

# Reconstructing the history of variation in effective population size along phylogenies.

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**Running head:** A phylogenetic history of  $N_e$

Table S1. Correlation coefficients between  $dS$ ,  $dN/dS$ ,  $\pi_S$ ,  $\pi_N/\pi_S$ , life-history traits and  $N_e$  under a uniform prior over divergence times.

	$dS$	$dN/dS$	Maturity	Mass	Longevity	$\pi_S$	$\pi_N/\pi_S$	Gen. time	$N_e$
$dS$		0.27	-0.33	-0.57**	-0.20	-0.63*	0.51	-0.38	-0.78**
$dN/dS$			0.16	0.10	0.50*	-0.49	0.42	0.43	-0.57*
Maturity				0.61**	0.53**	0.04	0.10	0.65**	-0.01
Mass					0.52**	0.35	-0.18	0.64**	0.30
Longevity						-0.23	0.25	0.87**	-0.30
$\pi_S$							-0.79**	-0.02	0.91**
$\pi_N/\pi_S$								0.09	-0.74**
Gen. time									-0.13

Asterisks indicate strength of support (\*\*:  $pp > 0.975$ , \*:  $pp > 0.95$ )

Table S2. Estimates of mutation rate per year  $r$  and per generation  $u$  (posterior median and 96% credible interval), for extant and ancestral species, under a uniform prior over divergence times.

species	$r$ (per $10^9$ years)		$u$ (per $10^8$ generation)		pedigrees <sup>c</sup>
	without anc. pol. <sup>a</sup>	with anc. pol. <sup>b</sup>	without anc. pol. <sup>a</sup>	with anc. pol. <sup>b</sup>	
<i>Homo</i>	0.79 ( 0.59, 1.11)	0.65 ( 0.48, 0.90)	2.29 ( 1.70, 3.21)	1.90 ( 1.38, 2.61)	1.23 - 1.29
<i>Pan</i>	0.75 ( 0.61, 0.90)	0.63 ( 0.50, 0.76)	1.79 ( 1.48, 2.15)	1.51 ( 1.21, 1.83)	1.26 - 1.48
<i>Gorilla</i>	0.76 ( 0.43, 1.19)	0.54 ( 0.29, 0.90)	1.44 ( 0.82, 2.27)	1.03 ( 0.56, 1.70)	1.13
<i>Pongo</i>	0.86 ( 0.54, 1.23)	0.73 ( 0.45, 1.06)	2.14 ( 1.36, 3.08)	1.83 ( 1.12, 2.65)	1.66
<i>Homo - Pan</i>	0.70 ( 0.50, 0.98)	0.60 ( 0.41, 0.85)	1.68 ( 1.25, 2.22)	1.43 ( 1.03, 1.91)	
<i>Homo - Gorilla</i>	0.73 ( 0.51, 1.03)	0.66 ( 0.46, 0.95)	1.65 ( 1.23, 2.17)	1.46 ( 1.07, 1.96)	
<i>Homo - Pongo</i>	0.78 ( 0.49, 1.20)	0.71 ( 0.43, 1.12)	1.61 ( 1.11, 2.25)	1.44 ( 0.94, 2.07)	
Hominoidea	0.71 ( 0.42, 1.15)	0.67 ( 0.39, 1.08)	1.31 ( 0.85, 1.94)	1.20 ( 0.77, 1.75)	
<i>Macaca</i>	0.62 ( 0.48, 0.77)	0.53 ( 0.40, 0.68)	0.87 ( 0.68, 1.08)	0.74 ( 0.56, 0.95)	0.37
<i>Papio</i>	0.91 ( 0.50, 1.69)	0.70 ( 0.37, 1.30)	1.24 ( 0.73, 1.98)	0.97 ( 0.54, 1.58)	0.55
Cercopithecidae	1.06 ( 0.71, 1.59)	1.00 ( 0.66, 1.56)	1.22 ( 0.90, 1.67)	1.13 ( 0.80, 1.61)	
Catarrhini	0.87 ( 0.52, 1.42)	0.91 ( 0.54, 1.60)	1.18 ( 0.78, 1.73)	1.20 ( 0.76, 1.86)	
<i>Aotus</i>	0.96 ( 0.52, 1.67)	0.91 ( 0.46, 1.61)	1.03 ( 0.58, 1.65)	0.96 ( 0.50, 1.56)	0.81
Platyrrhini	1.49 ( 1.01, 2.21)	1.43 ( 0.93, 2.18)	1.56 ( 1.14, 2.15)	1.50 ( 1.06, 2.12)	
Simiiformes	1.53 ( 0.87, 2.76)	1.66 ( 0.88, 3.10)	1.56 ( 1.03, 2.46)	1.70 ( 1.08, 2.72)	
Haplorrhini	2.77 ( 1.33, 5.76)	2.97 ( 1.44, 6.46)	1.78 ( 1.03, 3.09)	2.05 ( 1.16, 3.68)	
Lorisiformes	2.18 ( 1.25, 3.85)	2.28 ( 1.26, 4.22)	1.21 ( 0.80, 1.86)	1.29 ( 0.80, 2.11)	
Lemuriformes	1.22 ( 0.70, 2.12)	1.31 ( 0.72, 2.39)	1.11 ( 0.72, 1.73)	1.16 ( 0.73, 1.86)	
Strepsirrhini	3.42 ( 1.64, 7.04)	3.80 ( 1.81, 8.45)	1.98 ( 1.16, 3.48)	2.33 ( 1.32, 4.34)	
Primates	3.04 ( 1.47, 6.39)	3.22 ( 1.54, 7.08)	1.86 ( 1.09, 3.29)	2.10 ( 1.18, 3.86)	

