Supplementary Appendix

Data

The sample sizes and distribution of traits used in the analyses are summarised in Table S1. Primate trait data were extracted from the literature and from primary sources (Dataset S1).

Table S1. Coding for binary traits and number by coding (Dataset S1).

Binary trait	**Coding**				
	State (0)	N	State (1)	N	Polymorphic (01)
Mating system	Polygyny	152	Pair living	34	28
Paternal care	No care	192	Care	27	-
Female ranging patterns	Discrete ranges	49	Overlapping ranges	164	-
Infanticide	Low infanticide	120	High infanticide	56	-

Paternal care

Ross and MacLarnon (1) use a four point scale: 1 (no or very low care, 0 – 5% of infant time), 2 (low care, 5-30% of infant time), 3 (medium care 30-55% of infant time), and 4 (high care, > 55% of infant time) for allocare (by all carers) in anthropoid primates, including feeding, carrying, playing and grooming. They suggest that category 3 (30 - 55% of infant time) and above represents significant allocare. We have redefined this scheme to focus on paternal care across the primate order, defining significant care as adult males providing care for at least 30% of infant time (Dataset S1).

Female Ranging Patterns

Female ranges are designated as either discrete or overlapping. Discrete female ranges are defined as overlapping by less than 5% (following Komers and Brotherton (2)). Data were collected from the literature (Dataset S1).

Infanticide

Reports of infanticide were taken from the literature and were included where infanticide was observed in wild populations (Dataset S1). Furthermore, because of the rarity of infanticide, it is not possible to be certain that a lack of reporting of infanticide, even in well-studied species, confirms that infanticide does not take place in that species. This issue has been highlighted by a recent study using long-term data (spanning 29 years) on *Hylobates lar (3)*. Although this well-studied species (726 publications - Dataset S1) was presumed to have no infanticide, by using the full data set Borries and colleagues (3) were able to show that male infanticide did take place, even if very rarely. We have therefore categorised species as “high infanticide”, where infanticide has be widely documented, and “low infanticide” where infanticide has not been reported or is thought to be rare. We classified species as ‘low rates of infanticide’ in order to reflect the possibility that there is some low-level of infanticide pressure even in species where it is unreported. Species with less than 20 publications have been excluded from these analyses on the grounds that they have not been sufficiently studied to determine the level of infanticide that takes place in the species.

Since infanticide is a rare event, even in those populations where infanticide is a significant cause of infant death, the reporting of infanticide for species may be influenced by the intensity of study. In particular, it may be that polygynous species have been more intensely studied than monogamous species, since they are more likely to occupy open habitats, and therefore infanticide is more likely to have been seen in those species. We therefore performed a literature search for the number of publications for each primate species using Web of Science (http://apps.webofknowledge.com).

Those species with >100 publications were deemed well studied. There was no association between being well studied and being polygynous (Table S2, $X^2 = 0.87$, df = 1, p = 0.35). Moreover, there was no significant difference in the mean $\log_{10}$ number of publications for monogamous versus polygynous species (two tailed t=0.22, p = 0.82, Figure S1).

Table S2. Study intensity of primate species by mating system.

Study Intensity	Polygynous	Monogamous
Limited study	97	36
Well studied	66	17

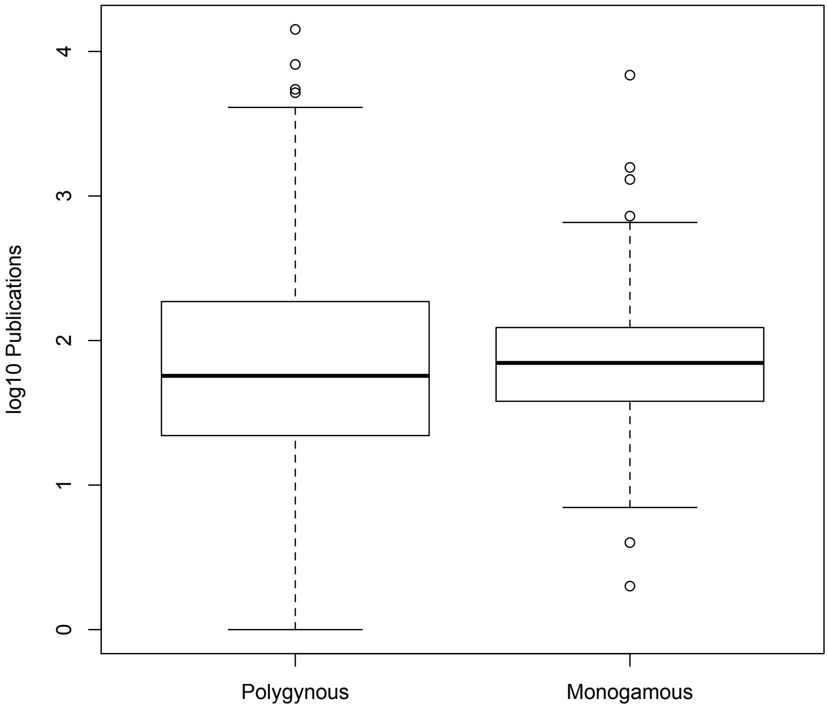


Figure S1. Plot of number of publications for individual primate species by mating system.

