



FIGURE S4.— Comparisons between recurrent selective sweeps when  $\frac{H_{RHH}}{H_{NEU}} = 0.25$  and  $s = 0.01, 0.0001$ . (A) The SFS of the RHH model when  $s = 0.0001$  is similar to that of the standard neutral SFS whereas a large excess of singletons appears when  $s = 0.01$ . (B) When the SFS of the data itself is used in the *SweepFinder* calculations then the model with  $s = 0.0001$  shows higher values of  $\Lambda_{MAX}$ . This is because the genomic regions affected by positive selection are smaller for smaller  $s$  values and a large fraction of the genome remains still unaffected by positive selection.