<sup>a</sup> naive-phylogenetic method (not accounting for ancestral polymorphism); <sup>b</sup> mean-coalescent method (accounting for ancestral polymorphism); <sup>c</sup> from Table 1 of Wu et al (2019)

Table S3. Estimates of effective population size ( $\times 10^{-3}$ , posterior median and 95% credible interval) for extant taxa and ancestors, under a uniform prior over divergence times.

species	mechanistic	mech. w/o anc. pol.	phenomenological	uncoupled	coal. <sup>a</sup>	hmmcoal <sup>b</sup>
<i>Homo</i>	23 ( 17, 32)	19 ( 14, 26)	19 ( 12, 35)	21 ( 13, 35)	(13, 16)	8
<i>Pan</i>	69 ( 57, 86)	58 ( 48, 70)	72 ( 45, 114)	61 ( 39, 103)	(31, 62)	30
<i>Gorilla</i>	69 ( 24, 184)	67 ( 26, 177)	102 ( 34, 334)	48 ( 20, 117)	(28, 57)	21
<i>Pongo</i>	42 ( 14, 113)	37 ( 13, 93)	50 ( 19, 125)	32 ( 10, 106)	(42, 85)	19
<i>Homo-Pan</i>	46 ( 28, 74)	45 ( 28, 72)	49 ( 29, 88)	40 ( 24, 65)	(10, 47)	50
<i>Homo-Gorilla</i>	47 ( 26, 78)	47 ( 28, 80)	53 ( 29, 98)	41 ( 24, 71)	(27, 61)	47
Hominidae	53 ( 26, 106)	45 ( 23, 86)	53 ( 27, 111)	48 ( 22, 105)		
Hominoidea	62 ( 30, 131)	57 ( 29, 112)	70 ( 34, 159)	58 ( 25, 137)		
Cercopithecidae	67 ( 35, 125)	74 ( 42, 128)	79 ( 41, 156)	73 ( 37, 152)		
Catarrhini	74 ( 35, 156)	73 ( 38, 145)	69 ( 33, 155)	58 ( 26, 131)		
Platyrrhini	42 ( 21, 83)	37 ( 20, 71)	32 ( 16, 61)	31 ( 13, 75)		
Simiiformes	60 ( 26, 138)	56 ( 27, 124)	37 ( 15, 87)	36 ( 14, 90)		
<i>Tarsius</i>	536 ( 99, 4855)	407 ( 88, 2558)	107 ( 22, 561)	56 ( 5, 599)		
Haplorrhini	92 ( 37, 239)	83 ( 36, 207)	32 ( 9, 97)	34 ( 11, 103)		
Lorisiformes	125 ( 58, 279)	124 ( 61, 286)	46 ( 14, 120)	49 ( 20, 121)		
Lemuriformes	94 ( 41, 202)	90 ( 41, 187)	89 ( 34, 218)	123 ( 51, 310)		
<i>Daubentonia</i>	1251 ( 208, 11831)	1296 ( 237, 8859)	1030 ( 181, 8983)	443 ( 56, 3733)		
Strepsirrhini	91 ( 35, 246)	82 ( 34, 214)	27 ( 7, 91)	33 ( 12, 92)		
Primates	93 ( 35, 240)	80 ( 34, 201)	29 ( 7, 94)	32 ( 11, 97)		

<sup>a</sup> from Prado-Martinez et al, 2013, table 1, for extant hominids, and from Rannala and Yang, 2003 for ancestral species; <sup>b</sup> from Prado-Martinez et al, 2013, figure 2

