

**Table 1. Probability of obtaining the observed difference in frequency ( $f$ ) and Fay and Wu's  $H$  statistic when comparing P and U mutations**

Demographic conditions	Recombination	$P(\Delta f \geq 0.122)$	$P(\Delta H \geq 0.281)$
Constant population size	0	0.0012	0.0002
	1 cM	0.0007	<0.0001
	10 cM	0.0006	<0.0001
	Unlinked	<0.0001	<0.0001
Growth <sup>‡</sup>	0	<0.0001	<0.0001
Severe growth	0	<0.0001	<0.0001
Bottleneck and growth	0	<0.0001	<0.0001
Bottleneck and severe growth	0	<0.0001	<0.0001

Probabilities were obtained by coalescent simulations under the neutral model (see *Materials and Methods*).

\*Total rate of cross-over per generation between the most distant polymorphisms, expressed in cM and assuming ancestral population size of 10,000.

<sup>†</sup>Simulations assuming unlinked genes and complete linkage within genes.

<sup>‡</sup>Demographic conditions are detailed in *Materials and Methods*.