

Figure S2 Bayesian inference phylogenetic tree obtained for exons 6 and 7 of *ZP3* of the studied muroid rodents, with indels coded using the SIC method. Shown are posterior probabilities for cricetid clades that were greater than 0.5. Clades and haplotypes of Cricetinae and Tylomyinae are respectively indicated by black and white circles because these two cricetid subfamilies were not monophyletic.

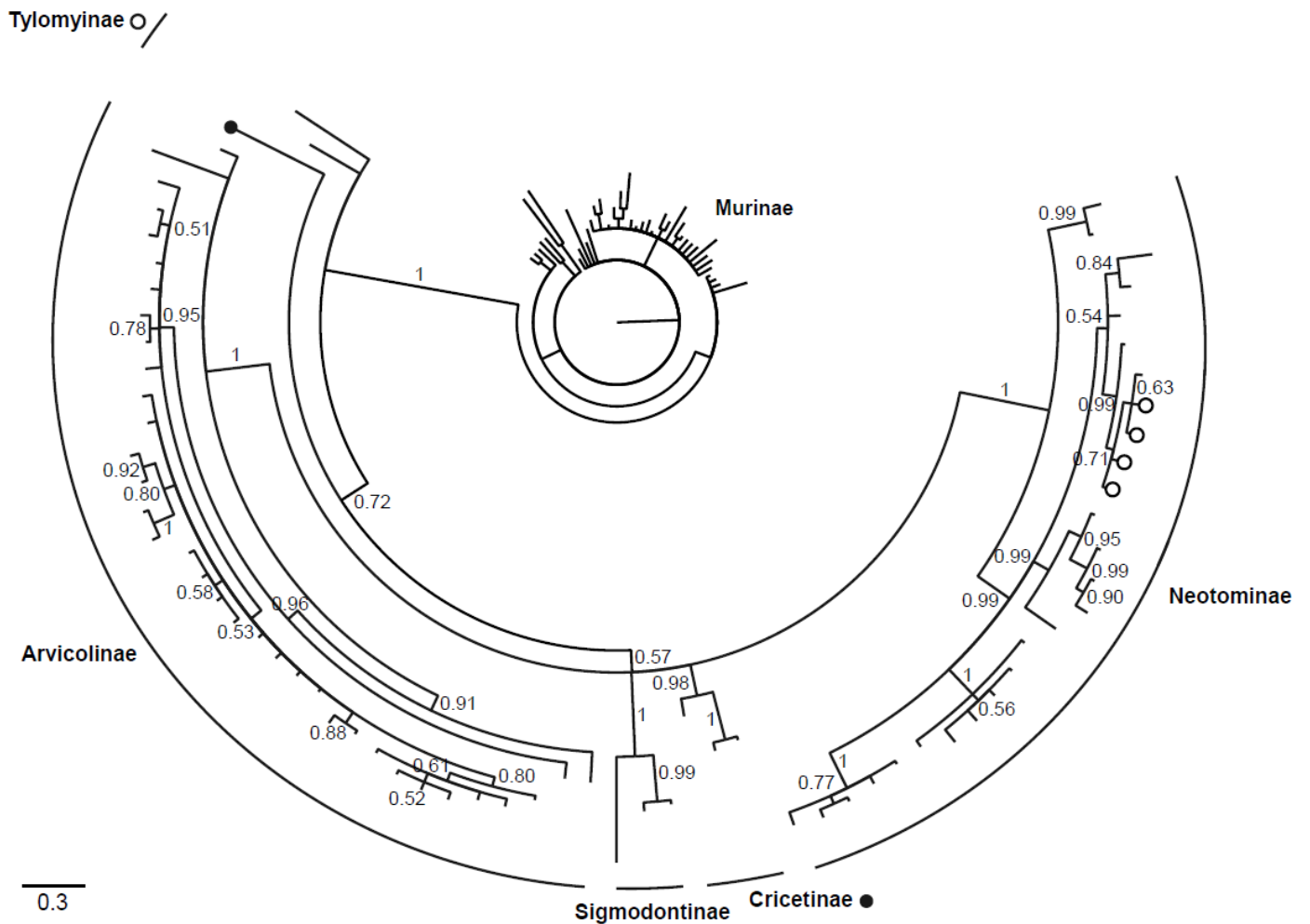
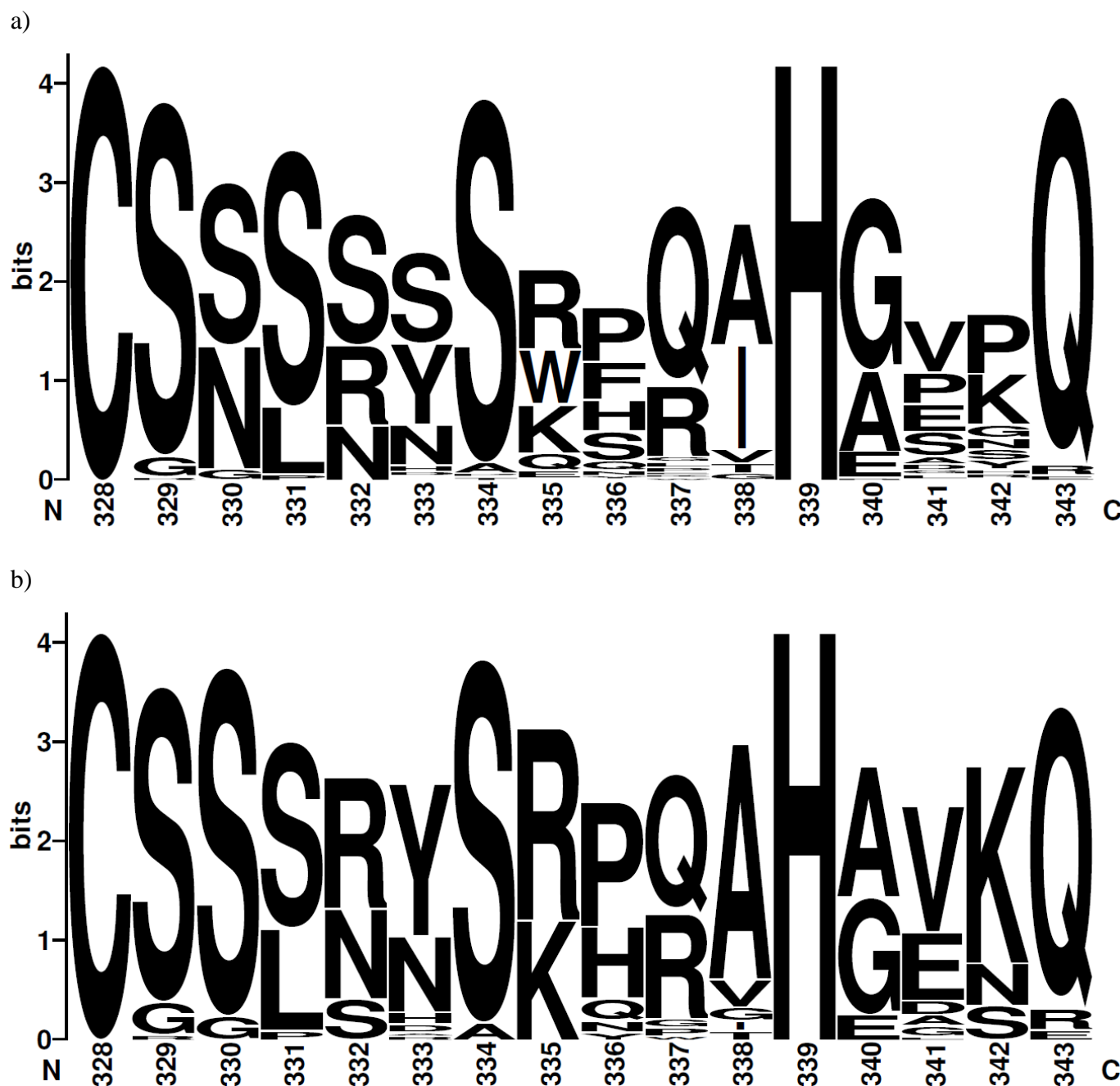