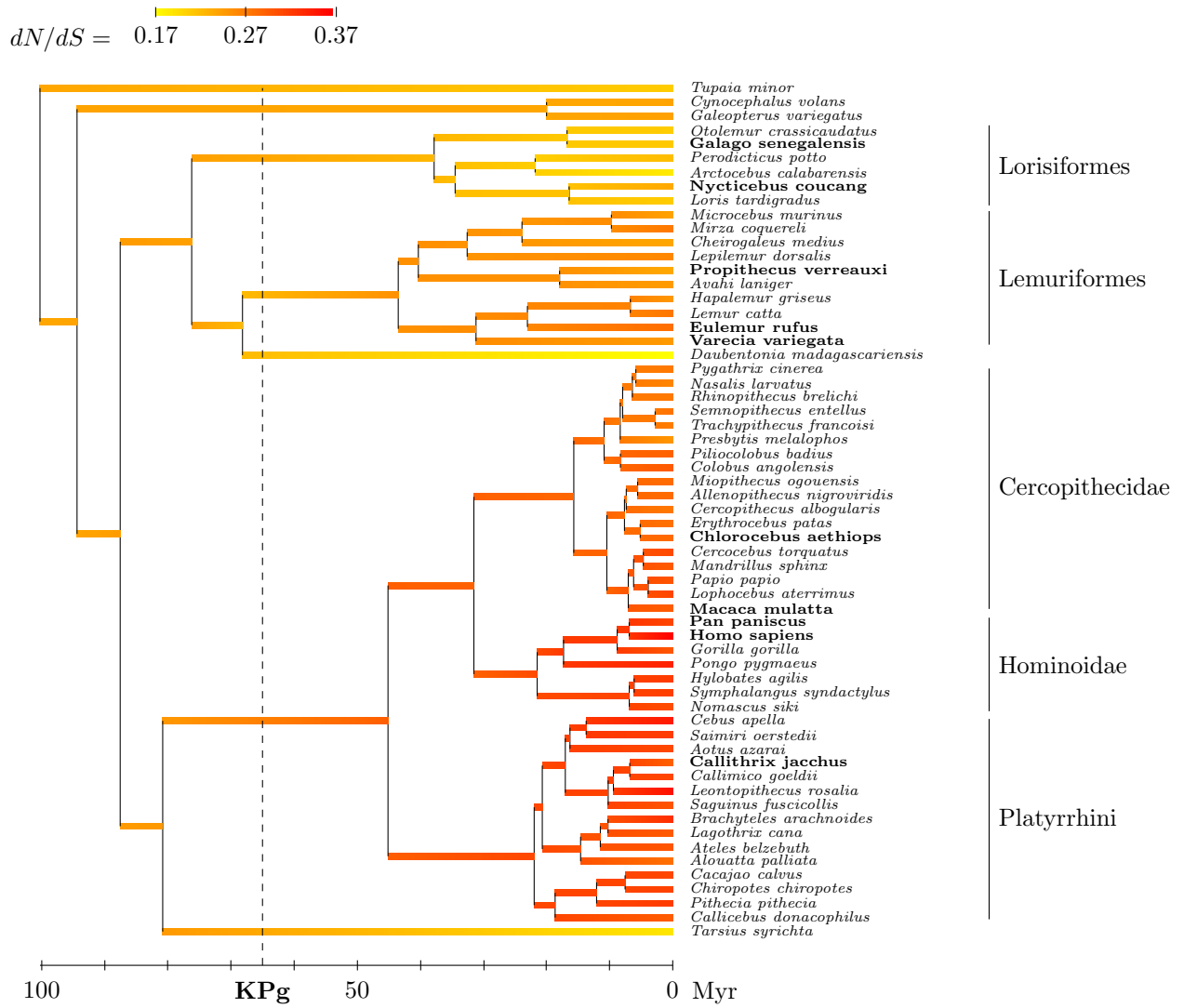


Figure S1. Reconstructed phylogenetic history of  $dN/dS$  (posterior median estimate) under the phenomenological model.

