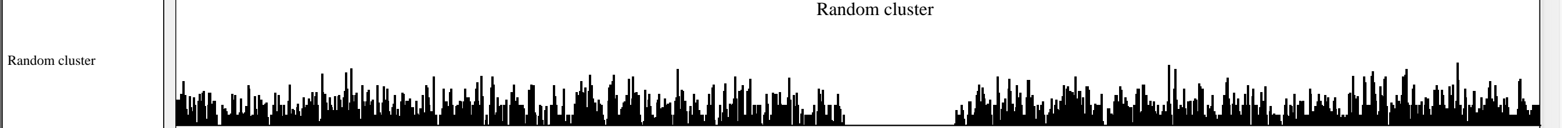
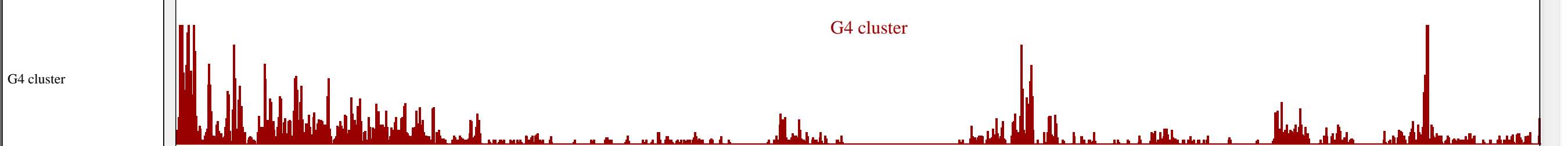
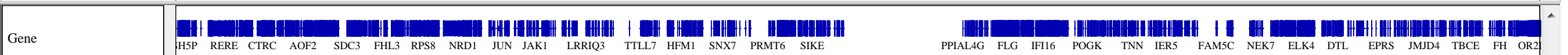
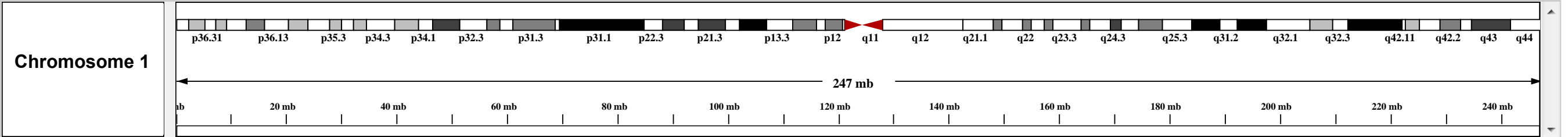
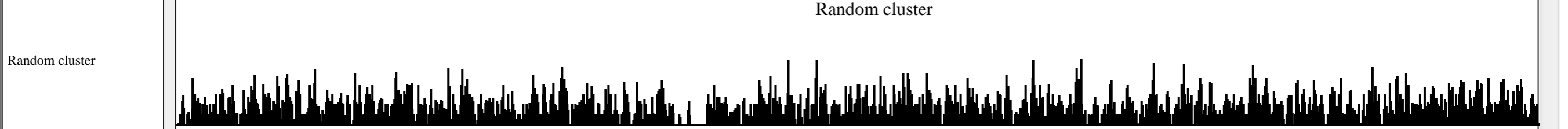
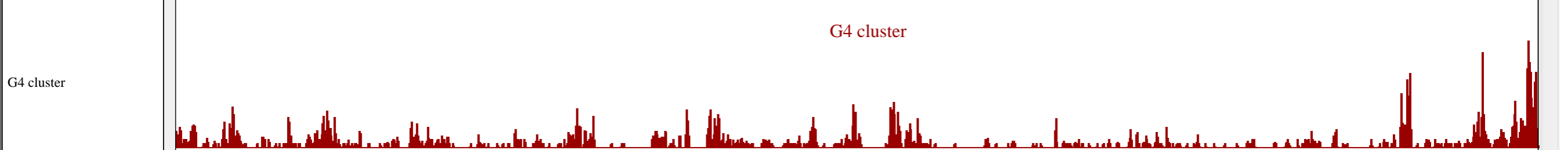
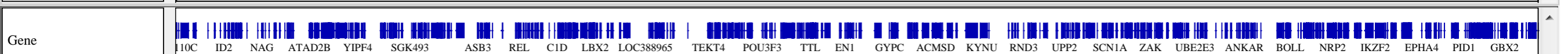
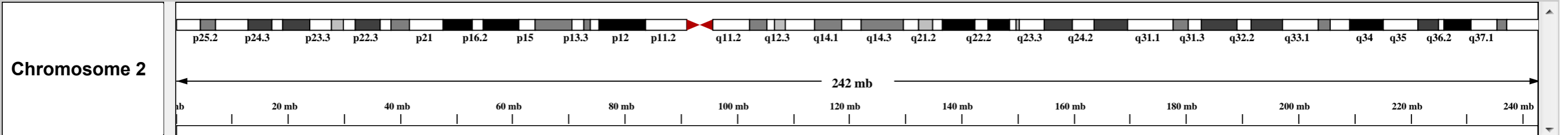


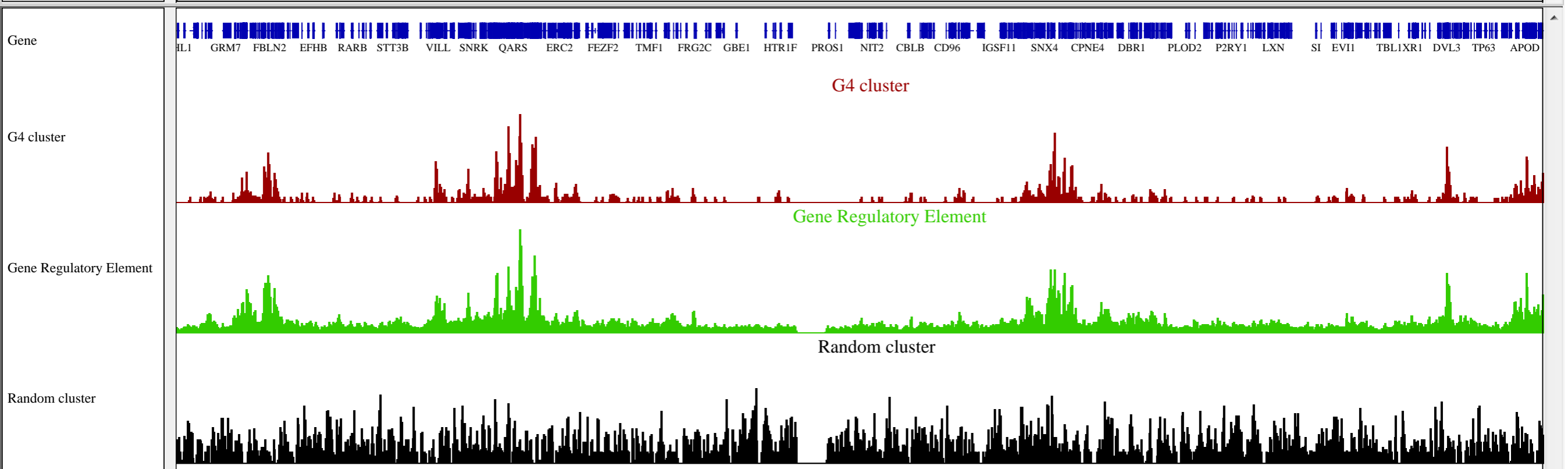
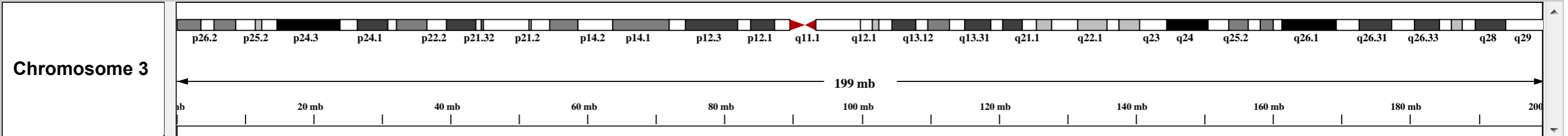
Chromosome	Spearman ρ	<i>P</i> value	Chromosome	Spearman ρ	<i>P</i> value
chr1	0.569	<0.001	chr13	0.602	<0.001
chr2	0.539	<0.001	chr14	0.631	<0.001
chr3	0.600	<0.001	chr15	0.487	<0.001
chr4	0.532	<0.001	chr16	0.655	<0.001
chr5	0.562	<0.001	chr17	0.653	<0.001
chr6	0.417	<0.001	chr18	0.514	<0.001
chr7	0.492	<0.001	chr19	0.670	<0.001
chr8	0.460	<0.001	chr20	0.639	<0.001
chr9	0.608	<0.001	chr21	0.728	<0.001
chr10	0.480	<0.001	chr22	0.466	<0.001
chr11	0.569	<0.001	chrX	0.610	<0.001
chr12	0.502	<0.001	chrY	0.139	<0.001

