S10 Fig. **CLiP-Y scores for quantitative phenotypes with weight functions over individuals contributing to the correlation, as a function of SNP variance explained.** Means and standard deviations of scores are shown as a function of variance explained: **(A)** homogeneous cohorts, **(B)** heterogeneous cohorts, and **(C)** the difference between scores of heterogeneous cohorts and expected homogeneous scores in A. Colors indicate the type of weight function, with blue lines indicating learned polynomial functions. In panel A, black dotted lines indicate calculated expected scores for each homogeneous cohort, given effect sizes and allele frequencies. In practice, these expected scores will serve as the null scores subtracted from that of test data to produce analogous results to panel C. Each condition was run for 20 trials, and all cohorts were simulated with 100 SNPs and a sample size of 100,000 cases and 100,000 controls.