

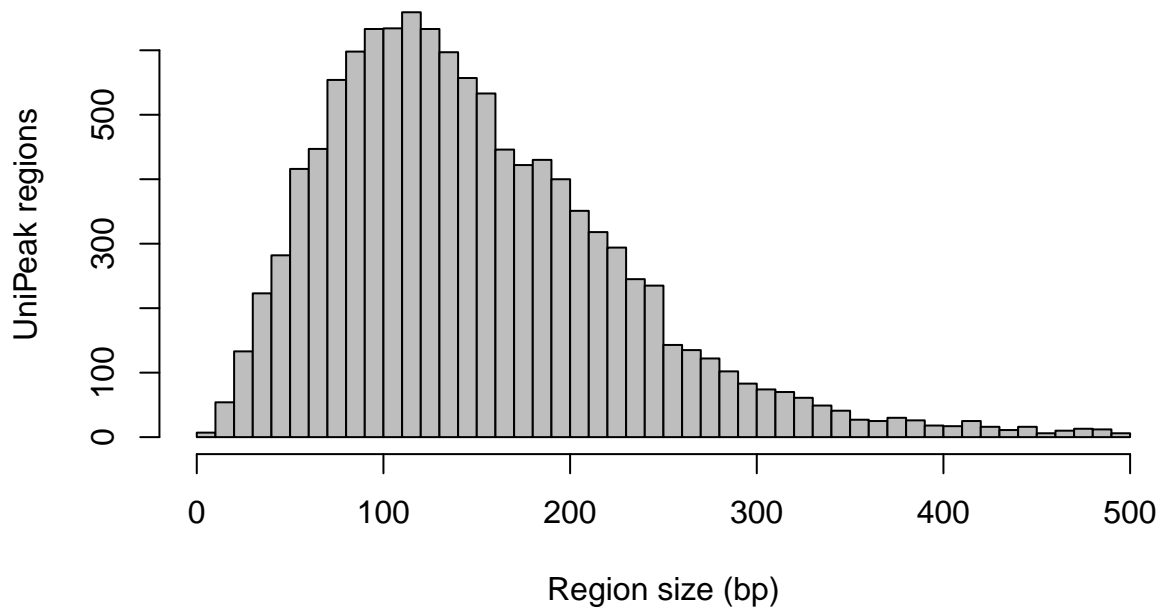
Table S1: ChIP-seq samples used in this analysis. Most TFs were not tested in most of the 5 cell lines. Symbols indicate which laboratory performed the experiment: M, Myers (HudsonAlpha); S, Snyder (Yale/Stanford); B, Bernstein (Broad); the number of symbols shows the number of replicates. Different antibodies to the same protein (e.g. MafK_ab50322, MafK_SC-477) showed very similar results and therefore were not treated distinctly for analysis.

	GM12878	H1-hESC	HeLa-S3	HepG2	K562
	canonical transcription factor				
ATF2	MM	MM			
ATF3	MM	MM		MM	MM
BATF	MM				
BCL11A	MM	MM			
BCL3	MM				
BCLAF1	MM				MM
BHLHE40	SS			MMSS	SS
CEBPB			SS	MMSS	SS
CEBPD				MM	
E2F6					MM
EBF1	MMSS				
EGR1	MMM	MM			MM
ELF1	MM			MM	MM
ETS1	MM				MM
FAM48A (SPT20)			SS		
FOS (c-Fos)	SSS		SS		SSS
FOSL1		MM			MM
FOSL2				MM	
FOXA1				MMMM	
FOXA2				MM	
GABPA (GABP)	MM	MM	MM	MM	MM
GATA2					MM
HEY1				MM	
HNF4A				MM	
HNF4G				MM	
IRF3	SS		SS	SS	
IRF4	MM				
JUN (c-Jun)		SS	SS	SS	SS
JUND	SS	MMSS	SS	MMSS	SS
MAFF				SS	SS
MAFK				SSSS	SS
MAX	SS		SSSS	SS	MMSSSS
MEF2A	MM				MM
MEF2C	MM				
MTA3	MM				
MXI1	SS		SS		SS
MYC (c-Myc)		SS	SS		SSSS
NANOG		MM			
NFATC1	MM				
NFE2	SS				SS
NFIC				MM	
NFYA					SS

	GM12878	H1-hESC	HeLa-S3	HepG2	K562
NFYB					SS
NRF1	SS	SS	SS	SS	SS
PAX5	MMMM				
PBX3	MM				
PML	MM				MM
POU2F2	MMM				
POU5F1		MM			
PRDM1			SS		
REST (NRSF)	MMMM	MM	MM	MMMM	MM
RFX5	SS	SS	SS	SS	SS
RUNX3	MM				
RXRA	MM	MM		MM	
SIN3A		MM		MM	MM
SIX5	MM	MM			MMMM
SP1	MM	MM		MM	MM
SP2		MM		MM	MM
SP4		MM			
SPI1 (PU.1)	MMM				MM
SRF	MMMM	MM		MM	MM
STAT1	SS				
STAT3	SS		SS		
STAT5A	MM				
TAL1					SS
TCF12	MM	MM		MM	
TCF3	MM				
TEAD4					MM
THAP1					MM
USF1	MM	MM		MM	MM
USF2	SS	SS	SS	SS	SS
YY1	MM	MM		MM	MMMM
ZBTB33	MM			MMMM	MM
ZBTB7A				MM	MM
ZEB1	MM				
ZNF143	SS	SS	SS		SS
cohesin complex					
CTCF	SS	MM		MM	MMSS
CTCFL					MM
RAD21	MMSS	MMSS	SS	MMSS	MMSS
SMC3	SS		SS	SS	SS
chromatin remodeler					
BRCA1	SS	SS	SS	SS	
CHD2	SS		SS	SS	SS
EP300 (p300)	MMSSSSSS	MM	SS	MMSS	SSSS
HDAC2		MM		MM	MM
KAT2A (GCN5)			SS		
MBD4				MM	
SMARCA4 (BRG1)			SSS		SS
SMARCB1 (INI1)			SSS		SS
SMARCC1 (BAF155)			SSS		

	GM12878	H1-hESC	HeLa-S3	HepG2	K562
SMARCC2 (BAF170)			SSS		
WRNIP1 (WHIP)	SS				
XRCC4					SS
preinitiation complex					
GTF2F1			SS		SS
TAF1	MM	MM	MM	MM	MM
TAF7		MM			MM
TBP	SS	SS	SS	SS	SS
polymerase					
Pol II-S2P	SS	SS	SS		SS
Pol II-S5P	MMSSSSSSS	MM	MMSSS	MMSS	MMSSSS
control					
input	MMMMMMSSSS	MS	MSSSS	MMMMMMS	MMMMSSSSS
histone mark					
H3K27ac	BB	BB	BB	BB	BB
H3K4me1	BB	BB	BB	BB	BB
H3K4me3	BB	BB	BB	BB	BB

All proteins



Transcription factors

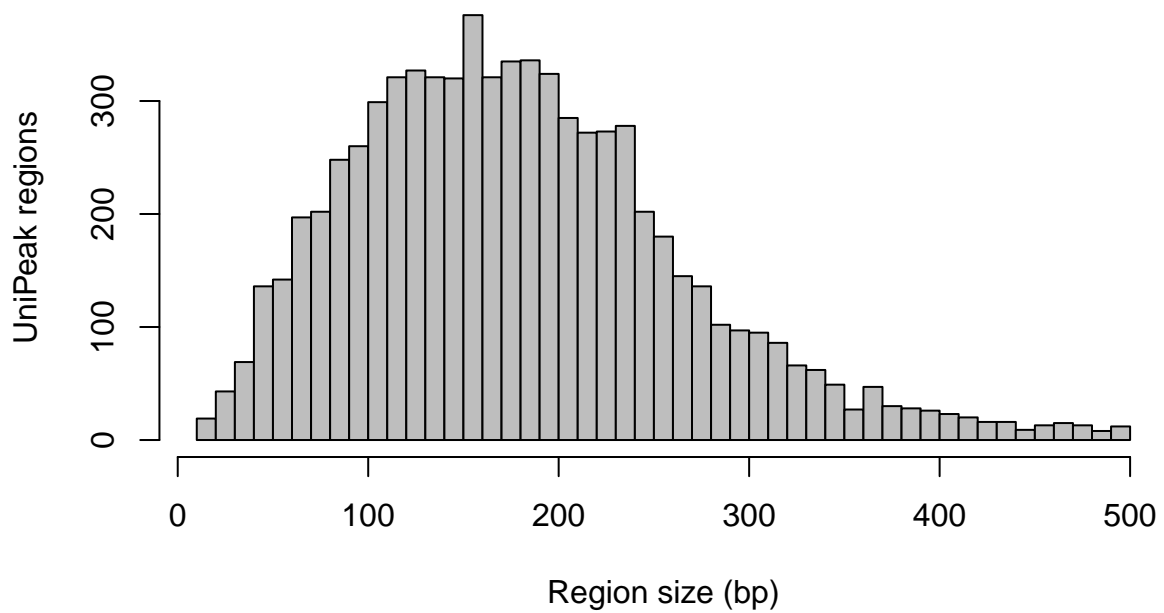
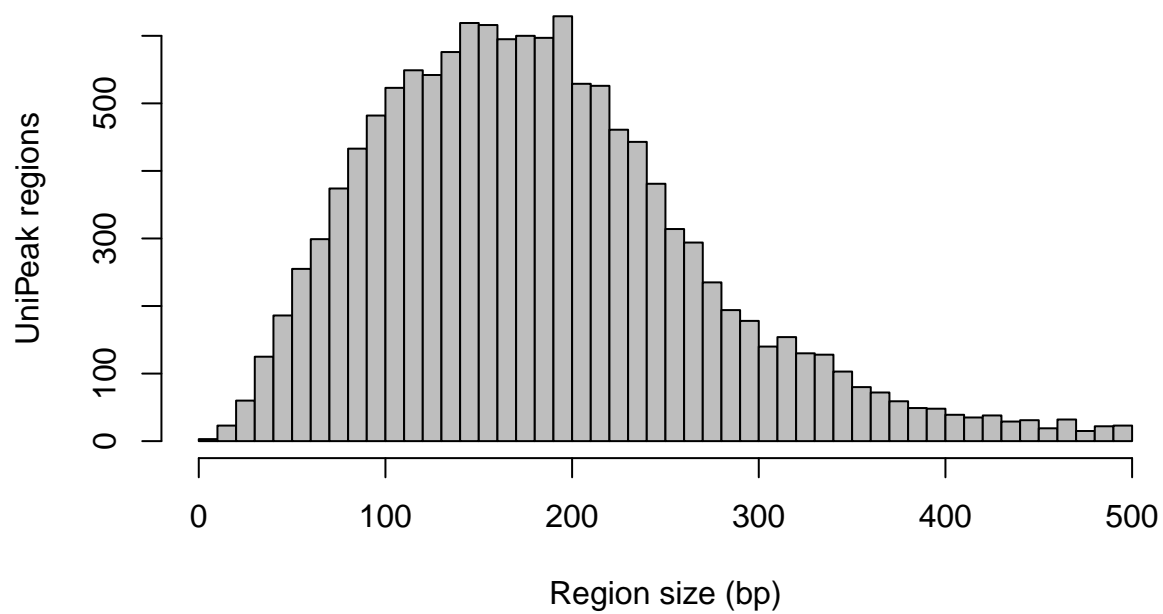