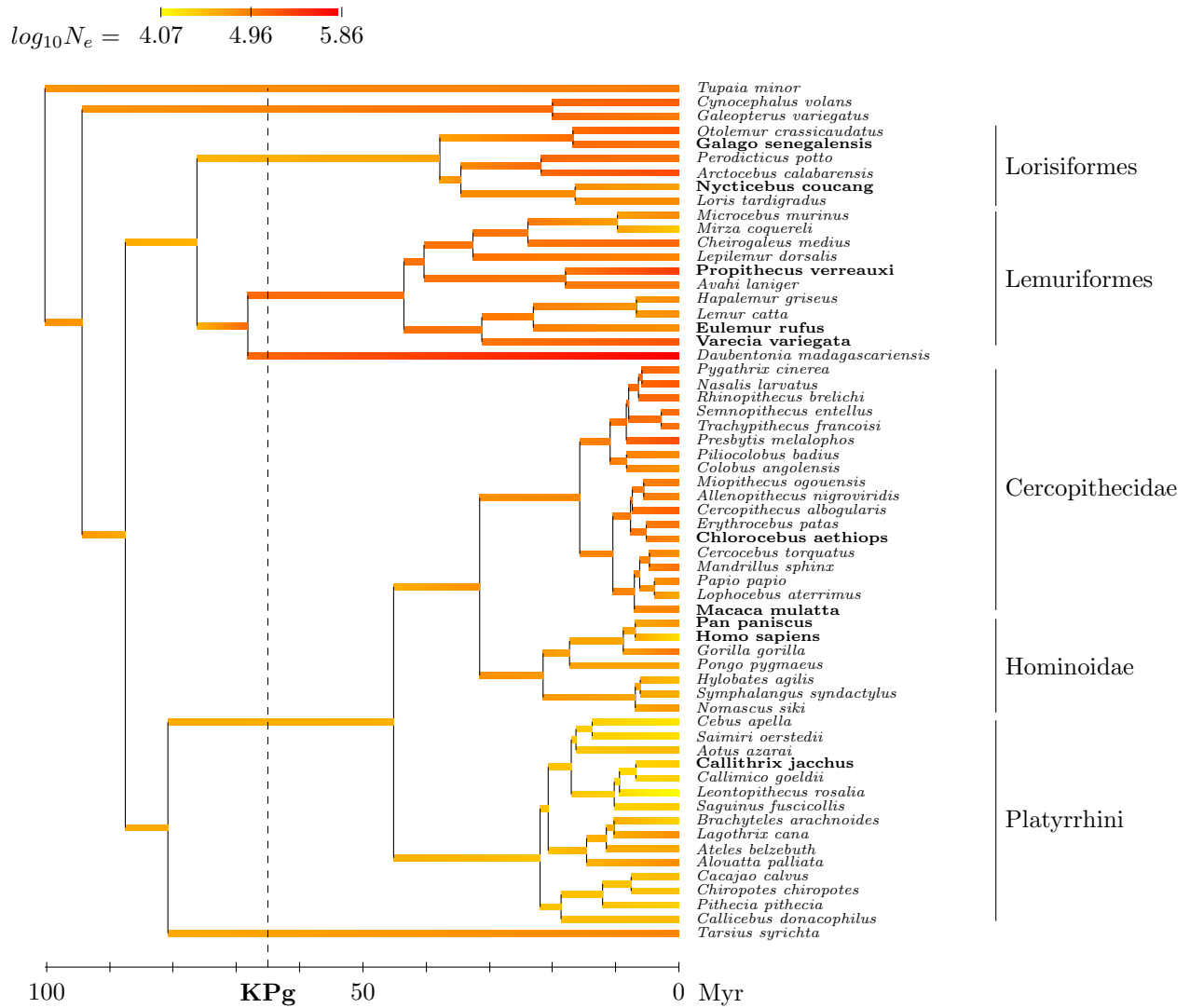


Figure S2. Reconstructed phylogenetic history of  $N_e$  (posterior median estimate) under the phenomenological model.

