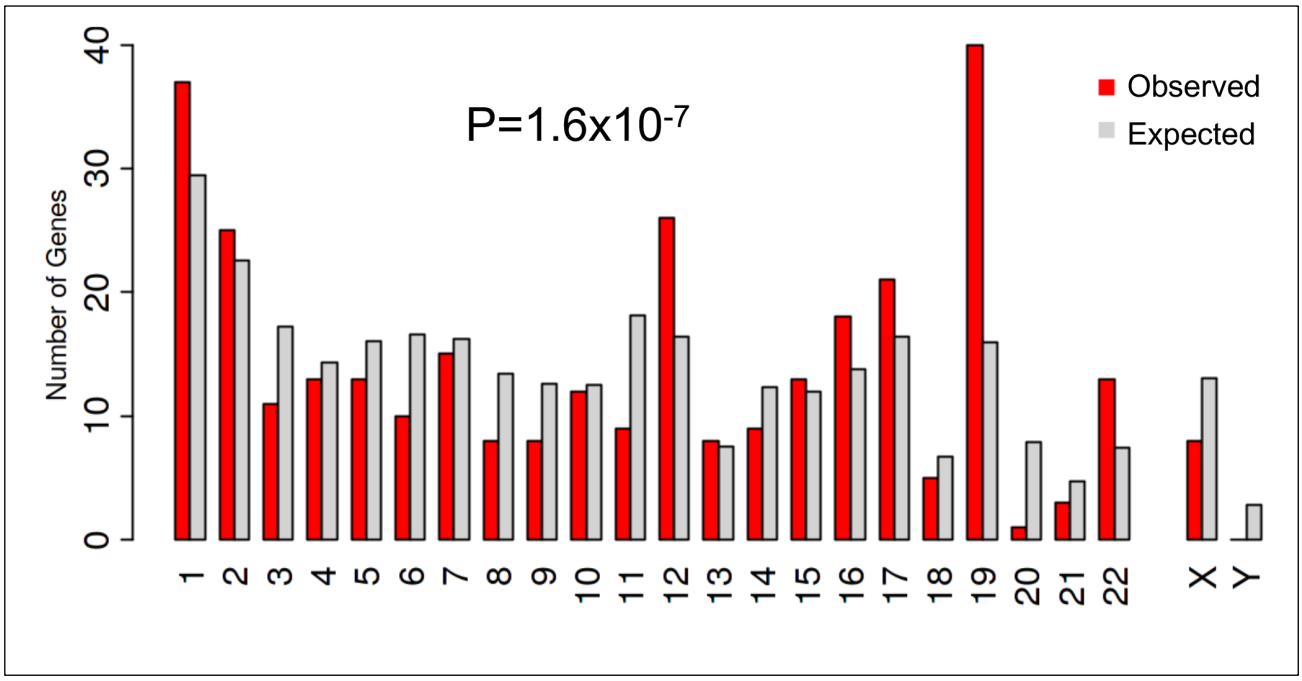
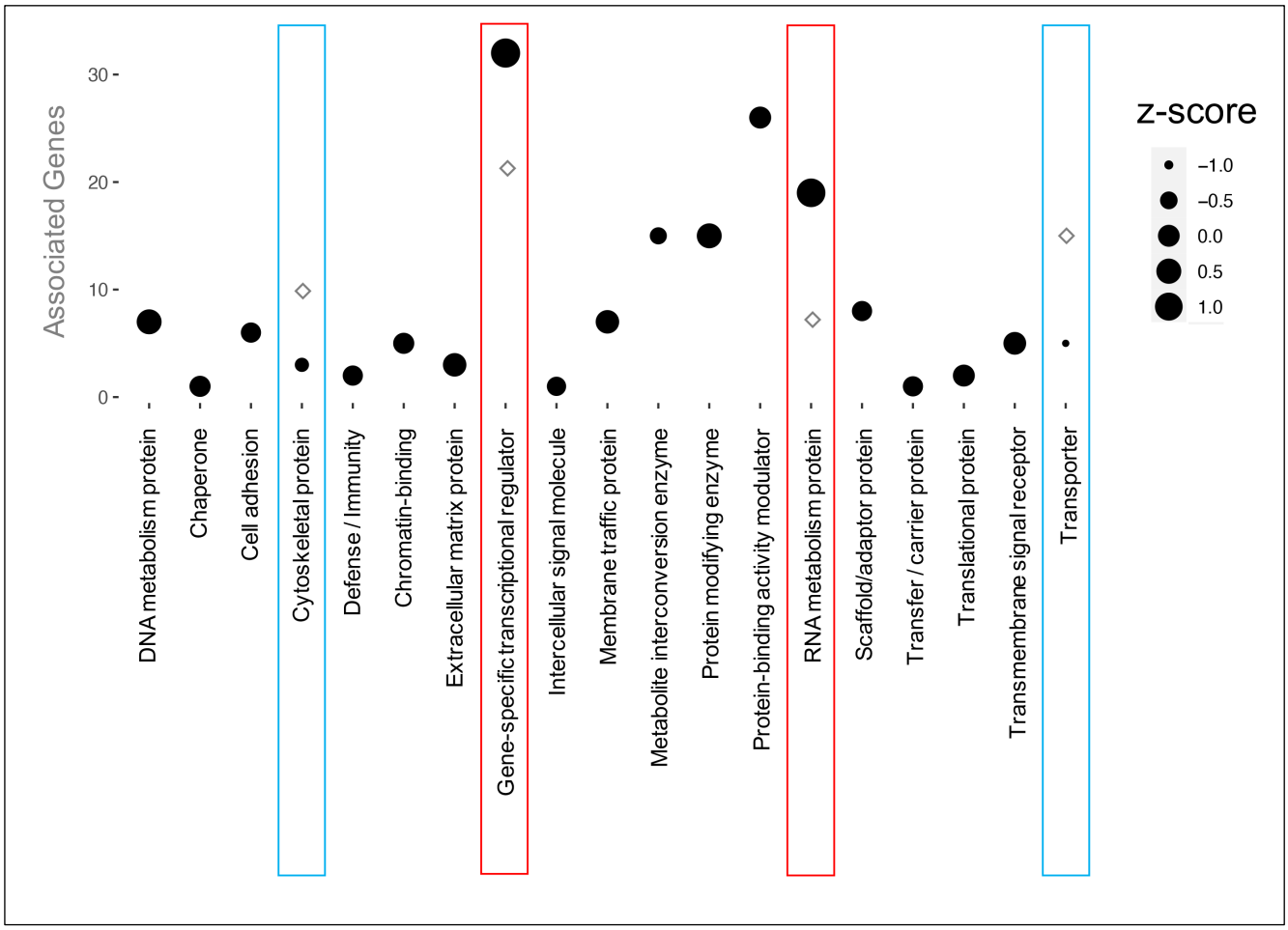
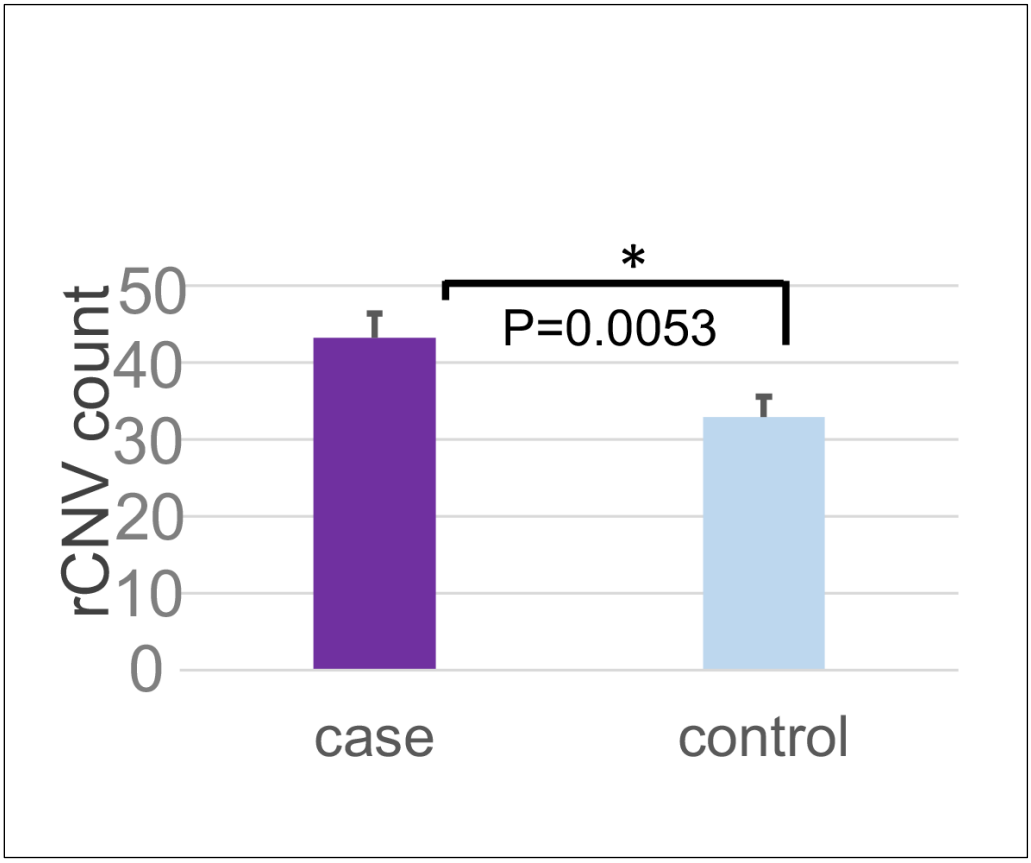


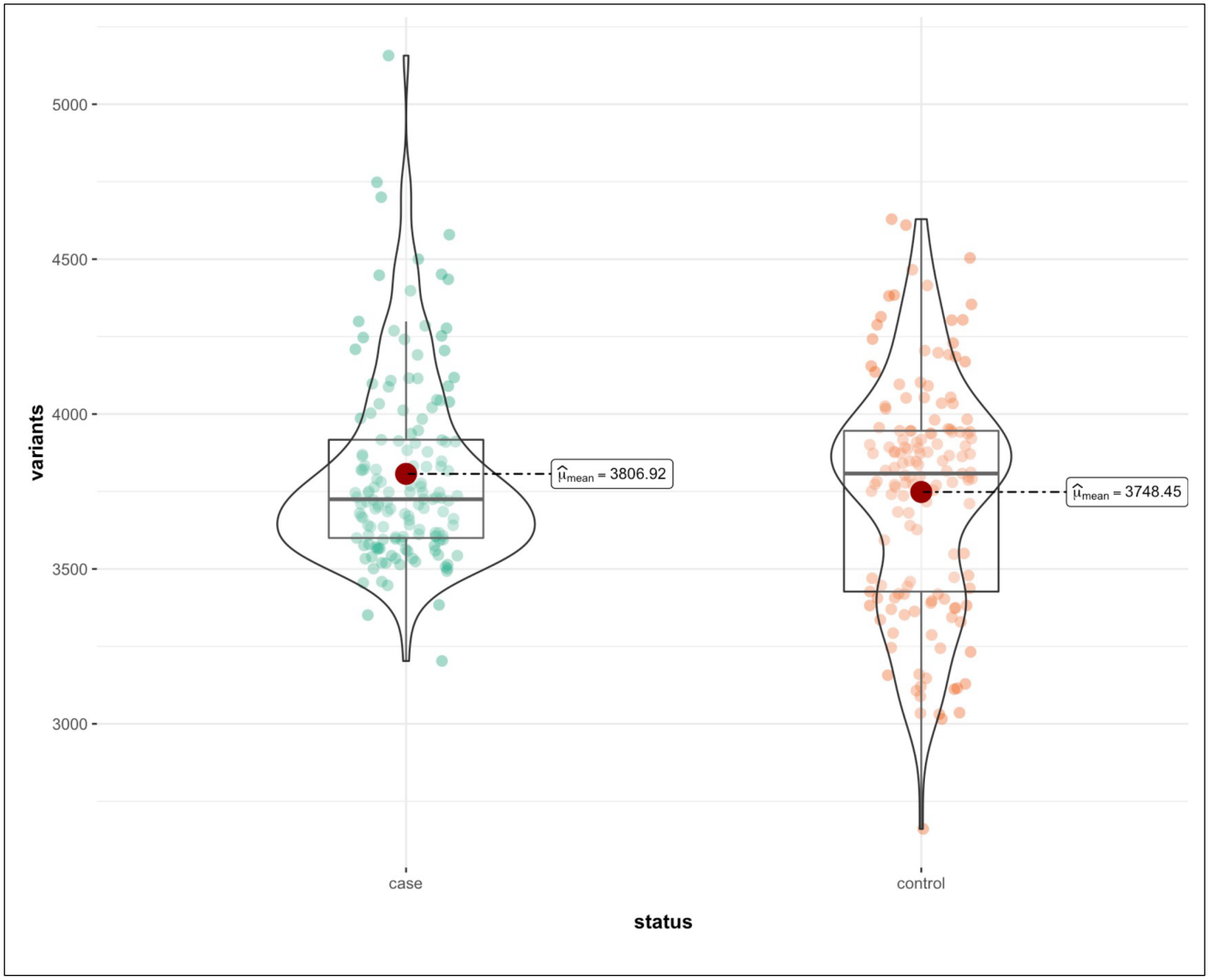
Supplementary Figure 1: A chromosomal assessment of predicted target genes of TFBS-rSNVs in SB cases. A chi-squared test was used to determine a genome-wide p-value for chromosomal differences between the expected and observed distribution of target genes affected in SB cases.



