

Table S1. Sequences retrieved from GeneBank. The voucher number or collection code is presented for the nuclear sequences of *Blarinella* spp. according to Fig. 4 and literature source.

species	GeneBank Acc No	Source
<i>cytb</i>		
<i>Blarinella wardi</i>	JF719714	Chen et. al. 2012
<i>B. quadraticauda</i>	JF719701–F719713, JF719715–JF719725	Chen et. al. 2012
	NC_023950	Wang et al., 2014
	GU981258, GU981259	He et al., 2010
	AB175144	Ohdachi et al., 2006
<i>Cryptotis parva</i>	AB175135	Ohdachi et al., 2006
<i>ApoB</i>		
<i>B. quadraticauda</i>	JF719697 (ElsmypA02001)	Chen et al., 2012
	DQ630187 (BLG)	Dubey et al., 2007
	LC124841 (AMNH101610)	Sato et al., 2016
	GU981108 (Blagris1), GU981109 (Blagris2)	He et al., 2010
<i>Blarinella wardi</i>	JF719698	Chen et al., 2012
<i>Crocidura fuliginosa</i>	GU981117	He et al., 2010
<i>Pseudosoriculus fumidus</i>	GU981121	
<i>Soriculus nigrescens</i>	GU981132	
<i>Nectogale elegans</i>	GU981128	
<i>Episoriculus leucops</i>	GU981122	
<i>Chimarrogale himalayica</i>	GU981112	
<i>Chodsigoa hypsibia</i>	GU981110	
<i>Episoriculus macrurus</i>	GU981125_	
<i>Episoriculus caudatus</i>	GU981119	
<i>Chodsigoa parca</i>	KX765554	Chen et al., 2017
<i>Chodsigoa sodalis</i>	DQ630191	Dubey et al., 2007
<i>BRCA1</i>		
<i>Blarinella quadraticauda</i>	DQ630268 (BLG)	Dubey et al., 2007
	LC124932 (AMNH101610)	Sato et al., 2016
	GU981183 (Blagris1), GU981184 (Blagris2)	He et al., 2010
<i>Cryptotis parva</i>	DQ630261	Dubey et al., 2007
<i>Crocidura fuliginosa</i>	GU981192	He et al., 2010
<i>Episoriculus macrurus</i>	GU981202	
<i>Episoriculus leucops</i>	GU981197	
<i>Nectogale elegans</i>	GU981203	
<i>Soriculus nigrescens</i>	GU981209	
<i>Episoriculus caudatus</i>	GU981195	
<i>Pseudosoriculus fumidus</i>	DQ630277	
<i>Chodsigoa parca</i>	GU981189	
<i>Chodsigoa hypsibia</i>	KX765637	Chen et al., 2017
<i>Chodsigoa sodalis</i>	DQ630271	Dubey et al., 2007
<i>Chimarrogale himalayica</i>	DQ630260	
<i>RAG2</i>		
<i>Blarinella quadraticauda</i>	GU981441 (Blagris1)	He et al., 2010
<i>Crocidura fuliginosa</i>	GU981450	
<i>Pseudosoriculus fumidus</i>	GU981454	

<i>Soriculus nigrescens</i>	GU981467	
<i>Nectogale elegans</i>	GU981461	
<i>Episoriculus macrurus</i>	GU981458	
<i>Episoriculus leucops</i>	GU981455	
<i>Episoriculus caudatus</i>	GU981452	
<i>Chodsigoa parca</i>	GU981446	
<i>Chodsigoa hypsibia</i>	GU981443	
<i>Chodsigoa sodalis</i>	GU981449	
<i>Chimarrogale himalayica</i>	KY082637	Abramov et al., 2017

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- He K, Li Y-J, Brandley MC, Lin L-K, Wang Y-X, Zhang Y-P, Jiang X-L (2010) A multi-locus phylogeny of Nectogalini shrews and influences of the paleoclimate on speciation and evolution. *Molecular Phylogenetics and Evolution* 56: 734–746. doi.org/10.1016/j.ympev.2010.03.039
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- Wang Q, Fu C, Chen S, Yong B, Chen G, Hao Z (2014) The complete mitogenome of Asiatic Short-tailed Shrew *Blarinella quadratacauda* (Soricidae). *Mitochondrial DNA* 27: 282–283. <https://doi.org/10.3109/19401736.2014.892078>.

Table S2. The original primers designed for amplification and sequencing of *cytb* in *Blarinella*.