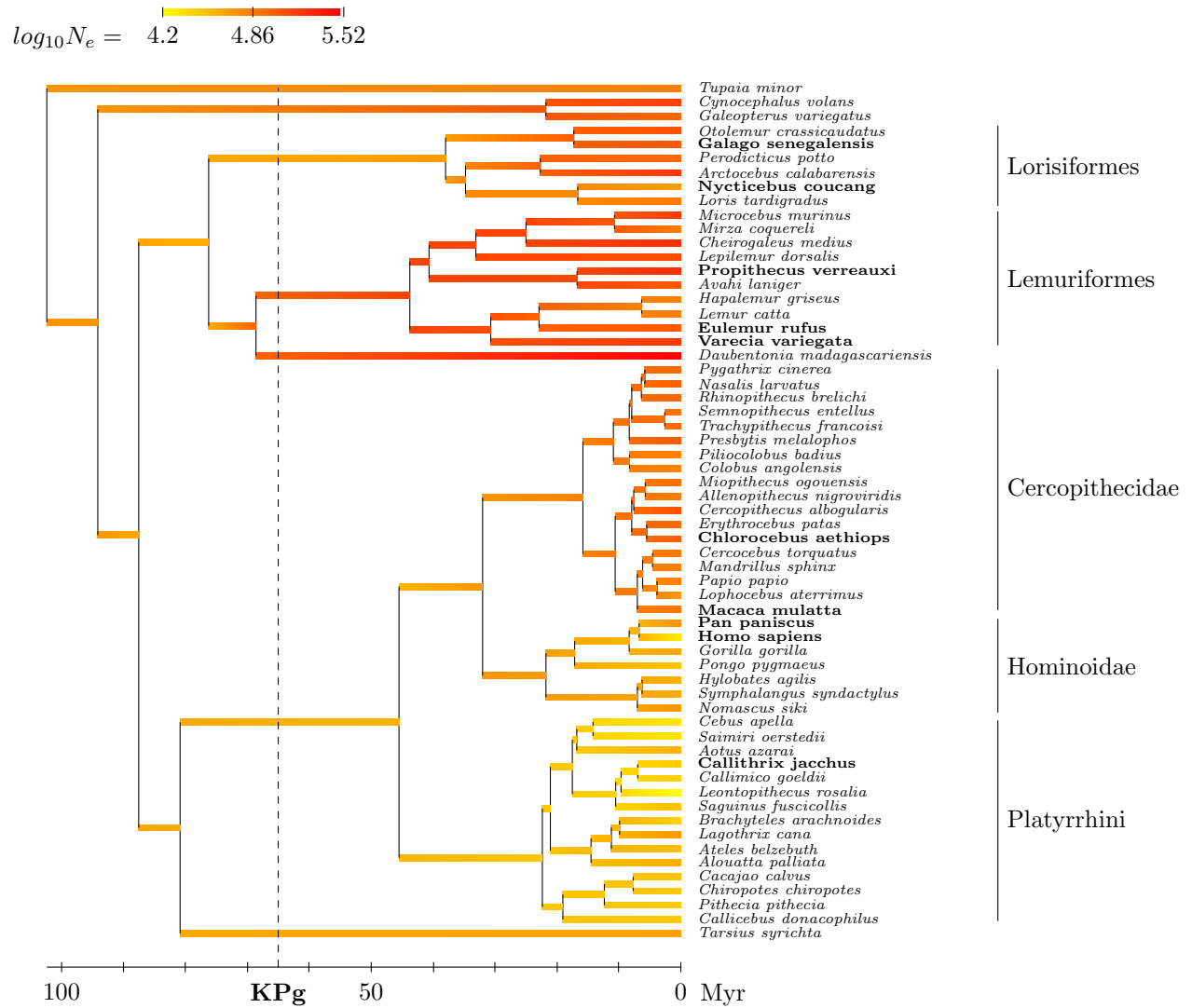


Figure S3. Reconstructed phylogenetic history of  $N_e$  (posterior median estimate) under the uncoupled model.

