

**Supplemental Table 6.** Power analysis for 4,000 individuals with family structure. We used SOLAR<sup>32</sup> to simulate phenotypes conditional on the observed family structures in the FHS sample. The phenotypes were simulated to have variance of 1 and polygenic heritability of 0.25. We considered the QTL (additive model) with MAF of 0.01, 0.05, 0.1, 0.2, 0.3 and 0.4, and QTL variance of 0.0025, 0.005, 0.0075 and 0.01. 1,000 of replicates were used to estimate power for each considered scenario. Simulated phenotypes were analyzed using a linear mixed effects model implemented in the *lmekin* function from the *coxme* R package where a relationship coefficient matrix was used to account for familial correlation.

maf	qtl_var	power
0.01	0.0025	0.03
0.01	0.005	0.25
0.01	0.0075	0.577
0.01	0.01	0.813
0.05	0.0025	0.03
0.05	0.005	0.243
0.05	0.0075	0.595
0.05	0.01	0.848
0.1	0.0025	0.023
0.1	0.005	0.232
0.1	0.0075	0.601
0.1	0.01	0.863
0.2	0.0025	0.022
0.2	0.005	0.23
0.2	0.0075	0.598
0.2	0.01	0.843
0.3	0.0025	0.02
0.3	0.005	0.227
0.3	0.0075	0.594
0.3	0.01	0.861
0.4	0.0025	0.027
0.4	0.005	0.244
0.4	0.0075	0.586
0.4	0.01	0.856