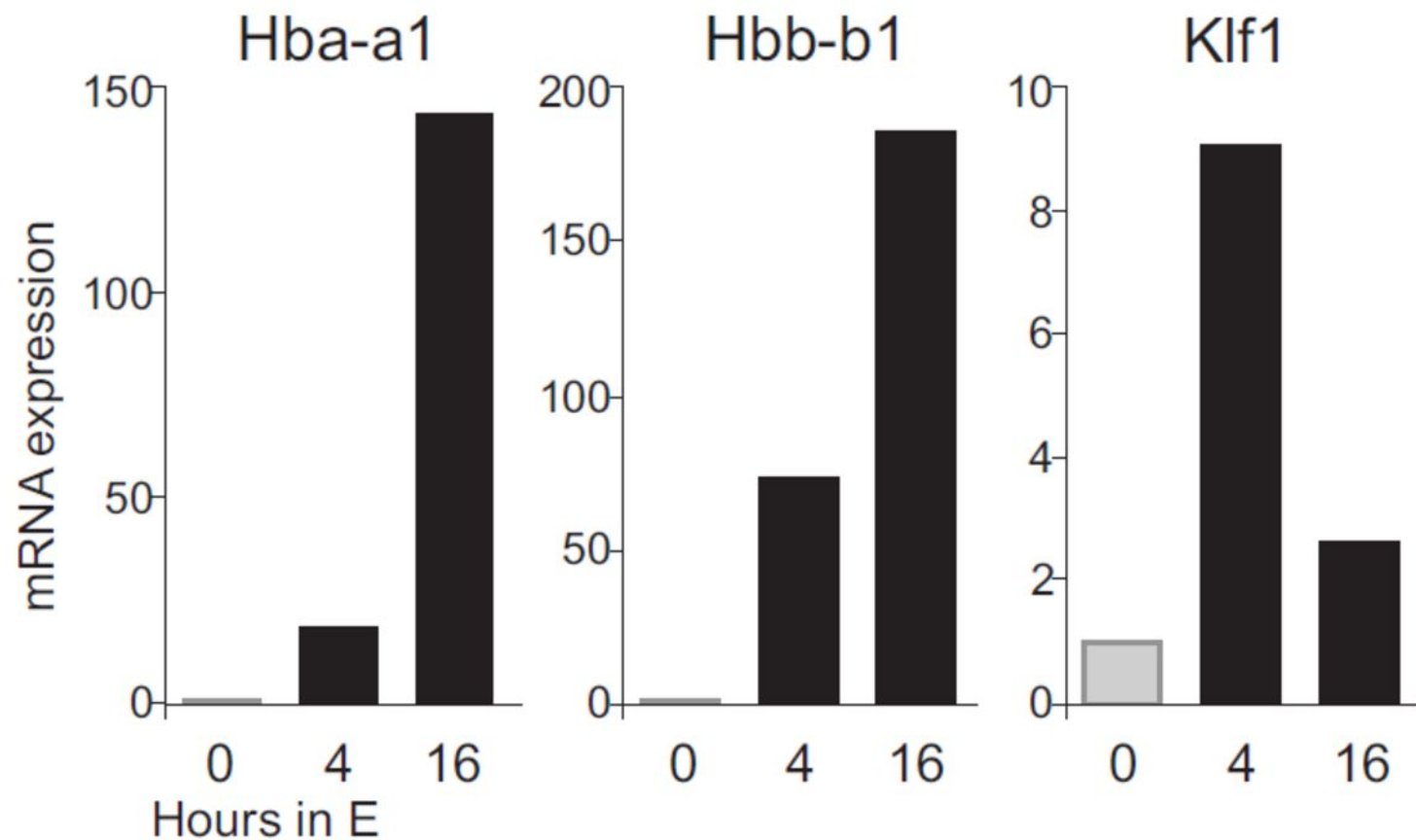


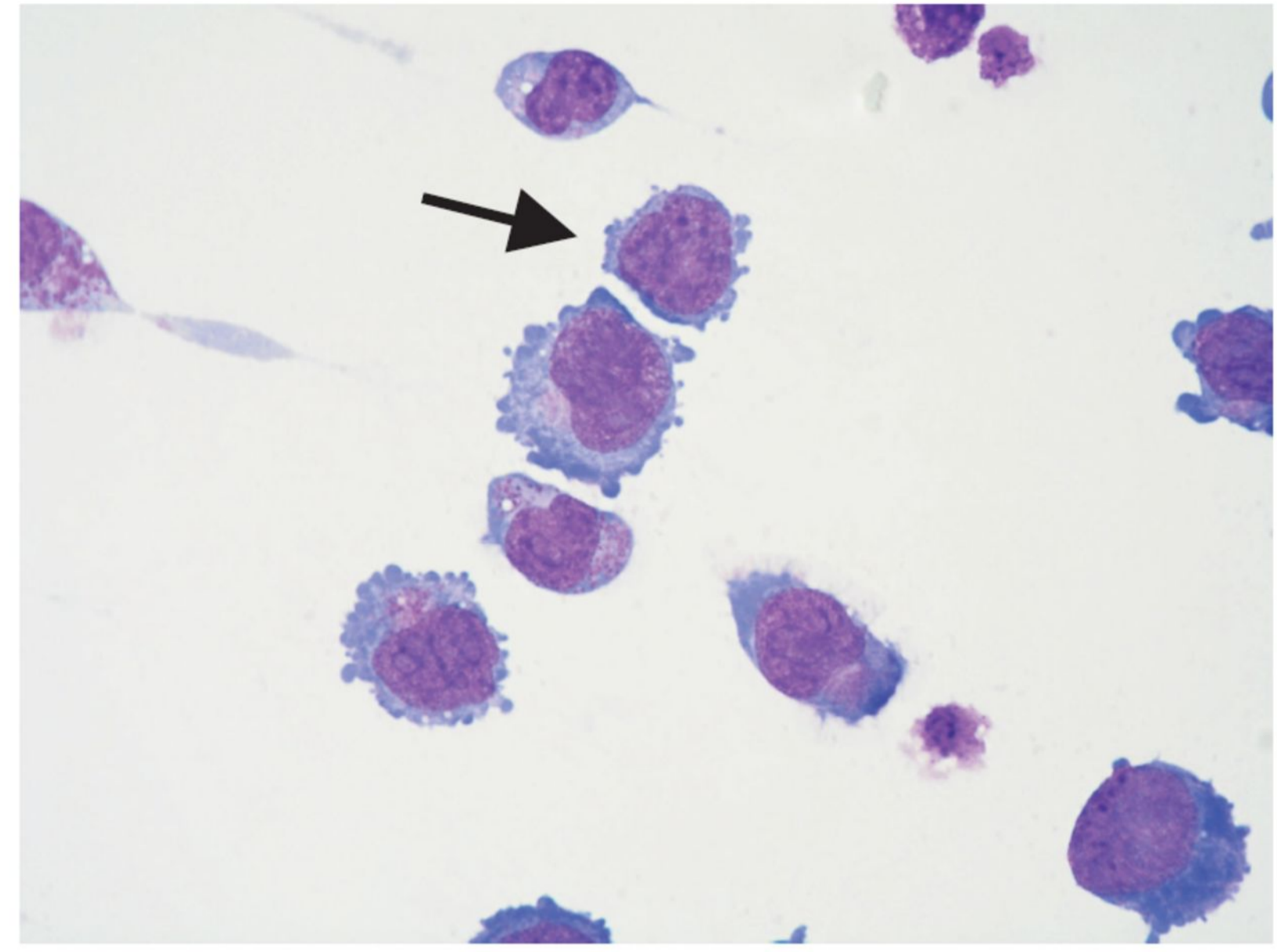
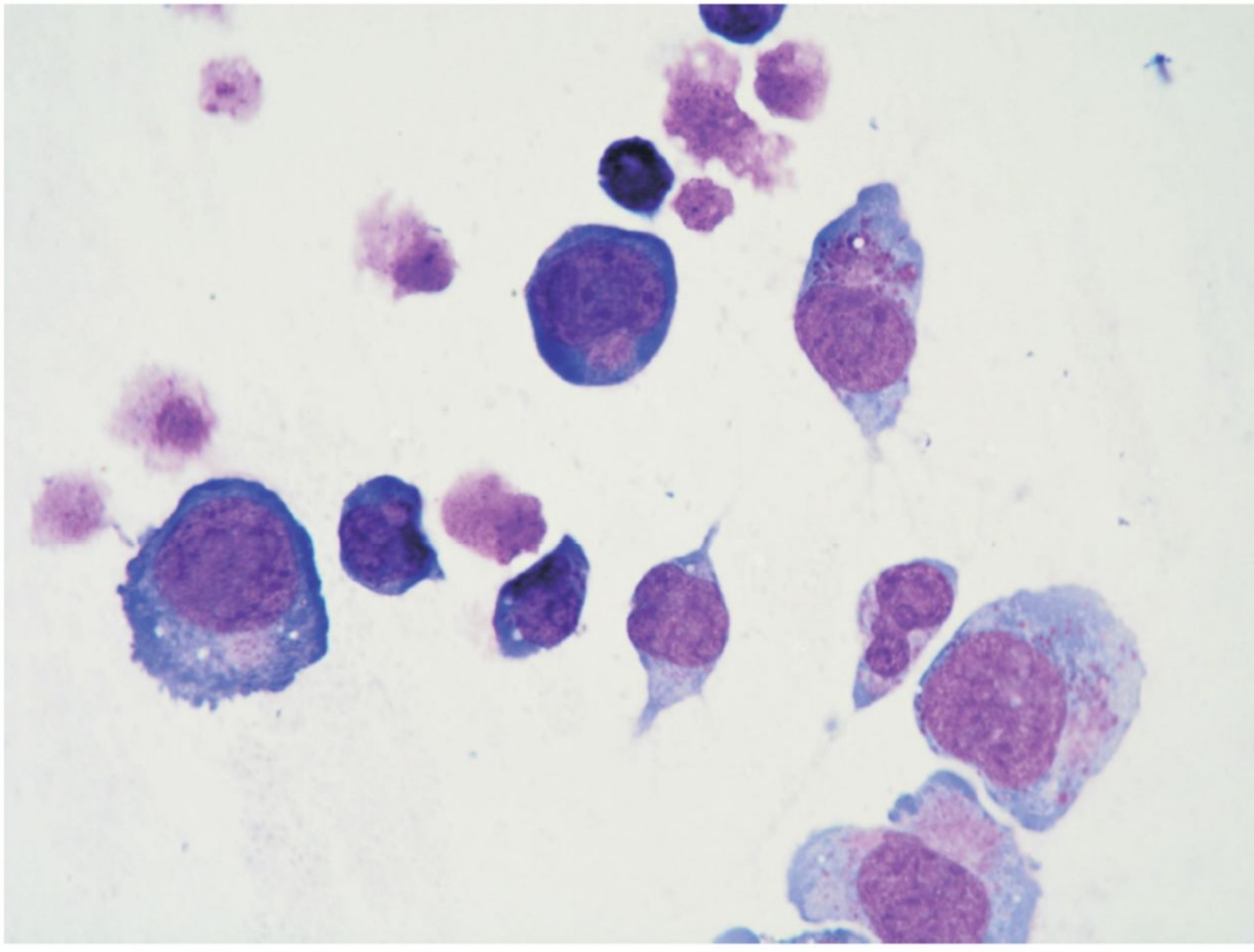
SF1



