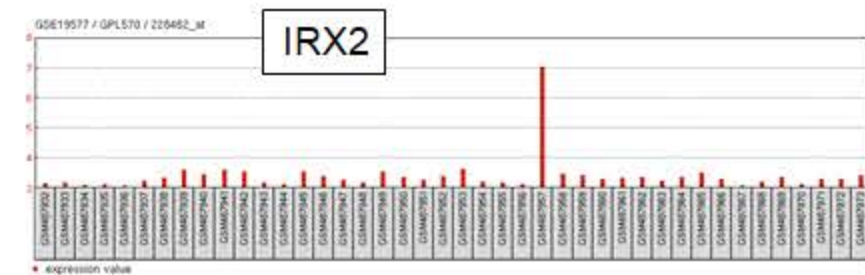
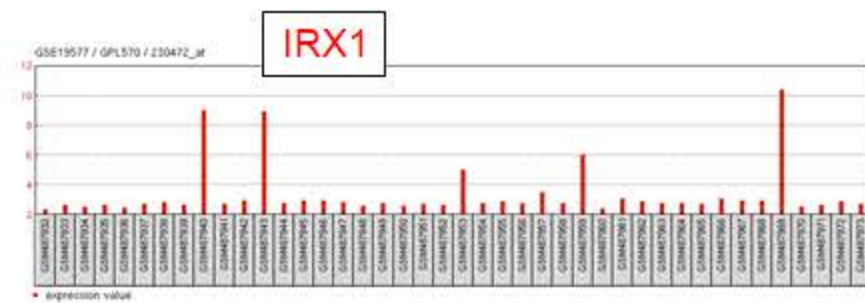




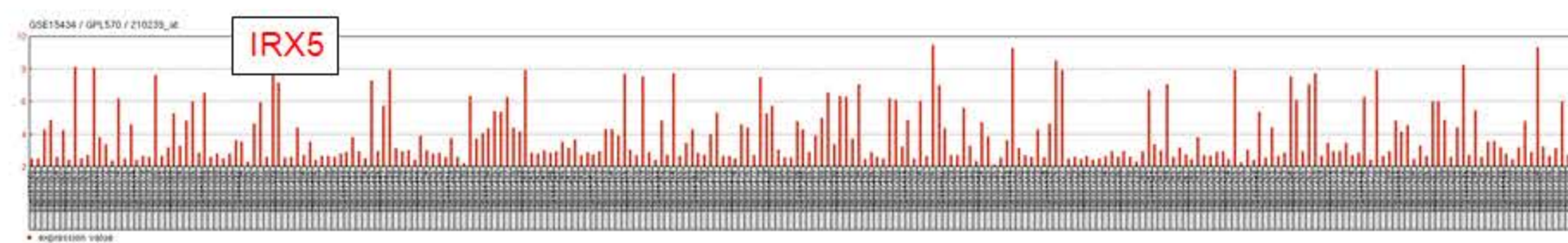
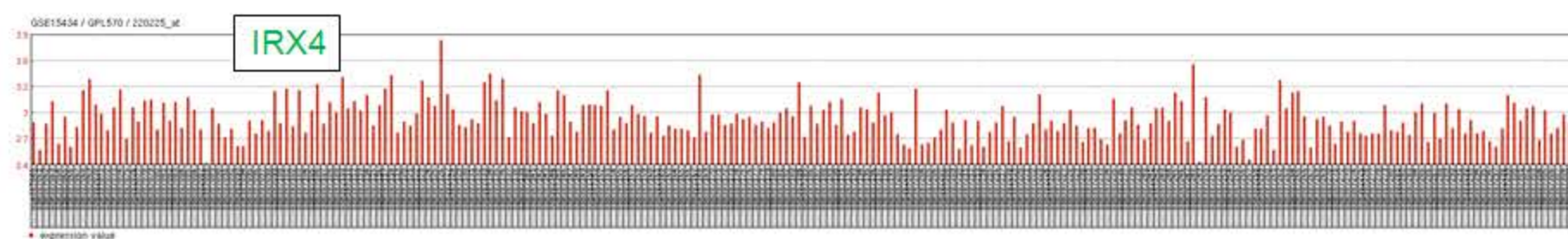
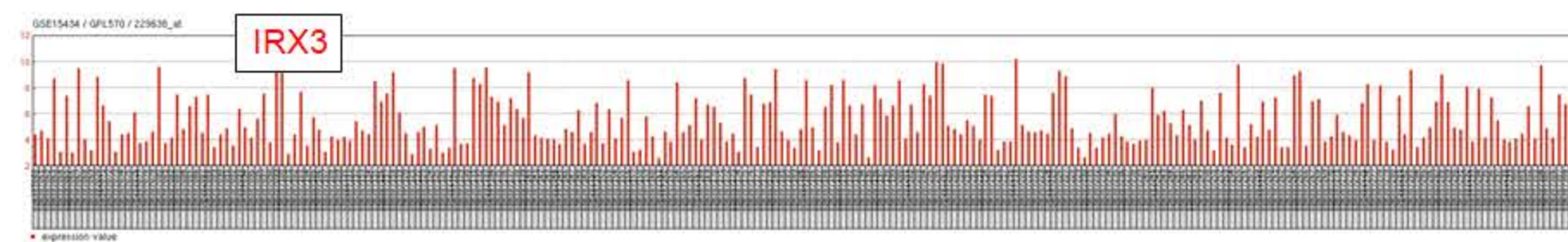
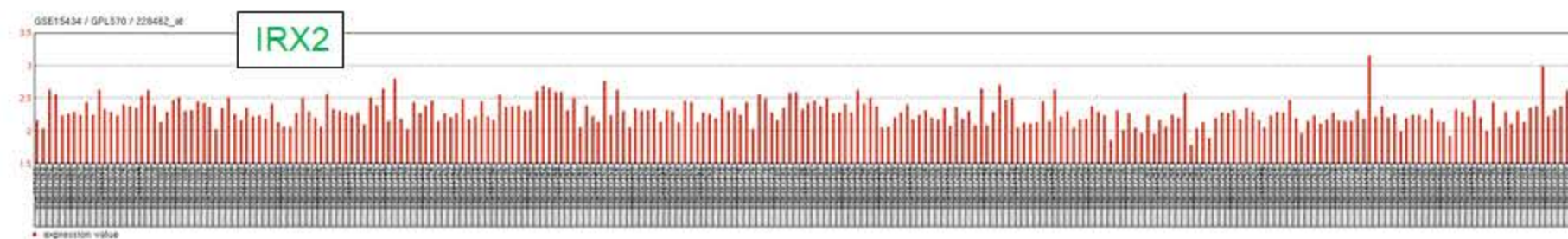
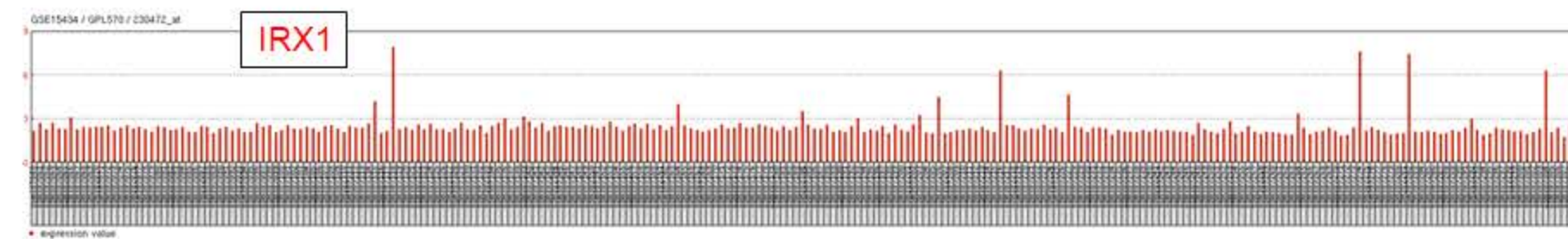
RNA-seq expression data for IRX1, IRX2, IRX3, IRX4, IRX5 and IRX6 were obtained from the Human Protein Atlas. For each gene, activities are shown in entities belonging to the hematopoietic (above) or alternative tissue compartment (below). Blue arrows indicate selected tissues which were analyzed in this study.