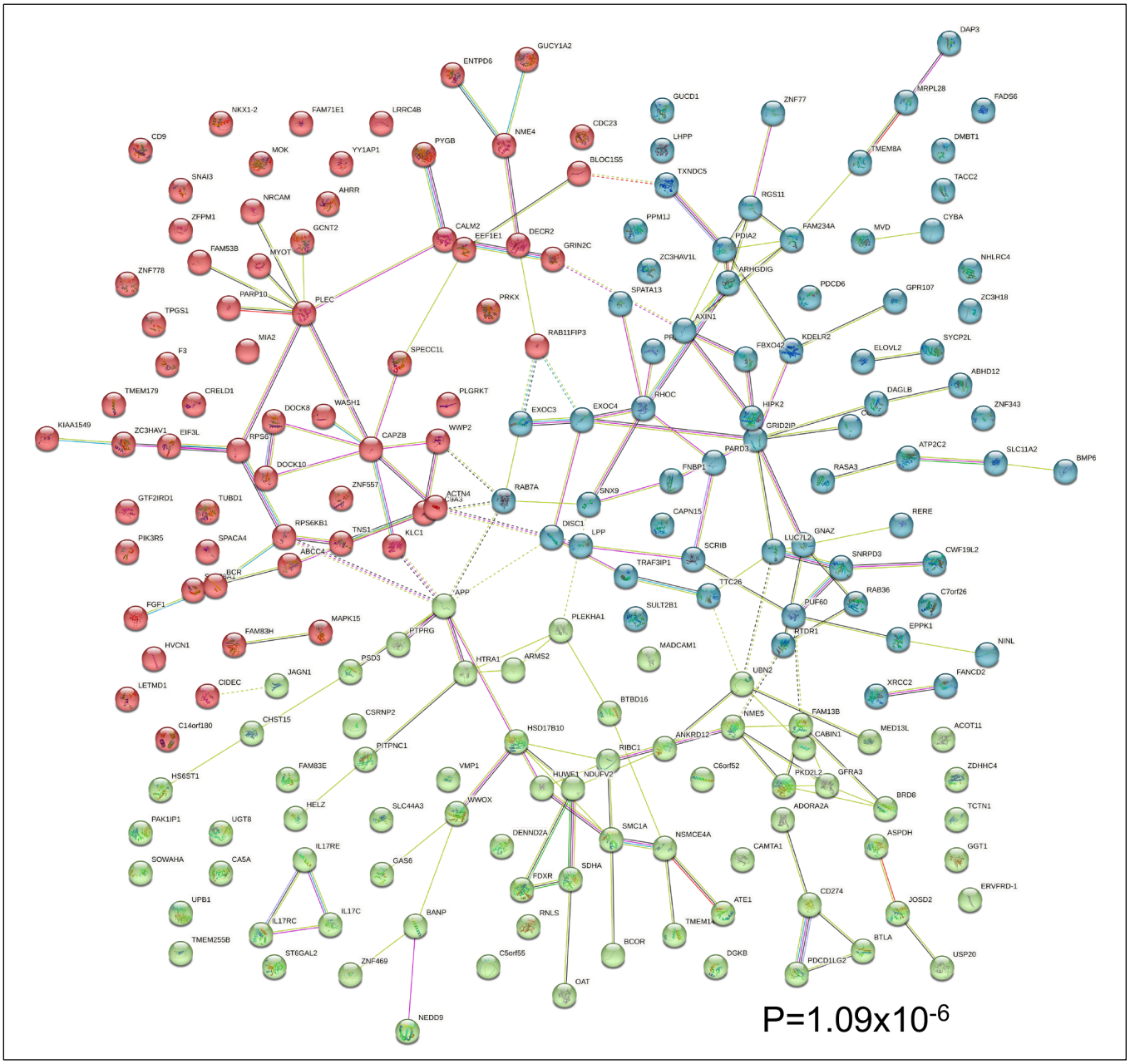
Supplementary Figure 2: Protein classes differentially impacted in the TFBS-rSNV target genes between SB cases and controls. Red boxes indicate an increase in SB cases and blue boxes represent a decrease in SB cases as compared to controls. Diamonds represent the values observed in controls.