Figure S3

GM12878



K562

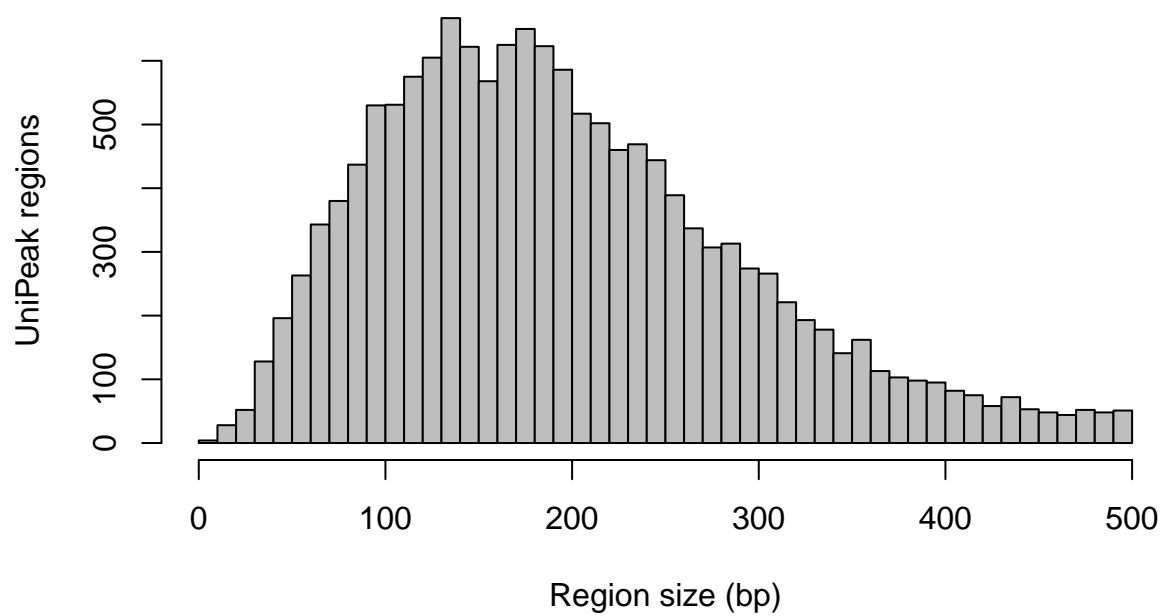
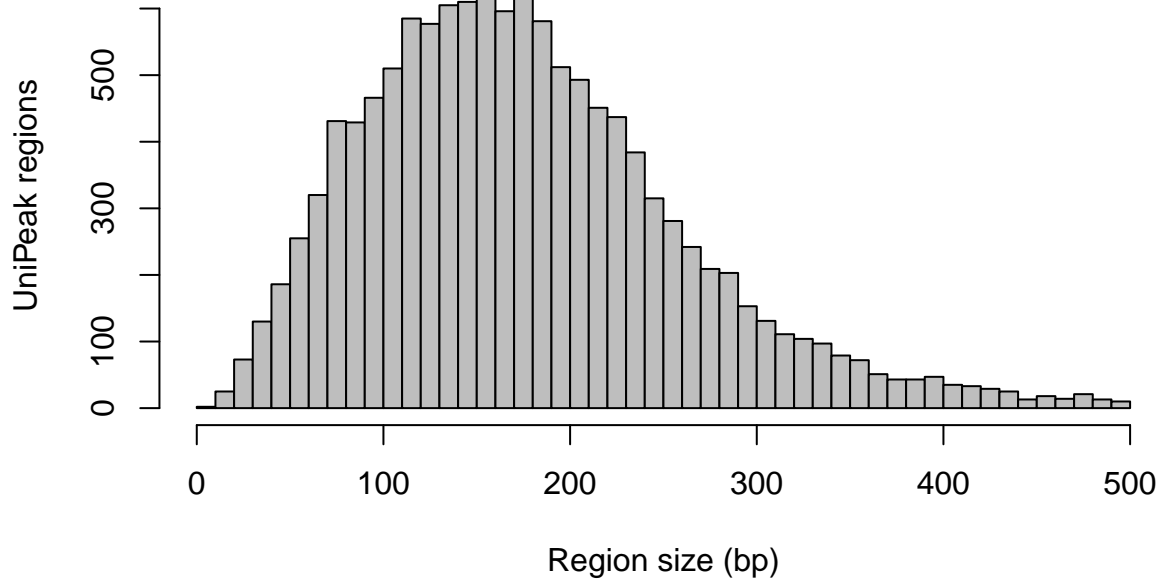


Figure S3

HepG2



H1-hESC

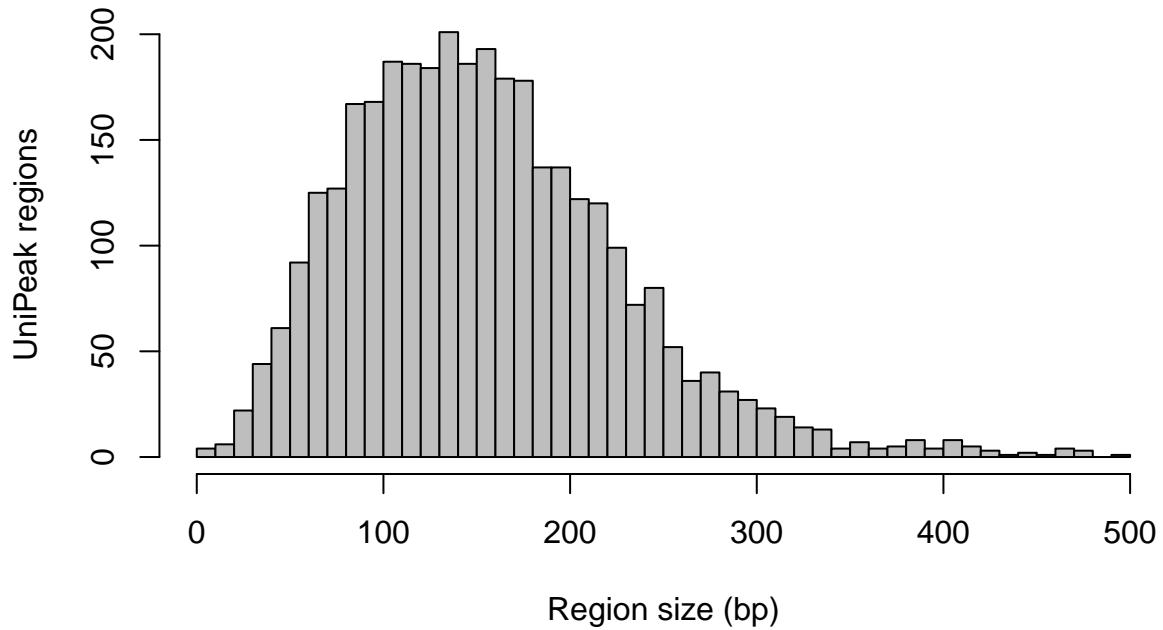


Figure S3

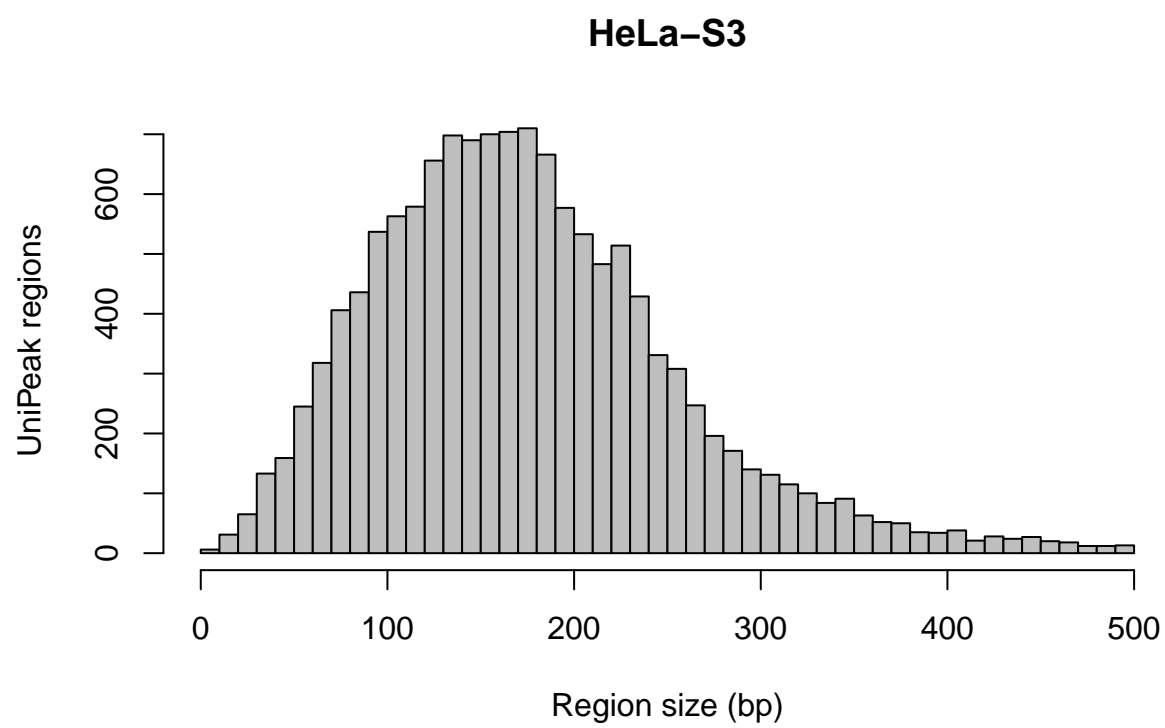


Figure S3: Distribution of UniPeak region sizes in all analyses.

