

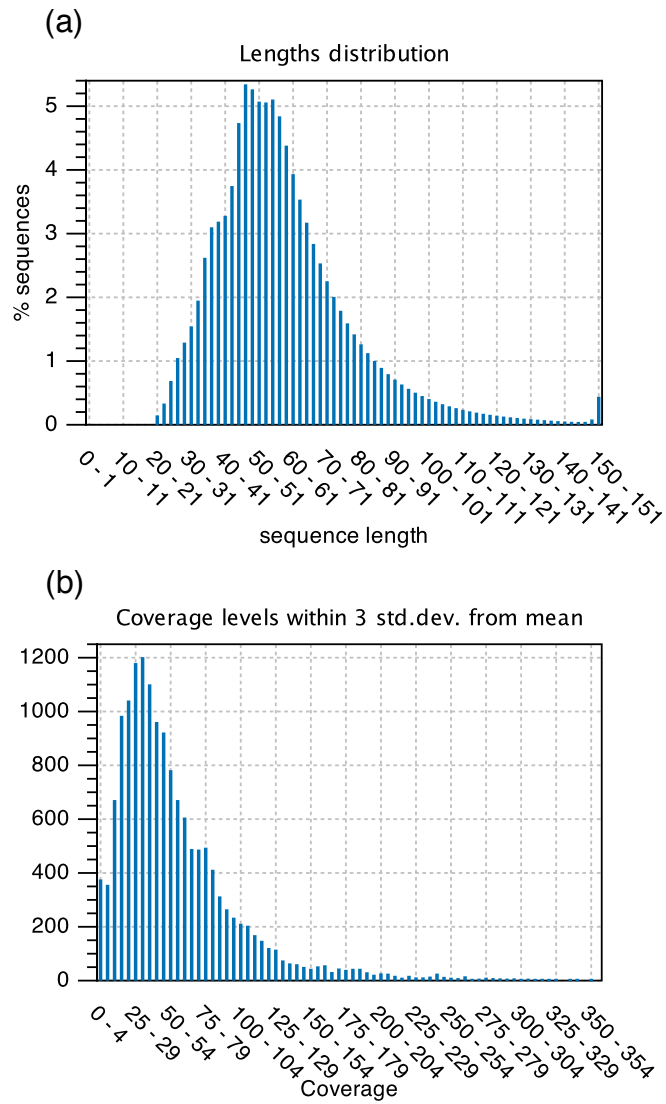


Figure S1. (a) Distribution of read lengths in paired-reads dataset. **(b)** Level of coverage across reference mitochondrial genome in mapped-reads dataset.

