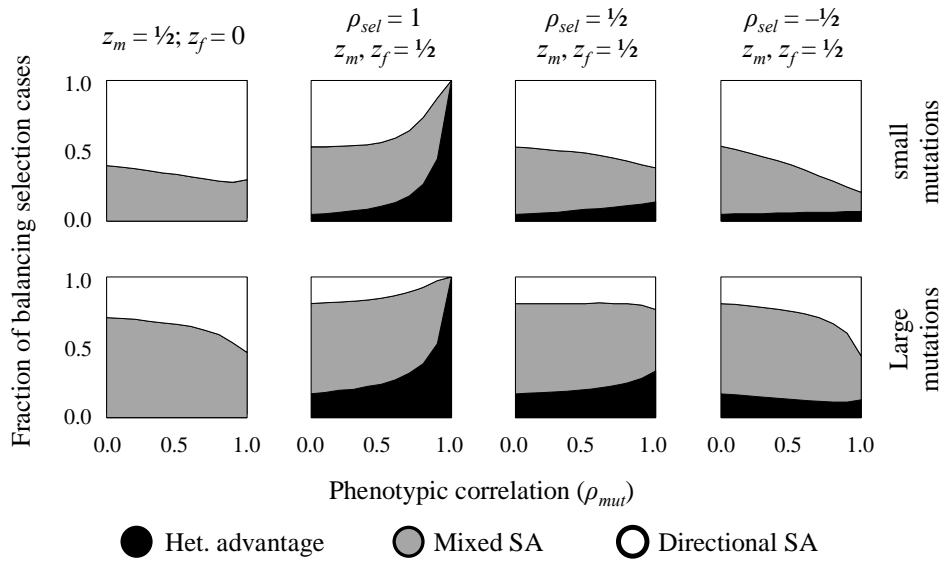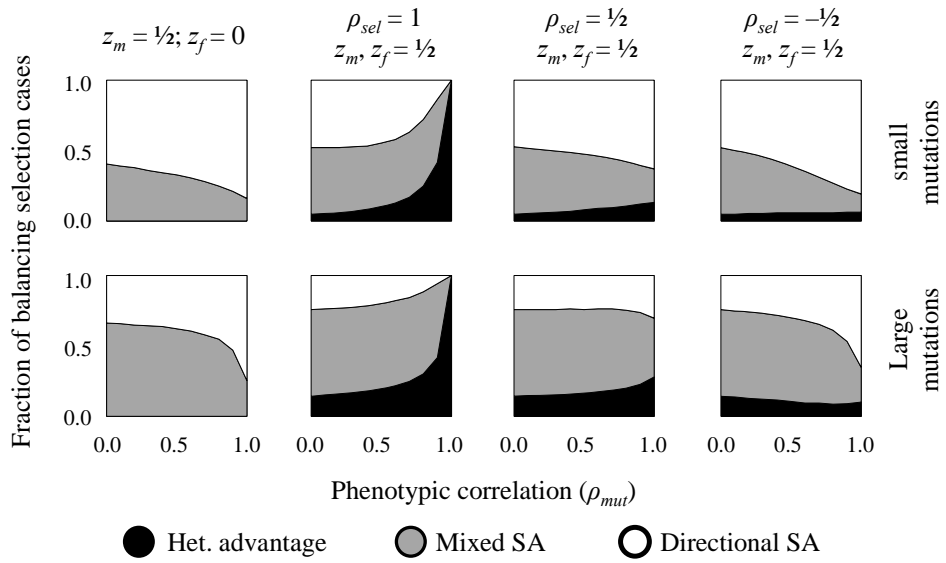**Figure S1** Mechanisms of balancing selection, and their relative probabilities, for n = 5, and h = 0.25. For each parameter set (z_m, z_f, ρ_{sel}, ρ_{mut}), 100,000 balanced polymorphisms were randomly generated using the simulation approach described in the main text and in the Fig. 4 legend, but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

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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.
