Quina *et al.*

Supplementary Table S4 Results from mismatch distribution analysis and neutrality tests for *p53* in *M. duodecimcostatus* and *M. lusitanicus*. Significant p-values are shown in bold. Numbers in parenthesis are the upper and lower bound of the 95% confidence interval (1000 bootstrap replicates). Parameters: θ_0, pre-expansion population size; θ_1, post-expansion population size; τ, expansion age; θ, population size (assuming constant deme); M, migration rate. *SSD*: sum of square deviations; *hg*: Harpending's raggedness index.

Species	Sudden-expansion model							Spatial-expansion model							Neutrality tests			
	Parameters			Goodness-of-fit tests				Parameters			Goodness-of-fit tests				Tajima's *D* test		Fu's Fs test	
	θ_0	θ_1	τ	*SSD*	p	*hg*	p	θ	M	τ	*SSD*	p	*hg*	p	Tajima's *D*	p	Fs	p
Microtus duodecimcostatus	0.000	2.339	1.934 (0.000-4.521)	0.02	0.24	0.11	0.41	0.001	3.825	1.656 (0.299-3.678)	0.02	0.34	0.11	0.53	-0.88	0.20	-3.41	0.07
Microtus lusitanicus[1]	0.000	99999.0	0.680 (0.430-1.086)	0.01	0.14	0.12	0.19	0.003	99999.0	0.681 (0.294-0.982)	0.01	**0.03**	0.12	0.18	-1.28	0.10	-4.17	0.03
Northern group[1]	0.000	99999.0	0.801 (0.414-1.430)	0.01	0.10	0.13	0.10	0.001	99999.0	0.800 (0.305-1.305)	0.01	**0.03**	0.13	0.11	-1.12	0.13	-3.07	0.04
Southern group	0.000	99999.0	0.504 (0.215-0.977)	0.00	0.65	0.14	0.54	0.014	99999.0	0.512 (0.165-1.170)	0.00	0.46	0.14	0.49	0.05	0.62	0.18	0.46

[1]Segment of extra repeat motifs (10bp) was removed from aligned sequences.