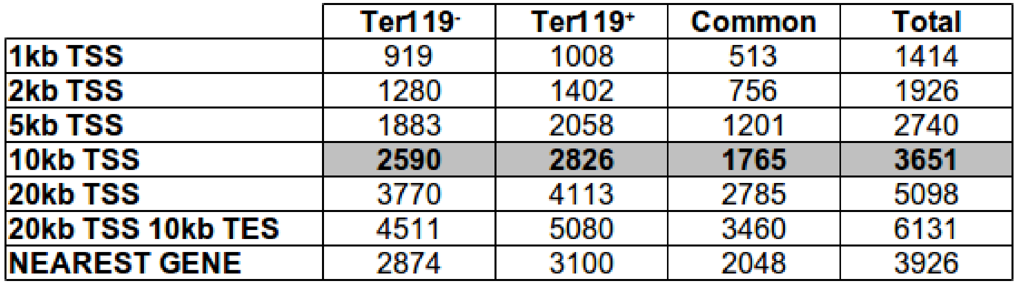
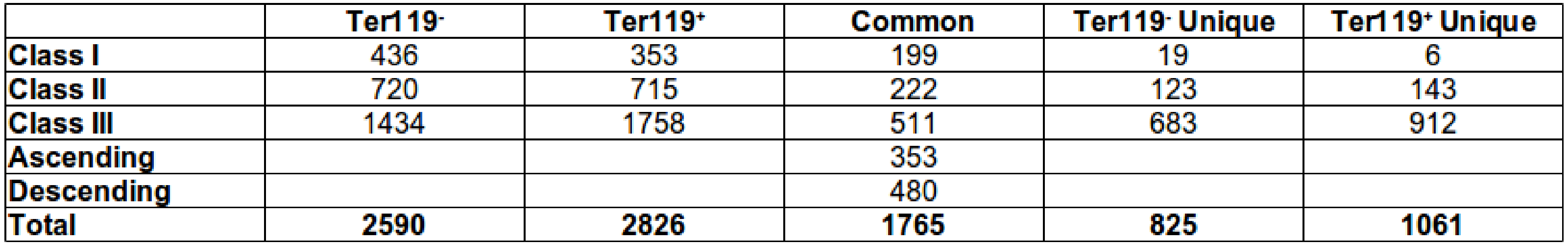
TABLE S1



	Ter119^{-}	Ter119^{+}	Common	Total
1kb TSS	919	1008	513	1414
2kb TSS	1280	1402	756	1926
5kb TSS	1883	2058	1201	2740
10kb TSS	**2590**	**2826**	**1765**	**3651**
20kb TSS	3770	4113	2785	5098
20kb TSS 10kb TES	4511	5080	3460	6131
NEAREST GENE	2874	3100	2048	3926

Table S1. Number of GATA-1 target genes proposed by different target gene assignment method

TABLE S2



	Ter119^{-}	Ter119^{+}	Common	Ter119^{-} Unique	Ter119^{+} Unique
Class I	436	353	199	19	6
Class II	720	715	222	123	143
Class III	1434	1758	511	683	912
Ascending			353		
Descending			480		
Total	**2590**	**2826**	**1765**	**825**	**1061**

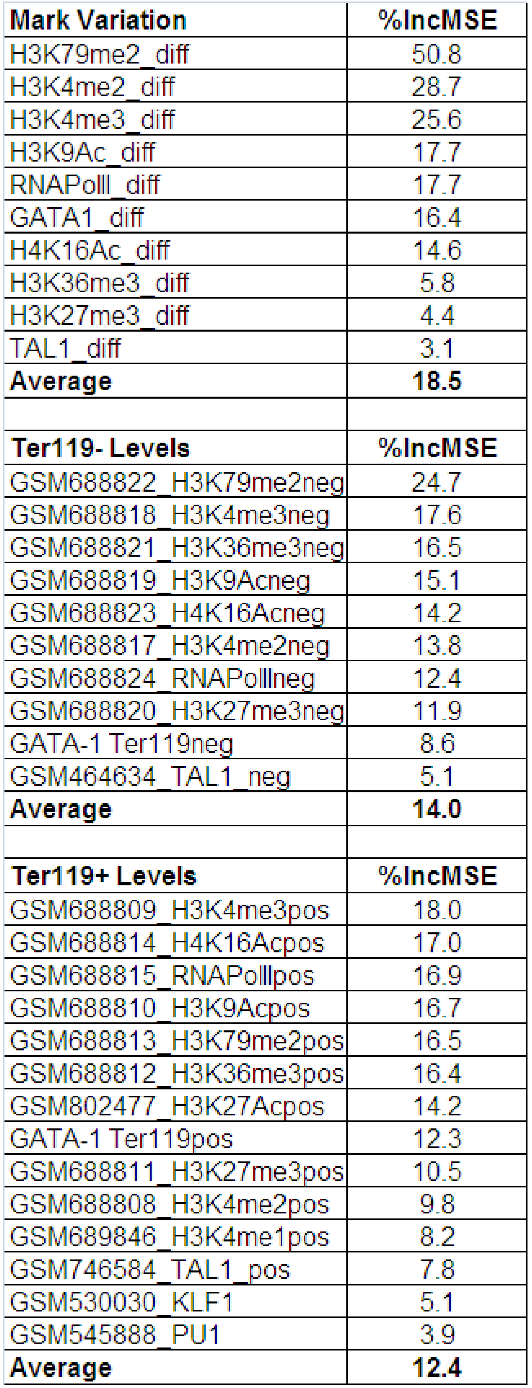
Table S2. Number of GATA-1 target genes in TGS Classes