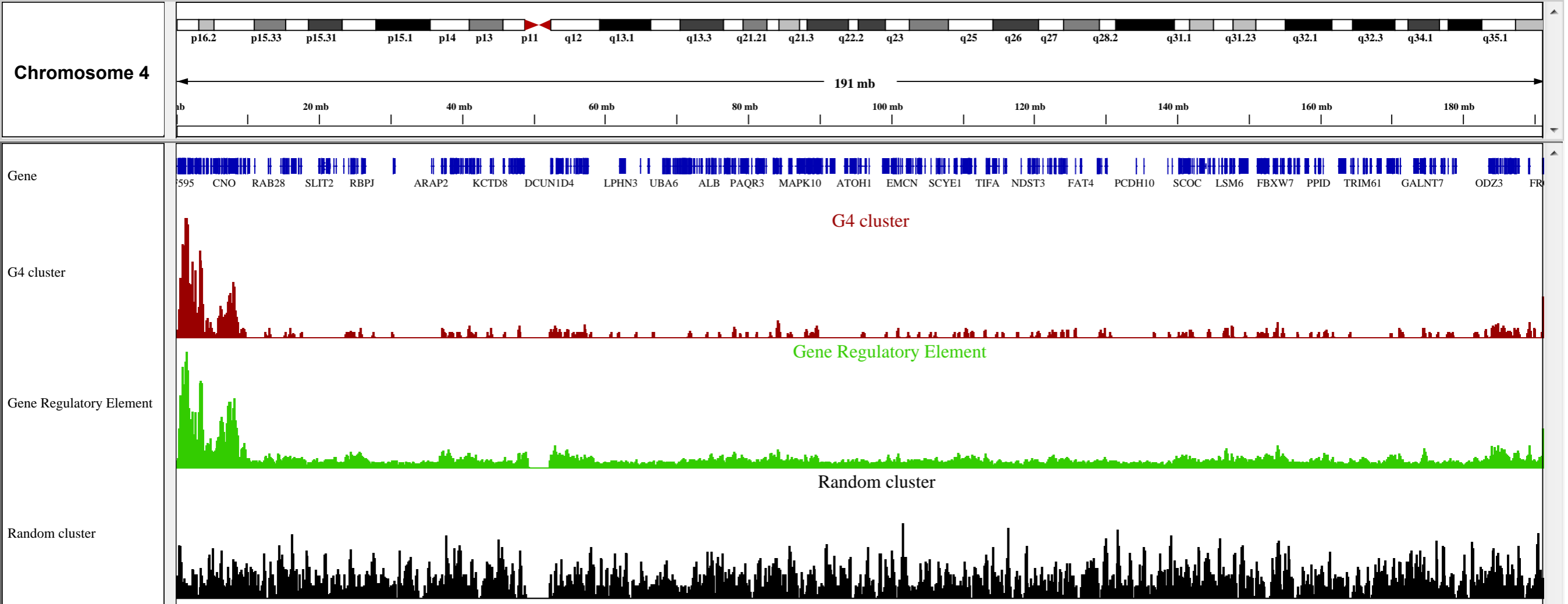
Supplementary Material Figure S1. The distribution of PG4Ms correlates with that of genes across the human genome.

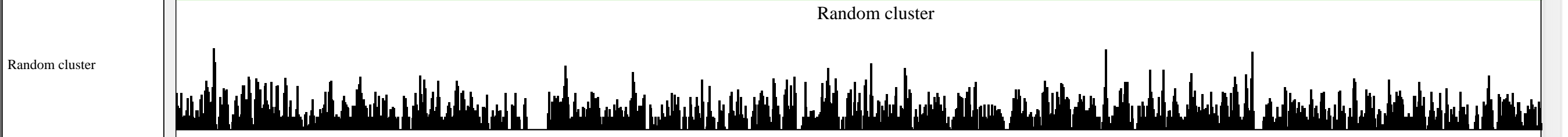
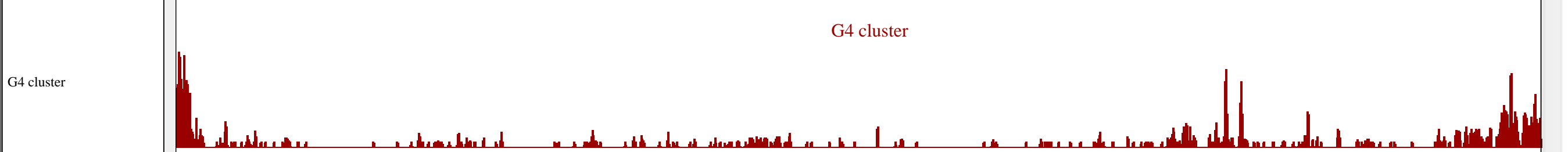
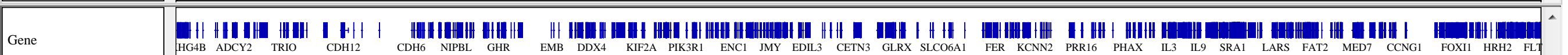
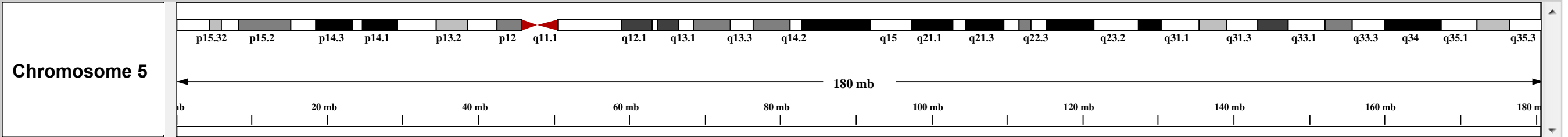
Number of PG4Ms and gene regions was calculated in the human genome in 500-kb windows with a 50 kb step size. The distribution of PG4Ms (dark blue bars) and gene regions (dark red bars) are shown for each chromosome (this figure was prepared by the UCSC genome browser). Correlation coefficient between PG4Ms and gene regions for each chromosome are shown on the bottom. The low correlation coefficient of Y chromosome might have been due to low gene density.

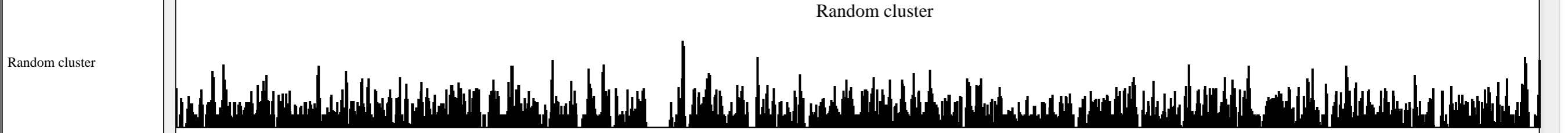
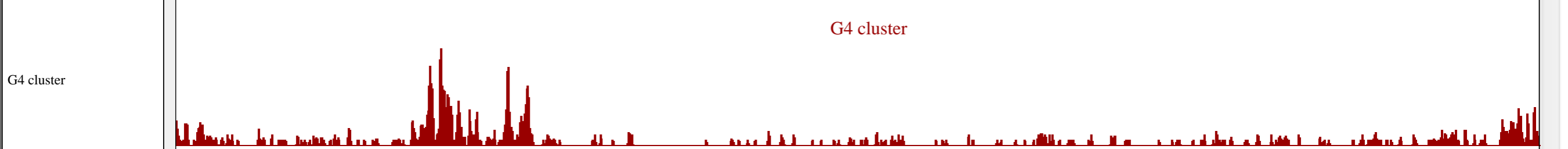
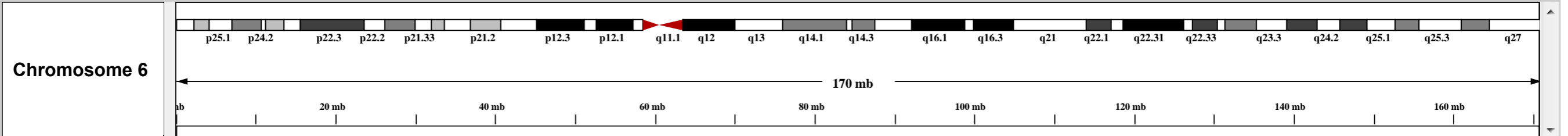


