

**Table 6.** Mitochondrial codon sequences (codon-substitution +  $\Gamma$  model)

Tree topology	$\Delta\ln L(\pm SE)$	PP	BP	AU	KH	WSH
1 (Eul,((Chi,(Per,Car)),Cetart),Out)	-23.4( $\pm$ 9.2)	7e-11	0	1e-04	0.011	0.045
2 (Eul,(Chi,(Cetart,(Per,Car))),Out)	<-118056.2>	0.971	0.533	0.804	0.671	0.961
3 (Eul,(Chi,((Cetart,Per),Car)),Out)	-3.5( $\pm$ 7.9)	0.029	0.291	0.507	0.329	0.746
4 (Eul,((Chi,Cetart),(Per,Car)),Out)	-12.8( $\pm$ 11.7)	3e-06	0.078	0.231	0.136	0.473
5 (Eul,((Chi,Car),(Cetart,Per)),Out)	-25.5( $\pm$ 13.6)	8e-12	0.002	0.016	0.034	0.087
6 (Eul,((Chi,(Cetart,Car)),Per),Out)	-29.3( $\pm$ 13.7)	2e-13	0.001	0.015	0.019	0.124
7 (Eul,((Chi,(Cetart,Per)),Car),Out)	-25.9( $\pm$ 13.6)	5e-12	0.001	0.007	0.031	0.082
8 (Eul,(((Chi,Car),Cetart),Per),Out)	-30.7( $\pm$ 14.1)	5e-14	0	0.009	0.017	0.118
9 (Eul,(((Chi,Cetart),Per),Car),Out)	-19.5( $\pm$ 14.6)	3e-09	0.021	0.105	0.093	0.378
10 (Eul,((Chi,Per),(Cetart,Car)),Out)	-33.3( $\pm$ 12.8)	3e-15	0	2e-06	0.007	0.052
11 (Eul,(((Chi,Cetart),Car),Per),Out)	-18.0( $\pm$ 15.0)	1e-08	0.048	0.158	0.112	0.431
12 (Eul,(((Chi,Car),Per),Cetart),Out)	-35.0( $\pm$ 12.6)	6e-16	0	1e-04	0.005	0.039
13 (Eul,(((Chi,Per),Car),Cetart),Out)	-36.4( $\pm$ 12.3)	1e-16	0	2e-04	0.003	0.028
14 (Eul,(((Chi,Per),Cetart),Car),Out)	-34.5( $\pm$ 13.4)	1e-15	0	4e-05	0.007	0.059
15 (Eul,(Chi,((Cetart,Car),Per)),Out)	-8.1( $\pm$ 6.4)	3e-04	0.026	0.127	0.105	0.391

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). With the codon-substitution model, Eulipotyphla was assumed to be basal in Laurasiatheria because of the heavy computational burden (only the 15 trees were examined).

## References

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