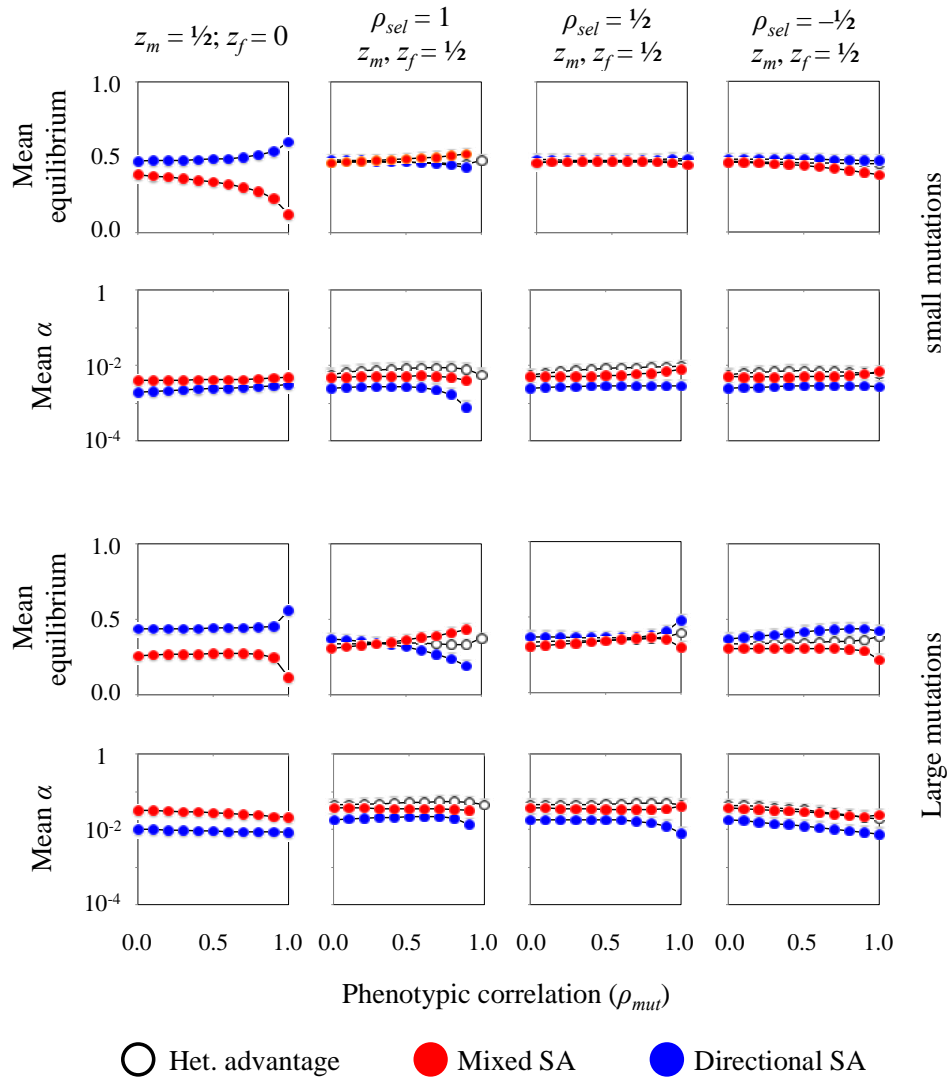
Figure S3 Mechanisms of balancing selection, and their relative probabilities, for *n* = 5, and *h* = 0.75. Details otherwise follow those in the Figure S1 legend.

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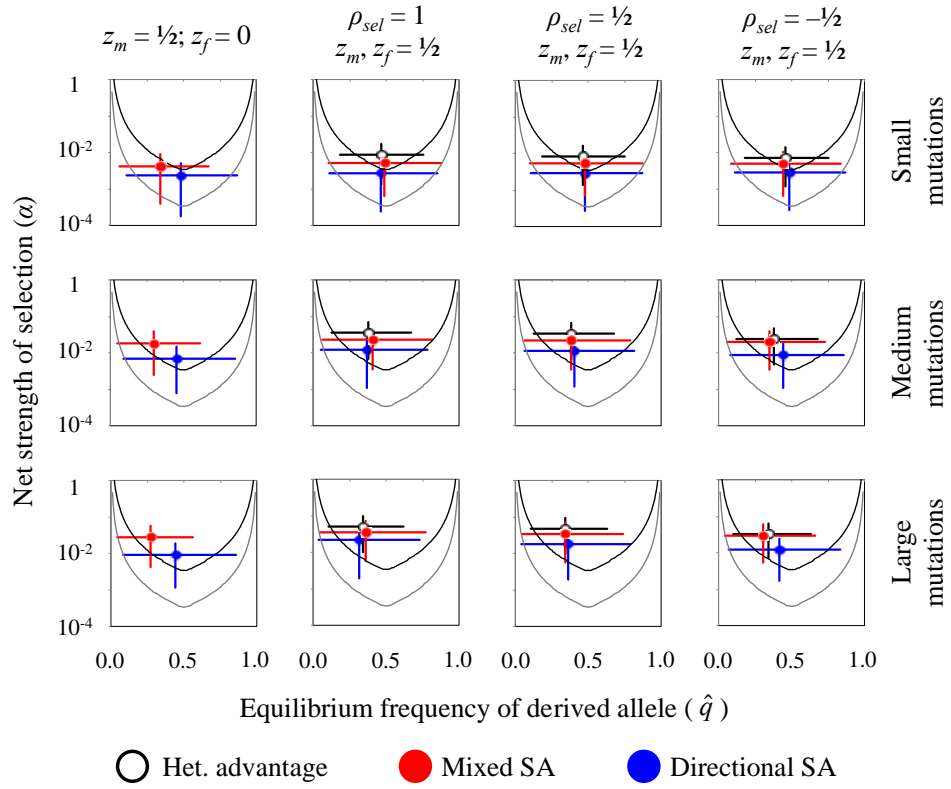
Figure S4 Efficacy of balancing selection, showing results for ρ_{mut} = 0.5, and all other details described in Fig. 5 of the main text.
