Appendix S2. Assessment of effect of phylogenetic uncertainty in the form of alternative tree topologies on phylogenetic signals within the Hylobatidae.

Due to the apparent difficulty of resolving the pattern of phylogenetic branching within the Hylobatidae [1],[2], limitations associated with the most complete gibbon phylogenetic tree available in terms of species assemblage (single locus data used to construct the phylogeny; some nodes of tree are poorly supported) [3], and concerns regarding the sensitivity of comparative analyses to the choice of phylogenetic tree [4],[5], we performed a preliminary investigation to explore the impact of phylogenetic uncertainty upon our principal comparative analysis testing phylogenetic signal. Using a range of alternative phylogenetic tree topologies drawn from the available literature, each representing different possible relationships among gibbons, we tested for the presence and strength of any phylogenetic signal in the traits of interest, including: body mass (as a control); home range; group size; and mating system.

An additional five published phylogenetic trees [6-10] incorporating gibbons and the two *Pongo* species (as an outgroup) were tested, in addition to the published tree of Thinh *et al.* (2010) [3] and our *a priori* preferred tree, a modified version of this tree also including *N. annamensis* (see Figures S1-7). These alternative trees differed both in the number of gibbon species incorporated (and generally did not include the main species of interest, *Nomascus hainanus*) and in the topology of relationships between different species, but all of these trees included ≥8 gibbon species (i.e. they represented at least half of all gibbon species recognized before the recent establishment of three new species, *Hylobates abbotti*, *H. funereus* [11], and *Nomascus annamensis* [12]. This set of seven possible trees included phylogenies derived from a variety of methodological approaches, including several trees that used multiple genetic markers/regions (e.g. [8],[9]).

We tested for phylogenetic signal across the seven alternative trees using Pagel's lambda (λ) [13],[14] for continuous traits and *D* [15],[16] for categorical traits and using high and low estimates for Hainan gibbon home range [17],[18], as described in the main methods section. The frequency distribution of resultant λ and *D* signal values was then plotted to investigate variation in the strength of the phylogenetic signal in each trait when alternative phylogenetic trees were utilized. For *D*, only six trees in total returned signals due to the absence of *Nomascus* from one tree [6] which prevented variation in this trait being captured and thus adequate representation of this binary-coded variable in this instance.

Our results of phylogenetic signal in all four traits were consistent, despite the phylogenetic uncertainty introduced by testing alternative gibbon species assemblages and relationships across the different tree topologies. We observed very similar values of λ for body mass, home range (for both high and low Hainan gibbon estimates), and group size across all trees tested, with tight clustering of signals around λ=1 (Figures S8-11), supporting strong patterns of phylogenetic signal in each of these traits. Similarly, values of *D* for mating system varied from -0.5 to -2.0 but clustered around -1.0 to -1.5 (Figure S12), again indicating strong phylogenetic conservatism in this trait. The strength of the phylogenetic signals observed across all trees for the three continuous traits was consistent ($\lambda \geq 0.82$), as was the direction (negative) and magnitude of the signal observed for the categorical trait ($D \leq -0.54$). This consistency indicates that the choice of tree topology in these cases is not critical to the phylogenetic signals observed; indeed it appears to have little impact on these signals, apparently because the signals are so strong. The signals returned for each trait by our *a priori* preferred phylogeny (indicated by the red lines in Figures S8-12) align with the most frequently observed signal value for all four traits, indicating that use of this preferred tree alone for all subsequent comparative analyses within this study is valid, and will not reduce the power, reliability, or relevance of results of any of these analyses.

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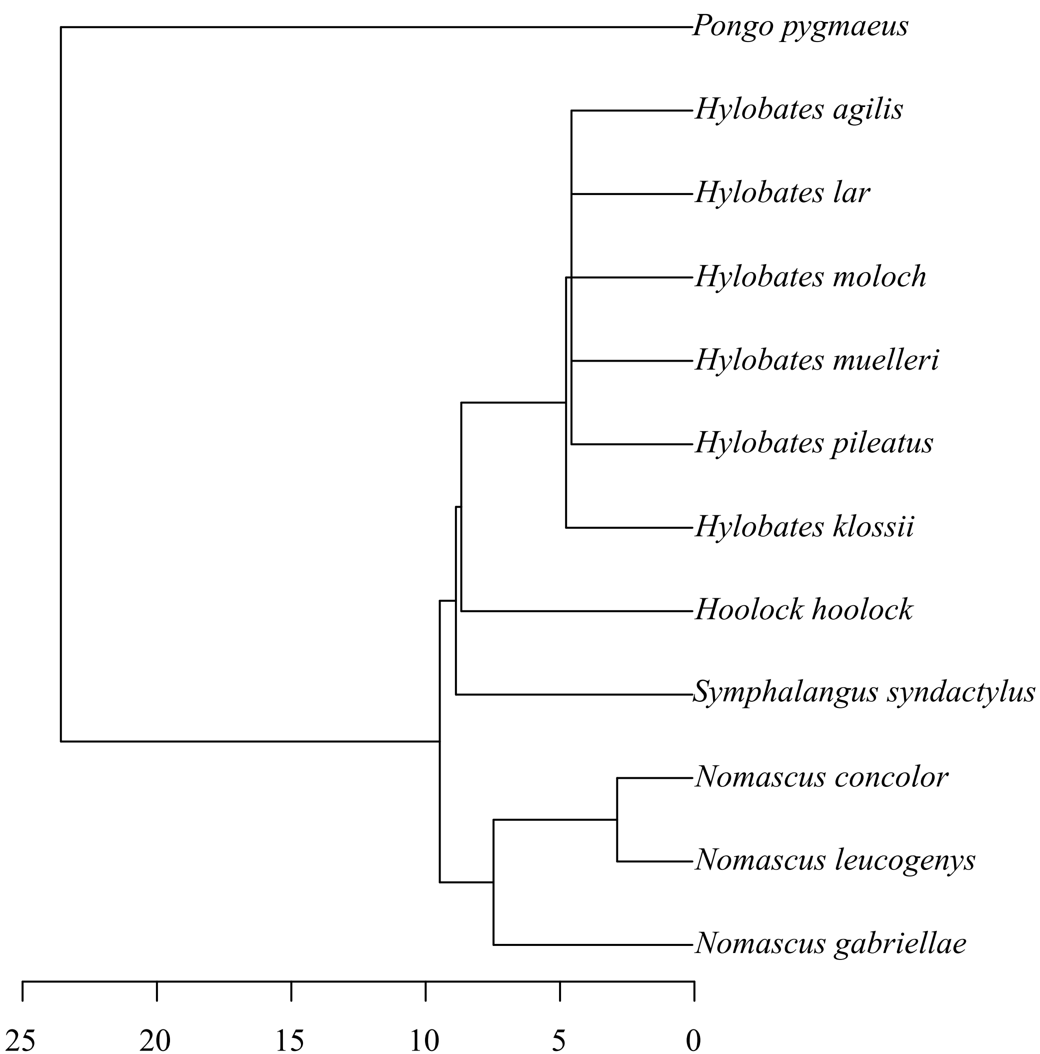
Figures S1-7 **Phylogenetic uncertainty:** Seven alternative phylogenetic trees representing possible relationships among gibbons used for tests of phylogenetic signal in four traits (body mass, home range group size, and mating system) across the Hylobatidae. Trees standardised as chronograms, scales indicate branch length in million years before present (MYA).