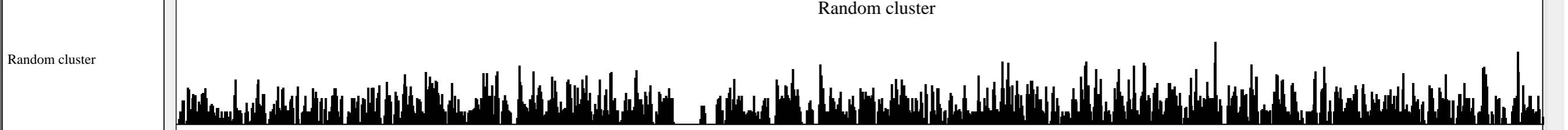
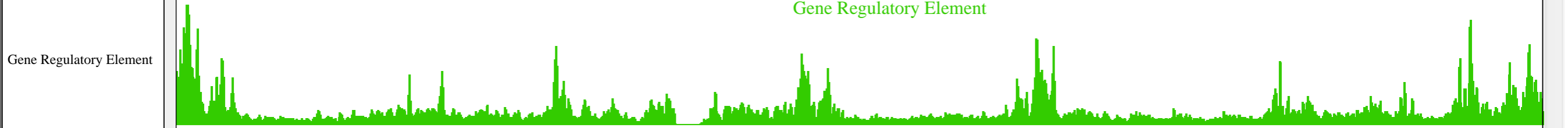
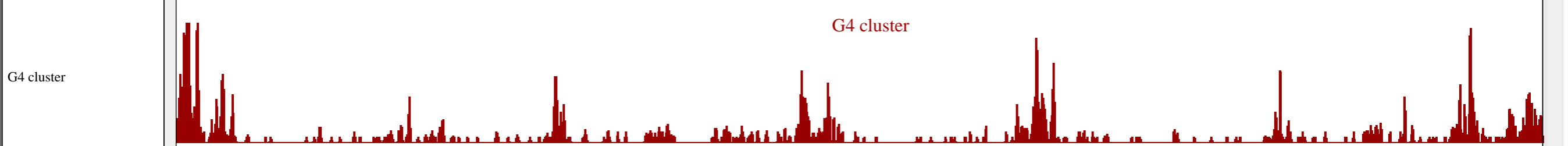
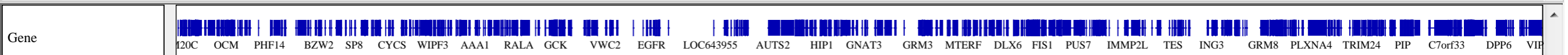


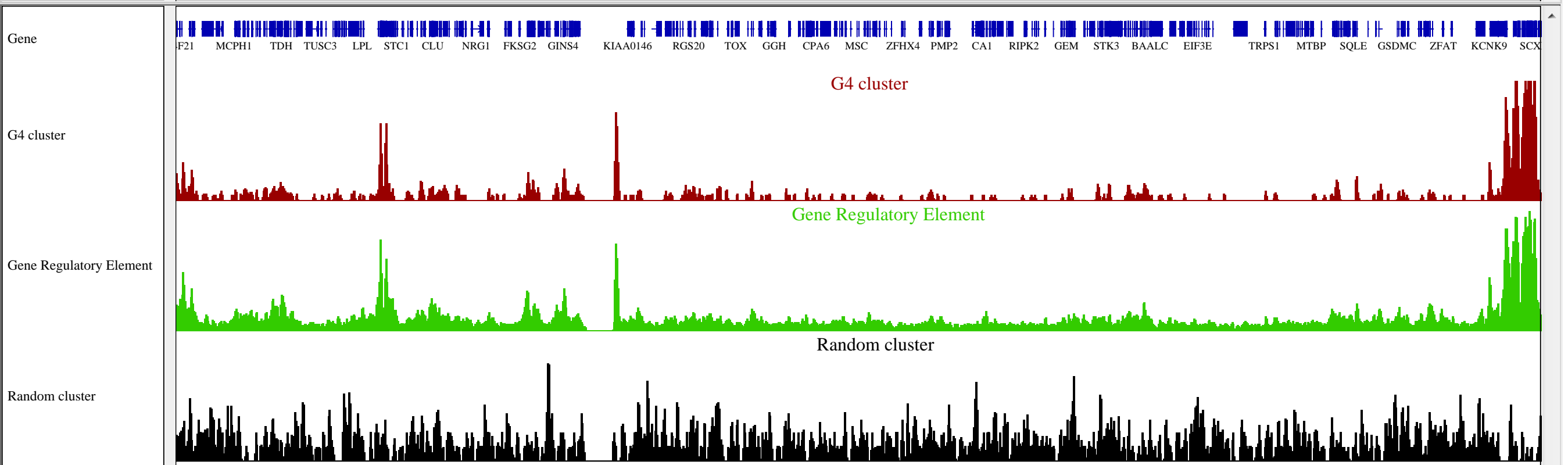
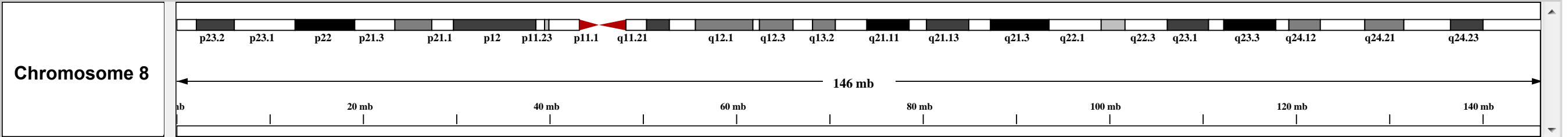


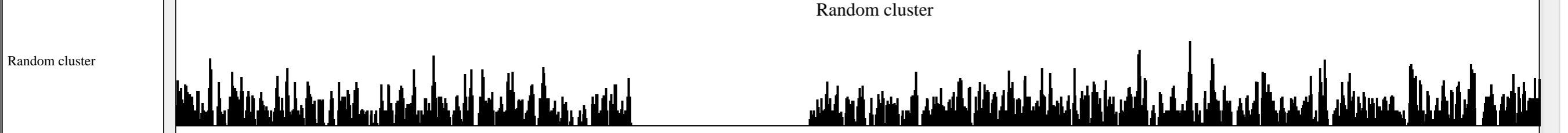
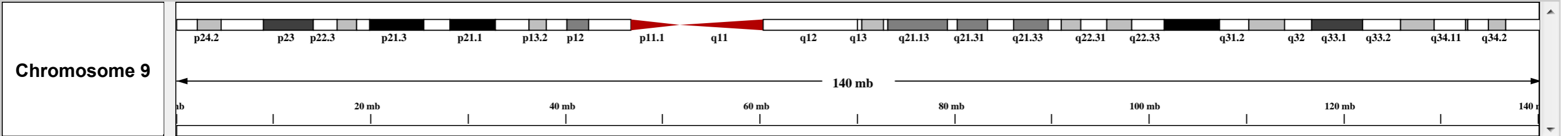


