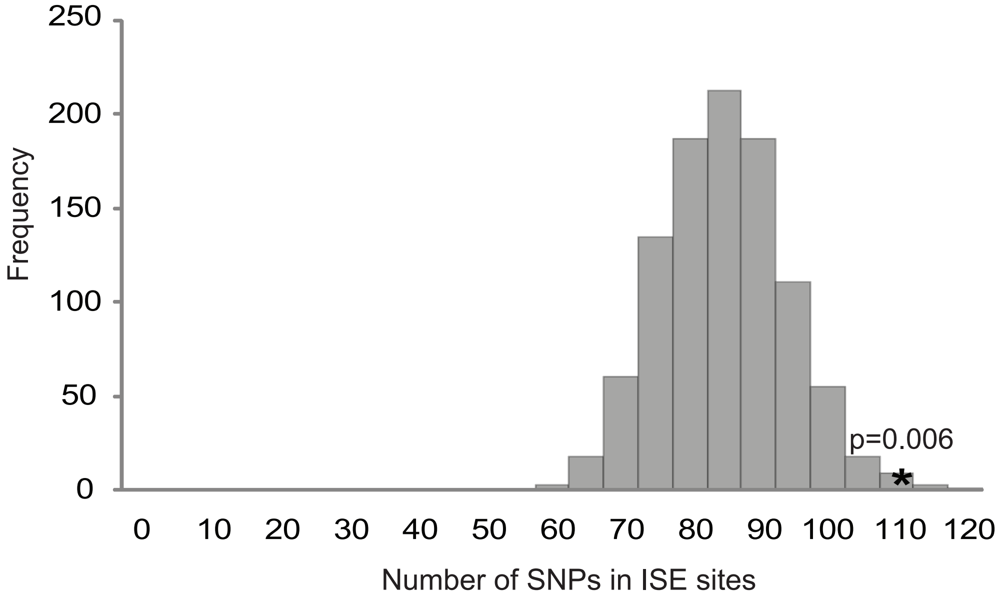

Figure S1. Enrichment of Exon Skipping-Associated ISE SNPs among Complex Human Trait-Associated SNPs. The distribution of the number of predicted exon-skipping associated ISE SNPs observed for each of the 1,000 random sets (each consisting of 3,353 SNPs, equal to the number of trait-associated SNPs) while conditioning on MAF (using HapMap CEU MAF data) and distance to the nearest exon is shown in the bar graphs. The actual number of 111 predicted exon-skipping ISE SNPs observed in the 3,353 SNPs from the NHGRI catalog is shown as a solid asterisk.