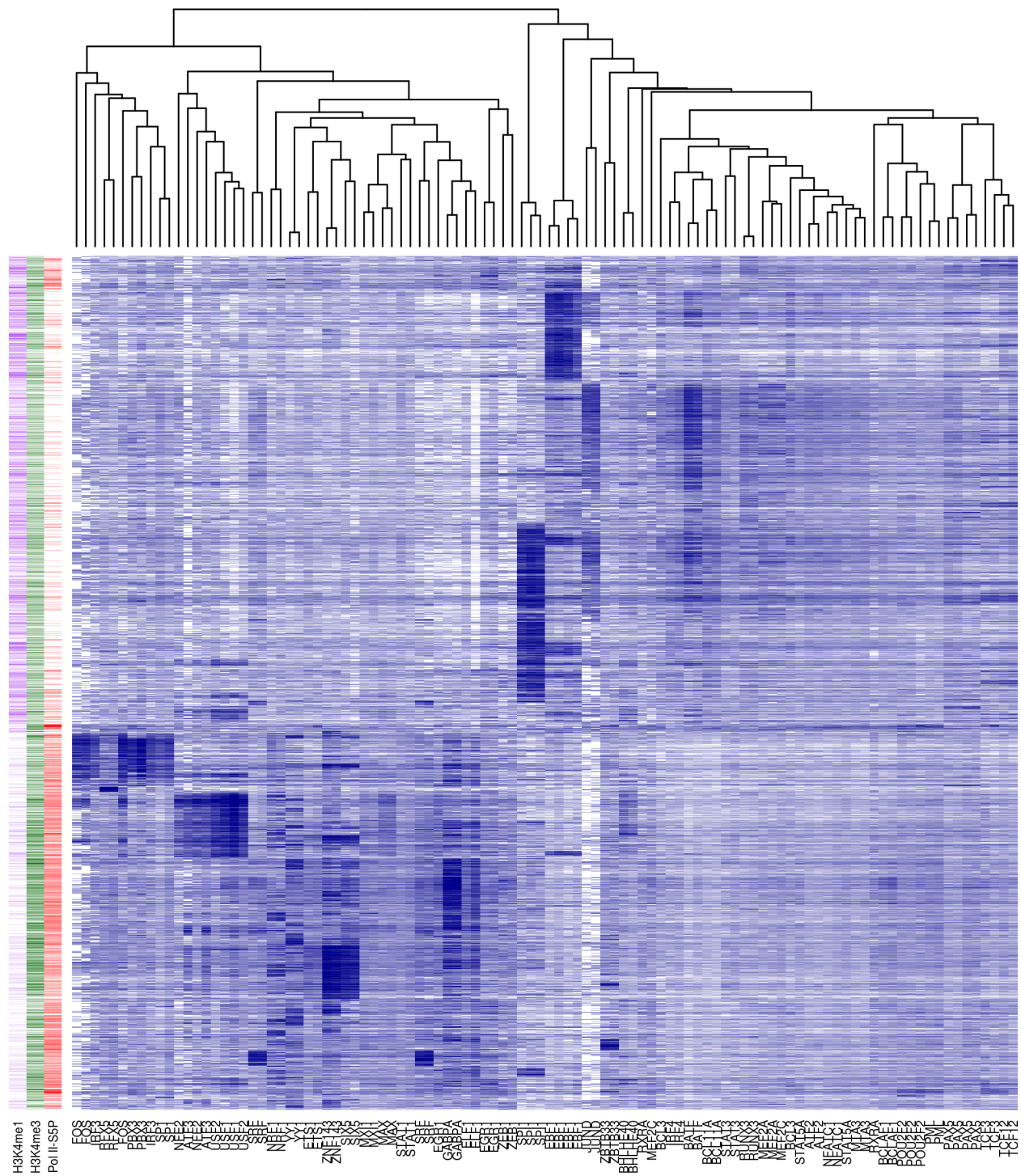


Figure S4

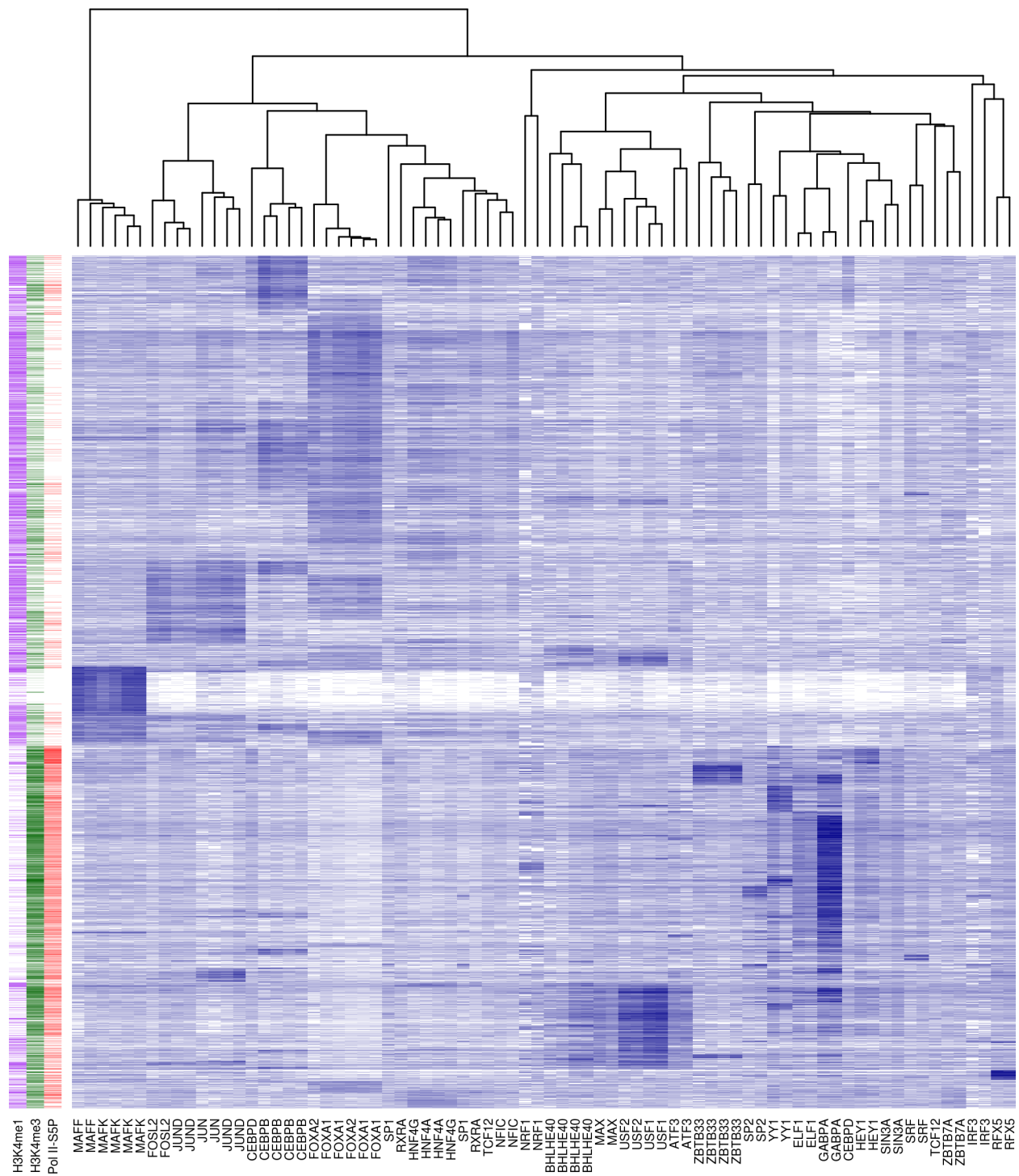


Figure S4

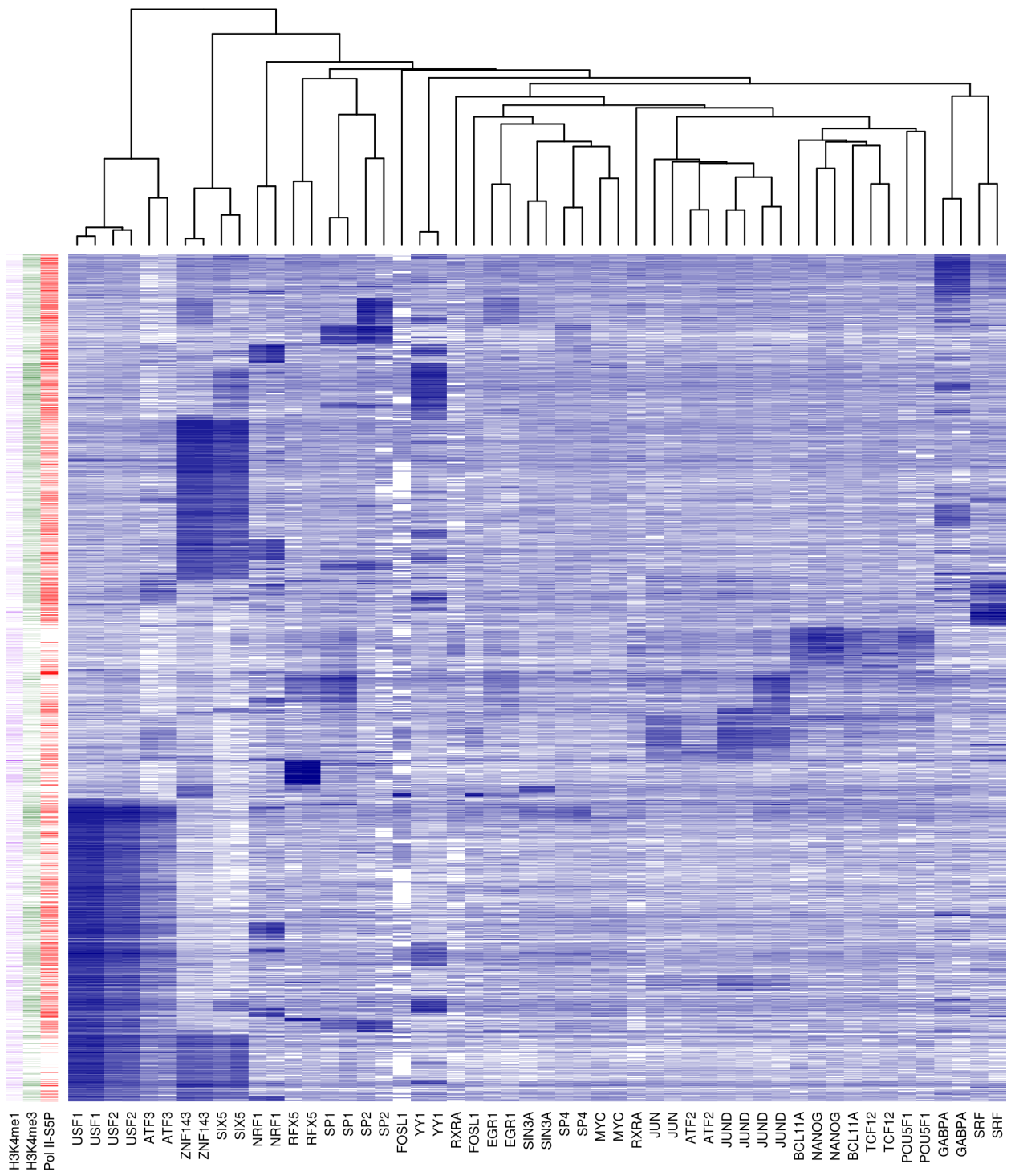


Figure S4

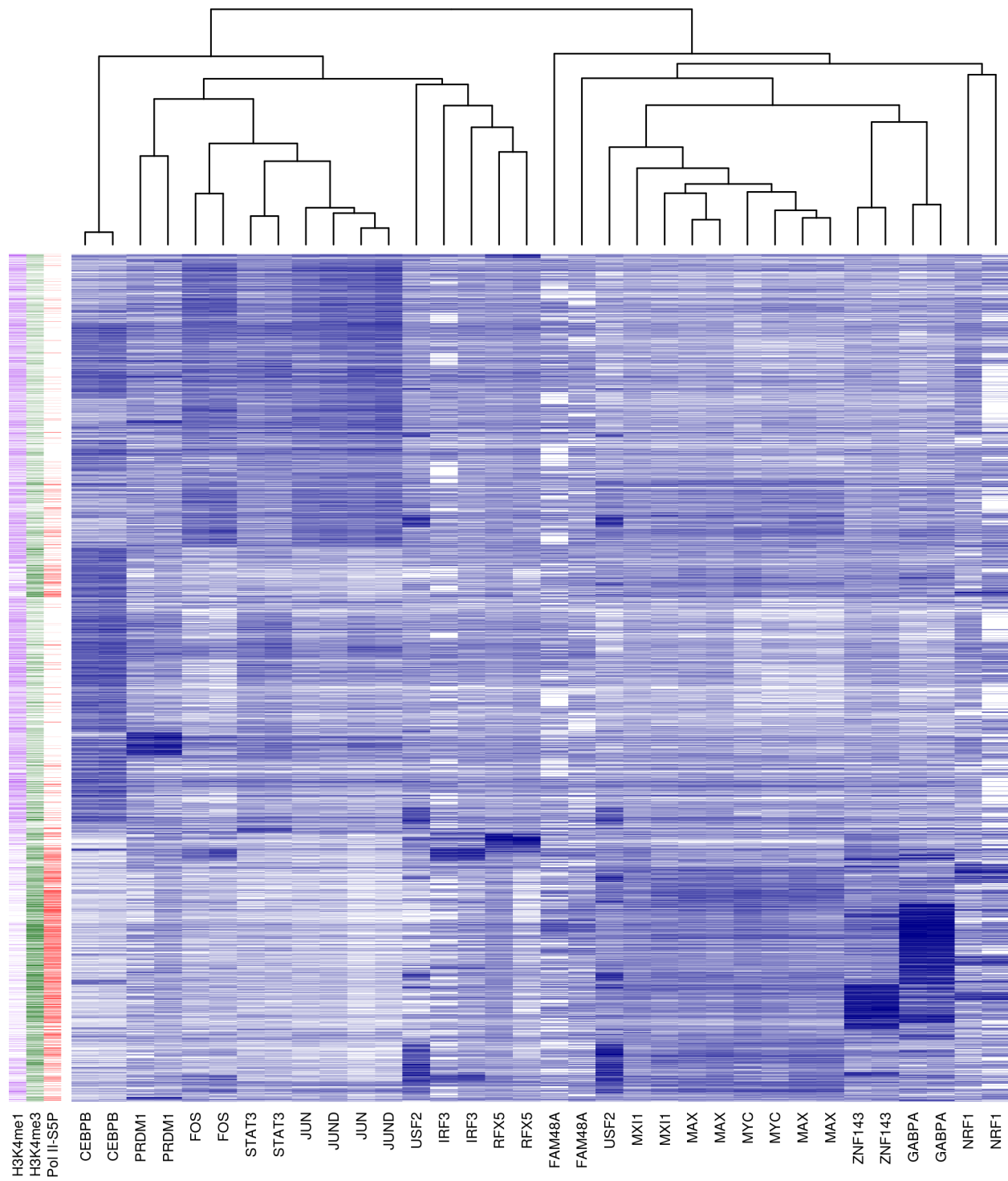
