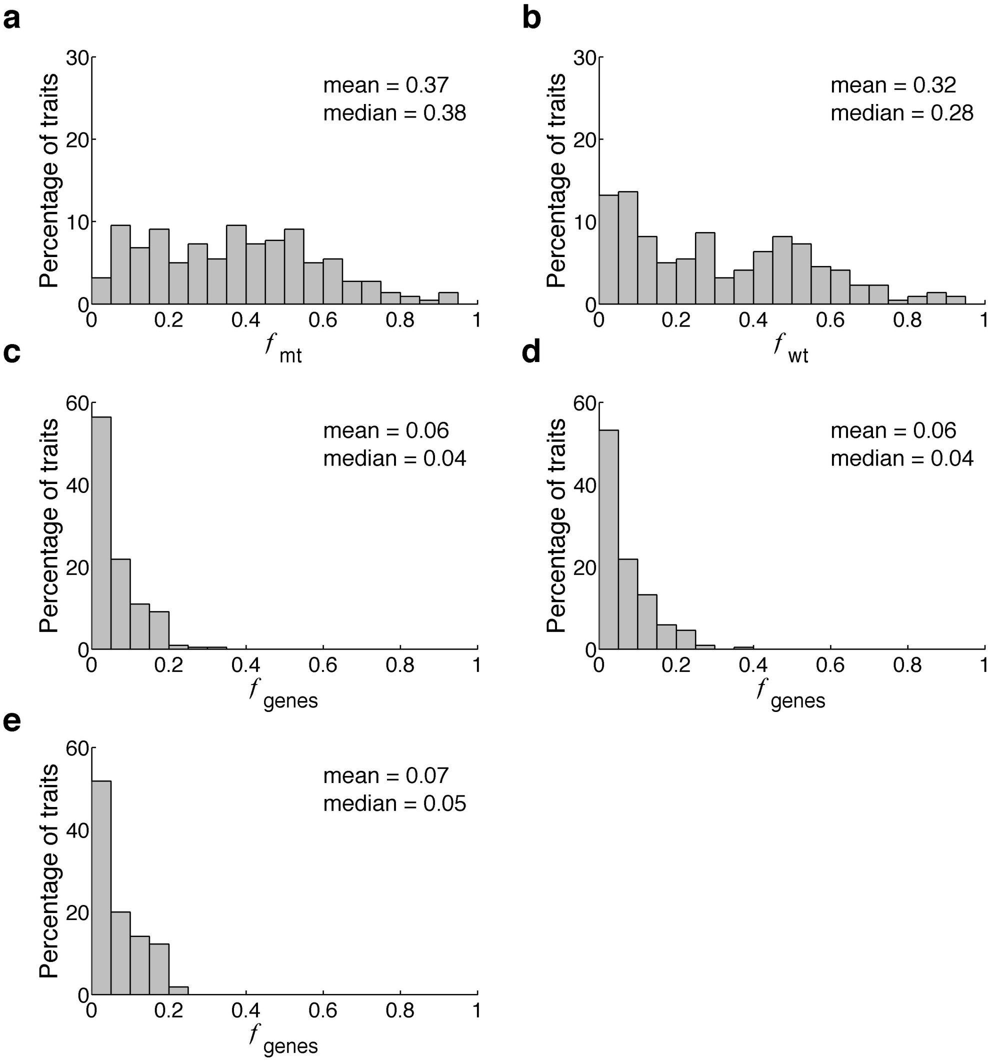

Figure S1. Fraction of genes affecting a trait under different cutoffs, with or without corrections for environmental variation and multiple testing. (**a**) Fraction of genes (f_{mt}) affecting a trait under $p < 0.05$, without corrections. (**b**) Fraction (f_{wt}) of wild-type replicate populations that show significant deviations from an arbitrarily selected wild-type population. The corrected fraction of genes affecting a trait (f_{genes}) is shown in Fig. 1c. (**c**) Corrected fraction of genes (f_{genes}) affecting a trait under $p < 0.01$. (**d**) Corrected fraction of genes (f_{genes}) affecting a trait under $p < 0.1$. (**e**) Corrected fraction of genes (f_{genes}) affecting a trait estimated by examining whether the mean trait value of a mutant would be an outlier in the distribution of the 123 means of the wild-type replicate populations. A deletion is annotated to affect a trait if the mean trait value of the mutant is in either the left or right 2.5% tail of the distribution of the 123 mean trait values of the 123 wild-type replicate populations. However, given that 4718 deletions are tested per trait, there are 236 expected deletions located in these two tails simply by chance. Therefore, the total number of genes affecting a trait is either corrected by subtracting 236 or set as zero if the original number is less than 236.