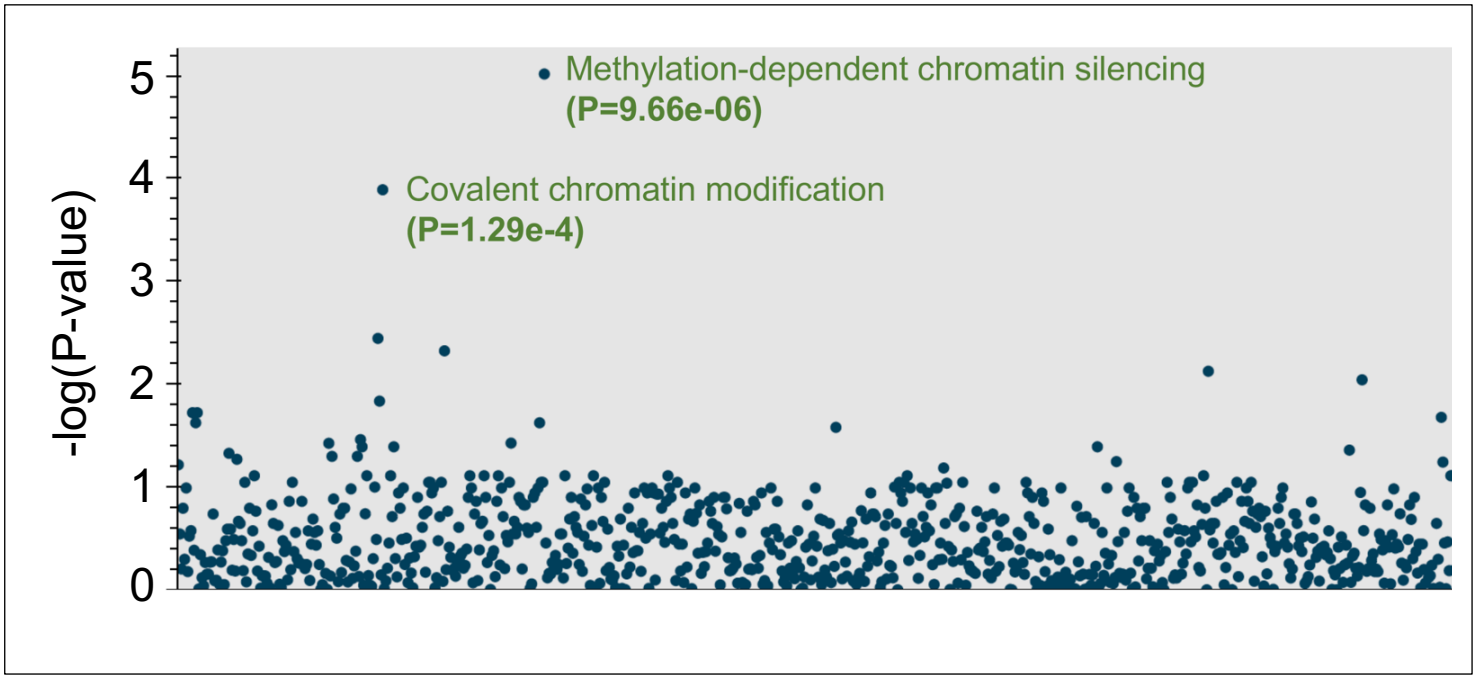
Supplementary Figure 3: rCNVs in SB cases and controls overlapping putative critical regions (pCRs). Data relevant to pCRs were obtained from Yousefi *et al.*, 2021.



Supplementary Figure 4: Rare (AF < 1%) brain enhancer SNVs detected in SB cases and controls.



Supplementary Figure 5: Protein-protein interactions within the set of enhancer-associated rare CNVs. Red nodes represent interactions detected by fusion, green nodes represent interactions detected by neighborhood, and blue nodes represent interactions detected by co-occurrence.



Supplementary Figure 6: Annotations of rare CNVs in SB cases that impact gene promoters. The statistically significant annotations are emphasized and include methylation-dependent chromatin silencing and covalent chromatin modification (each dot represents a different annotation).