Supporting Information

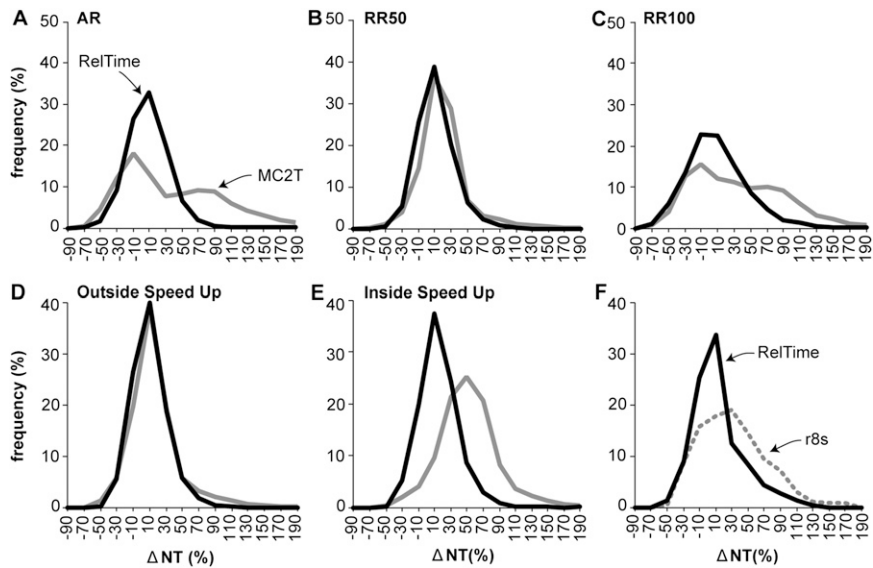## Tamura et al. 10.1073/pnas.1213199109

Fig. S1. Distributions of the normalized differences between estimated and true node times for internal nodes (NTs). (*A–C*) Comparisons of RelTime (black curve) and MC2T (gray curve) performances for datasets simulated with autocorrelated (AR) and random rates (RR50, RR100). Relative performances of MC2T and RelTime for estimating times outside (*D*) and inside (*E*) the speed-up clades. (*F*) Comparison of the accuracy of RelTime (black solid) and r8s (gray dotted) for RR100 and RR50+50 datasets.
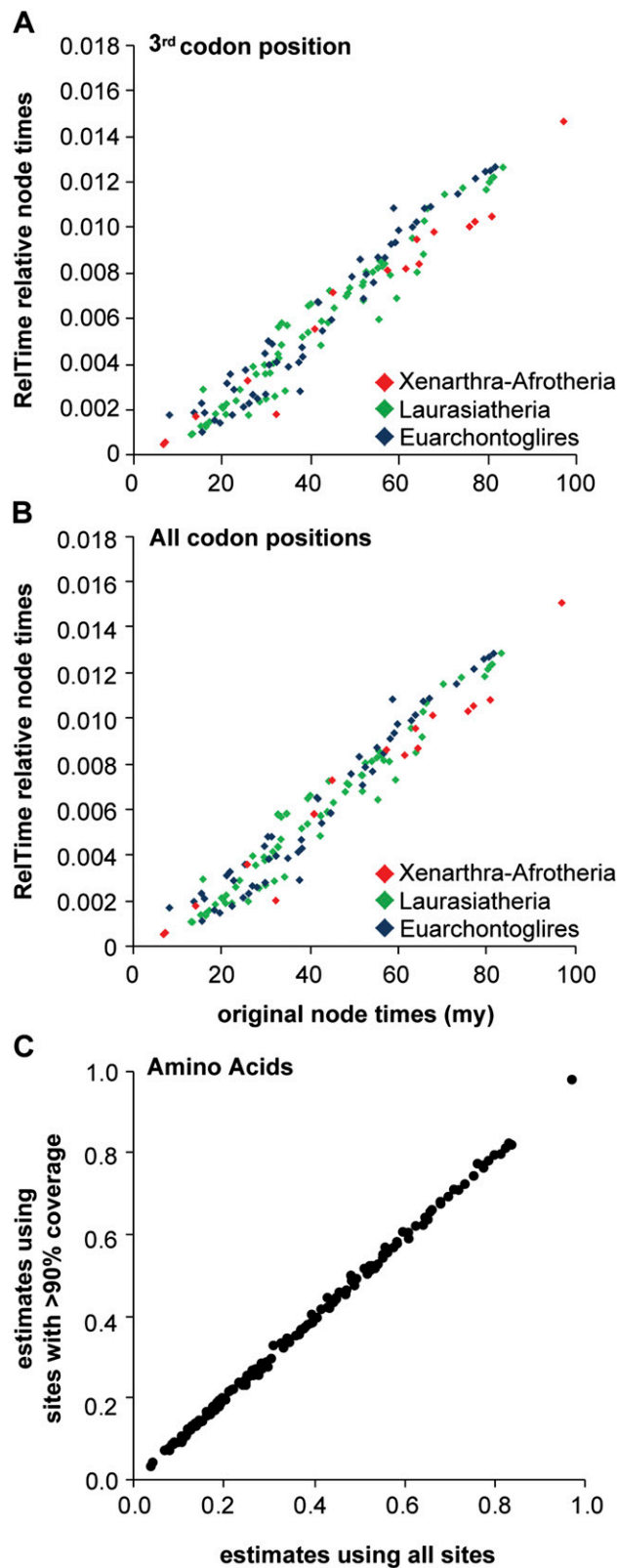
Fig. S2. (*A* and *B*) Comparisons of node times in RelTime (*y* axis) and MC2T (*x* axis) for placental mammals. Estimates were obtained by using data from third codon positions (*A*) and all codon (*B*) positions at the DNA sequence level for the DNA sequence data, which were analyzed under a GTR+Γ model. (*C*) A comparison of relative times obtained by using all amino acid positions (*x* axis) and excluding positions containing missing data or alignment gaps in greater than 10% positions (90% coverage; *y* axis), which removes 34% positions from the sequence alignment.

