

Table S1: Genomic control factors achieved in analysis of the real data, or a single replicate of the simulated data, when feeding externally estimated kinships into FaST-LMM

Kinship estimation method	Trait analysed		
	Real	Simulated weak	Simulated quantitative
Unadjusted	1.23	1.12	1.43
Wrong ^a	1.23	1.12	1.43
FLMM-R ^b	0.99	0.99	1.00
KING (homogeneous)	0.99	0.99	0.99
KING (robust)	0.99	0.99	1.00
Theoretical (pedigree-based) kinships	1.11	1.00	0.99
PLINK	1.18	1.12	1.42

^a Wrong = misspecified kinships, chosen to be inversely related to the theoretical kinship value.

^b FLMM-R = FaST-LMM's own realised relationship matrix