№	primer	sequence (5`-3`)
<i>Blarinella</i> spp.		
external primers for complete <i>cytb</i> gene (1140 bp)		
1.	L14132_B	GACCTATGACATGAAAAATCATCGTTGT
2.	L14734_B	CATGAAAAATCATCGTTGTTATTCAACT
3.	H15327_B	GGTTTACAAGACCAGTGTAATAATTATACTAC
4.	H15347_B	GAATCTCCATTTCTGGTTTACAAGAC
5.	H15416_B	AGAATTCCAGCTTTGGGTGTTG
Internal primers for fragment 1-670 bp		
7	H400a	GCCTCAAAAAGACATTTGTCCTCAT
8	L240a	CTACAYGCCAACGGAGCATCAATA
9	H330a	AATAATACCCCGATRITTCATGTTTCTA
10	L170ax	GACACAATAACAGCCTTTTCATCAGTAAC
11	H190a	ATCYCGGCARATGTGTGTTACTGATGA
12	L62a	TACCYGCTCCATCTAAYATTTTCATCAT
13	H95a	GCAGACACCTAATAAAGAACCGAAGT
14	L360a	TTCGCRGTTATAGCYACAGCCTTTATA
15	H511a	AAYCGTGTGAGTGTTGCTTTGTC
16	L467a	TTGGCTCRGACCTWGTMCAATGAATCT
17	L580a	GAGTTCACCTATTATTCCTCCACGA
18	H601a	GGGTTGTTGGAACCAGTTTCGTG
19	H716a	TCAGGGGAGAATAATACTAATGATGTTA
20	H670a	GGAGAACACCTAGAATATCTTTRATTGTATA
<i>Blarinella griselda</i>		
Internal primers for fragment 1-670 bp		
21.	H670x	AGTGCTCCTAGAATGTCTTTGATTGTATA
22.	H400x	GCGCCTCAAATGATATTTGTCCTC
23.	L240x	ATACATGCAAATGGAGCATCAATA
24.	H330x	AGCAGTACTCCGATATTTTCATGTTTCTA
25.	H601x	GATGGATTGTTTGATCCTGTTTCGTG
26.	H190x	CTCGGCAAATGTGTGTTACTGATGA
27.	L62x	TACCTGCTCCATCCAAYATTTTCATCAT
28.	H95x	GCAGATTCCTAATAGTGARCCGAAGT
29.	L360x	TTCGCAGTTATAGCYACTGCCTTTATA
30.	H511x	AACCGTGTGAGTGTTGCTTTGTC

31.	L467x	TTGGCTCAGACCTAGTAGAATGAATCT
32.	L580x	GGAGTCCACCTCTTATTTCTACACGA

Table S3. GenBank AccNos of the original sequences used in the study.

species	ID	voucher	<i>cytb</i>	<i>ApoB</i>	<i>IRBP</i>	<i>RAG2</i>	<i>BRCA1</i>
<i>B. quadraticauda</i>	36 (BI-1)	ZIN 91211	<i>KY249525</i>	–	–	–	–
<i>B. quadraticauda</i>	42 (BI-2)	ZIN 96272	–	<i>KY249531</i>	////////	<i>KY249542</i>	////////
<i>B. quadraticauda</i>	43 (BI-3)	ZIN 96273	<i>KY249526</i>	–	–	<i>KY249543</i>	–
<i>B. quadraticauda</i>	136 (BI-5)	ZIN 97788	<i>KY249527</i>	<i>KY249532</i>	–	<i>ZIN 97788</i>	////////
<i>B. quadraticauda</i>	V12-40	ZIN 101574	<i>KY249528</i>	<i>KY249533</i>	<i>KY249551</i>	<i>KY249545</i>	////////
<i>B. quadraticauda</i>	V12-61	ZIN 101575	<i>KY249529</i>	<i>KY249534</i>	<i>KY249552</i>	<i>KY249546</i>	////////
<i>B. quadraticauda</i>	G17-12	ZMMU G17-12	////////	////////	////////	////////	////////
<i>Parablarinella griselda</i>	Chi111	ZMMU 195179	<i>KY249530</i>	<i>KY249535</i>	////////	<i>KY249547</i>	////////
<i>P. griselda</i>	G17-87	ZMMU G17-87	////////	////////	////////	////////	–
<i>P. griselda</i>	G18-252	ZMMU G18-252	////////	////////	////////	////////	–
<i>P. griselda</i>		NHMUK 1912.8.5.23	////////				–
<i>Chodsigoa parca</i>	AVA10-29	ZIN99787	–	<i>KY082620</i>	–	<i>KY082638</i>	–
<i>Chodsigoa hysibia</i>	Chi11-72	ZMMU 195190	////////	<i>MF577031</i>	<i>KY082659</i>	<i>KY082640</i>	////////
<i>Chodsigoa hysibia</i>	G17-13	ZMMU G17-13	////////	–	–	–	–

sequences used from our previous study are marked in *Italic*

Table S4. The best-fit substitution models employed for each of the five partitions found by IQTREE.

model	Partitions (gene and codon position)
TIM3+F+G4	<i>ApoB</i> 1 st and 2 ^d codon positions; <i>IRBP</i> 2 ^d codon position
HKY+F+G4	<i>BRCA1</i> and <i>IRBP</i> 1 st codon position
K2P+I	<i>RAG2</i> 1 st and 2 ^d codon positions
TPM2+F	<i>IRBP</i> 3 rd codon position
K3Pu+F+G4	<i>BRCA1</i> 2 ^d codon position; <i>ApoB</i> , <i>BRCA1</i> , <i>RAG2</i> 3 rd codon positions

