

## Supporting Information

### S5 Table

Power Comparison with Partially Missing Data, When the Relevant Covariates are Omitted from the Fitted Model, Where Traits are Generated by the Mixed-Effects Logistic Model.

Setting of ( $\theta_a, \theta_c$ )	MQLS-LIN	MQLS-LOG	CERAMIC	GMMAT	EMMAX	MASTOR	CARAT
(0, .1)	<b>.66</b>	<b>.66</b>	<b>.66</b>	.11	.11	<b>.66</b>	.11
(.2, .8)	<b>.53</b>	<b>.53</b>	<b>.53</b>	.11	.12	<b>.53</b>	.14
(.4, .6)	<b>.46</b>	<b>.46</b>	<b>.46</b>	.13	.13	<b>.46</b>	.16
(.6, .4)	<b>.38</b>	<b>.38</b>	<b>.39</b>	.13	.15	<b>.39</b>	.17
(.8, .2)	.34	.34	<b>.36</b>	.13	.19	<b>.36</b>	.19
(1, 0)	.29	.29	<b>.34</b>	.13	.23	<b>.34</b>	.19

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 1,200 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  $\sim 0.007$ .  $\theta_a$  is the ratio of the variance explained by polygenic effects to the total variance of polygenic and covariate effects on the logit scale, and  $\theta_c = 1 - \theta_a$ .