Scenario III: 2 correlated quantitative traits from the same study (n_{Trait}, n_{Trait2} = 2000, 2000) (p_{trait} = -0.9 (p_{trait} = -0.4 (p_{trait} = 0.4 (p_{trait} = 0.9 (p

S2 Fig: Scenario III: QQ plots for the pleiotropic analysis of null data on 2 correlated traits where each trait is measured on the same 2,000 individuals. Observed($-\log_{10}$ p-values) are plotted on the y-axis and Expected($-\log_{10}$ p-values) on the x-axis. Type I error performance of tests of pleiotropic effect of a genetic variant on the 2 traits is based on 9.99 million null variants with genetic effects that are either $\{\beta_1 = 0 = \beta_2\}$ or $\{\beta_1 = 0, \beta_2 \text{ explains } 0.1\%$ of Trait 2 variance} or $\{\beta_1 \text{ explains } 0.1\%$ of Trait 1 variance, $\beta_2 = 0\}$. The gray shaded region represents a conservative 95% confidence interval for the expected distribution of p-values. P-values $\geq 10^{-12}$ are shown here.

PLACO (trait correlation ignored)

PLACO

Sobel

maxP