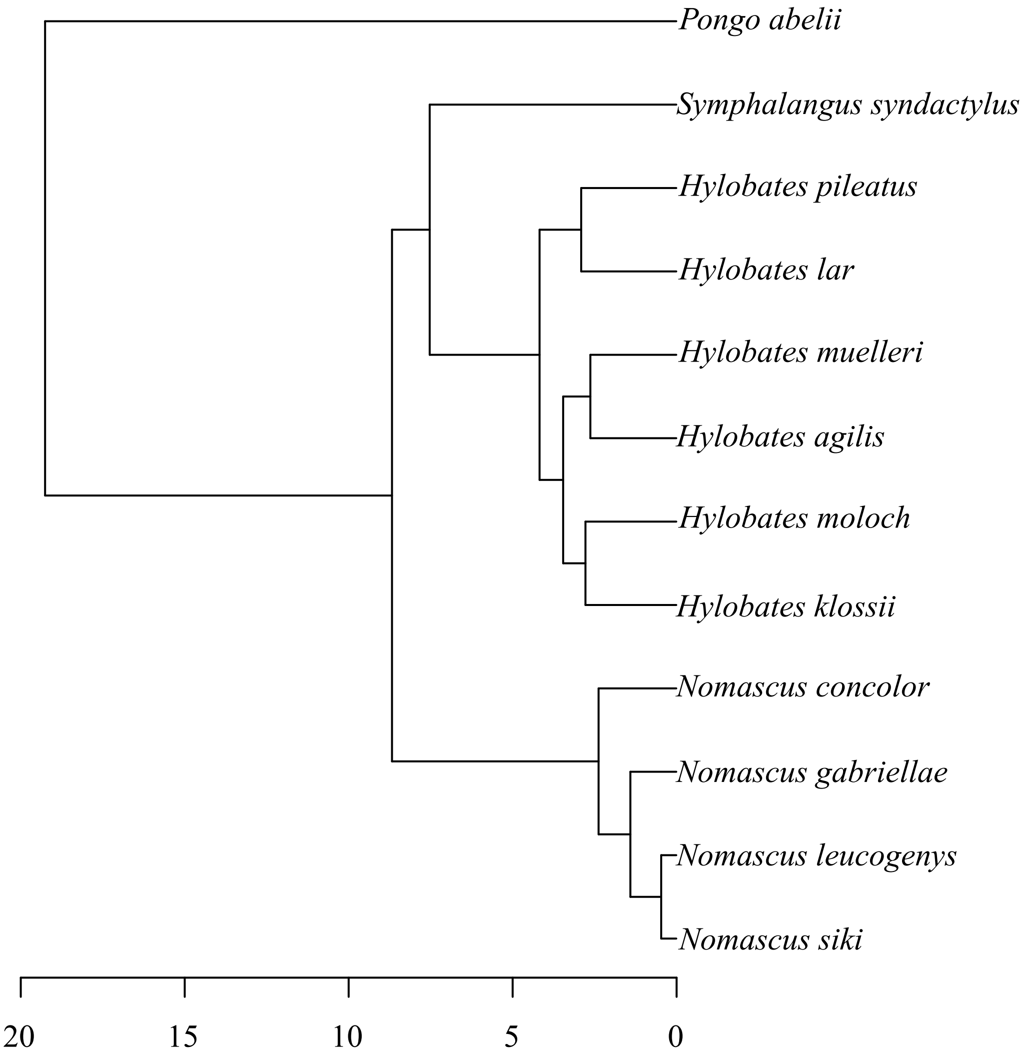
Figures S8-11 **Effect of phylogenetic uncertainty on phylogenetic signal in continuous traits:** Histograms showing the frequency distribution of values of Pagel's lambda (λ) from the tests of phylogenetic signal using seven different phylogenetic tree topologies for the continuous traits of body mass, home range (using two estimates of Hainan gibbon home range), and group size. The red line indicates the signal (λ) returned by our *a priori* preferred phylogeny.

