Mendeley Data F2. Related to Figure 3. Distribution of fitness effects (DFE). (A)-(C), Inference of distribution of fitness effects (DFE) with Anavar on the allele frequency spectra of genome-wide synonymous and non-synonymous sites. Simulations were performed assuming a sequencing error rate of (A) 0.001, (B) 0.0033 and (C) 0.01. Calibration factors were computed for each allele frequency bin, and were multiplied to the observed AFS for correction (Table S78-89). Variation of parameter estimates was estimated by one hundred bootstraps of multinomial resampling of the AFS. Black dots are estimates from the dataset before bootstrapping. In all simulations, the dry populations have a higher proportion of sites assigned to the slightly deleterious category (one-tail p values obtained from the resampled parameter distributions).