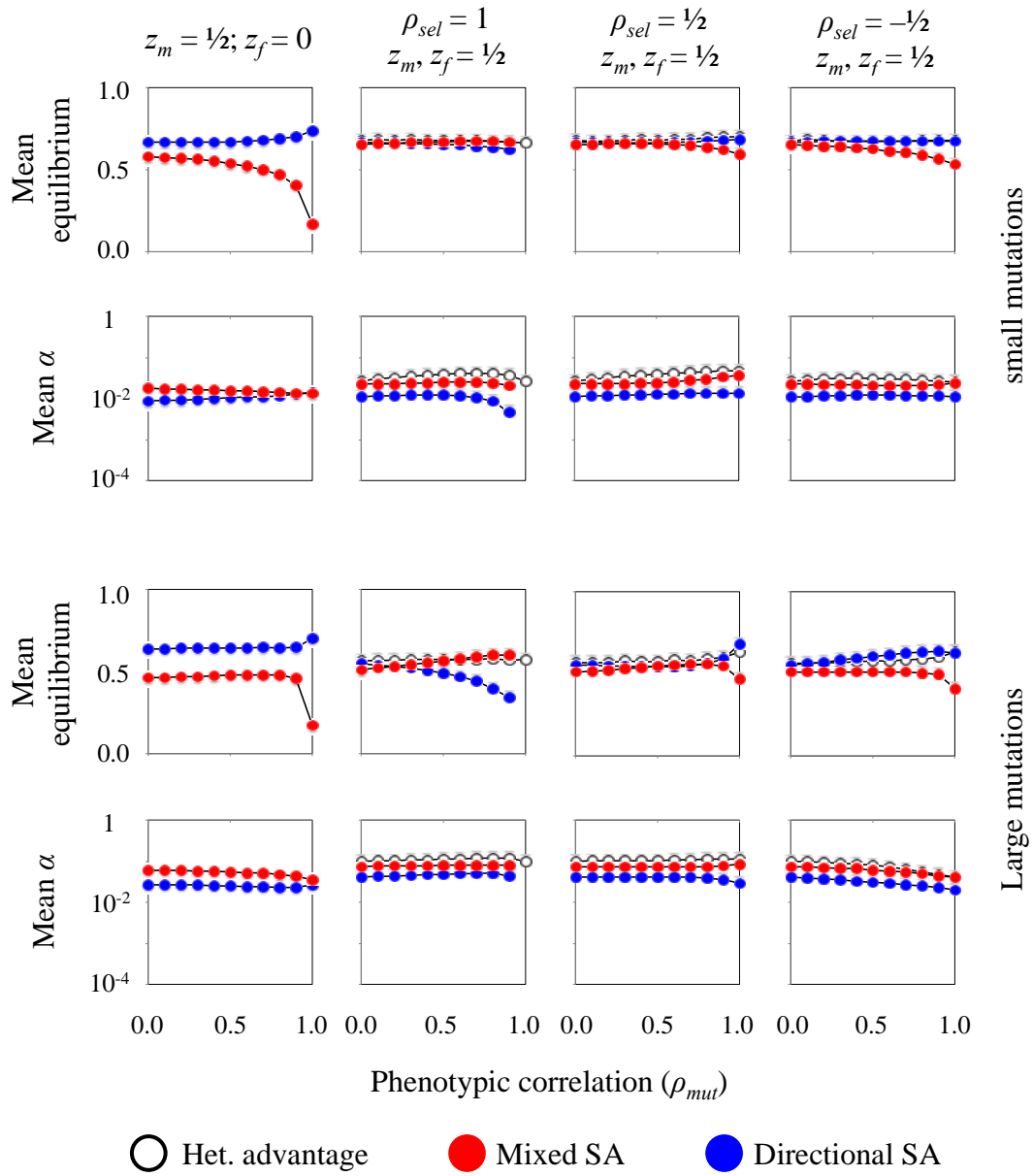
Figure S5 Mean alpha and $\hat{q}$, for $n = 25$, $h = 0.5$, and $\omega_m = \omega_f = \frac{1}{2}$. Each datapoint is based on 500,000 randomly simulated balanced polymorphisms for the given parameter set (z_m, z_f, ρ_{sel}, ρ_{mut}). For each parameter combination, mutation magnitudes were generated using a bivariate exponential distribution (gamma with shape parameter $k = 1$), with equal marginal distributions, and correlation of $\rho_{mut} = \text{corr}(r_m, r_f)$. 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).
