



FIGURE S5.— The fraction of predicted targets within 5 kb from the true location of the selective sweep for a recurrent selective sweep scenario where $\frac{H_{RHH}}{H_{NEU}} = 0.25$ (for A and B) and $\frac{H_{RHH}}{H_{NEU}} = 0.50$ (for C and D). (A) and (C): Comparison of the precision of *SweepFinder* when only polymorphic sites are used (dark bars) and a fraction of monomorphic sites is embedded (light bars). (B) and (D): Comparison between the variable-size sliding window approach and the constant-size sliding window approach. The precision of the two approaches is similar for low threshold values (high sensitivity, low specificity). However, for higher cutoff values the variable-size sliding window method is slightly more precise. Simulations assume a 100-kb genomic fragment. Selective sweeps have occurred uniformly within this region or within its flanking regions following a homogeneous Poisson distribution in time. The selection coefficient is $s = 0.01$, $\theta = 0.008/\text{bp}$, and $\rho = 0.08/\text{bp}$.