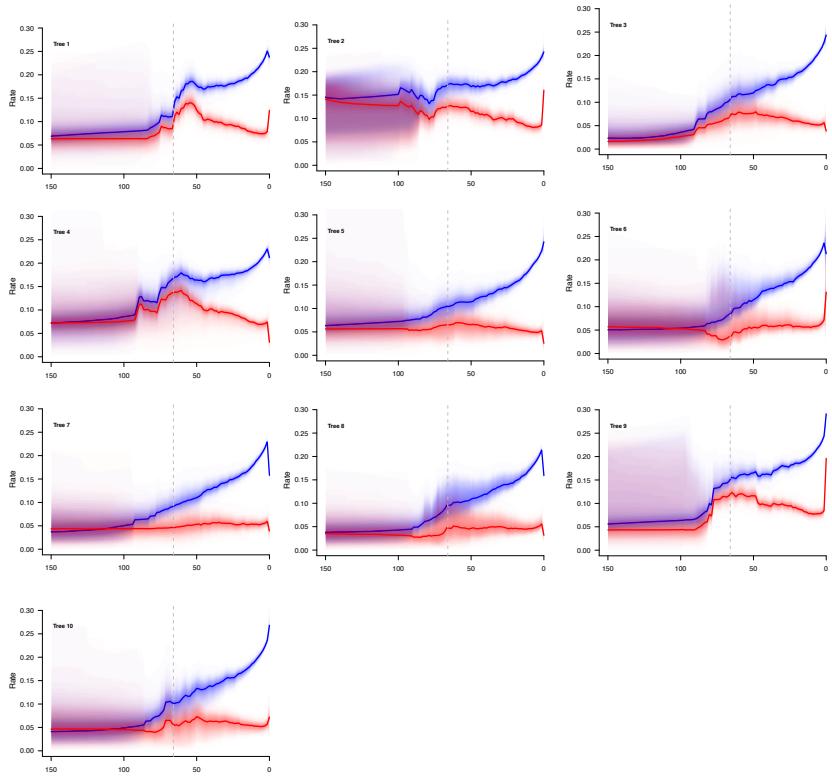
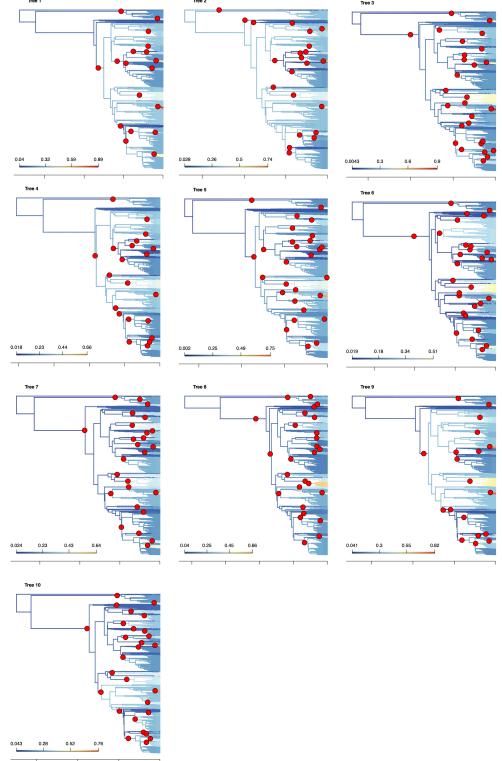