The main text shows a clear association between low infanticide and monogamous mating. In order to test whether this association was influenced by intensity of study we also subset the data to well-studied species. The association between low infanticide and monogamy still holds when the data was subset to well-studied species. Correlated evolution is strong between infanticide and mating system ($\log_{10}$ Bayes Factor 2.98) and there is a clear association between low infanticide and monogamy, with low transition rates out of the derived state of monogamy with low infanticide (Figure S2).

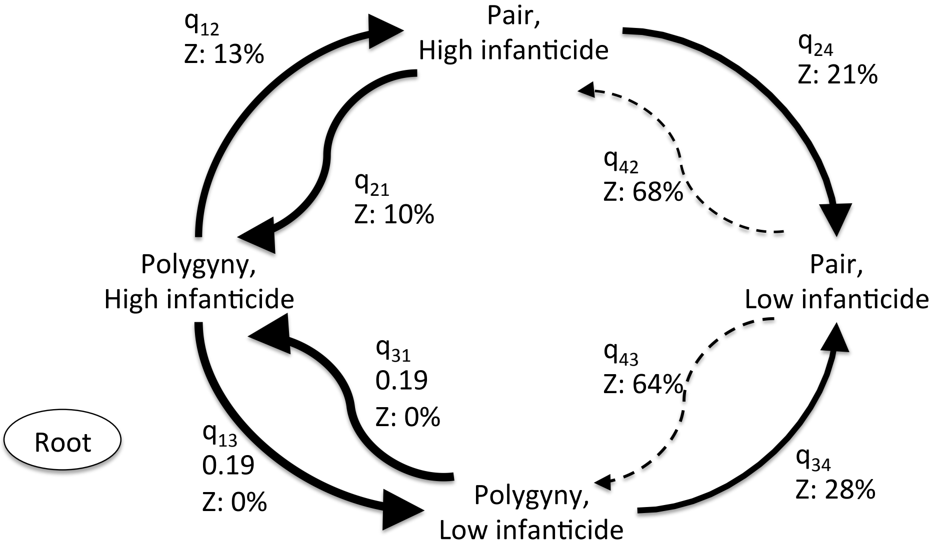
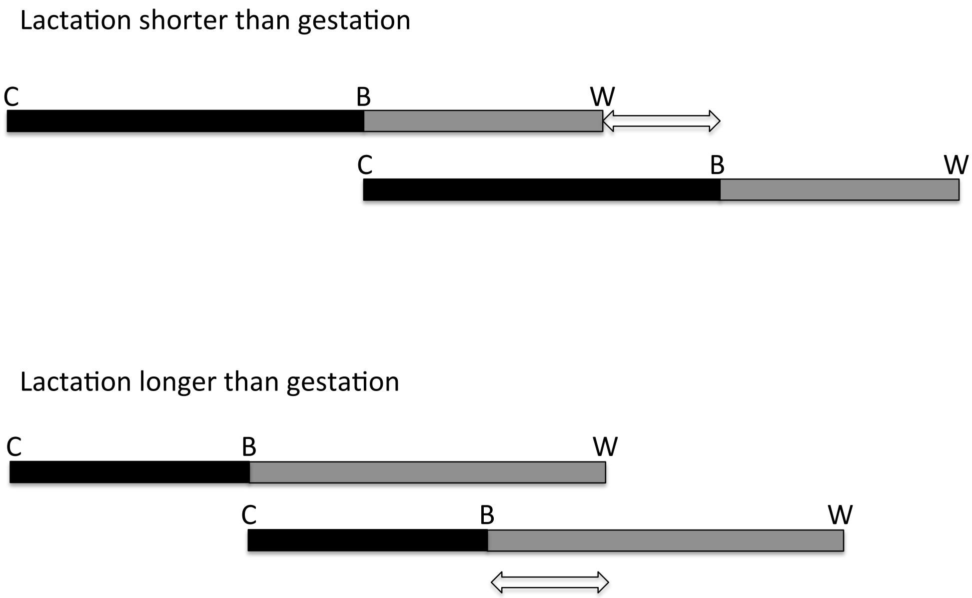


Figure S2. Correlated evolution between primate mating system and male infanticide in well-studied species. Z denotes visits assigned to zero as a proportion of the posterior probability distribution. Thickness of arrows reflects proportion of time transition rate is not assigned to zero, with dashed line > 50% zeros. Number below rate name (q_{ij}) is the mean transition rate where rate distribution has zero or very low Z value.

Weaning proportion

Data for gestation length (G) and lactation length (L) were collected from the literature (Dataset S1). The weaning proportion (L/(L+G)) shows the relative length of lactation to the inter-birth interval and indicates infanticide risk (Figure S3). Data were Arc Sine transformed.