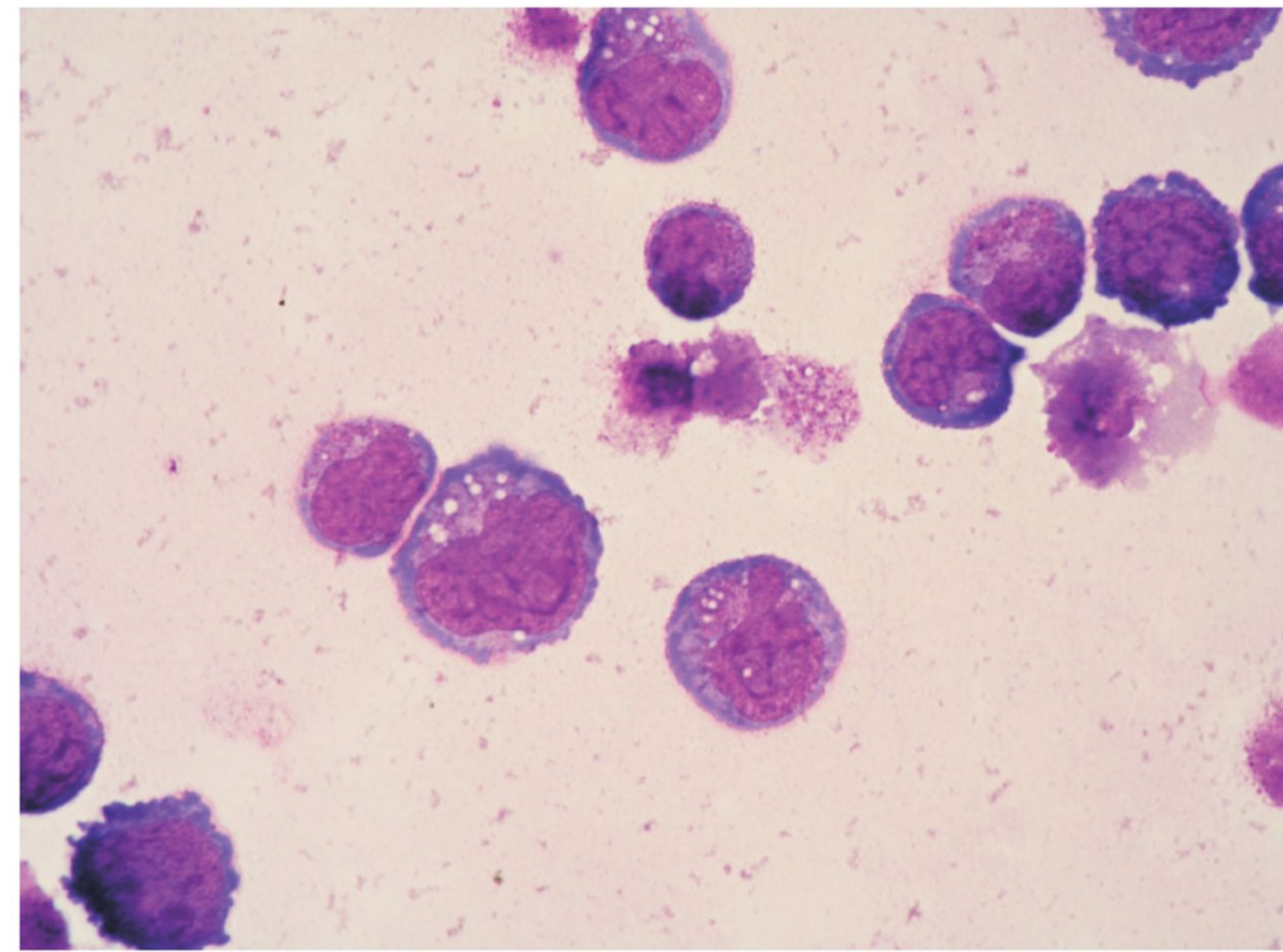
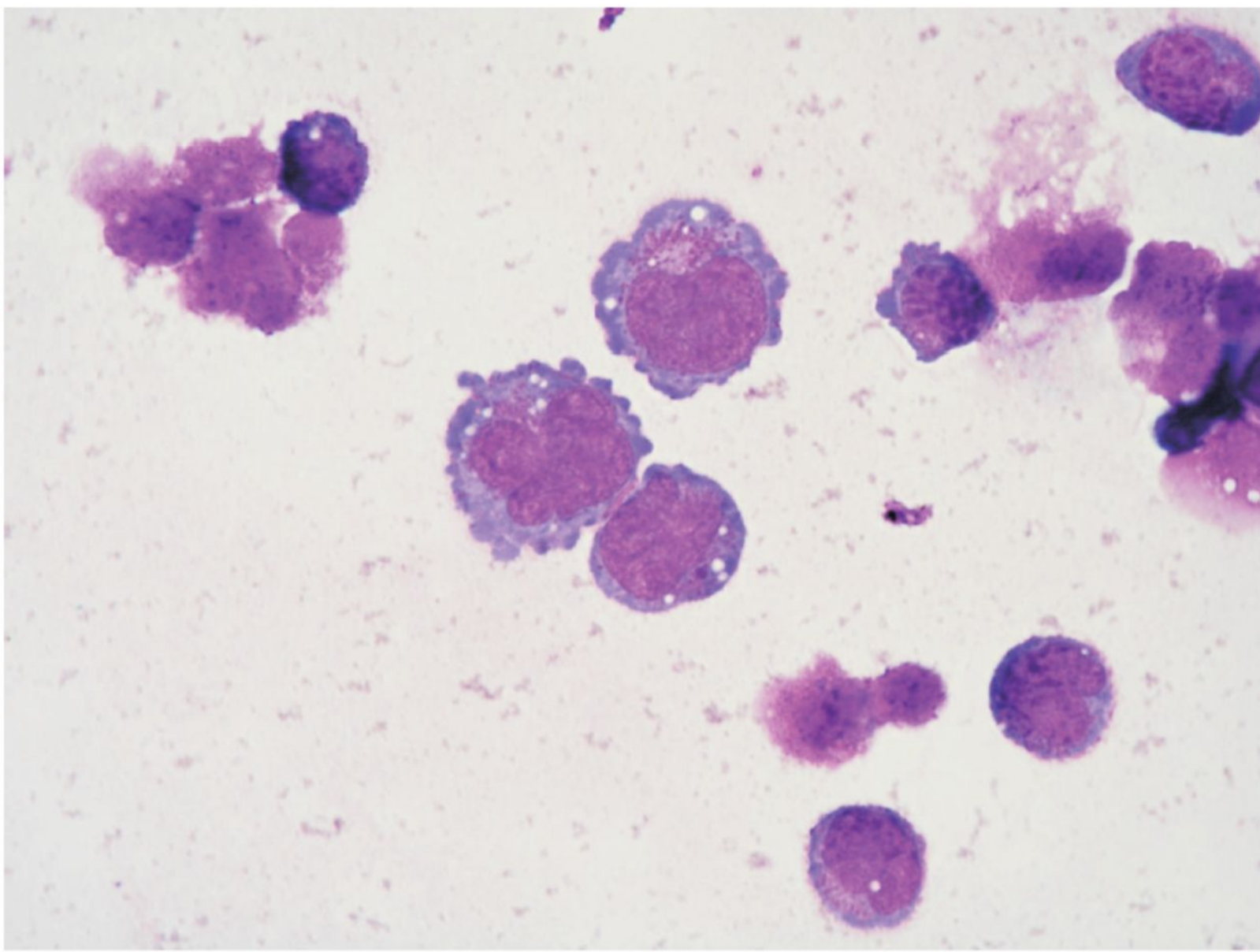
SF2

→ Proerythroblasts → Basophilic erythroblasts ↗ Atypical

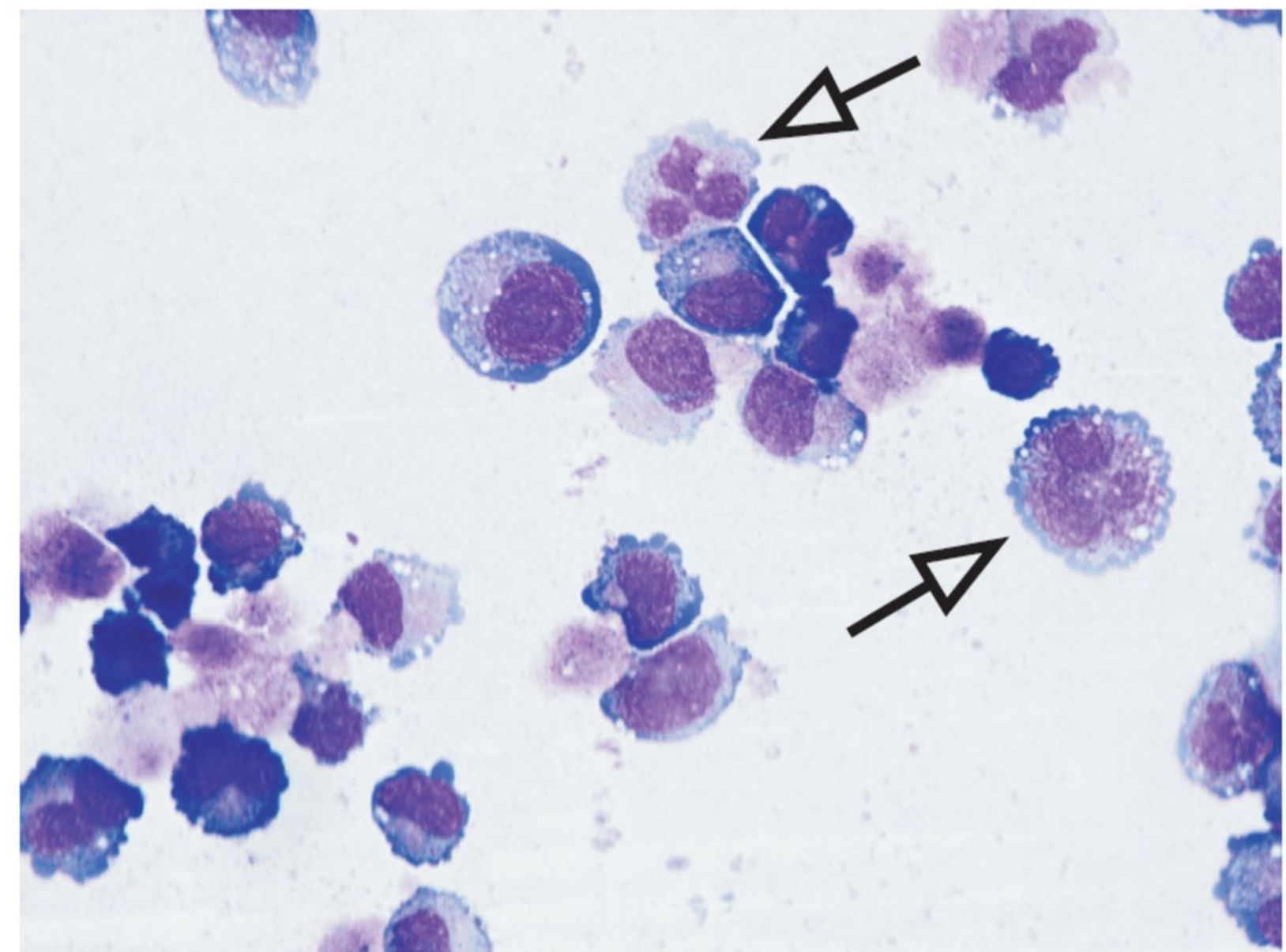
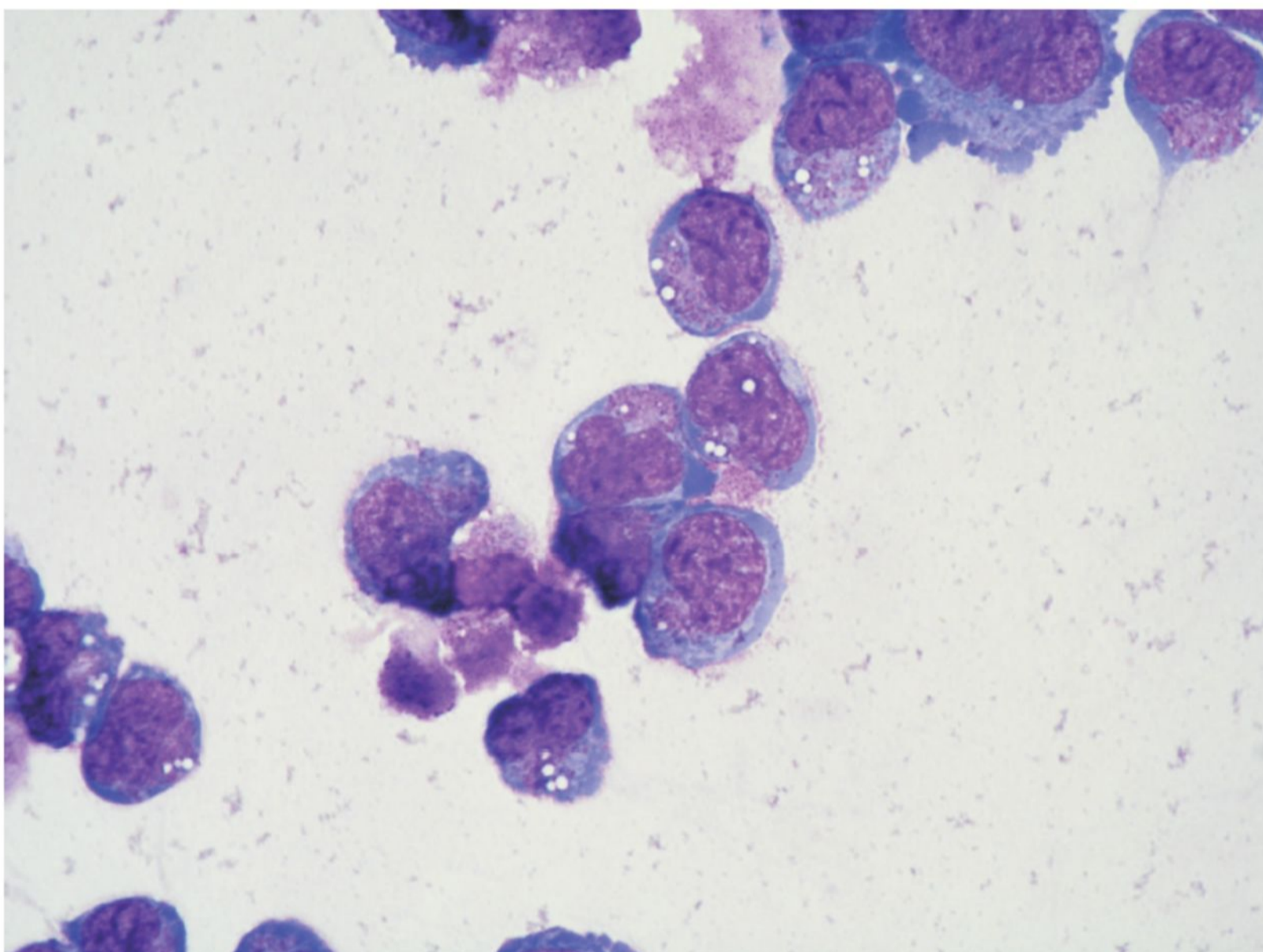
MEL