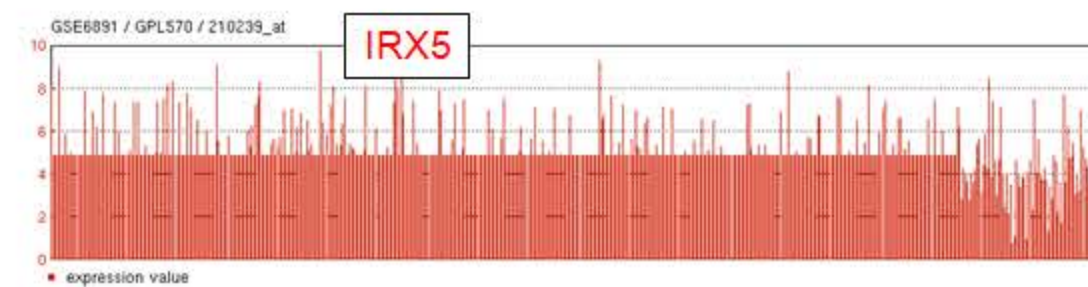
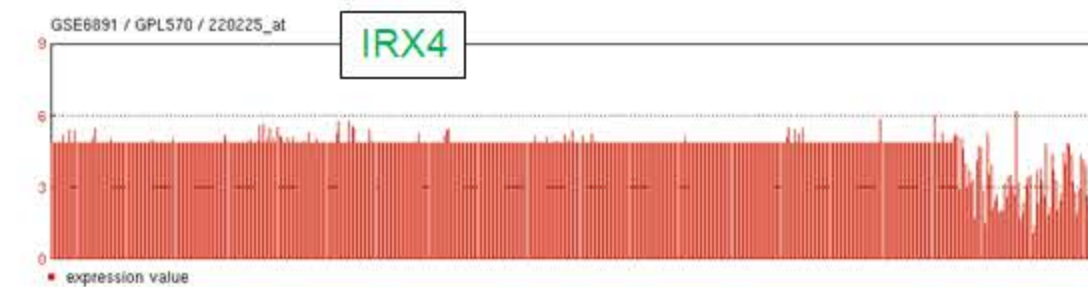
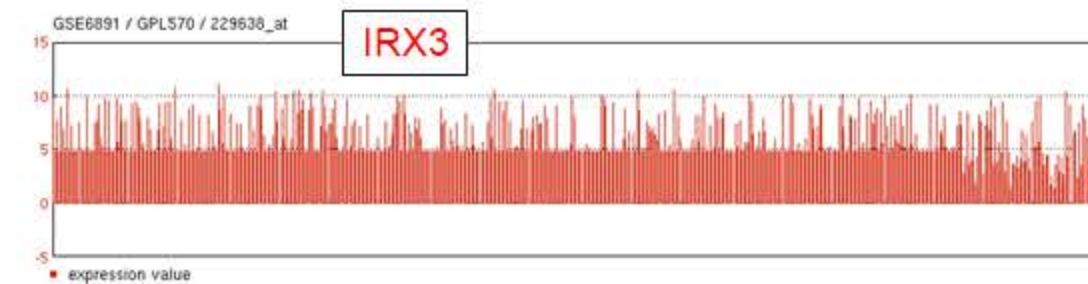
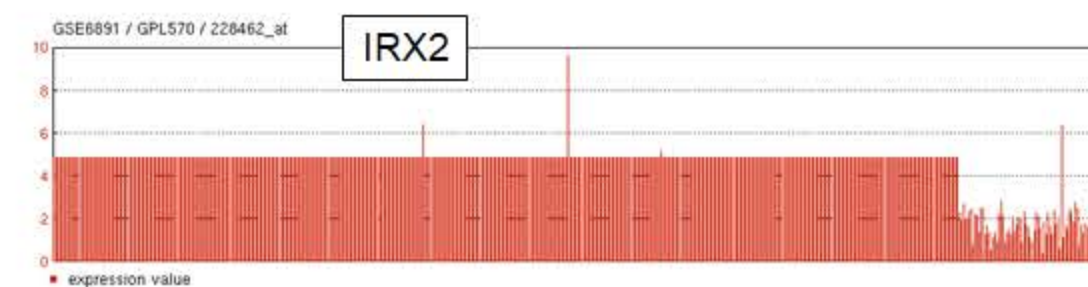
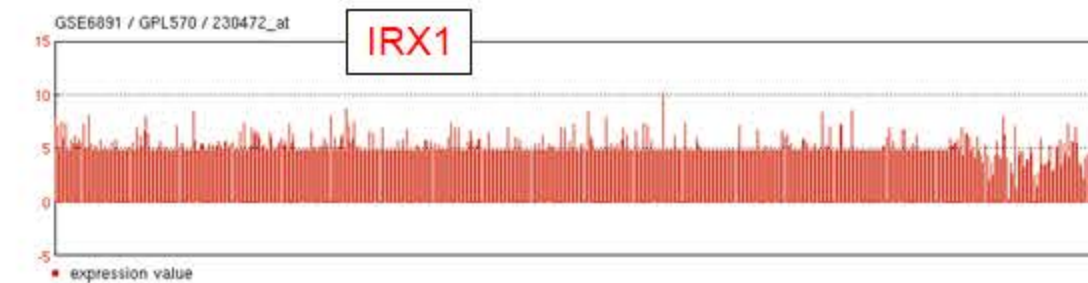
AML dataset GSE19577