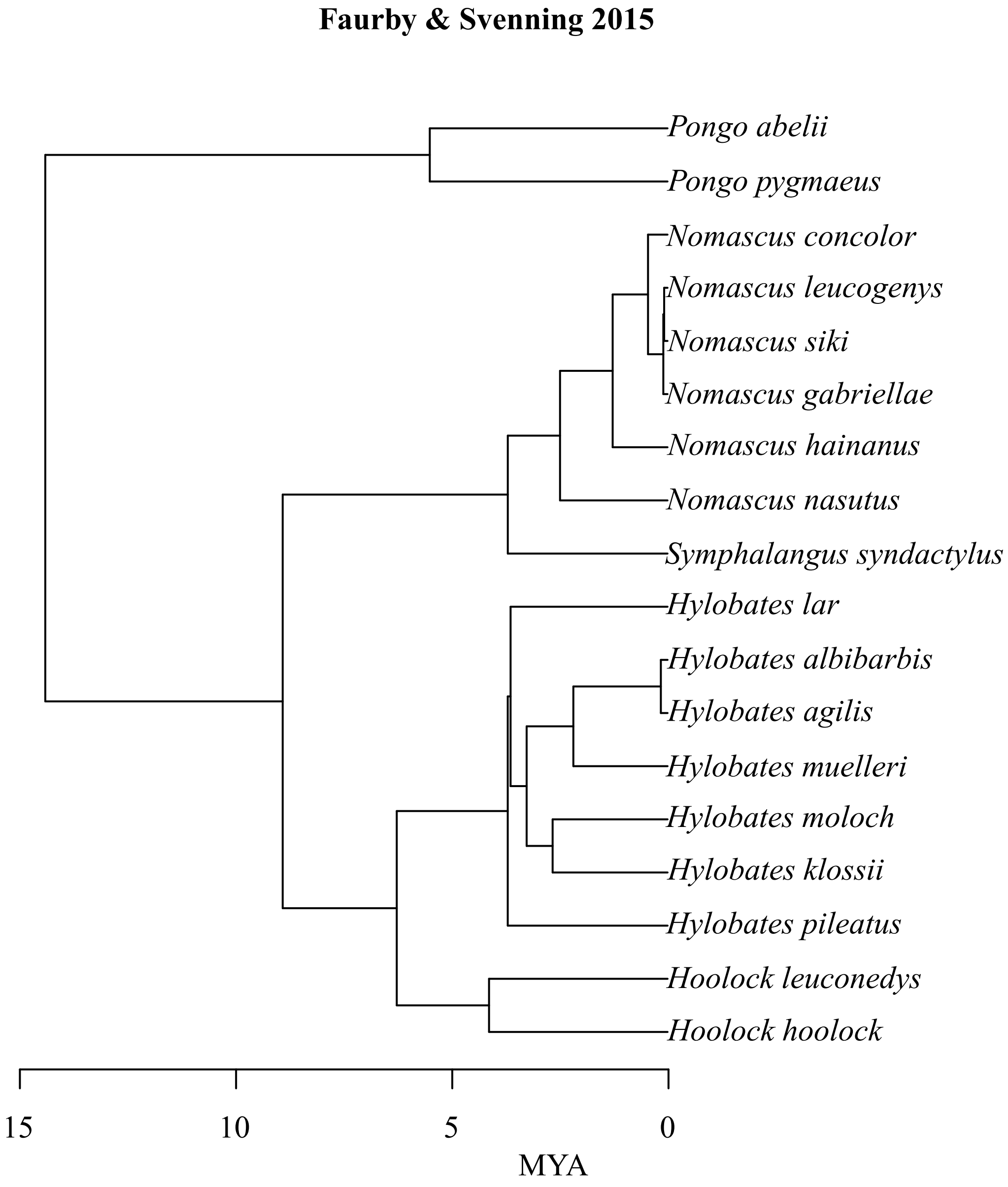
Figure S12 Effect of phylogenetic uncertainty on phylogenetic signal in a categorical trait: Histogram showing the frequency distribution of values of *D* from the tests of phylogenetic signal using six different phylogenetic tree topologies for the categorical trait of mating system. The red line indicates the signal (*D*) returned by our *a priori* preferred phylogeny.

