**Table 3**. The nucleotide sequences of Murphy *et al*. (1) (excluding gaps and missing sites) (GTR + Γ model)

| | Tree topology | ΔlnL(± SE) | PP | BP | AU | KH | WSH |
|---|---|---|---|---|---|---|---|
| 1 | (Eul,(((Chi,(Per,Car)),Cetart),Out) | <-65312.6> | 0.452 | 0.252 | 0.786 | 0.594 | 0.988 |
| 2 | (Eul,(Chi,(Cetart,(Per,Car))),Out) | -0.5(± 2.2) | 0.275 | 0.167 | 0.652 | 0.406 | 0.94 |
| 3 | (Eul,(Chi,((Cetart,Per),Car)),Out) | -7.1(± 6.4) | 4e-04 | 0.003 | 0.115 | 0.138 | 0.711 |
| 4 | (Eul,(((Chi,Cetart),(Per,Car)),Out) | -0.6(± 2.2) | 0.256 | 0.156 | 0.643 | 0.391 | 0.938 |
| 5 | (Eul,(((Chi,Car),(Cetart,Per)),Out) | -4.3(± 7.2) | 0.006 | 0.109 | 0.493 | 0.272 | 0.861 |
| 6 | (Eul,(((Chi,(Cetart,Car)),Per),Out) | -8.6(± 6.3) | 9e-05 | 0.003 | 0.09 | 0.09 | 0.595 |
| 7 | (Eul,(((Chi,(Cetart,Per)),Car),Out) | -6.2(± 6.7) | 0.001 | 0.023 | 0.269 | 0.177 | 0.781 |
| 8 | (Eul,(((Chi,Car),Cetart),Per),Out) | -6.2(± 6.9) | 0.001 | 0.032 | 0.284 | 0.19 | 0.765 |
| 9 | (Eul,(((Chi,Cetart),Per),Car),Out) | -7.7(± 6.2) | 2e-04 | 0.005 | 0.15 | 0.111 | 0.648 |
| 10 | (Eul,(((Chi,Per),(Cetart,Car)),Out) | -6.6(± 6.4) | 0.001 | 0.011 | 0.222 | 0.156 | 0.749 |
| 11 | (Eul,((((Chi,Cetart),Car),Per),Out) | -8.3(± 6.2) | 1e-04 | 0.002 | 0.074 | 0.091 | 0.595 |
| 12 | (Eul,((((Chi,Car),Per),Cetart),Out) | -4.8(± 6.0) | 0.004 | 0.05 | 0.358 | 0.208 | 0.801 |
| 13 | (Eul,((((Chi,Per),Car),Cetart),Out) | -5.6(± 5.8) | 0.002 | 0.032 | 0.311 | 0.171 | 0.751 |
| 14 | (Eul,((((Chi,Per),Cetart),Car),Out) | -5.6(± 6.7) | 0.002 | 0.058 | 0.406 | 0.2 | 0.806 |
| 15 | (Eul,(Chi,((Cetart,Car),Per)),Out) | -9.1(± 5.9) | 5e-05 | 0 | 0.02 | 0.068 | 0.477 |
| 45 | ((Eul,Cetart),Chi,(Out,(Per,Car))) | -15.0(± 11.0) | 1e-07 | 0.029 | 0.219 | 0.088 | 0.535 |
| 54 | ((Eul,Cetart),(Chi,(Per,Car)),Out) | -15.2(± 9.6) | 1e-07 | 0.01 | 0.151 | 0.059 | 0.419 |
| 20 | (Eul,Chi,((Out,(Per,Car)),Cetart)) | -16.0(± 11.0) | 5e-08 | 0.022 | 0.172 | 0.074 | 0.481 |
| 53 | (Eul,Chi,(Out,(Cetart,(Per,Car)))) | -18.7(± 10.4) | 3e-09 | 0.002 | 0.081 | 0.04 | 0.338 |
| 37 | ((Eul,Cetart),((Chi,Car),Per),Out) | -19.1(± 11.2) | 2e-09 | 0.004 | 0.07 | 0.046 | 0.374 |
| 21 | (Eul,Chi,((Out,Cetart),(Per,Car))) | -19.2(± 10.5) | 2e-09 | 0.001 | 0.074 | 0.036 | 0.34 |
| 101 | ((Eul,Cetart),Chi,((Out,Car),Per)) | -20.3(± 12.7) | 7e-10 | 0.006 | 0.142 | 0.059 | 0.465 |
| 76 | ((Eul,Cetart),((Chi,Per),Car),Out) | -20.4(± 11.2) | 6e-10 | 0.001 | 0.05 | 0.037 | 0.337 |
| 83 | ((Eul,Cetart),(Chi,Per),(Out,Car)) | -21.1(± 12.7) | 3e-10 | 0.007 | 0.129 | 0.052 | 0.44 |
| 74 | (Eul,Chi,(((Out,Car),Per),Cetart)) | -21.7(± 12.9) | 2e-10 | 0.005 | 0.1 | 0.051 | 0.409 |
| 42 | ((Eul,Cetart),Chi,((Out,Per),Car)) | -22.1(± 12.5) | 1e-10 | 0.001 | 0.075 | 0.042 | 0.394 |
| 71 | (Eul,Chi,(((Out,Car),Cetart),Per)) | -23.8(± 13.0) | 2e-11 | 0.002 | 0.061 | 0.039 | 0.354 |
| 86 | (Eul,(Chi,Per),((Out,Car),Cetart)) | -26.2(± 12.4) | 2e-12 | 6e-05 | 0.054 | 0.022 | 0.263 |

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).

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