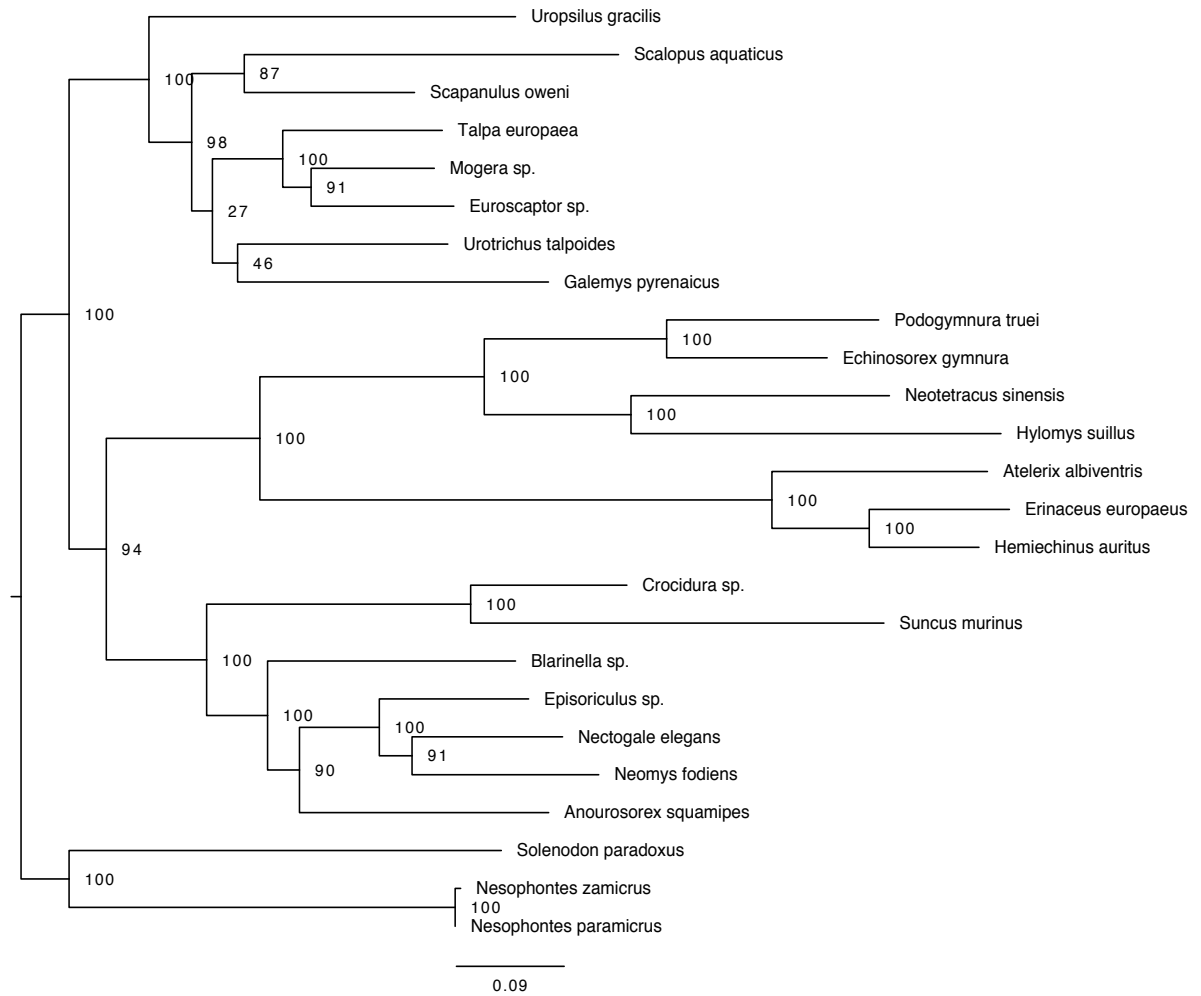


Figure S2. Maximum likelihood phylogeny generated using RAxML, including *Nesophontes paramicros*, *N. zamicros*, and extant eulipotyphlans with available whole mitochondrial genome data. Node values represent bootstrap support (100 replicates).

Table S1. Morphometric measurements taken on Hispaniolan *Nesophontes* mandibles.

Character	Description
1	Alveolar length of canine – m3
2	Alveolar length of m1 – m3
3	Length of canine – posterior margin of angular margin
4	Length of canine – posterior margin of condyle
5	Length of canine – dorsal margin of coronoid
6	Length of m3 – posterior margin of angular margin
7	Length of m3 – posterior margin of condyle
8	Length of m3 – dorsal margin of coronoid
9	Buccal width between m2 and m3
10	Width of condyle
11	Length of dorsal margin of coronoid – ventral margin of condyle
12	Length of dorsal margin of coronoid – ventral margin of angular margin
13	Length of dorsal margin of condyle – ventral margin of angular margin

Table S3. Genes used in phylogenetic analysis, including GenBank accession numbers. Asterisk indicates chimeric taxon made up of multiple species.