Figure S3 Amino acid sequence logos showing patterns of conservation and variation in the putative sperm-binding region of ZP3, for different data sets: a) Cricetidae + Murinae; b) Cricetidae; c) Murinae; d) Arvicolinae; e) Cricetinae; f) Neotominae; g) Sigmodontinae; and h) Tylomyinae. The overall height of each stack indicates the sequence conservation at the position, and the height of symbols within a stack reflects the relative frequency of the corresponding amino acid at each position, with the most frequent (‘consensus’) amino acid being on top of the stack. The amino acids are represented by their one-letter codes.



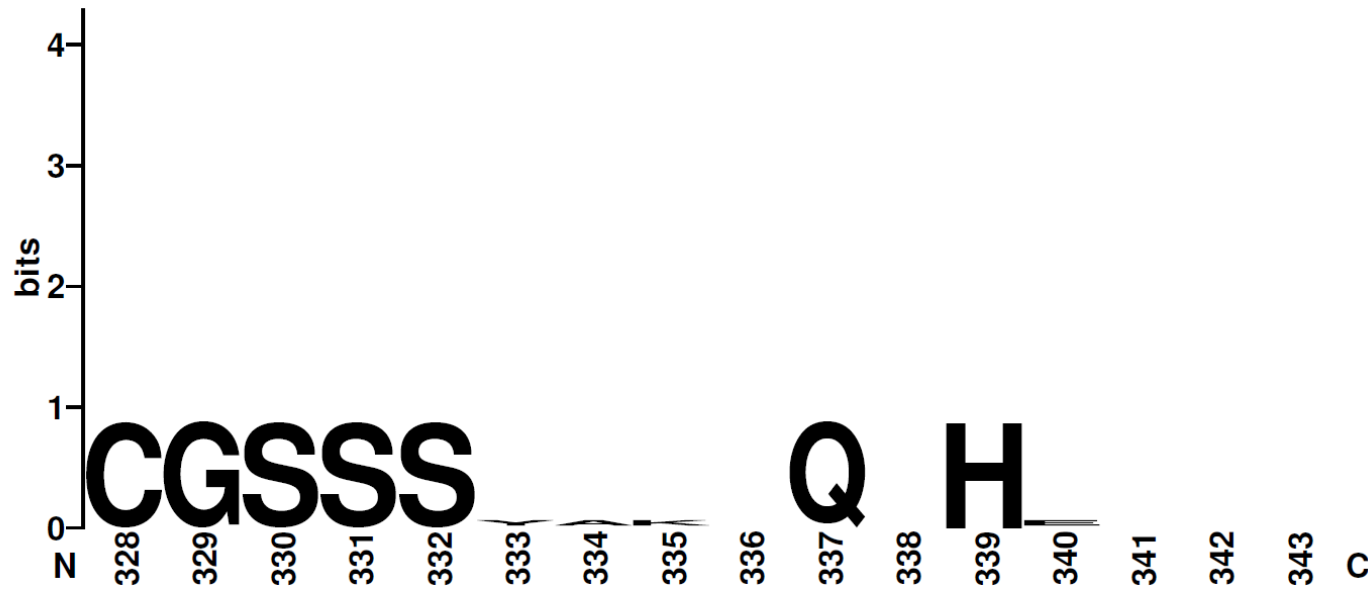
c)



d)



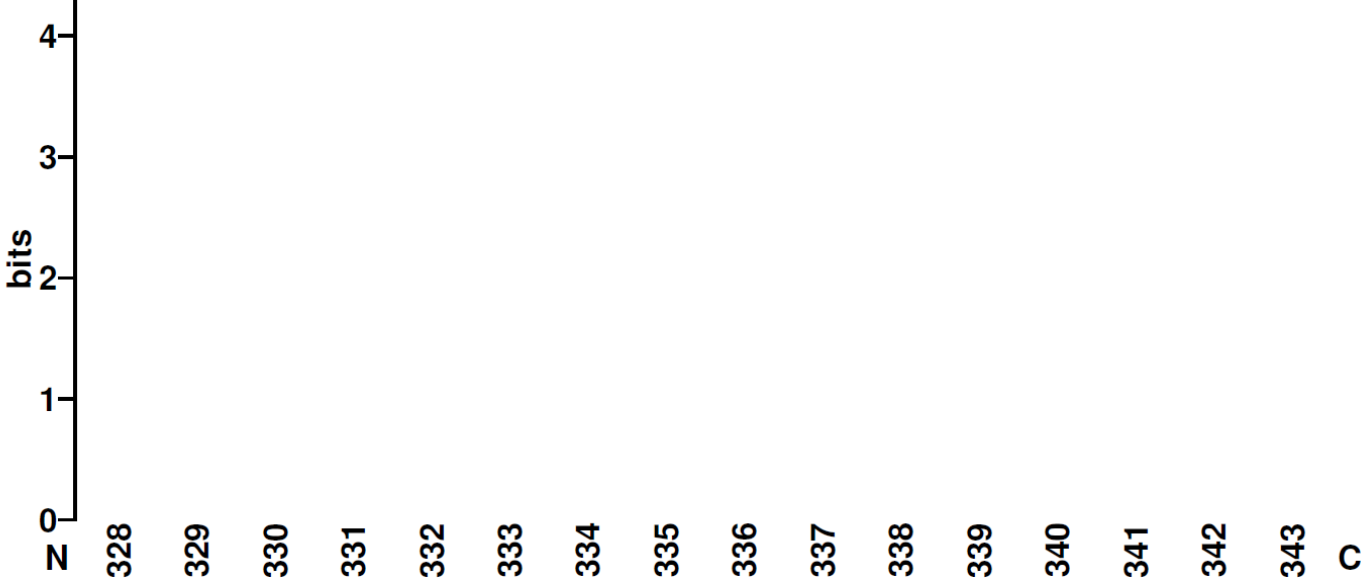
e)



f)



g)



h)



Table S1 List of species examined in this study. This table provides information on the subfamily and family to which the species belong, whether the ZP3 sequence fragment was obtained in this study from specimens (in which case the acronym of the institution that provided the sample, and its voucher number if available, is given) or retrieved from Genbank, number of specimens sequenced per species (N), the accession numbers of the GenBank sequences, and the DNA and amino acid haplotypes found in each species. MTTU = Museum of Texas Tech University, USA; MNCN = Museo Nacional de Ciencias Naturales, Spain; CMPG = Institute of Ecology and Evolution, University of Bern, Switzerland; IZ-MLU = Institute of Zoology, Martin-Luther University, Germany; MUHNAC = Museu Nacional de História Natural e da Ciência, Portugal.