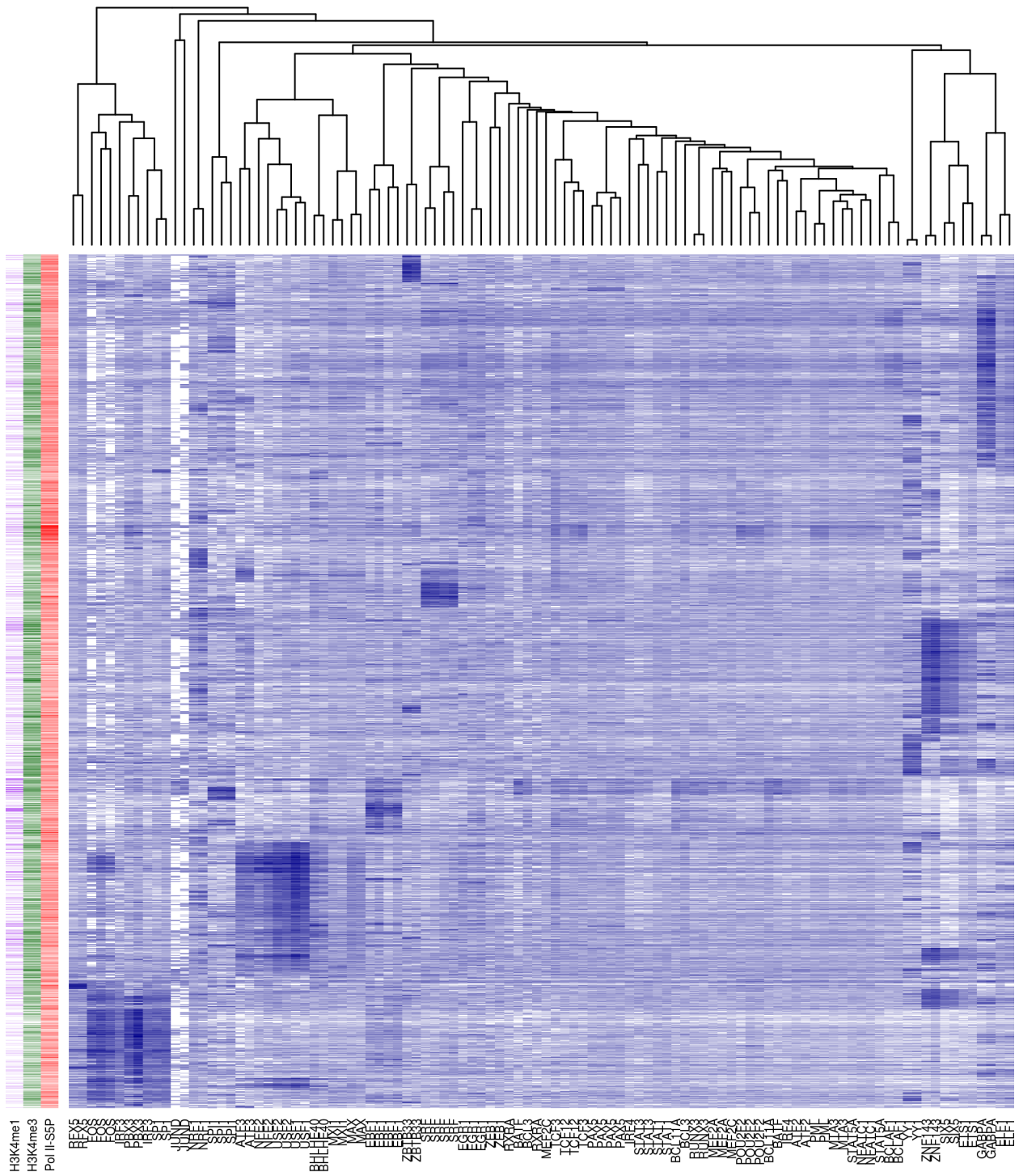


Figure S4: Clustered heatmaps for cell-specific analyses. S4a: GM12878. S4b: K562. S4c: HepG2. S4d: H1-hESC. S4e: HeLa-S3.