Lactation shorter than gestation

Lactation longer than gestation

Figure S3. The relative length of lactation and gestation affects the occurrence of two lactating offspring of different ages in non-seasonal breeding primates indicating infanticide risk (following van Schaik (4)). (C=conception, B=birth, and W=weaning). Where lactation is short relative to gestation (top) conception can occur soon after the birth of the previous offspring without lactation periods overlapping (as shown by open arrow). Male infanticide would have no effect on birth timing of the subsequent offspring and is therefore predicted to be low. Where lactation is long relative to gestation (bottom) post-partum conception would lead to two lactating offspring for a period (as shown by the open arrow), and therefore conception is delayed. However, this delay then enables a male to hasten a return to oestrus in a female by killing her lactating infant.

For seasonal breeding species with a single reproductive event each year followed by a 'timeout period', lactation longer than gestation would falsely suggest that there was infanticide risk, but the killing of her infant would not speed a female's return to oestrus. Seasonal breeders (with a timeout period) are identified in the Dataset S1, and these species were removed from this analysis (following van Schaik (4)).

Phylogenetic Signal

Phylogenetic signal was tested in discrete traits (Table S3) by calculating D using the function *phylo.d* (5) in the *Caper* package (6) in *R* (7). A D value significantly different from random indicates that related species are more similar in a particular trait than would be expected by chance (5). For the continuous trait the *Continuous* procedure in BayesTraits (8) was used to test for phylogenetic signal by calculating Pagel's λ (9, 10). A λ value of 1 indicates the probability of shared inheritance is proportional to relatedness, while a λ value of 0 suggests evolution is independent of the phylogenetic tree.

Each of the discrete traits tested have a phylogenetic structure that has a zero probability of being generated from a random distribution (no phylogenetic structure) (Table S3), while the continuous trait has a λ value close to 1 (Table S4). These results suggest that for the traits used here phylogenetic ancestry is a significant factor in their distribution across extant taxa.

Table S3. D statistic for phylogenetic structure of binary traits.

Trait Data	**Est. D**	**Probability of Est. D resulting from:**	
		No phylogenetic structure (random)	Brownian motion
Mating system	-0.11	0.000	0.722
Paternal care	-0.55	0.000	0.994
Female ranging patterns	-0.17	0.000	0.807
Infanticide	0.54	0.000	0.001

Table S4. Bayesian analyses of traits with results for root values and phylogenetic signal (λ)

Analysis	**Lh**	**Harmonic mean**	**Alpha (Root)**	**Lambda (λ)**
Weaning Proportion	74.95	73.56	0.54	0.92

Transition Rates

Transition rates between states can be used to determine the relative timing of changes between states where there is correlated evolution between two binary traits (Figure 1, Table S5).

Table S5. The posterior probability of transition rate being zero for correlated evolution analyses between mating system and other traits. Transition rates are referred to as q_{ij}, where i and j refer to the beginning and end trait states of the transition respectively (1 is the ancestral state, 4 is the derived state and 2 and 3 are the intermediate states) in correlated evolution Figure 1.

Co-evolutionary analyses (with mating system)	**Posterior probability of a zero rate (%)**							
	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}
Paternal care	99.7	0.0	39.5	34.5	3.8	0.0	89.5	87.5
Female ranging patterns	99.6	0.0	14.5	1.4	26.4	0.0	76.5	14.1
Infanticide	0.0	75.8	0.0	0.12	93.2	90.1	20.7	0.8

Evolutionary Models

As outlined in the methods section, analyses were carried out in BayesTraits (8, 11) using a Markov Chain Monte Carlo (MCMC) (12) sampling algorithm together with a reversible jump (RJ) procedure. The RJ procedure searches the posterior distribution of possible models by linking (setting to equal) or removing (setting to zero (Z)) transition rate parameters. Models were sampled in proportion to their posterior probability, accounting for variation in the number of parameters (Tables S6-S8).

Table S6. Top ten and fiftieth model of mating system and paternal care with their posterior probabilities. (Note: Z = transition rate assigned to zero. 0, 1 and 2 are non-zero rates.) Subscripts on the transition rates refer to the four possible states of the two binary traits. Frequency = visits to the model in the posterior sample of 50,000 observations. Approximately 87 visits are expected by chance (following Pagel and Meade (11)).