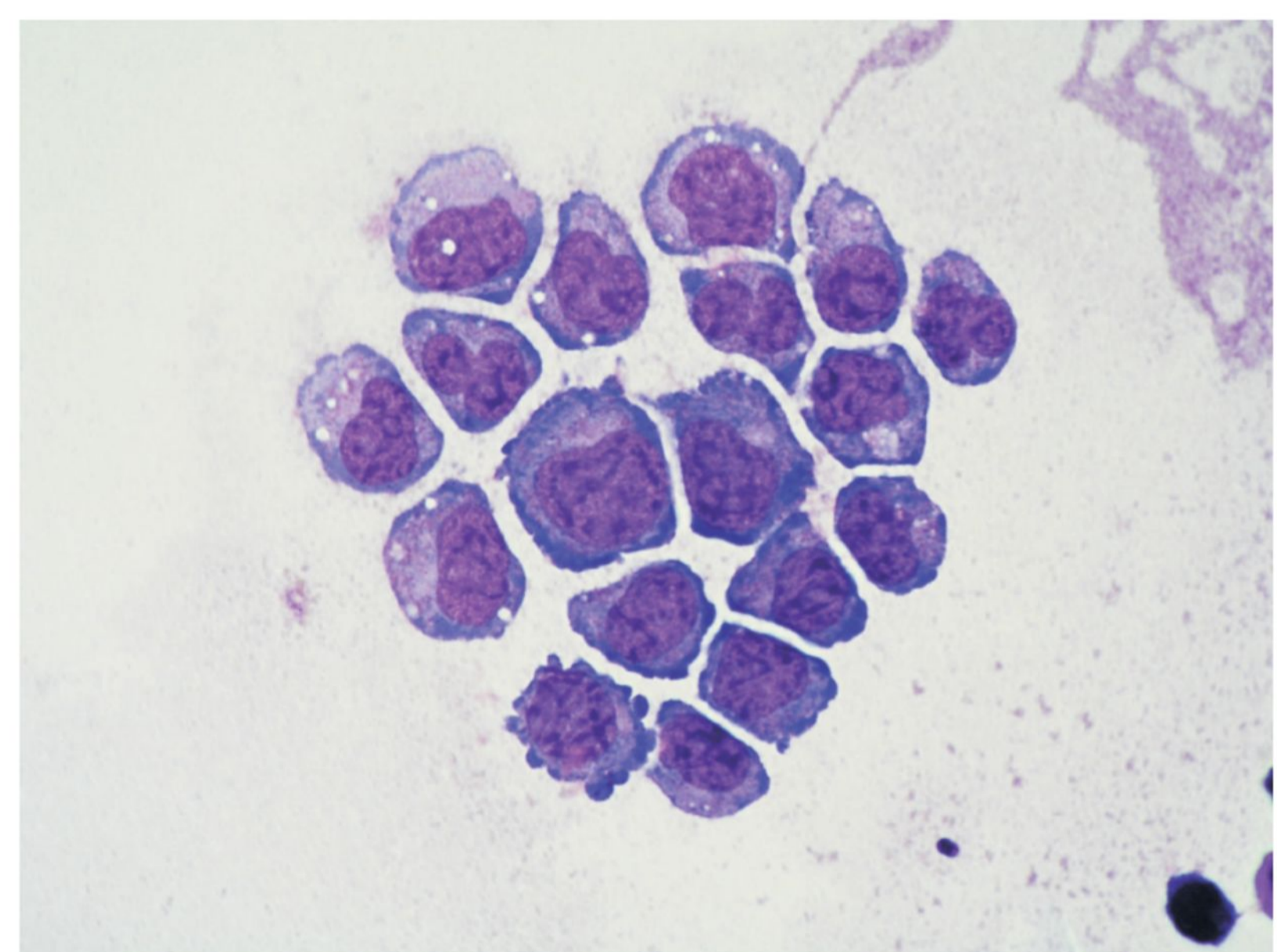
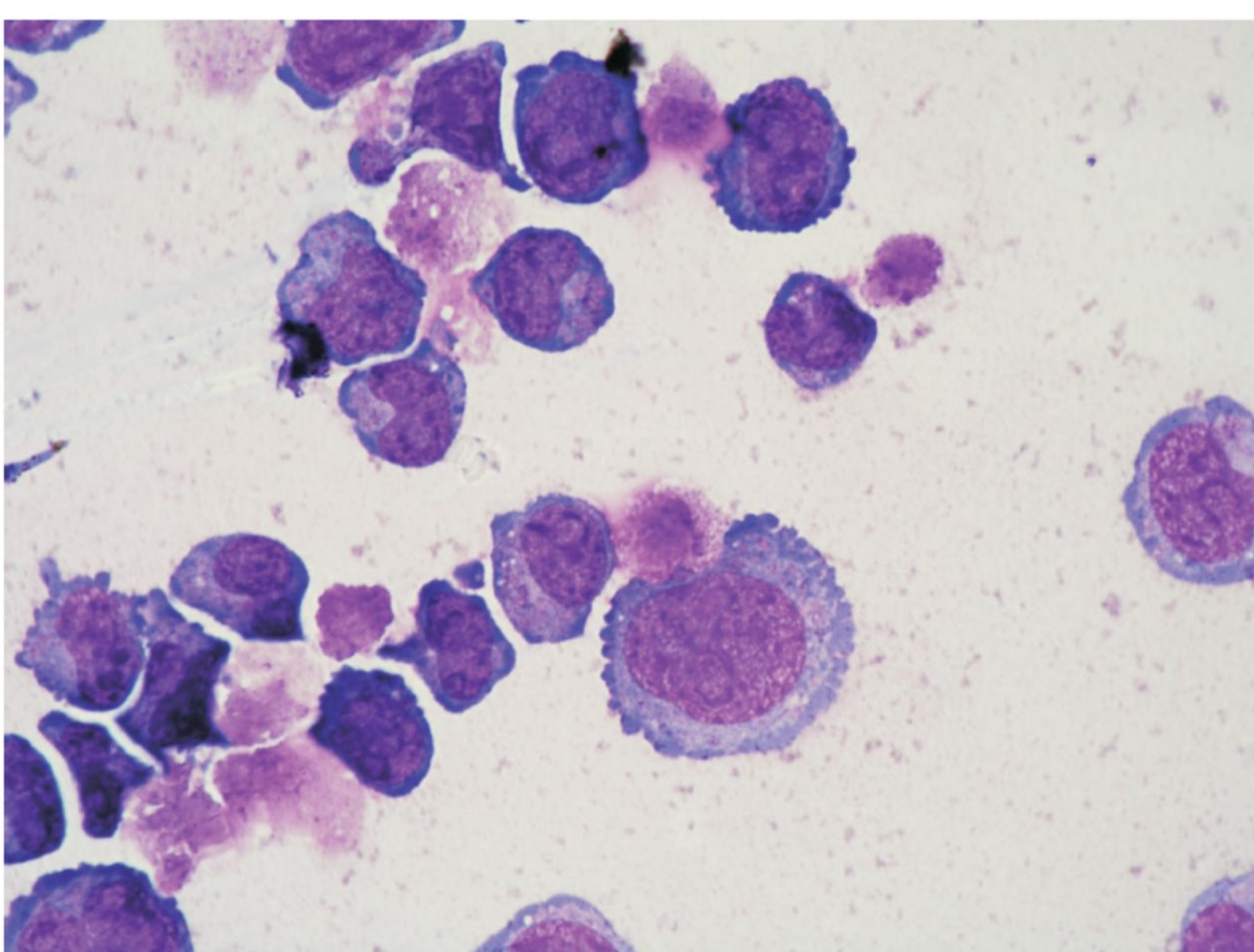
MEL^{PUER}



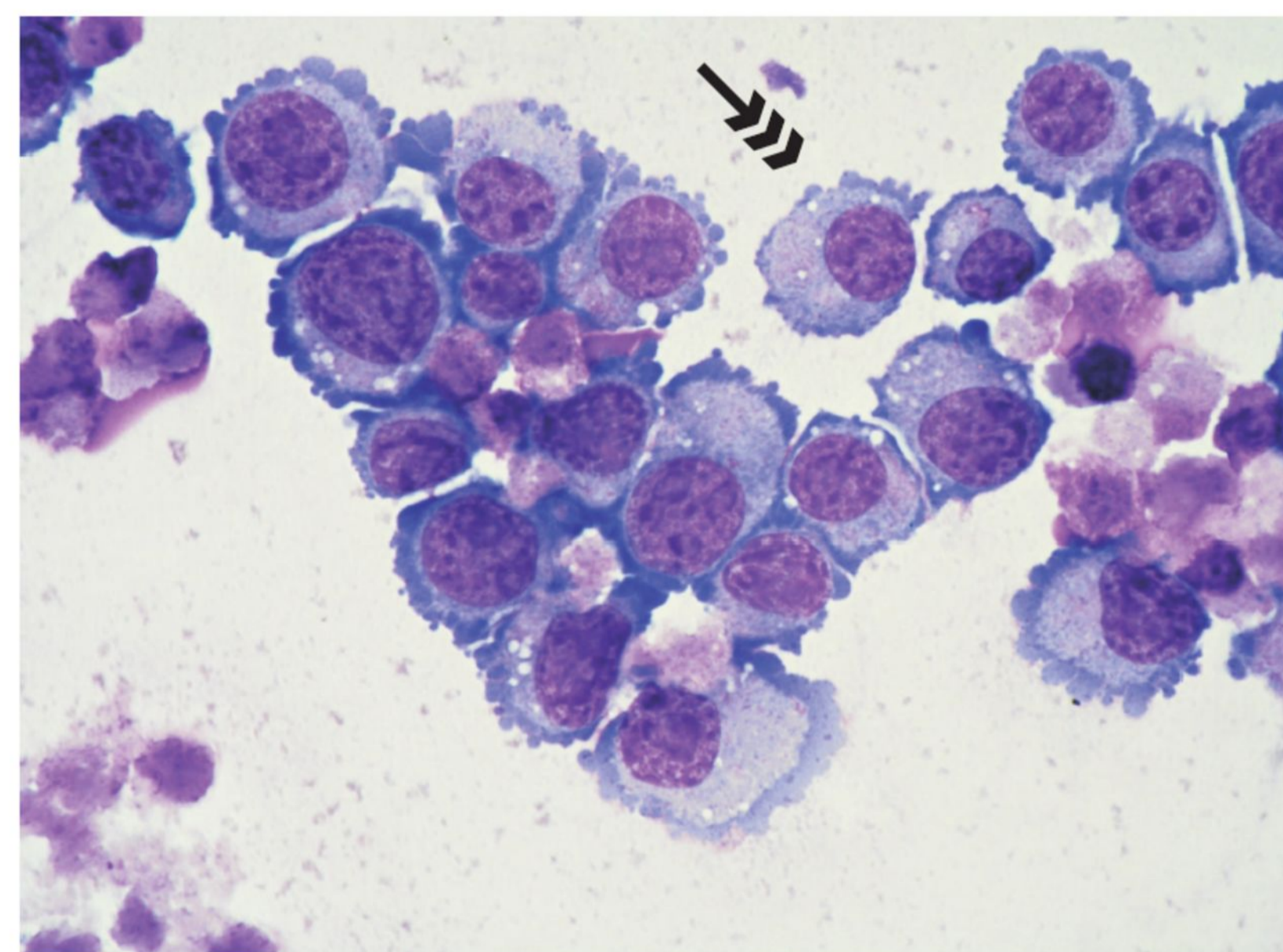
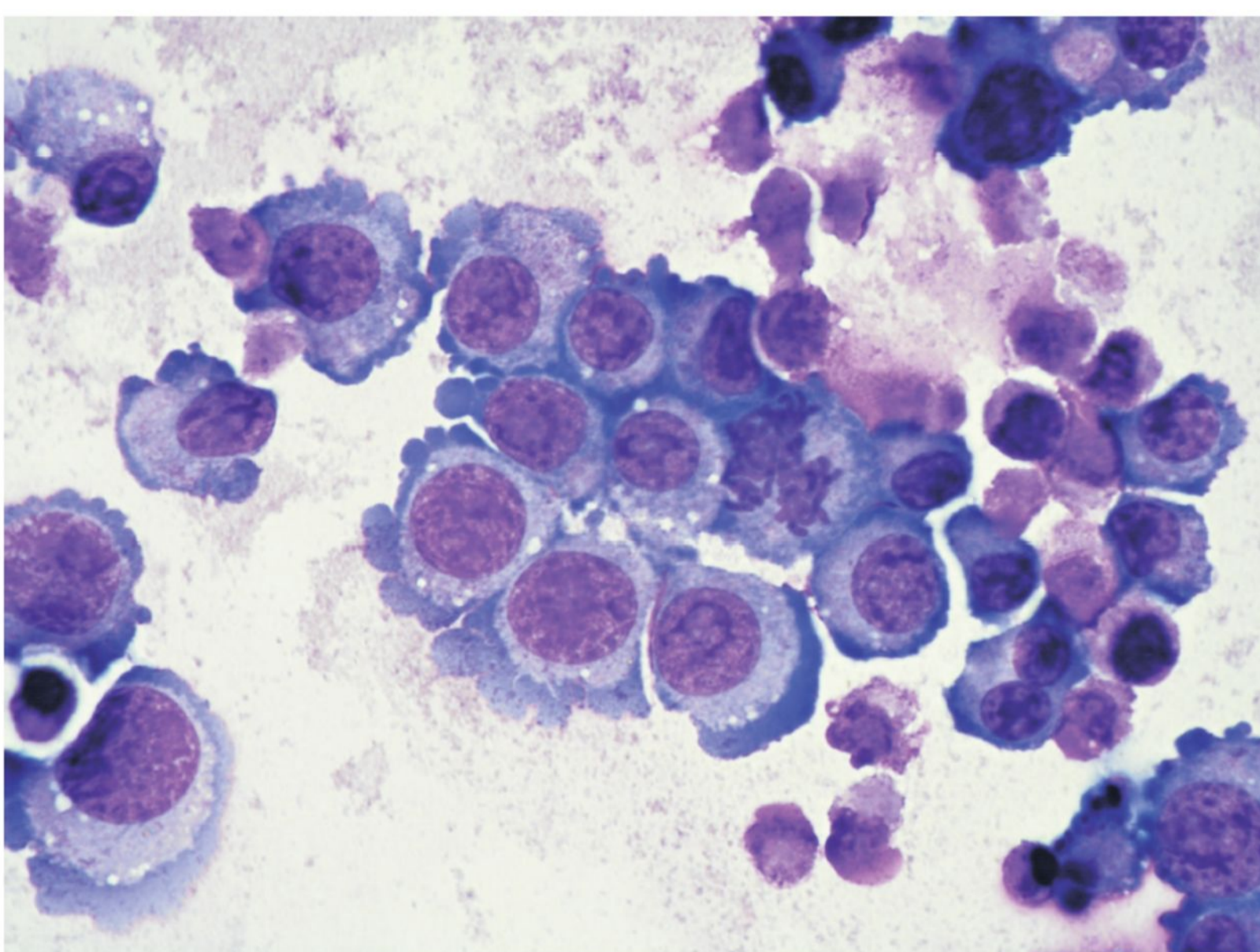
MEL^{PUER}+E



