



**Figure S6** Mean alpha and  $\hat{q}$ , for  $n = 5$ ,  $h = 0.25$ , and  $\omega_m = \omega_f = 1/2$ . 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  $\rho_{mut} = \text{corr}(r_m, r_f)$ . 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).