Figure S1  Mechanisms of balancing selection, and their relative probabilities, for \( n = 5 \), and \( h = 0.25 \). For each parameter set \((z_m, z_f, \rho_{sel}, \rho_{mut})\), 100,000 balanced polymorphisms were randomly generated using the simulation approach described in the main text and in the Fig. 4 legend, but with small mutations using \( E[r] = 0.05 \rho^{0.5} \) and large mutations using \( E[r] = 0.4 \rho^{0.5} \) (these values correspond to male-specific scaled sizes of \( E[x_m] = 0.25 \), and \( E[x_m] = 2 \), respectively).
Fraction of balancing selection cases

Phenotypic correlation ($\rho_{\text{mut}}$)

$z_m = \frac{1}{2}; z_f = 0$

$\rho_{\text{sel}} = 1$

$z_m, z_f = \frac{1}{2}$

$\rho_{\text{sel}} = \frac{1}{2}$

$z_m, z_f = \frac{1}{2}$

$\rho_{\text{sel}} = -\frac{1}{2}$

$z_m, z_f = \frac{1}{2}$

$\rho_{\text{sel}} = 1$

$z_m, z_f = \frac{1}{2}$

Figure S2  Mechanisms of balancing selection, and their relative probabilities, for $n = 5$, and $h = 0.5$. Details otherwise follow those in the Figure S1 legend.
Figure S3  Mechanisms of balancing selection, and their relative probabilities, for $n = 5$, and $h = 0.75$. Details otherwise follow those in the Figure S1 legend.
Figure S4  Efficacy of balancing selection, showing results for $\rho_{\text{mut}} = 0.5$, and all other details described in Fig. 5 of the main text.
Figure S5  Mean alpha and \( \hat{q} \), for \( n = 25 \), \( h = 0.5 \), and \( \omega_m = \omega_f = \frac{1}{2} \). Each datapoint is based on 500,000 randomly simulated balanced polymorphisms for the given parameter set (\( z_m, z_f, \rho_{sel}, \rho_{mut} \)). For each parameter combination, mutation magnitudes were generated using a bivariate exponential distribution (gamma with shape parameter \( k = 1 \)), with equal marginal distributions, and correlation of \( \rho_{mut} = \text{corr}(\sigma_m, \sigma_f) \). Small mutations use \( E[r] = 0.05 \), and large mutations use \( E[r] = 0.4 \) (corresponding to male-specific scaled sizes of \( E[x_m] = 0.25 \), and \( E[x_m] = 2 \), respectively).
Figure S6  Mean $\alpha$ and $\hat{q}_i$, for $n = 5$, $h = 0.25$, and $\omega_m = \omega_f = \frac{1}{2}$. Each datapoint is based on 100,000 randomly simulated balanced polymorphisms for the given parameter set ($z_m, z_f, \rho_{sel}, \rho_{mut}$). For each parameter combination, mutation magnitudes were generated using a bivariate exponential distribution (gamma with shape parameter $k = 1$), with equal marginal distributions, and correlation of $\rho_{mut} = corr(r_m, r_f)$. Small mutations use $E[r] = 0.05n^{0.5}$, and large mutations use $E[r] = 0.4n^{0.5}$ (corresponding to male-specific scaled sizes of $E[x_m] = 0.25$, and $E[x_m] = 2$, respectively).
Figure S7  Mean alpha and $\hat{q}$, for $n = 5$, $h = 0.5$, and $\omega_m = \omega_f = \frac{1}{2}$. Additional details follow those in the Figure S6 legend.
Figure S8  Mean alpha and $\hat{q}$, for $n = 5$, $h = 0.75$, and $\omega_m = \omega_f = \frac{1}{2}$. Additional details follow those in the Figure S6 legend.