

**S2 Table: Locus architectures modeled at simulated loci.**

Architecture	Direction of effects	Selection parameter (from Agarwala et al)	Description (also see S3 Figure)
AR1	All deleterious	$\tau = 1$	Rare variants (MAF<1%) explain >90% of heritability and have large additive effects relative to common variants
AR2	All deleterious	$\tau = 0.5$	Rare variants explain ~50% of heritability and have moderate additive effect sizes relative to common variants
AR3	All deleterious	$\tau = 0$	Rare variants explain <15% of heritability and have additive effects comparable to common variants
AR4	All deleterious	$\tau = 1$ , all causal variants have MAF < 1%	Same effect size distribution as AR1; but only rare (MAF<1%) are causal at the simulated locus
AR5	All deleterious	$\tau = 0.5$ , all causal variants have MAF < 1%	Same effect size distribution as AR2; but only rare (MAF<1%) are causal at the simulated locus
AR6	50% deleterious, 50% protective	$\tau = 0.5$	Same effect size distribution as AR2; but 50% of variants have protective effects on disease