

Table 8. 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 large dataset between the different time periods

Ne	$\mu = 29.8\%$ subst./MY			$\mu = 10.0\%$ subst./MY		
	Holocene/Modern	Pleistocene/Holocene	Pleistocene/Modern	Holocene/Modern	Pleistocene/Holocene	Pleistocene/Modern
100	0.142	0.715	0.110	0.048	0.625	0.032
500	0.126	0.446	0.102	0.083	0.491	0.065
1,000	0.062	0.294	0.046	0.050	0.444	0.067
2,000	0.007	0.113	0.004	0.044	0.319	0.042
5,000	0.000	0.014	0.000	0.006	0.152	0.004
10,000	0.000	0.000	0.000	0.001	0.044	0.000
15,000	0.000	0.000	0.000	0.000	0.021	0.000
20,000	0.000	0.000	0.000	0.000	0.006	0.000
25,000	0.000	0.000	0.000	0.000	0.006	0.000
30,000	0.000	0.000	0.000	0.000	0.002	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	0.001	0.000
45,000	0.000	0.000	0.000	0.000	0.000	0.000

Same analyses as for SI Table 2 but assuming the age of the sample Asiako at 40 KY. Frequencies superior to 0.05 are shown in red.