

Supplementary figures

Figure S1. Distribution of effect sizes in typical simulation runs. Two scenarios represented, one with low (L, blue bars) and one with high (H, red bars) statistical power, representing $m_I=3,000$ and 100 effect SNPs, respectively, at various dimensionalities. Effect sizes are sampled from an exponential distribution with mean 1. Effect size is the Euclidean distance between the mean phenotypes of the two genotypes at a SNP.

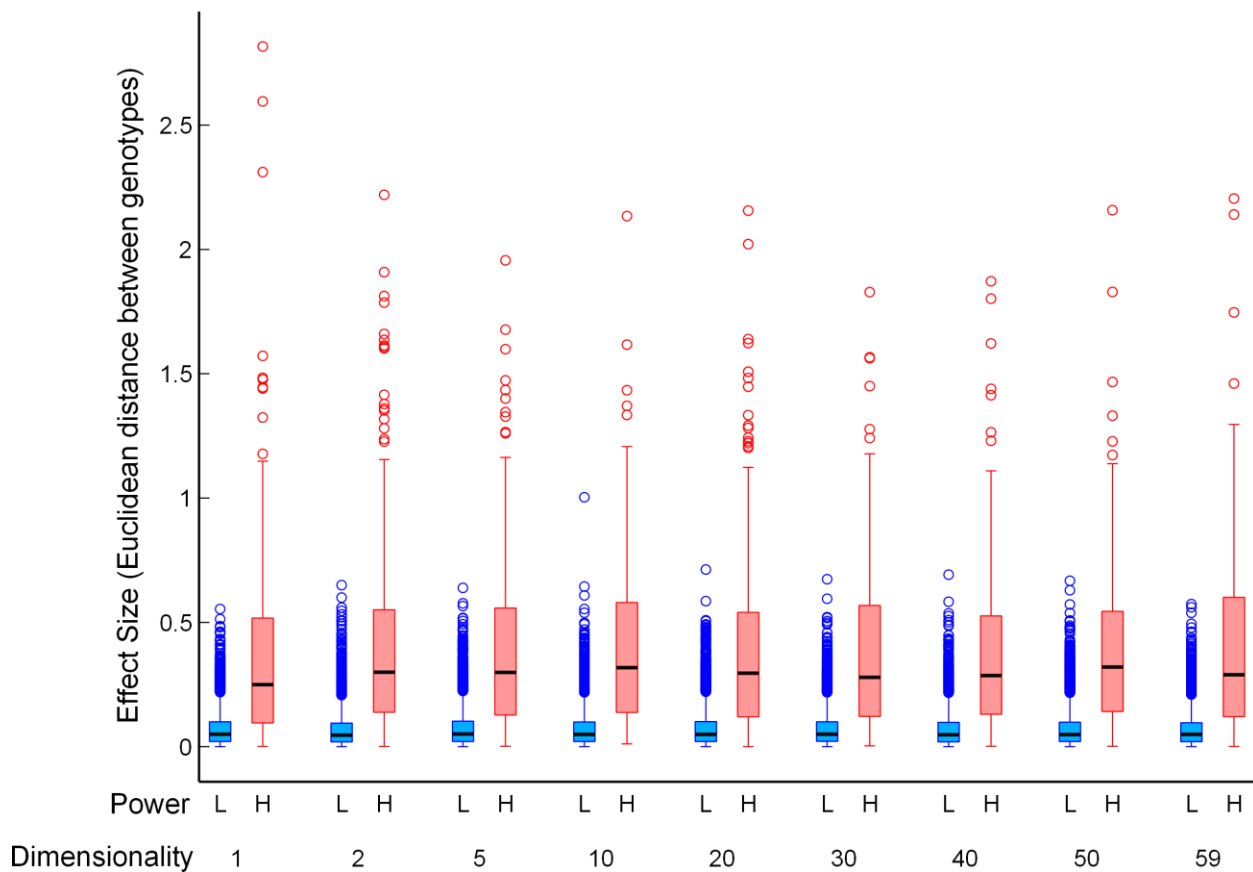


Figure S2. Proportion of the total genetic variance (i.e., trace of G) explained by SNPs obtained from typical simulation runs. Same scenarios as in Figure S1 are represented, assuming low (L, blue bars) and high (H, red bars, $m_2=100$) statistical power, respectively, at various dimensionalities.