TABLE S3

Dependent Variable	Predictors	# of Predictors	# of Samples	ntree	mtry	Training (85%)	Testing (15%)	Sampling	Training R^2	Testing R^2	Full Dataset R^2
Gene Expression Change (log2(FC))	GATA-1 (1kb TSS)	11	1414	1000	1	1202	212	100	0.06	0.06	0.06
Gene Expression Change (log2(FC))	GATA-1 (2kb TSS)	11	1926	1000	1	1637	289	100	0.07	0.07	0.08
Gene Expression Change (log2(FC))	GATA-1 (5kb TSS)	11	2740	1000	1	2329	411	100	0.12	0.12	0.12
Gene Expression Change (log2(FC))	GATA-1 (10kb TSS)	11	3651	1000	1	3103	548	100	0.13	0.14	0.14
Gene Expression Change (log2(FC))	GATA-1 (20kb TSS)	11	5098	1000	1	4333	765	100	0.13	0.13	0.13
Gene Expression Change (log2(FC))	GATA-1 (20kb TSS 10kb TES)	11	6131	1000	1	5211	920	100	0.12	0.12	0.12
Gene Expression Change (log2(FC))	GATA-1 (NEAREST GENE)	11	3926	1000	1	3337	589	100	0.13	0.13	0.13
Gene Expression Change (log2(FC))	4 TFs, RNApol2, 9 Hist. Mod., DNA m	61	2261	2000	30	1922	339	100	0.617	0.616	0.620
GSM688817_H3K4me2 (ΔTGS)	GATA-1	5	6282	1000	2	5340	942	100	0.36	0.35	0.37
GSM688818_H3K4me3 (ΔTGS)	GATA-1	5	5795	1000	2	4926	869	100	0.29	0.29	0.31
GSM688819_H3K9Ac (ΔTGS)	GATA-1	5	4742	1000	1	4031	711	100	0.22	0.20	0.23
GSM688823_H4K16Ac (ΔTGS)	GATA-1	5	4889	1000	1	4156	733	100	0.29	0.28	0.30
GSM688821_H3K36me3 (ΔTGS)	GATA-1	5	4041	1000	1	3435	606	100	0.18	0.19	0.21
GSM688822_H3K79me2 (ΔTGS)	GATA-1	5	5031	1000	1	4276	755	100	0.31	0.31	0.32
GSM688820_H3K27me3 (ΔTGS)	GATA-1	5	3905	1000	1	3319	586	100	0.06	0.07	0.07
GSM688824_RNAPolII (ΔTGS)	GATA-1	5	3588	1000	1	3050	538	100	0.23	0.24	0.26
GSM688817_H3K4me2 (ΔTGS)	GATA-1, TAL-1, EKLF	11	6282	1000	3	5340	942	100	0.56	0.55	0.56
GSM688818_H3K4me3 (ΔTGS)	GATA-1, TAL-1, EKLF	11	5795	1000	4	4926	869	100	0.47	0.47	0.48
GSM688819_H3K9Ac (ΔTGS)	GATA-1, TAL-1, EKLF	11	4742	1000	2	4031	711	100	0.43	0.43	0.44
GSM688823_H4K16Ac (ΔTGS)	GATA-1, TAL-1, EKLF	11	4889	1000	8	4156	733	100	0.47	0.48	0.47
GSM688821_H3K36me3 (ΔTGS)	GATA-1, TAL-1, EKLF	11	4041	1000	2	3435	606	100	0.29	0.29	0.3
GSM688822_H3K79me2 (ΔTGS)	GATA-1, TAL-1, EKLF	11	5031	1000	2	4276	755	100	0.45	0.46	0.46
GSM688820_H3K27me3 (ΔTGS)	GATA-1, TAL-1, EKLF	11	3905	1000	6	3319	586	100	0.20	0.19	0.21
GSM688824_RNAPolII (ΔTGS)	GATA-1, TAL-1, EKLF	11	3588	1000	10	3050	538	100	0.47	0.49	0.45
GSM688810_H3K9Ac (Ter119+ TGS)	GATA-1	4	4179	1000	1	3552	627	100	0.31	0.30	0.34
GSM688814_H4K16Ac (Ter119+ TGS)	GATA-1	4	3756	1000	1	3193	563	100	0.41	0.41	0.42
GSM802477_H3K27Ac (Ter119+ TGS)	GATA-1	4	3715	1000	1	3158	557	100	0.44	0.45	0.46
GSM688810_H3K9Ac (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	4179	1000	3	3552	627	100	0.66	0.66	0.67
GSM688814_H4K16Ac (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	3756	1000	3	3193	563	100	0.58	0.58	0.59
GSM802477_H3K27Ac (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	3715	1000	3	3158	557	100	0.64	0.64	0.66
GSM689846_H3K4me1 (Ter119+ TGS)	GATA-1	4	2963	1000	1	2519	444	100	0.30	0.30	0.31
GSM688817_H3K4me2 (Ter119+ TGS)	GATA-1	4	5478	1000	1	4656	822	100	0.42	0.42	0.43
GSM688818_H3K4me3 (Ter119+ TGS)	GATA-1	4	5207	1000	1	4426	781	100	0.35	0.35	0.37
GSM689846_H3K4me1 (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	2963	1000	3	2519	444	100	0.51	0.52	0.52
GSM688817_H3K4me2 (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	5478	1000	3	4656	822	100	0.64	0.64	0.65
GSM688818_H3K4me3 (Ter119+ TGS)	GATA-1, TAL-1, EKLF	10	5207	1000	3	4426	781	100	0.58	0.58	0.60