Bininda−Emonds *et al.* 2007

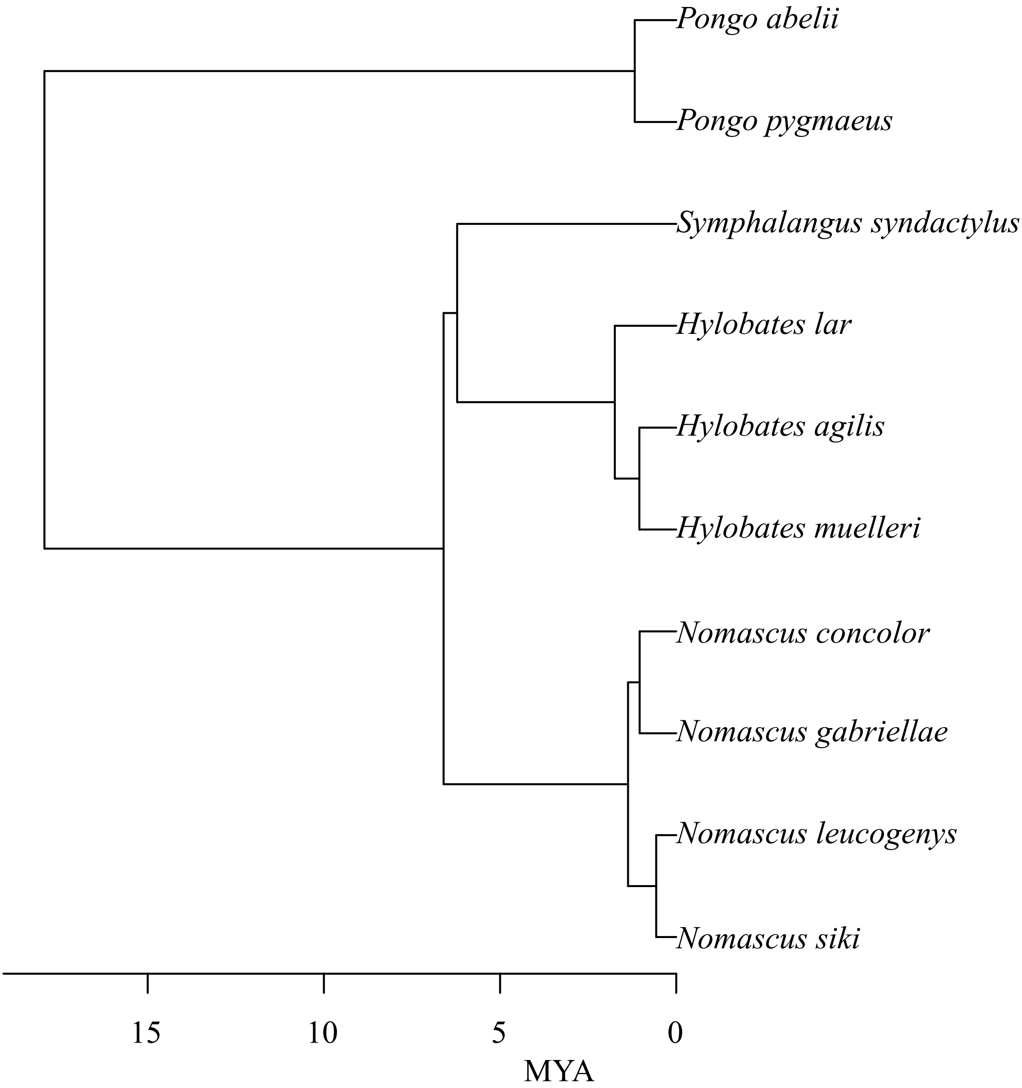


Chan *et al.* 2010

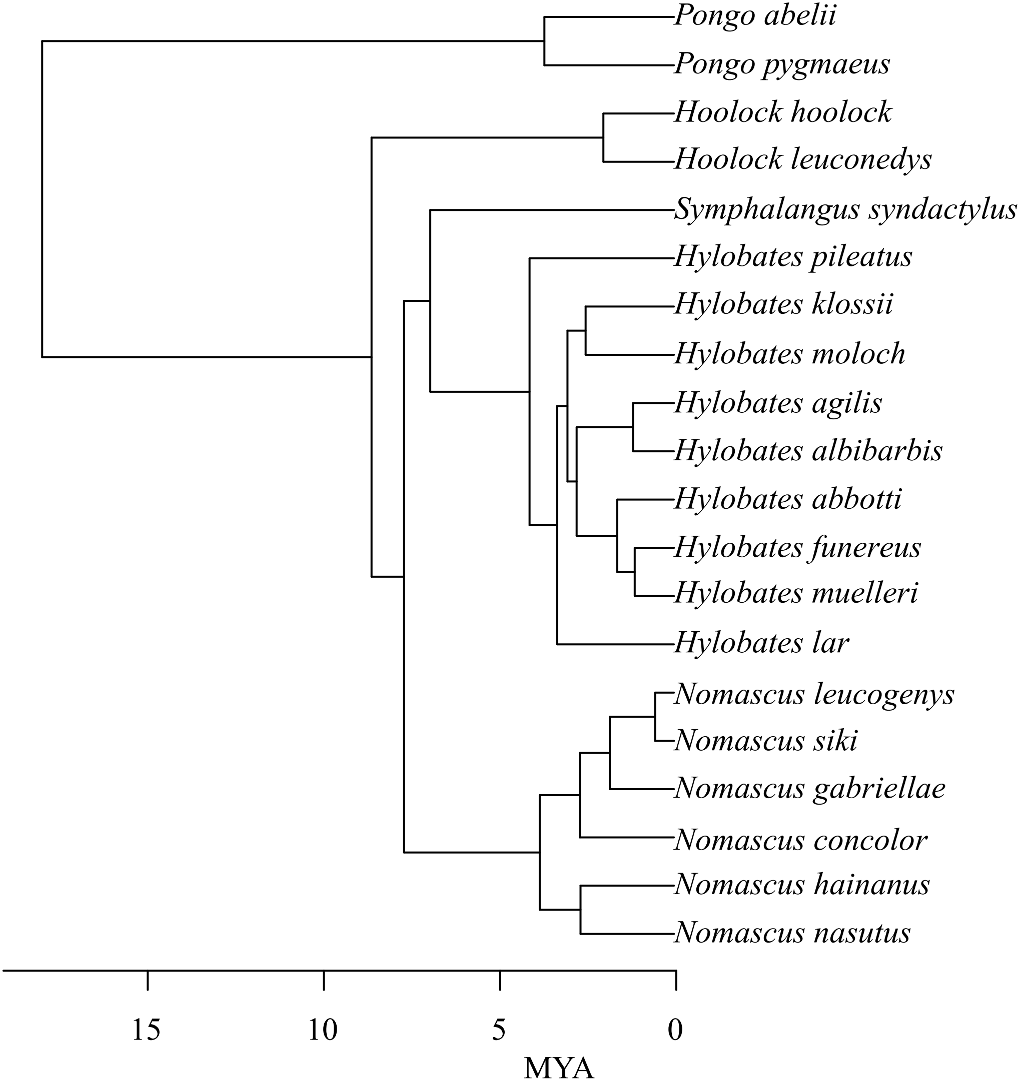



Faurby & Svenning 2015
Pongo abelii
Pongo pygmaeus
Nomascus concolor
Nomascus leucogenys
Nomascus siki
Nomascus gabriellae
Nomascus hainanus
Nomascus nasutus
Symphalangus syndactylus
Hylobates lar
Hylobates albibarbis
Hylobates agilis
Hylobates muelleri
Hylobates moloch
Hylobates klossii
Hylobates pileatus
Hoolock leuconedys
Hoolock hoolock
15
10
5
0
MYA