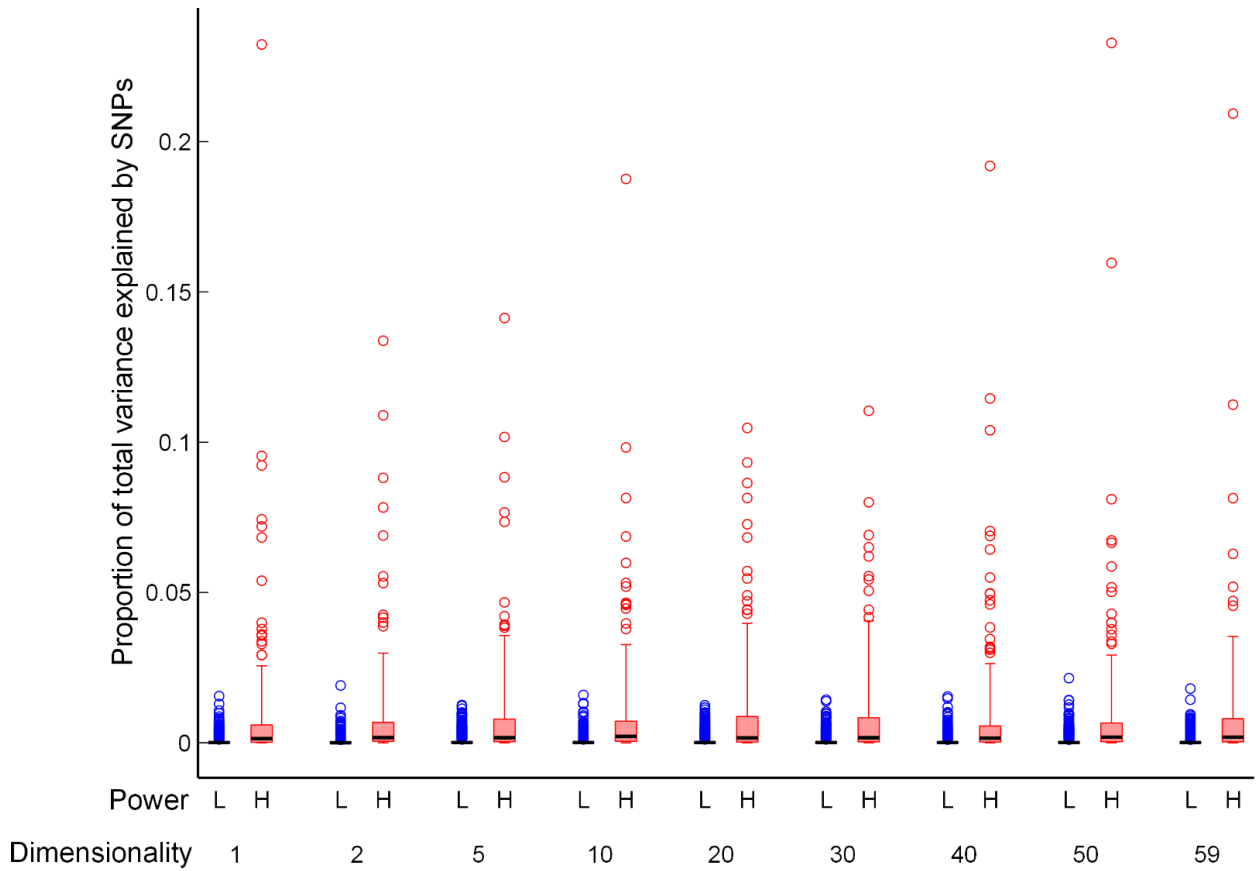


Figure S3. Eigenvalues (λ) of the phenotypic (P, red circles), genetic (G, blue circles), and environmental (E=P-G, green circles) covariance matrices for the wing shape data used to parameterize the simulations. Eigenvalues expressed as base-10 logarithms.