### A Lineage-specific rates through time (BAMM)

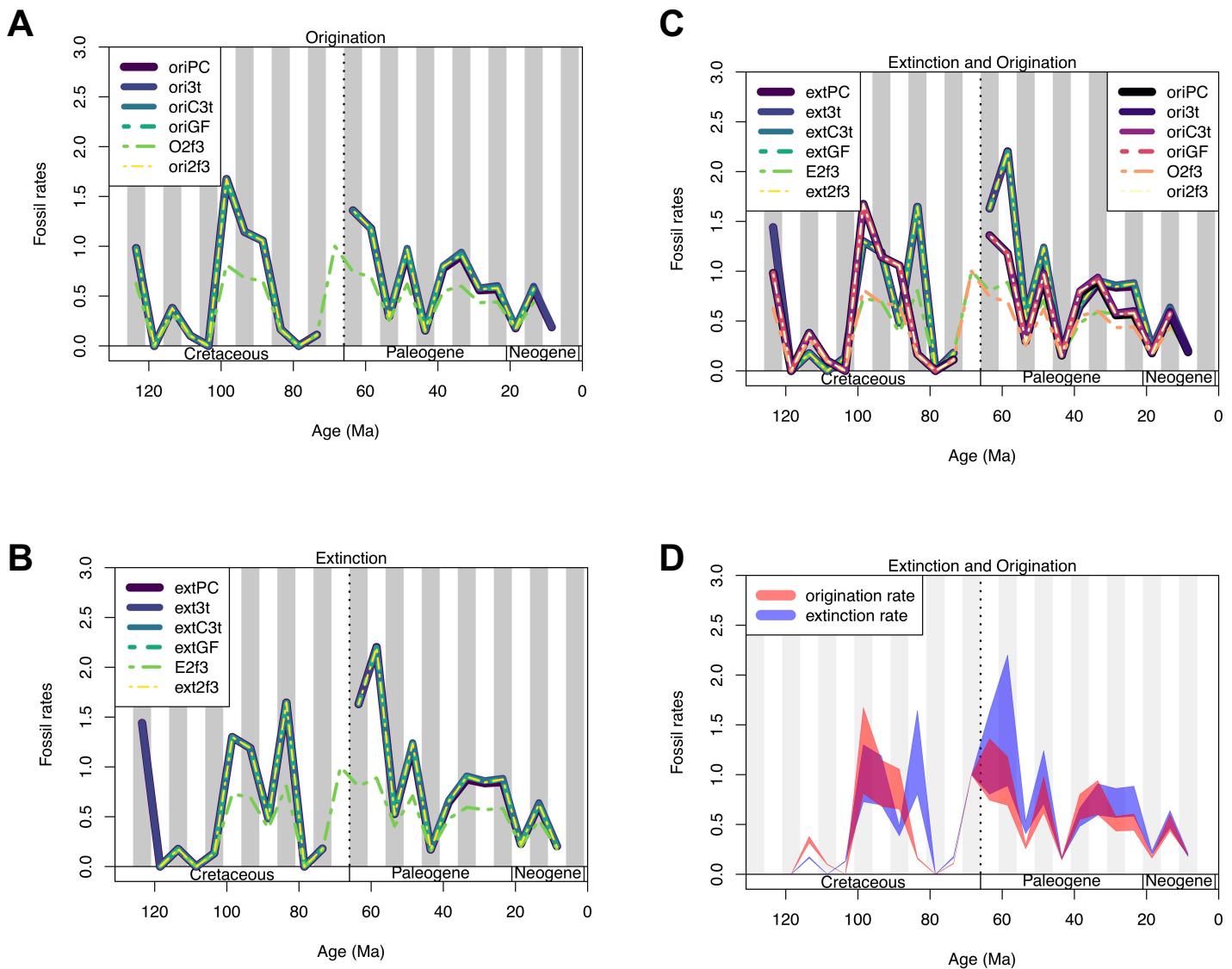


### B Lineage-specific rate shifts (BAMM)

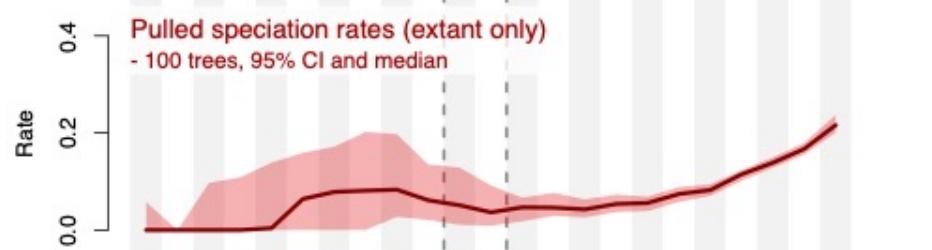
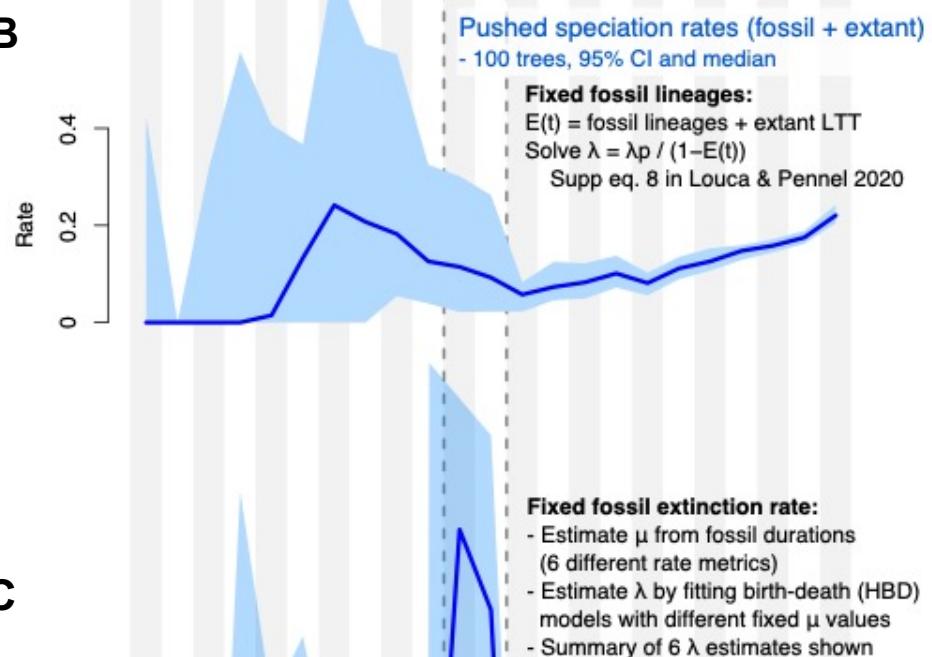
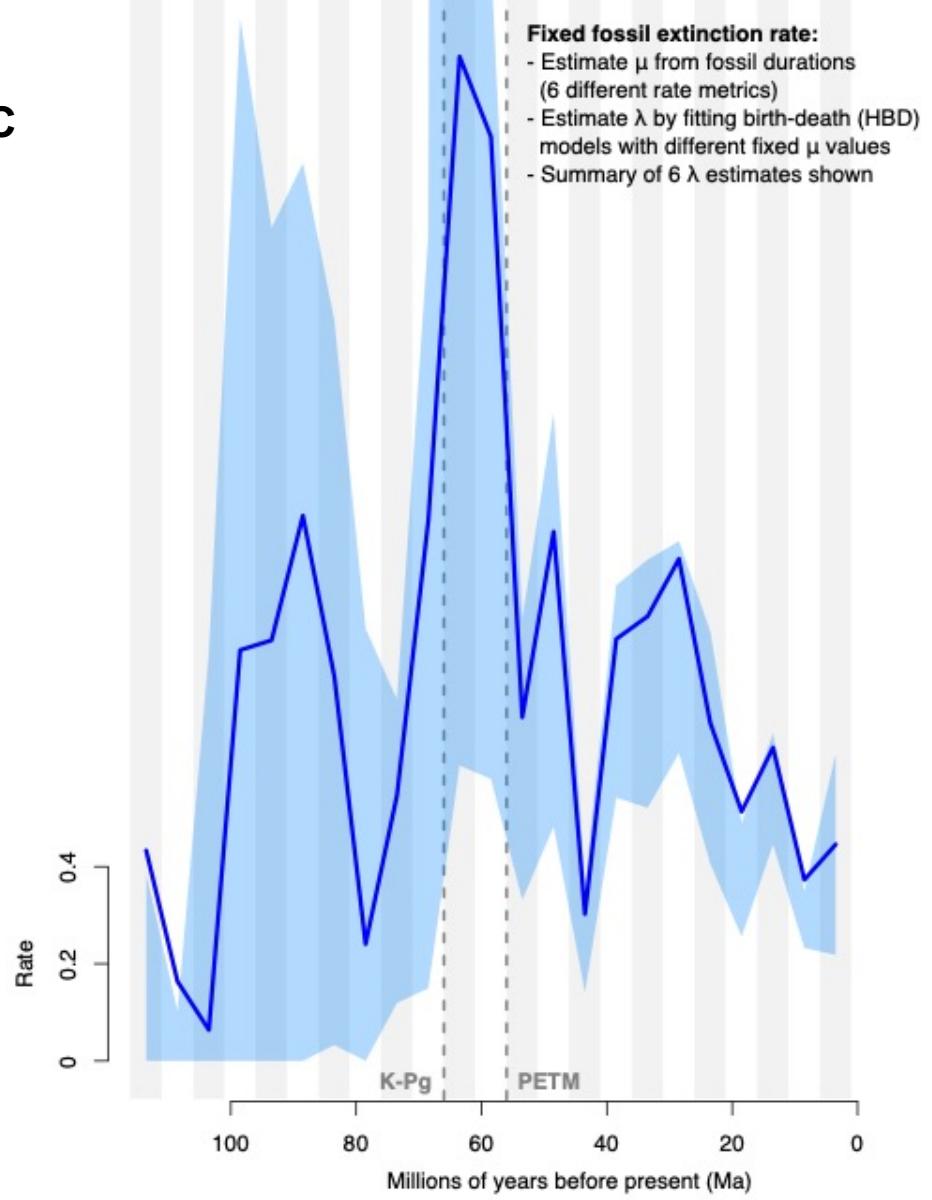


