



**Figure S6** – SNP enrichment (enrichment in genomic heritability by class of SNPs), for additive effects and dominance effects (D), by bin for structural and evolutionary features in Ames-H and NAM-H, while accounting for enrichment by gene proximity by adding one bin in functional enrichment models for SNPs  $\leq 1$  kb from an annotated gene (Proximal). Gene+Rec.: recombination rate; Gene+MNase HS: chromatin openness; Gene+MAF: minor allele frequency; Gene+GERP: genomic evolutionary rate profiling score. In Ames-H, the fitting algorithm could not converge for Gene+Rec. (PH) and Gene+MAF (DTS).