Figure S5  Distribution of fitness effects (DFE) of new nonsynonymous mutations or simulated outcrossing (t=1.00) and selfing (t=0.02) populations under various fixed dominance coefficients (h=0.2, 0.5, or 0.8) when both mutations unique to each population and mutations shared between populations were used to estimate selective and demographic parameters. $N_{es}$ is the product of $N_e$ and the selection coefficient ($s$). Shown are A) the expected DFEs, B) $h=0.2$, C) $h=0.5$, and D) $h=0.8$. Simulations illustrate the change in DFE for both populations after 6N generations after a split from the common outcrossing ancestor. We generated the expected DFE for the outcrossing population represented as a gamma distribution using supplied $\beta$ and $N_s$ parameters. We generated the expected DFE for the selfing population by scaling supplied $N_s$ parameter by the observed 75% reduction in synonymous diversity in selfers and multiplying it by 1.96 to account for effective dominance levels of mutations in selfing genomes while leaving $\beta$ unchanged. We generated observed DFEs by randomly sampling and generating allele frequency spectra using eight genomes from populations of size 1000. The coding regions were under various selection coefficients ($N_s=0.5-95$) all sampled from a gamma distribution with shape parameter ($\beta$) 0.3. Shown are the mean proportions of sites for each $N_{es}$ category and their respective confidence intervals based on 120 simulations.