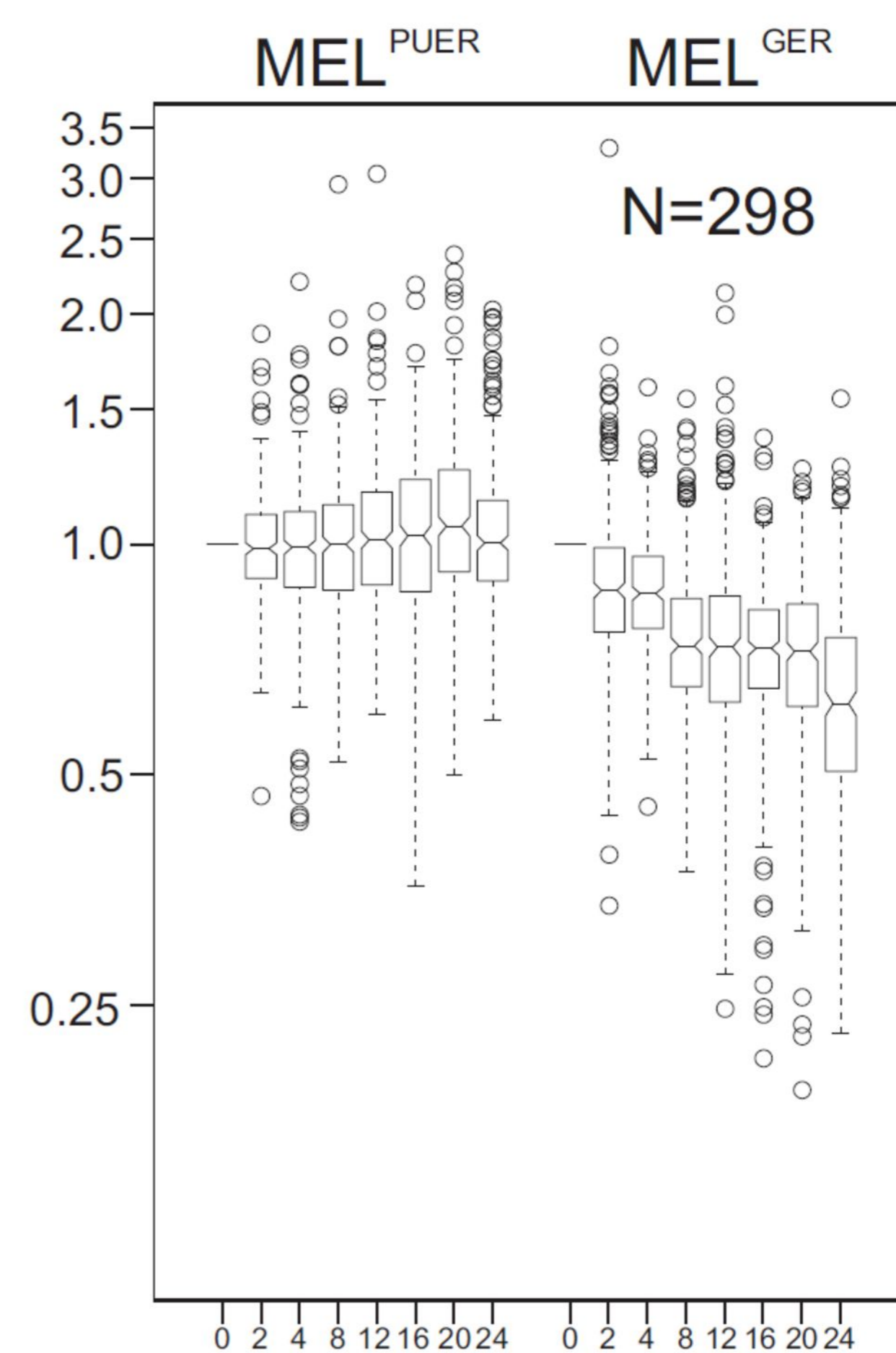
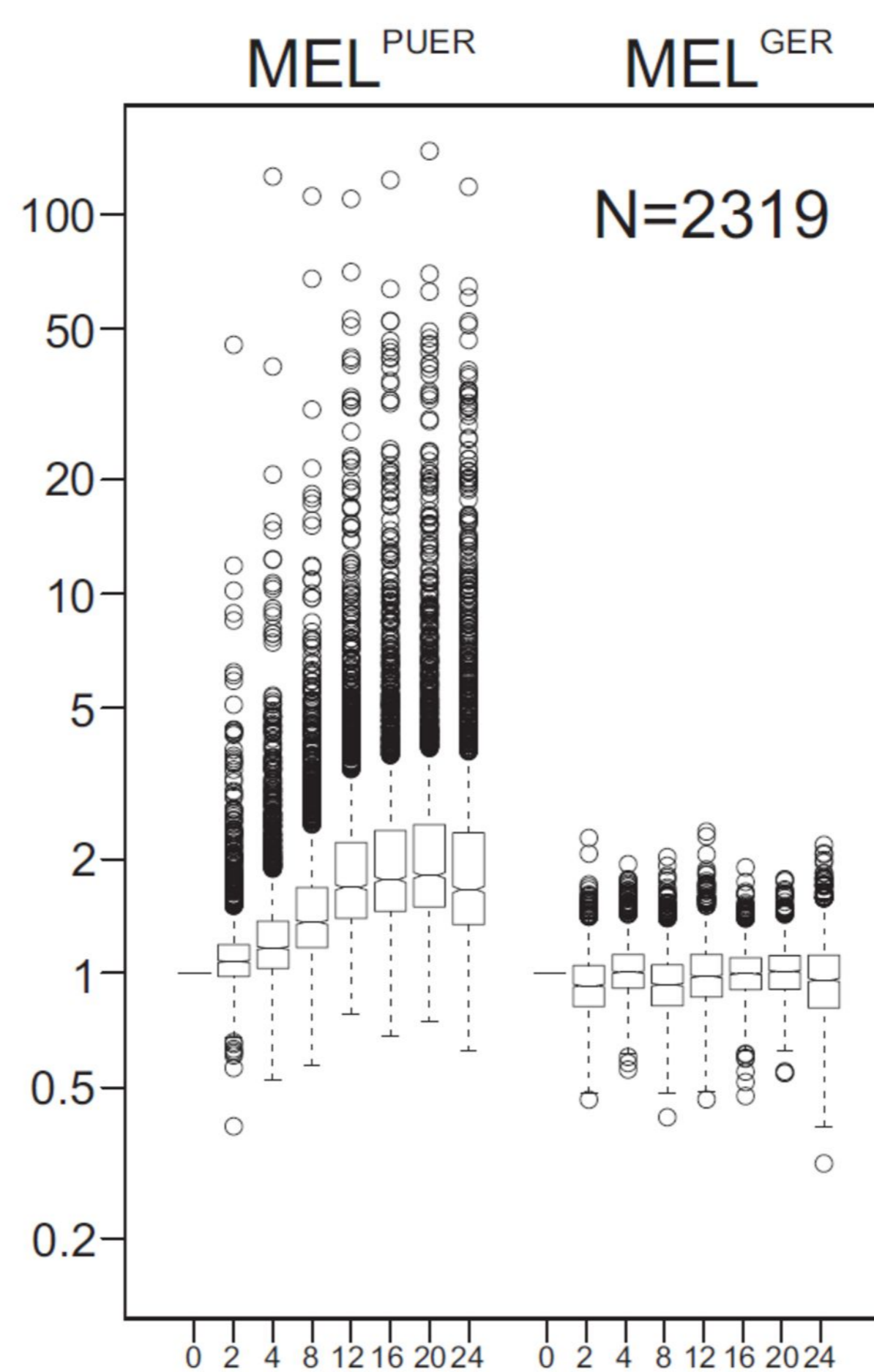
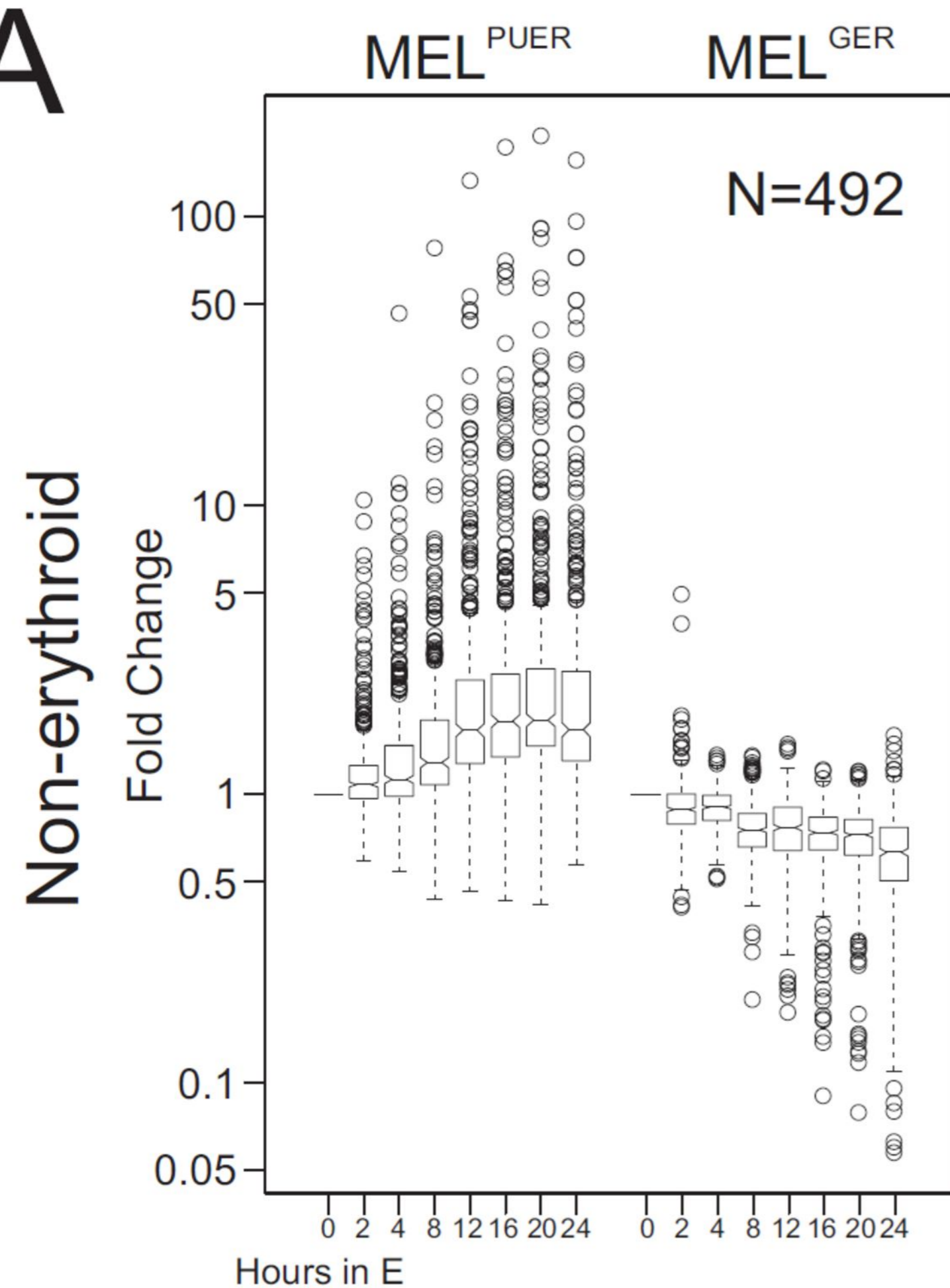
MEL^{GER}



