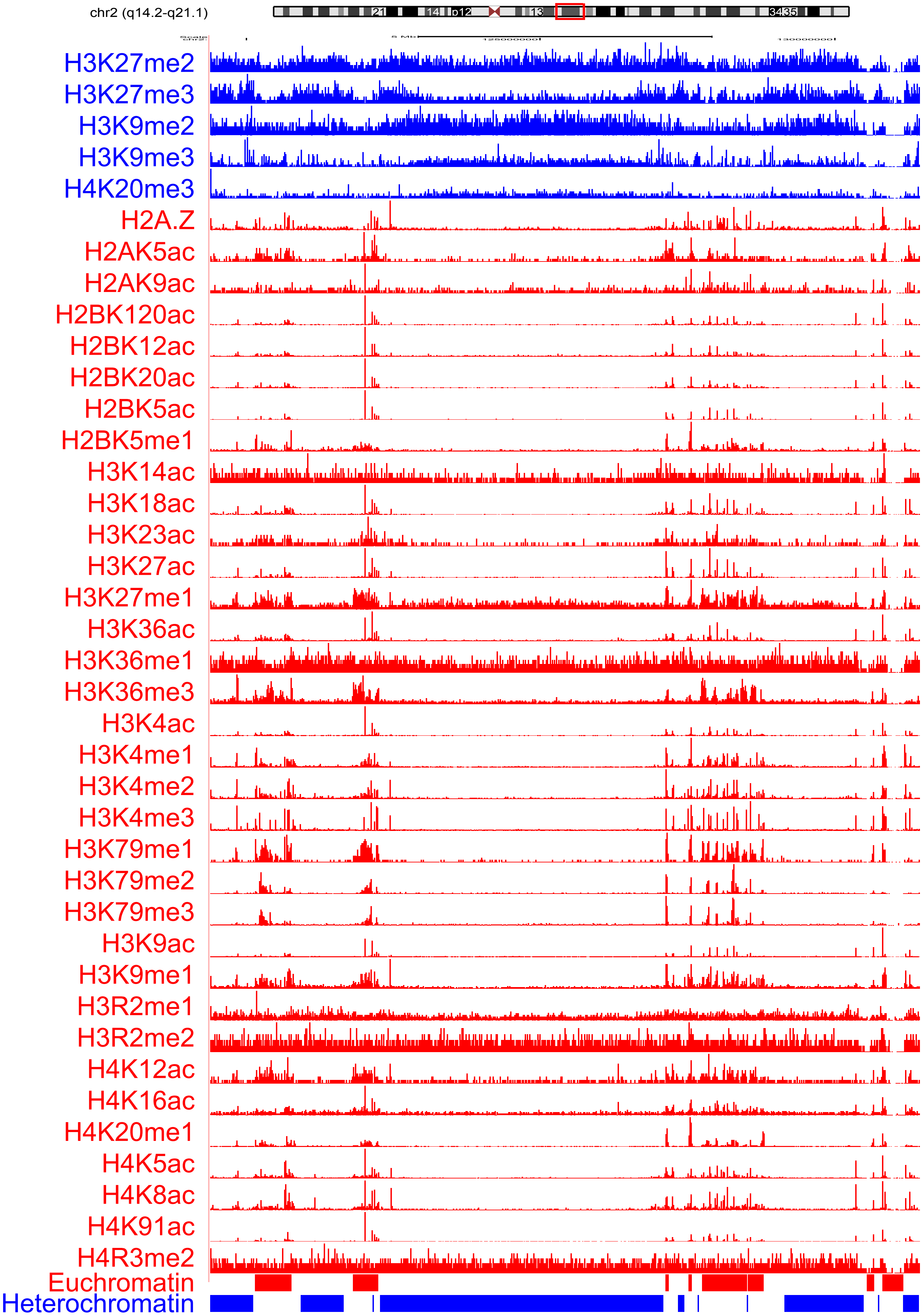
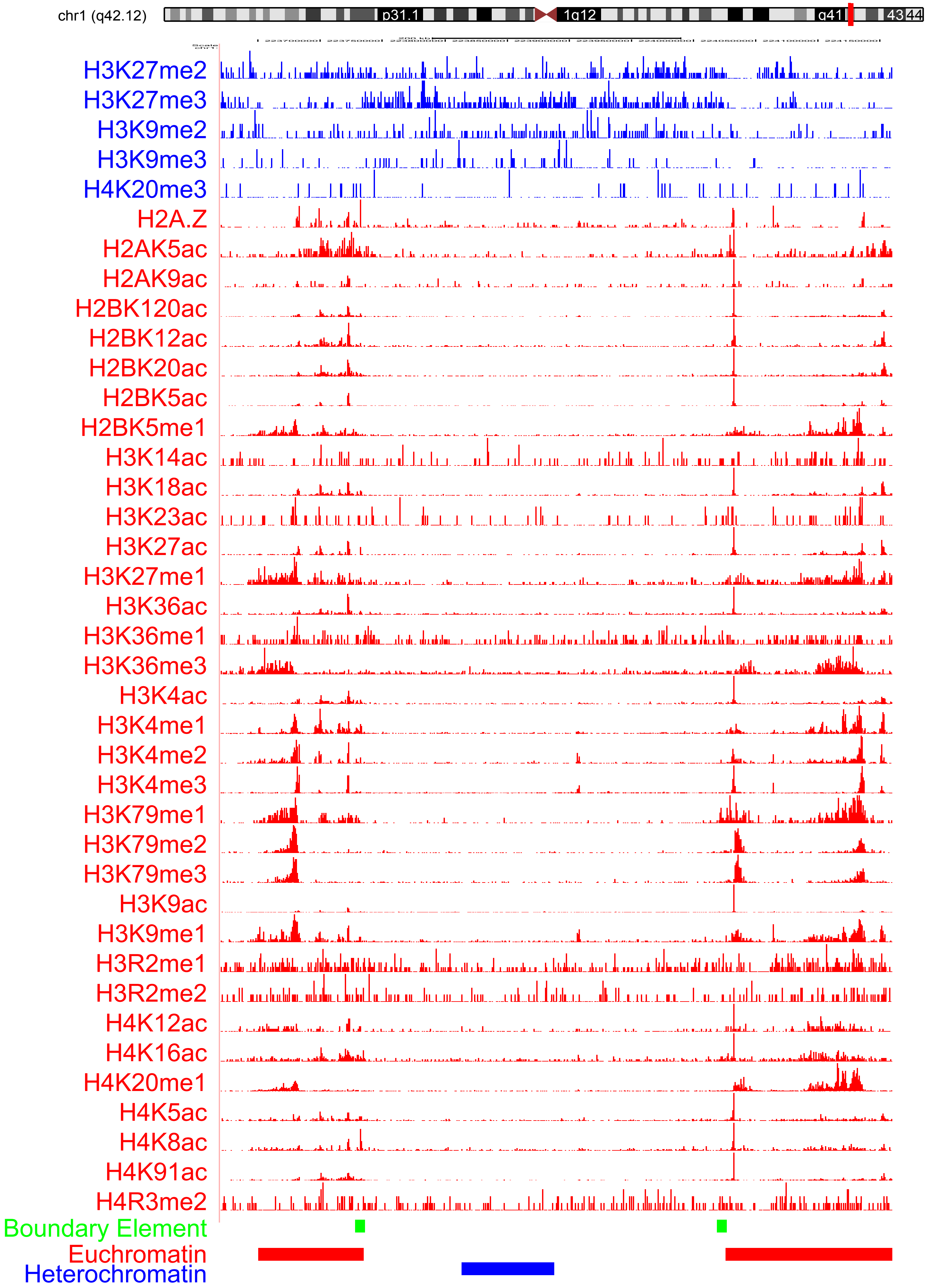
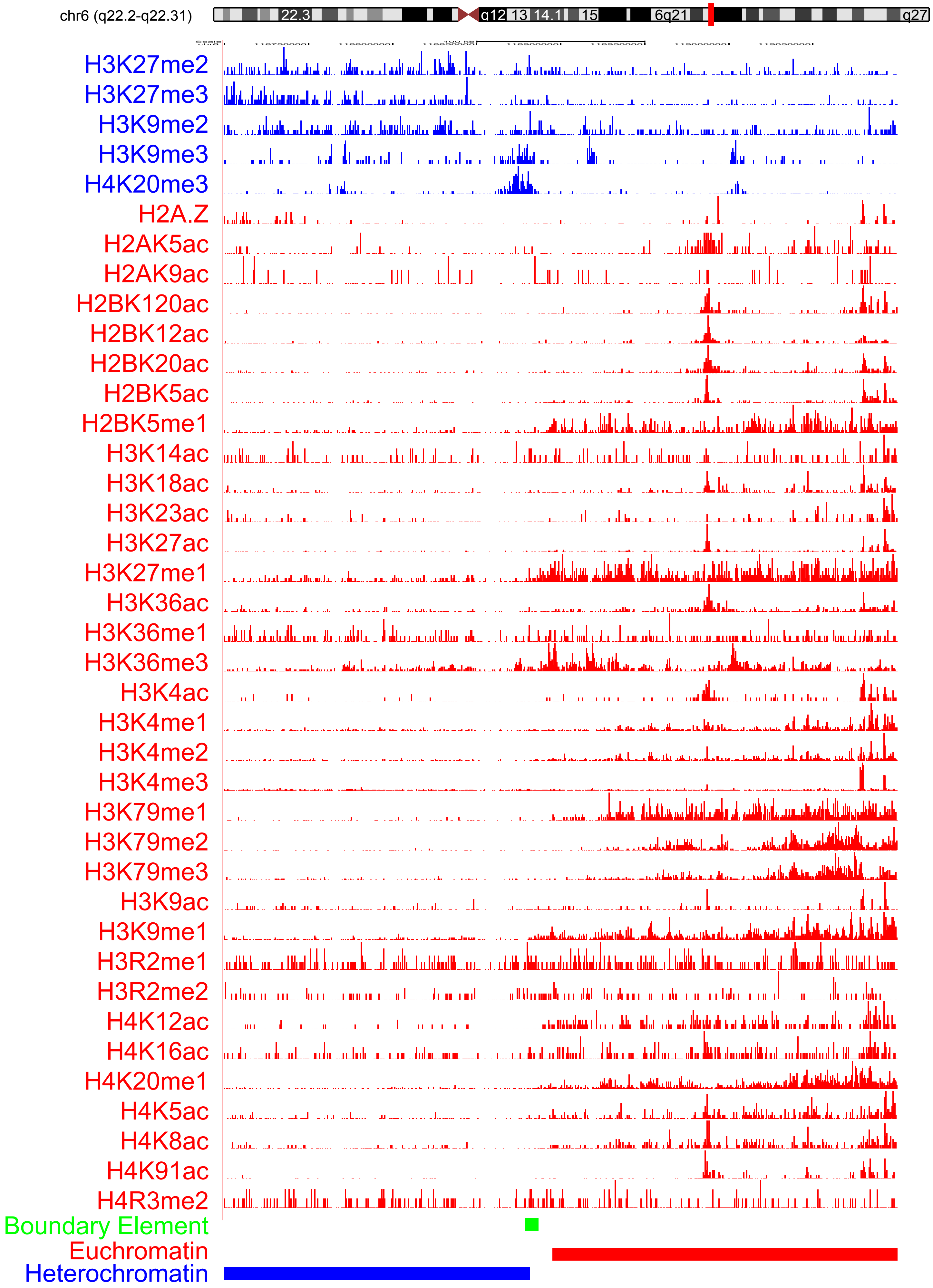
Supplementary Figure 1: Example of predicted chromatin domains. An ideogram of chromosome 2 shows the cytogenetic banding pattern along with the location of this specific example. The distributions of ChIP-seq tag mapping peaks for the active histone modification (red bars), the repressive histone modification (blue bars) are shown in separate tracks. The predicted euchromatic domains (red bands) and heterochromatic domains (blue bands) are shown in the tracks denoted as ‘Euchromatin’ and ‘Heterochromatin’.



