

Table S7 – Significance of variance partition by panel and functional feature

Panel	Trait	p-value for variance partition				
		Gene	Rec.	MNase HS	MAF	GERP
Ames-H	DTS	0.21	0.29	0.15	0.035	0.12
	PH	6.0×10^{-5}	9.1×10^{-4}	6.0×10^{-5}	0.80	8.6×10^{-5}
	GY	0.18	0.24	0.12	0.088	0.11
NAM-H	DTS	4.6×10^{-3}	4.1×10^{-4}	7.8×10^{-5}	7.7×10^{-4}	3.8×10^{-4}
	PH	1.6×10^{-11}	1.9×10^{-7}	5.6×10^{-10}	0.70	7.5×10^{-12}
	GY	6.1×10^{-5}	1.4×10^{-4}	1.8×10^{-5}	0.033	3.4×10^{-6}
Combined (Fisher's method)	DTS	7.8×10^{-3}	1.2×10^{-3}	1.4×10^{-4}	3.1×10^{-4}	5.1×10^{-4}
	PH	3.3×10^{-14}	4.0×10^{-9}	1.1×10^{-12}	0.88	2.3×10^{-14}
	GY	1.3×10^{-4}	3.7×10^{-4}	3.0×10^{-5}	0.020	6.0×10^{-6}
		Gene	Gene+ Rec.	Gene+ MNase HS	Gene+ MAF	Gene+ GERP
Ames-H	DTS	–	0.31	0.39	N/A	0.57
	PH	–	N/A	0.46	1.0	0.97
	GY	–	0.72	0.41	0.054	0.61
NAM-H	DTS	–	8.0×10^{-3}	6.0×10^{-3}	1.0×10^{-4}	0.032
	PH	–	1.0	0.83	1.0	0.20
	GY	–	0.26	0.13	0.024	0.019
Combined (Fisher's method)	DTS	–	0.017	0.017	N/A	0.091
	PH	–	N/A	0.75	1.0	0.51
	GY	–	0.50	0.21	9.8×10^{-3}	0.063

Significance of variance partition by gene proximity (Gene), structural features (Rec., MNase HS), and evolutionary features (MAF, GERP); p-values were obtained by likelihood ratio test comparing the functional enrichment model (partitioning variance of additive and dominance marker effects in Ames-H, or additive marker effects only in NAM-H) to the baseline model: no partition (top) or variance partition by gene proximity (bottom). N/A: the fitting algorithm could not converge to a solution.