Family	Genus	Species	mt genome	APP	BMI1	CREM	PLCB4	ADORA3	APOB	ADRA2B	ADRB2
Nesophontidae	<i>Nesophontes</i>	<i>zamicrus</i>		X		X			X	X	X
Solenodontidae	<i>Solenodon</i>	<i>paradoxus</i>	X	AY530068	AY530071	AY451973, AY530072	AY530074	AY530066	JN414026	AY530081	AY530067
Erinaceidae	<i>Erinaceus</i>	<i>europaeus</i>	NC.002080	XM.007519783 AY011319	XM.007526364	XM.007523995	XM.007539576	XM.007526934	JN414024	XM.007529903	XM.007516378
	<i>Hemiechinus</i>	<i>auritus</i>	NC.005033								
	<i>Atelerix</i>	<i>albiventris</i>	X					X	X	X	X
	<i>Echinosorex</i>	<i>gymnura</i>	NC.002808		AY986735	AY451978	AY451986				
	<i>Hylomys</i>	<i>suillus</i>	NC.010298				AY451987		DQ630204	AJ505819	
	<i>Neotetracus</i>	<i>sinensis</i>	NC.019626								
	<i>Podogymnura</i>	<i>truei</i>	AF434823, AF434829, AF298578-9	JN633548	AY986742	AY451980	JN633106	JN633426	JN414025	JN413881	JN633682
Soricidae	<i>Crociodura</i>	<i>russula/ *fuliginosa/ *gueldenstaedtii</i>	NC.006893		AY986736* <i>gueldenstaedtii</i>	AY451977* <i>gueldenstaedtii</i>	AY451985* <i>gueldenstaedtii</i>		GU981117* <i>fuliginosa</i>	AY121766	
	<i>Suncus</i>	<i>murinus/*remyi</i>	AB175074 AB032842 EF507245 AB032845 AB033720 F444469		AY986741	AY451981	AY451992		DQ630181		
			FJ814528 J813943								
			FJ813963 AB011390								
	<i>Episoriculus</i>	<i>fumidus</i>	NC.003040						DQ630193		
	<i>Sorex</i>	<i>araneus/ *unquiculatus</i>	NC.005435*	XM.004621155	AY011509	AY011631	AY011754	AY011200	JN414027	XM.004609236	XM.004620597
	<i>Nectogale</i>	<i>elegans</i>	NC.023351						GU981129		
	<i>Blarinella</i>	sp.	NC.023950						DQ630187		
	<i>Anourosorex</i>	<i>squamipes</i>	NC.024563								
	<i>Neomys</i>	<i>fodiens</i>	NC.025559						DQ630177		
Talpidae	<i>Mogera</i>	<i>wogura</i>	NC.005035	HG738058	HG738000	HG738020	HG738041	HG737959		AB638542	
	<i>Talpa</i>	<i>europaea/ *altaica</i>	NC.002391	HG738065*	HG738009	AY011629*	AY011752*	HG737968	JN414028*	JN413891*	AY011259*
	<i>Euroscaptor</i>	<i>mizura/</i>	AB106233	HG738051	HG737991	HG738012	HG738032	HG737949	DQ630168		

		<i>*parvidens</i>	DQ630336, AB076828 DQ630413								
	<i>Scalopus</i>	<i>aquaticus</i>	AF069539 AY170059 AB076809							AF496636	
	<i>Scapanulus</i>	<i>oweni</i>	NC.025777								
	<i>Condylura</i>	<i>cristata</i>	X	XM.004675316	AY011508	AY011630	AY011753	AY011199	XM.004686059	XM.004686125	XM.004686868
	<i>Galemys</i>	<i>pyrenaicus</i>	NC.008156	AY833412		AY833411	AY833416	AY833418		AY121767	AY833413
	<i>Urotrichus</i>	<i>talpoides</i>	AB099483								
	<i>Uropsilus</i>	<i>gracilis</i>	NC.018598		KF778096	KF778144	KF778255	KF777913	DQ630199	AY121768	
<i>Outgroups:</i>											
Manidae	<i>Manis</i>	<i>pentadactyla</i>	NC.016008	AY011374	EF104992	AY011684	AY011807	AY011251	JN413999	JN413856	AY011311
Felidae	<i>Felis</i>	<i>catus</i>	NC.001700	AY011369	AY011553	AY011679	AY011802	AY011246	XM.003984468	XM.006930331	AY011306
Canidae	<i>Canis</i>	<i>lupus</i>	KF857179	GU167668	NM.001287063	GU167419	AY011805	NM.001003178	XM.005630596	XM.005642442	NM.001003234
Delphinidae	<i>Tursiops</i>	<i>truncatus</i>	NC.012059	AY011360	JQ002729	AY011670	AY011793	AY011237	JN413972	XM.004311473	AY011297
Bovidae	<i>Bos</i>	<i>taurus</i>	GU947019	NM.001076796		XM.005214245	NM.001166510	NM.001104611	XM.002691511	NM.001206628	NM.174231
Suidae	<i>Sus</i>	<i>scrofa</i>	NC.012095	AY011364	NM.001285971	AY011674	AY011797	AY011241	XM.001501679	NM.001037148	AY011301
Equidae	<i>Equus</i>	<i>caballus</i>	NC.001640	AY011366	XM.005606891	AY011676	AY011799	AY011243	JN414029	NM.001164012	AY011303
Vespertilionidae	<i>Myotis</i>	<i>davidii</i>	KF111724	XM.006758757	XM.006759928	XM.006774616	XM.006758082		XM.006767541	XM.006761143	XM.006766218
Pteropodidae	<i>Pteropus</i>	<i>alecto/ *giganteus</i>	NC.023122	XM.006908243	XM.006907001	XM.006911376	XM.006921597	XM.006919638	XM.006910423	XM.006909438	XM.006906373
Elephantidae	<i>Loxodonta</i>	<i>africana</i>	NC.000934	AY011326	AY011513	AY011635	AY011758	AY011204	JN413956	JN413853	AY011264

