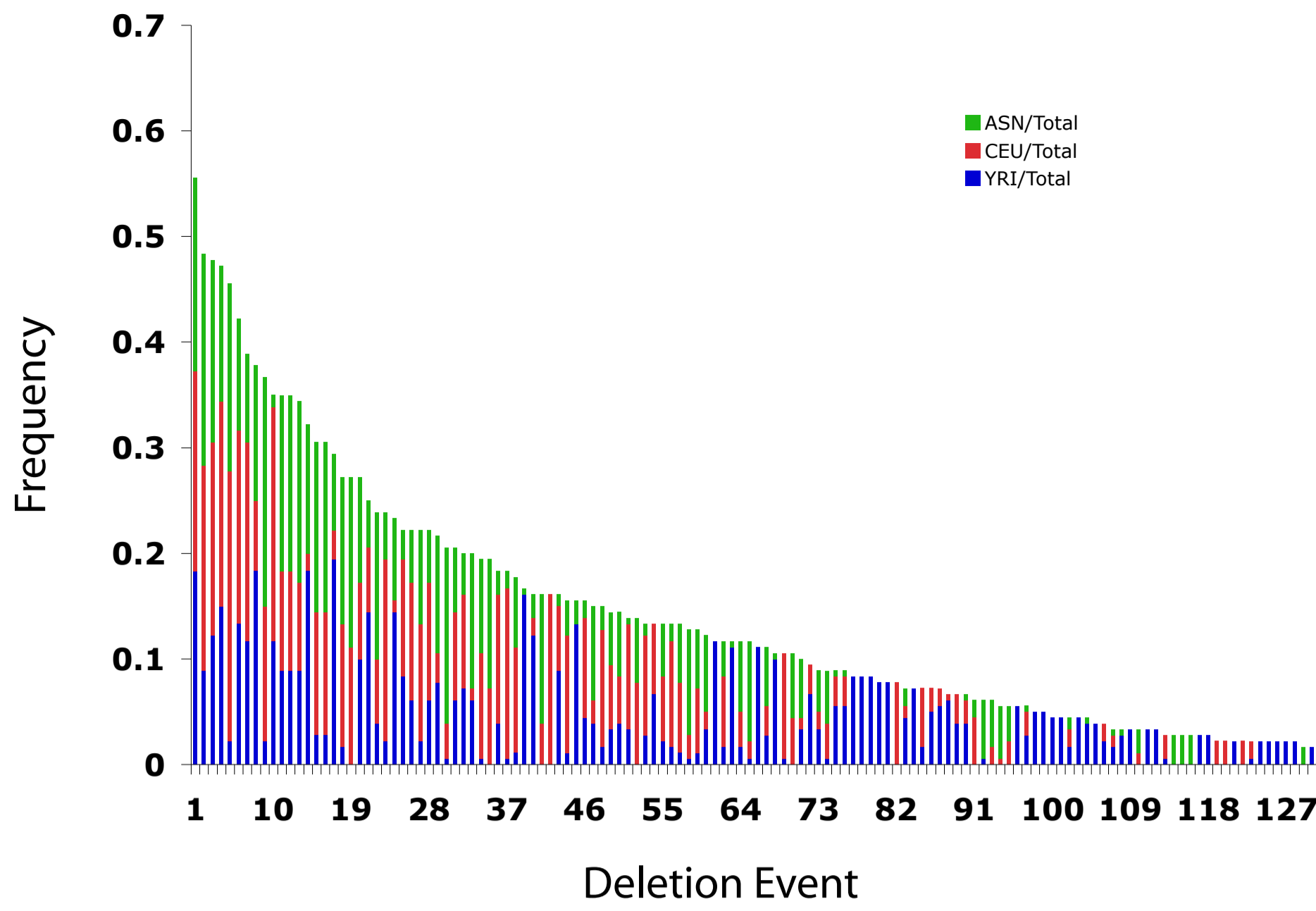
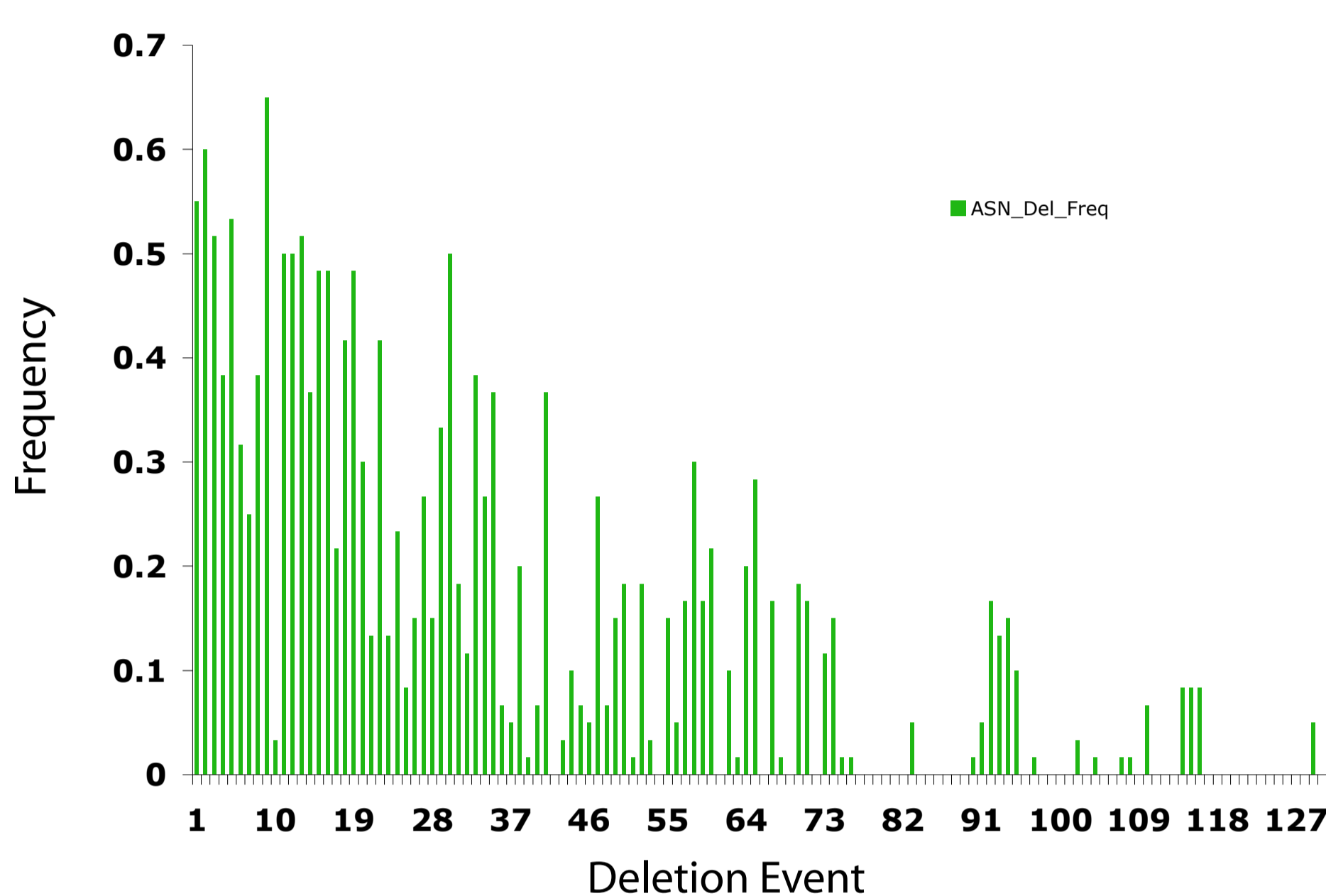
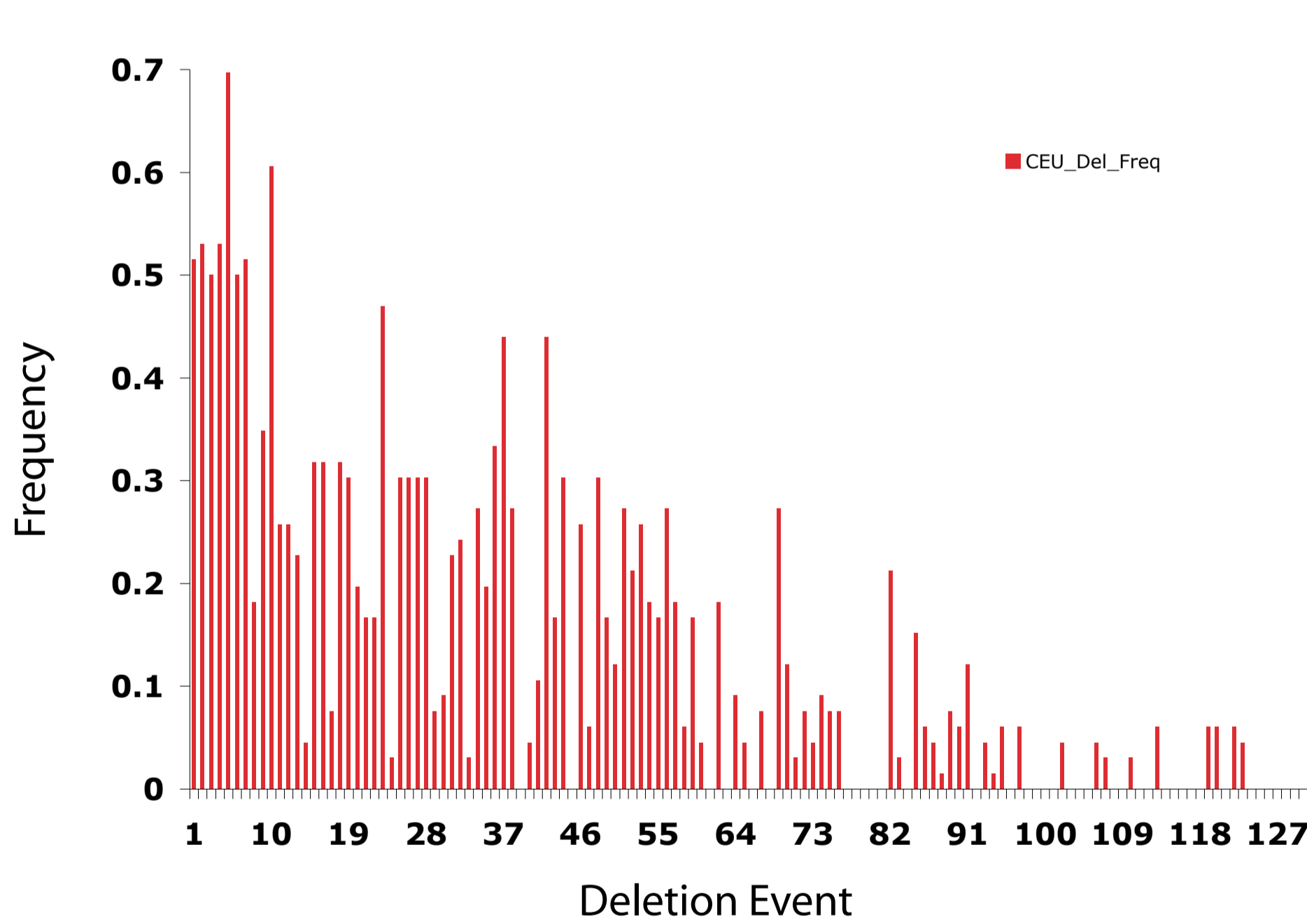


Figure S5. Genotyping Structural Variation. Frequency spectrum for 130 deletion events identified through ESP, validated and breakpoint-refined using sequence or arrayCGH, and present in at least 1% of unrelated chromosomes. Each deletion event is indicated with tick marks along the X-axis, with the global allele frequency for that event indicated by the total height of the corresponding vertical bar (a). The allele proportions within the three distinct populations are indicated in blue (YRI), red (CEU), or green (CHB+JPT), respectively. b-d) Frequency of deletion event within each population plotted separately.

A**B****C****D**