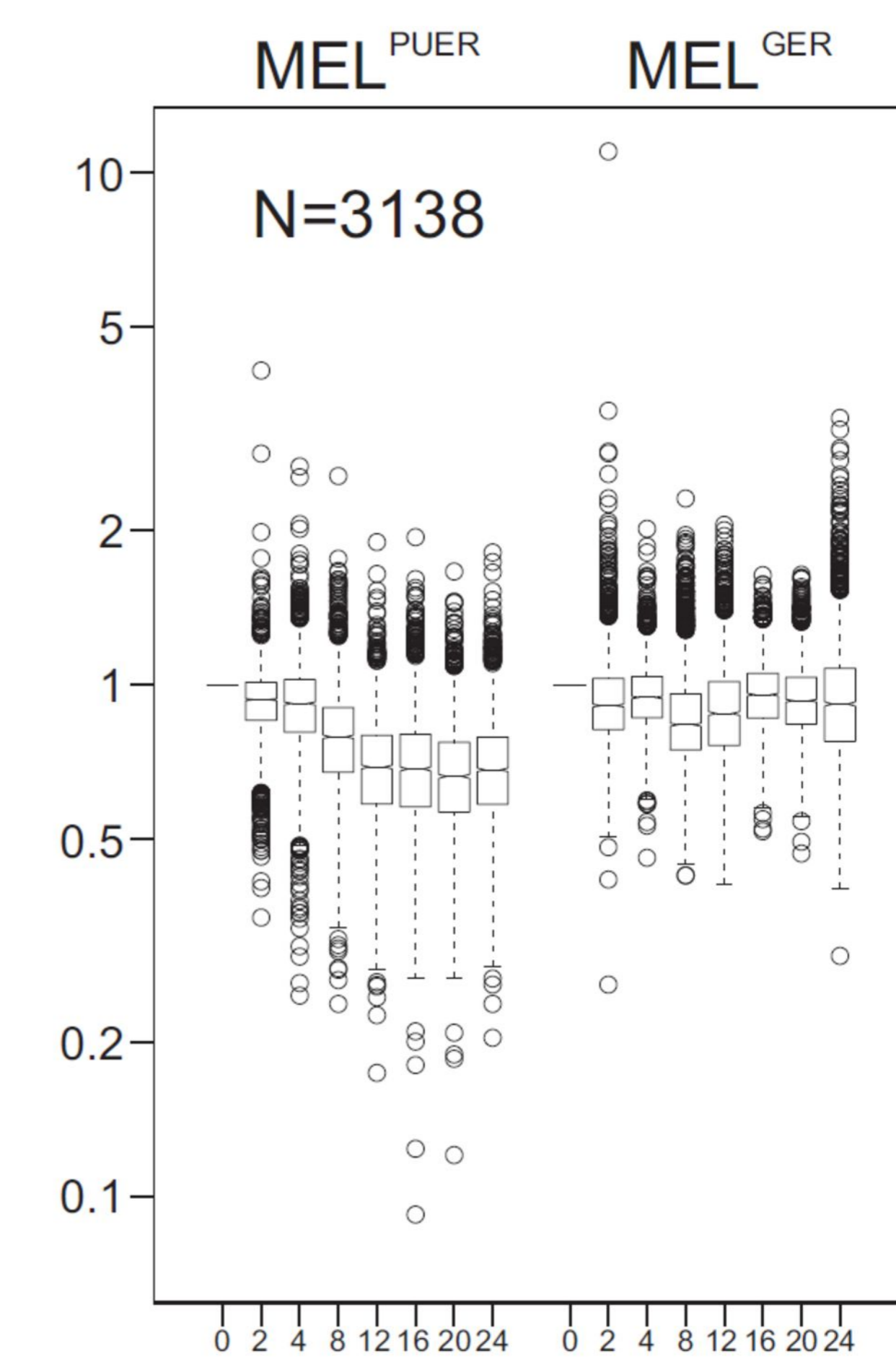
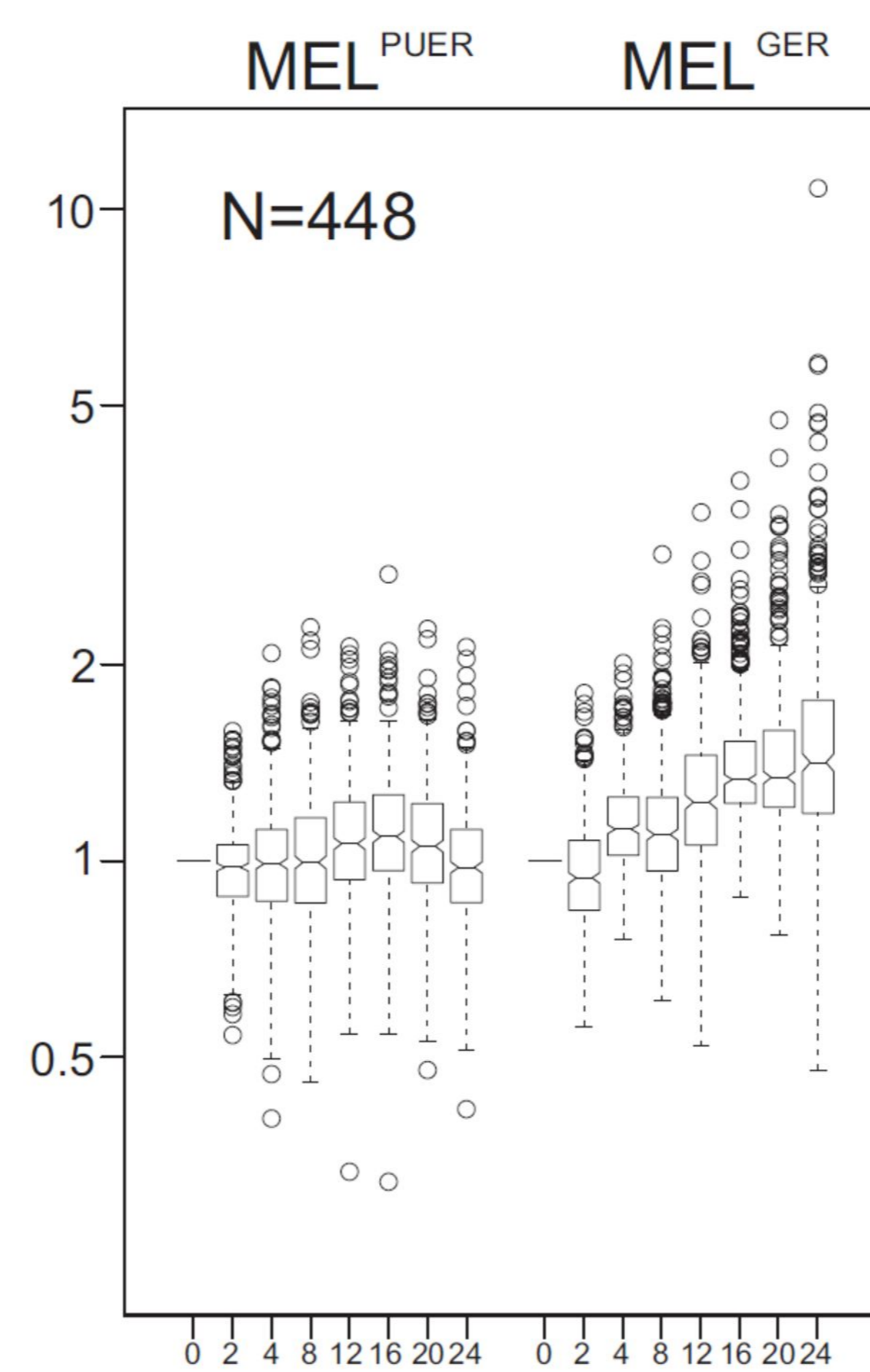
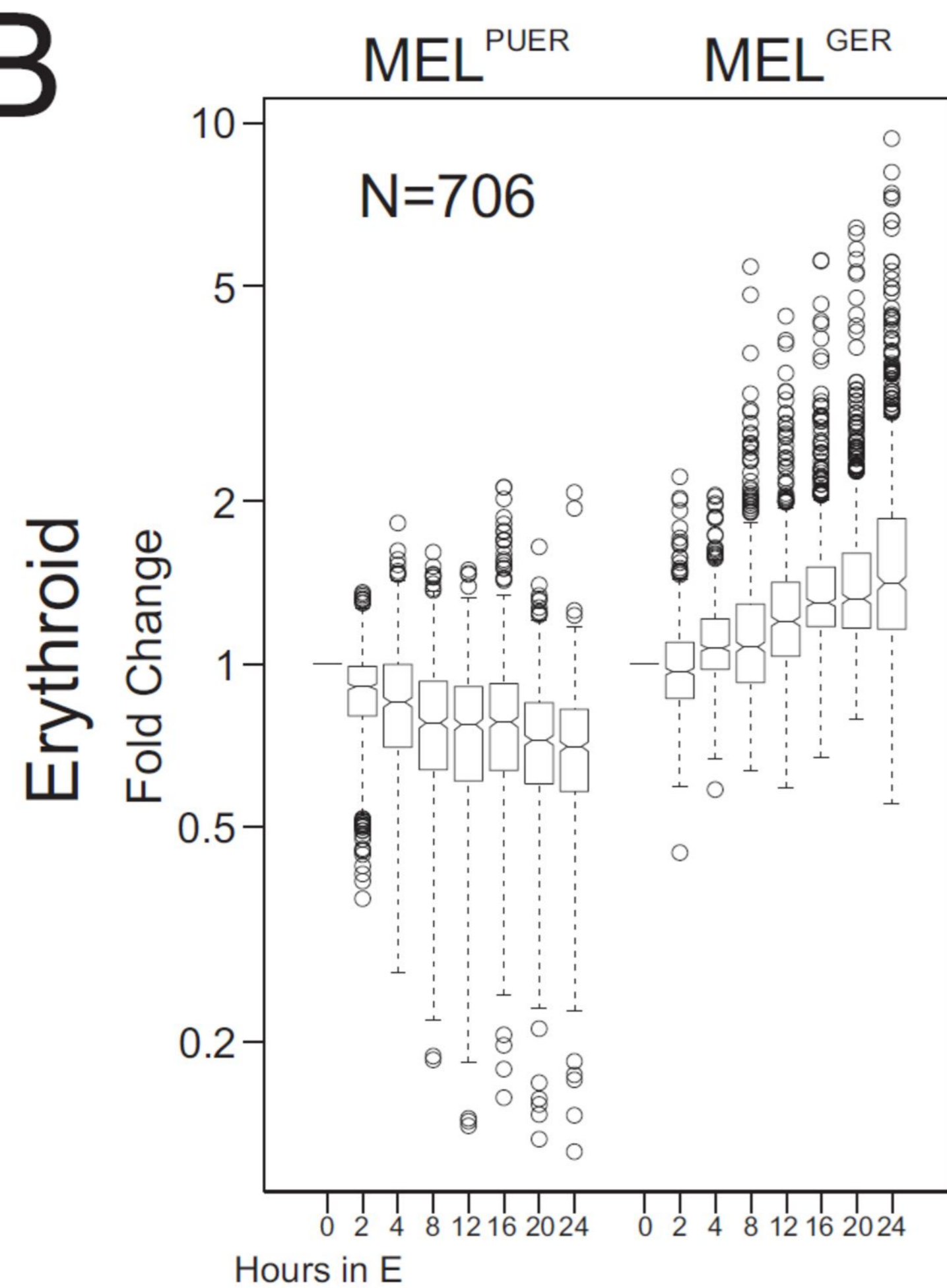
MEL^{GER}+E



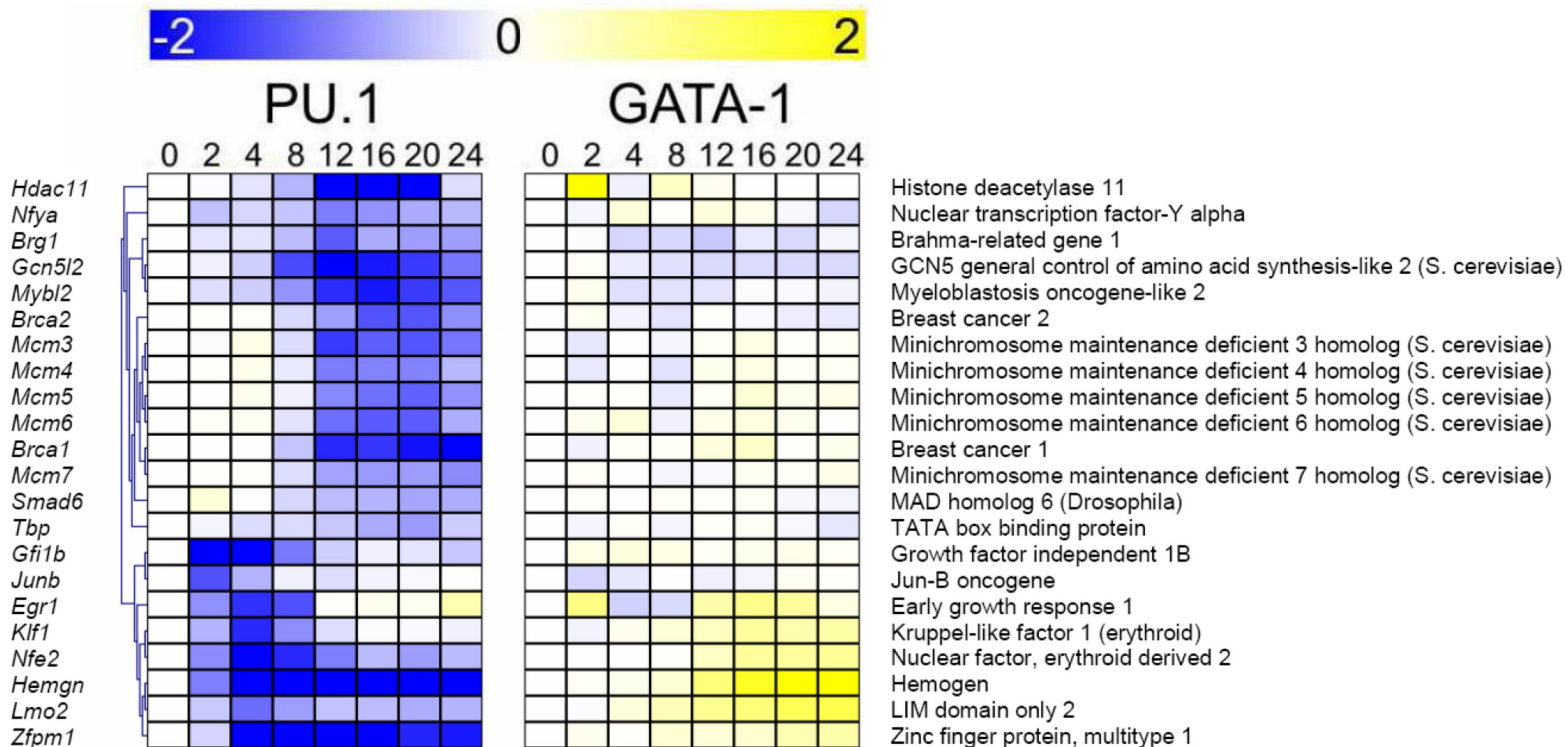
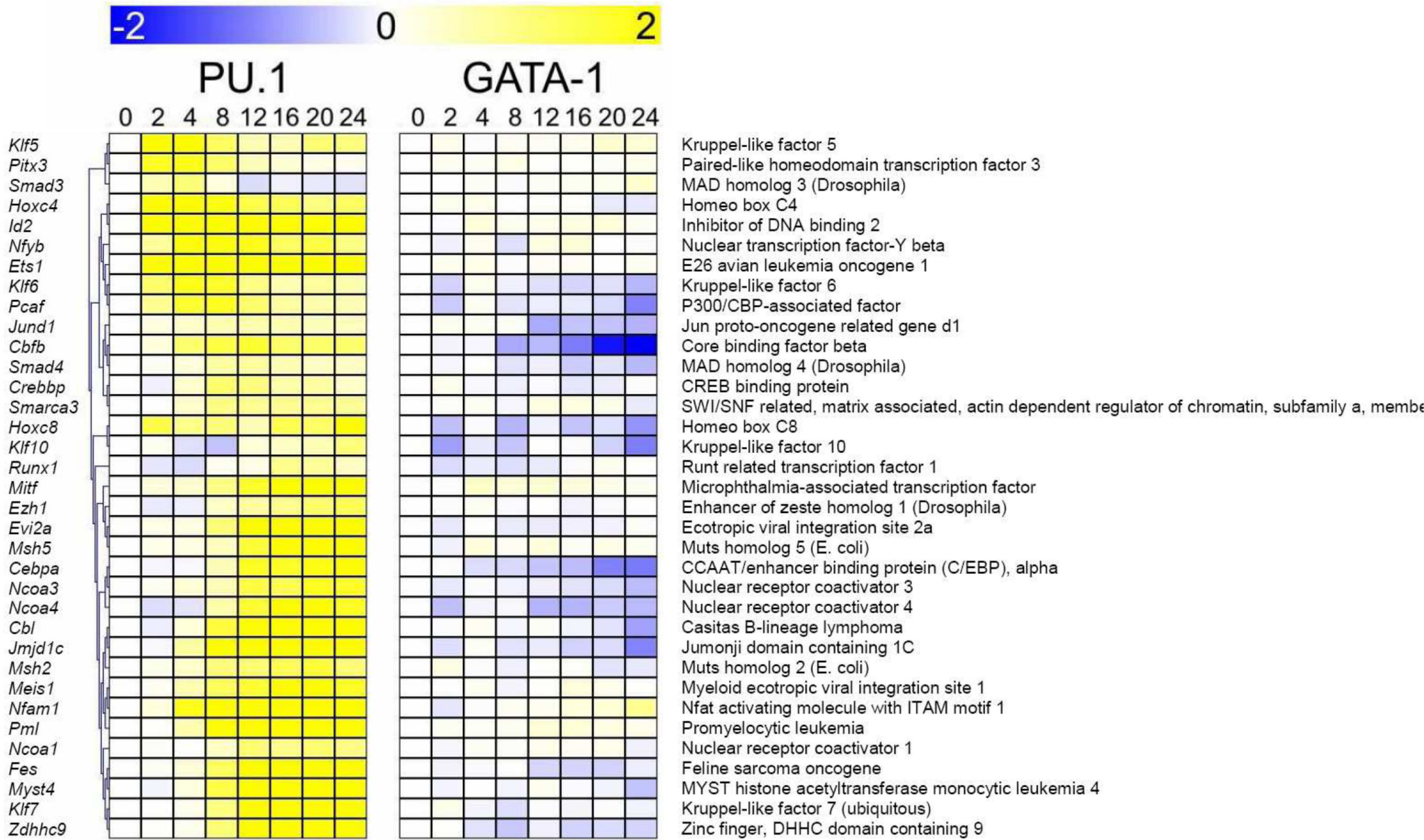
A