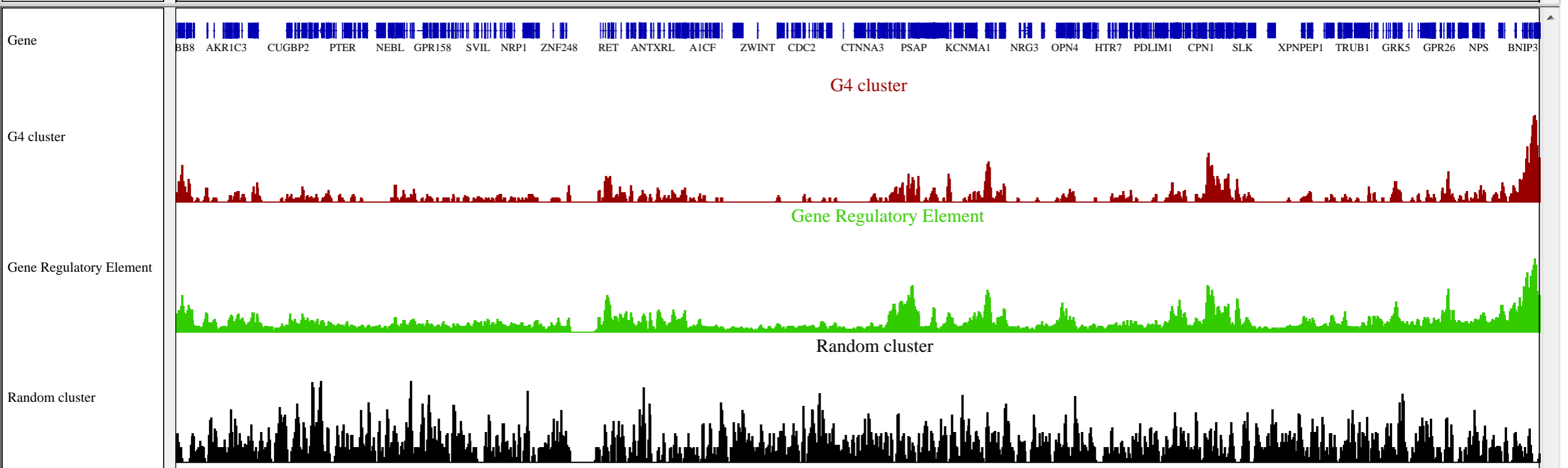
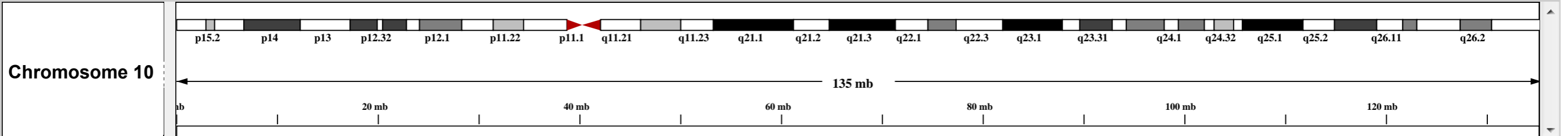


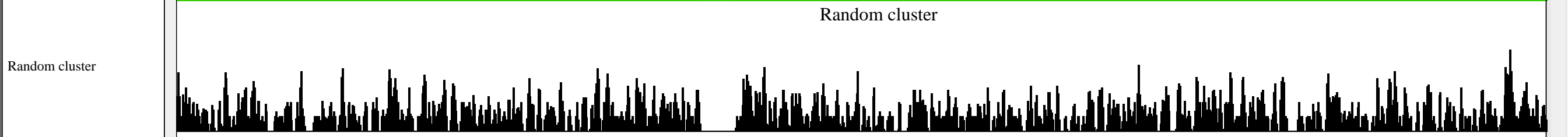
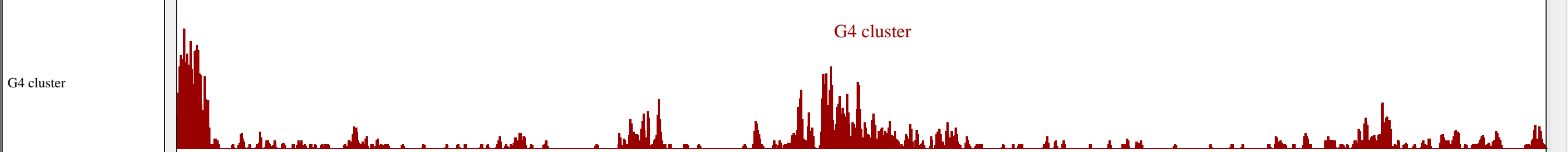
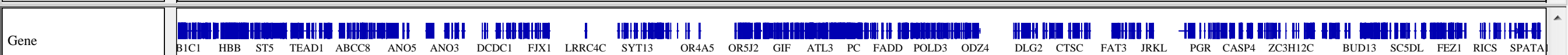
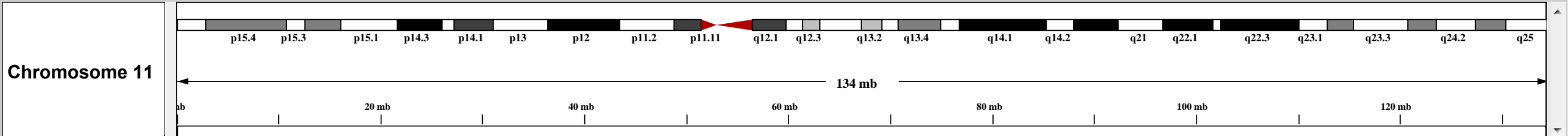


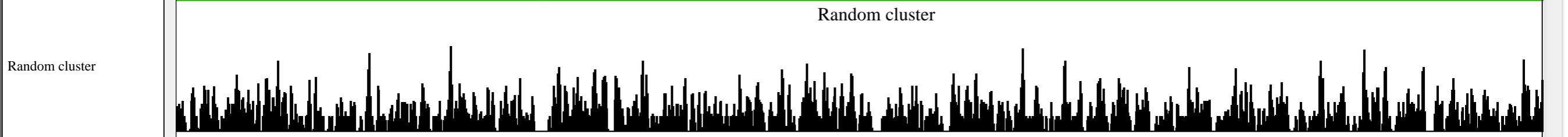
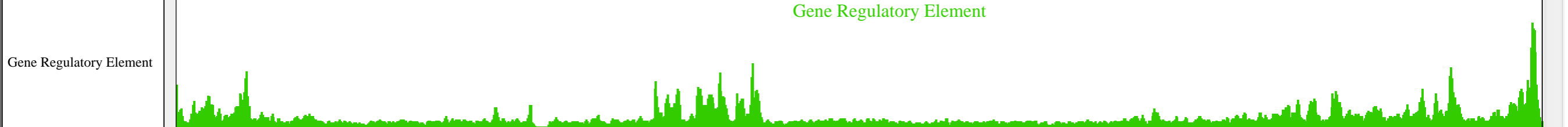
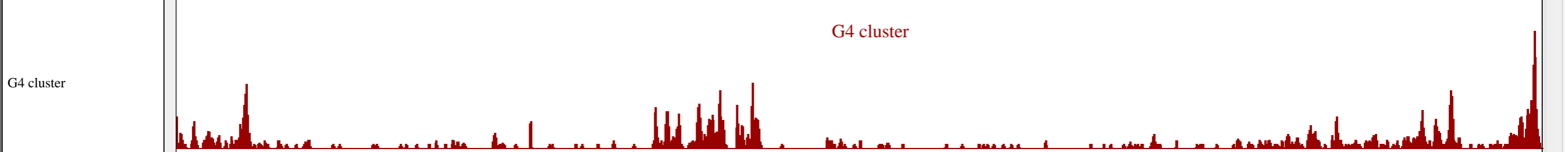
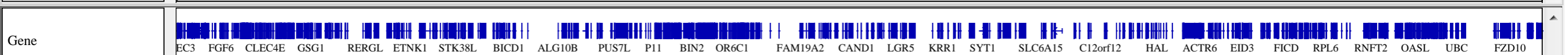
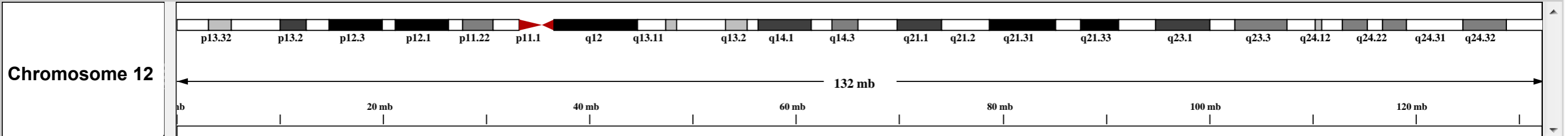