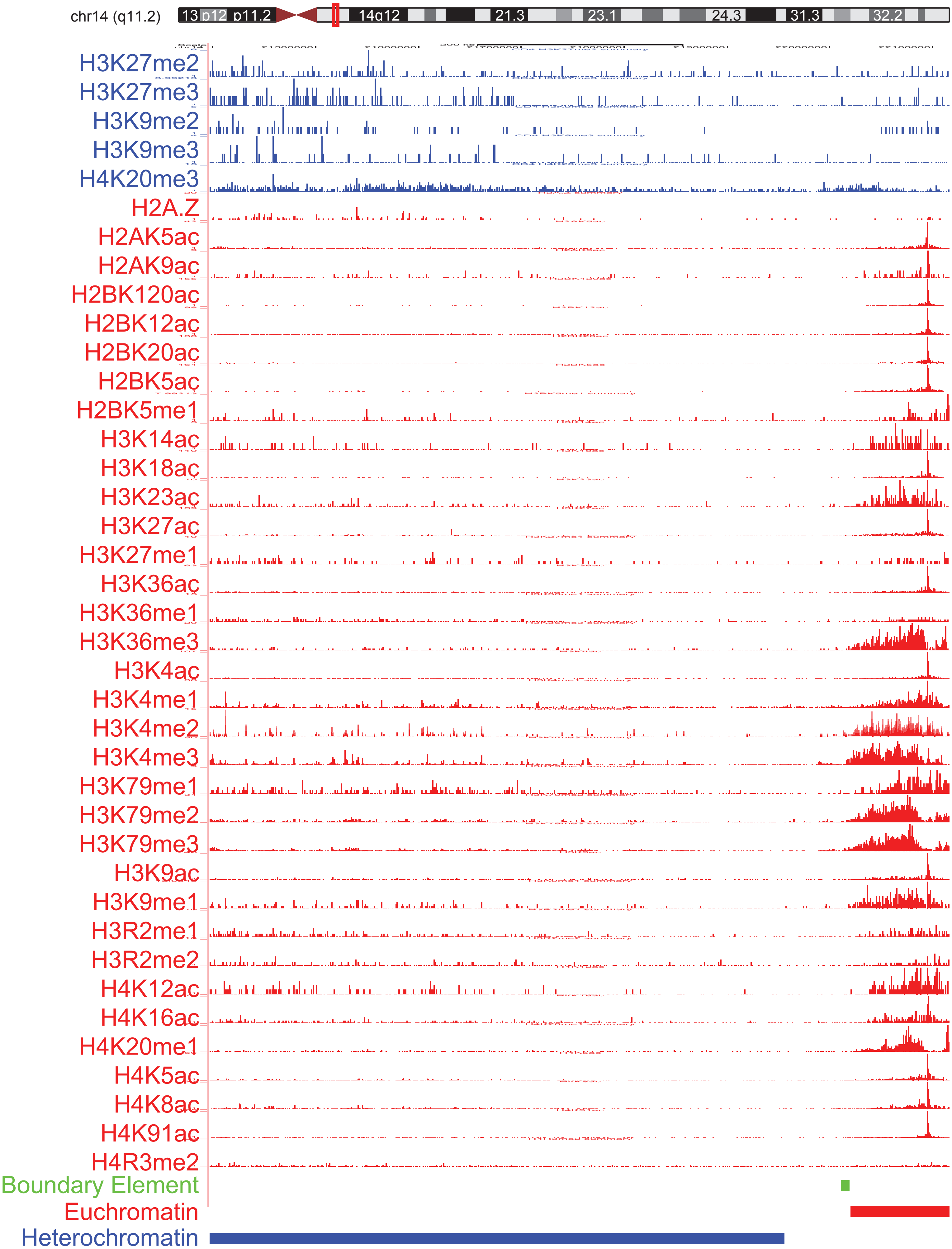
Supplementary Figure 2: Examples of predicted boundary elements with CTCF binding. The predicted boundary elements are shown as green bands. ChIP-seq peaks for active and repressive histone modifications, along with the locations of euchromatic domains and heterochromatic domains are illustrated as separate tracks (as in Supplementary Figure 1)



