# Supplementary Material: Methods

We obtained correlated and independent ASE datasets from supplemental datasets 1 and 2 in [8]. We also generated correlated and independent ASE datasets by partitioning 48 biological replicates of expression data from yeast [10]. Four replicates were discarded based on quality reported in the paper. To produce a dataset resulting in correlated estimates of cis and trans variation, the 44 remaining samples were partitioned into four subsets of 11 samples each, representing two “alleles” (strain 1 and strain 2) by two “conditions” (hybrid and parental). To produce a dataset resulting in independent estimates of cis and trans, 42 of the 44 remaining samples were partitioned into six subsets of 7 samples each, representing two “alleles” (strain 1 and strain 2) by three “conditions” (hybrid 1, hybrid 2, and parental). Estimates of ASE were calculated on the sums of individual partitions according to [8], with the modification that dHybrid and dParent were calculated according to the expression:

 .