Species	Subfamily, Family	Source	N	GenBank accession number	DNA haplotype	Amino acid haplotype
<i>Arvicola sapidus</i>	Arvicolinae, Cricetidae	MUHNAC	2	MT226293	H1	A1
<i>Chionomys nivalis</i>		CMPG	2	MT226294	H2	A2
<i>Lagurus lagurus</i>		GenBank	-	AF515621	H3	A3
<i>Lasiopodomys brandti</i>		CMPG	1	MT226295	H4	A2
<i>Microtus agrestis</i>		MNCN (ES-20909)	1	MT226296 MT226297	H5 H6	A2
<i>Microtus arvalis</i>		CMPG	2	MT226298 MT226299 MT226300 MT226301 MT226302 MT226303 MT226304 MT226305	H7 H8 H9 H10 H11 H12 H13 H14	A2 A4
<i>Microtus cabreræ</i>		MUHNAC	3	MT226306 MT226307	H15 H16	A5
<i>Microtus californicus</i>		CMPG	1	MT226308	H17	A2
<i>Microtus duodecimcostatus</i>		MUHNAC	2 5	MT226298 MT226301 MT226309	H7 H10 H18	A2 A6
<i>Microtus felteni</i>		CMPG	1	MT226298 MT226305	H7 H14	A2
<i>Microtus kikuchii</i>		CMPG	1	MT226310 MT226311	H19 H20	A4
<i>Microtus lusitanicus</i>		MUHNAC	2 9	MT226298 MT226312	H7 H21	A2
<i>Microtus montanus</i>		CMPG	2	MT226313	H22	A7
<i>Microtus montebelli</i>		CMPG	1	MT226313	H22	A7
<i>Microtus multiplex</i>		CMPG	2	MT226314 MT226315	H23 H24	A8
<i>Microtus ochrogaster</i>		CMPG	2	MT226316 MT226317	H25 H26	A2

				MT226318	H27	
<i>Microtus oeconomus</i>		CMPG	1	MT226319	H28	A9
<i>Microtus richardsoni</i>		CMPG	1	MT226310 MT226311	H19 H20	A4
<i>Microtus rossiaemeridionalis</i>		CMPG	2	MT226298 MT226299	H7 H8	A2 A4
<i>Microtus schelkovnikovi</i>		CMPG	1	MT226295	H4	A2
<i>Microtus socialis</i>		CMPG	2	MT226320 MT226321 MT226322 MT226323 MT226324 MT226325	H29 H30 H31 H32 H33 H34	A2 A8 A10 A11 A12 A13
<i>Microtus subterraneus</i>		CMPG	1	MT226295	H4	A2
<i>Microtus tatricus</i>		CMPG	2	MT226298	H7	A2
<i>Microtus thomasi</i>		CMPG	2	MT226298	H7	A2
<i>Myodes glareolus</i>		MNCN (MNCN-144800/ MNCN-144801)	2	MT226326	H35	A14
<i>Mesocricetus auratus</i>	Cricetinae, Cricetidae	IZ-MLU	2	MT226280	H36	A15
<i>Phodopus campbelli</i>			1	MT226281	H37	A16
<i>Phodopus roborovskii</i>			3	MT226282	H38	A17
<i>Phodopus sungorus</i>			3	MT226283	H39	A16
<i>Nyctomys sumichrasti</i>	Tylomyinae, Cricetidae	MTTU (TK 19590 / TK 113595)	2	MT226284 MT226285 MT226286 MT226287 MT226288	H40 H41 H42 H43 H44	A18 A19 A20 A36 A37
<i>Tylomys watsoni</i>		MTTU (TK 136061)	1	MT226289	H45	A21
<i>Oryzomys couesi</i>	Sigmodontinae, Cricetidae	MTTU (TK 92437)	1	MT226290 MT226291	H46 H47	A22
<i>Sigmodon arizonae</i>		MTTU (TK 112658)	1	MT226292	H48	A23
<i>Onychomys torridus</i>	Neotominae, Cricetidae	GenBank	-	DQ668293+ DQ668343 DQ668292+ DQ668342	H49 H50	A24 A25
<i>Peromyscus aztecus</i>				DQ668245+ DQ668332	H51	A26
<i>Peromyscus boylii</i>				DQ668250+ DQ668323	H52	A27
<i>Peromyscus californicus</i>				DQ668253+ DQ668341	H53	A28

