Table 5. Mitochondrial amino acid sequences (mtREV + Γ model)

	Tree topology	ΔlnL(± SE)	PP	BP	AU	KH	WSH
1	(Eul,(((Chi,(Per,Car)),Cetart),Out)	-23.8(± 8.8)	5e-11	0	7e-07	0.005	0.063
2	(Eul,(Chi,(Cetart,(Per,Car))),Out)	<-44796.2>	0.962	0.395	0.822	0.629	0.992
3	(Eul,(Chi,((Cetart,Per),Car)),Out)	-3.2(± 9.4)	0.037	0.232	0.595	0.371	0.925
4	(Eul,((Chi,Cetart),(Per,Car)),Out)	-16.1(± 10.7)	1e-07	0.021	0.173	0.065	0.477
5	(Eul,((Chi,Car),(Cetart,Per)),Out)	-20.7(± 14.3)	1e-09	0.008	0.069	0.075	0.323
6	(Eul,(((Chi,(Cetart,Car)),Per),Out)	-26.7(± 14.8)	3e-12	4e-04	0.029	0.036	0.359
7	(Eul,(((Chi,(Cetart,Per)),Car),Out)	-24.4(± 13.7)	2e-11	2e-04	0.007	0.039	0.123
8	(Eul,((((Chi,Car),Cetart),Per),Out)	-21.8(± 15.6)	3e-10	0.025	0.175	0.082	0.537
9	(Eul,((((Chi,Cetart),Per),Car),Out)	-21.8(± 14.0)	3e-10	0.011	0.131	0.066	0.477
10	(Eul,(((Chi,Per),(Cetart,Car)),Out)	-35.2(± 12.6)	5e-16	0	0.003	0.004	0.074
11	(Eul,((((Chi,Cetart),Car),Per),Out)	-20.3(± 15.1)	2e-09	0.032	0.216	0.091	0.566
12	(Eul,((((Chi,Car),Per),Cetart),Out)	-30.7(± 13.0)	5e-14	0	0.001	0.013	0.161
13	(Eul,((((Chi,Per),Car),Cetart),Out)	-36.4(± 12.1)	2e-16	0	4e-04	0.002	0.046
14	(Eul,((((Chi,Per),Cetart),Car),Out)	-32.4(± 13.4)	8e-15	0	0.024	0.01	0.11
15	(Eul,(Chi,(((Cetart,Car),Per)),Out)	-10.8(± 7.1)	2e-05	0.005	0.087	0.073	0.48
53	(Eul,Chi,(Out,(Cetart,(Per,Car))))	-7.2(± 11.4)	0.001	0.147	0.467	0.265	0.846
44	(Eul,Chi,(Out,((Cetart,Per),Car)))	-10.3(± 14.7)	3e-05	0.085	0.342	0.242	0.833
59	(Eul,Chi,(((Out,Per),Car),Cetart))	-27.8(± 20.7)	8e-13	0.029	0.17	0.09	0.556
25	(Eul,Chi,((Out,Per),(Cetart,Car)))	-33.8(± 20.7)	2e-15	0.002	0.063	0.052	0.412

Differences in log-likelihood scores of alternative trees from the highest likelihood tree [and their SEs calculated by the Kishino and Hasegawa (1) formula in parentheses] are given. The log-likelihood of the highest likelihood tree is shown in brackets. PP, Bayesian posterior probability; BP, RELL bootstrap probability (2); AU, *P* values of the approximately unbiased test (3); KH, Kishino and Hasegawa test (1); WSH, weighted Shimodaira and Hasegawa test (4); Eul, Eulipotyphla; Chi, Chiroptera; Car, Carnivora; Cetart, Cetartiodactyla; and Per, Perissodactyla. Tests were done with the CONSEL program (5). Among the 105 possible trees, only 15 are shown, including the Eulipotyphla basal tree and others having *P* > 0.05 (from the AU test).

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