Table S4 Likelihood scores for assessing models of genome-wide nucleotide diversity ($\theta = 4N_e u$) that are constant or variable across loci using the method outlined by Hudson (1990). Estimates of nucleotide diversity are per locus.

Model	log$L$	-2log$L$	P
All sites			
Constant θ	-15627.58		
	θ = 1.33		
Variable θ	-8301.572	14652.02	P<2.2e-16
(*df* = 5,455)			
NS sites			
Constant θ	-4175.475		
	θ = 0.39		
Variable θ	-1745.141	4860.67	P<2.2e-16
(*df* = 2,480)			
SY sites			
Constant θ	-4030.923		
	θ = 0.44		
Variable θ	-2086.158	3889.53	P<2.2e-16
(*df* = 2,480)			
NC sites			
Constant θ	-6102.177	8125.56	
	θ = 0.49		
Variable θ	-2039.397		P<2.2e-16
(*df* = 2,480)			

Abbreviations: *df*, degrees of freedom; NC, noncoding; NS, nonsynonymous; SY, synonymous.