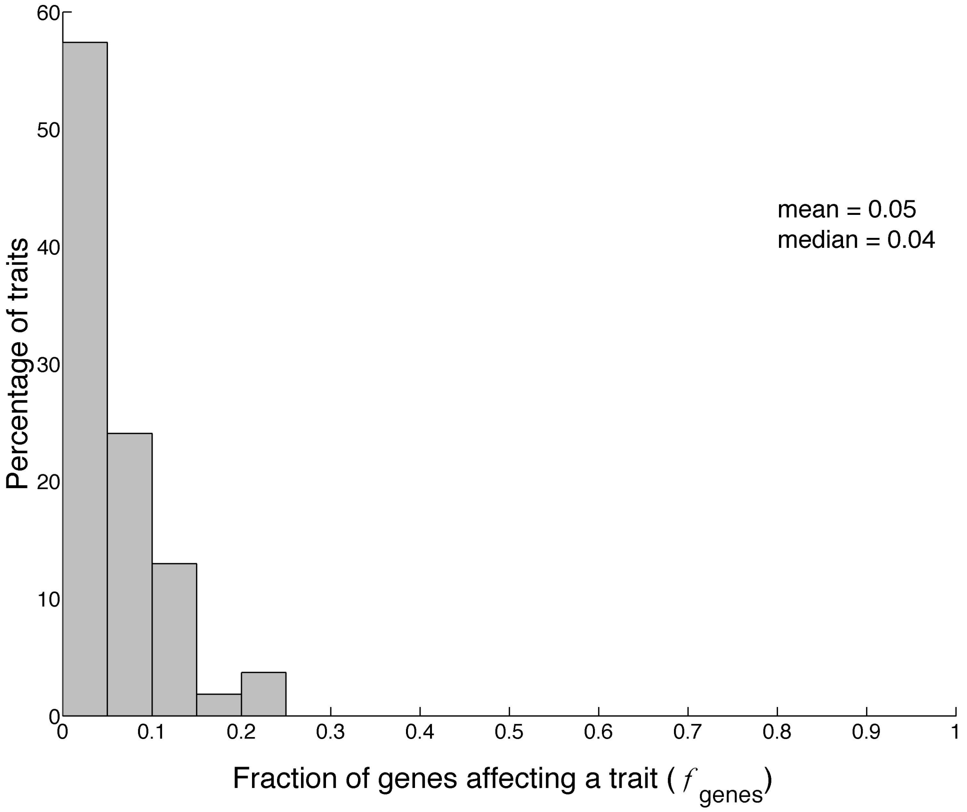

Figure S2. Fraction of genes (f_{genes}) affecting a trait after the removal of highly correlated traits.