AML dataset GSE15434

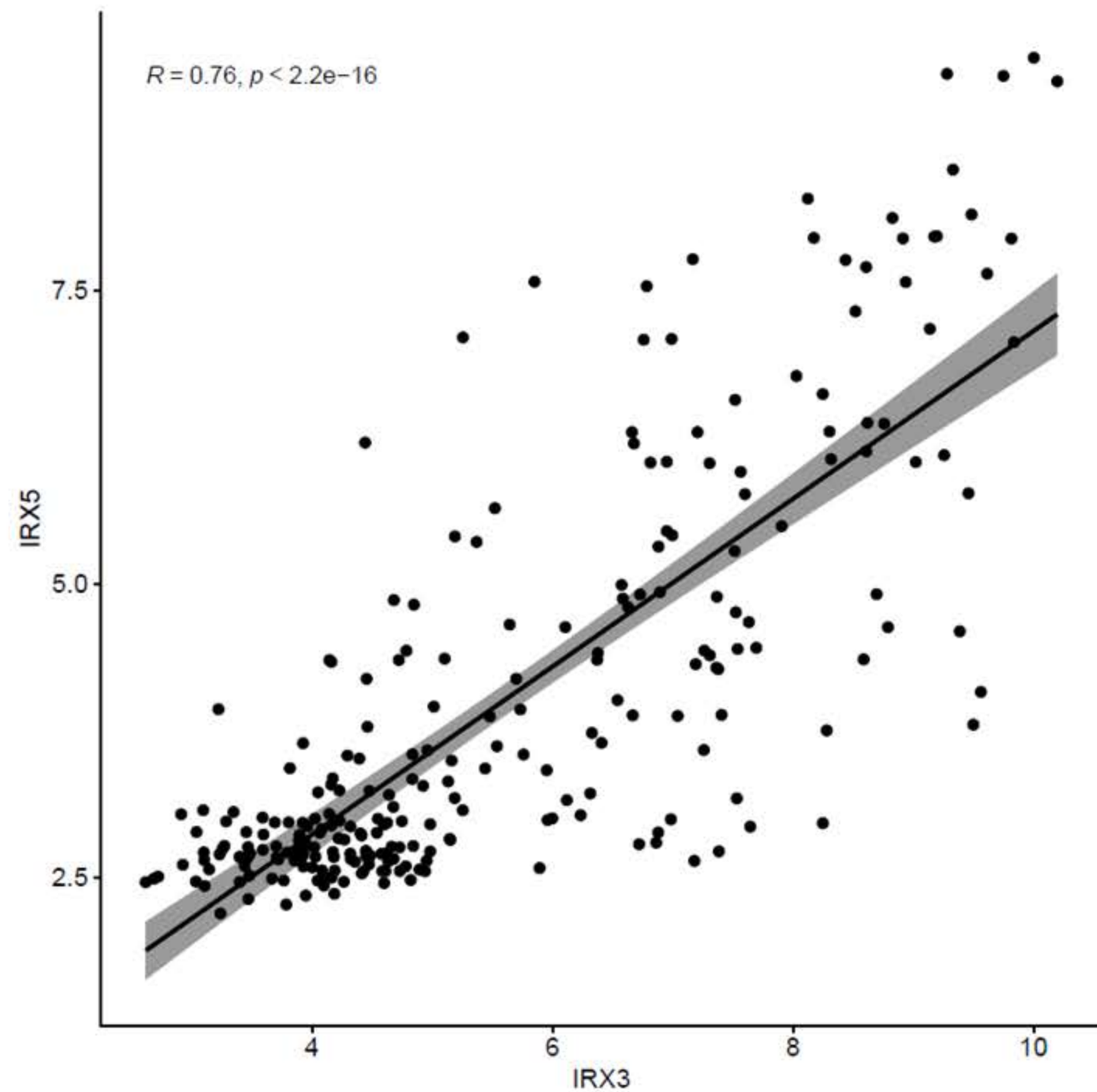


AML dataset GSE6891

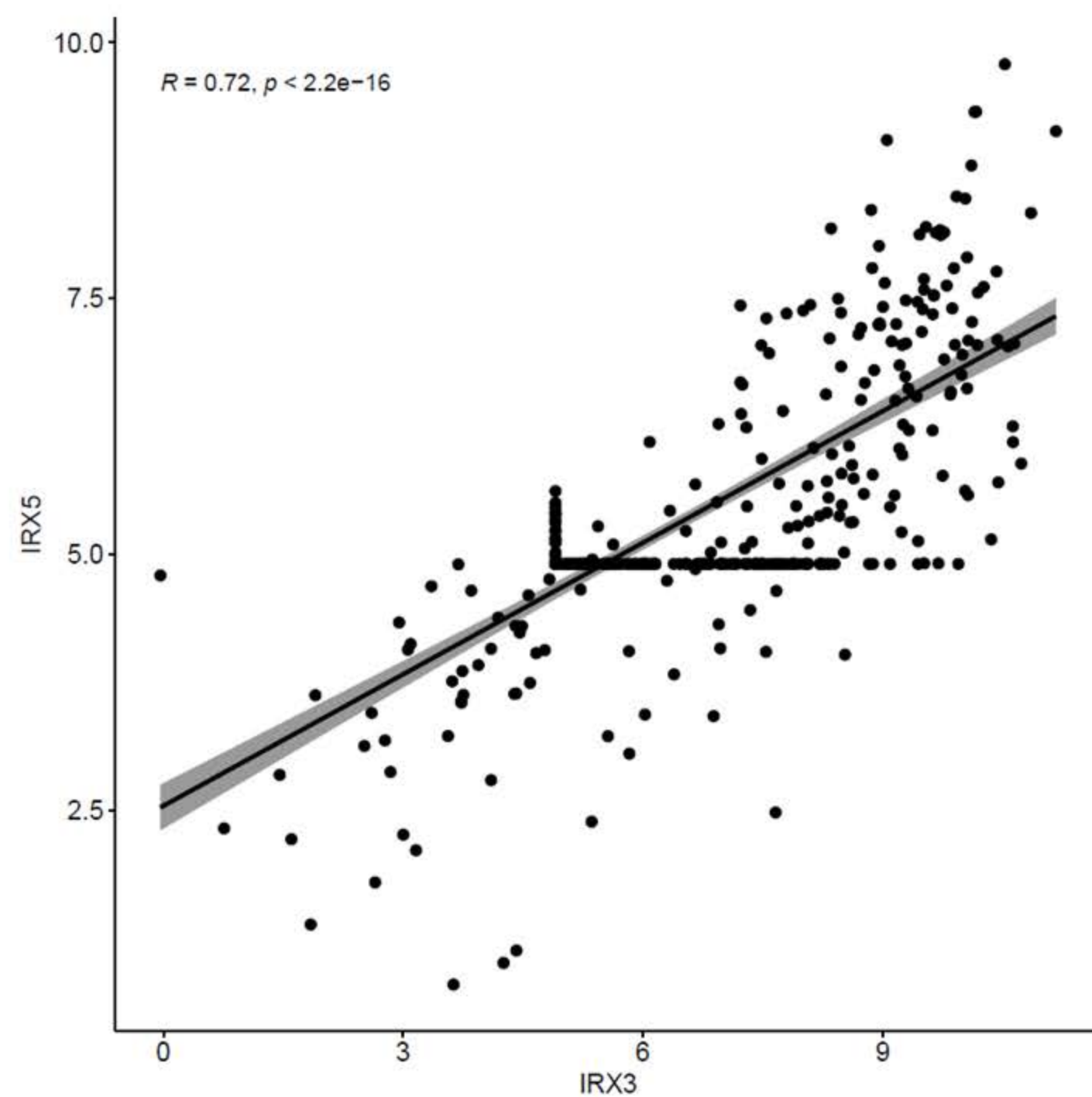