Table S3. Overview of Random Forest parameters and results

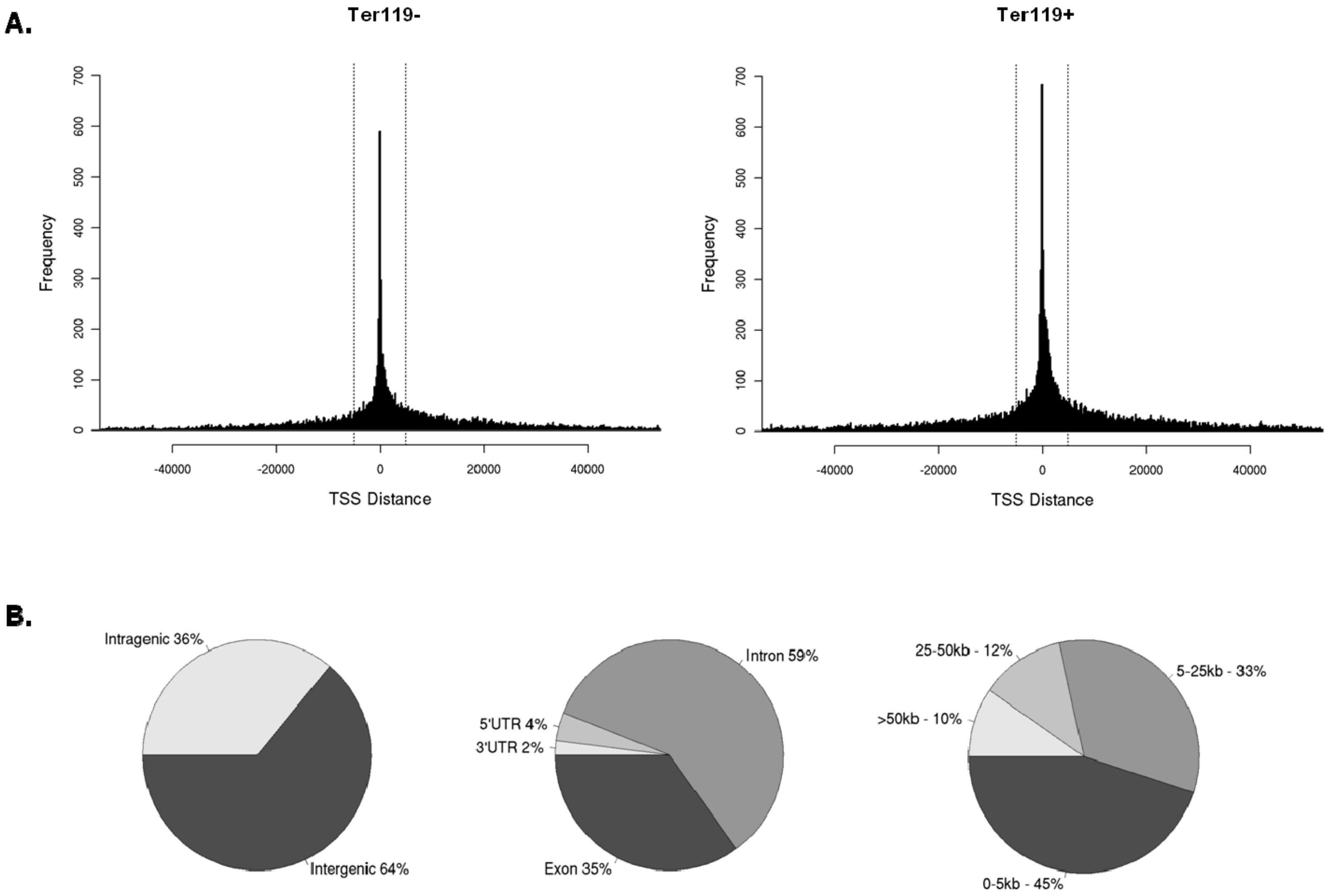
TABLE S4



Mark Variation	%IncMSE
H3K79me2_diff	50.8
H3K4me2_diff	28.7
H3K4me3_diff	25.6
H3K9Ac_diff	17.7
RNAPolII_diff	17.7
GATA1_diff	16.4
H4K16Ac_diff	14.6
H3K36me3_diff	5.8
H3K27me3_diff	4.4
TAL1_diff	3.1
Average	**18.5**
Ter119- Levels	**%IncMSE**
GSM688822_H3K79me2neg	24.7
GSM688818_H3K4me3neg	17.6
GSM688821_H3K36me3neg	16.5
GSM688819_H3K9Acneg	15.1
GSM688823_H4K16Acneg	14.2
GSM688817_H3K4me2neg	13.8
GSM688824_RNAPolIIneg	12.4
GSM688820_H3K27me3neg	11.9
GATA-1 Ter119neg	8.6
GSM464634_TAL1_neg	5.1
Average	**14.0**
Ter119+ Levels	**%IncMSE**
GSM688809_H3K4me3pos	18.0
GSM688814_H4K16Acpos	17.0
GSM688815_RNAPolIIpos	16.9
GSM688810_H3K9Acpos	16.7
GSM688813_H3K79me2pos	16.5
GSM688812_H3K36me3pos	16.4
GSM802477_H3K27Acpos	14.2
GATA-1 Ter119pos	12.3
GSM688811_H3K27me3pos	10.5
GSM688808_H3K4me2pos	9.8
GSM689846_H3K4me1pos	8.2
GSM746584_TAL1_pos	7.8
GSM530030_KLF1	5.1
GSM545888_PU1	3.9
Average	**12.4**

Table S4. Variable importance measures (%IncMSE) in predicting gene expression changes between Ter119- and Ter119+ erythroid cells

