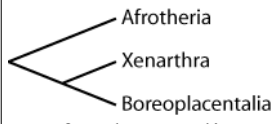
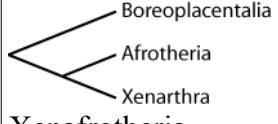
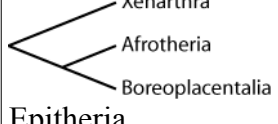
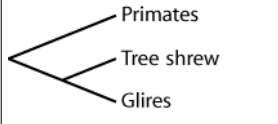
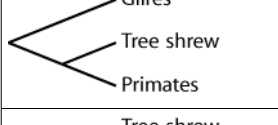
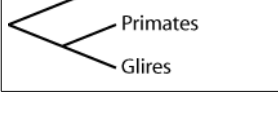


Supplemental Table 1 – ML test statistics (pSH) for all alternative relationships among Afrotheria, Xenarthra, and Boreoplacentalia.

Tree	pSH aa	pSH NT12	pSH NT123
 <p>Exafroplacentalia</p>	1.000	1.000	1.000
 <p>Xenafrotheria</p>	0.586	0.437	0.606
 <p>Epitheria</p>	0.223	0.154	0.581

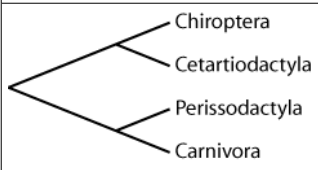
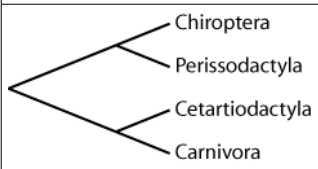
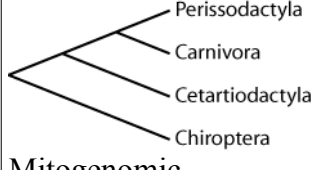
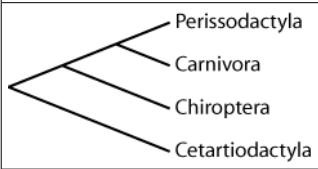
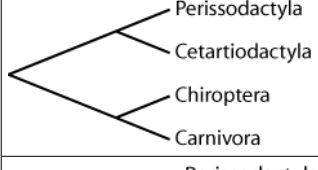
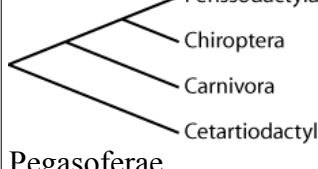
Note – NT12 and NT123 indicate analyses on first and second and all three codon positions, respectively. Bold figures indicate pSH values that do not allow significant rejection of a hypothesis.

Supplemental Table 2. – ML test statistics (pSH) for all alternative relationships of the tree shrew (Scandentia).

Tree	pSH aa	pSH NT12	pSH NT123
	1.000	1.000	1.000
	0.090	0.144	<0.001
	0	0	0

Note – NT12 and NT123 indicate analyses on first and second and all three codon positions, respectively. Bold figures indicate pSH values that do not allow significant rejection of a hypothesis.

Supplemental Table 3. – ML test statistics (pSH) for alternative relationships within Laurasiaplacentalia. Only pSHs > 0.05 are shown.

Tree	pSH aa	pSH NT12	pSH NT123
 <p>ML tree</p>	1.000	1.000	1.000
	0.422	0.224	0.546
 <p>Mitogenomic</p>	0.347	0.359	0.350
	0.011	0.049	0.558
	0.004	0.015	0.067
 <p>Pegasoferae</p>	<0.001	<0.001	0.067

Note – NT12 and NT123 indicate analyses on first and second and all three codon positions, respectively. Bold figures indicate pSH values that do not allow significant rejection of a hypothesis.

Supplemental Table 4 – Computer simulation of number of aa sequence sites needed to significantly resolve the relationship between Xenarthra, Boreoplacentalia, and Afrotheria and increasingly shorter branch lengths.

Branch length	Time interval (Ma)	Without gaps	With gaps
Observed	2.7	7,000	12,500
1/2	1.4	15,000	25,000
1/3	0.90	35,000	45,000
1/4	0.68	45,000	75,000
1/5	0.54	60,000	105,000

Note – the length of the Xenarthra plus Boreoplacentalia branch (figure 2) was reduced to 1/2, 1/3, 1/4, and 1/5th of the observed length. The corresponding time interval was calculated according to the branch length.