

**Table S8 – Genomic heritability captured by functional classes**

Feature	Bin	Genomic heritability (Proportion of genomic heritability explained)					
		Ames-H			NAM-H		
		DTS	PH	GY	DTS	PH	GY
<b>Gene</b>	Non-genic	<b>0.40 (43%)</b>	0.00 (0%)	0.03 (5%)	<b>0.19 (25%)</b>	0.00 (0%)	0.00 (0%)
	Genic	<b>0.20 (22%)</b>	<b>0.58 (76%)</b>	<b>0.36 (55%)</b>	<b>0.56 (75%)</b>	<b>0.72 (100%)</b>	<b>0.49 (100%)</b>
	Non-genic (D)	0.01 (1%)	0.00 (0%)	0.10 (16%)			
	Genic (D)	<b>0.32 (34%)</b>	<b>0.18 (24%)</b>	<b>0.16 (25%)</b>			
<b>Rec.</b>	< 0.45	0.11 (12%)	0.00 (0%)	0.01 (2%)	0.04 (5%)	0.03 (5%)	0.01 (2%)
	(0.45, 1.65)	<b>0.41 (44%)</b>	<b>0.17 (22%)</b>	<b>0.14 (21%)</b>	<b>0.42 (55%)</b>	<b>0.22 (31%)</b>	<b>0.13 (27%)</b>
	> 1.65	0.08 (9%)	<b>0.40 (53%)</b>	<b>0.23 (35%)</b>	<b>0.30 (39%)</b>	<b>0.46 (64%)</b>	<b>0.35 (71%)</b>
	< 0.45 (D)	0.07 (8%)	0.02 (3%)	0.06 (9%)			
	(0.45, 1.65) (D)	0.10 (11%)	0.02 (3%)	0.07 (11%)			
	> 1.65 (D)	<b>0.15 (16%)</b>	<b>0.15 (19%)</b>	<b>0.14 (22%)</b>			
<b>MNase HS</b>	Dense	<b>0.17 (18%)</b>	0.00 (0%)	<b>0.27 (42%)</b>	0.06 (7%)	0.00 (0%)	0.00 (0%)
	Open	<b>0.43 (46%)</b>	<b>0.58 (75%)</b>	<b>0.12 (19%)</b>	<b>0.70 (93%)</b>	<b>0.71 (100%)</b>	<b>0.51 (100%)</b>
	Dense (D)	<b>0.32 (35%)</b>	0.00 (0%)	0.00 (0%)			
	Open (D)	0.01 (1%)	<b>0.19 (25%)</b>	<b>0.26 (40%)</b>			
<b>MAF</b>	< 0.01	0.00 (0%)	0.00 (0%)	0.00 (0%)	0.00 (0%)	0.05 (7%)	<b>0.17 (36%)</b>
	(0.01, 0.05)	<b>0.46 (50%)</b>	0.07 (10%)	0.09 (14%)	<b>0.34 (46%)</b>	0.00 (0%)	0.00 (0%)
	> 0.05	<b>0.14 (15%)</b>	<b>0.40 (54%)</b>	0.06 (9%)	<b>0.40 (54%)</b>	<b>0.64 (93%)</b>	<b>0.31 (64%)</b>
	< 0.01 (D)	0.00 (0%)	0.00 (0%)	0.00 (0%)			
	(0.01, 0.05) (D)	0.00 (0%)	<b>0.13 (18%)</b>	<b>0.36 (53%)</b>			
	> 0.05 (D)	<b>0.32 (35%)</b>	<b>0.14 (19%)</b>	<b>0.16 (24%)</b>			
<b>GERP</b>	0	<b>0.46 (49%)</b>	0.00 (0%)	<b>0.16 (24%)</b>	0.15 (19%)	0.00 (0%)	0.00 (0%)
	> 0	0.14 (15%)	<b>0.58 (76%)</b>	<b>0.23 (36%)</b>	<b>0.61 (81%)</b>	<b>0.72 (100%)</b>	<b>0.51 (100%)</b>
	0 (D)	0.00 (0%)	0.01 (1%)	0.00 (0%)			
	> 0 (D)	<b>0.32 (35%)</b>	<b>0.17 (23%)</b>	<b>0.26 (40%)</b>			

Variance partition by functional features. Gene: proximity to genes ( $\leq 1$  kb); Rec.: recombination rate; MNase HS: chromatin openness; MAF: minor allele frequency; GERP: genomic evolutionary rate profiling score. Genomic heritability: variance component at a given bin from functional enrichment models, normalized by the total phenotypic variance. Proportion of genomic heritability explained: ratio of genomic variance at a given bin over the sum of genomic variances across bins.