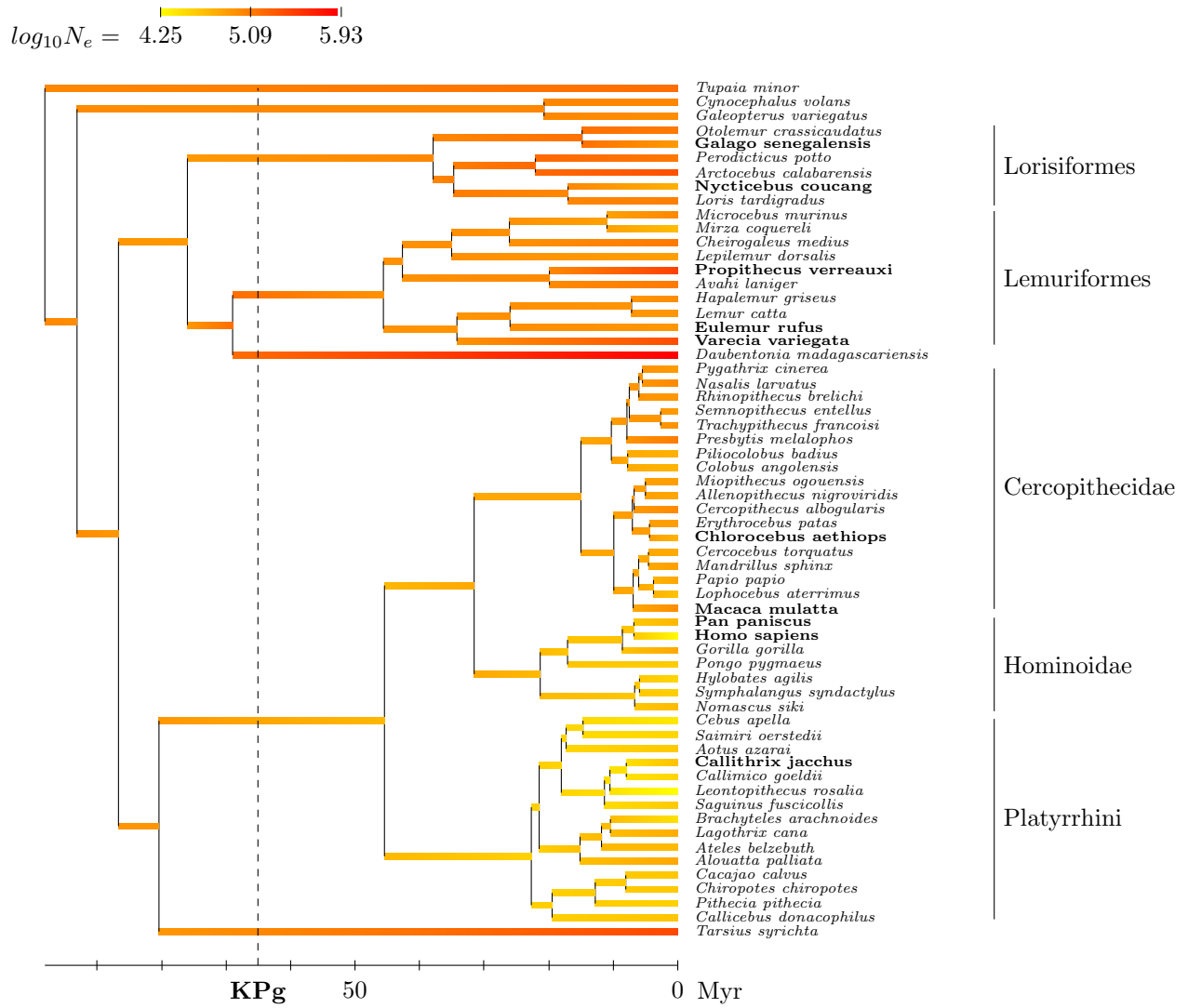


Figure S4. Reconstructed phylogenetic history of  $N_e$  (posterior median estimate) under the mechanistic model, without ancestral polymorphism.