Table S4. Evolutionary models chosen for each gene in the alignment using Partitionfinder.

Gene partition	Model
Mitochondrial genome	
rrnS, trnC, trnF, trnL2, trnM, trnN, trnQ, trnR, trnS2, trnY	GTR + G
rrnL, trnD, trnH, trnI, trnK, trnL1, trnT, trnV, trnW	GTR + G
atp6, cob, nad1, nad3, nad4, trnA	GTR + G + I
atp8, nad2, nad4l, nad5, trnP	GTR + G
cox1, cox2, cox3, trnG	GTR + G + I
Nuclear genes	
ADORA3, ATP7A, GHR, VWF, BMI1, EDG1	GTR + G
CREM, APP, BRCA1, TTN	K80 + G
ADRB2, BDNF, RAG1, RAG2, BCHE	GTR + I

Table S5. Fossil constraints and priors used in divergence date analysis.

Root	Node	Fossil and deposit locality	Age (My)	Prior distribution
1	Laurasiatheria	Minimum: Earliest carnivoramorphan (<i>Protictis</i> from Fort Union/ Polecat Bench Formation)	Basal Torrejonian (To1) – Barremian	logNormalPrior mean="16.02" stdev="1.0" offset="62.5"
		Soft maximum: offset="62.5" Liaoning fossils of <i>Eomaia</i> and <i>Sinodelphys</i> (Theria)	62.5 – 131.5	
2	Laurasiatheria minus Eulipotyphla	<i>As above</i>	<i>As above</i>	<i>As above</i>
3	Ferungulata	<i>As above</i>	<i>As above</i>	<i>As above</i>
4	Erinaceidae/Soricidae	Minimum: Oldest erinaceomorph (<i>Adunator</i> from Torrejonian)	Early Danian – Barremian	logNormalPrior mean="16.25" stdev="1.0" offset="61.5"
		Soft maximum: <i>As above</i>	61.5 – 131.5	
5	Carnivora	Minimum: <i>Hesperocyon</i> from earliest Duchesnean	Earliest Duchesnean – Early Paleocene, 39.68 – 65.8	logNormalPrior mean="6.067" stdev="1.0" offset="39.68"
		Soft maximum: Oldest stem carnivorans in Torrejonian		
6	Cetartiodactyla	Minimum: <i>Himalayacetus</i> from base of Subathu Formation	Early Eocene – Early Paleocene, 52.4 – 65.8	logNormalPrior mean="3.111" stdev="1.0" Soft maximum: offset="52.4"
		Soft maximum: absence of crown Cetartiodactyla in Paleocene		
7	Chiroptera	Minimum: <i>Icaronycteris</i>	48.6 – 65.8	logNormalPrior mean="3.995" stdev="1.0" offset="48.6"
		Soft maximum: as for other members of Laurasiatheria		

Table S6. Eulipotyphlan species used in pairwise genetic distance analysis.