FIGURE S1

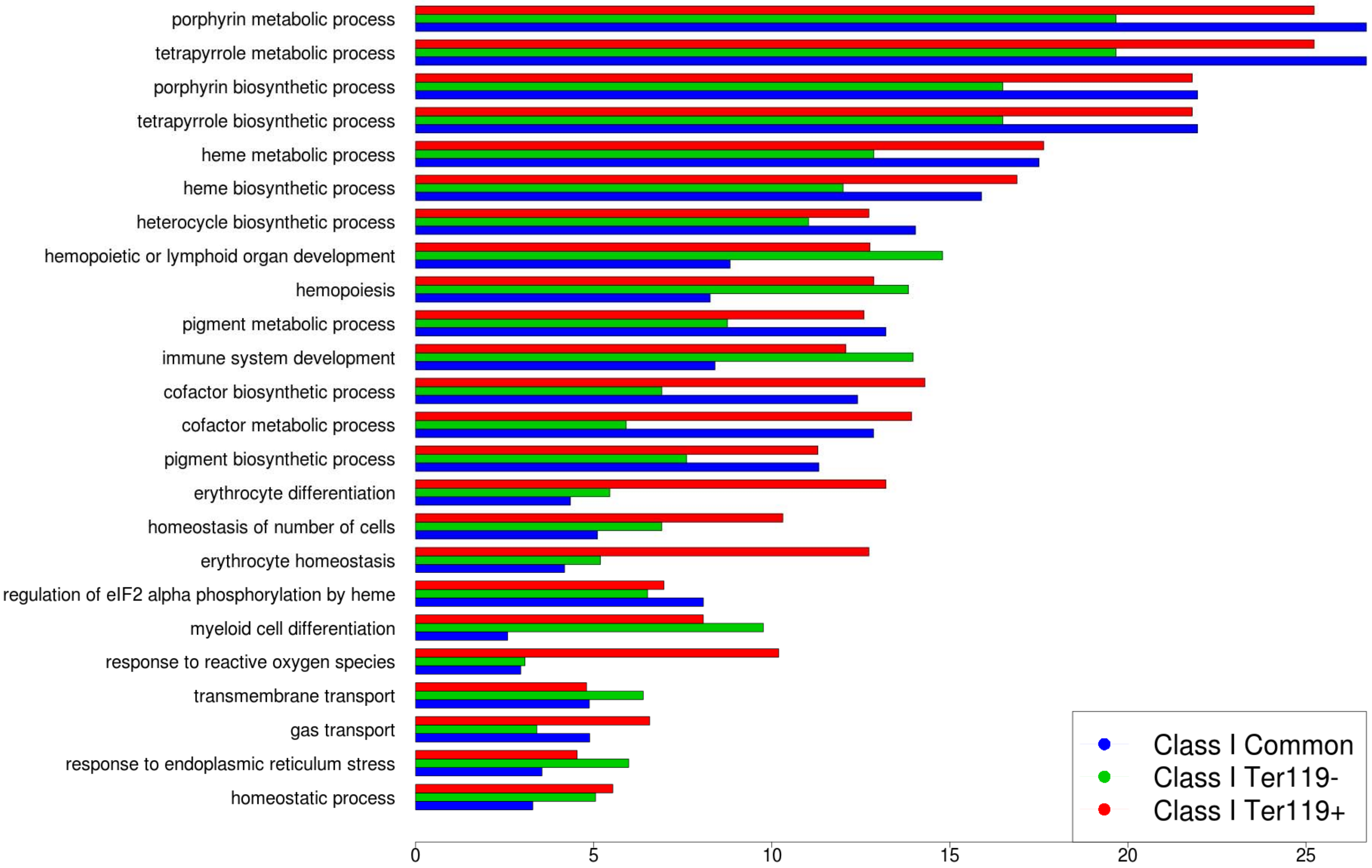


Supplementary Figure S1. Distribution of GATA-1 chromatin occupancy in Ter119- and Ter119+ cells

A. Distribution of the distances between GATA-1 identified peaks from annotated gene TSSs

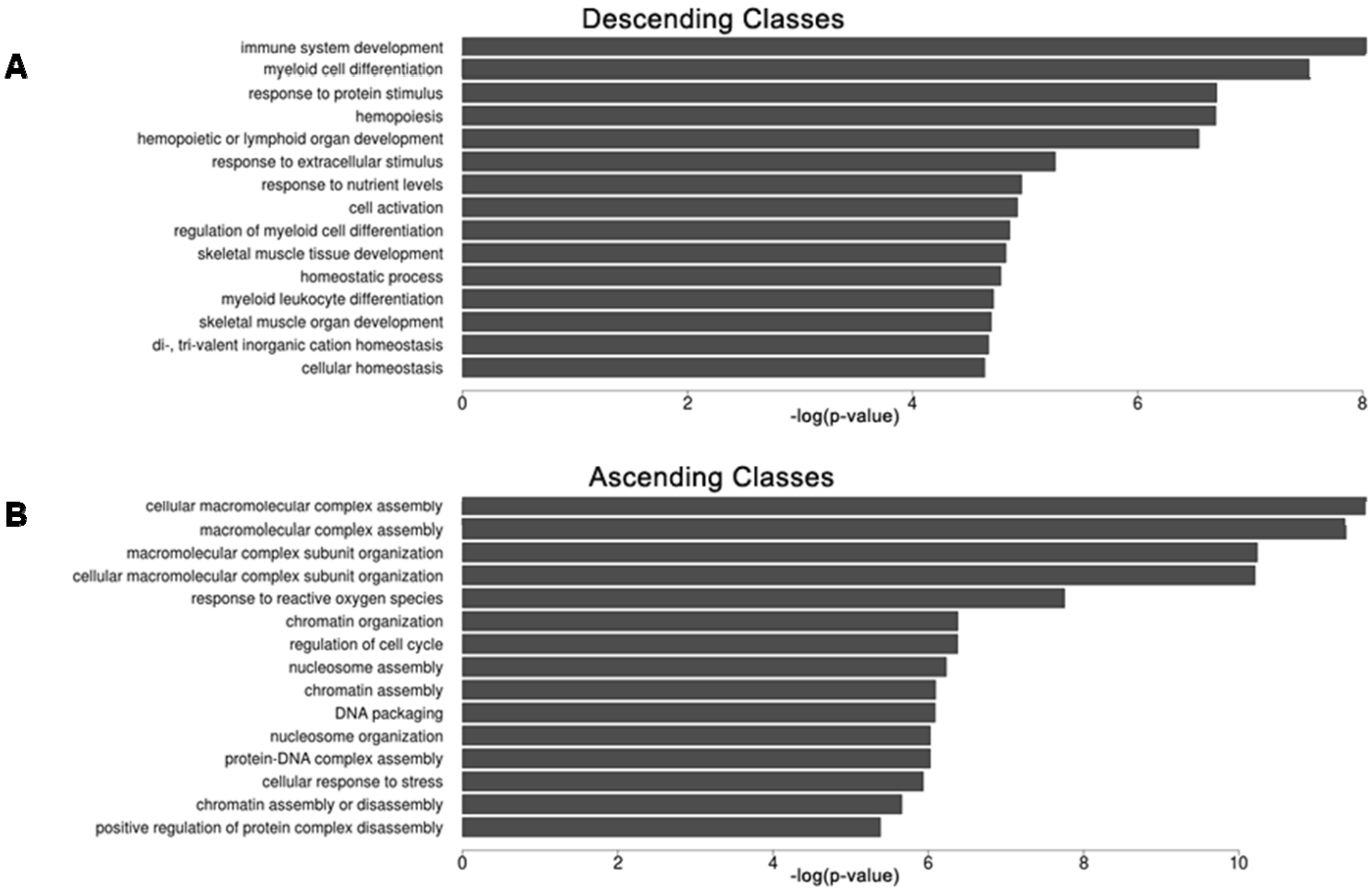
B. Location analysis of GATA-1 peaks. Left: Percentage of intragenic and intergenic peaks. Middle: Distribution of intragenic GATA-1 peaks in 5'UTR, 3'UTR, introns and exons. Right: Distribution of intergenic GATA-1 peaks in 0-5kb, 5-25kb, 25-50kb and >50kb windows from TSS.

