



Figure S5 Mean alpha and \hat{q} , for $n = 25$, $h = 0.5$, and $\omega_m = \omega_f = 1/2$. 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 $\rho_{mut} = \text{corr}(r_m, r_f)$. 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).