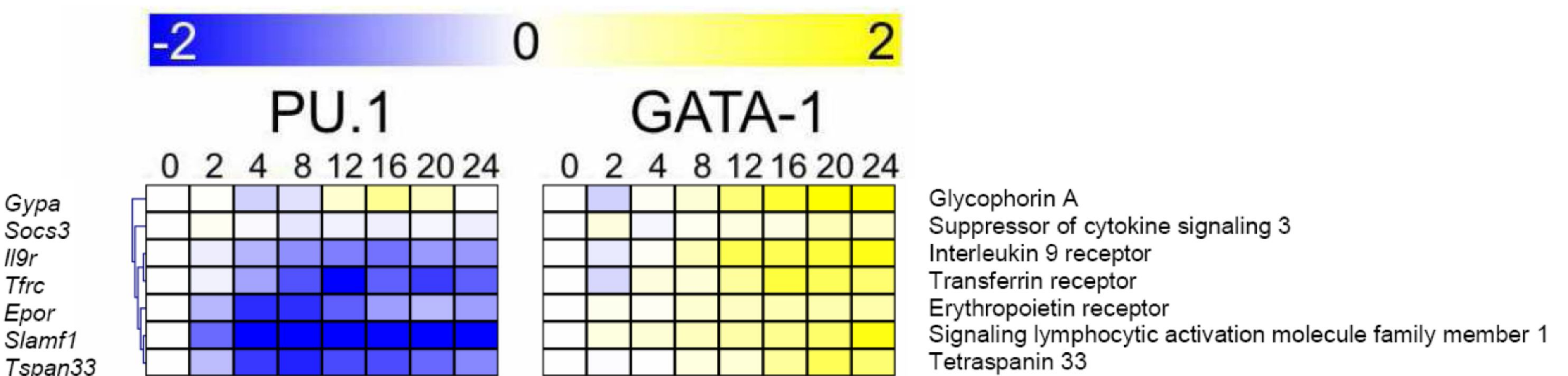
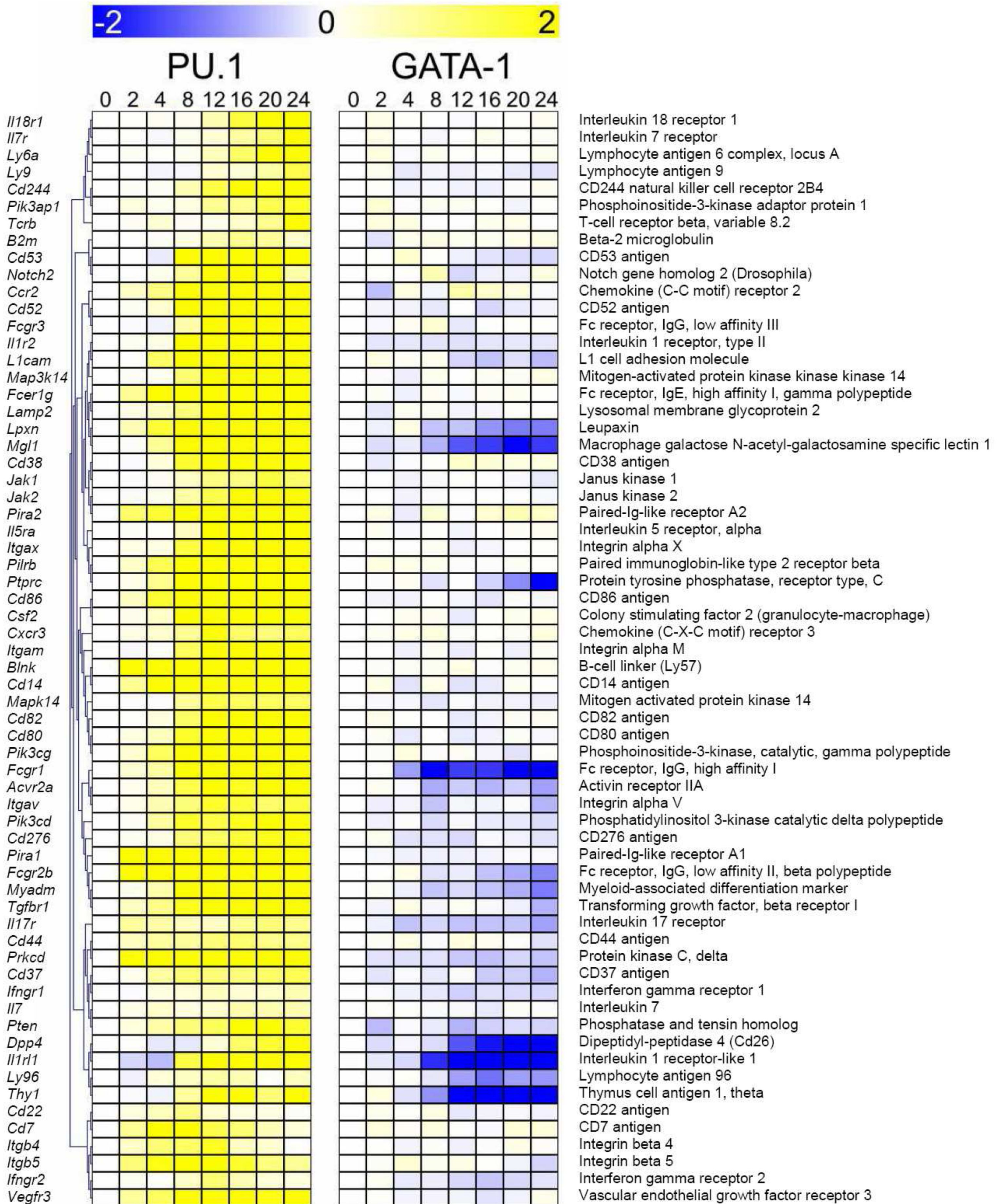
B



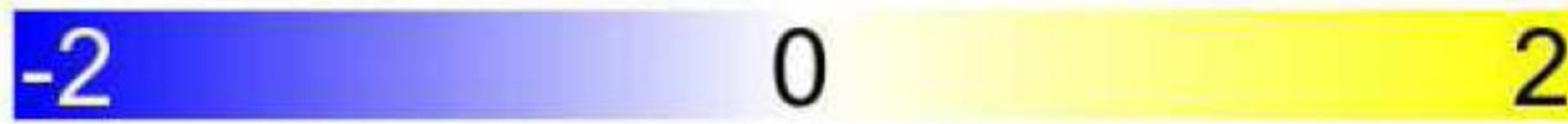
C: Transcription and chromatin remodelling factors



D: Cell surface receptors and signal transduction proteins



E: Celular metabolism



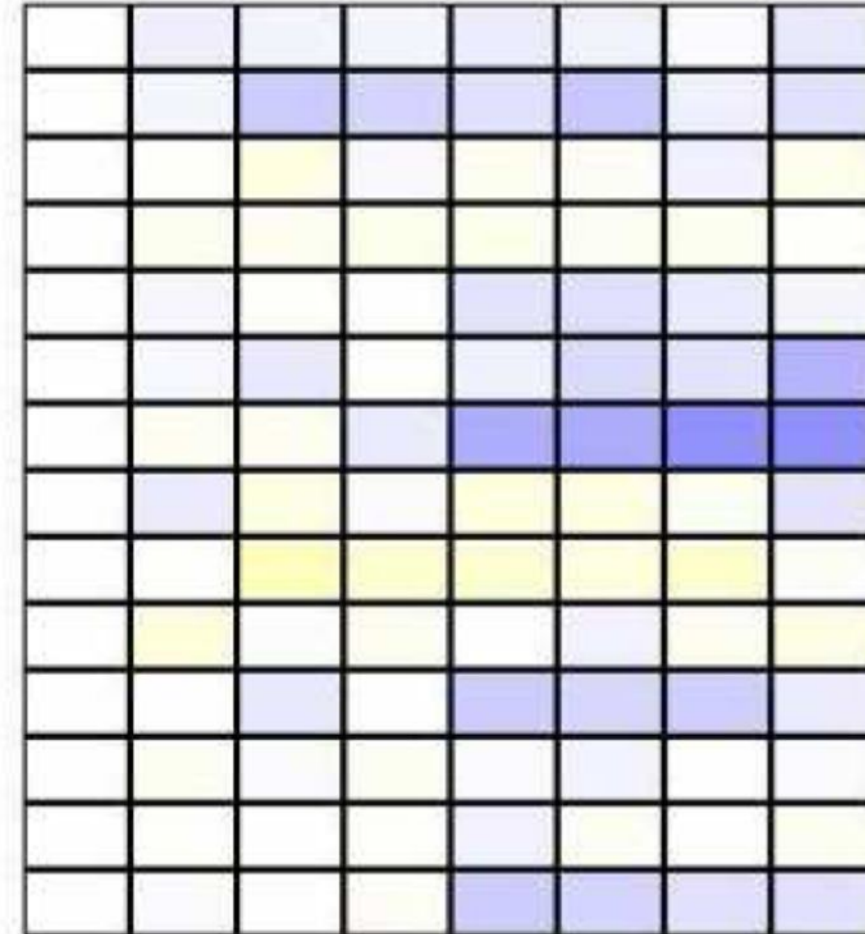
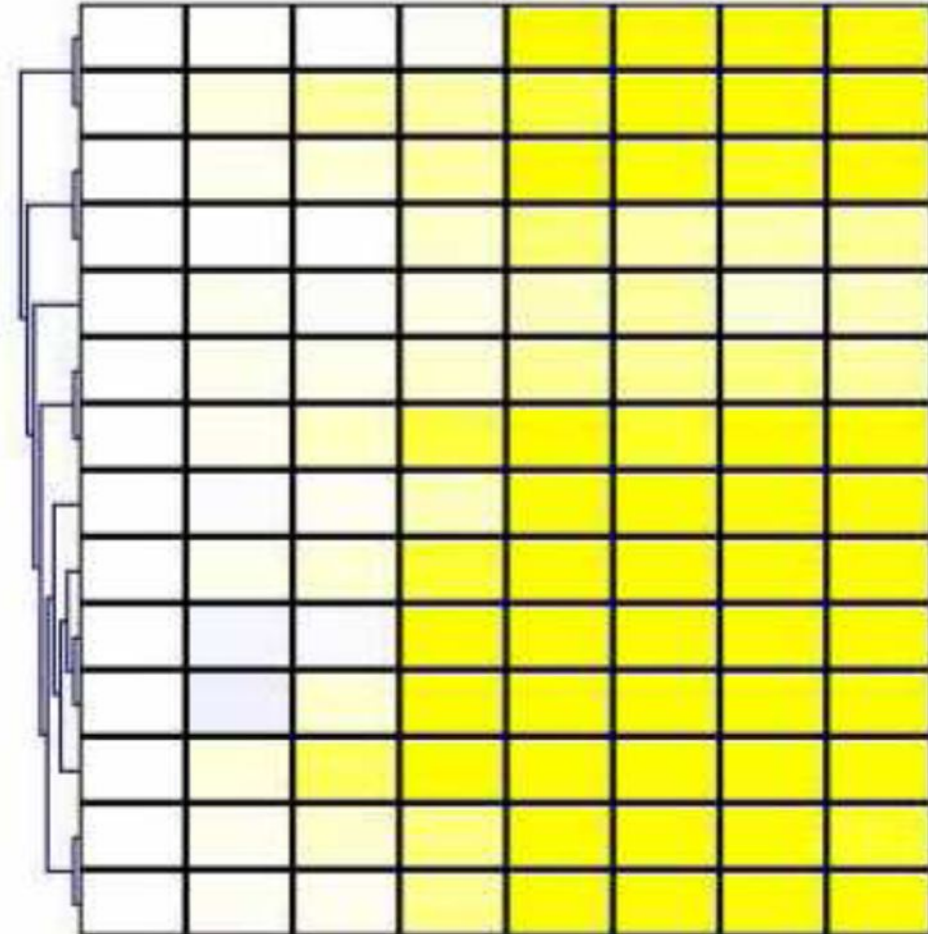
PU.1

