



FIGURE S1.—Starting a single mutation at a given time (labeled “single”) and allowing multiple mutations to occur in a selected region for five generations (labeled “multiple”) show similar proportions of selected datasets rejecting neutrality. The fact that both simulation approaches yield similar results supports the validity of our approach. SNM denotes the rejection region defined by the standard neutral model, TRUE the rejection region defined by the true demographic model for each population, and EST the rejection region defined by a growth model where the parameters were estimated from the SFS of neutral data (see

Methods). Error bars denote approximate 95% CIS on the binomial proportion and were calculated from $\hat{p} \pm 1.96 \sqrt{\frac{\hat{p}(1-\hat{p})}{N}}$,

where \hat{p} is the proportion of simulation replicates rejecting neutrality, and N is the total number of simulation replicates (1000 in our case).