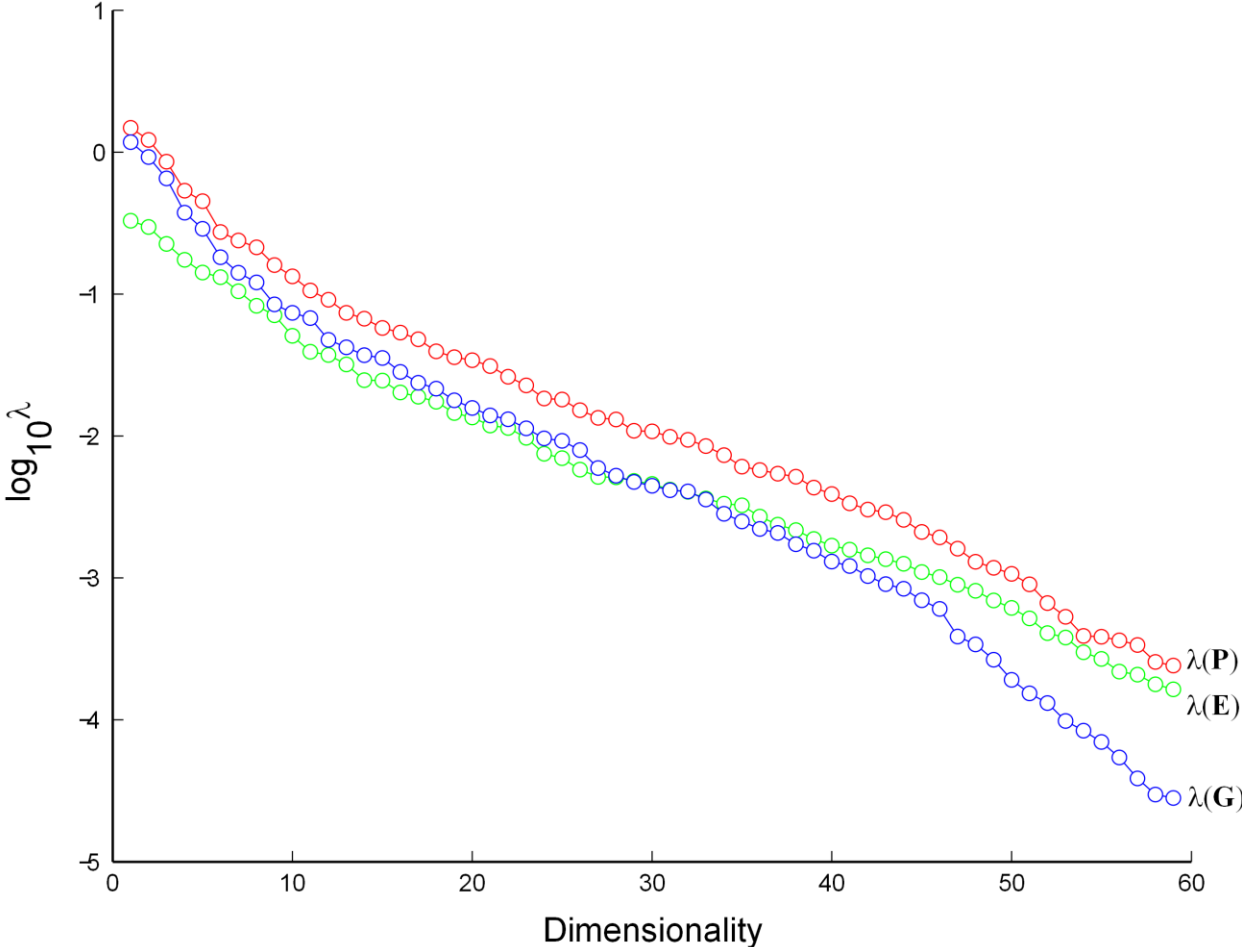


Figure S4. Estimates of heritability (h^2) for each of the 59 “traits” (i.e., Principal Components of \mathbf{G}) used as basis for simulations. Shape data was projected onto the eigenvectors of \mathbf{G} , and h^2 computed as the ratio of the projected score variances to the corresponding eigenvalue of \mathbf{G} (λ).