**Figure S1. Details of the branch-specific rate shifts in Mammalia, Related to Figures 1, 3B, 4A.**

Results from analyses on 10 trees relative to the Cretaceous-Paleogene boundary (K-Pg, ~66 Ma; vertical dotted lines): (A) BAMM models showing reconstructed speciation (blue) and extinction (red) rates through time (medians and 95% confidence intervals of the rates from 1,000 event data samples; Figure 4a upper panel shows the same data overlaid across 10 trees); and (B) placement of BAMM maximum shift credibility rate-shift sets from each tree (red dots) on the background of different rate regimes (branch colors, hotter colors are faster rates; time scale in intervals of 50 Ma; trees differ in root age but are ladderized for comparison to Figure 1 in the main text; Figure 4a lower panel shows the same data as tick marks).



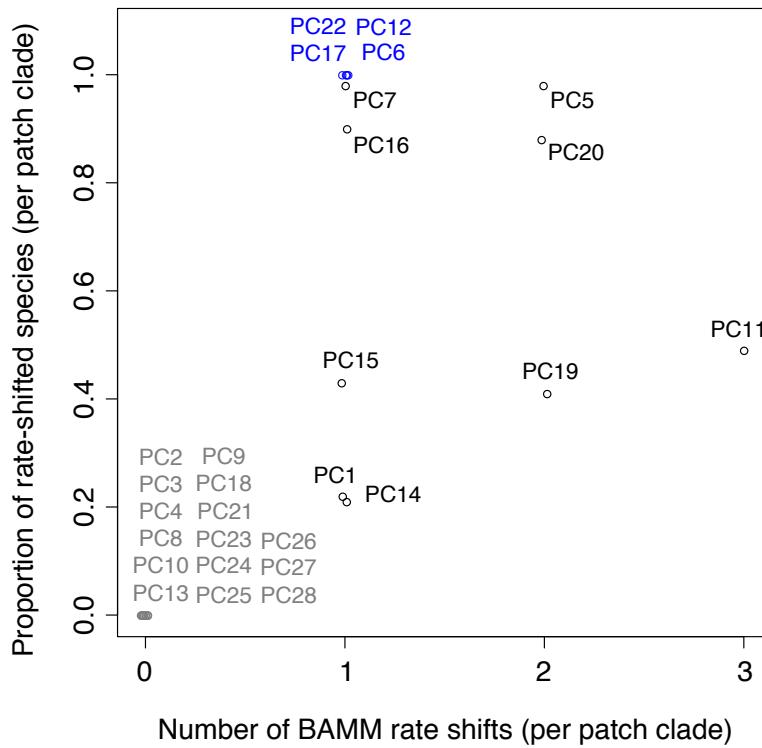
**Figure S2. Comparing the 6 different rate metrics for calculating rates from fossil durations, Related to Figures 2B, 4B.** Shown across the 5-million-year bins are the (A) origination rates separately plotted; (B) extinction rates separately plotted; (C) all rates overlaid separately; and (D) minimum and maximum values of the 6 metrics used to construct a confidence interval of origination and extinction values through time. This same confidence interval is plotted in Figure 2b of the main text. All metrics were calculated in the ‘divDyn’ R Package (Kocsis et al. 2019) with rate names as follows: oriPC, extPC: per capita rates of Foote (2000); ori3t, ext3t: three-timer rates of Alroy (2008); oriC3t, extC3t: corrected three-timer rates of Alroy (2008); oriGF, extGF: gap-filler rates of Alroy (2014); O2f3, E2f3: second-for-third proportions of Alroy (2015); ori2f3, ext2f3: second-for-third rates (based on Alroy, 2015).