Model	Transition Rates								Frequency	Probability (%)	Cumulative probability (%)
	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}			
1	Z	0	0	0	0	0	Z	Z	11025	22.1	22.1
2	Z	0	Z	0	0	0	Z	Z	10678	21.4	43.4
3	Z	0	0	Z	0	0	Z	Z	8561	17.1	60.5
4	Z	0	Z	Z	0	0	Z	Z	5773	11.5	72.1
5	Z	0	0	0	0	0	Z	0	1884	3.8	75.8
6	Z	0	0	0	0	0	0	Z	1163	2.3	78.2
7	Z	1	0	1	1	1	1	Z	625	1.3	79.4
8	Z	0	Z	Z	0	0	0	Z	623	1.2	80.7
9	Z	0	Z	0	Z	0	Z	0	572	1.1	81.8
10	Z	0	Z	Z	Z	0	Z	0	538	1.1	82.9
50	Z	1	Z	1	0	1	Z	Z	45	0.1	91.9

Table S7. Top ten and fiftieth model of mating system and female ranging patterns with their posterior probabilities. (Note: Z = transition rate assigned to zero. 0, 1 and 2 are non-zero rates.) Subscripts on the transition rates refer to the four possible states of the two binary traits. Frequency = visits to the model in the posterior sample of 50,000 observations. Approximately 95 visits are expected by chance (following Pagel and Meade (11)).

Model	Transition Rates								Frequency	Probability (%)	Cumulative Probability (%)
	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}			
1	Z	1	1	1	0	0	Z	1	10082	20.2	20.2
2	Z	1	1	1	1	0	Z	1	6253	12.5	32.7
3	Z	1	1	1	Z	0	Z	1	6050	12.1	44.8
4	Z	0	0	0	1	1	Z	0	4215	8.4	53.2
5	Z	1	1	1	Z	0	Z	Z	2299	4.6	57.8
6	Z	0	0	0	Z	1	Z	0	1926	3.9	61.7
7	Z	0	0	0	0	1	Z	0	1837	3.7	65.3
8	Z	1	Z	1	1	0	1	1	1503	3.0	68.3
9	Z	1	1	1	1	0	Z	Z	1489	3.0	71.3
10	Z	1	1	1	0	0	1	1	1291	2.6	73.9
50	Z	1	Z	2	0	0	1	2	39	0.1	94.9

Table S8. Top ten and fiftieth model of mating system and infanticide with their posterior probabilities. (Note: Z = transition rate assigned to zero. 0, 1 and 2 are non-zero rates.) Subscripts on the transition rates refer to the four possible states of the two binary traits. Frequency = visits to the model in the posterior sample of 50,000 observations. Approximately 124 visits are expected by chance (following Pagel and Meade (11)).

Models	Transition Rates								Frequency	Probability (%)	Cumulative Probability (%)
	q_{12}	q_{13}	q_{21}	q_{24}	q_{31}	q_{34}	q_{42}	q_{43}			
1	1	Z	1	0	Z	Z	1	1	11364	22.7	22.7
2	1	Z	1	0	Z	Z	0	1	8880	17.8	40.5
3	1	Z	1	0	Z	Z	Z	0	5737	11.5	52.0
4	1	Z	1	1	Z	Z	0	1	2524	5.0	57.0
5	1	0	1	0	Z	Z	0	1	2186	4.4	61.4
6	1	0	1	0	Z	Z	Z	1	2050	4.1	65.5
7	0	Z	0	1	Z	Z	0	0	1594	3.2	68.7
8	1	0	1	0	Z	Z	1	1	1444	2.9	71.6
9	1	Z	1	0	Z	0	0	1	932	1.9	73.4
10	0	Z	0	1	Z	Z	1	0	911	1.8	75.2
50	2	Z	2	0	Z	Z	2	1	71	0.1	94.8

Ancestral States

We used an RJ MCMC approach within the Multistate procedure in BayesTraits (8, 11) to infer states at ancestral nodes for each binary trait (Figures S4-S7). For the continuous trait we also used an MCMC approach in the Continuous procedure in BayesTraits (8, 11) to infer states at ancestral nodes (Figure S8).