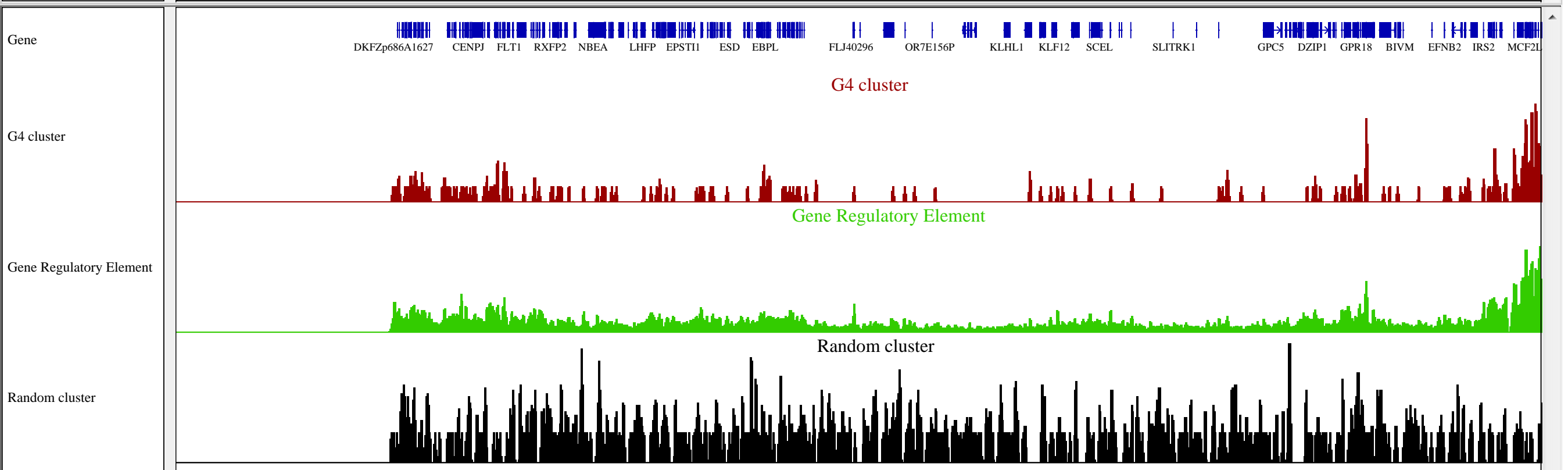
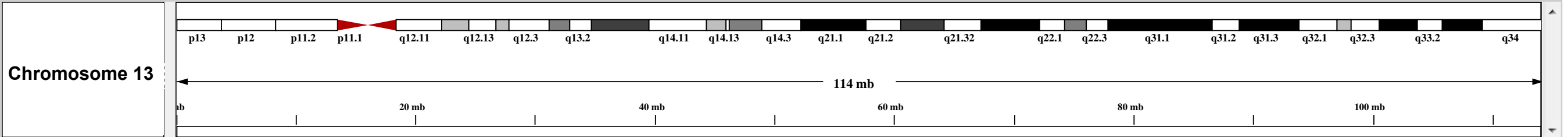


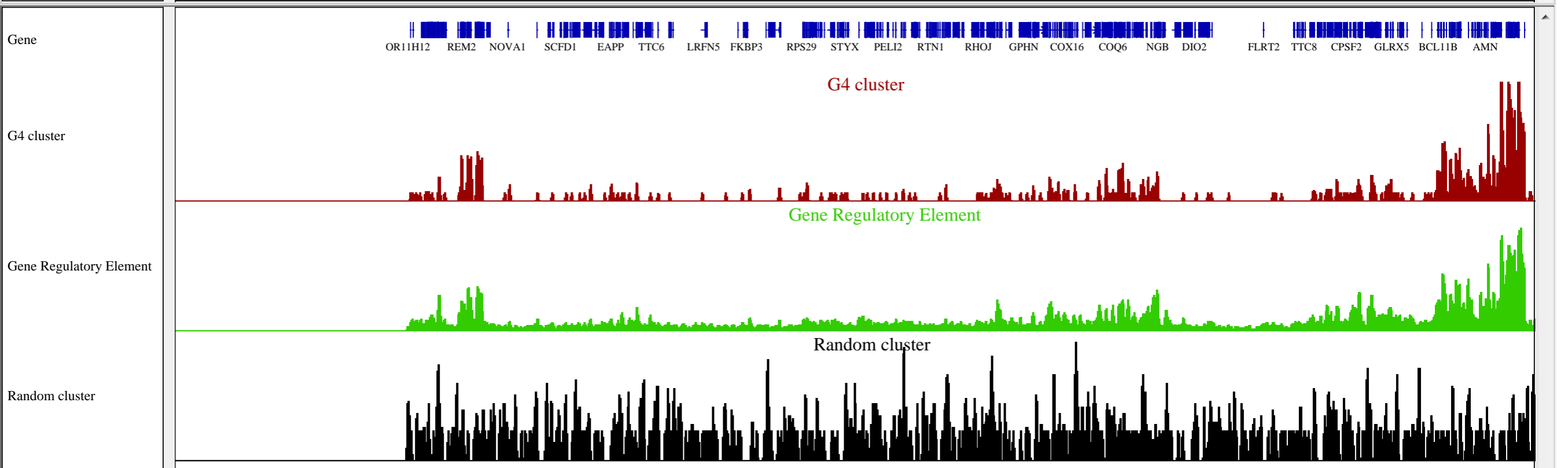
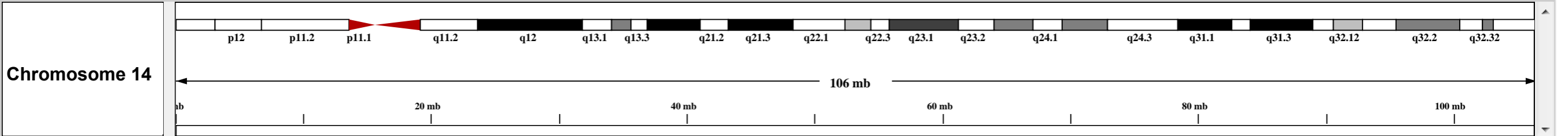


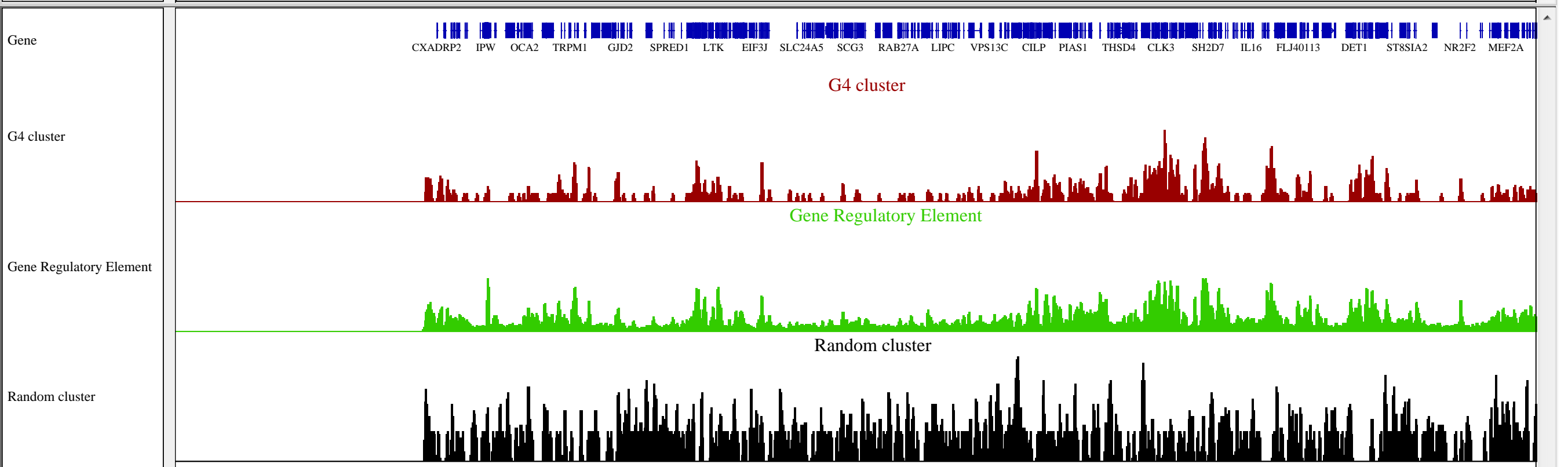
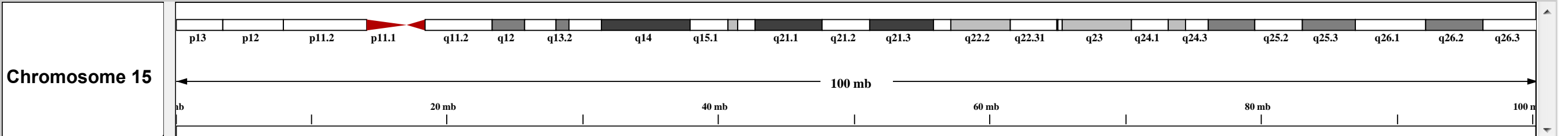


