

Quina et al.

Supplementary Table S5 Likelihood ratio statistics from branch, site-specific and branch-site tests using PAML software on *p53* exonic sequences (189 bp) of *Microtus*, rodent and mammalian lineages.

	N¹	Model tests	d.f.²	2ΔI	p³	Positively-selected sites⁴
Microtus	7	Branch test				
		M0-Model=2	1			
		Selected branch:				
		<i>M. duodecimcostatus</i>		5.735	0.017	
		<i>M. lusitanicus</i>		0	1	
		Site-specific tests				
		M0-M3	4	0	1	M3: -
		M1-M2	2	0.00005	0.99998	M2: -
		M7-M8	2	ND	-	M8: -
		Branch-site test				
		Foreground branch:				
		<i>M. duodecimcostatus</i>		0.665	0.415	Model A: 228E (0.943)
		<i>M. lusitanicus</i>		0	1	Model A: -
Rodents	20	Branch test				
		M0-Model=2	1			
		Selected branch:				
		<i>M. duodecimcostatus</i>		3.981	0.046	
		<i>M. lusitanicus</i>		0	1	
		Site-specific tests				
		M0-M3	4	14.611	0.005	M3: -
		M1-M2	2	0	1	M2: -
		M7-M8	2	ND	-	M8: -
		Branch-site test				
		Foreground branch:				
		<i>M. duodecimcostatus</i>		0.743	0.389	Model A: 228E (0.976)
		<i>M. lusitanicus</i>		0	1	Model A: -
		<i>Spalax judaei</i>		0	1	Model A: 174K (0.569)
Mammals	52	Branch test				
		M0-Model=2	1			
		Selected branch:				
		<i>M. duodecimcostatus</i>		3.771	0.052	
		<i>M. lusitanicus</i>		0.000002	0.997	
		Site-specific tests				
		M0-M3	4	110.867	0	M3: 209R (0.999)
		M1-M2	2	0	1	M2: -
		M7-M8	2	ND	-	M8: -
		Branch-site test				
		Foreground branch:				
		<i>M. duodecimcostatus</i>		0.724	0.395	Model A: 228E (0.982)
		<i>M. lusitanicus</i>		0.000002	0.999	Model A: -
		<i>Spalax judaei</i>		0	1	Model A: 174K (0.624)

¹ Number of sequences; ² degrees of freedom; ³ p-value; ⁴ Posterior probability in parenthesis; ND – not detected ($2\Delta I < 0$)