**A****B****C**

**Figure S3. Comparing two methods of ‘pushing’ the pulled rates of speciation, Related to Figure 4B.** (A) The pulled rates of speciation,  $\lambda_p$ , are compared to (B) a pushed-rate method based on fixing the total lineages through time,  $\lambda_{\text{fixedE}(t)}$ , and (C) a pushed-rate method based on fixing the extinction rate through time,  $\lambda_{\text{fixedMu}(t)}$ . This shows that  $\lambda_{\text{fixedE}(t)}$  are of larger magnitude than  $\lambda_p$  but follow a similar pattern of peak rates ca. 85 Ma, followed by a decline after the Cretaceous-Paleogene boundary (K-Pg) and Paleocene-Eocene Thermal Maximum (PETM; dashed gray lines). In contrast,  $\lambda_{\text{fixedMu}(t)}$  shows a different pattern of peak speciation rates from ca. 66–56 Ma after the K-Pg and before the PETM, during which time fossil extinction rates were also elevated, indicating high lineage turnover. Rates here are shown on a linear scale rather than the log scale displayed in Figure 4b, for easier comparison across rate calculations. The upper 95%  $\lambda_{\text{fixedMu}(t)}$  confidence value is truncated in the 66–61 Ma bin for display purposes (see Table S4 for complete values of all bins through time).

**A**

		Clade richness	B	D	E	F	G	H	J	L	M	N	O	P	Q	R	T	V	W	X	Unshifted species	# Shifts
PC1	Marsupialia	362	78	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	284	78%	1
PC2	Afrotheria	92	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	92	100%	0
PC3	Xenarthra	33	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	33	100%	0
PC4	Scandentia	20	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	20	100%	0
PC5	Primates	458	.	.	.	.	.	.	.	.	313	135	.	.	.	.	.	.	.	10	2%	2
PC6	Lagomorpha	91	.	.	.	.	.	.	.	.	.	.	91	.	.	.	.	.	.	0	0%	1
PC7	Castorimorpha	109	.	.	.	.	.	.	.	.	.	.	.	.	.	107	.	.	.	2	2%	1
PC8	Dipodidae	51	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	51	100%	0
PC9	Spalacidae	21	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	21	100%	0
PC10	Nesomyidae	63	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	63	100%	0
PC11	Muridae	779	.	.	.	.	.	.	.	.	.	.	.	.	.	.	196	104	80	399	51%	3
PC12	Cricetidae	726	.	.	.	.	.	.	.	.	.	.	.	.	.	726	.	.	.	0	0%	1
PC13	Squirrel-related	320	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	320	100%	0	
PC14	Guinea pig-related	304	.	.	.	.	.	.	.	.	.	.	65	.	.	.	.	.	239	79%	1	
PC15	Eulipotyphla	491	.	.	.	.	.	.	.	213	.	.	.	.	.	.	.	.	278	57%	1	
PC16	Noctilionoidea	227	.	.	.	.	205	.	.	.	.	.	.	.	.	.	.	.	22	10%	1	
PC17	Vespertilioidea	605	.	.	.	605	.	.	.	.	.	.	.	.	.	.	.	.	0	0%	1	
PC18	Emballonuroidea	70	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	70	100%	0		
PC19	Yinpterochiroptera	385	.	.	.	.	.	69	87	.	.	.	.	.	.	.	.	.	229	59%	2	
PC20	Artiodactyla	348	.	215	91	.	.	.	.	.	.	.	.	.	.	.	.	.	42	12%	2	
PC21	Perissodactyla	24	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	24	100%	0	
PC22	Carnivora	298	298	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	0	0%	1	
PC23	Monotremata	5	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	5	100%	0	
PC24	Pholidota	8	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	8	100%	0	
PC25	Dermoptera	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2	100%	0	
PC26	Anomaluromorphia	9	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	9	100%	0	
PC27	Calomyscidae	8	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	8	100%	0	
PC28	Platacanthomyidae	2	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	2	100%	0	

**B**

**Figure S4. Membership in phylogenetic patch clades vs. BAMM rate-shifted clades, Related to STAR Methods.** The overall location of rate shifts present in  $\geq 5$  of 10 trees analyzed appears unrelated to the patch clade delimitations used in the construction of the mammal phylogeny (Upham et al. 2019). **(A)** Summary of patch clades PC1-28 relative to the contained species in rate-shifted clades B-X (letters correspond to Figure 1 and Table S2). Out of 28 patch clades, we find that 15 do not contain any tipward rate shift (grey), 9 contain one or more shift for a subset of patch clade species (white), and 4 have all species contained in a rate shift (blue). **(B)** Plot of the 18 shifts most tipward in a given lineage (e.g., shift C is Placentalia and not shown) shows substantial variation in number of rate shifts per patch clade, indicating that patch clade delimitations are not by themselves causing rate heterogeneity to be detected in the mammal phylogeny.

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