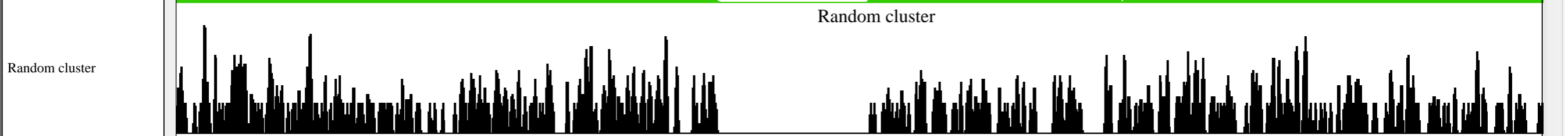
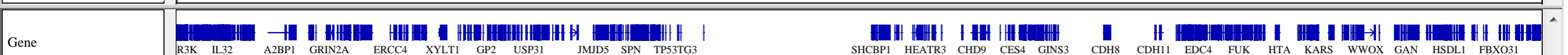
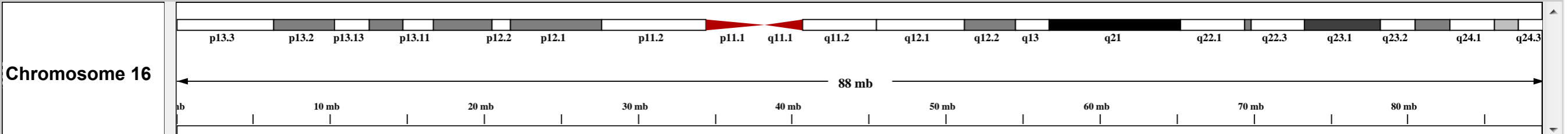


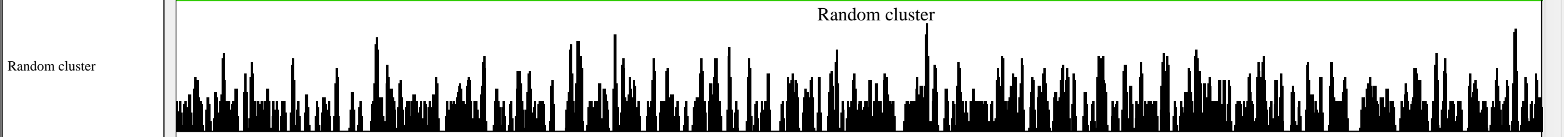
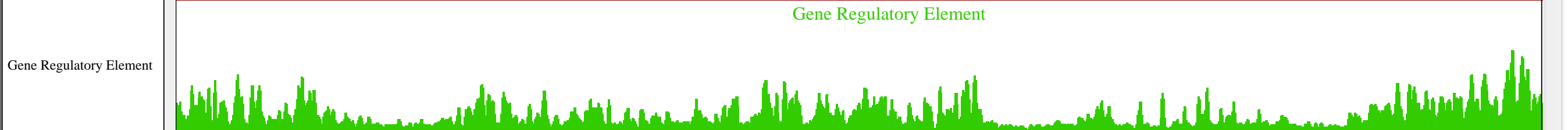
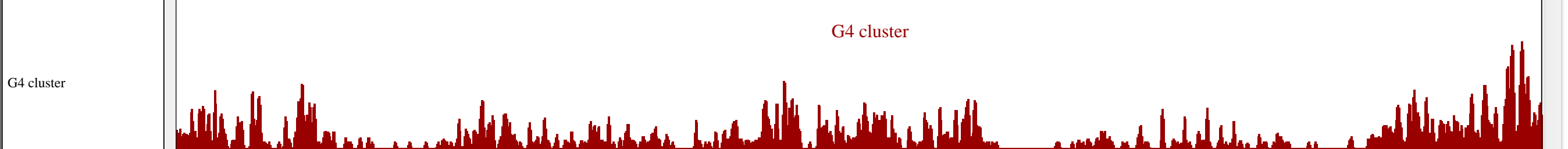
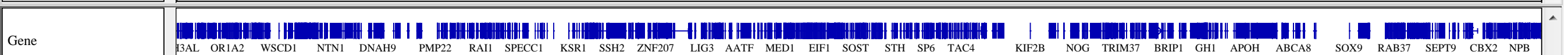
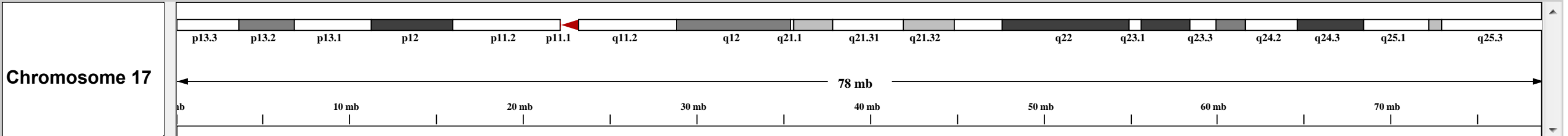


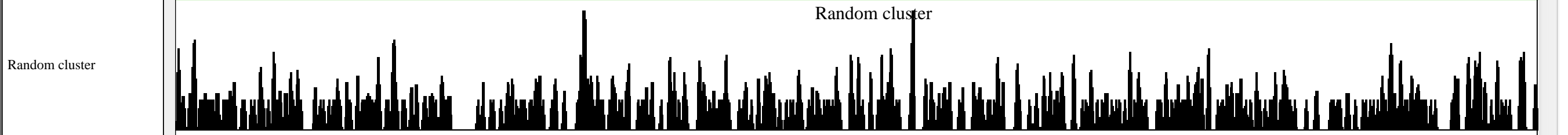
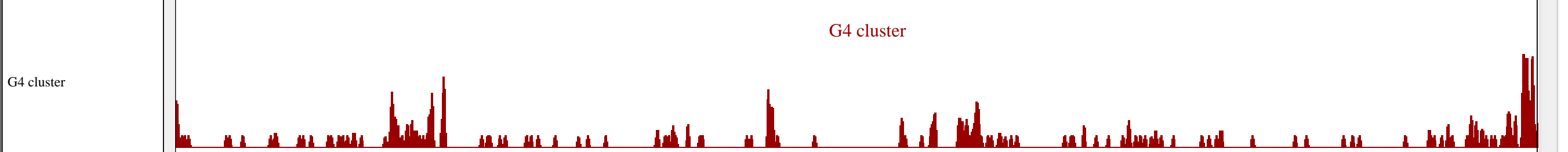
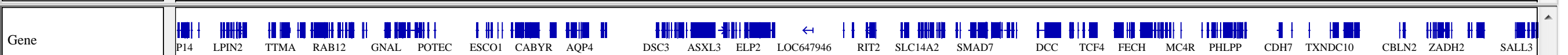
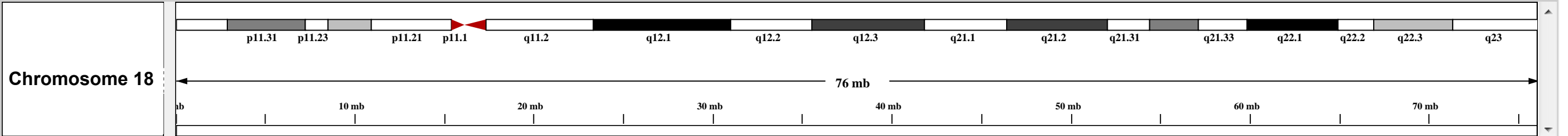