<i>Peromyscus crinitus</i>				DQ668255+ DQ668306	H54	A29
<i>Peromyscus difficilis</i>				DQ668259+ DQ668313	H55 H56 H57 H58	A30 A31
<i>Peromyscus eremicus</i>				DQ668262+ DQ668310	H59	A32
<i>Peromyscus eva</i>				DQ668263+ DQ668337	H60	A32
<i>Peromyscus fraterculus</i>				DQ668264+ DQ668338	H61	A32
<i>Peromyscus gossypinus</i>				DQ668267+ DQ668319	H62	A33
<i>Peromyscus gratus</i>				EU568656	H63	A34
<i>Peromyscus leucopus</i>				DQ668270+ DQ668316	H62 H64	A33
<i>Peromyscus maniculatus</i>				DQ668276+ DQ668299	H65 H66	A33
<i>Peromyscus melanophrys</i>				DQ668279+ DQ668336	H67	A35
<i>Peromyscus mexicanus</i>				DQ668283+ DQ668330	H68 H69	A36 A37
<i>Peromyscus polionotus</i>				EU489722	H70	A38
<i>Peromyscus truei</i>				EU568744	H71	A39
<i>Aethomys ineptus</i>	Murinae, Muridae	GenBank	-	EU004038	H72	A40
<i>Anisomys imitator</i>				EF364448	H73	A41
<i>Apodemus chevrieri</i>				EU004040	H74	A42
<i>Bandicota indica</i>				EU004041	H75	A43
<i>Bunomys andrewsi</i>				EU004042	H76	A44
<i>Chiruromys vates</i>				EF364449	H77	A45
<i>Coccymys ruemmleri</i>				EF364450	H78	A46
<i>Conilurus penicillatus</i>				EF364451	H79	A47
<i>Crossomys moncktoni</i>				EF364452	H80	A48
<i>Dasymys incomtus</i>				EU004043	H81	A49
<i>Hydromys chrysogaster</i>				EF364453	H82	A48
<i>Hylomyscus alleni</i>				AY057789	H83	A50
<i>Hyomys goliath</i>				EF364454	H84	A41
<i>Leggadina forresti</i>				EF364455	H85	A48
<i>Lemniscomys griselda</i>				EU004044	H86	A51
<i>Leopoldamys sabanus</i>				EU004046	H87	A52
<i>Leporillus conditor</i>				EF364457	H88	A53
<i>Leptomys elegans</i>				EF364458	H89	A48
<i>Lorentzimys nouhuysi</i>				EF364459	H90	S54
<i>Macruromys major</i>				EF364460	H91	A55

<i>Mallomys aroensis</i>				EF364461	H78	A46
<i>Mammelomys rattoides</i>				EF364464	H92	A56
<i>Mastacomys fuscus</i>				EF364465	H93	A57
<i>Mastomys hildebrandtii</i>				AY057790	H94	A58
<i>Maxomys bartelsii</i>				EU004047	H95	A59
<i>Melomys cervinipes</i>				EF364469	H96	A60
<i>Mesembriomys gouldii</i>				EF364472	H97	A61
<i>Micaelamys namaquensis</i>				EU004039	H98	A62
<i>Mus musculus</i>				M20026	H111	A72
<i>Niviventer fulvescens</i>				EU004049	H100	A63
<i>Notomys alexis</i>				EF364474	H99	A57
<i>Parahydromys asper</i>				EF364479	H101	A48
<i>Paramelomys rubex</i>				EF364482	H102	A64
<i>Paruromys dominator</i>				EU004050	H103	A43
<i>Pogonomys macrourus</i>				EF364484	H104	A65
<i>Pseudohydromys ellermani</i>				EF364466	H82	A48
<i>Pseudomys laborifex</i>				EF364499	H105	A66
<i>Rhabdomys pumilio</i>				EU004064	H107	A68
<i>Rattus rattus</i>				Y10823	H106	A67
<i>Solomys salebrosus</i>				EF364507	H108	A69
<i>Uromys anak</i>				EF364508	H109	A70
<i>Xeromys myoides</i>				EF364510	H82	A48
<i>Zyzomys pedunculatus</i>				EF364514	H110	A71

Table S2 Detailed results of selection tests. For the PAML models, the log-likelihood (l) of each model is given, as well as the position of positively selected codons (where $\omega > 1$) identified by the Naive Empirical Bayes (NEB) and Bayes Empirical Bayes (BEB) methods. For the HyPhy tests, both positively and negatively selected sites are shown. Sites inferred to be under selection by the different site models in PAML or by the various site tests in HyPhy are underlined, while sites inferred to be under selection by the different site tests in both PAML and HyPhy are double underlined. $p0$ = proportion of sites where $\omega < 1$ (ω_0), $p1$ = proportion of sites where $\omega = 1$ (ω_1), $p2$ = proportion of sites where $\omega > 1$ (ω_2), p/q = parameters of the beta distribution, ⁿ = positively selected site identified by NEB, ^b = positively selected site identified by BEB, * = probability > 95%, ** = probability > 99%, N.A. = not applicable.

