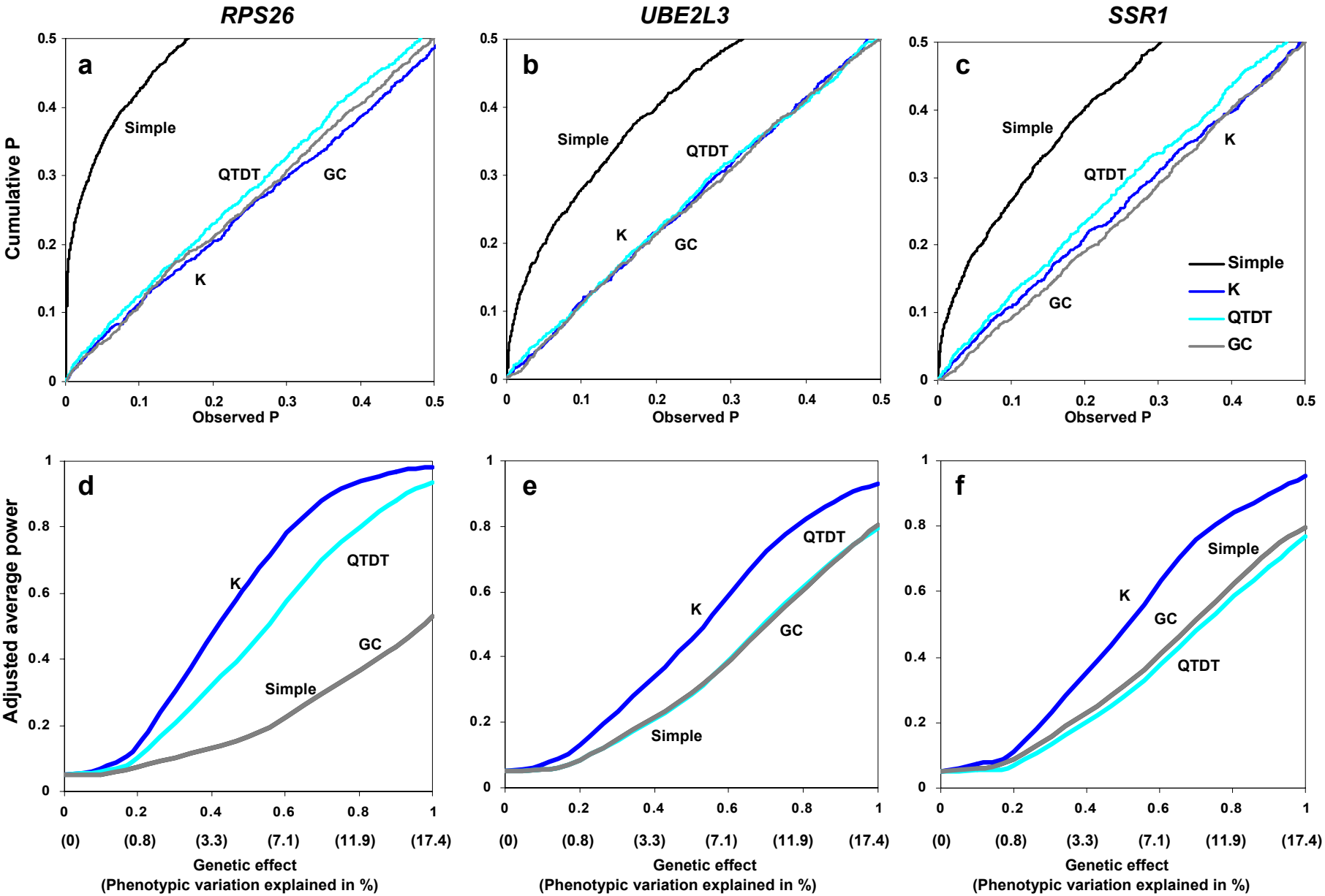
Supplementary Figure 1



Supplementary Figure 1 Model comparison with three additional human gene expression phenotypes. 1a-c Evaluation of the model Type I error rates using random SNPs for gene expression phenotypes, *RPS26* (**1a**)**,** *UBE2L3* (**1b**), and *SSR1* (**1c**). The cumulative distributions of observed *P* values are presented for the simple model, the K model, QTDT, and the simple model with genomic control (GC). Under the expectation that random SNPs are unlinked to the polymorphisms controlling these traits (H_0: no SNP effect), approaches that appropriately control for Type I errors should exhibit a uniform distribution of *P* values (a diagonal line in these cumulative plots). The simple model was included only for the purpose of illustrating the effect of ignoring family relationships, as it is not a standard practice. **1d-f** The adjusted average power of the models for *RPS26* (**1d**)**,** *UBE2L3* (**1e**), and *SSR1* (**1f**). A genetic effect was added to each random SNP (QTN effect), where k = 0.1, 0.2, 0.5, 0.7, 0.9 and 1.0 times of the standard deviation of the phenotypic mean of a trait. Each model was adjusted based on its empirical Type I error rate. The adjusted average power for GC is the same as that of the simple model with the empirical threshold *P* value. For convenience of comparison we listed the point value of phenotypic variation explained by a QTN at the allele frequency of p = 0.3.