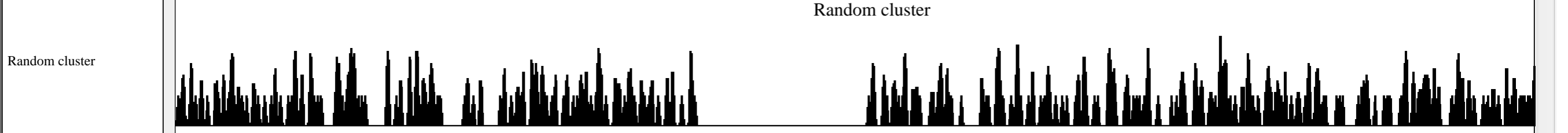
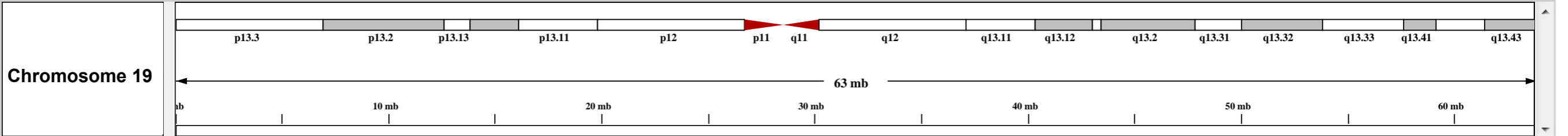


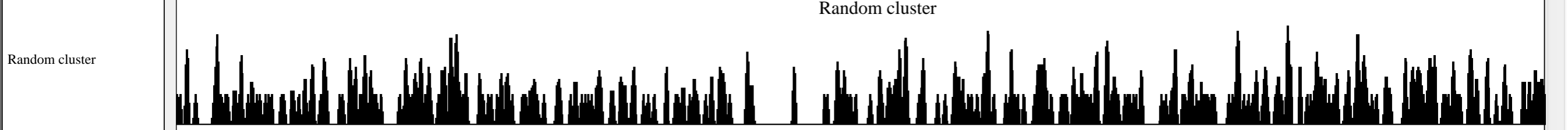
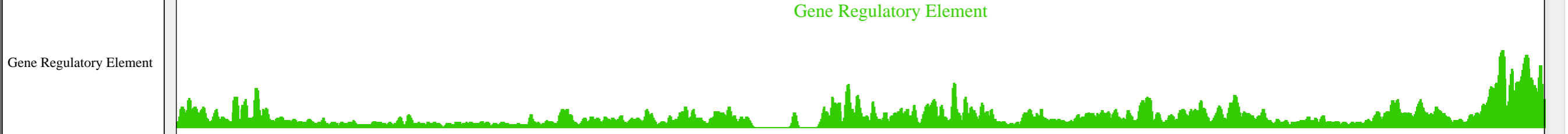
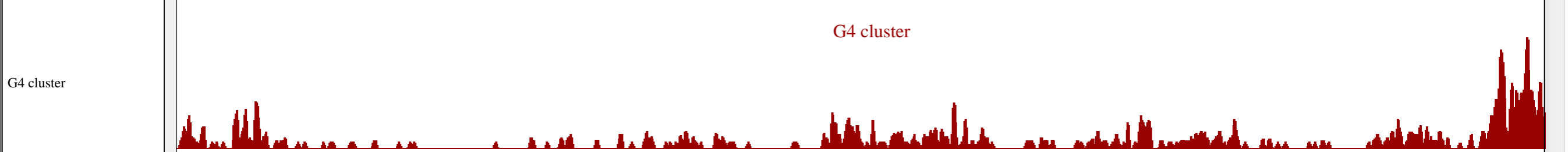
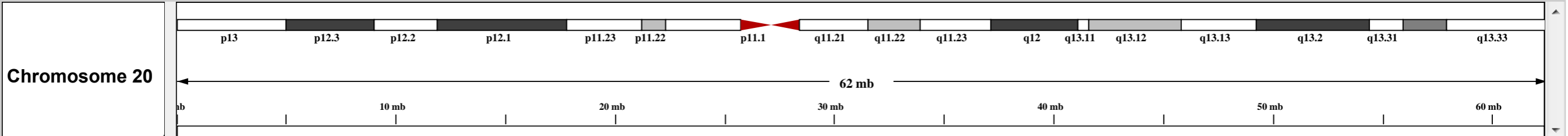


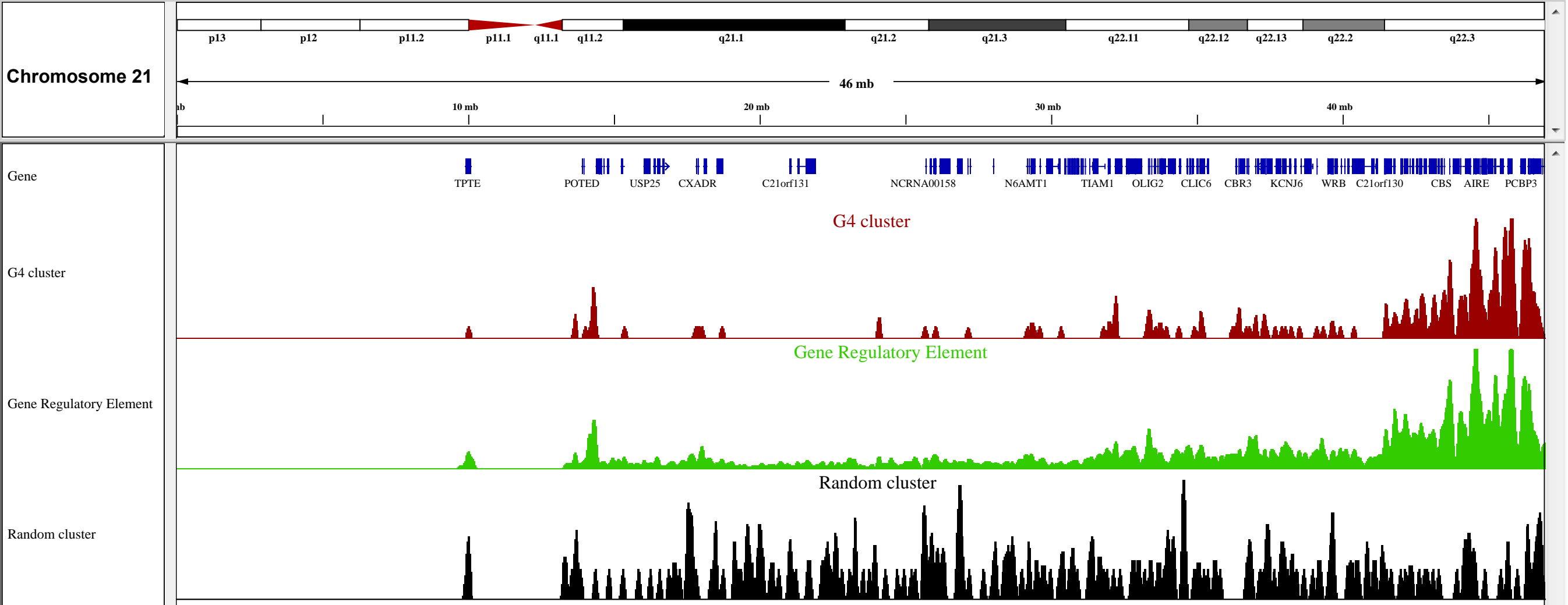


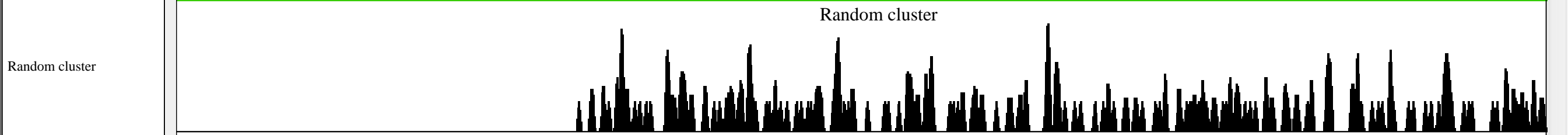
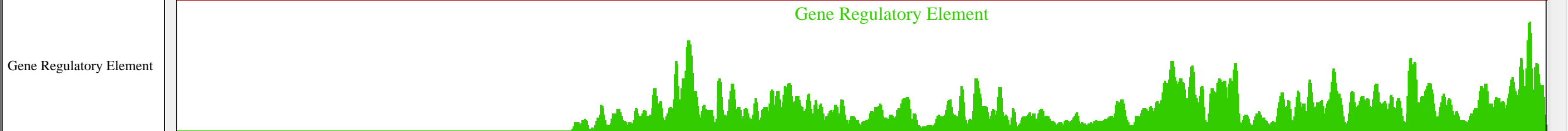
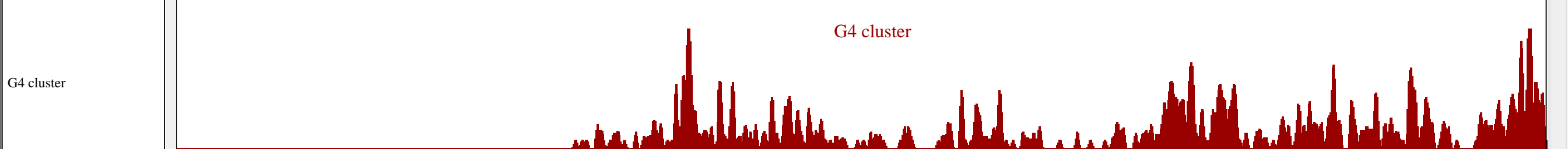
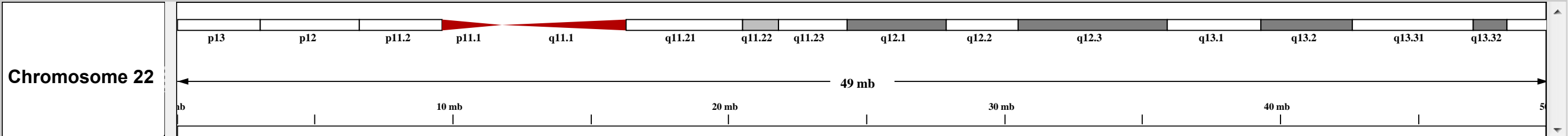


