**Supplementary Figure 10. Distribution of TASs and tested SNPs for five quantitative traits across genomic annotation sets.** Results are based on the maize Working Gene Set. (A) non-genic versus genic; (B) different annotation sets; and (C) synonymous *versus* nonsynonymous. Non-genic and promoter 5kb regions are over-represented among TASs. The nonsynonymous set is under-represented among TASs. Note that non-genic region includes promoter 5kb, which in turn includes promoter 1kb, and genic region includes the untranslated region (UTR), coding region (CDS), and intron. Stars denote the proportion of TASs from the annotation set differs significantly from that of tested SNPs. Arrow denotes transcription start site.