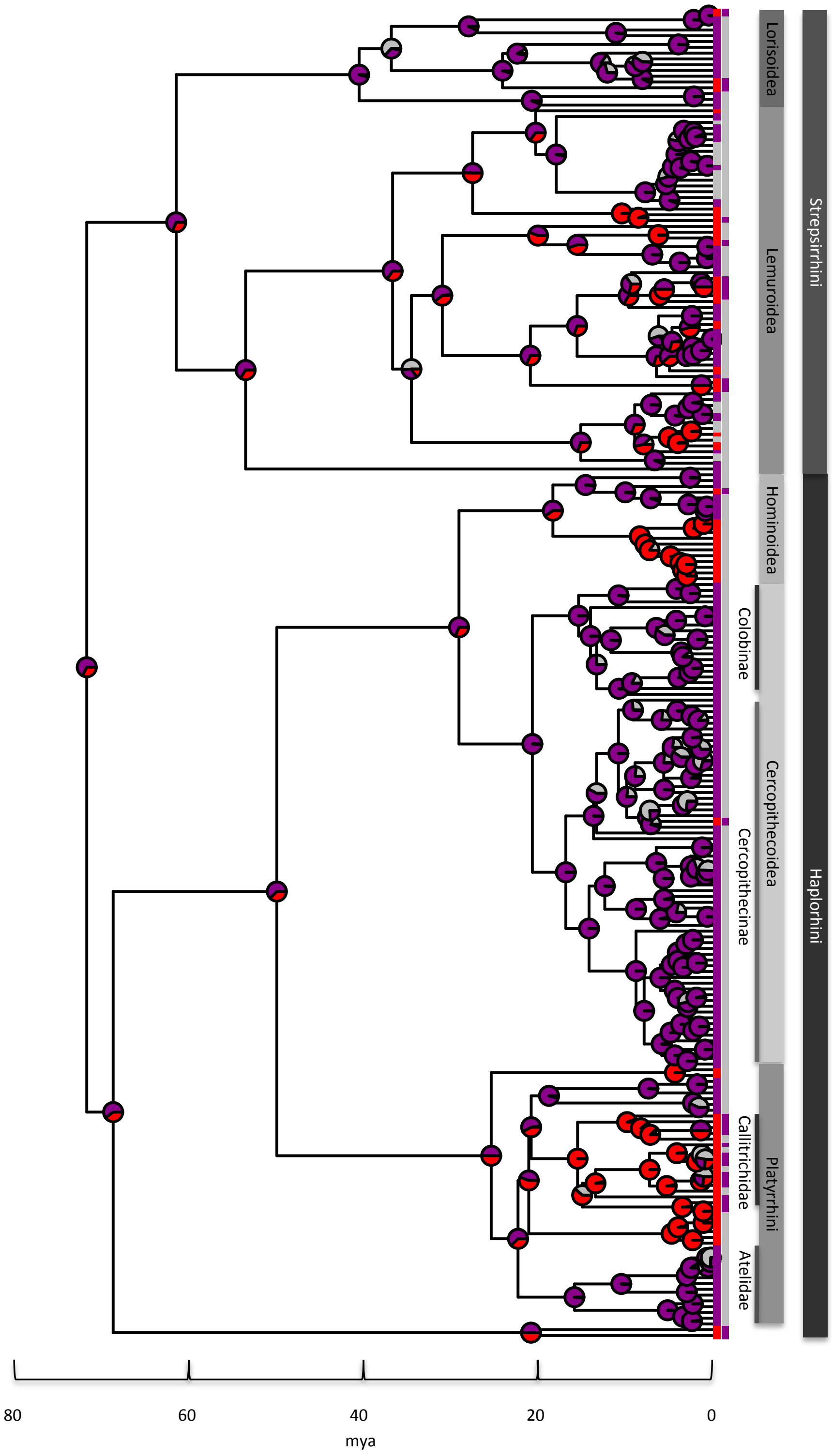


Figure S4. Ancestral node reconstructions for primate mating systems from MCMC analysis plotted on the maximum clade credibility tree derived from the full posterior sample of trees. The pies at ancestral nodes are the combined posterior probability of each state at that node with the posterior probability that the node itself exists. Red shading indicates probability of monogamy at each node and tip; purple indicates probability of polygyny. Two columns used at tips for polymorphic species. Grey represents missing data or monomorphic species (if in 2nd column) at tips, and node uncertainty derived from the full phylogeny.