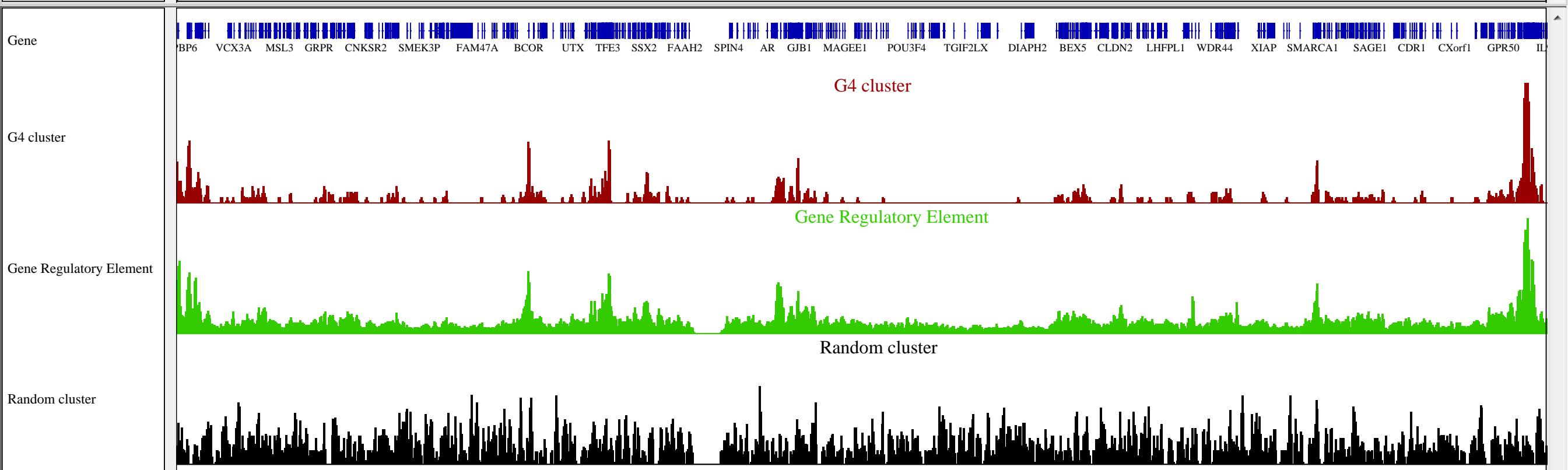
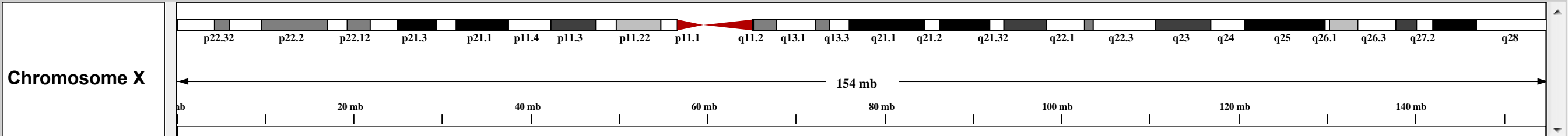


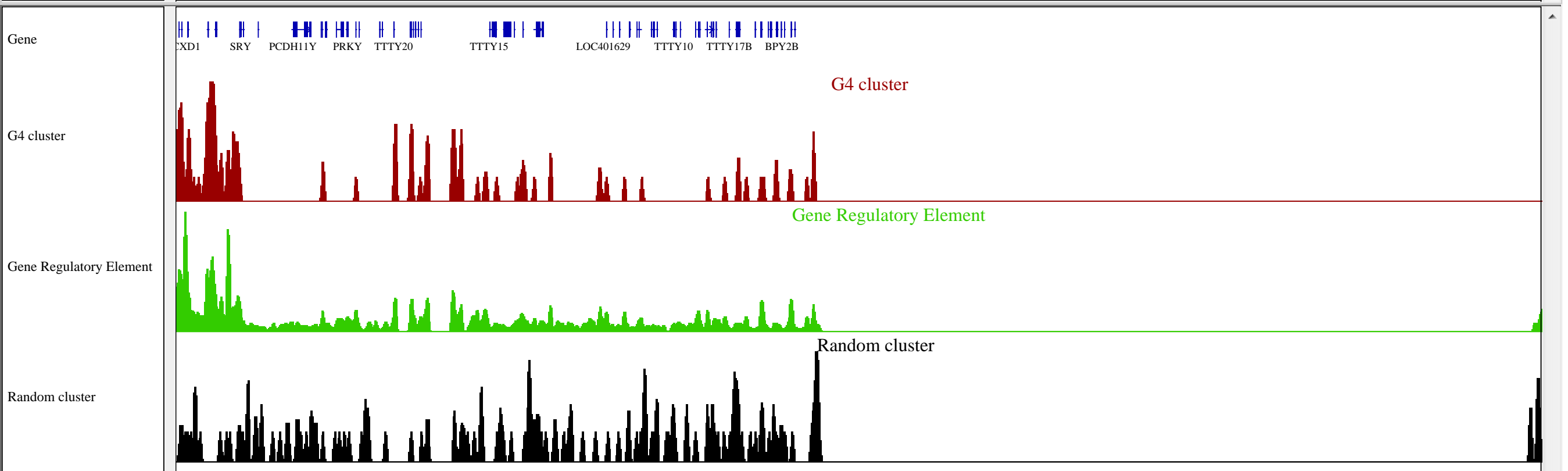
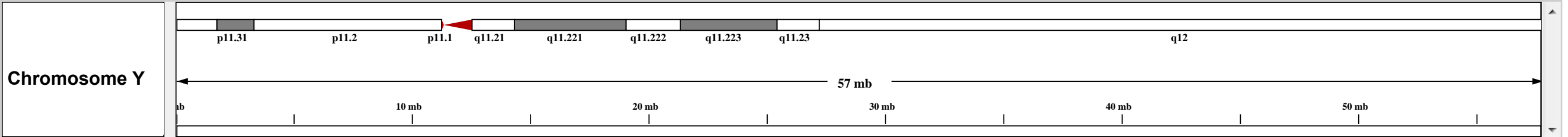












Supplementary Material Figure S2. The distribution of G4 clusters correlates with that of GREs across the human genome.

Number of G4 clusters and GREs was calculated in the human genome in 100-kb windows with a 10 kb step size. All overlapping GREs were merged into a single entity for this analysis and a set of randomly selected genomic regions (random cluster, with an equal length as the corresponding G4 cluster) were used as a control. The distribution of G4 clusters (red), GREs (green), and random clusters (black) are shown for each chromosome. We found a positive correlation between G4 clusters and GREs (Spearman $\rho = 0.40$, $P < 0.001$). Since the number of NCRs is very large, which could influence the results, we re-performed the correlation analysis by excluding NCRs. We obtained a similar result (Spearman $\rho = 0.432$, $P < 0.001$), indicating a co-localization tendency between G4 clusters and GREs at the genome level.