Dataset	Software	Model or test	Parameters	κ (ts/tv)	Log-likelihood (l)	Positively selected sites	Negatively selected sites
Cricetidae + Murinae	PAML	M0: one ratio	$\omega = 0.45307$	4.27867	-2823.044887	N.A.	N.A.
		M1a: nearly neutral	$p0 = 0.69290$ $\omega_0 = 0.10473$ $p1 = 0.30710$ $\omega_1 = 1.00000$	4.19730	-2715.812590	N.A.	N.A.
		M2a: positive selection	$p0 = 0.64858$ $\omega_0 = 0.10658$ $p1 = 0.25716$ $\omega_1 = 1.00000$ $p2 = 0.09426$ $\omega_2 = 2.74189$	4.77821	-2697.066353	<u>311</u> ^{nb} <u>325</u> ^{nb**} <u>336</u> ^{nb*} <u>337</u> ^{nb**} <u>341</u> ^{nb**} <u>342</u> ^{nb**} <u>346</u> ^{nb}	N.A.
		M3: discrete	$p0 = 0.37891$ $\omega_0 = 0.00000$ $p1 = 0.46362$ $\omega_1 = 0.39586$ $p2 = 0.15747$ $\omega_2 = 2.05395$	4.56989	-2686.221770	<u>311</u> ^{n**} <u>324</u> ^{n**} <u>325</u> ^{n**} <u>333</u> ⁿ <u>335</u> ^{n**} <u>336</u> ^{n**} <u>337</u> ^{n**} <u>338</u> ^{n*} <u>341</u> ^{n**} <u>342</u> ^{n**} <u>346</u> ^{n**} <u>347</u> ⁿ	N.A.
		M7: beta	$p = 0.22452$ $q = 0.42241$	4.07948	-2708.700999	N.A.	N.A.
		M8: beta and $\omega > 1$	$p0 = 0.87831$ $p = 0.32736$ $q = 0.92237$ $p1 = 0.12169$ $\omega = 2.27682$	4.61074	-2687.502429	<u>311</u> ^{nb} <u>324</u> ^{nb} <u>325</u> ^{nb**} <u>335</u> ^{nb} <u>336</u> ^{nb**} <u>337</u> ^{nb**} <u>341</u> ^{nb**} <u>342</u> ^{nb**} <u>346</u> ^{nb}	N.A.
		M8a: beta and $\omega = 1$	$p0 = 0.79168$ $p = 0.46594$ $q = 2.64845$	4.05849	-2705.263257	N.A.	N.A.

			$pI = 0.20832$ $\omega = 1.00000$				
		MA1, foreground branch = Murinae	N.A.	4.383	-1631.463527	315 ^{bn} 322 ^{bn}	N.A.
		MA1, foreground branch = Cricetidae	N.A.	4.082	-1626.069192	287 ^{bn} 307 ^{bn*/**} 311 ^{bn*}	N.A.
		MA1, foreground branch = Arvicolinae	N.A.	4.226	-1628.893840	287 ^{bn**}	N.A.
		MA1, foreground branch = Cricetinae	N.A.	4.242	-1631.709580	296 ^b 309 ^b	N.A.
		MA1, foreground branch = Neotominae	N.A.	4.237	-1632.173401	None	N.A.
		MA1, foreground branch = Sigmodontinae	N.A.	4.231	-1632.171253	None	N.A.
		MA1, foreground branch = Tylomyinae	N.A.	4.162	-1632.052340	307 ^b 311 ^{bn}	N.A.
	HyPhy	SLAC	N.A.	N.A.	N.A.	<u>337*</u>	<u>287*</u> <u>288**</u> <u>289**</u> <u>294**</u> <u>295**</u> <u>301**</u> <u>302**</u> <u>307*</u> <u>312*</u> <u>315*</u> <u>323**</u> <u>326**</u> <u>328**</u> <u>329*</u> <u>334**</u> <u>339**</u> <u>354**</u>
		FEL	N.A.	N.A.	N.A.	317* 336* <u>337**</u>	280* 283* <u>287**</u> 288* <u>289**</u> 290* <u>294**</u> <u>295**</u> 296* <u>301**</u> <u>302**</u> <u>307**</u>

							<u>312</u> ** <u>315</u> ** <u>323</u> ** <u>326</u> ** <u>328</u> ** <u>334</u> ** <u>339</u> ** <u>354</u> **
		MEME	N.A.	N.A.	N.A.	336* <u>337</u> *	N.A.
		FUBAR	N.A.	N.A.	N.A.	336** <u>337</u> ** 342**	<u>287</u> ** <u>289</u> ** <u>294</u> ** <u>295</u> * <u>301</u> * <u>302</u> ** <u>307</u> * <u>312</u> ** <u>315</u> * <u>323</u> * <u>326</u> ** <u>328</u> * <u>334</u> ** <u>339</u> ** <u>354</u> **
Cricetidae	PAML	M0: one ratio	$\omega = 0.40848$	4.11044	-1840.140915	N.A.	N.A.
		M1a: nearly neutral	$p0 = 0.58454$ $\omega0 = 0.02766$ $p1 = 0.41546$ $\omega1 = 1.00000$	4.21389	-1772.708134	N.A.	N.A.
		M2a: positive selection	$p0 = 0.58109$ $\omega0 = 0.02853$ $p1 = 0.35888$ $\omega1 = 1.00000$ $p2 = 0.06003$ $\omega2 = 2.11546$	4.31392	-1772.345302	<u>333</u> ^{nb} <u>337</u> ^{nb}	N.A.
		M3: discrete	$p0 = 0.52941$ $\omega0 = 0.01315$ $p1 = 0.25547$ $\omega1 = 0.55291$ $p2 = 0.21512$ $\omega2 = 1.48408$	4.29966	-1770.261410	296 ⁿ 297 ⁿ 308 ⁿ 321 ⁿ 324 ⁿ 325 ^{n*} <u>333</u> ^{n**} 336 ⁿ <u>337</u> ^{n**} 338 ^{n*} 341 ⁿ 342 ⁿ 344 ⁿ 346 ⁿ 347 ⁿ	N.A.
		M7: beta	$p = 0.09348$ $q = 0.14198$	4.11249	-1772.441428	N.A.	N.A.
		M8: beta and $\omega > 1$	$p0 = 0.88218$ $p = 0.12025$ $q = 0.27748$ $p1 = 0.11782$ $\omega = 1.70965$	4.30832	-1770.207833	293 ^b 296 ^b 297 ^b 308 ^b 317 ^b 321 ^b 324 ^b 325 ^{nb} 329 ^b <u>333</u> ^{nb} 336 ^{nb} <u>337</u> ^{nb*}	N.A.