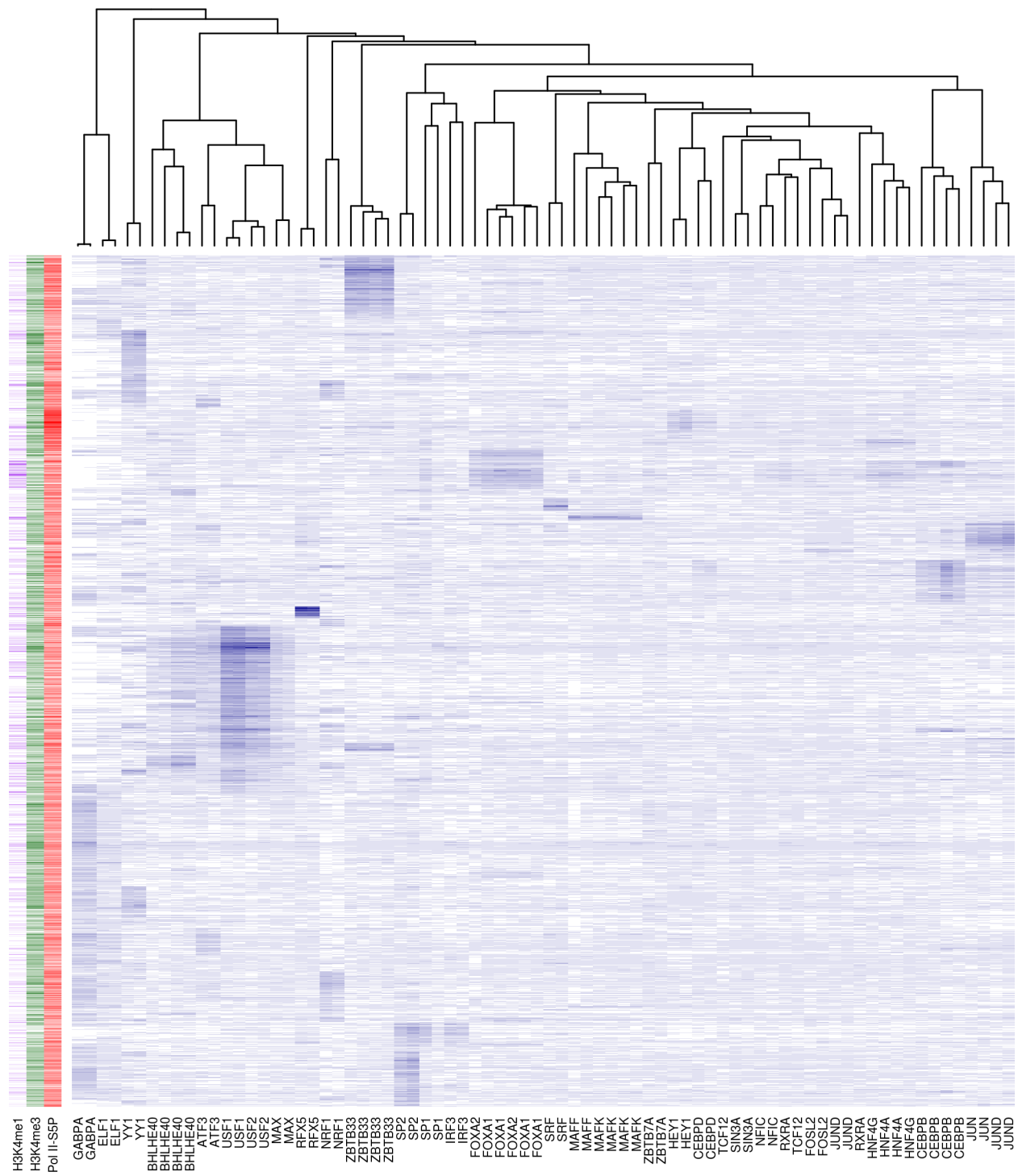


Figure S5

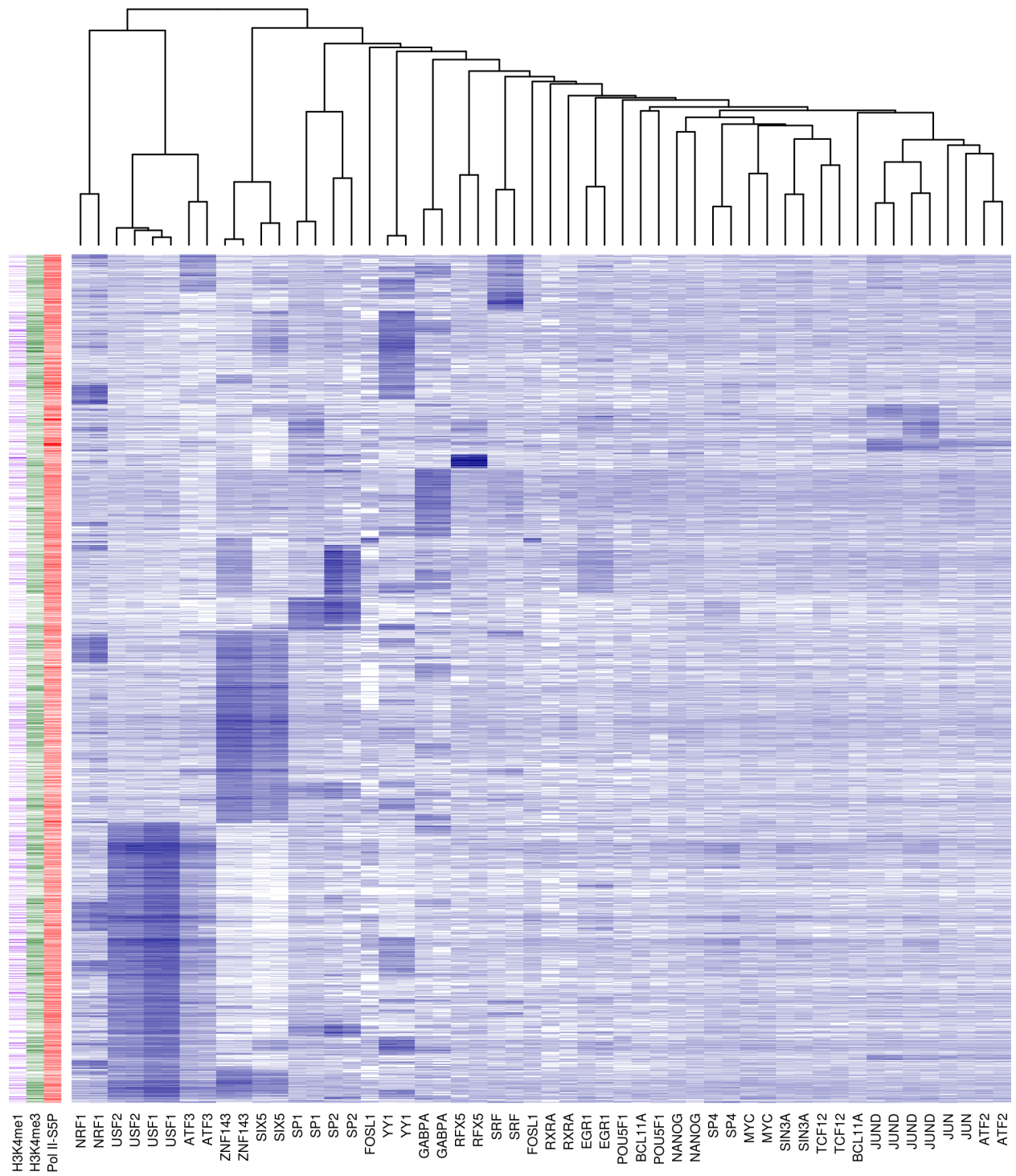


Figure S5

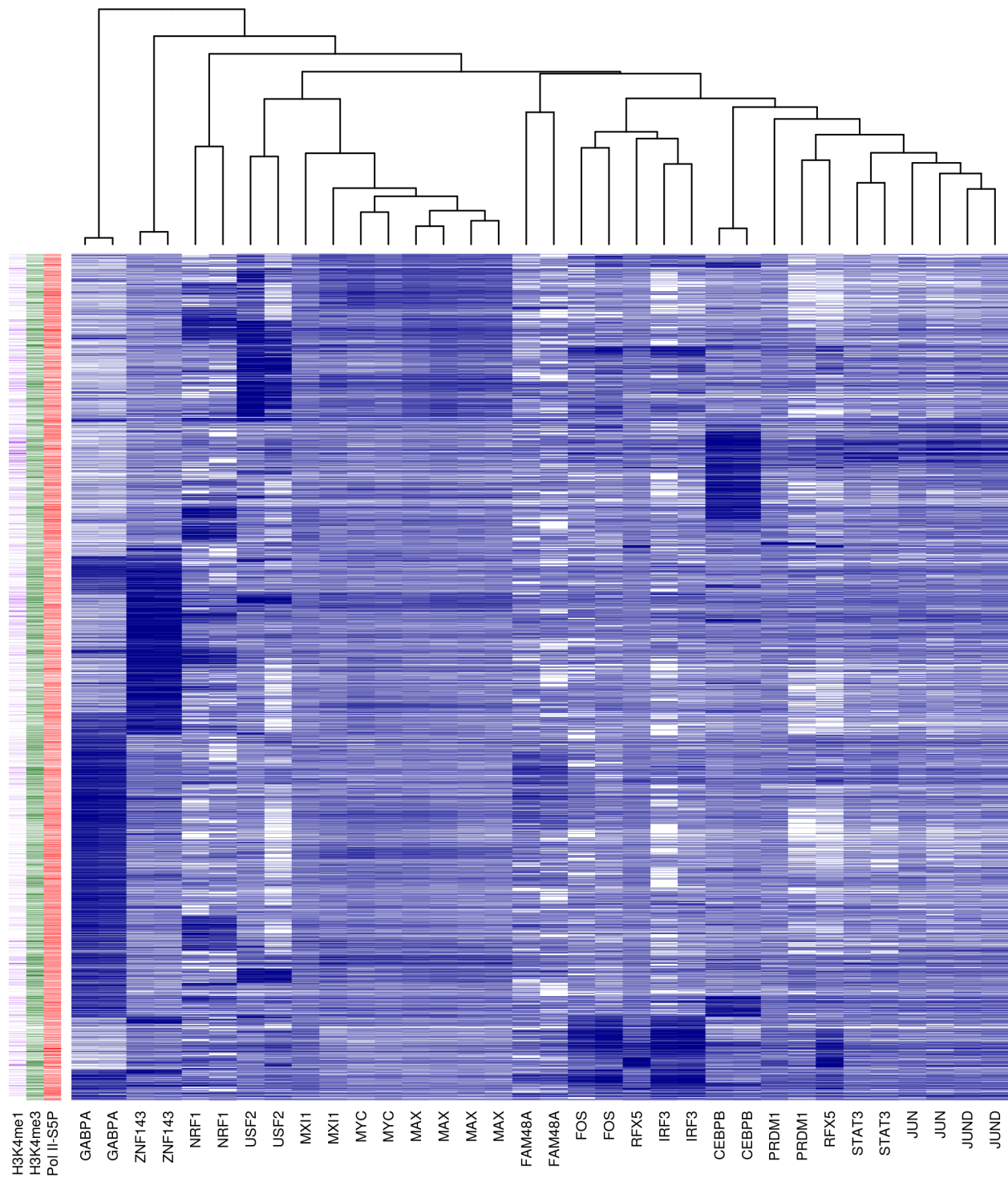


Figure S5: Clustered heatmaps for cell-specific analyses, consensus promoters only. S5a: GM12878. S5b: K562. S5c: HepG2. S5d: H1-hESC. S5e: HeLa-S3.

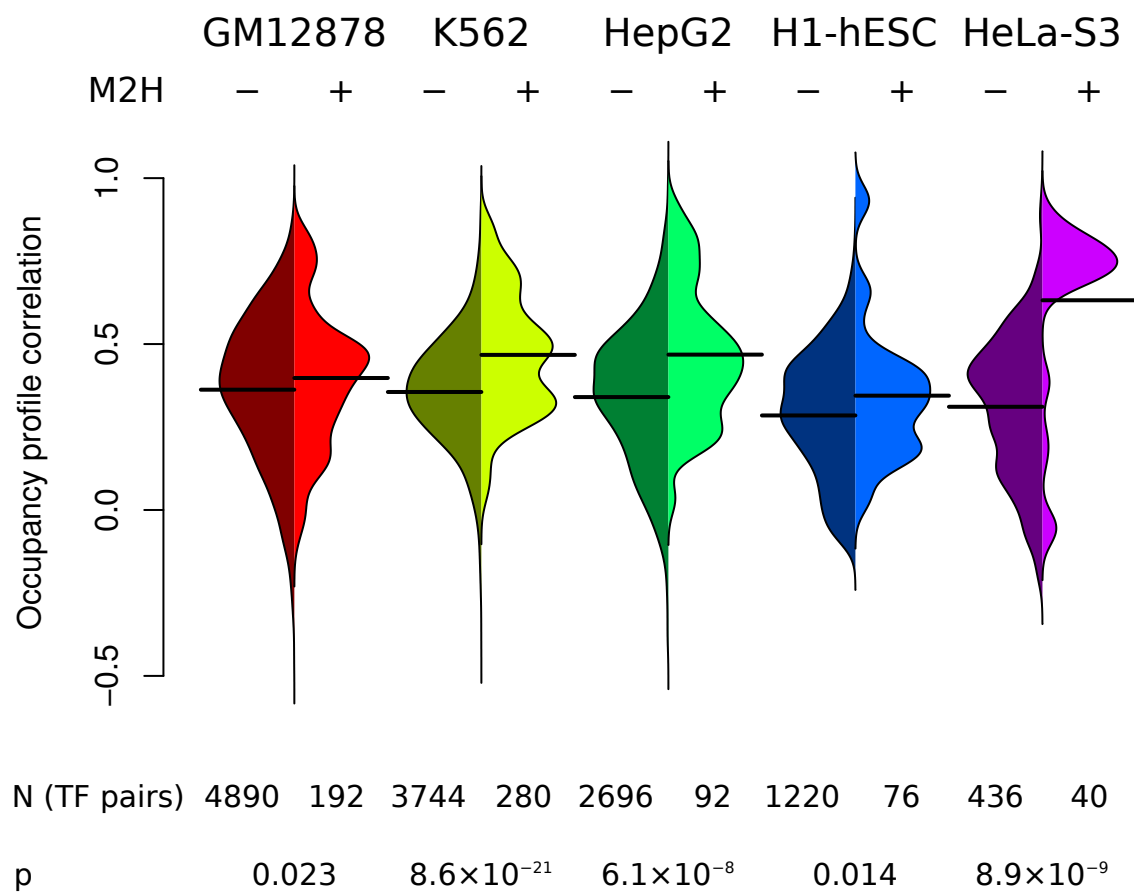


Figure S6: Occupancy profile correlations of interacting and non-interacting TFs. All pairwise correlations of occupancy profiles across all regions are plotted for each cell type, grouped by whether a mammalian two-hybrid (M2H) screen found the two TFs capable of directly binding each other. p -values are from the t -test.