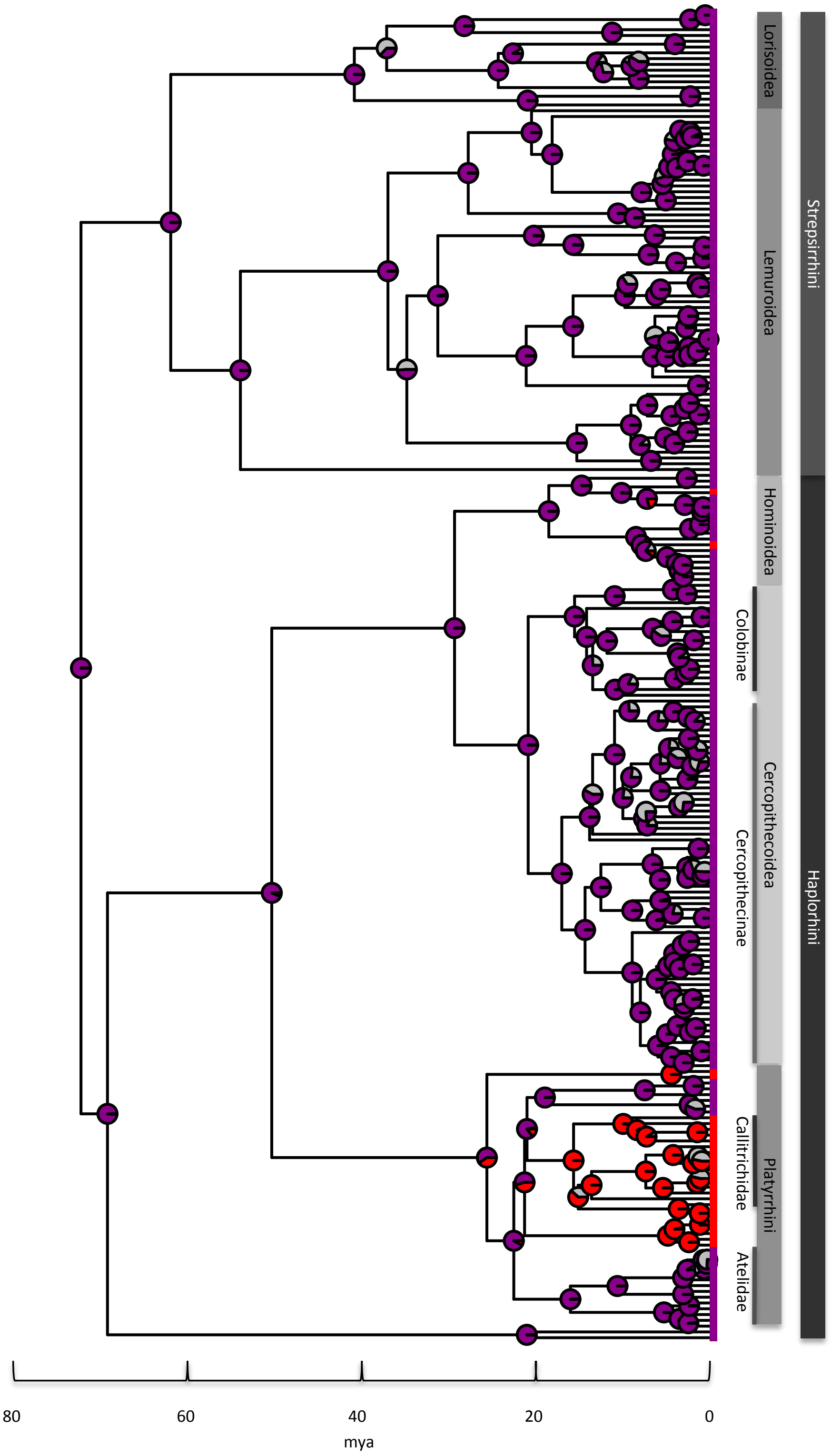


Figure S5. Ancestral node reconstructions for paternal care from MCMC analysis plotted on the maximum clade credibility tree derived from the full posterior sample of trees. Red shading indicates probability of paternal care at each node and tip; purple indicates probability of no care. Grey represents node uncertainty derived from the full phylogeny.