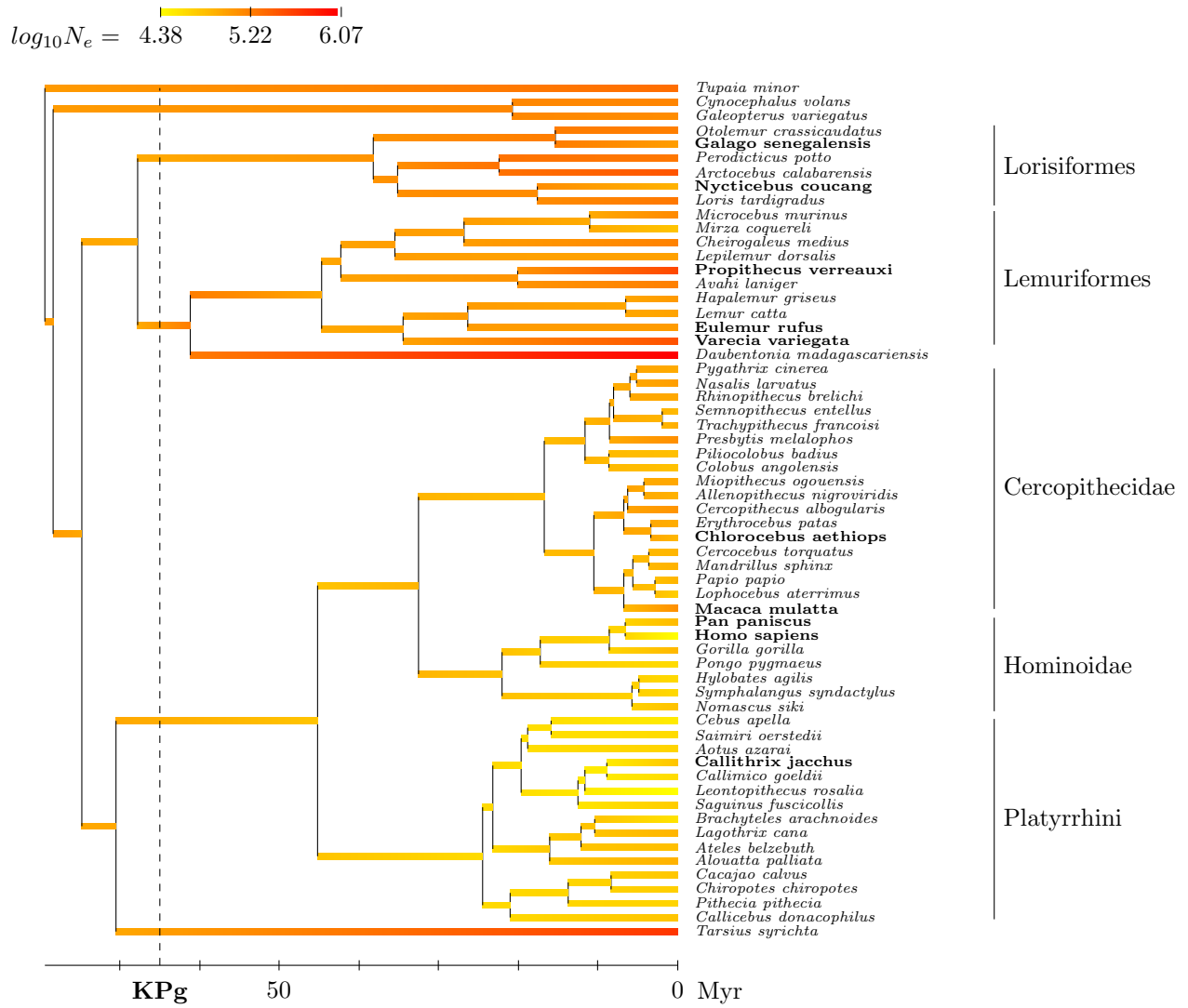


Figure S5. Reconstructed phylogenetic history of  $N_e$  (posterior median estimate) under the mechanistic model and using a uniform prior over divergence times.

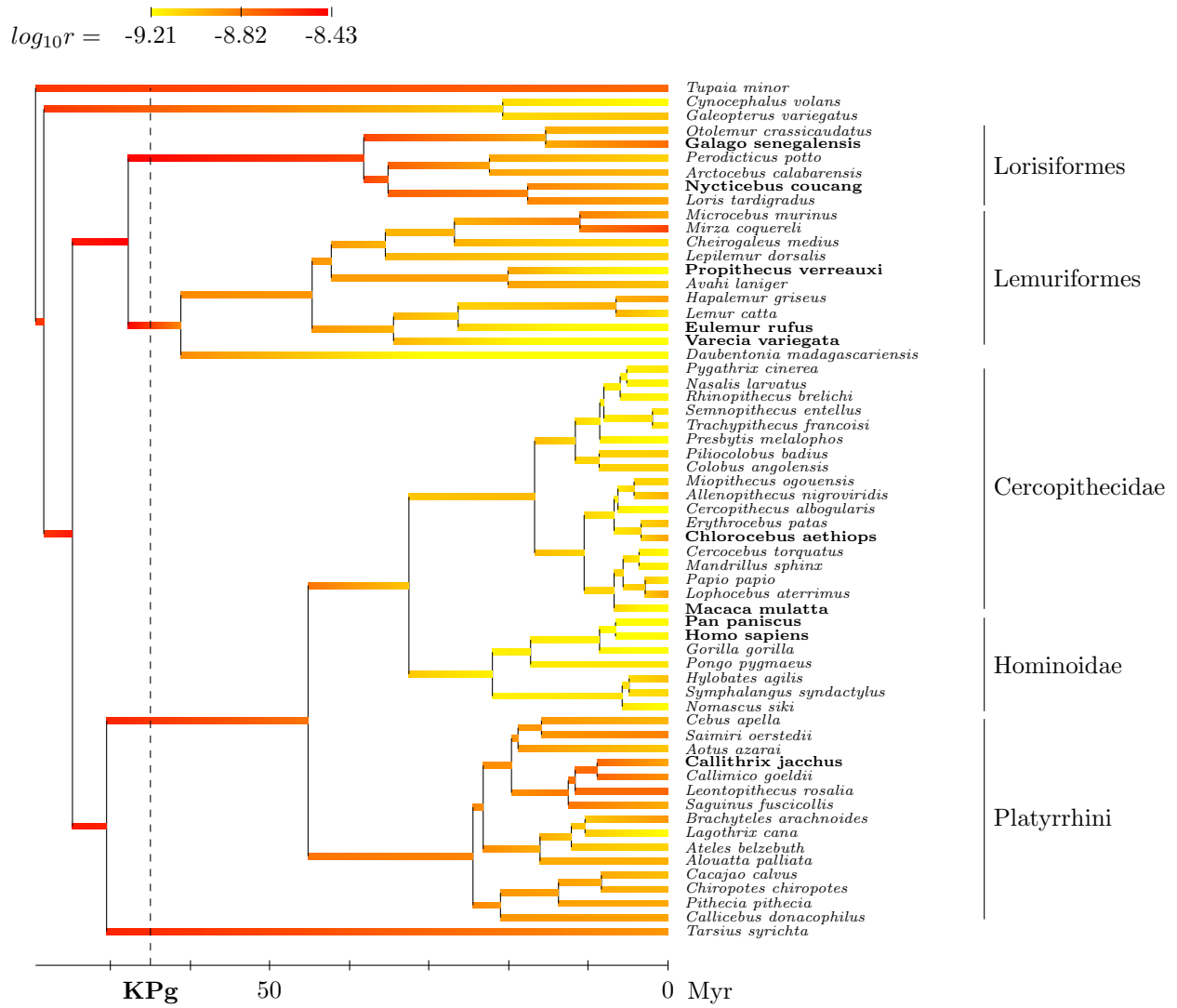


Figure S6. Reconstructed phylogenetic history of  $r$  (posterior median estimate) under the mechanistic model and using a uniform prior over divergence times.