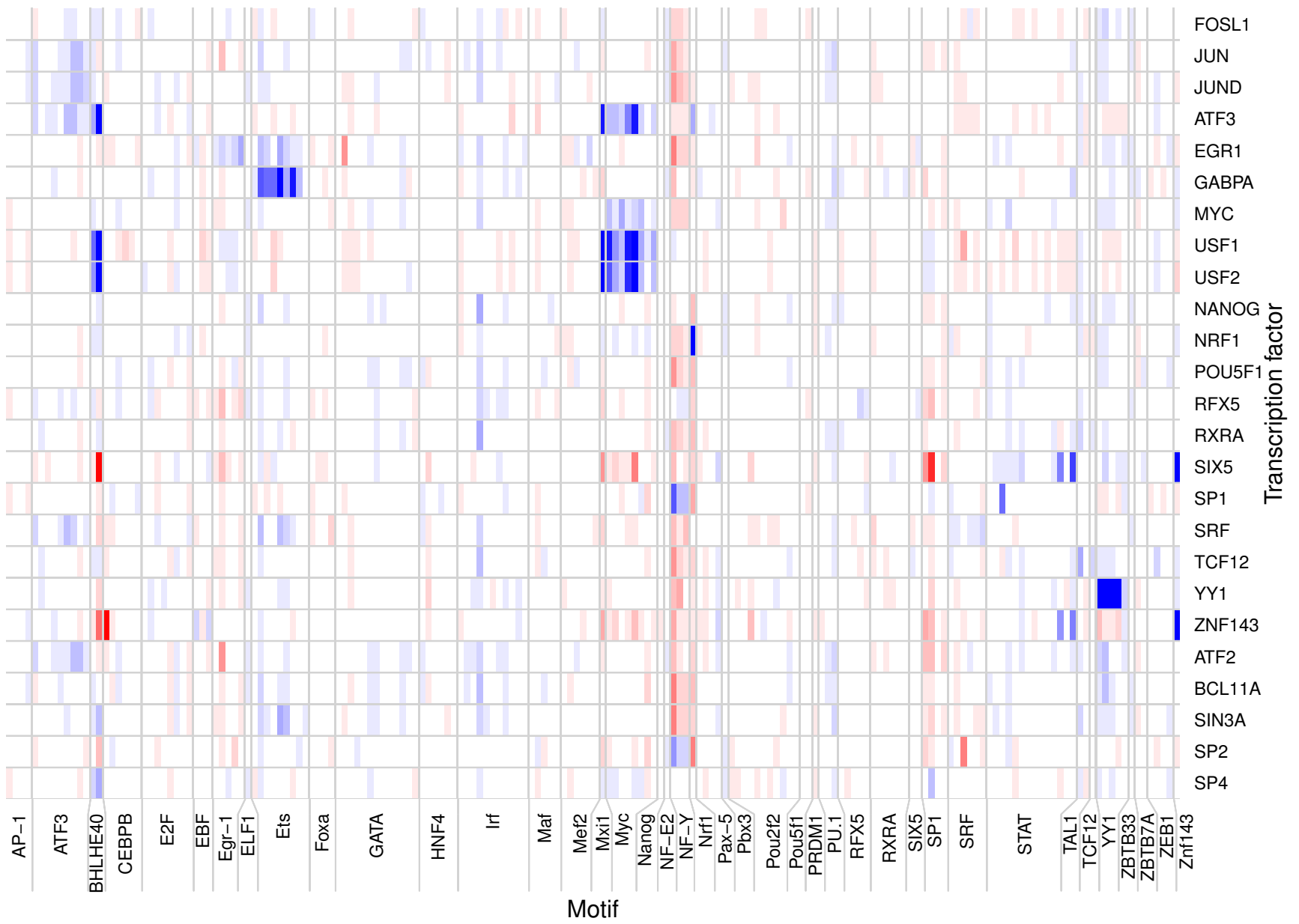


Figure S7

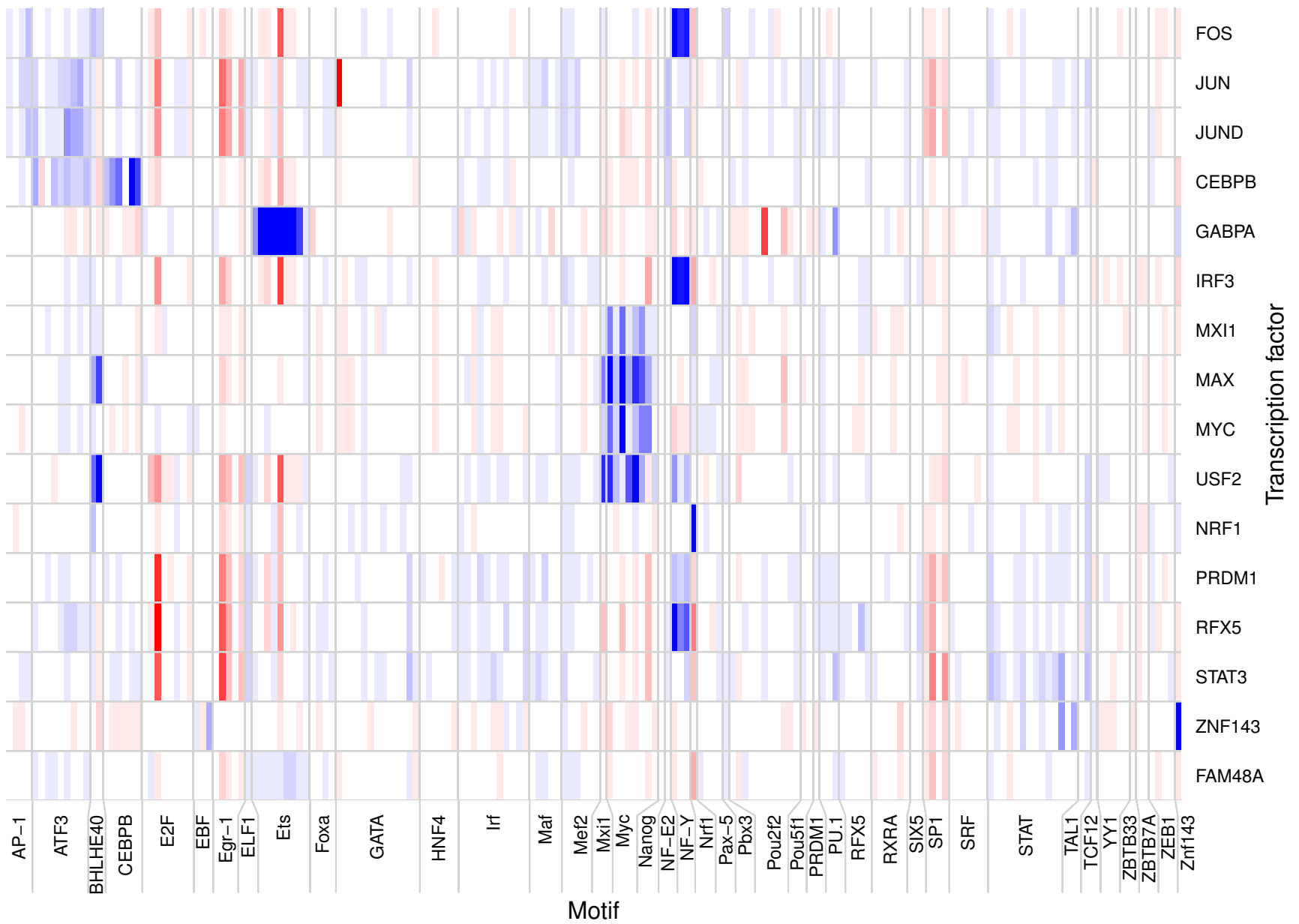


Figure S7: Sequence motifs vs. TF occupancy, by cell. S7a: K562. S7b: HepG2. S7c: H1-hESC. S7d: HeLa-S3.

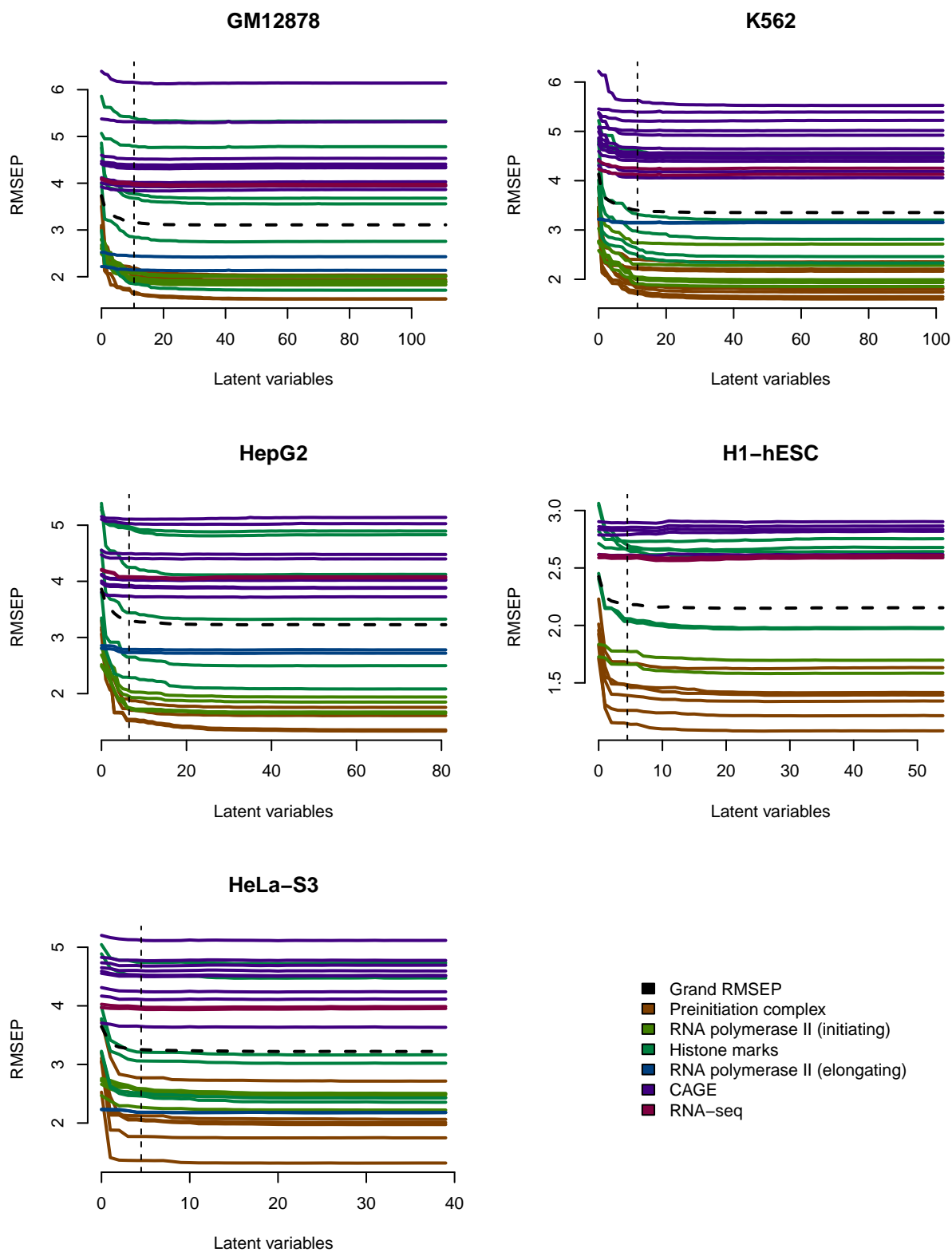


Figure S8: Root-mean-square error of prediction for partial least-squares regression analyses.

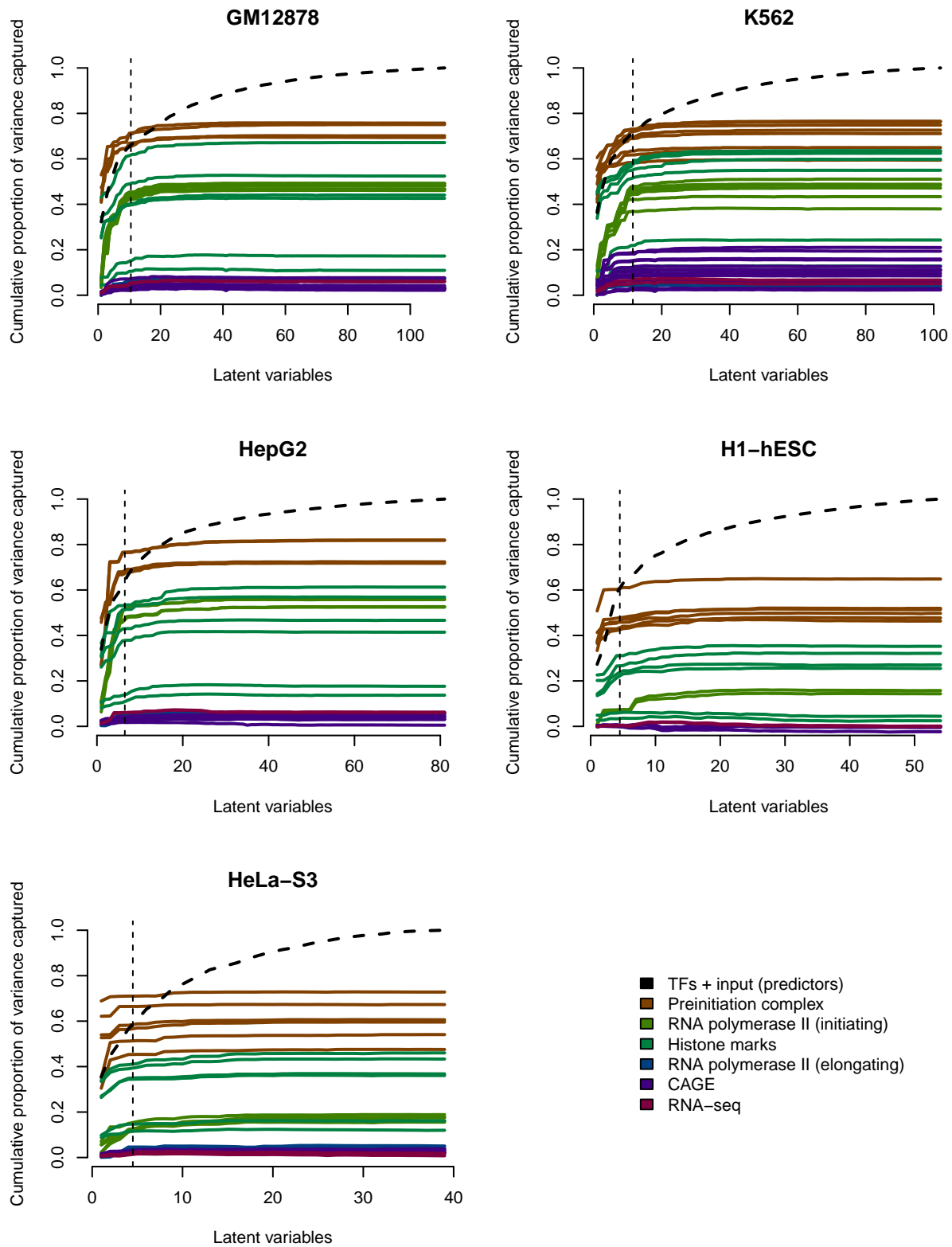


Figure S9: Variance captured by partial least-squares regression analyses.

