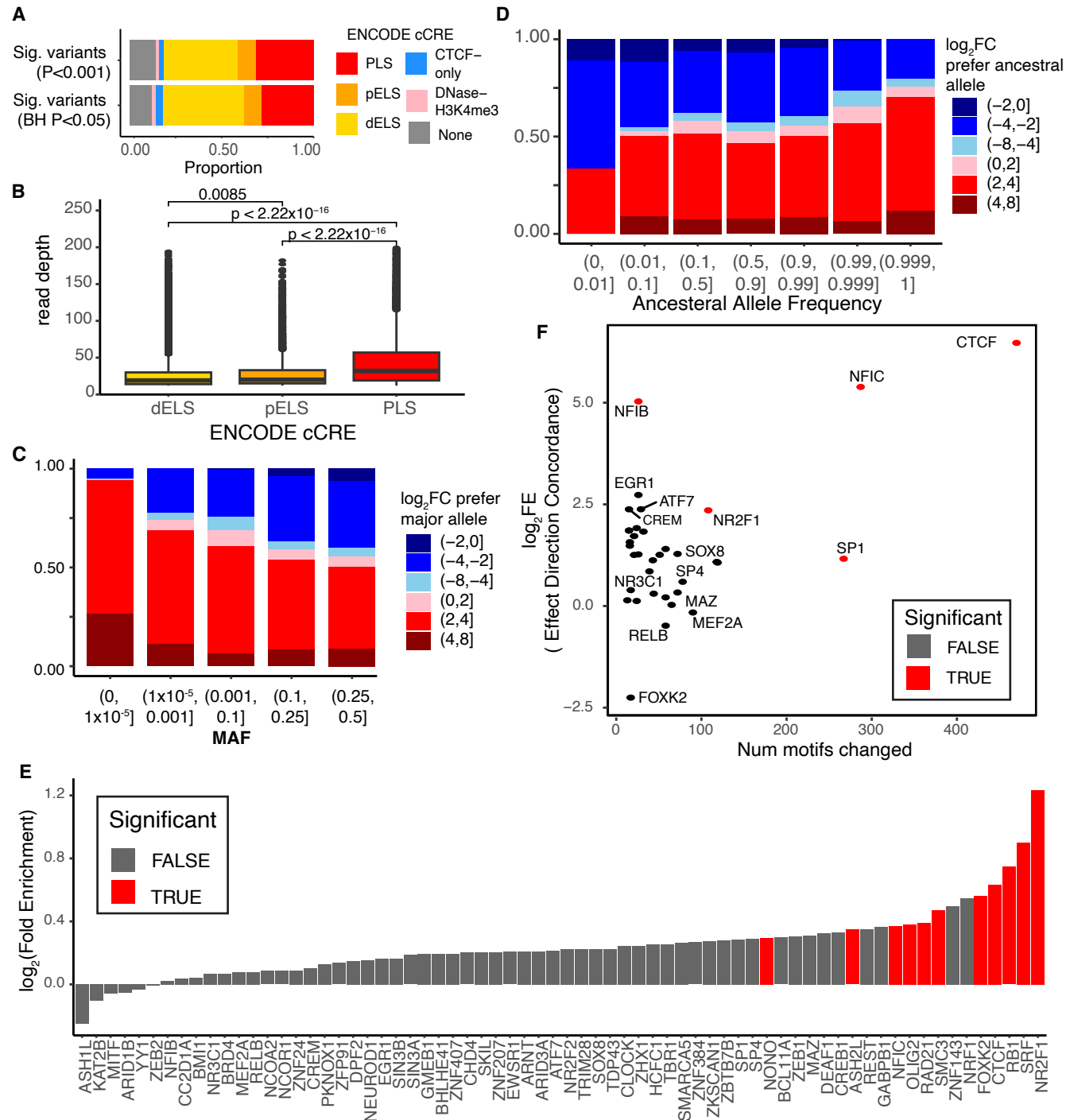




Supplemental Figure 3. Supplemental to Figure 2 A. Stacked bar plots showing the fraction of regions which overlap a particular cCRE annotation for ASB variants at nominal p-value<0.001 and BH p-value<0.05. **B.** Distribution of read depth at heterozygous variants in dELS, pELS, and PLS. P-values above the boxplots are for the t-test between the two indicated groups. **C.** Bar plot showing the proportion of ASB variants favoring the major and minor allele. **D.** Same as Figure 2B but excluding mono-allelic ASB variants. **E.** The log₂ fold enrichment for ASB variants under purifying selection (Gerp > 4) for each TF. Bars in red indicate those with a Chi-squared p-value < 0.01. **F.** The number of motifs changed for each TF (x-axis) versus the log₂ fold enrichment of effect direction concordance. Effect direction concordance is between the direction of the motif change and the direction of the allele-specific binding. Points in red indicate those with a Chi-squared p-value < 0.01.