GATA-1

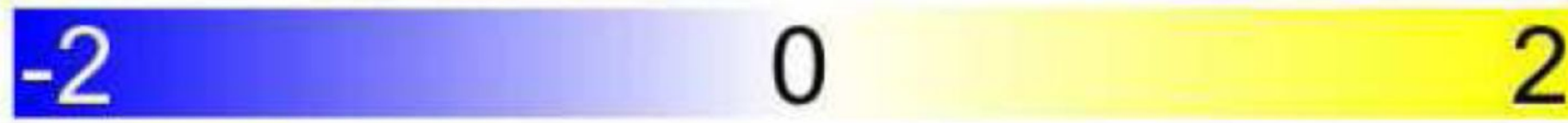
0 2 4 8 12 16 20 24

0 2 4 8 12 16 20 24

Ctsj
Ncf1
Hfe
Mmp9
Mpo
Ctsb
Myo1g
Cat
Hexb
Lyzs
Lzp-s
Man2b1
Ncf2
Ncf4



Cathepsin J
Neutrophil cytosolic factor 1
Hemochromatosis
Matrix metalloproteinase 9
Myeloperoxidase
Cathepsin B
Myosin IG
Catalase
Hexosaminidase B
Lysozyme
P lysozyme structural
Mannosidase 2, alpha B1
Neutrophil cytosolic factor 2
Neutrophil cytosolic factor 4



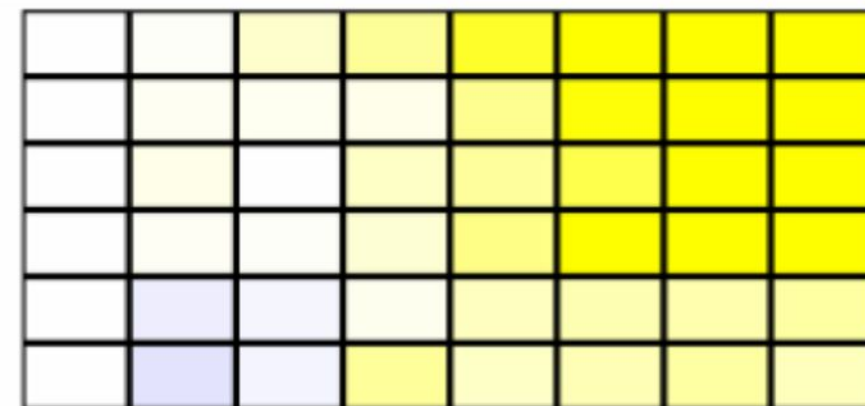
PU.1

GATA-1

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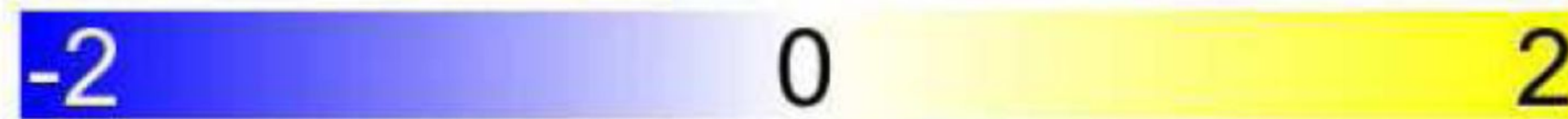
0 2 4 8 12 16 20 24

Eraf
Hba-a1
Alas2
Hbb-b1
Hk1
Hk2



Erythroid associated factor
Hemoglobin alpha, adult chain 1
Aminolevulinic acid synthase 2, erythroid
Hemoglobin, beta adult major chain
Hexokinase 1
Hexokinase 2

F: Cell cycle regulatory proteins



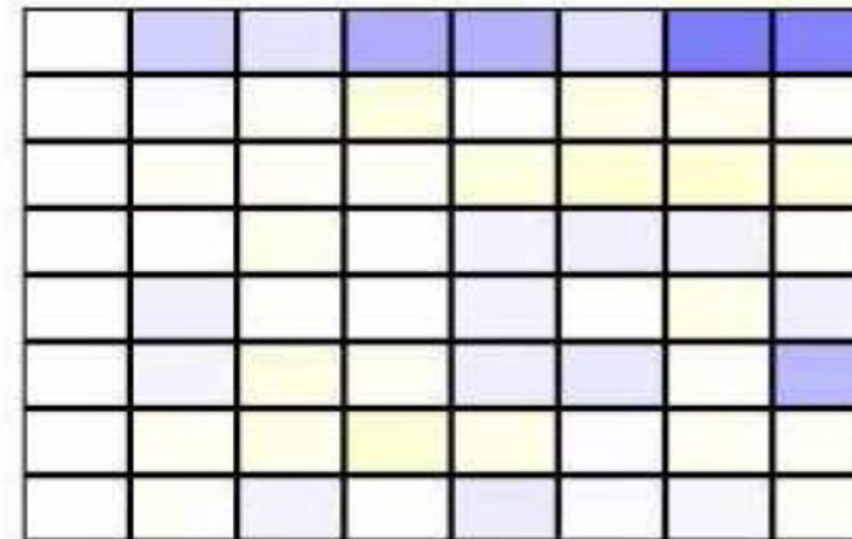
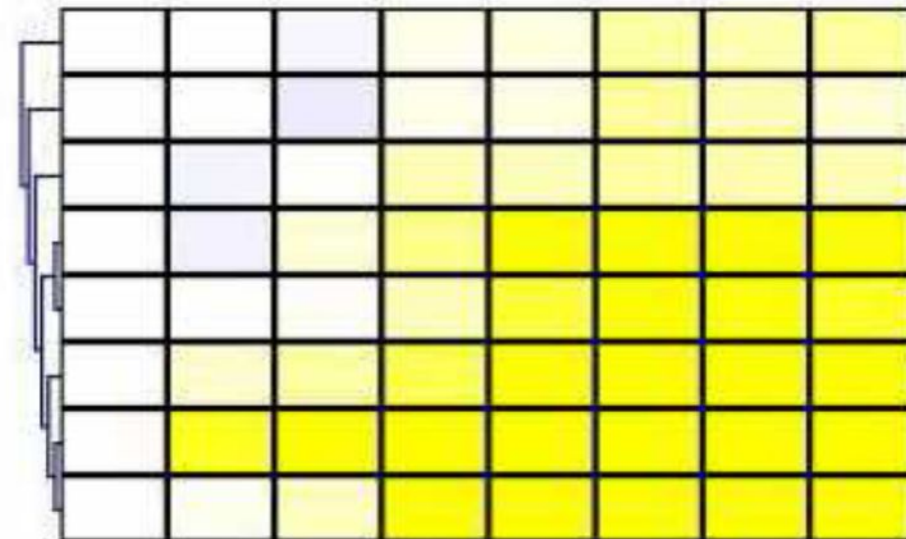
PU.1

GATA-1

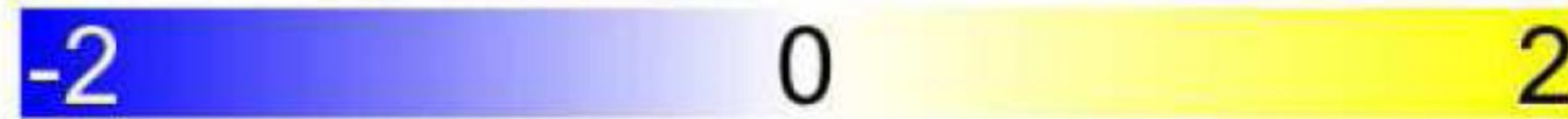
0 2 4 8 12 16 20 24

0 2 4 8 12 16 20 24

Cdkn2a
Cdkn1b
Cdkn2c
Cdkn2b
Pink1
Btg1
Pak1
Srgap3



Cyclin-dependent kinase inhibitor 2A (p16)
Cyclin-dependent kinase inhibitor 1B (p27)
Cyclin-dependent kinase inhibitor 2C (p18)
Cyclin-dependent kinase inhibitor 2B (p15)
PTEN induced putative kinase 1
B-cell translocation gene 1, anti-proliferative
p21 (CDKN1A)-activated kinase 1
SLIT-ROBO Rho gtpase activating protein 3



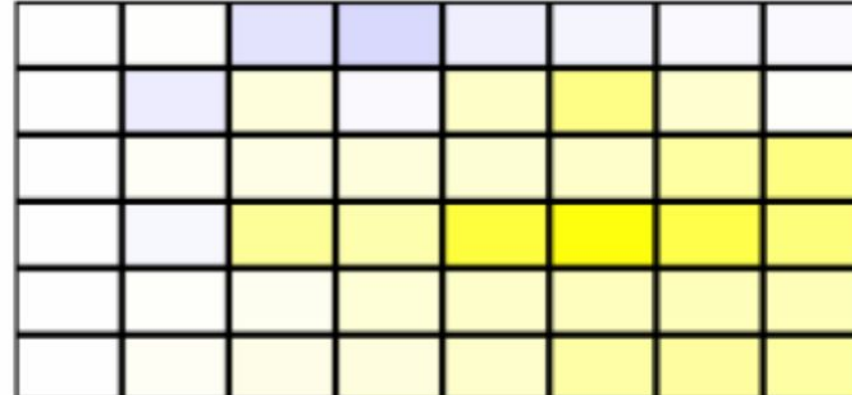
PU.1

GATA-1

0 2 4 8 12 16 20 24

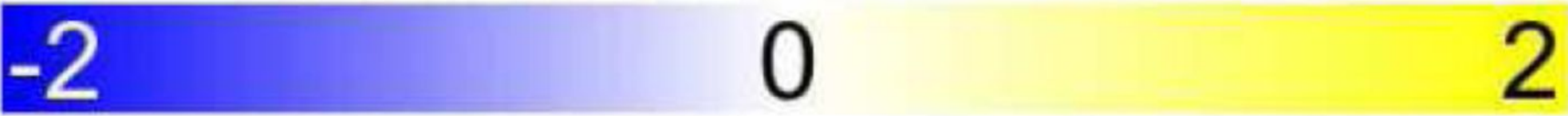
0 2 4 8 12 16 20 24

Cdc25a
Ccne2
Cdc25b
Cdc6
Cdkn1a
Cdkn2d



Cell division cycle 25 homolog A (*S. cerevisiae*)
Cyclin E2
Cell division cycle 25 homolog B (*S. cerevisiae*)
Cell division cycle 6 homolog (*S. cerevisiae*)
Cyclin-dependent kinase inhibitor 1A (p21)
Cyclin-dependent kinase inhibitor 2D (p19)

G: Apoptosis regulatory proteins



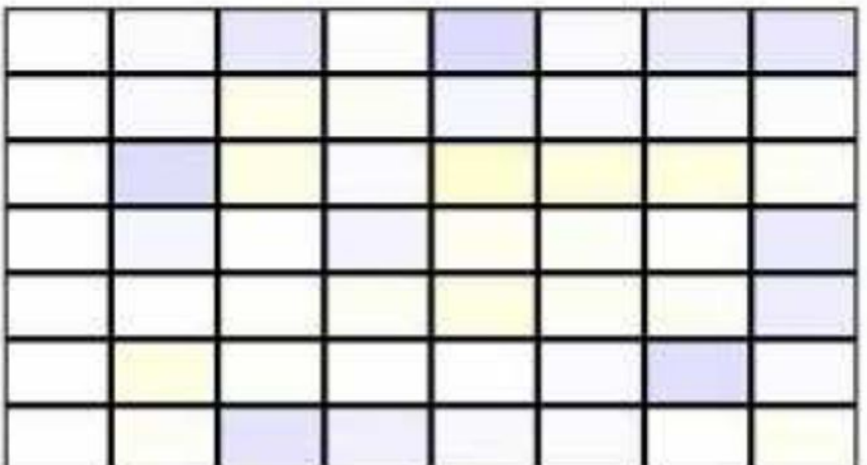
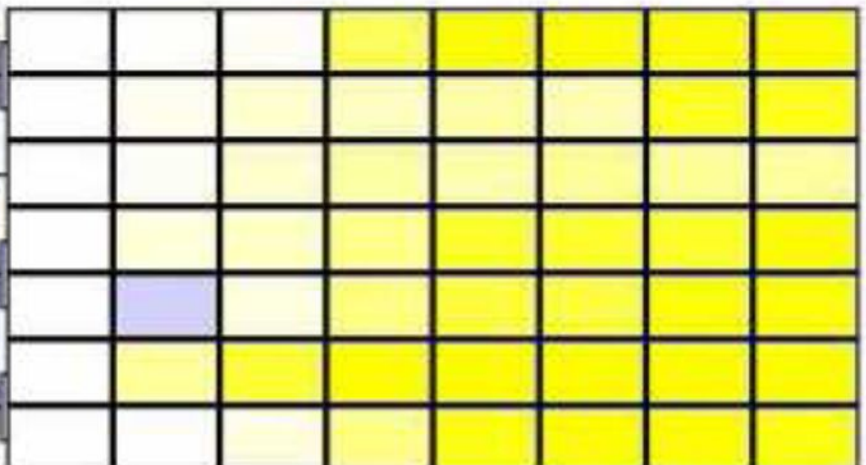
PU.1

