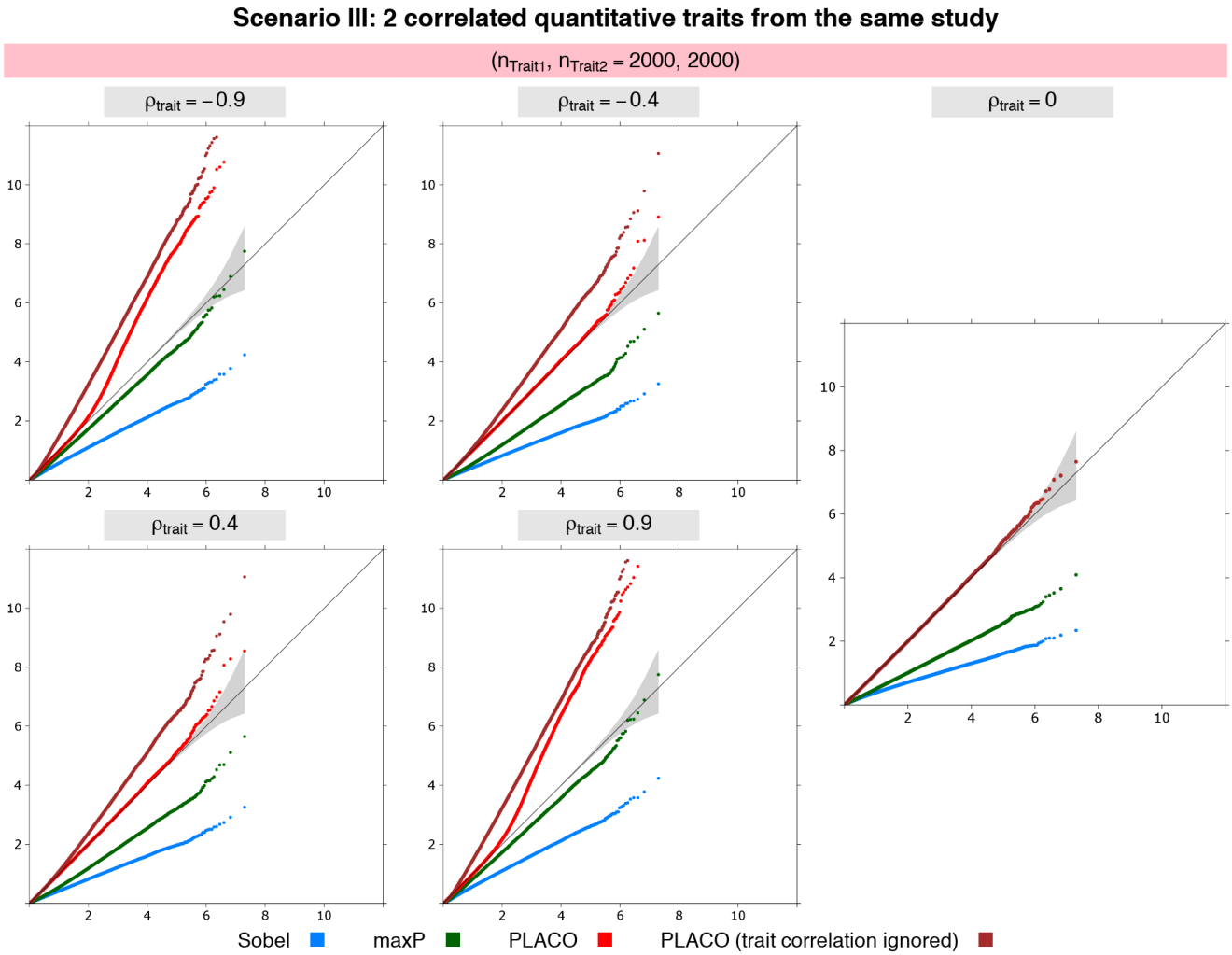

S2 Fig: Scenario III: QQ plots for the pleiotropic analysis of null data on 2 correlated traits where each trait is measured on the same $2,000$ individuals. Observed($-\log_{10}$p-values) are plotted on the y-axis and Expected($-\log_{10}$p-values) on the x-axis. Type I error performance of tests of 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 $\{\beta_1 = 0, \beta_2$ explains 0.1% of Trait 2 variance$\}$ or $\{\beta_1$ 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.