FIGURE S2



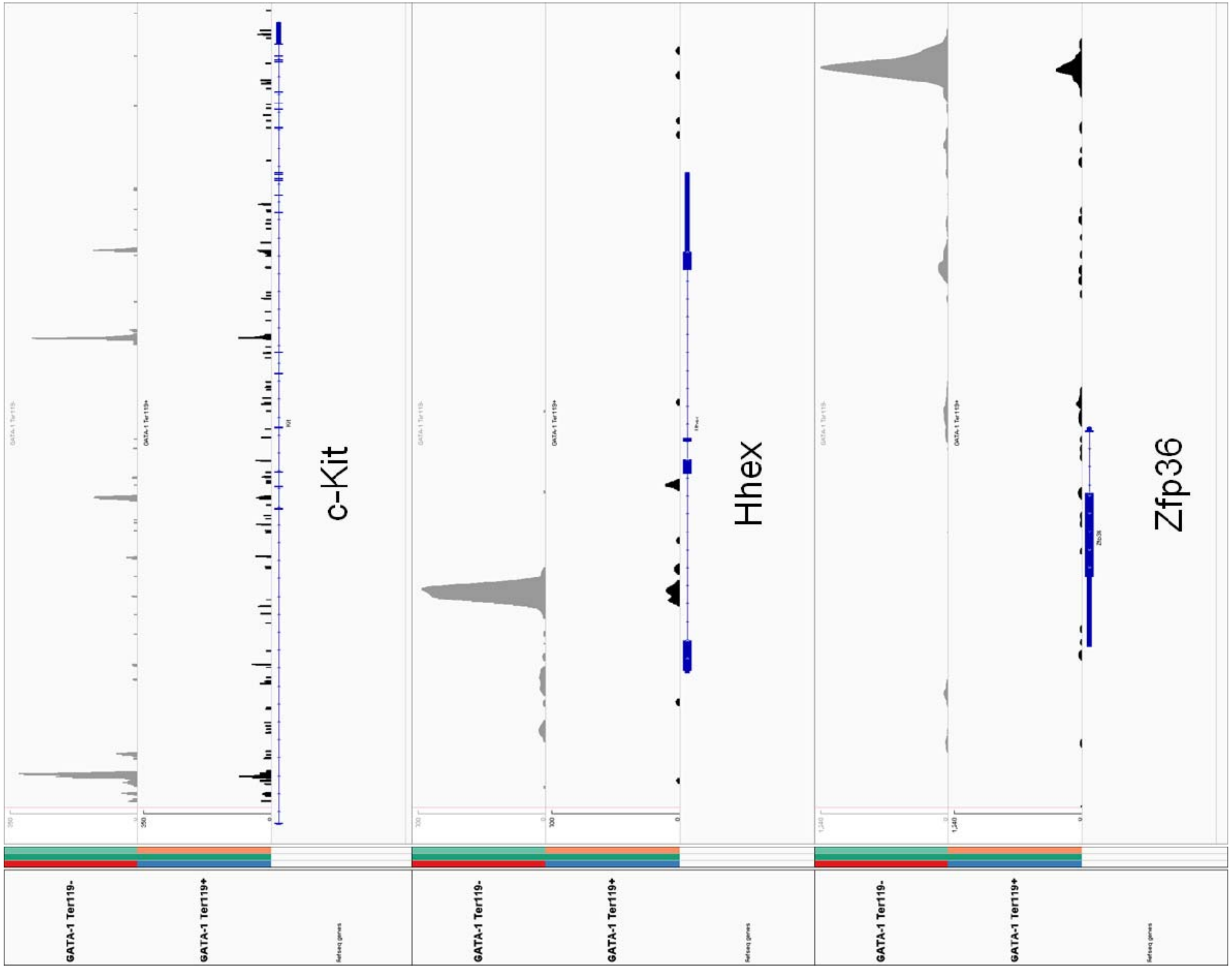
Supplementary Figure S2. GO analysis of GATA-1 target genes composing the TGS Class I
Results are shown for genes identified in Ter119- (green bars) and Ter119+ (red bars). Blue bars refer to genes identified in both Ter119- and Ter119+ cells with a TGS score higher than 500 (Class I threshold).