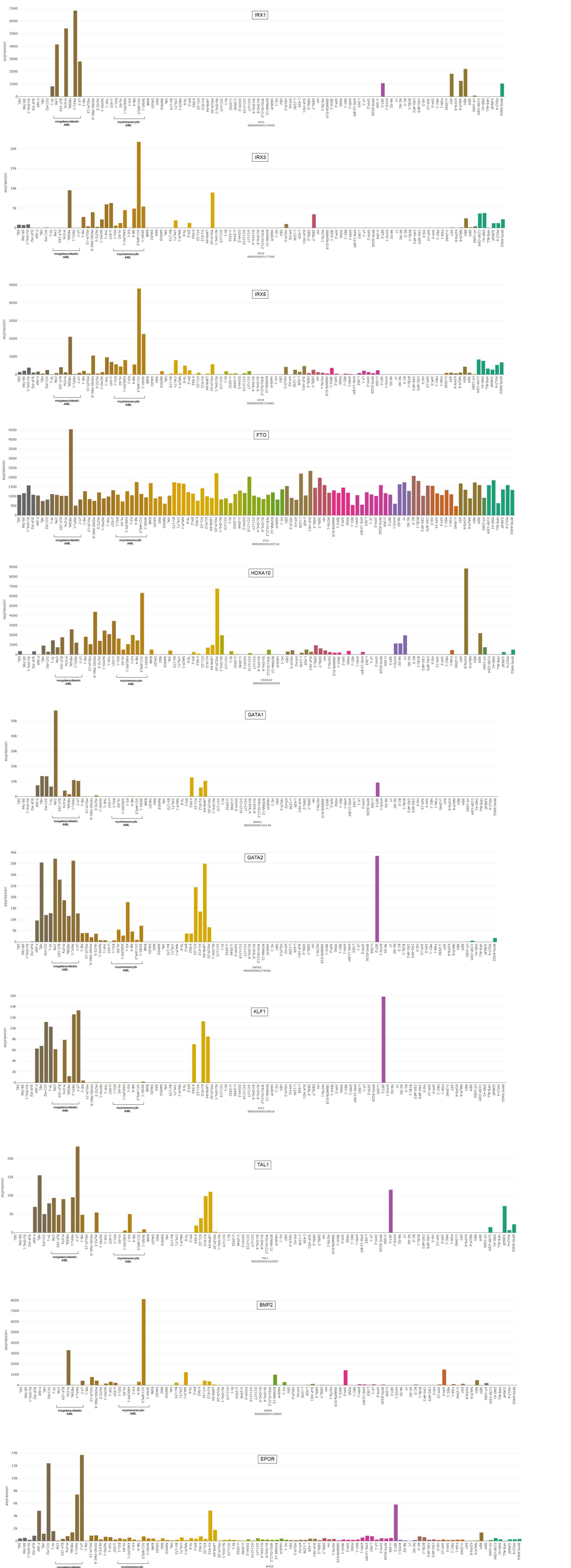
Coexpression-analysis of IRX3 and IRX5 for AML dataset GSE15434