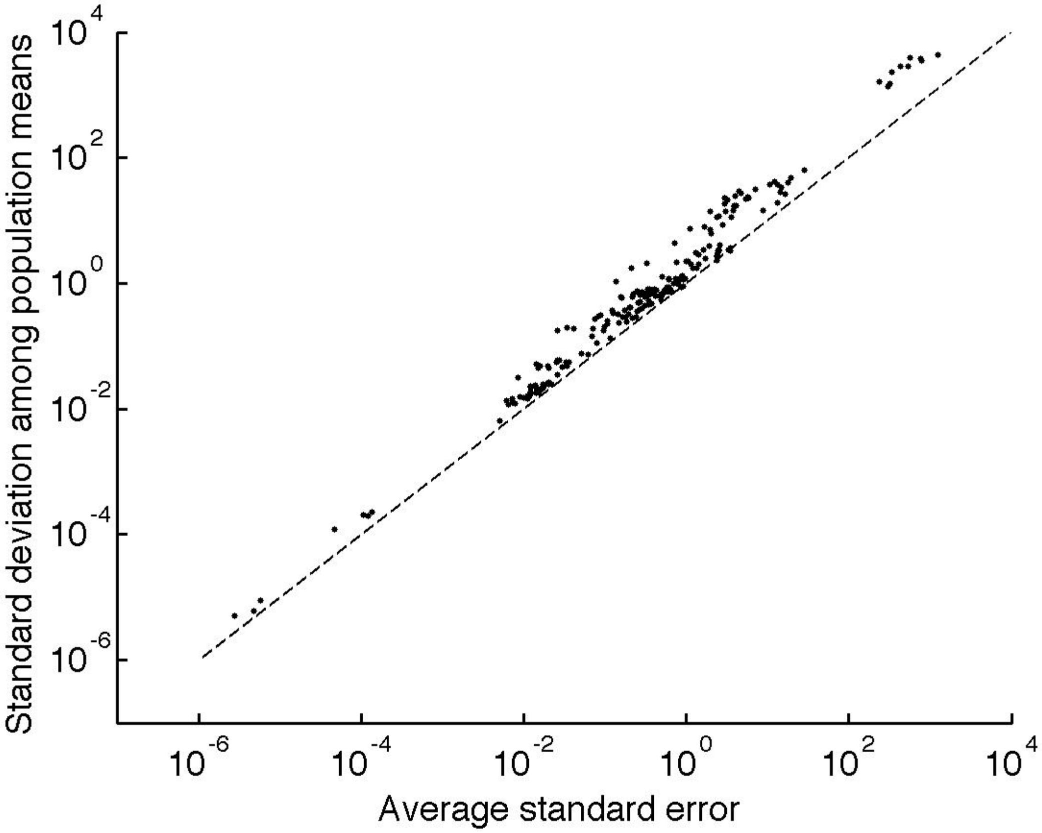

Figure S3. Sources of phenotypic variations of wild-type cells. Standard deviation among population means generally exceeds the average standard error of individual replicate populations, indicating the existence of environmental variation among replicate populations. The dotted line shows the expectation when there is no environmental difference among replicate populations.

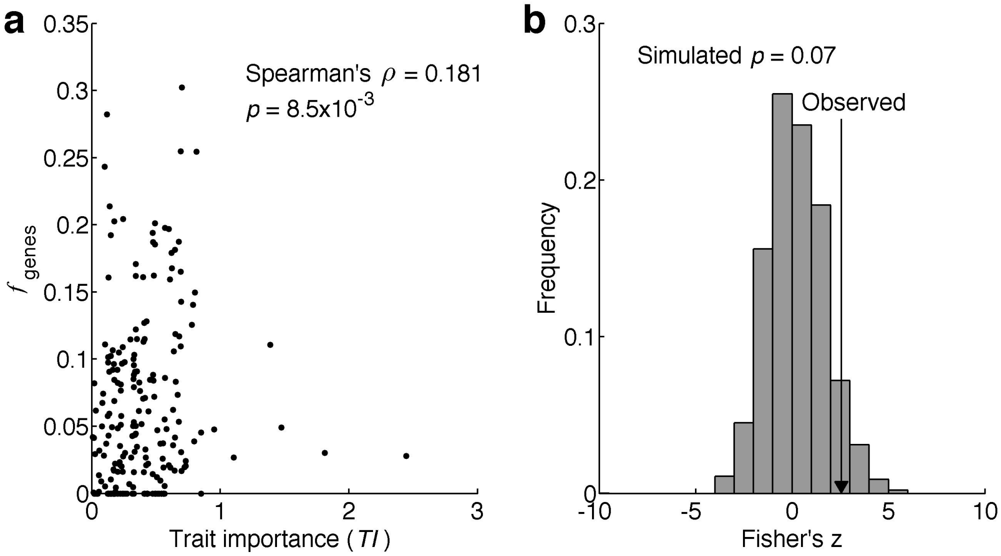

Figure S4. No significant correlation between the corrected fraction of genes affecting a trait (f_{genes}) and trait importance (*TI*). (**a**) Weak positive correlation between the corrected fraction of genes affecting a trait (f_{genes}) and trait importance (*TI*). Each dot is a trait. (**b**) Distribution of Fisher's *z* derived from the rank correlation between the corrected fraction of genes affecting a trait (f_{genes}) and trait importance (*TI*). The real *z* observed from the actual data is indicated by an arrowhead and the *p*-value is the probability that a randomly picked pseudo *z* is more positive than the real *z*.

