

Supplementary Table 5. SNP-heritability estimates

	MAF bin	LD bin ^a	# SNVs	V_g	V_g (s.e.)	V_p	V_p (s.e.)	Heritability	s.e.
Single GRM	-	-	7702027	0.087	0.028	0.836	0.011	0.104	0.034
GREML-LDMS	-	-	5806750	-	-	0.835	0.011	0.128	0.045
	0.01-0.1	High	1410877	1.0E-06	0.034	-	-	1.0E-06	0.041
		Low	1410886	0.005	0.012	-	-	0.006	0.015
	0.1-0.2	High	538069	0.050	0.018	-	-	0.060	0.022
		Low	538070	0.001	0.008	-	-	0.001	0.010
	0.2-0.3	High	372154	0.024	0.016	-	-	0.029	0.019
		Low	372154	1.0E-06	0.007	-	-	1.0E-06	0.008
	0.3-0.4	High	306954	0.017	0.015	-	-	0.021	0.018
		Low	306957	0.004	0.007	-	-	0.005	0.009
	0.4-0.5	High	275312	0.005	0.013	-	-	0.006	0.015
		Low	275317	0.001	0.006	-	-	0.001	0.007

^a High represents above median LD scores within MAF bin. Low represents below median LD scores within MAF bin

GRM, genomic relationship matrix; LD, linkage disequilibrium; MAF, minor allele frequency; s.e., standard error; V_g , genetic variance; V_p , phenotypic variance