Supplementary Figure 3: Example of a predicted boundary element without CTCF binding. The predicted boundary element is shown as green bands. ChIP-seq peaks for active and repressive histone modifications, along with the locations of euchromatic domains and heterochromatic domains are illustrated as separate tracks (as in Supplementary Figure 1)

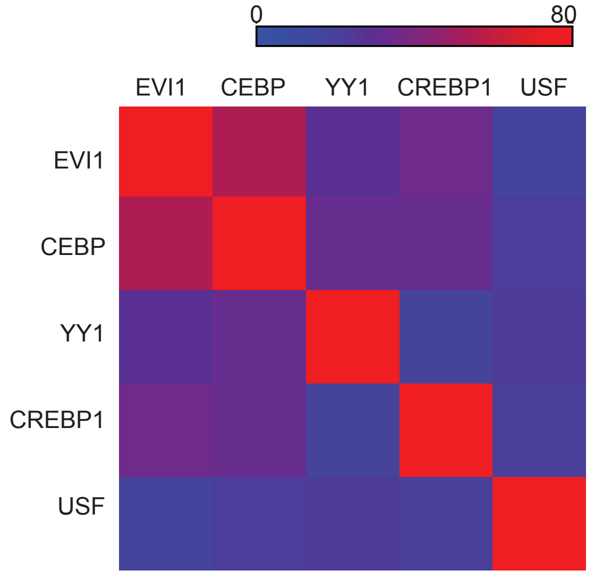


Supplementary Figure 4: The predicted boundary element overlapping with BEAD-1. The predicted boundary element is shown as the green band. ChIP-seq peaks for active and repressive histone modifications, along with the locations of euchromatic domains and heterochromatic domains are illustrated as separate tracks (as in Supplementary Figure 1)



Supplementary Figure 5: Overlaps between conserved TFBSs. A. Heatmap showing the degrees of pairwise overlaps between TFBSs; **B**. Matrix showing the numbers of pairwise overlaps between TFBSs; **C**. List of numbers of all observed combinations of TFBSs.