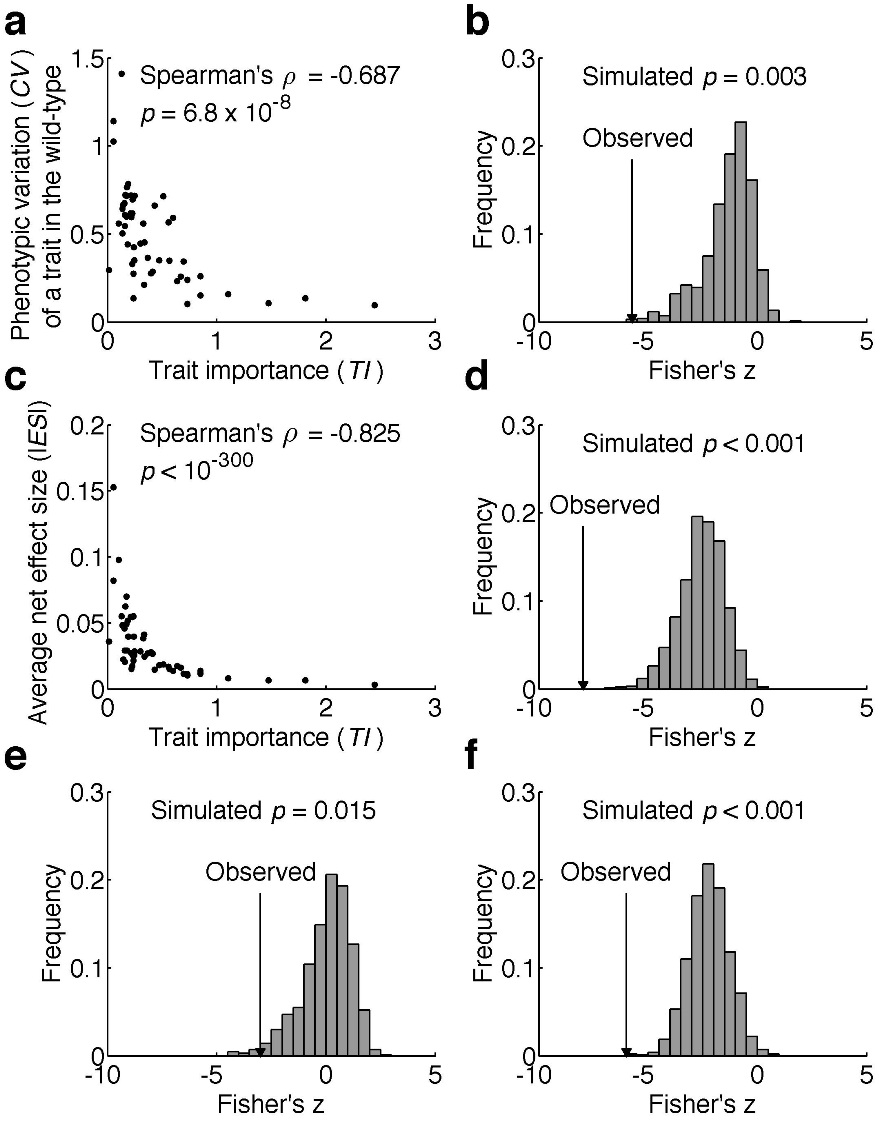

Figure S5. Environmental/stochastic robustness and genetic robustness of yeast morphological traits using less correlated traits. (**a**) The phenotypic variation (*CV*) of a trait among isogenic wild-type cells decreases with the rise of trait importance (*TI*), demonstrating environmental/stochastic robustness. Each dot is a trait. (**b**) Distribution of Fisher's *z* derived from the rank correlation between *CV* and pseudo *TI*. (**c**) The mean net |*ES*| of gene deletion on a trait decreases with the rise of trait importance (*TI*), demonstrating genetic robustness. Each dot is a trait. (**d**) Distribution of Fisher's *z* derived from the rank correlation between mean net |*ES*| and pseudo *TI*. (**e**) Distribution of Fisher's *z* derived from the partial rank correlation between *CV* and pseudo *TI*, after the control of mean net |*ES*|. (**f**) Distribution of Fisher's *z* derived from the partial rank correlation between mean net |*ES*| and pseudo *TI*, after the control of *CV*. In (b), (d), (e), and (f), the real *z* observed from the actual data is indicated by an arrowhead and the *p*-value is the probability that a randomly picked pseudo *z* is more negative than the real *z*.

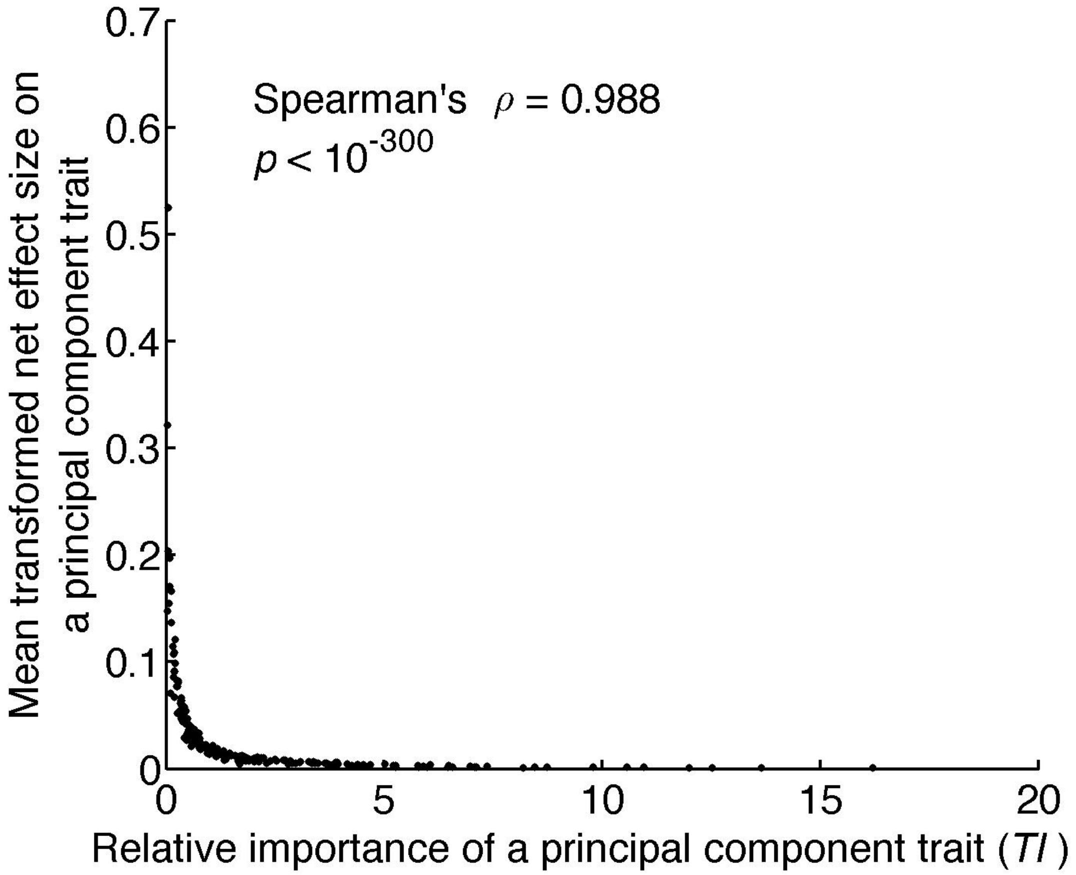

Figure S6. Negative correlation between transformed mean net effect size ($|ES|$) and the importance of principal component traits. Each dot is a principal component trait.