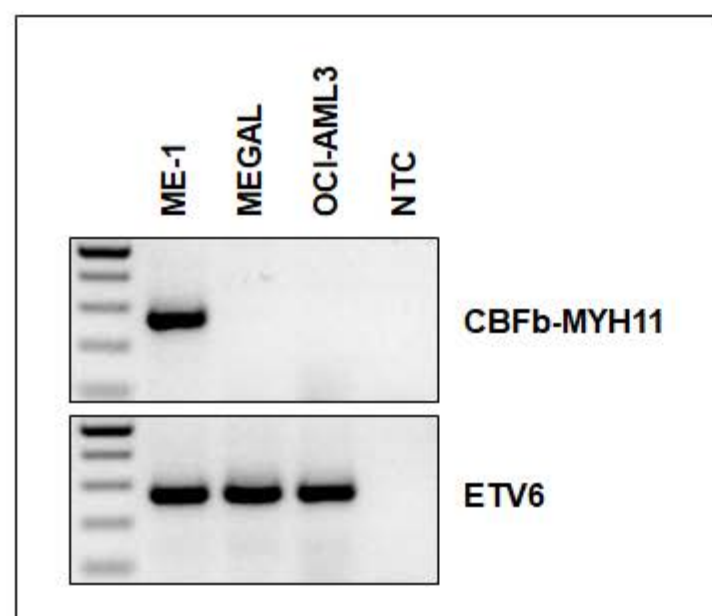
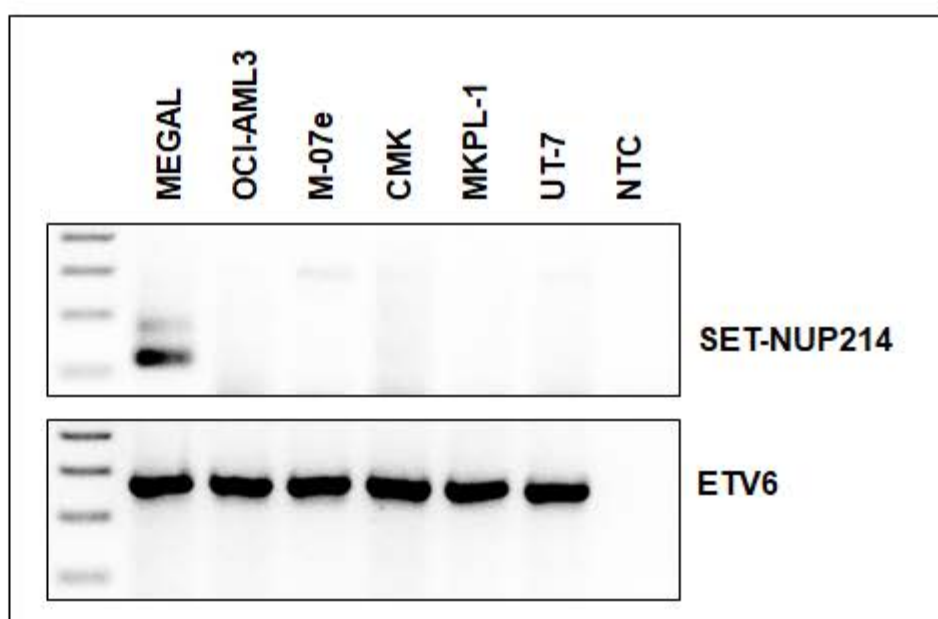
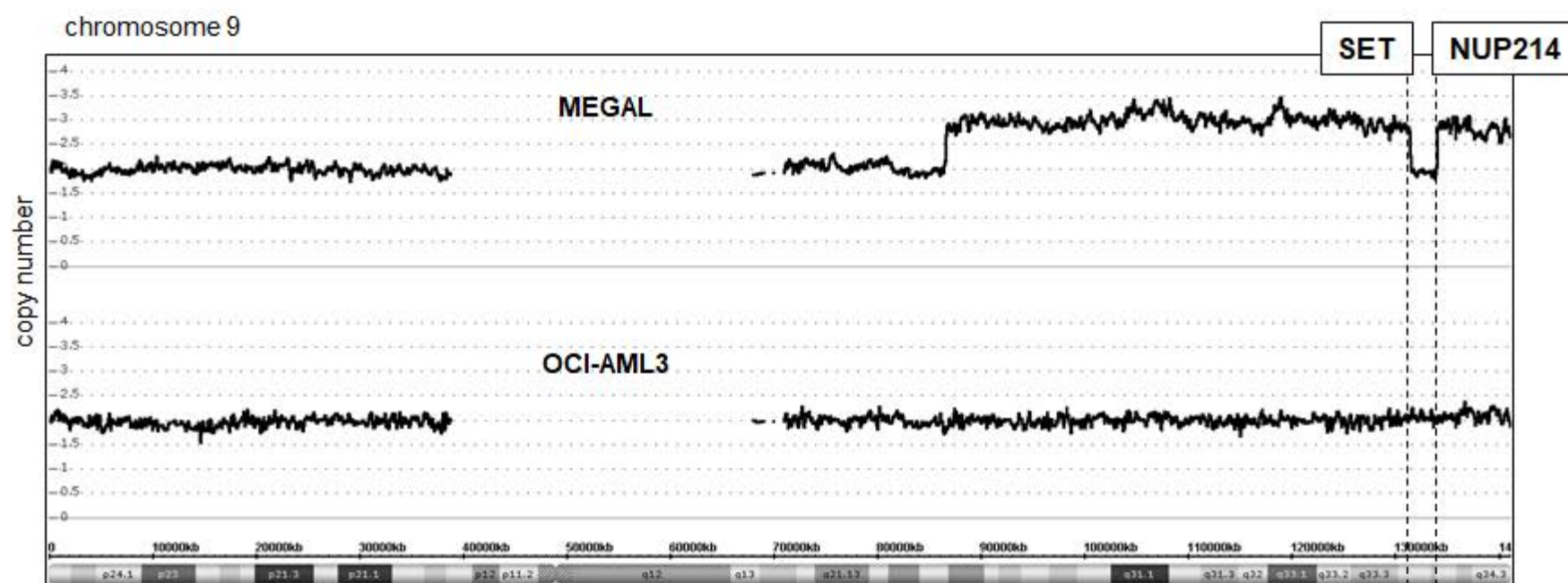
Coexpression-analysis of IRX3 and IRX5 for AML dataset GSE6891