A



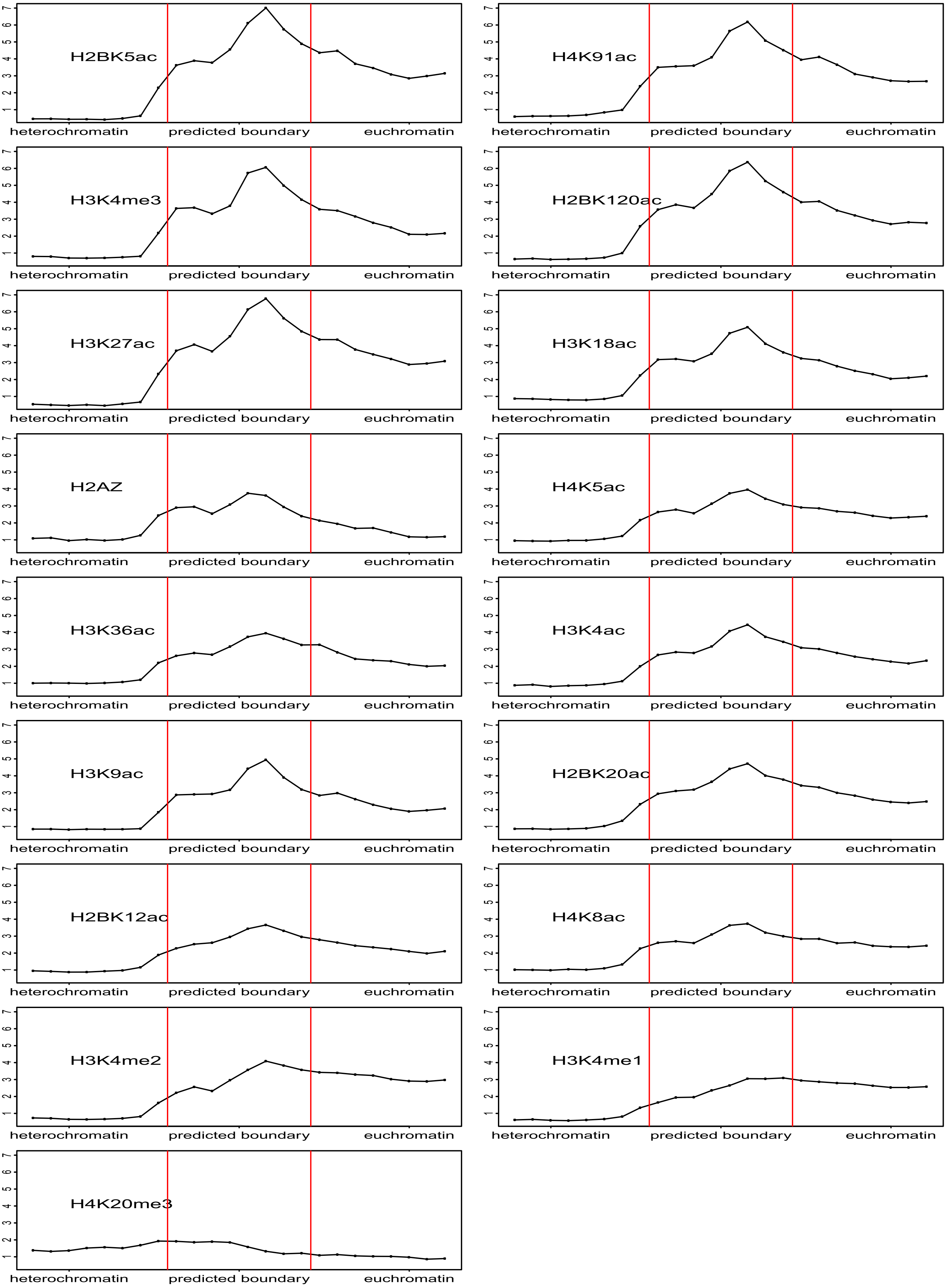
B

Pairwise Comparisons	EVI1	CEBP	YY1	CREBP1	USF
EVI1	382	54	28	35	17
CEBP	54	249	33	33	22
YY1	28	33	157	18	23
CREBP1	35	33	18	150	20
USF	17	22	23	20	140