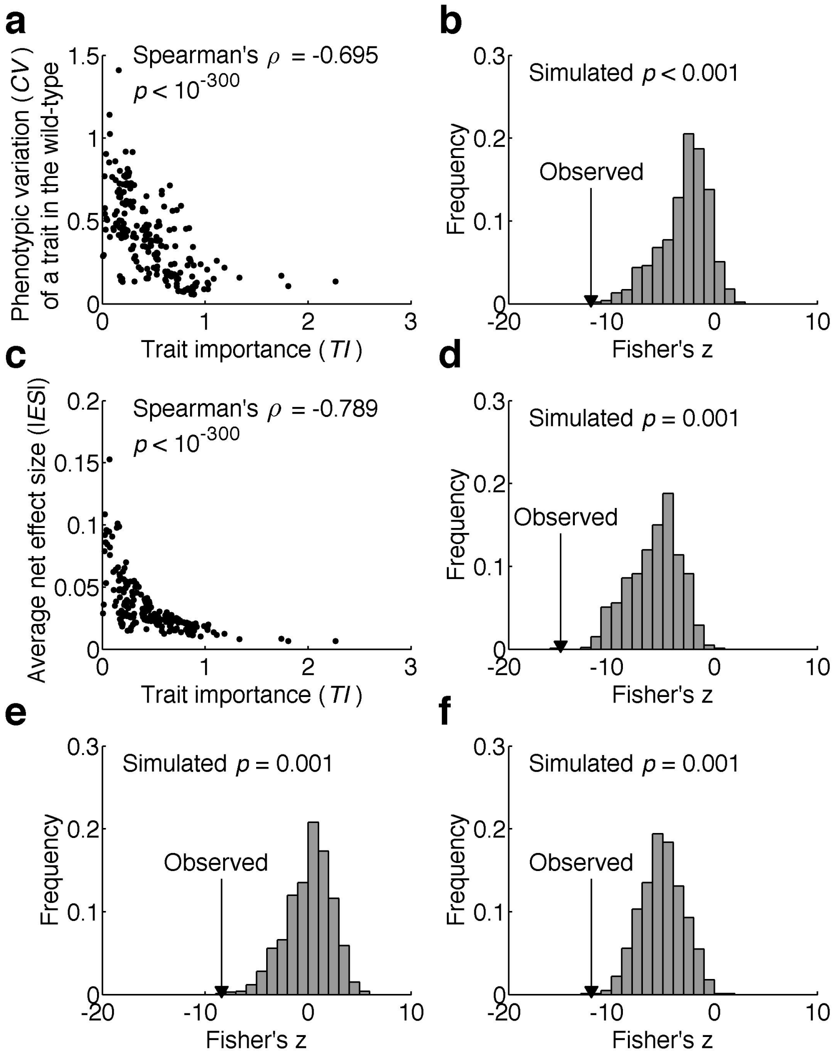

Figure S7. Environmental/stochastic robustness and genetic robustness of yeast morphological traits when trait importance is estimated using a log model (see Materials and Methods). (**a**) The phenotypic variation (*CV*) of a trait among isogenic wild-type cells decreases with the rise of trait importance (*TI*), demonstrating environmental/stochastic robustness. Each dot is a trait. (**b**) Distribution of Fisher's *z* derived from the rank correlation between *CV* and pseudo *TI*. (**c**) The mean net |*ES*| of gene deletion on a trait decreases with the rise of trait importance (*TI*), demonstrating genetic robustness. Each dot is a trait. (**d**) Distribution of Fisher's *z* derived from the rank correlation between mean net |*ES*| and pseudo *TI*. (**e**) Distribution of Fisher's *z* derived from the partial rank correlation between *CV* and pseudo *TI*, after the control of mean net |*ES*|. (**f**) Distribution of Fisher's *z* derived from the partial rank correlation between mean net |*ES*| and pseudo *TI*, after the control of *CV*. In (b), (d), (e), and (f), the real *z* observed from the actual data is indicated by an arrowhead and the *p*-value is the probability that a randomly picked pseudo *z* is more negative than the real *z*.