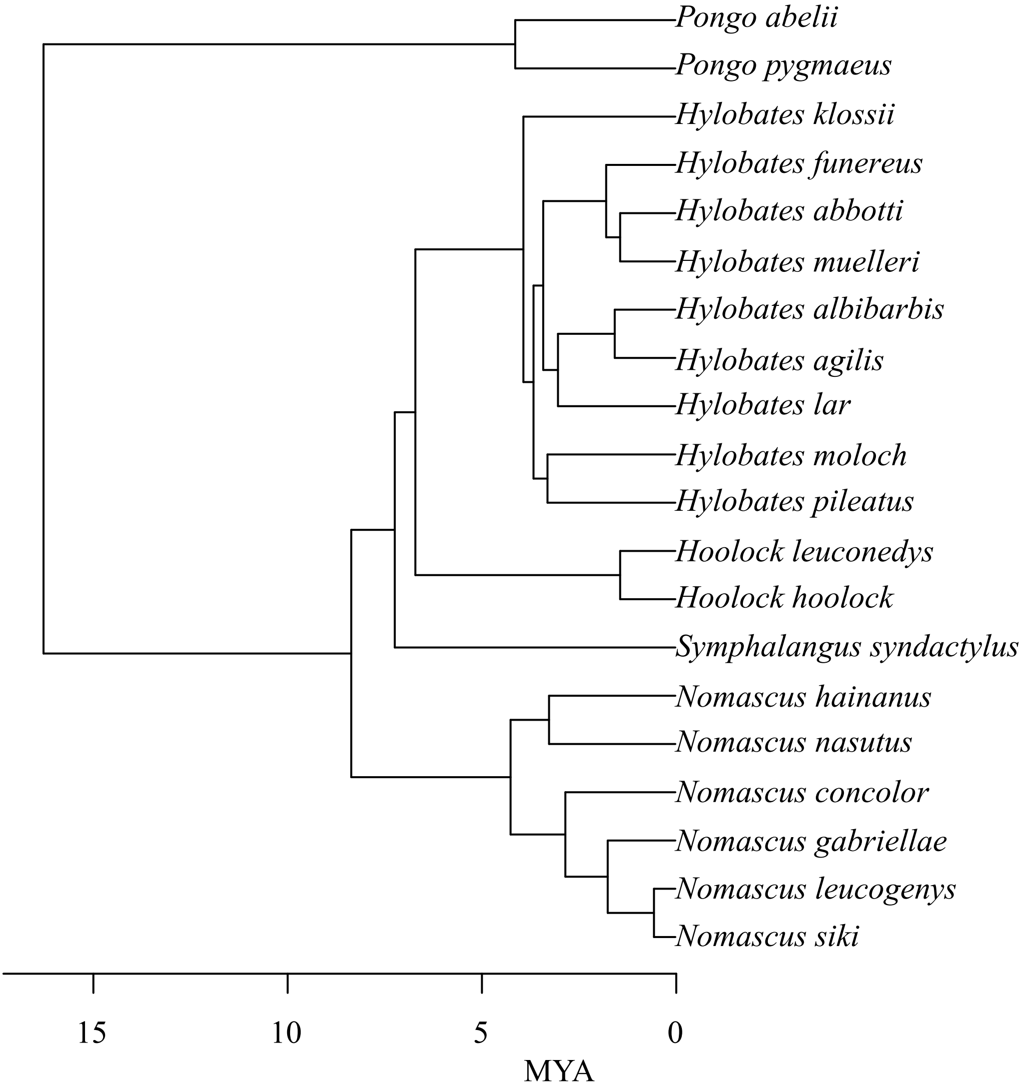
Perelman *et al.* 2011



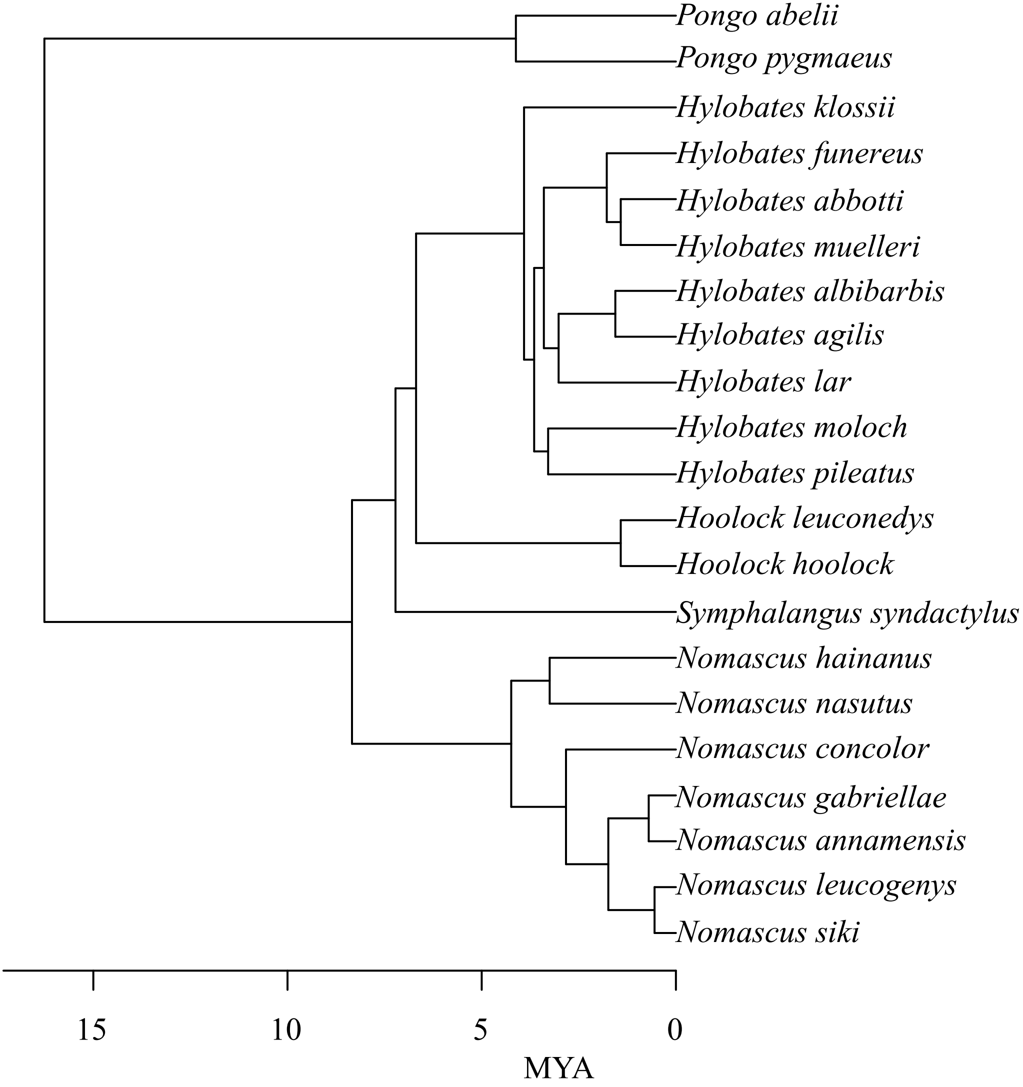
Springer *et al.* 2012

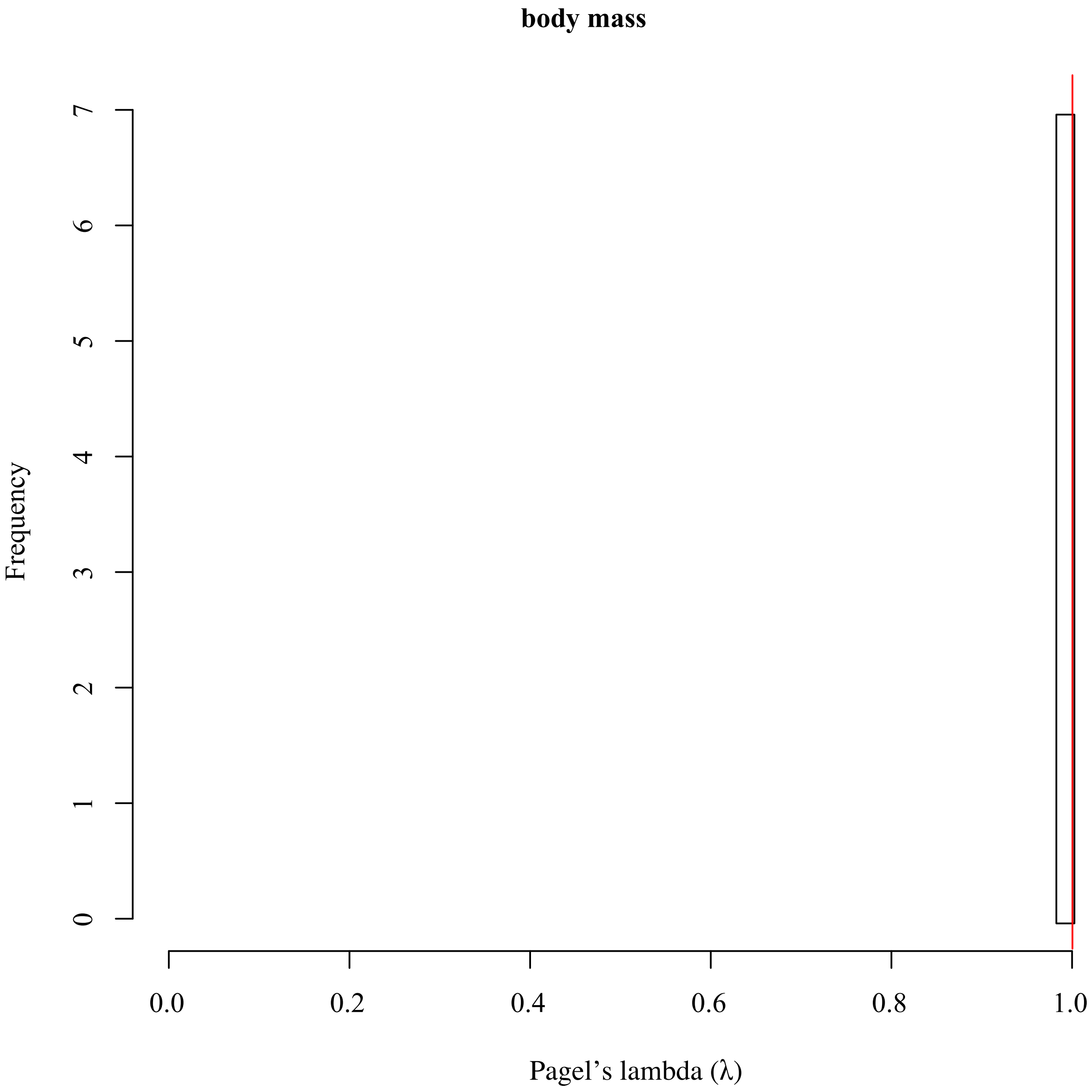


Thinh *et al.* 2010



Thinh *et al.* 2010 edited (*Nomascus annamensis* added)