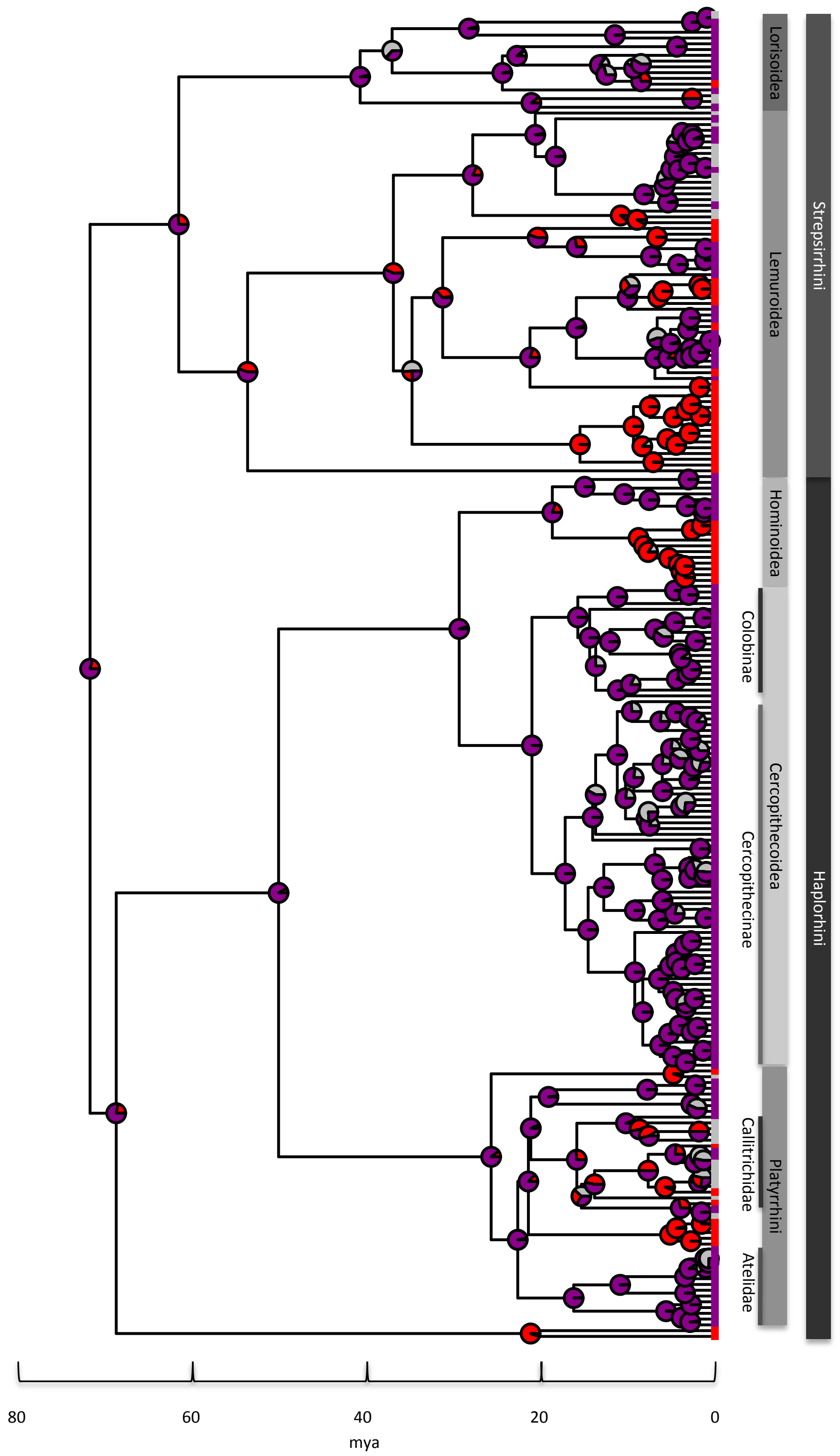


Figure S6. Ancestral node reconstructions for female ranging patterns from MCMC analysis plotted on the maximum clade credibility tree derived from the full posterior sample of trees. Purple shading indicates probability of overlapping female ranges at each node and tip; red indicates probability of discrete female ranges. Grey represents missing data at tips and node uncertainty derived from the full phylogeny.

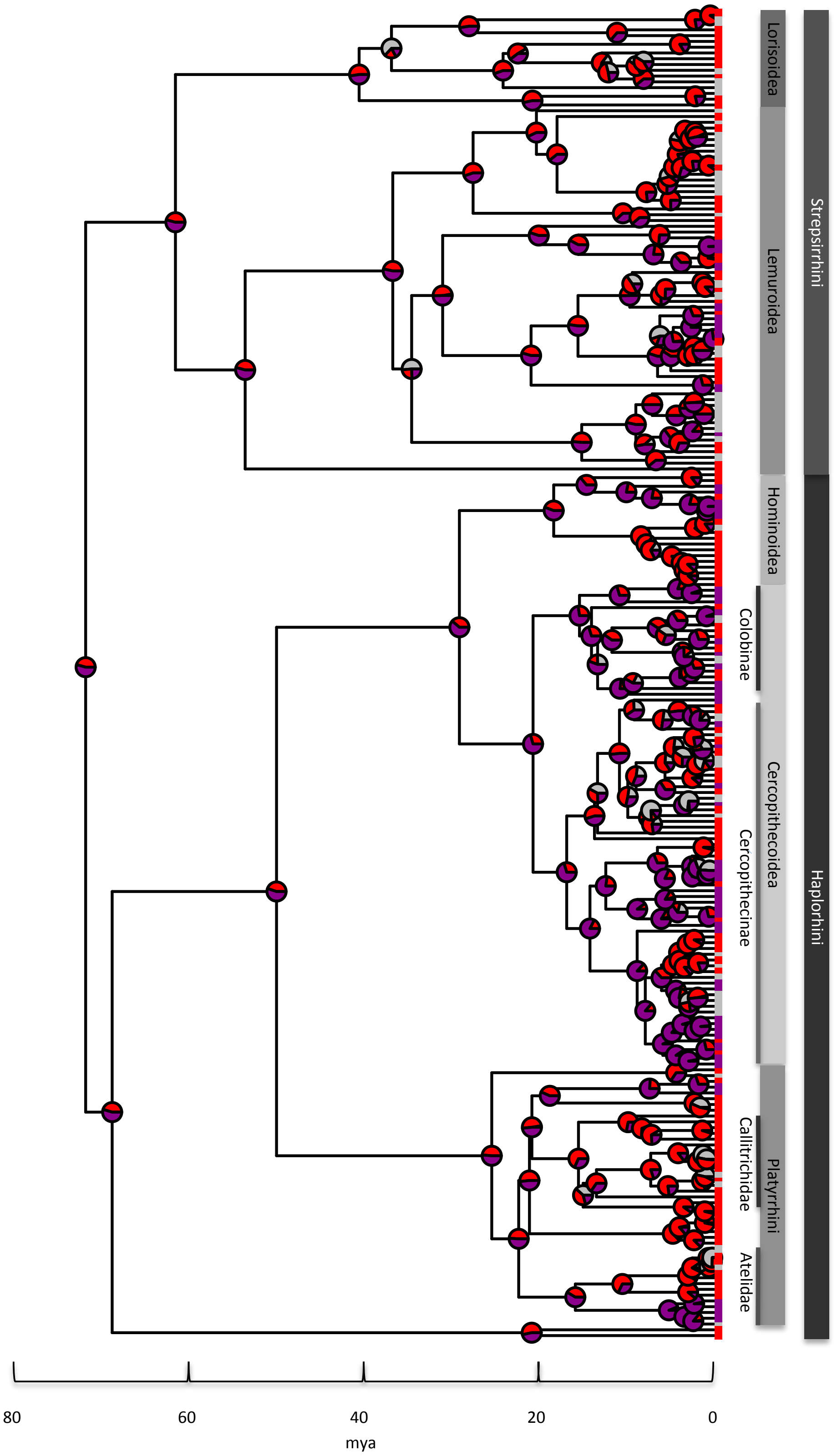


Figure S7. Ancestral node reconstructions for infanticide from MCMC analysis plotted on the maximum clade credibility tree derived from the full posterior sample of trees. Purple shading indicates probability of high infanticide at each node and tip; red indicates probability of low infanticide. Grey represents missing data at tips and node uncertainty derived from the full phylogeny.