FIGURE S3



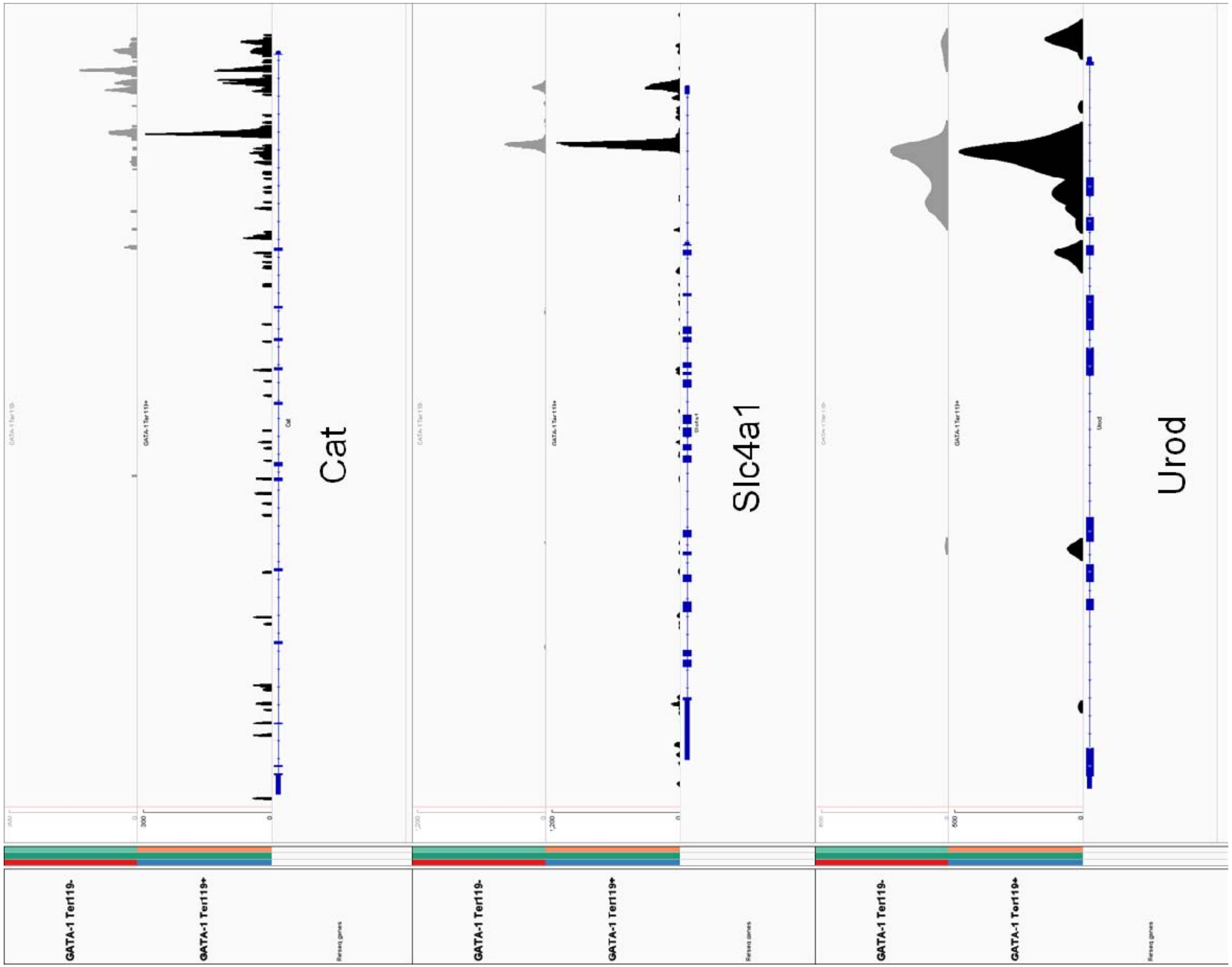
Supplementary Figure S3. GO analysis of GATA-1 target genes switching TGS Classes
Results are shown for genes identified in Ter119- and Ter119+ that fall in different TGS classes in each dataset.
A. Descending genes transition to a lower TGS class with differentiation.
B. Ascending genes represent genes transitioning to a higher TGS class with differentiation