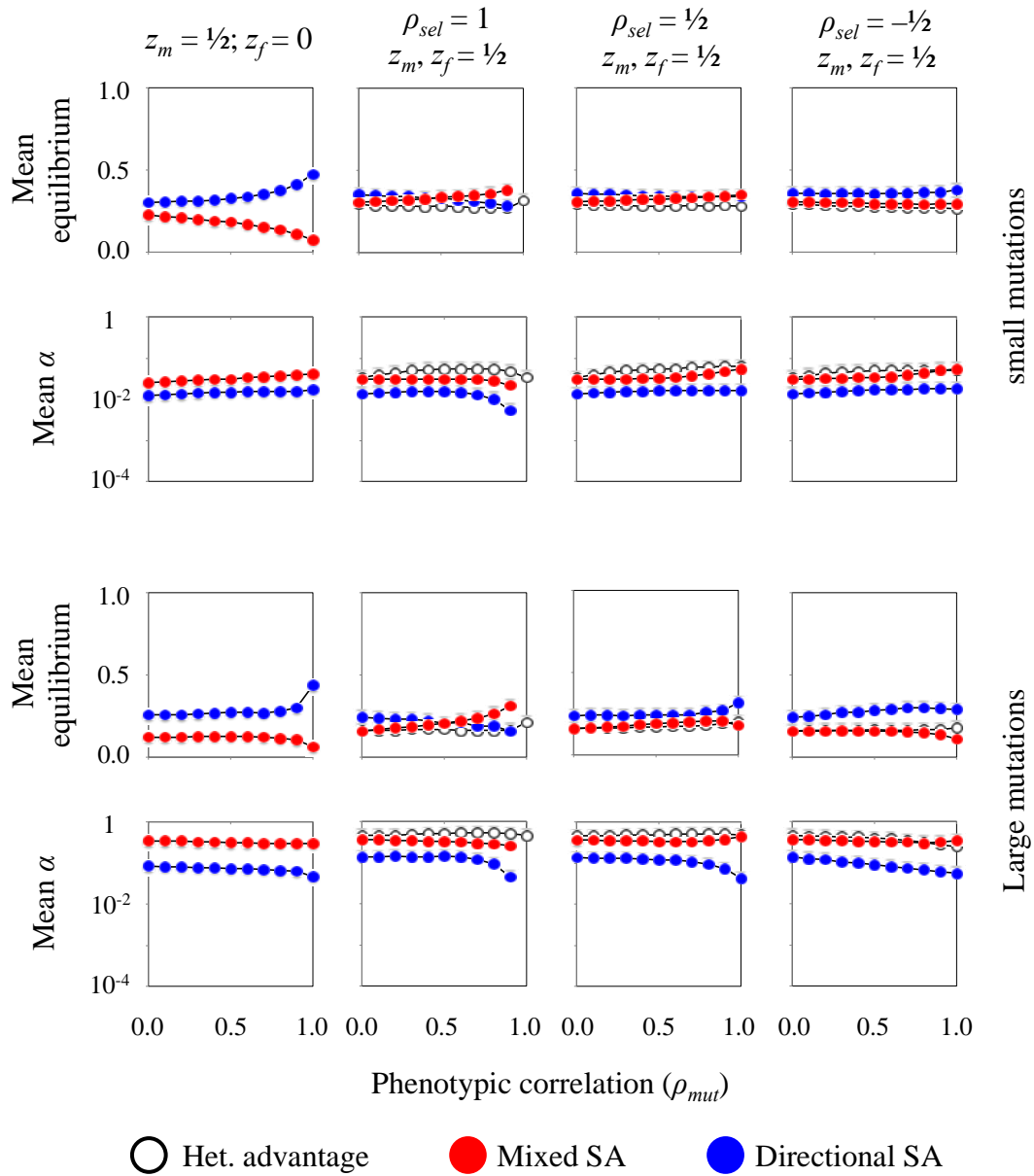
Figure S6 Mean alpha and $\hat{q}$, for $n = 5$, $h = 0.25$, and $\omega_m = \omega_f = \frac{1}{2}$. Each datapoint is based on 100,000 randomly simulated balanced polymorphisms for the given parameter set (z_m, z_f, ρ_{sel}, ρ_{mut}). For each parameter combination, mutation magnitudes were generated using a bivariate exponential distribution (gamma with shape parameter $k = 1$), with equal marginal distributions, and correlation of $\rho_{mut} = \mathrm{corr}(r_m, r_f)$. 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).