body mass
Frequency
0
1
2
3
4
5
6
7
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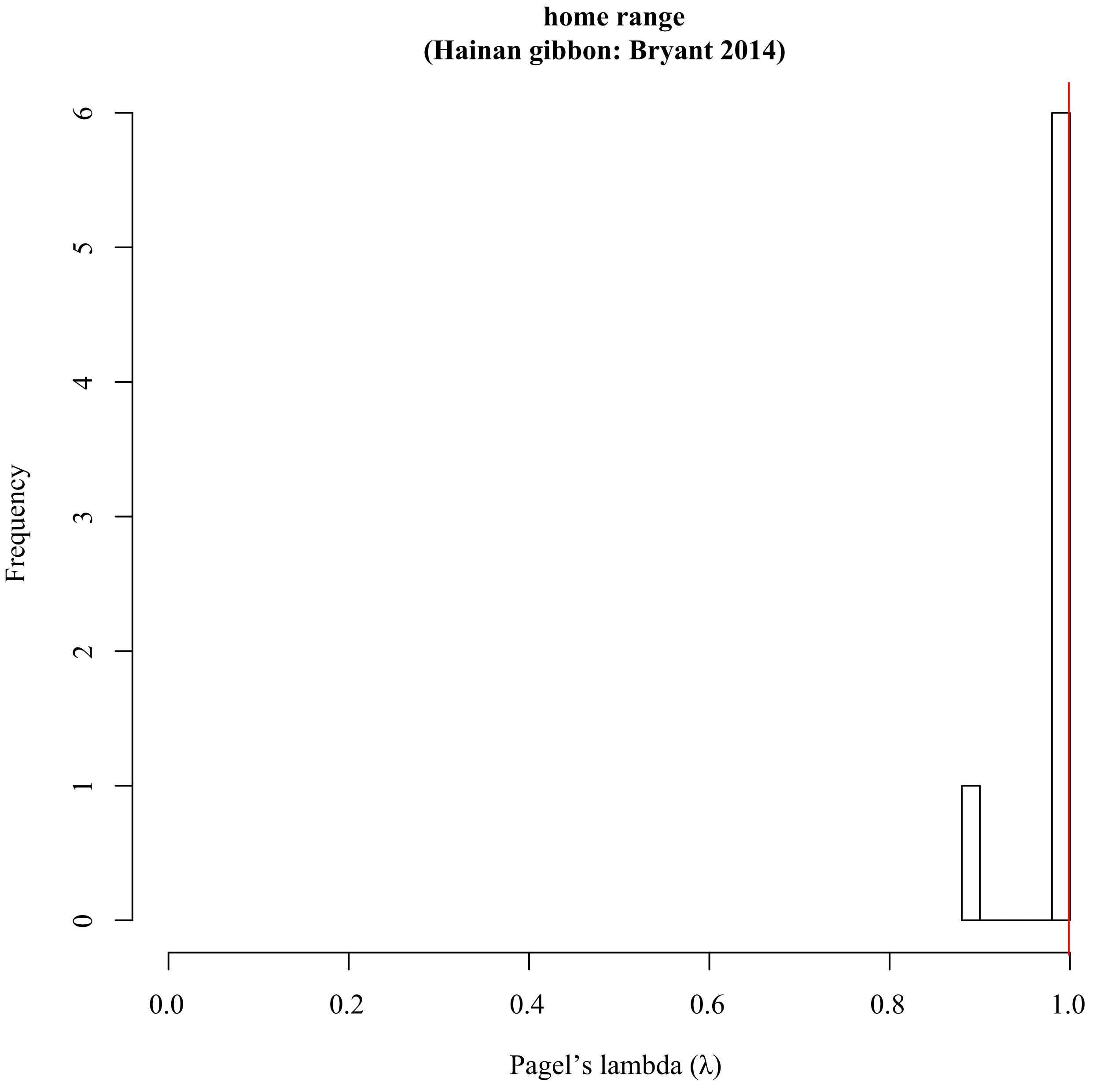