Species	Genetic distance ID	Species	Genetic distance ID
<i>Mogera imaizumii</i>	M1	<i>Neomys anomalus</i>	Neo1
<i>Mogera wogura</i>	M2	<i>Neomys teres</i>	Neo2
<i>Mogera insularis</i>	M3	<i>Neomys fodiens</i>	Neo3
<i>Mogera tokudae</i>	M4	<i>Suncus etruscus</i>	Su1
<i>Euroscaptor klossi</i>	Eu1	<i>Suncus murinus</i>	Su2
<i>Euroscaptor malayana</i>	Eu2	<i>Suncus montanus</i>	Su3
<i>Euroscaptor longirostris</i>	Eu3	<i>Suncus fellowesgordoni</i>	Su4
<i>Euroscaptor mizura</i>	Eu4	<i>Suncus varilla</i>	Su5
<i>Euroscaptor parvidens</i>	Eu5	<i>Suncus remyi</i>	Su6
<i>Euroscaptor subanura</i>	Eu6	<i>Suncus dayi</i>	Su7
<i>Talpa stankovici</i>	T1	<i>Suncus stoliczkanus</i>	Su8
<i>Talpa europaea</i>	T2	<i>Nesophontes paramicrus</i>	Nes1
<i>Talpa altaica</i>	T3	<i>Nesophontes zamicros</i>	Nes2
<i>Talpa caucasica</i>	T4	<i>Atelerix albiventris</i>	A1
<i>Talpa davidiana</i>	T5	<i>Atelerix algirus</i>	A2
<i>Uropsilus gracilis</i>	U1	<i>Atelerix frontalis</i>	A3
<i>Uropsilus nivatus</i>	U2	<i>Erinaceus concolor</i>	Er1
<i>Uropsilus soricipes</i>	U3	<i>Erinaceus amurensis</i>	Er2
<i>Uropsilus atronates</i>	U4	<i>Erinaceus europaeus</i>	Er3
<i>Uropsilus investigator</i>	U5	<i>Erinaceus roumanicus</i>	Er4
<i>Uropsilus aequodonenia</i>	U6	<i>Anourosorex squamipes</i>	An1
<i>Episoriculus caudatus</i>	Ep1	<i>Anourosorex yamashinai</i>	An2
<i>Episoriculus leucops</i>	Ep2	<i>Blarinella griselda</i>	B1
<i>Episoriculus macrurus</i>	Ep3	<i>Blarinella quadratacauda</i>	B2
<i>Episoriculus fumidus</i>	Ep4	<i>Blarinella wardi</i>	B3

Table S7. Pairwise distances for eulipotyphlan sister species pairs in the mitochondrial *cyt b* gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

An1	An1			
An2	-			
	0.061			
B1	B1 B2			
B2	-			
B3	0.048	-		
	0.117	0.119		
Ep1	Ep1 Ep2			
Ep2	-			
Ep3	0.133	-		
	0.156	0.156		
Neo1	Neo1			
Neo3	-			
	0.146			
Su2	Su2			
Su8	-			
	0.086			
Eu1	Eu1 Eu2			
Eu2	-			
Eu4	0.084	-		
	0.134	0.125		
M1	M1 M2 M4			
M2	-			
M4	0.073	-		
M3	0.098	0.096	-	
	0.096	0.111	0.111	
T3	T3			
T2	-			
	0.137			
Nes1	Nes1			
Nes2	-			
	0.022			
U1	U1 U2 U6 U4			
U2	-			
U6	0.025	-		
U4	0.102	0.103	-	
U3	0.138	0.132	0.142	-
	0.126	0.124	0.121	0.096
A1	A1			
A3	-			
	0.125			
Er3	Er3 Er4 Er2			
Er4	-			
Er2	0.003	-		
Er1	0.109	0.110	-	
	0.128	0.129	0.131	

Table S8. Pairwise distances for eulipotyphlan sister species pairs in the mitochondrial 12S gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