GATA-1

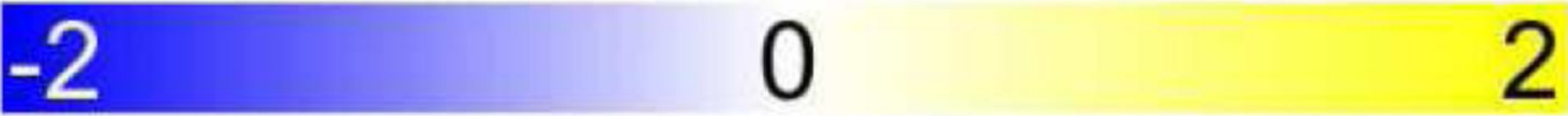
0 2 4 8 12 16 20 24

0 2 4 8 12 16 20 24

Bcl2a1
Birc1e
Birc4
Birc1b
Cflar
Birc3
Mcl1



B-cell leukemia/lymphoma 2 related protein A1
Baculoviral IAP repeat-containing 1e
Baculoviral IAP repeat-containing 4
Baculoviral IAP repeat-containing 1b
CASP8 and FADD-like apoptosis regulator (Flip)
Baculoviral IAP repeat-containing 3
Myeloid cell leukemia sequence 1



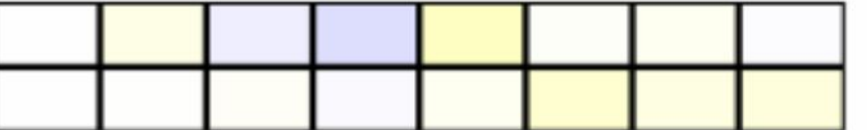
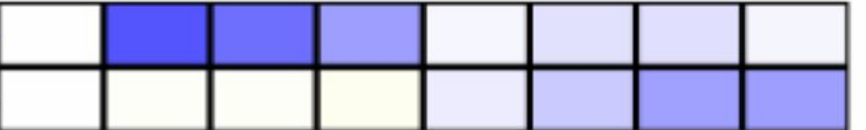
PU.1

GATA-1

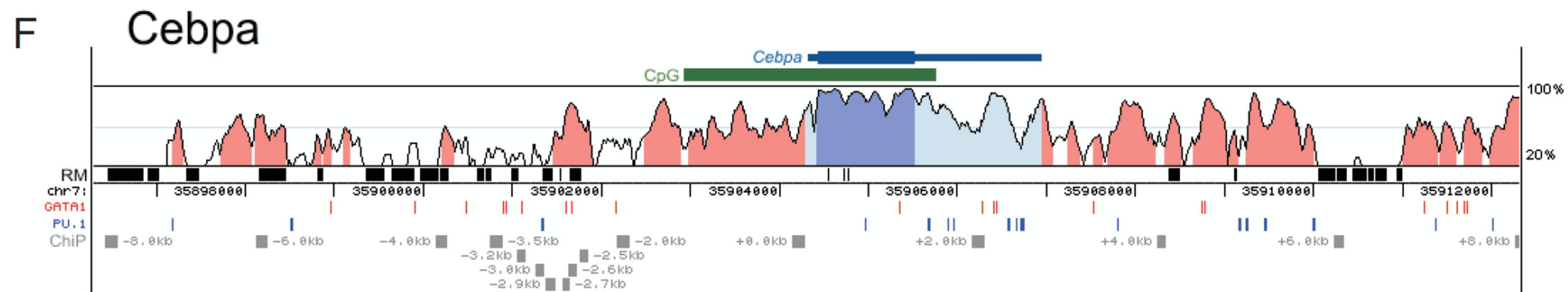
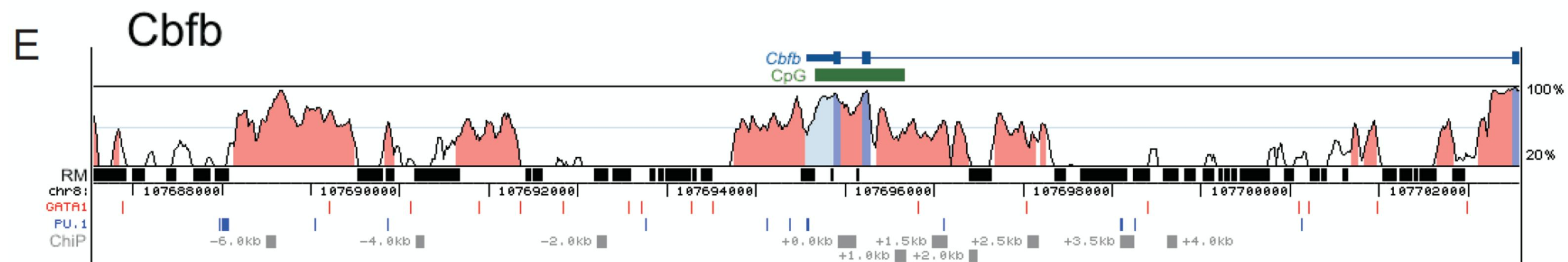
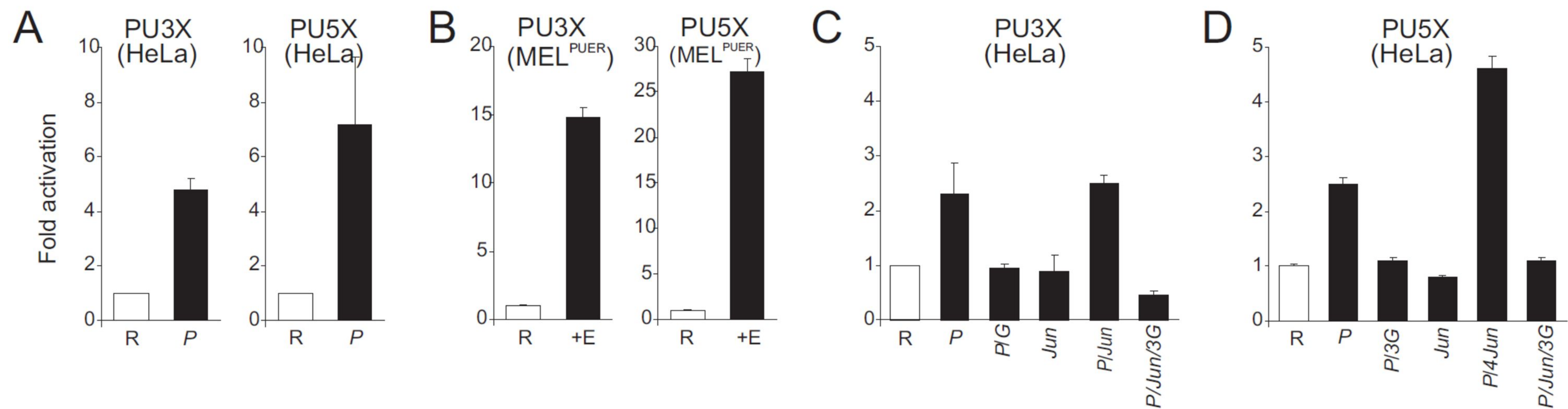
0 2 4 8 12 16 20 24

0 2 4 8 12 16 20 24

Bcl2
Birc5



B-cell leukemia/lymphoma 2
Baculoviral IAP repeat-containing 5



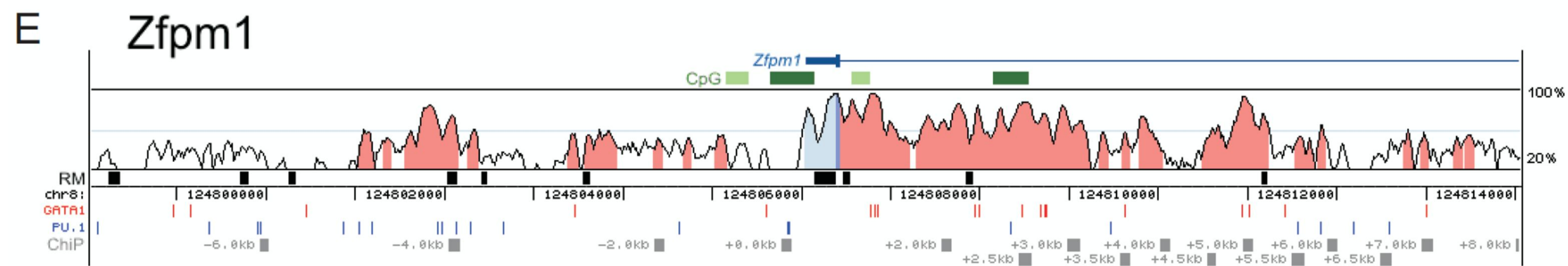
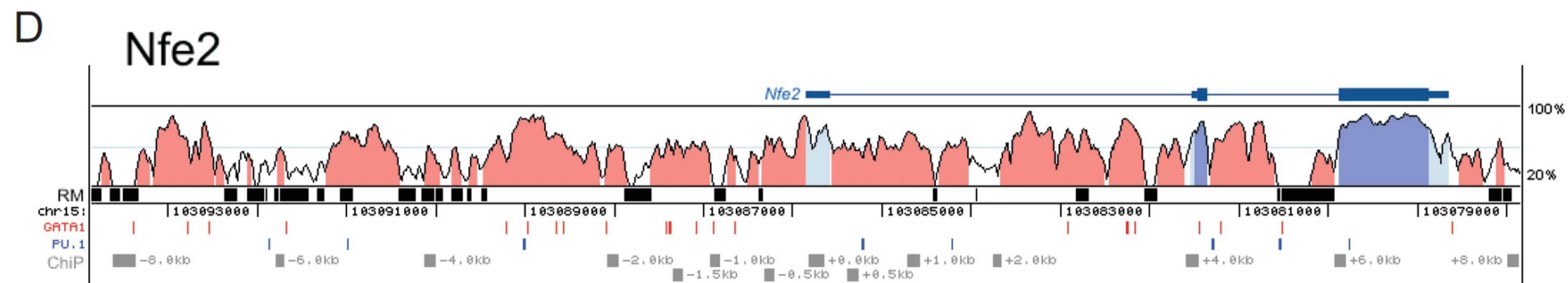
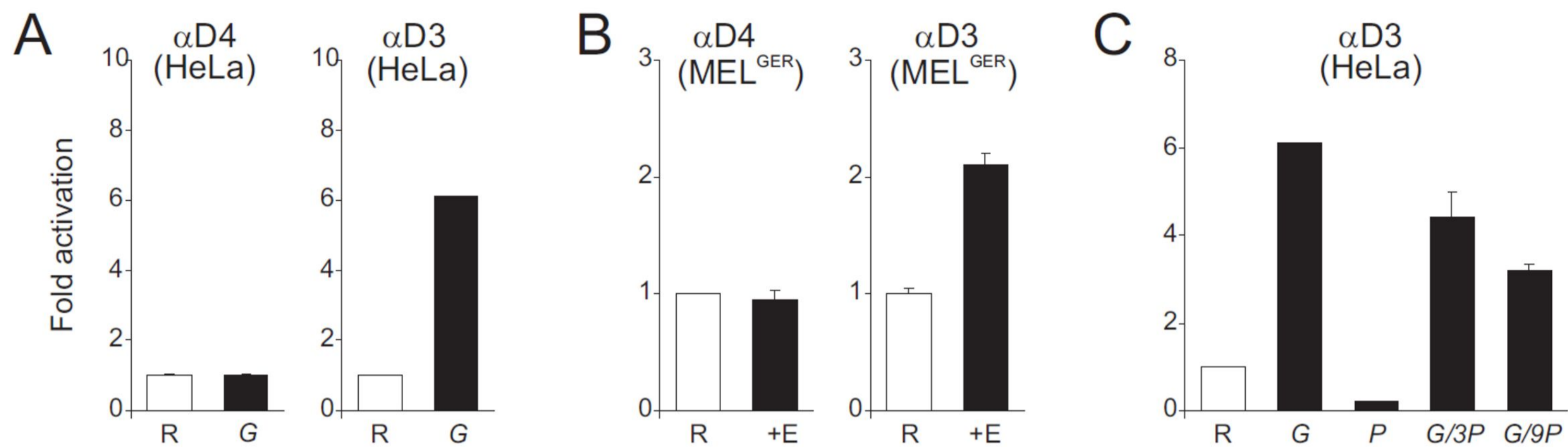


Table 1

Gene name	Amplicon (+/- bp relative to TSS)	Binding site (+/- bp relative to TSS)
<i>Zfpml</i>	3537 — 3630	+3579, AGATAA
<i>Nfe2</i>	-2233 — -2111 -1502 — -1390 -1084 — -966 -475 — -359 22 — 194	-1589, AGATAA -1532, AGATAG -1525, AGATAA -1052, AGATAG -804, AGATAG
<i>Cbfb</i>	1812 — 1913	+1531, GAGGAACT
<i>Cebpa</i>	-3260 — -3170	-2978, GAGGAAGT

Table 2

Gene	Oligo sequence	Relative position from TSS
<i>Zfpml</i>	CTCTTTGAAATAAGATCAGCTGAGATAAGCATTCCGGGCTACAGGAAGCC GAGAACTTTATTCTAGTCGACTCTATTTCGTAAGGCCCGATGTCCTTCGG	+3557 to +3606
<i>Nfe2</i>	TGAAATTATCTGTAATCTGATATTATGTTACTATCTCTTATCTCCTATTCTGCCATCTTATT ACTTAATAGACATTAGACTATAATAACAATGATAGAGAATAGAGGATAAGACGGATAGAATAA ATTGATACGGCGTTAGATAGACCGTCTGATACAGAAAAGGATACCTCCTCAGATACCTG TAACTATGCCGCAATCTATCTGGCAGACTATGTCTTTTCTTATGGAGGAGTCTATGGAC	Three segments: -1583 to -1559, -1537 to -1515 and -1055 to -1042 Five segments: -828 to -818, -807 to -796, -687 to -676, -428 to -417 and -327 to -316
<i>Cbfb</i>	TTGAAAAATATCGAAGTGATCTAGTTCCTCTCTTGCCTCTTCGTTATCCTC AACTTTTTTATAGCTTCACTAGATCAAGGAGAGAACGGAGAAGCAATAGGAG	+1509 to +1559
<i>Cebpa</i>	CCTCTGTAGCCGCTCCTGGAAAGAGGAAGTGGGGTTGAAACAAGTCCTTTTG GGAGACATCGGCGAGGACCTTCTCCTTCACCCCAACTTTGTTTCAGGAAAAC	-2999 to -2949