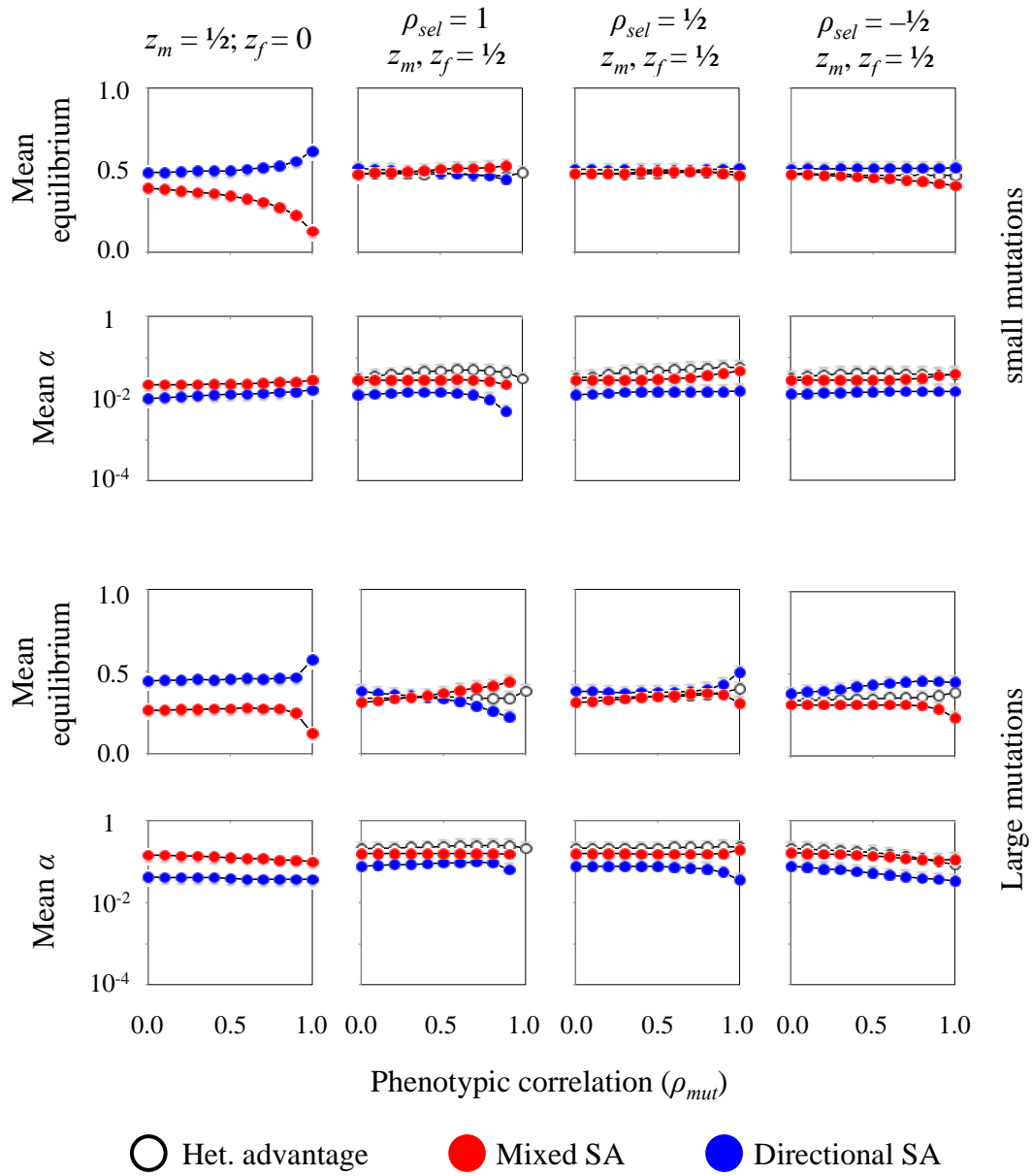
Figure S7 Mean alpha and $\hat{q}$, for $n = 5$, $h = 0.5$, and $\omega_m = \omega_f = \frac{1}{2}$. Additional details follow those in the Figure S6 legend.

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.