

Table S4. Power calculations. A) Association using a multiplicative model. Conservatively defining genome-wide significance as 5×10^{-8} , we calculate power in our sample (1,829 cases and 2,250 controls), assuming prevalence ~ 4 in 100,000 and a multiplicative model of gene effect as shown. B) Regression analysis of survival. Conservatively defining genome-wide significance as 5×10^{-8} , we calculate power in our sample (1014 cases) with four predictors (genotype, site of collection, first 2 dimensions of stratification analysis) using linear regression as shown.

A)

| <u>MAF</u> | <u>Odds ratio</u> | <u>Power (1E-05)</u> | <u>Power (5E-08)</u> |
|------------|-------------------|----------------------|----------------------|
| 0.1 | 1.1 | 0% | 0% |
| | 1.3 | 23% | 4% |
| | 1.5 | 93% | 66% |
| 0.3 | 1.1 | 0% | 0% |
| | 1.3 | 87% | 53% |
| | 1.5 | 100% | 100% |

B)

| <u>R²</u> | <u>F2 (effect size)</u> | <u>Power (1E-05)</u> | <u>Power (5E-08)</u> |
|----------------------|-------------------------|----------------------|----------------------|
| 0.01 | 0.01010 | <15% | <15% |
| 0.02 | 0.02041 | 30% | <15% |
| 0.03 | 0.03093 | 69% | 31% |
| 0.04 | 0.04167 | 92% | 64% |
| 0.05 | 0.05263 | 98.5% | 87% |