Table S1. Time estimates and ranges for major groups of placental mammals in millions of years, My

Taxon	Amino acids		Third codon positions		All codon positions	
	Mean	Range	Mean	Range	Mean	Range
Placentalia	114.4	99.1–133.1	115.2	92.0–142.8	114.0	95.8–135.7
Xenarthra	75.3	65.2–87.6	75.2	60.1–93.3	75.2	63.2–89.5
Afrotheria	80.8	70.0–94.0	80.4	64.2–99.7	80.2	67.4–95.5
Afrosoricida	66.4	57.6–77.3	72.7	58.1–90.1	70.9	59.6–84.5
Macroscelidea	51.1	44.3–59.4	54.8	43.8–68.0	54.0	45.4–64.3
Paenungulata	64.1	55.5–74.5	64.4	51.5–79.9	64.5	54.2–76.7
Hyracoidea	4.2	3.6–4.8	3.8	3.0–4.7	4.0	3.3–4.7
Proboscidea	4.6	4.0–5.4	4.5	3.6–5.6	4.5	3.8–5.4
Sirenia	16.0	13.9–18.6	13.9	11.1–17.2	15.0	12.6–17.8
Boreoeutheria	105.1	91.1–122.3	106.9	85.4–132.6	105.1	88.3–125.1
Laurasiatheria	91.1	78.9–106.0	93.6	74.8–116.1	91.8	77.2–109.3
Eulipotyphla	85.9	74.4–99.9	90.0	71.9–111.6	87.6	73.6–104.2
Chiroptera	74.3	64.3–86.4	78.8	63.0–97.8	76.4	64.2–91.0
Perissodactyla	60.1	52.0–69.9	60.7	48.5–75.3	60.2	50.6–71.6
Pholidota	29.8	25.8–34.7	29.9	23.9–37.1	29.5	24.8–35.1
Carnivora	59.6	51.6–69.3	64.5	51.6–80.0	60.5	50.9–72.1
Cetartiodactyla	67.9	58.8–79.0	67.7	54.1–83.9	68.2	57.3–81.1
Euarchontoglires	95.5	82.7–111.0	97.0	77.5–120.3	95.4	80.1–113.5
Primatomorpha	92.7	80.3–107.8	95.4	76.3–118.4	93.6	78.6–111.4
Primates	83.6	72.5–97.3	88.0	70.3–109.1	85.4	71.8–101.7
Dermoptera	12.0	10.4–13.9	13.7	10.9–16.9	12.6	10.6–15.0
Scandentia	60.9	52.7–70.8	66.5	53.2–82.5	62.9	52.8–74.8
Glires	88.4	76.6–102.8	93.1	74.4–115.5	90.3	75.9–107.5
Rodentia	79.4	68.8–92.4	83.6	66.8–103.7	80.7	67.8–96.1
Lagomorpha	51.1	44.2–59.4	60.1	48.0–74.6	56.1	47.2–66.8

The RelTime estimates from amino acid analysis were converted into absolute times by using three calibrations: Perissodactyla (58.3 My), Whippomorpha (56.8 My), and Castorimorpha (56.8 My), where each calibrating time is the mean of upper and lower bound of time constraints in Meredith et al. (1). The mean divergence time and the range are obtained by using results from these three calibrations individually.

1. Meredith RW, et al. (2011) Impacts of the Cretaceous Terrestrial Revolution and KPg extinction on mammal diversification. *Science* 334(6055):521–524.