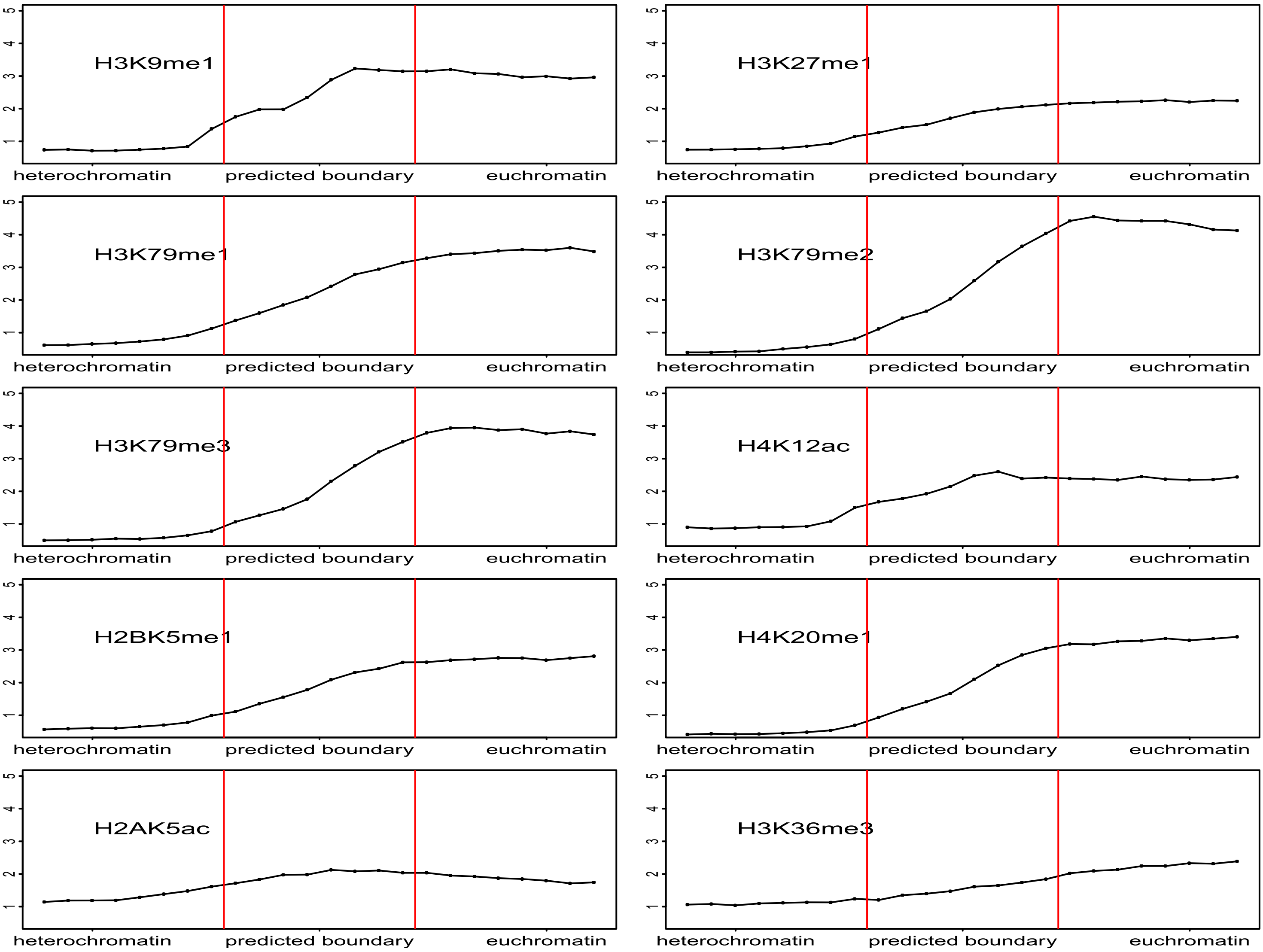
C

Combination	Number
EVI1 only	214
CEBP only	120
CEBP, EVI1	35
YY1 only	80
YY1,EVI1	13
YY1,CEBP	16
YY1,CEBP,EVI1	8
CREBP1 only	57
CREBP1,EVI1	23
CREBP1,CEBP	17
CREBP1,CEBP,EVI1	6
CREBP1,YY1	7
CREBP1,YY1,EVI1	1
CREBP1,YY1,CEBP	3
CREBP1,YY1,CEBP,EVI1	2
USF only	70
USF,EVI1	9
USF,CEBP	13
USF,CEBP,EVI1	1
USF,YY1	12
USF,YY1,EVI1	3
USF,YY1,CEBP	2
USF,YY1,CEBP,EVI1	1
USF,CREBP1	9
USF,CREBP1,EVI1	2
USF,CREBP1,CEBP	3
USF,CREBP1,CEBP,EVI1	1
USF,CREBP1,YY1	4
USF,CREBP1,YY1,CEBP	1