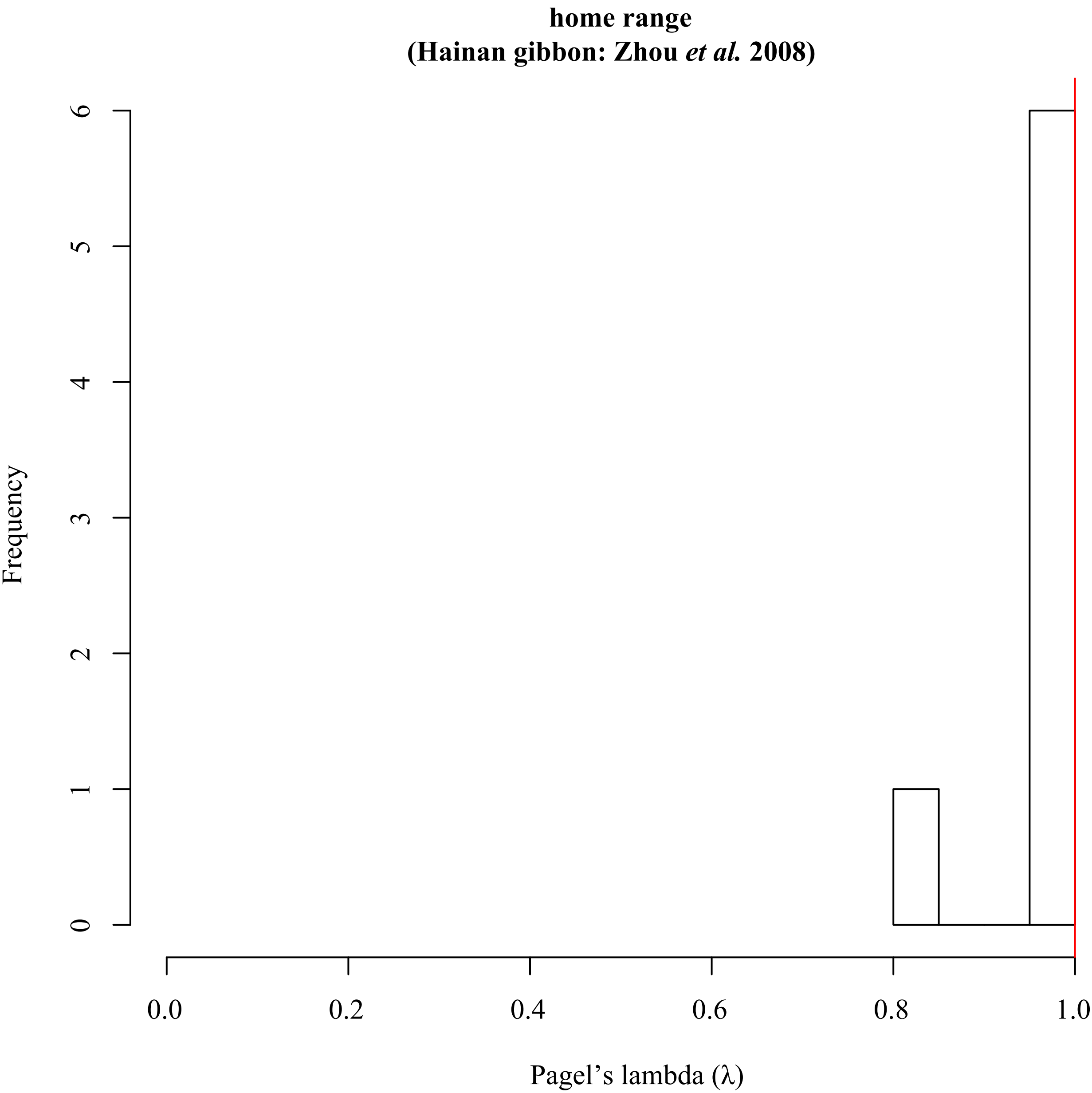
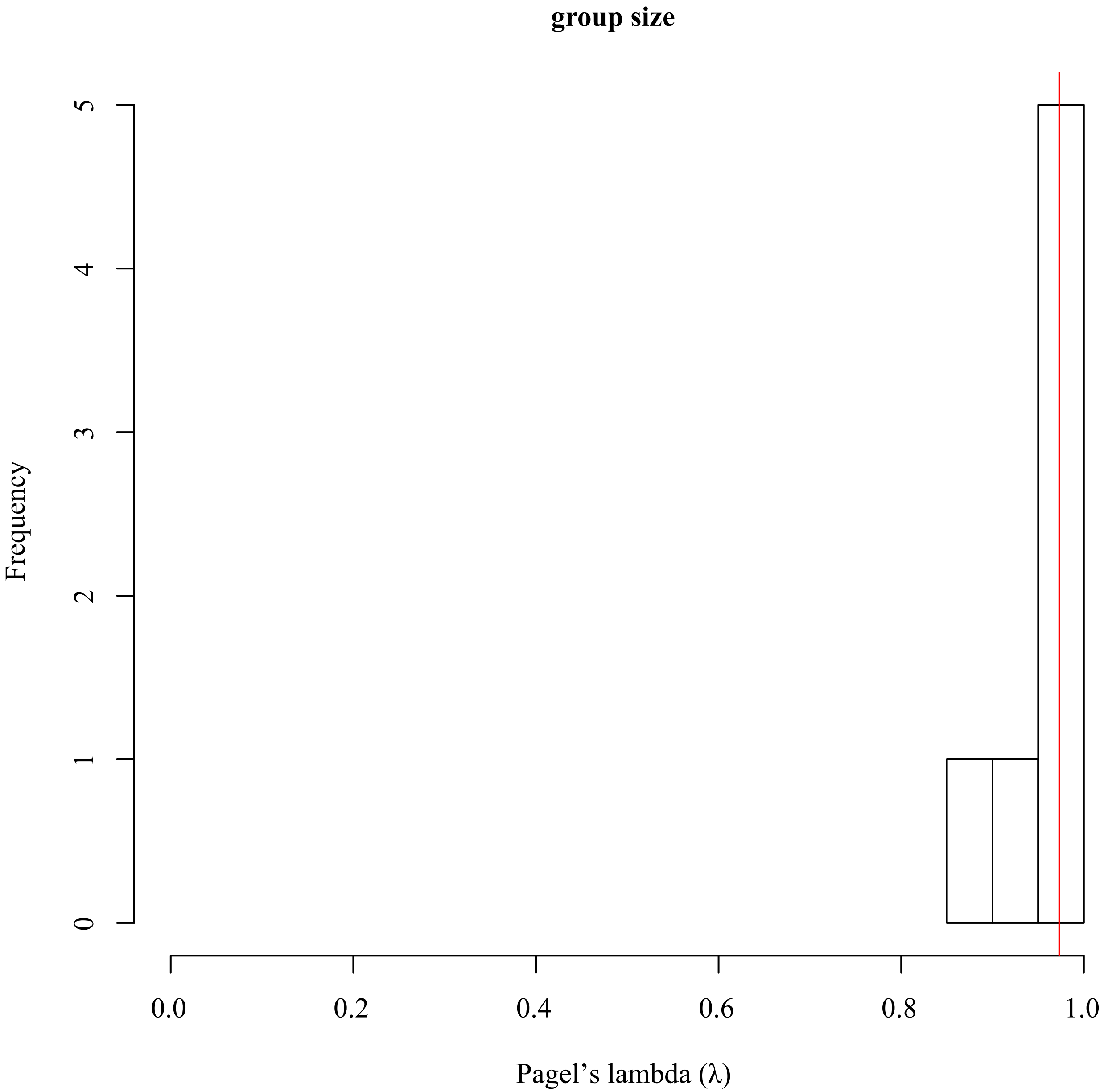
0.2
0.4
0.6
0.8
1.0
Pagel's lambda (λ)


