

Table S2: Results of inference on simulated phenotypes from the yeast genetic data

	Mean (SD) Estimates	Mean \hat{SE}
h^2	0.40 (0.05)	0.06
h_2^2	0.30 (0.07)	0.07
$h_{>}^2$	0.20 (0.09)	0.10

The columns are, from left to right, the sample mean (standard deviation) of the estimates, as well as the mean of the standard error estimates, from 500 simulated phenotypes. True values are $h^2 = 0.4$, $h_2^2 = 0.3$, $h_{>}^2 = 0.2$, with the variance from higher order interactions divided equally between third and fourth order interactions.