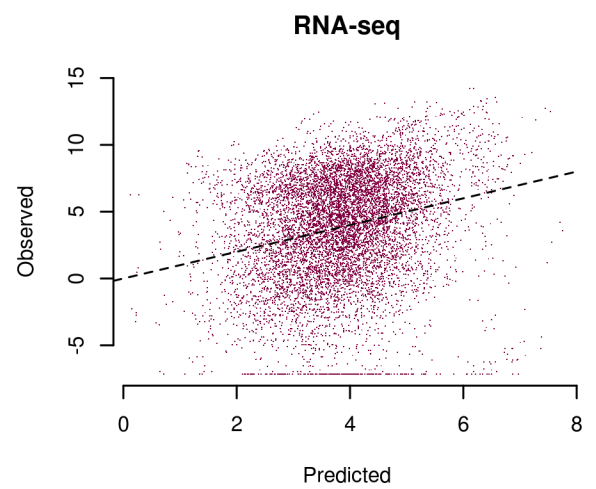
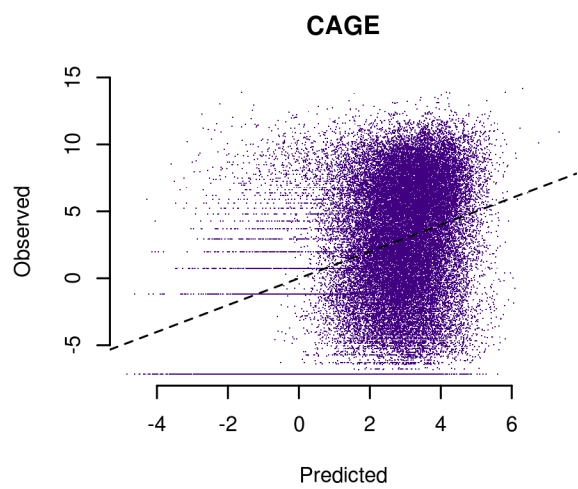
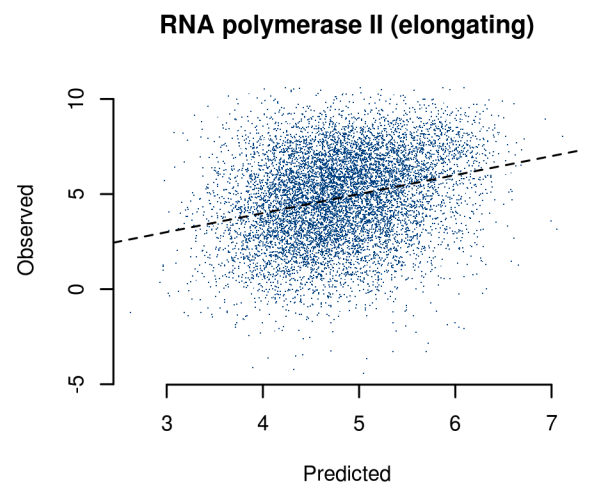
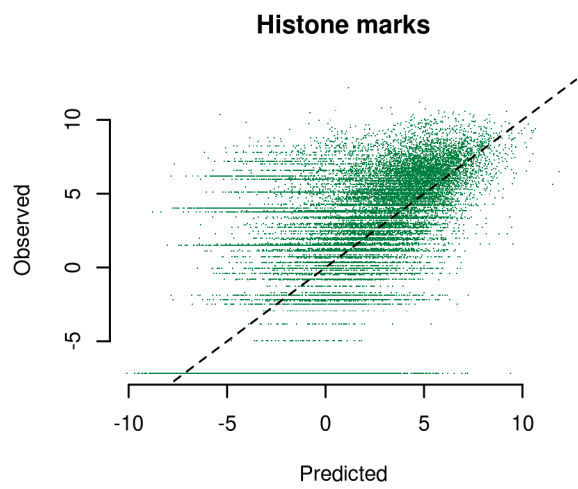
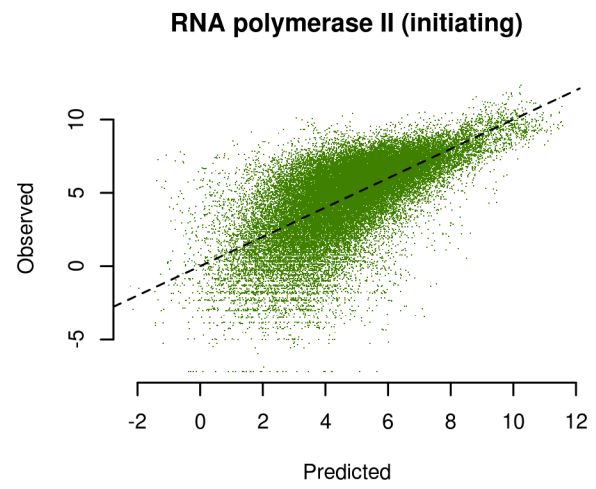
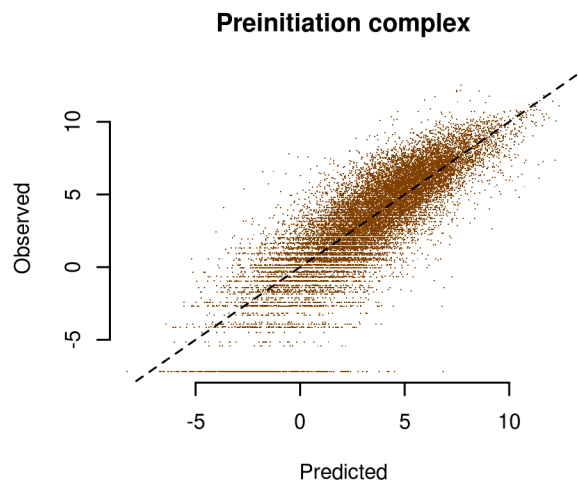


Figure S10

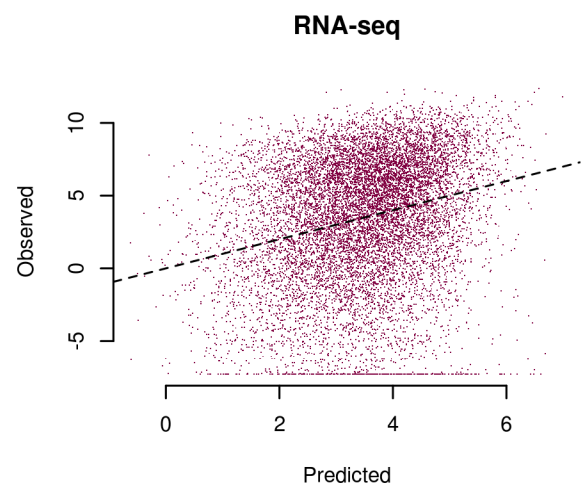
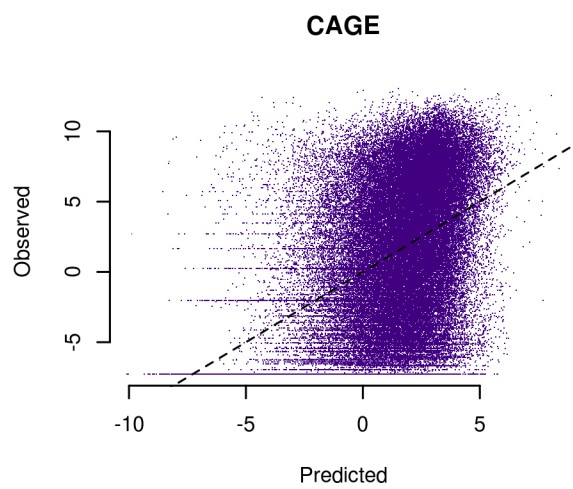
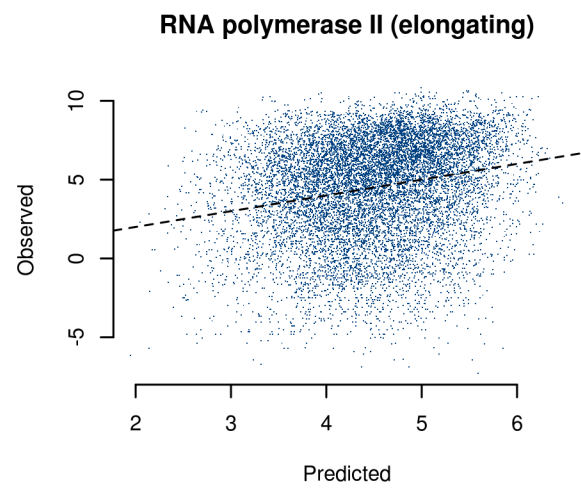
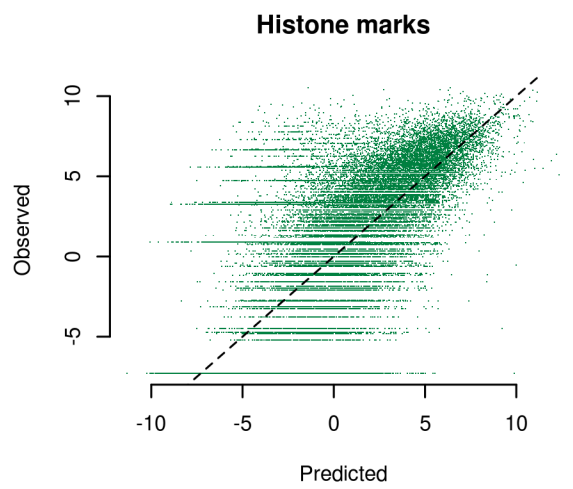
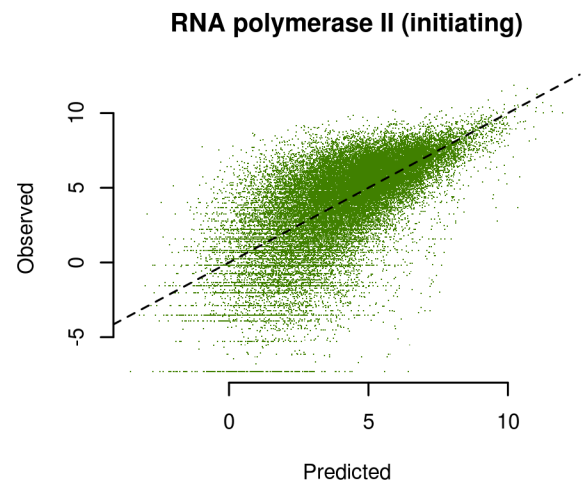
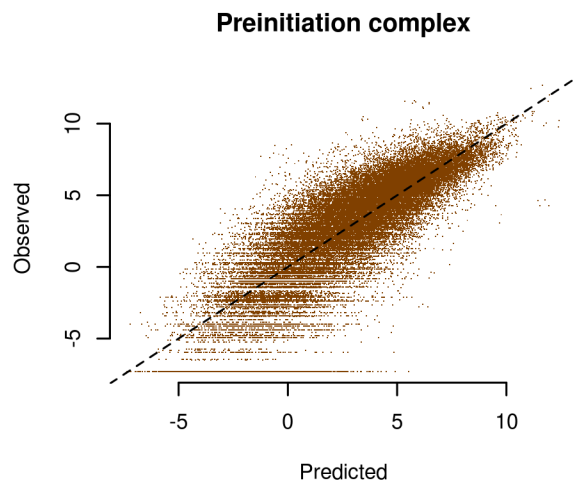