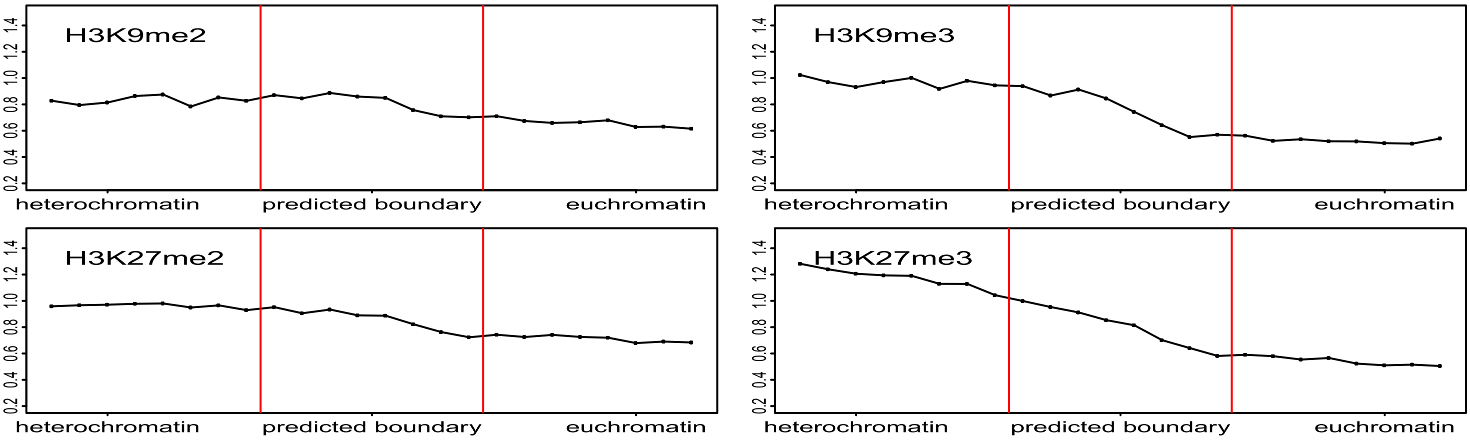
Supplementary Figure 6: Enrichment profiles around boundary elements of histone modifications which show distinct peaks. The average fold enrichments (y-axis) of individual histone modifications are ploted for the predicted boundary elements (8kb), the heterochromatin sides (8kb) and the euchromatin sides (8kb).



Supplementary Figure 7: Enrichment profiles around boundary elements of histone modifications which increase from heterochromatin to euchromatin. The average fold enrichments (y-axis) of individual histone modifications are ploted for the predicted boundary elements (8kb), the heterochromatin sides (8kb) and the euchromatin sides (8kb).



Supplementary Figure 8: Enrichment profiles around boundary elements of histone modifications which decrease from heterochromatin to euchromatin. The average fold enrichments (y-axis) of individual histone modifications are ploted for the predicted boundary elements (8kb), the heterochromatin sides (8kb) and the euchromatin sides (8kb).



Supplementary Table 1: Sequence Features of RITs and Predicted Boundary Elements.

	RIT	Boundary Element
Median Size	68.6 kb	8 kb
GC content	0.421	0.423
CpG O/E[1]	0.229	0.316
Genic Fractions[2]	43.0%	40.9%

[1] The ratio of observed CpG frequency to expected CpG frequency.

[2] The length fractions of regions within gene bodies.

Supplementary Table 2: Enriched Gene Ontology and KEGG Terms of Genes in Predicted Euchromatin Domains with High Gene Densities (>1 gene/20kb)

	Term	*P*-value
Gene Ontology	ATP dependent helicase activity	0.039
	Defense Response	0.045
	Glycerophospholipid Biosynthetic Process	0.056
	Regulation of Response to External Stimulus	0.069
	Inflammatory Response	0.070
KEGG Pathway	Systemic Lupus Erythematosus	0
	Antigen Processing and Presentation	0.017