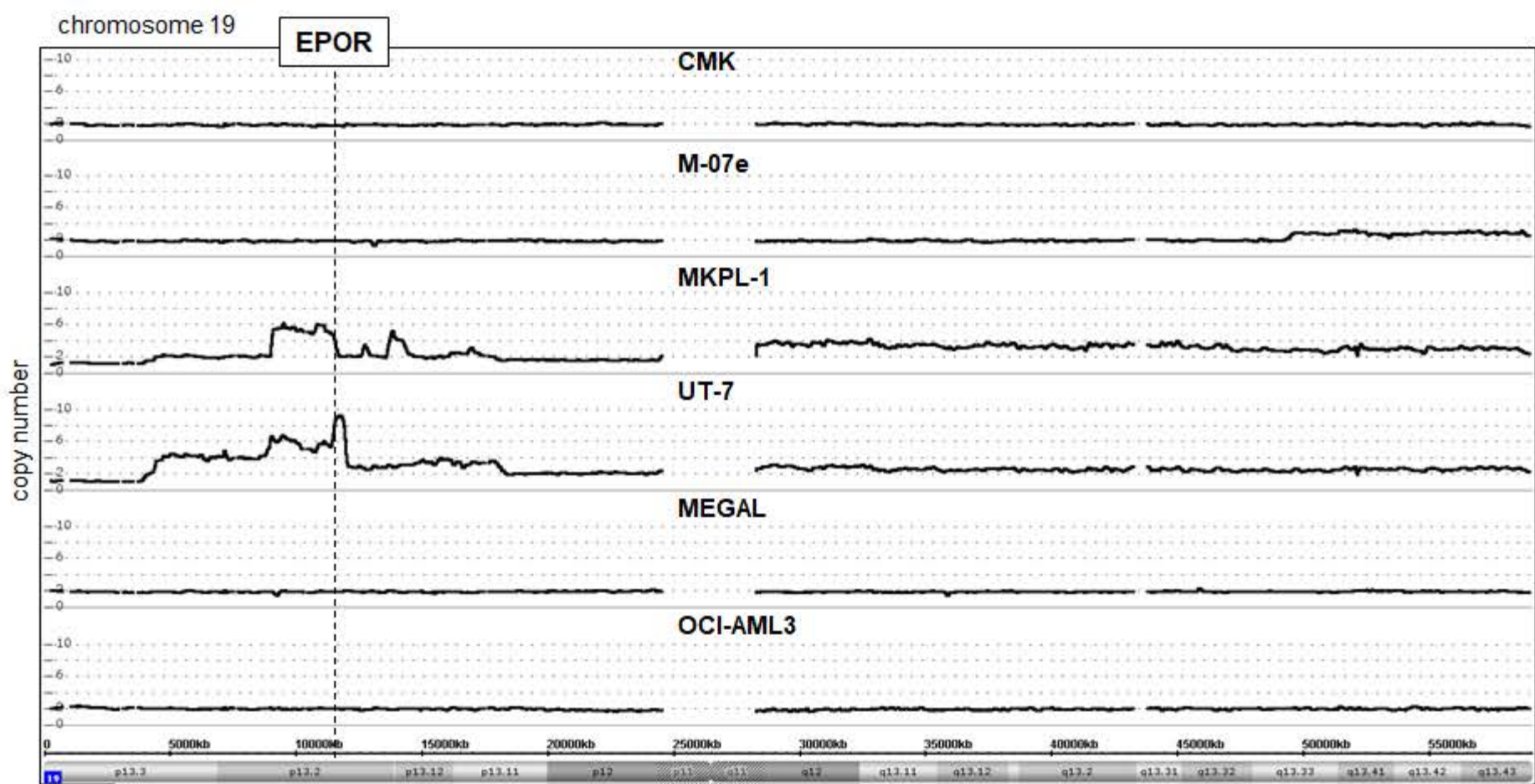
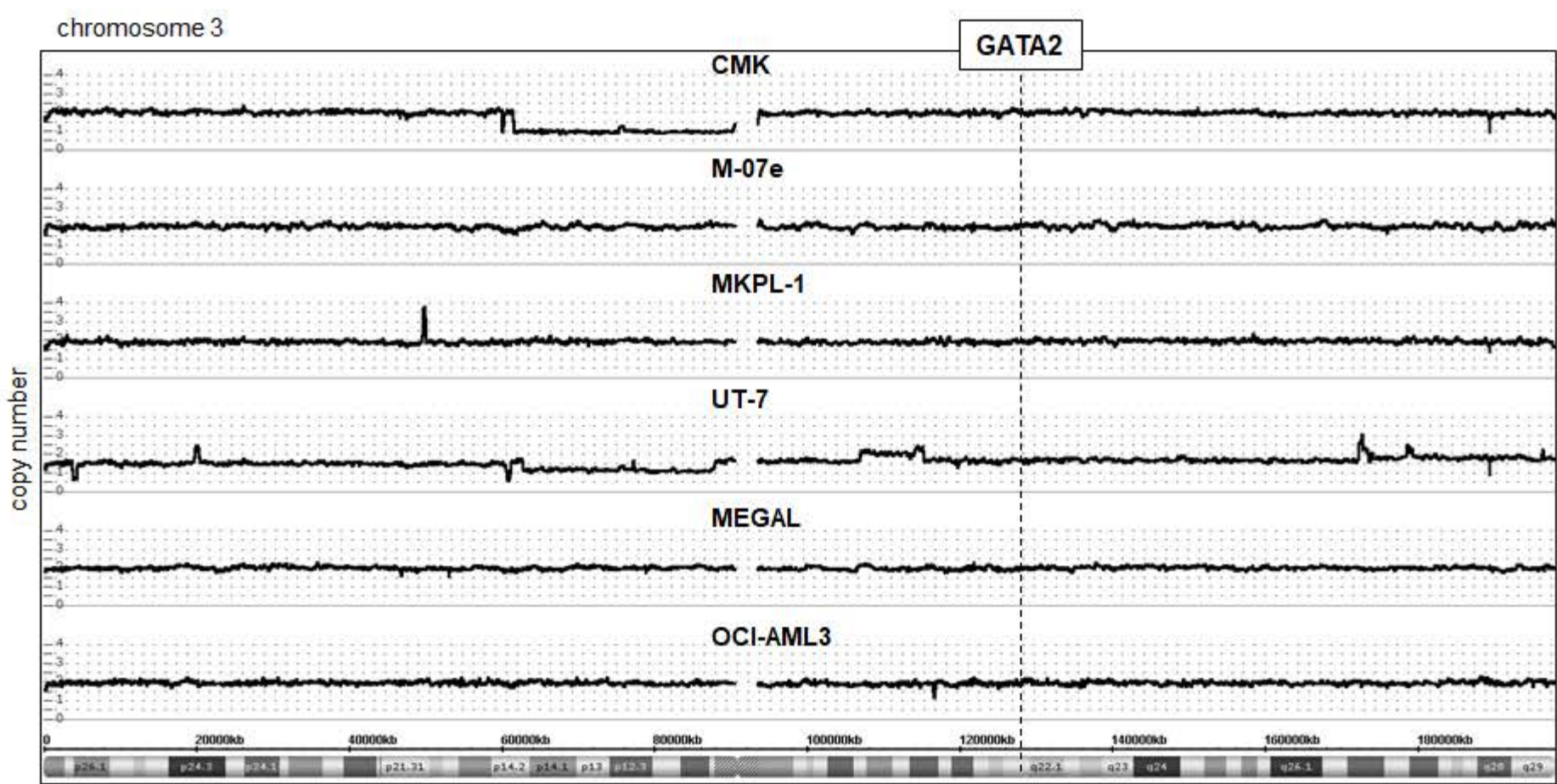