Figure S10

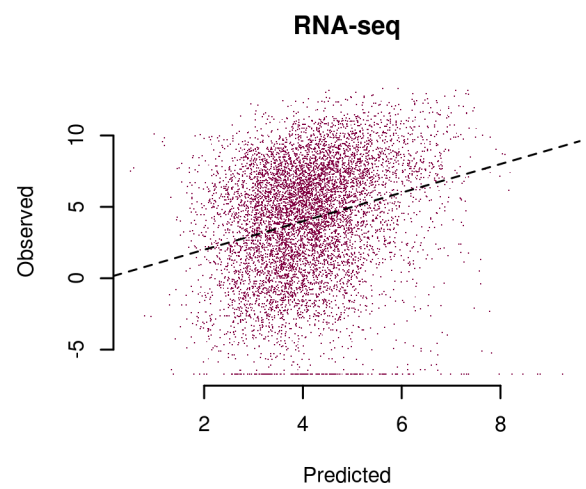
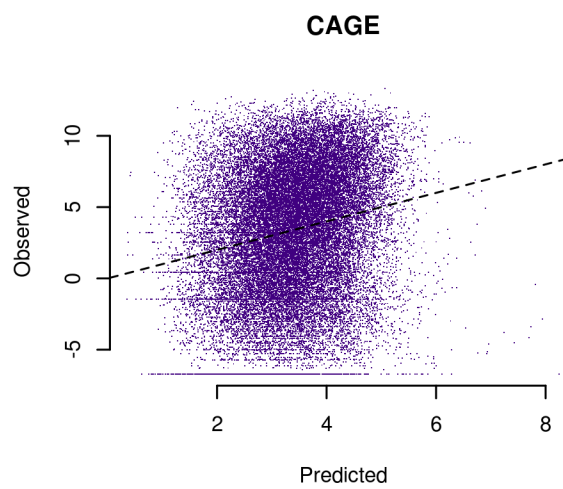
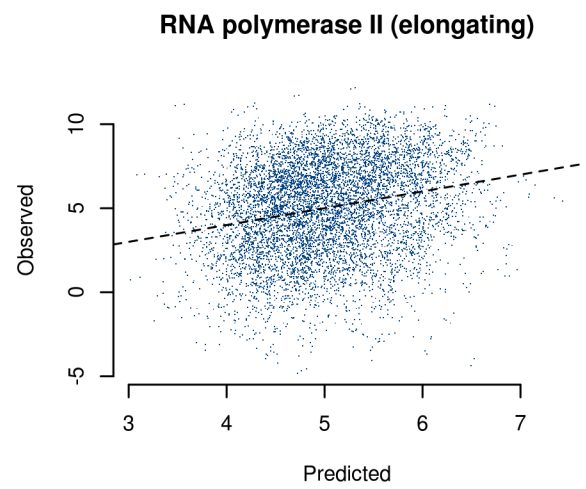
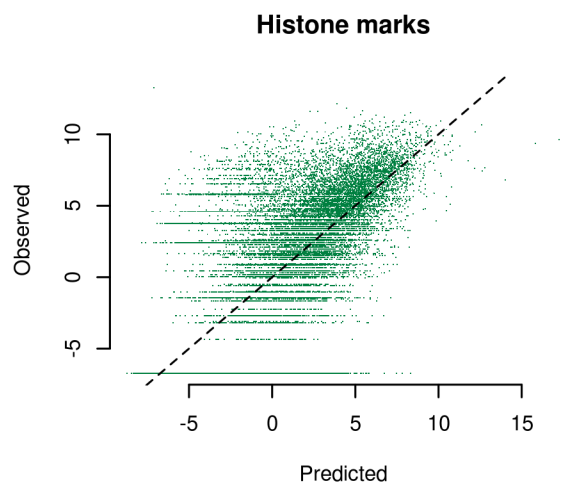
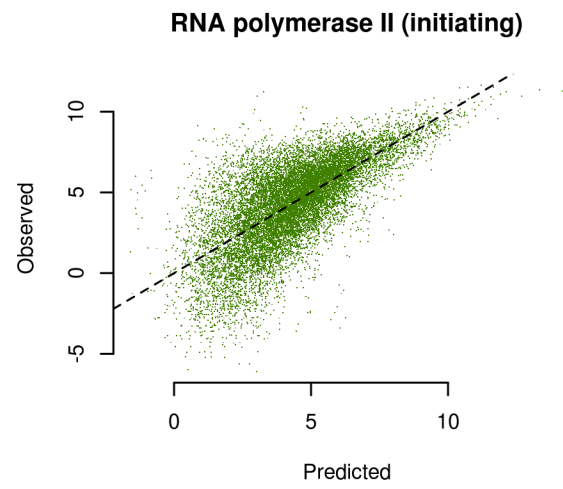
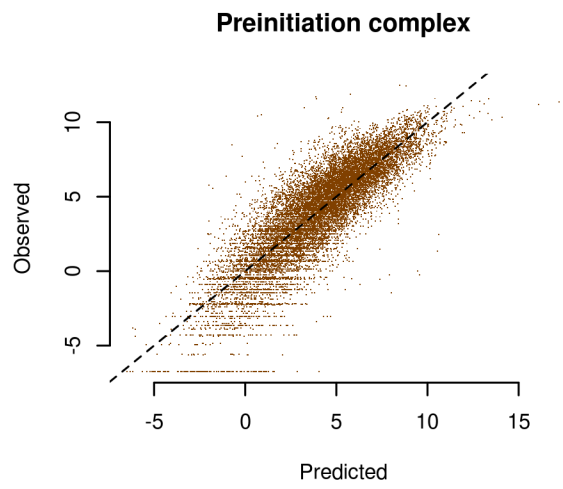


Figure S10

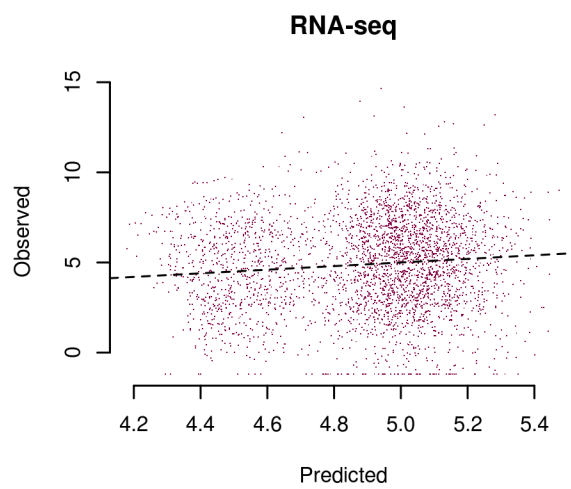
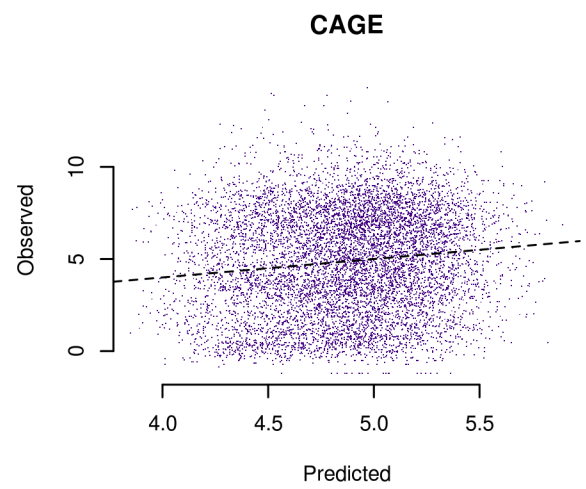
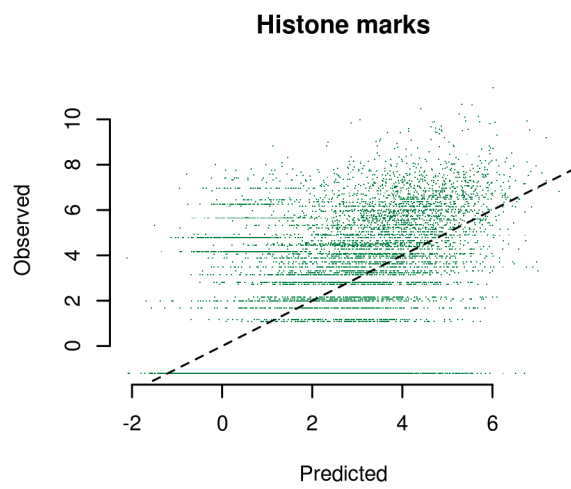
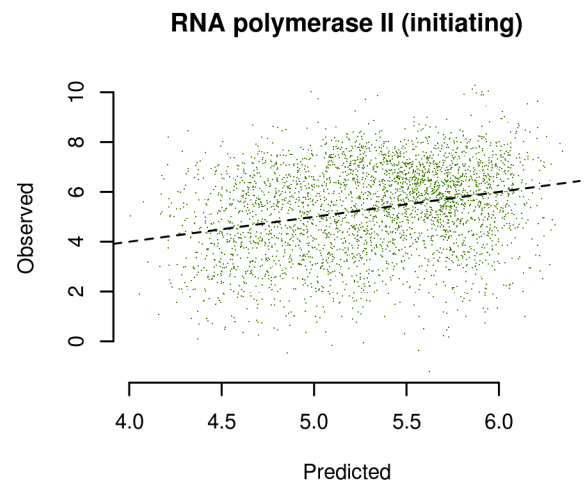
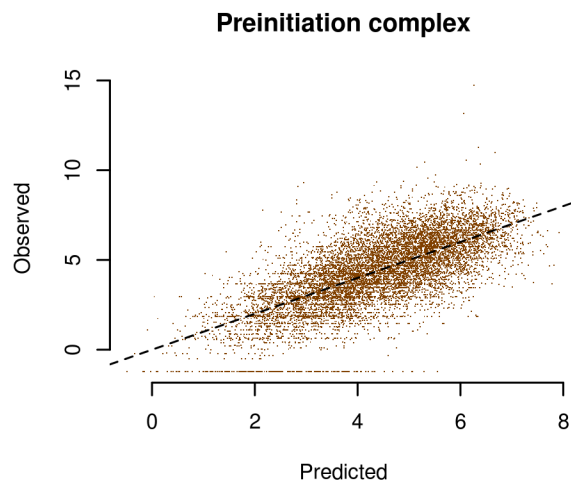


Figure S10

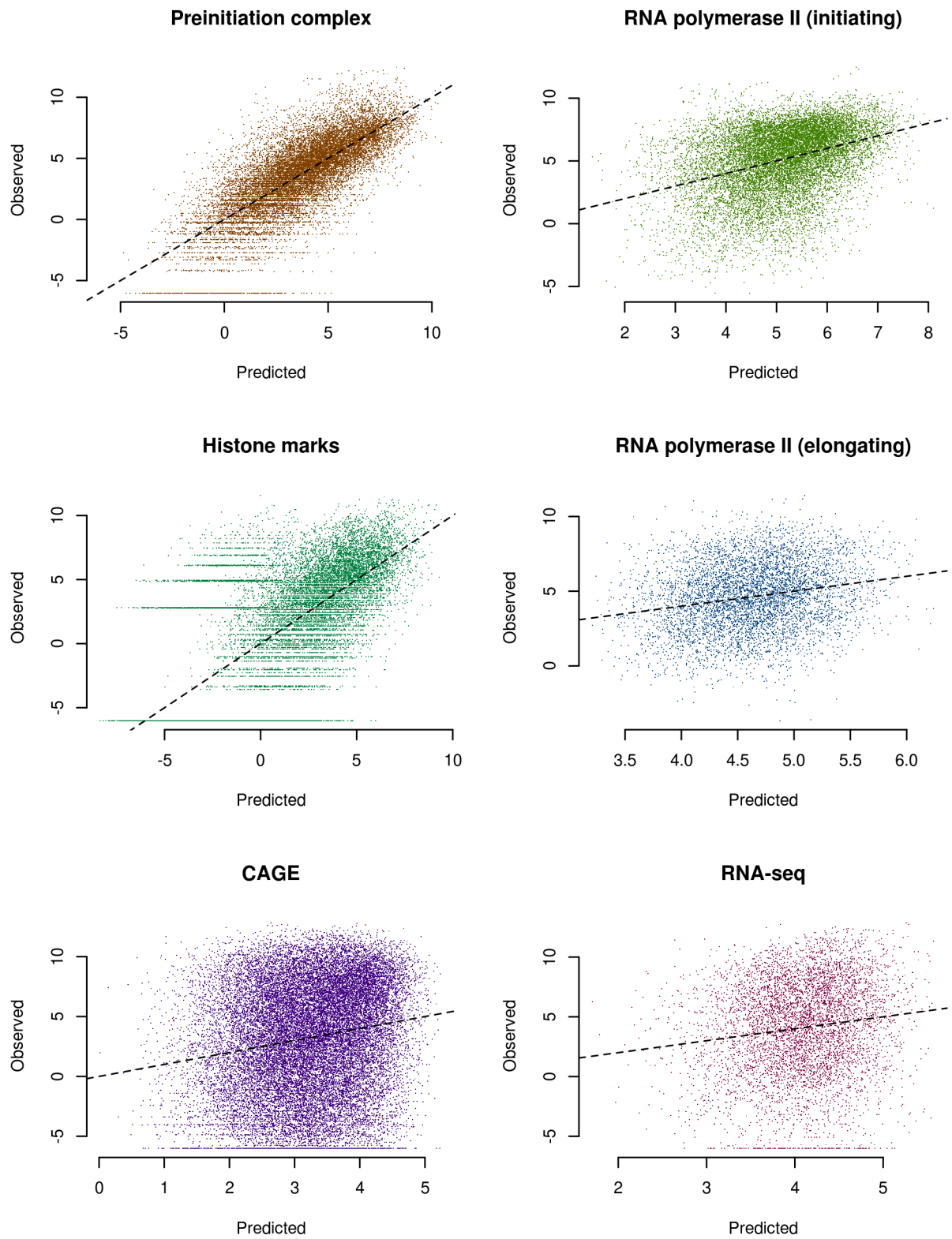


Figure S10: Leave-one-out cross-validation of PLS regression models. S10a: GM12878. S10b: K562. S10c: HepG2. S10d: H1-hESC. S10e: HeLa-S3.