Figure S8

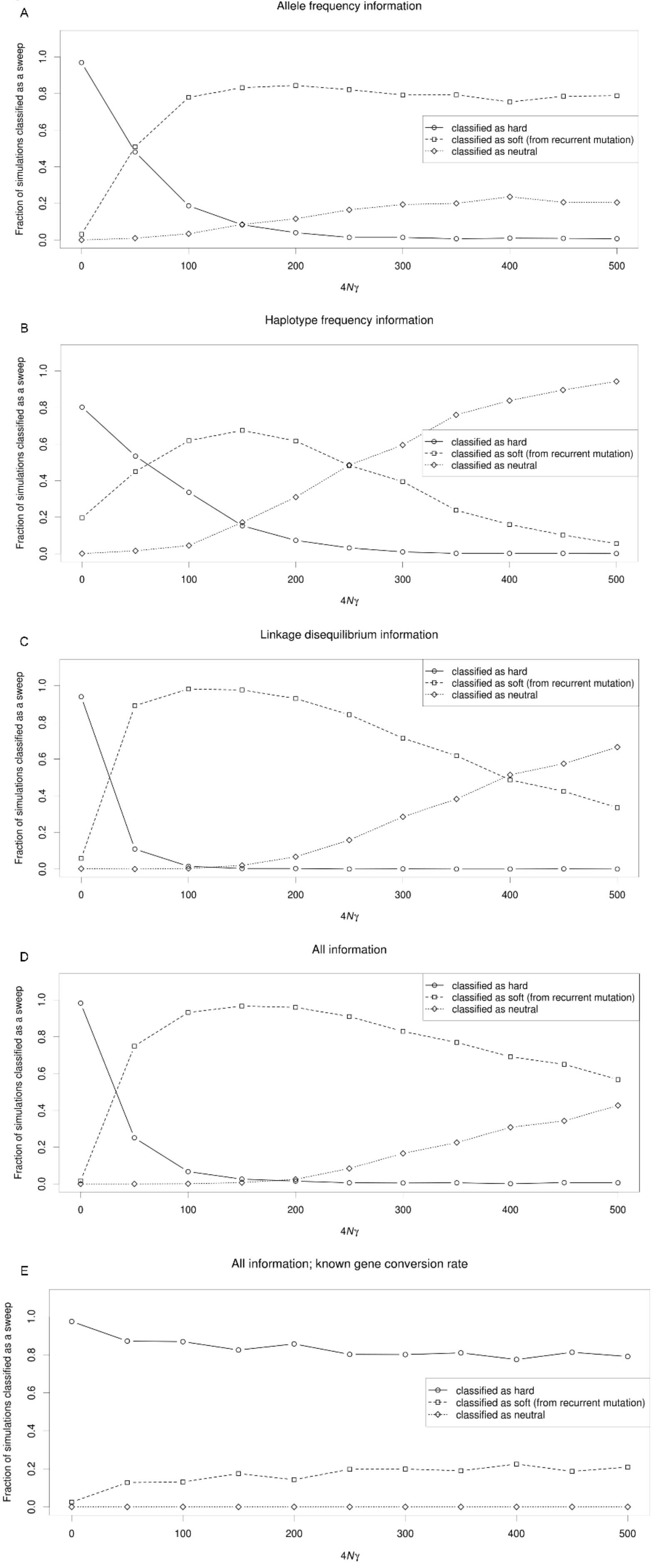
A
Allele frequency information
B
Haplotype frequency information
C
Linkage disequilibrium information
D
All information
E
All information; known gene conversion rate
Fraction of simulations classified as a sweep
0.0
0.2
0.4
0.6
0.8
1.0
4Nγ
0
100
200
300
400
500
classified as hard
classified as soft (from recurrent mutation)
classified as neutral

Figure S8 The relationship between gene conversion rate and sweep misclassification rate when modeling soft sweeps from recurrent adaptive mutation. (A) The relationship between the locus-wide gene-conversion rate and the fraction of simulated windows containing a hard sweep (α=1000) classified as hard, soft (from recurrent mutation), or neutral. (B) Same as panel A, but using a classifier leveraging haplotype information. (C) Results from an SVM leveraging LD information. (D) An SVM leveraging our full set of summary statistics (Methods). (E) An SVM leveraging our full set of summary statistics and trained from simulated regions experiencing the correct gene conversion rate.