						338 ^{nb} 341 ^{nb} 342 ^{nb} 344 ^b 346 ^{nb} 347 ^b	
		M8a: beta and $\omega = 1$	$p0 = 0.64093$ $p = 0.18762$ $q = 2.45890$ $p1 = 0.35907$ $\omega = 1.00000$	4.13917	-1771.953080	N.A.	N.A.
	HyPhy	SLAC	N.A.	N.A.	N.A.	<u>337</u> *	<u>287</u> * <u>289</u> ** 298* <u>301</u> ** <u>312</u> * <u>323</u> * <u>326</u> ** 330* <u>334</u> ** <u>339</u> ** <u>354</u> **
		FEL	N.A.	N.A.	N.A.	317* <u>337</u> *	<u>287</u> ** <u>289</u> ** 294* 295* 298* <u>301</u> ** 307* <u>312</u> * 314* 315* 318* <u>323</u> ** <u>326</u> ** 328* <u>334</u> * <u>339</u> ** <u>354</u> **
		MEME	N.A.	N.A.	N.A.	297* <u>337</u> *	N.A.
		FUBAR	N.A.	N.A.	N.A.	<u>337</u> **	<u>287</u> ** <u>289</u> * <u>301</u> * <u>312</u> * <u>323</u> * <u>326</u> ** <u>334</u> ** <u>339</u> ** <u>354</u> **
Murinae	PAML	M0: one ratio	$\omega = 0.40348$	3.31445	-1135.898833	N.A.	N.A.
		M1a: nearly neutral	$p0 = 0.76934$ $\omega0 = 0.07569$ $p1 = 0.23066$ $\omega1 = 1.00000$	3.06737	-1095.799952	N.A.	N.A.
		M2a: positive selection	$p0 = 0.77312$ $\omega0 = 0.10194$ $p1 = 0.13762$ $\omega1 = 1.00000$ $p2 = 0.08926$ $\omega2 = 3.13645$	3.69926	-1087.463200	<u>311</u> ^{nb} <u>325</u> ^{nb**} <u>335</u> ^{nb} <u>337</u> ^{nb} <u>342</u> ^{nb**} <u>346</u> ^{nb}	N.A.
		M3: discrete	$p0 = 0.48367$ $\omega0 = 0.00000$ $p1 = 0.39562$ $\omega1 = 0.36774$	3.70074	-1084.433658	279 ⁿ <u>311</u> ^{n**} 324 ⁿ <u>325</u> ^{n**}	N.A.

			$p2 = 0.12071$ $\omega2 = 2.68516$			<u>335</u> ^{n**} <u>337</u> ^{n*} <u>341</u> ⁿ <u>342</u> ^{n**} <u>346</u> ⁿ	
		M7: beta	$p = 0.12345$ $q = 0.29286$	3.11705	-1095.892379	N.A.	N.A.
		M8: beta and $\omega > 1$	$p0 = 0.89108$ $p = 0.30707$ $q = 1.32853$ $p1 = 0.10892$ $\omega = 2.81543$	3.69150	-1085.310331	<u>279</u> ^{nb} <u>311</u> ^{nb**/*} <u>324</u> ⁿ <u>325</u> ^{nb**} <u>335</u> ^{nb*} <u>337</u> ^{nb} <u>341</u> ^{nb} <u>342</u> ^{nb**} <u>346</u> ^{nb}	N.A.
		M8a: beta and $\omega = 1$	$p0 = 0.80021$ $p = 0.41353$ $q = 3.92123$ $p1 = 0.19979$ $\omega = 1.00000$	3.04708	-1094.453451	N.A.	N.A.
	HyPhy	SLAC	N.A.	N.A.	N.A.	None	<u>289</u> [*] <u>294</u> [*] <u>295</u> [*] <u>296</u> [*] <u>302</u> ^{**} <u>306</u> [*] <u>327</u> [*] <u>339</u> ^{**}
		FEL	N.A.	N.A.	N.A.	342 [*]	<u>288</u> ^{**} <u>289</u> ^{**} <u>294</u> [*] <u>295</u> [*] <u>296</u> ^{**} <u>302</u> ^{**} <u>306</u> ^{**} <u>307</u> [*] <u>327</u> [*] <u>339</u> ^{**}
		MEME	N.A.	N.A.	N.A.	<u>316</u> [*] <u>342</u> [*]	N.A.
		FUBAR	N.A.	N.A.	N.A.	<u>355</u> ^{**} <u>342</u> ^{**}	<u>288</u> [*] <u>289</u> [*] <u>294</u> [*] <u>295</u> [*] <u>296</u> [*] <u>302</u> ^{**} <u>306</u> [*] <u>339</u> ^{**}
<i>Microtus</i>	PAML	M0: one ratio	$\omega = 0.15381$	5.07385	-706.765944	N.A.	N.A.
		M1a: nearly neutral	$p0 = 0.90975$ $\omega0 = 0.00997$ $p1 = 0.09025$ $\omega1 = 1.00000$	4.70089	-680.735490	N.A.	N.A.
		M2a: positive selection	$p0 = 0.91830$ $\omega0 = 0.01498$ $p1 = 0.05719$ $\omega1 = 1.00000$ $p2 = 0.02452$ $\omega2 = 4.30461$	5.07955	-676.424362	<u>297</u> ^{nb} <u>337</u> ^{nb**}	N.A.
		M3: discrete	$p0 = 0.91526$ $\omega0 = 0.01413$ $p1 = 0.05823$ $\omega1 = 0.92183$ $p2 = 0.02652$	5.03878	-676.613865	<u>297</u> ⁿ <u>337</u> ^{n**}	N.A.