FIGURE S4



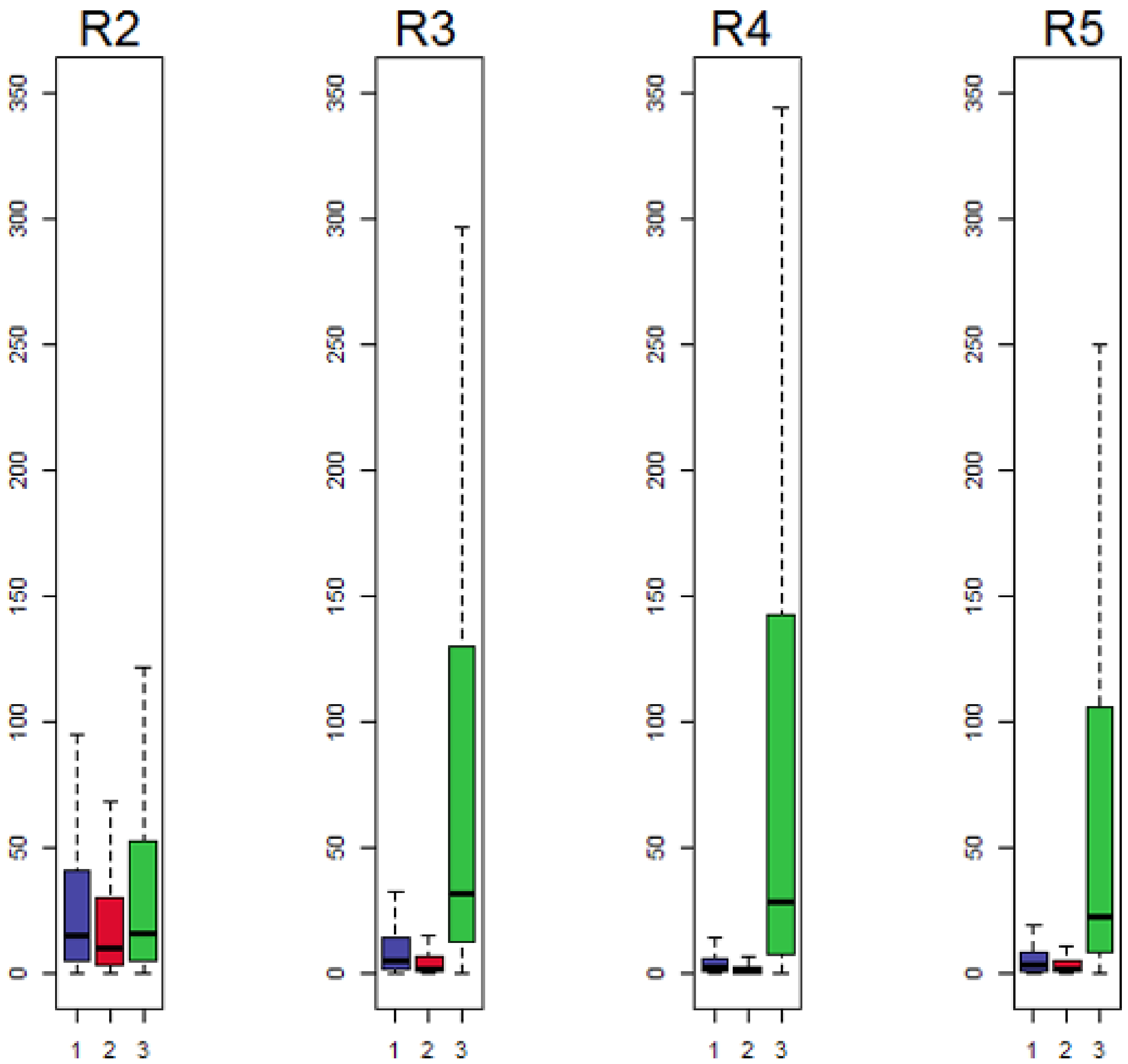
Supplementary Figure S4. Examples of GATA-1 enrichment profiles of genes showing decreasing GATA-1 levels

FIGURE S5



Supplementary Figure S5. Examples of GATA-1 enrichment profiles of genes showing increasing GATA-1 levels

FIGURE S6



Supplementary Figure S6. Absolute mRNA levels of clustered GATA-1 target genes
Boxplots illustrating the distribution of absolute mRNA levels between genes composing each of the three identified clusters along the R2 to R5 stages of erythroid differentiation