	M1	M2	M3	
M1	-			
M2	0.025	-		
M3	0.032	0.034	-	
M4	0.027	0.034	0.029	
	Eu1	Eu2	Eu3	
Eu1	-			
Eu2	0.022	-		
Eu3	0.027	0.022	-	
Eu4	0.059	0.053	0.055	
	T1			
T1	-			
T2	0.095			
	U1	U2	U3	U4
U1	-			
U2	0.000	-		
U3	0.033	0.033	-	
U4	0.039	0.039	0.043	-
U5	0.032	0.032	0.037	0.042
	Ep1	Ep2	Ep4	
Ep1	-			
Ep2	0.039	-		
Ep3	0.063	0.057	-	
Ep4	0.080	0.072	0.071	
	Neo1	Neo2		
Neo1	-			
Neo2	0.035	-		
Neo3	0.053	0.045		
	Su1			
Su1	-			
Su2	0.071			
	Nes1			
Nes1	-			
Nes2	0.053			
	A1			
A1	-			
A2	0.023			

Table S9. Pairwise distances for eulipotyphlan sister species pairs in the CREM (cAMP responsive element modulator) protein-coding nuclear gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

	T2			
T2		-		
T3		0.000		
	M2		M1	
M2		-		
M1		0.003		-
M3		0.000	0.003	
	Eu2		Eu3	Eu5
Eu2		-		
Eu3		0.000		-
Eu5		0.003	0.003	
Eu4		0.005	0.005	0.003
	Nes1			
Nes1		-		
Nes2		0.022		

Table S10. Pairwise distances for eulipotyphlan sister species pairs in the BRCA1 (Breast Cancer 1) protein-coding nuclear gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

	T2				
T2	-				
T4	0.004				
	M2				
M2	-				
M3	0.013				
	A3		A1		
A3	-				
A1	0.002	-			
A2	0.008	0.008			
	Er3		Er2		
Er3	-				
Er2	0.005	-			
Er4	0.005	0.005			
	Su5		Su6	Su2	Su7
Su5	-				
Su6	0.038	-			
Su2	0.072	0.088	-		
Su7	0.074	0.079	0.031	-	
Su1	0.075	0.082	0.056	0.058	
	Nes2				
Nes2	-				
Nes1	0.004				

Table S11. Pairwise distances for eulipotyphlan sister species pairs in the RAG1 (recombination activating gene 1) protein-coding nuclear gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

	T4	T3	T2
T4	-		
T3	0.018	-	
T2	0.022	0.021	-
T5	0.022	0.022	0.024
	M2	M1	M4
M2	-		
M1	0.003	-	
M4	0.008	0.005	-
M3	0.016	0.015	0.016
	Eu4	Eu2	
Eu4	-		
Eu2	0.012	-	
Eu6	0.019	0.019	
	U1		
U1	-		
U4	0.007		
	Su2	Su3	Su4
Su2	-		
Su3	0.005	-	
Su4	0.035	0.036	-
Su1	0.032	0.032	0.016
	Nes2		
Nes2	-		
Nes1	0.001		
	Er3	Er2	
Er3	-		
Er2	0.003	-	
Er4	0.004	0.001	
	A2	A1	
A2	-		
A1	0.002	-	
A3	0.006	0.007	

Table S12. Pairwise distances for eulipotyphlan sister species pairs in the BDNF (brain derived neurotrophic factor) protein-coding nuclear gene, showing number of base differences per site between sequences. Analysis involved 29 nucleotide sequences. All ambiguous positions were removed for each sequence pair. The final dataset contained 1009 positions. Evolutionary analyses conducted in MEGA7.

	Su3	Su4	Su1
Su3	-		
Su4	0.000	-	
Su1	0.000	0.000	-
Su2	0.000	0.000	0.000
	T2	T3	
T2	-		
T3	0.006	-	
	Eu2	Eu3	Eu4
Eu2	-		
Eu3	0.006	-	
Eu5	0.010	0.008	-
Eu4	0.015	0.014	0.010
	M2	M1	
M2	-		
M1	0.000	-	
M3	0.006	0.006	
	Nes2		
Nes2	-		
Nes1	0.006		
	Er1		
Er1	-		
Er2	0.002		