			$\omega_2 = 4.03886$				
		M7: beta	$p = 0.01066$ $q = 0.07279$	4.71871	-680.839279	N.A.	N.A.
		M8: beta and $\omega > 1$	$p0 = 0.96968$ $p = 0.03462$ $q = 0.51150$ $p1 = 0.03032$ $\omega = 3.80463$	5.01679	-676.664233	$\frac{297^{nb}}{337^{nb**}}$	N.A.
		M8a: beta and $\omega = 1$	$p0 = 0.90974$ $p = 1.03990$ $q = 99.00000$ $p1 = 0.09026$ $\omega = 1.00000$	4.69391	-680.780313	N.A.	N.A.
	HyPhy	SLAC	N.A.	N.A.	N.A.	$\frac{337^*}{337^*}$	$\frac{291^{**}}{318^{**}}$ $\frac{326^*}{334^*}$ $\frac{339^*}{339^*}$
		FEL	N.A.	N.A.	N.A.	$\frac{337^*}{337^*}$	$\frac{291^{**}}{303^*}$ $\frac{314^*}{315^*}$ $\frac{318^{**}}{326^*}$ $\frac{333^*}{334^*}$ $\frac{339^*}{339^*}$
		MEME	N.A.	N.A.	N.A.	$\frac{337^*}{337^*}$	N.A.
		FUBAR	N.A.	N.A.	N.A.	$\frac{337^{**}}{337^{**}}$	$\frac{291^{**}}{318^{**}}$ $\frac{326^{**}}{334^{**}}$ $\frac{339^*}{339^*}$
<i>Peromyscus</i>	PAML	M0: one ratio	$\omega = 0.35231$	3.83664	-735.567226	N.A.	N.A.
		M1a: nearly neutral	$p0 = 0.61897$ $\omega_0 = 0.00000$ $p1 = 0.38103$ $\omega_1 = 1.00000$	4.07239	-728.070941	N.A.	N.A.
		M2a: positive selection	$p0 = 0.61897$ $\omega_0 = 0.00000$ $p1 = 0.28498$ $\omega_1 = 1.00000$ $p2 = 0.09605$ $\omega_2 = 1.00000$	4.07238	-728.070941	333 ^b	N.A.
		M3: discrete	$p0 = 0.34058$ $\omega_0 = 0.00000$ $p1 = 0.27098$ $\omega_1 = 0.00000$ $p2 = 0.38844$ $\omega_2 = 0.94086$	4.02303	-728.050079	None	N.A.
		M7: beta	$p = 0.01629$ $q = 0.02858$	4.04372	-728.072655	N.A.	N.A.
		M8: beta and $\omega > 1$	$p0 = 0.87803$ $p = 0.01356$ $q = 0.03717$ $p1 = 0.12197$ $\omega = 1.00000$	4.04761	-728.060149	333 ⁿ 344 ⁿ 346 ⁿ	N.A.
		M8a: beta and $\omega = 1$	$p0 = 0.61897$ $p = 0.00500$ $q = 74.14239$ $p1 = 0.38103$ $\omega = 1.00000$	4.07239	-728.070936	N.A.	N.A.
	HyPhy	SLAC	N.A.	N.A.	N.A.	None	$\frac{287^*}{289^*}$ $\frac{298^*}{298^*}$

							<u>323</u> ** <u>328</u> * <u>354</u> *
		FEL	N.A.	N.A.	N.A.	None	<u>287</u> ** <u>289</u> ** <u>298</u> ** <u>323</u> ** <u>326</u> * <u>328</u> ** <u>354</u> **
		MEME	N.A.	N.A.	N.A.	None	N.A.
		FUBAR	N.A.	N.A.	N.A.	None	<u>287</u> ** <u>289</u> * <u>298</u> * <u>323</u> ** <u>328</u> * <u>342</u> * <u>354</u> *