Table 5. Proportion of simulations (of 1,000) that lead to a shift in gene diversity equal to or even greater than the one observed in the Iberian brown bear short dataset between the different time periods

		μ = 29.8% subst./MY			μ = 10.0% subst./MY	
Ne	**Holocene/Modern**	**Pleistocene/Holocene**	**Pleistocene/Modern**	**Holocene/Modern**	**Pleistocene/Holocene**	**Pleistocene/Modern**
100	**0.052**	**0.647**	0.030	0.019	**0.461**	0.010
500	**0.055**	**0.463**	0.050	0.018	**0.469**	0.030
1,000	0.033	**0.370**	0.033	0.020	**0.420**	0.034
2,000	0.007	**0.245**	0.010	0.008	**0.382**	0.035
5,000	0.000	**0.068**	0.001	0.003	**0.229**	0.006
10,000	0.000	0.008	0.000	0.002	**0.126**	0.001
15,000	0.000	0.006	0.000	0.000	**0.055**	0.000
20,000	0.000	0.001	0.000	0.000	0.036	0.000
25,000	0.000	0.000	0.000	0.000	0.009	0.000
30,000	0.000	0.000	0.000	0.000	0.005	0.000
35,000	0.000	0.000	0.000	0.000	0.006	0.000
40,000	0.000	0.000	0.000	0.000	0.006	0.000
45,000	0.000	0.000	0.000	0.000	0.002	0.000

The simulations have been conducted for the short dataset (115 nt) over a large space of possible effective size values, assuming (*i*) no demographic change over time, (*ii*) two possible mutation rates, and (*iii*) the age of the sample Asieko at 80 KY. Frequencies superior to 0.05 are shown in red.