

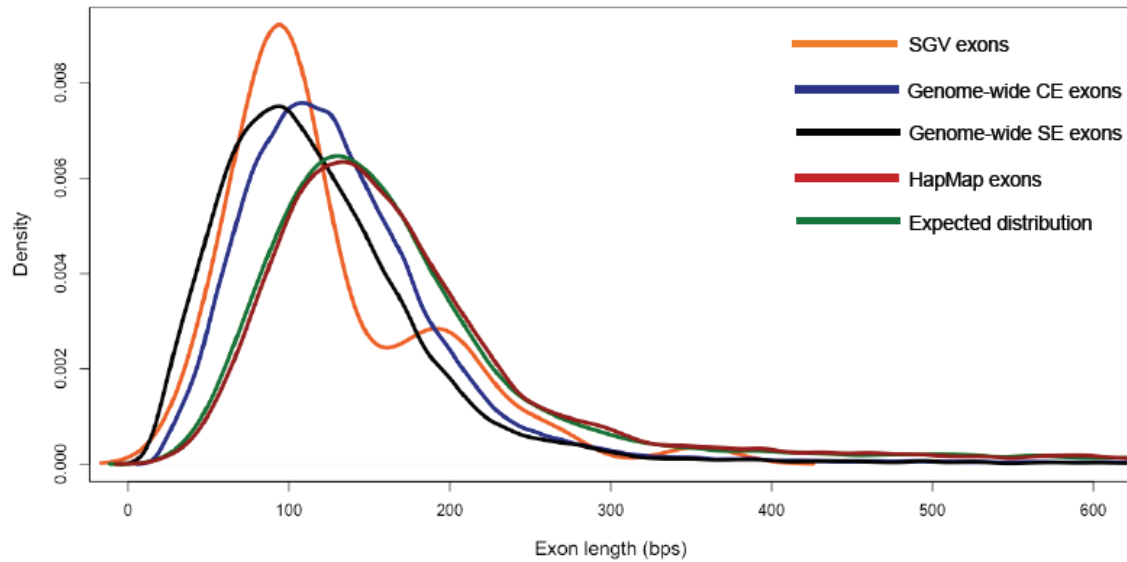


Figure S4. Distribution of exon lengths for SAV exons versus HapMap and genome-wide exons. Only distributions of exon lengths up to 600bp were plotted for clarity. Genome-wide exons were divided into constitutively spliced (CE) and alternatively spliced (AS) as defined by the Hollywood database. A fifth, expected set of exons represents a set of exon lengths we would expect given the average distribution of hSNPs across the genome and fits the real distribution of HapMap exons closely.