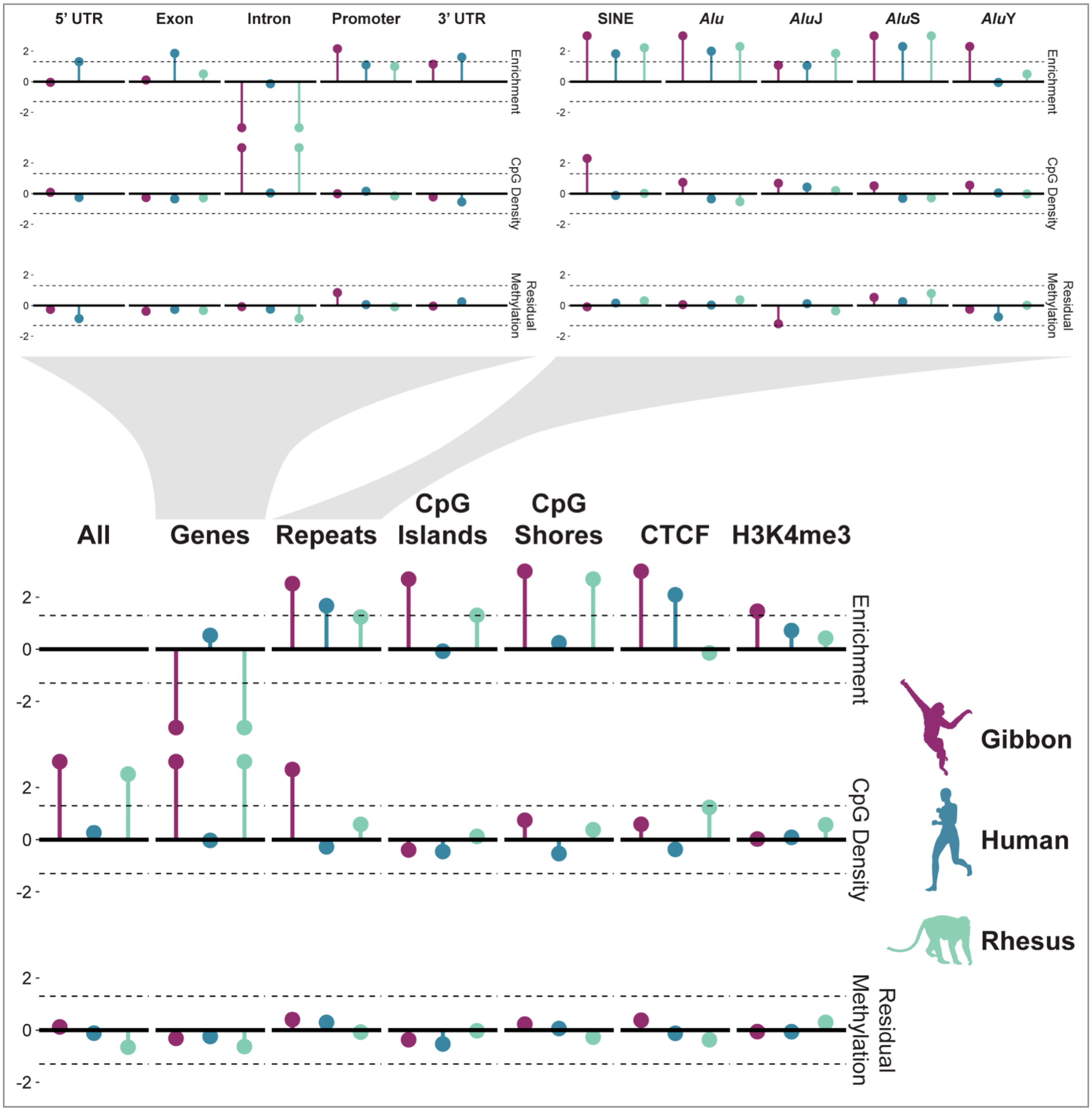

Supplemental Figure S6 - The 'lollipop' plot summarizes permutation analyses testing differences in enrichment of genomic features, CpG density, and residual methylation between the gibbon BOS and the rest of the genome. Regions orthologous to the gibbon BOS were used for human and rhesus. Negative $\log_{10}$ two-sided p-values from 1,000 permutations are represented as points above zero when values in BOS are greater than the permutation mean and below zero when less. Dotted lines mark 0.05 significance threshold with no multiple-test correction.