Table 7. 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 long 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	**0.131**	**0.512**	0.043	0.040	**0.566**	0.015
500	**0.099**	**0.329**	0.044	**0.081**	**0.452**	0.046
1,000	0.048	**0.221**	0.023	**0.044**	**0.358**	0.049
2,000	0.014	**0.095**	0.001	0.037	**0.271**	0.031
5,000	0.001	0.015	0.000	0.005	**0.121**	0.002
10,000	0.000	0.002	0.000	0.000	0.041	0.000
15,000	0.000	0.000	0.000	0.000	0.024	0.000
20,000	0.001	0.000	0.000	0.000	0.005	0.000
25,000	0.000	0.000	0.000	0.000	0.003	0.000
30,000	0.000	0.000	0.000	0.000	0.000	0.000
35,000	0.000	0.000	0.000	0.000	0.001	0.000
40,000	0.000	0.000	0.000	0.000	0.000	0.000
45,000	0.000	0.000	0.000	0.000	0.000	0.000

Same analysis as for SI Table 2 but with the population parameters used in LAMARC 2.0 (transition/transversion ratio = 0.289 and Gamma-shape parameter = 70.209). Frequencies superior to 0.05 are shown in red.