Table 4. The nucleotide sequences of Murphy *et al*. (1) (including gaps and missing sites) (GTR + Γ model)

	Tree topology	ΔlnL(± SE)	PP	BP	AU	KH	WSH
1	(Eul,(((Chi,(Per,Car)),Cetart),Out)	-3.0(± 8.1)	0.019	0.048	0.398	0.351	0.883
2	(Eul,(Chi,(Cetart,(Per,Car))),Out)	-0.5(± 6.8)	0.221	0.187	0.705	0.462	0.964
3	(Eul,(Chi,((Cetart,Per),Car)),Out)	<-101887.3>	0.379	0.164	0.7	0.538	0.979
4	(Eul,(((Chi,Cetart),(Per,Car)),Out)	-3.2(± 8.0)	0.015	0.036	0.358	0.336	0.861
5	(Eul,(((Chi,Car),(Cetart,Per)),Out)	-0.6(± 3.9)	0.198	0.147	0.581	0.415	0.96
6	(Eul,(((Chi,(Cetart,Car)),Per),Out)	-8.1(± 7.0)	1e-04	0.007	0.112	0.127	0.704
7	(Eul,(((Chi,(Cetart,Per)),Car),Out)	-1.3(± 3.6)	0.102	0.071	0.483	0.325	0.941
8	(Eul,((((Chi,Car),Cetart),Per),Out)	-8.8(± 7.2)	6e-05	0.002	0.088	0.112	0.554
9	(Eul,((((Chi,Cetart),Per),Car),Out)	-9.2(± 6.7)	4e-05	1e-04	0.053	0.089	0.533
10	(Eul,(((Chi,Per),(Cetart,Car)),Out)	-2.4(± 8.3)	0.033	0.114	0.553	0.382	0.943
11	(Eul,((((Chi,Cetart),Car),Per),Out)	-9.8(± 7.1)	2e-05	5e-04	0.067	0.087	0.57
12	(Eul,((((Chi,Car),Per),Cetart),Out)	-7.9(± 7.4)	1e-04	0.003	0.063	0.141	0.662
13	(Eul,((((Chi,Per),Car),Cetart),Out)	-3.1(± 8.7)	0.016	0.066	0.445	0.356	0.93
14	(Eul,((((Chi,Per),Cetart),Car),Out)	-3.3(± 8.3)	0.014	0.055	0.463	0.345	0.935
15	(Eul,(Chi,((Cetart,Car),Per)),Out)	-6.2(± 5.1)	0.001	0.004	0.084	0.118	0.66
27	(Eul,Chi,(((Out,Car),(Cetart,Per)))	-15.8(± 12.4)	5e-08	0.026	0.235	0.102	0.611
53	(Eul,Chi,(Out,(Cetart,(Per,Car))))	-17.3(± 12.2)	1e-08	0.007	0.13	0.078	0.4
44	(Eul,Chi,(Out,((Cetart,Per),Car)))	-17.4(± 10.2)	1e-08	0.005	0.067	0.048	0.384
18	(Eul,(Chi,(Cetart,Per)),(Out,Car))	-18.4(± 10.7)	4e-09	0.001	0.079	0.046	0.377
20	(Eul,Chi,((Out,(Per,Car)),Cetart))	-19.1(± 14.1)	2e-09	0.008	0.188	0.088	0.499
71	(Eul,Chi,(((Out,Car),Cetart),Per))	-19.8(± 14.6)	1e-09	0.01	0.128	0.086	0.587
83	((Eul,Cetart),(Chi,Per),(Out,Car))	-20.1(± 14.9)	7e-10	0.011	0.157	0.085	0.541
74	(Eul,Chi,(((Out,Car),Per),Cetart))	-20.5(± 14.4)	5e-10	0.004	0.127	0.076	0.561
45	((Eul,Cetart),Chi,(Out,(Per,Car)))	-21.1(± 14.1)	3e-10	0.003	0.099	0.066	0.424
34	(Eul,((Chi,Per),Cetart),(Out,Car))	-21.1(± 13.5)	3e-10	0.001	0.055	0.061	0.344
26	((Eul,(Cetart,Per)),Chi,(Out,Car))	-21.4(± 11.7)	2e-10	4e-04	0.052	0.036	0.383
59	(Eul,Chi,(((Out,Per),Car),Cetart))	-22.2(± 14.4)	9e-11	0.007	0.136	0.064	0.5
54	((Eul,Cetart),(Chi,(Per,Car)),Out)	-22.2(± 13.4)	8e-11	0.001	0.059	0.052	0.315
101	((Eul,Cetart),Chi,((Out,Car),Per))	-23.2(± 14.7)	3e-11	0.002	0.063	0.055	0.489
25	(Eul,Chi,((Out,Per),(Cetart,Car)))	-24.1(± 13.8)	1e-11	0.001	0.054	0.042	0.411
42	((Eul,Cetart),Chi,((Out,Per),Car))	-24.7(± 14.7)	7e-12	0.003	0.08	0.048	0.429
103	(((Eul,Car),Per),Chi,(Out,Cetart))	-38.2(± 12.9)	9e-18	0	0.059	0.002	0.07

Differences in log-likelihood scores of alternative trees from the highest likelihood tree [and their SEs calculated by the Kishino and Hasegawa (2) 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 (3); AU, *P* values of the approximately unbiased test (4); KH, Kishino and Hasegawa test (2); WSH, weighted Shimodaira and Hasegawa test (5); Eul, Eulipotyphla; Chi, Chiroptera; Car, Carnivora; Cetart, Cetartiodactyla; and Per, Perissodactyla. Tests were done with the CONSEL program (6). Among the 105 possible trees, only 15 are shown, including the Eulipotyphla basal tree and others having *P* > 0.05 (from the AU test).

References

1. Murphy, W. J., Eizirik, E., O'Brien, S. J., Madsen, O., Scally, M., Douady, C. J., Teeling, E., Ryder, O. A., Stanhope, M. J., de Jong, W. W. & Springer, M. S. (2001) *Science* **294,** 2348-2351.
2. Kishino, H. & Hasegawa, M. (1989) *J. Mol. Evol.* **29,** 170-179.
3. Kishino, H., Miyata, T. & Hasegawa, M. (1990) *J. Mol. Evol.* **31,** 151-160.
4. Shimodaira, H. (2002) *Syst. Biol.* **51,** 492-508.
5. Shimodaira, H. & Hasegawa, M. (1999) *Mol. Biol. Evol.* **16,** 1114-1116.
6. Shimodaira, H. & Hasegawa, M. (2001) *Bioinformatics* **17,** 1246-1247.