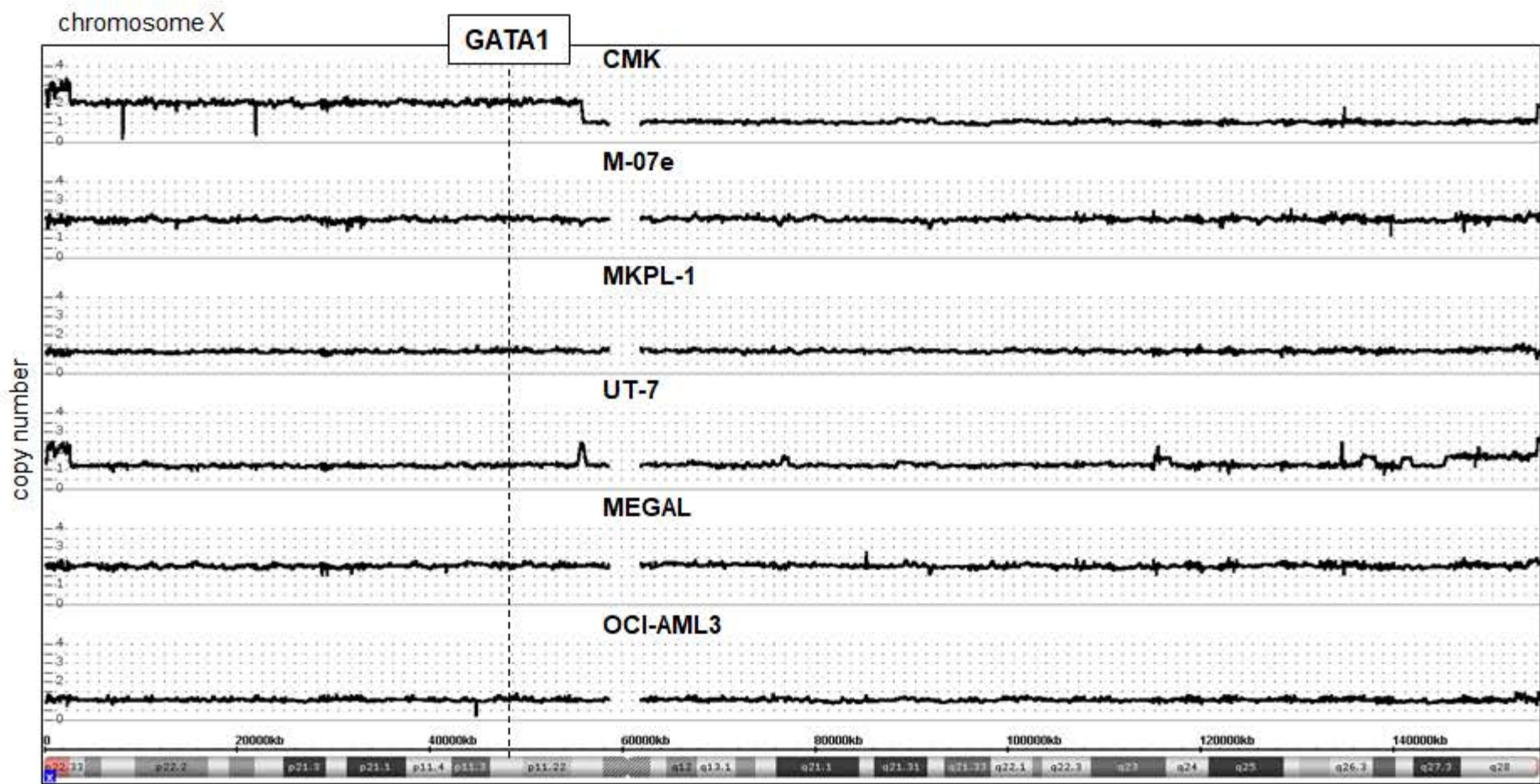