home range
(Hainan gibbon: Bryant 2014)
Frequency
0
1
2
3
4
5
6
0.0
0.2
0.4
0.6
0.8
1.0
Pagel's lambda (λ)


home range
(Hainan gibbon: Zhou *et al.* 2008)
Frequency
0
1
2
3
4
5
6
0.0
0.2
0.4
0.6
0.8
1.0
Pagel's lambda (λ)


group size
Frequency
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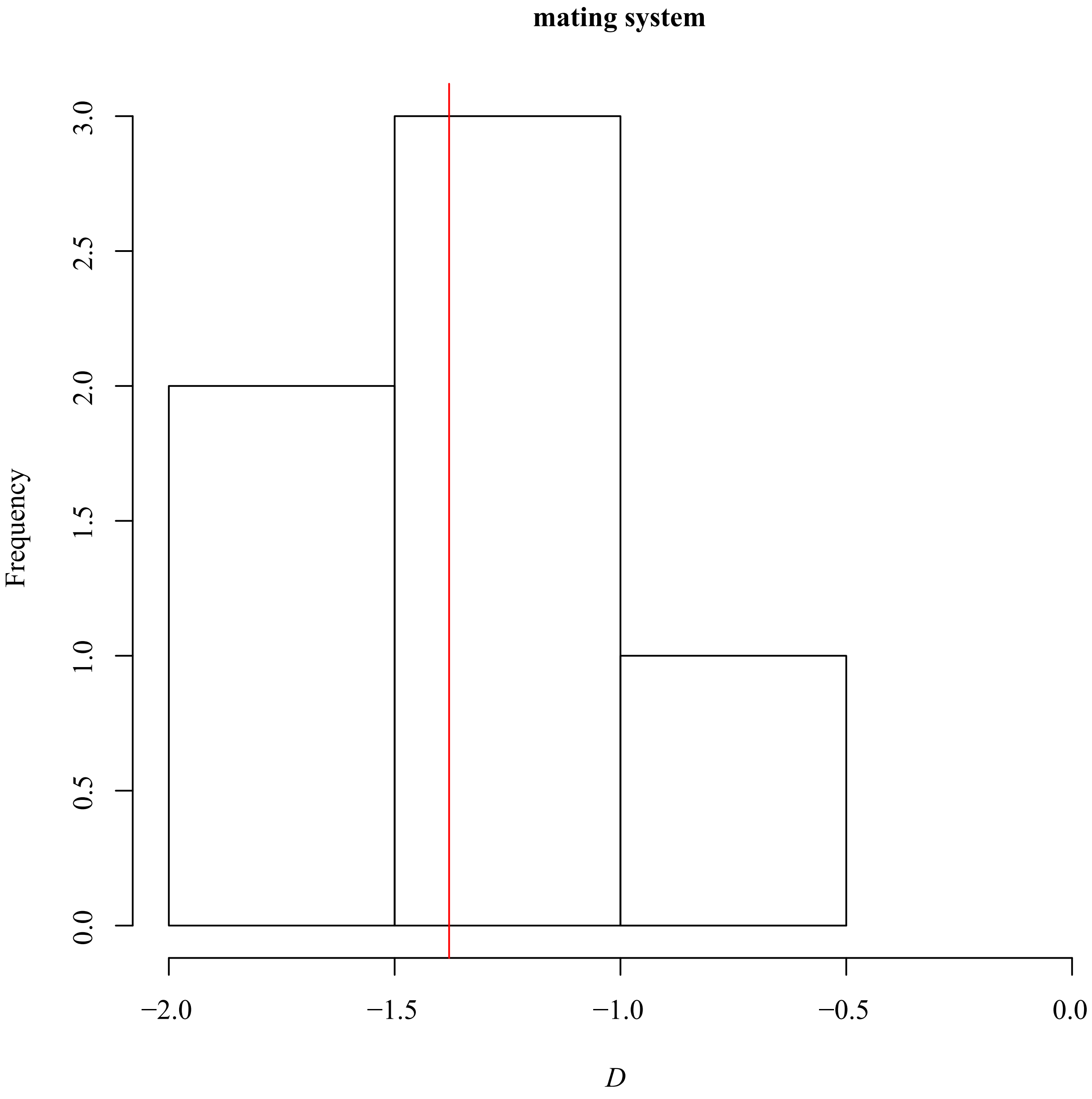
2
3
4
5
0.0
0.2
0.4
0.6
0.8
1.0
Pagel's lambda (λ)


mating system
Frequency
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0.5
1.0
1.5
2.0
2.5
3.0
−2.0
−1.5
−1.0
−0.5
0.0
D