Table 6. 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 = 19.5% subst./MY			μ = 6.5% subst./MY	
Ne	**Holocene/Modern**	**Pleistocene/Holocene**	**Pleistocene/Modern**	**Holocene/Modern**	**Pleistocene/Holocene**	**Pleistocene/Modern**
100	0.011	0.043	0.001	0.033	**0.453**	0.012
500	**0.092**	**0.404**	**0.062**	0.046	**0.409**	0.023
1,000	0.046	**0.275**	0.030	0.050	**0.360**	0.039
2,000	0.017	**0.154**	0.012	0.031	**0.312**	0.032
5,000	0.001	0.033	0.000	0.010	**0.180**	0.013
10,000	0.001	0.011	0.000	0.004	**0.085**	0.000
15,000	0.001	0.000	0.000	0.000	0.036	0.000
20,000	0.000	0.000	0.000	0.000	0.017	0.000
25,000	0.000	0.001	0.000	0.000	0.014	0.000
30,000	0.000	0.000	0.000	0.000	0.010	0.000
35,000	0.000	0.000	0.000	0.000	0.000	0.000
40,000	0.000	0.000	0.000	0.000	0.002	0.000
45,000	0.000	0.000	0.000	0.000	0.002	0.000

Same analysis as for SI Table 2 but assuming two different mutation rates (6.5% subst./MY and 19.5% subst./MY). Frequencies superior to 0.05 are shown in red.