**A****B**

(A) RQ-PCR analysis of fusion gene CBFb-MYH11. AML cell line ME-1 served as positive control for the fusion transcript. ETV6 served as control for cDNA integrity. (B) Genomic profiling data for chromosome 9 from cell lines MEGAL and OCI-AML3 show a deletion in MEGAL at 9q34 which targets the genes SET and NUP214 (above). RQ-PCR analysis of fusion gene SET-NUP214 confirmed the presence in cell line MEGAL (below). ETV6 served as control for cDNA integrity. NTC: no template control.

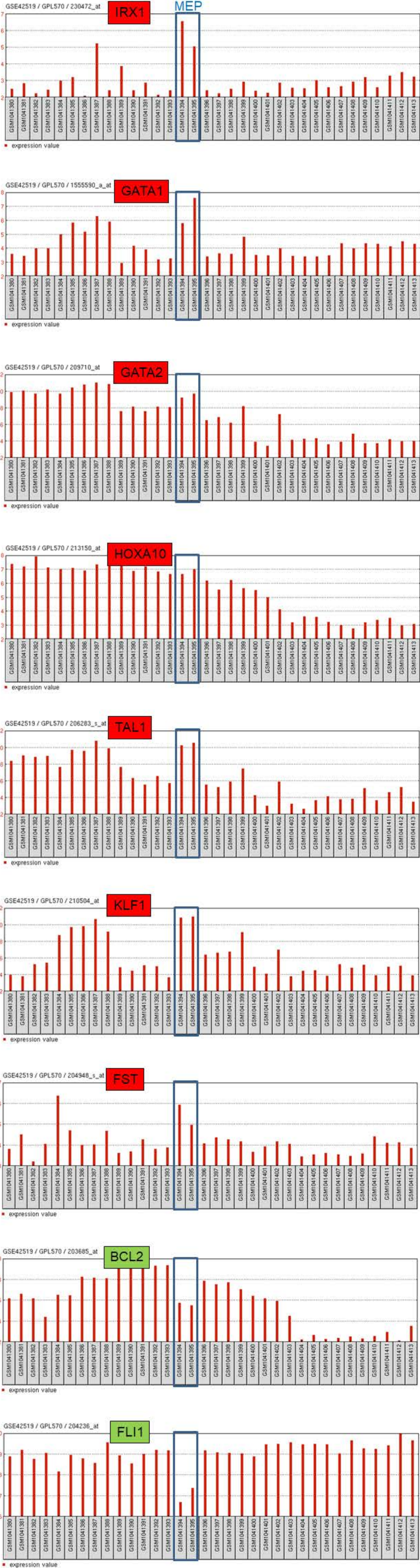




Genomic profiling data for chromosome X (above), chromosome 3 (middle), and chromosome 19 (below) from cell lines CMK, M-07e, MKPL-1, UT-7, MEGAL and OCI-AML3. The genes GATA1, GATA2 and EPOR are indicated.



Myelopoiesis dataset GSE42519



GSM1041383	HSC 4
GSM1041384	MPP 1
GSM1041385	MPP 2
GSM1041386	CMP 1
GSM1041387	CMP 2
GSM1041388	CMP 3
GSM1041389	GMP 1
GSM1041390	GMP 2
GSM1041391	GMP 3
GSM1041392	GMP 4
GSM1041393	GMP 5
GSM1041394	MEP 1
GSM1041395	MEP 2
GSM1041396	early_PM 1
GSM1041397	early_PM 2
GSM1041398	early_PM 3
GSM1041399	late_PM 1
GSM1041400	late_PM 2
GSM1041401	late_PM 3
GSM1041402	MY 1
GSM1041403	MY 2
GSM1041404	MM 1
GSM1041405	MM 2
GSM1041406	MM 3
GSM1041407	BC 1
GSM1041408	BC 2
GSM1041409	BC 3
GSM1041410	BC 4
GSM1041411	PMN 1
GSM1041412	PMN 2
GSM1041413	PMN 3

Gene expression profiling data for selected genes from dataset GSE42519. The data for MEP are highlighted in blue. Genes elevated or decreased in MEP are indicated in red or green, respectively.