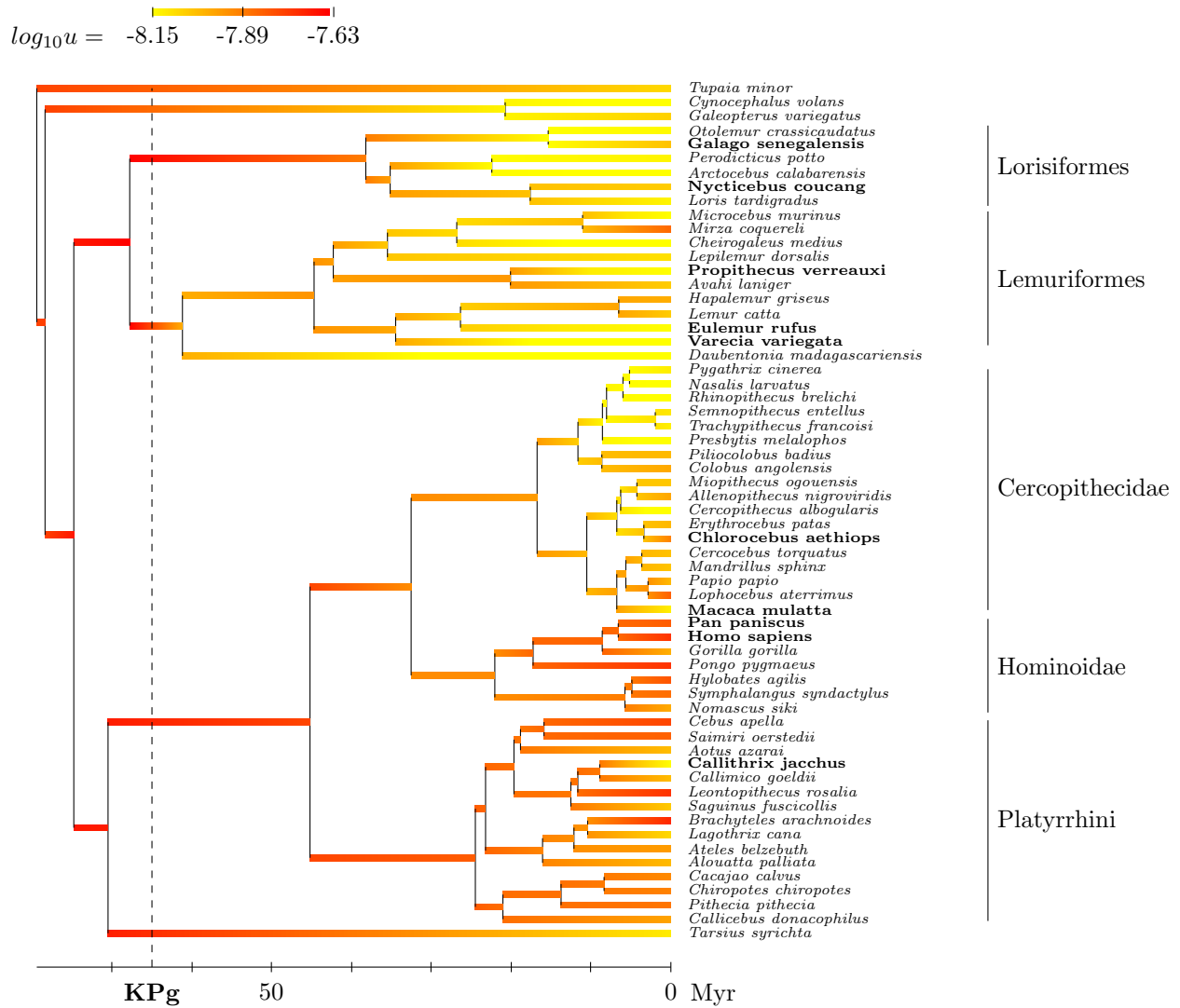


Figure S7. Reconstructed phylogenetic history of  $u$  (posterior median estimate) under the mechanistic model and using a uniform prior over divergence times.