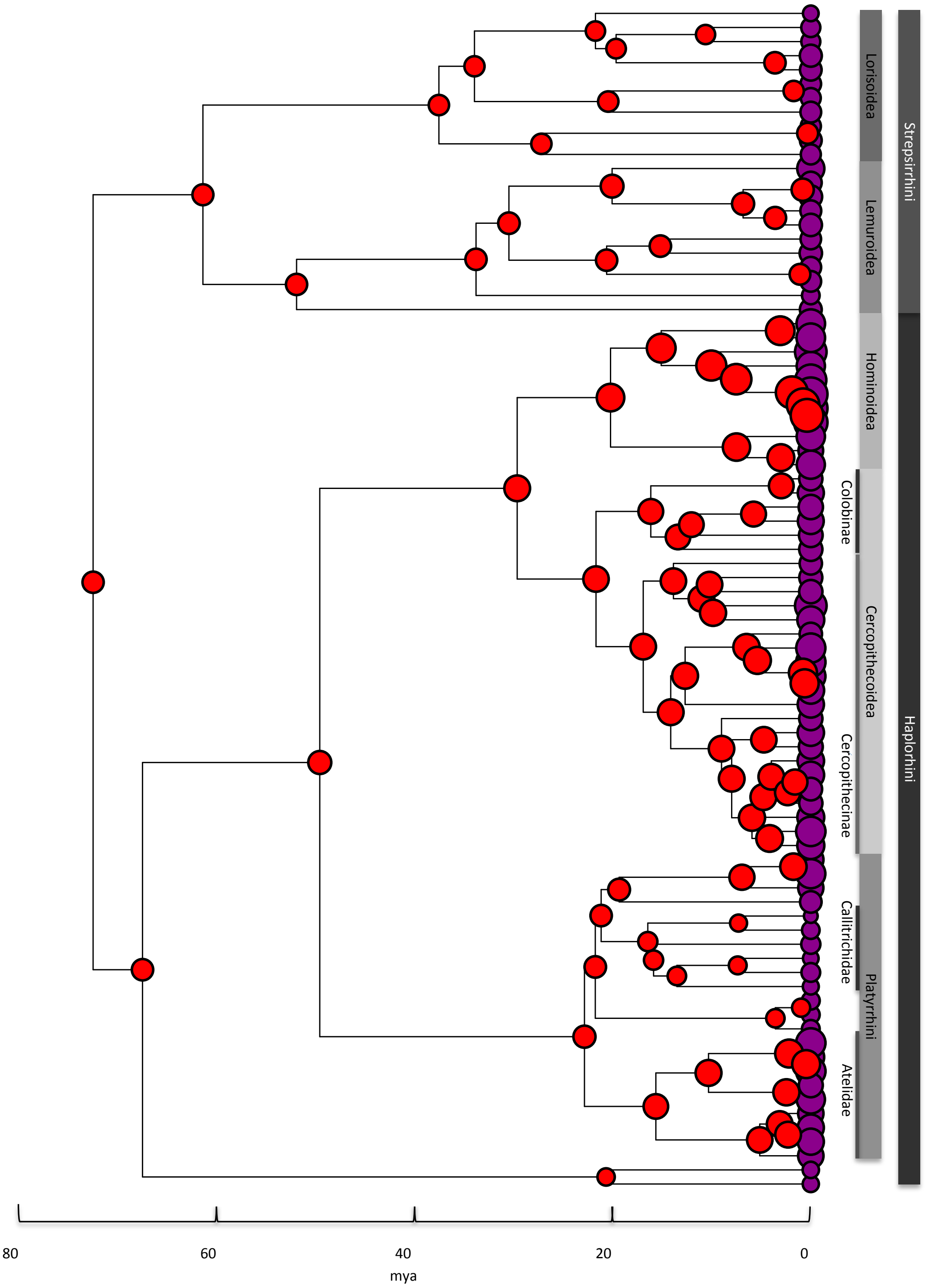


Figure S8. Inferred proportion of the breeding cycle dedicated to lactation at ancestral nodes of the primate phylogeny from MCMC analysis plotted on the maximum clade credibility tree derived from the full posterior sample of trees. Size of circle at nodes is proportional to value. Red denotes ancestral node; purple denotes extant taxa.

Supplementary References

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