Supporting Information

S11 Table

Power Comparison with Complete Data, When the Relevant Covariates are Omitted from the Fitted Model, Where Traits are Generated by the Liability Threshold Model.

Setting of (π_a, π_c)	**MQLS-LIN**	**MQLS-LOG**	**CERAMIC**	**GMMAT**	**EMMAX**	**MASTOR**	**CARAT**
$(0, .8)$	**.53**	**.53**	**.53**	.45	.45	**.53**	**.53**
$(.2, .6)$	**.46**	**.46**	**.46**	.41	.41	**.46**	**.46**
$(.4, .4)$	**.40**	**.40**	**.40**	**.39**	**.39**	**.40**	**.40**
$(.6, .2)$	**.34**	**.34**	**.34**	**.34**	**.35**	**.34**	**.35**
$(.8, 0)$	.29	.29	**.31**	.30	**.32**	**.31**	**.32**

Bold indicates the highest estimated power, or estimated power not significantly different from the highest, for each setting. In each case, the sample size is 600 individuals, and ascertainment setting A is used. Association is tested at causal SNP 2, which has MAF .2, and power is assessed empirically at significance level .05, based on 10,000 replicates. An upper bound (obtained based on power 0.5) for the standard error of each power estimate is 0.005. For a pairwise comparison, the upper bound is $\sim$0.007. π_a is the proportion of total liability variance that is due to polygenic effects and π_c is the proportion due to covariate effects.