Supplementary figure captions

Fig. S1. Subsampled richness at different quorum levels of shareholder quorum subsampling [1]. Although fewer time intervals are included when the quorum level is larger, the relative trends are not altered.

Fig. S2. Comparison of the effects of different choices for calculation of Good's u and other SQS procedures. (A) We calculated Good's u based on single-reference taxa, excluding the most common taxon and the largest collection ("Refs, common, largest"). However, the shape of the richness curve is unchanged if we calculate Good's u based on single-reference taxa, excluding the most common taxon but not the largest collection ("Refs, common"). It is likewise unchanged if we calculate Good's u only from single-reference taxa without any adjustments ("Refs"). Use of occurrences rather than references, regardless of other choices, also has little effect. (B) We did not downweight references that yielded many collections because most PBDB insect collections contain occurrences from multiple references. The subsampled richness curve is unchanged if we do downweight large references.

Fig. S3. Comparison of Paleobiology Database data with existing range-through diversity curves[2,3]. The Paleobiology Database (PBDB) yields comparable diversity curves to previously published studies when it is treated with range-through counting methods including extant records (the Pull of the Recent). The Nicholson et al. curve[3] reaches slightly greater heights because it includes some families known only from trace fossils and because the PBDB curve is only based on records identified to genus level or lower.

Fig. S4. Paleolatitudinal distribution of fossil insect occurrences from compression fossil localities (excluding amber). North America, Europe, and countries of the former Soviet Union all have a peak around 45 degrees paleolatitude, with fewer occurrences around 10-30 degrees. North American and Europe independently have a bimodal distribution with a smaller peak of occurrences centered around the paleo-equator.

Fig. S5. Paleolatitudinal distribution of compression fossil occurrences in PBDB "10 million year" time intervals. Distributions are shown as beanplots [4], which contour the occurrences with a Gaussian smoothing curve. The width of the bean is scaled to the number of occurrences at a given paleolatitude. Sampling is concentrated in the northern hemisphere, due to extensive research in North America, Europe, countries of the former Soviet Union, and China. Like in figure S4, insect occurrences preferentially derive from paleo-equatorial regions or mid-latitudes (around 45 degrees). Some time intervals (e.g., Permian 2 and Cretaceous 3) have bimodal distributions with a low at 10-30 degrees paleolatitude.

Fig. S6. Effect of the geographic extent of sampling on subsampled family richness. Geographic extent was calculated as the distance along the minimum spanning tree connecting unique paleolatitude/paleolongitude coordinates for insect collections. If multiple collections occurred at a single location, only one paleolat/paleolongitude value was used. Unlithified and poorly lithified occurrences were excluded from both analyses. (A) SQS family richness against minimum spanning tree distance for all insect localities. (B) SQS family richness for compression fossils against minimum spanning tree distance for compression fossil localities.

There is no clear relationship between minimum spanning tree distance and subsampled richness in either analysis.

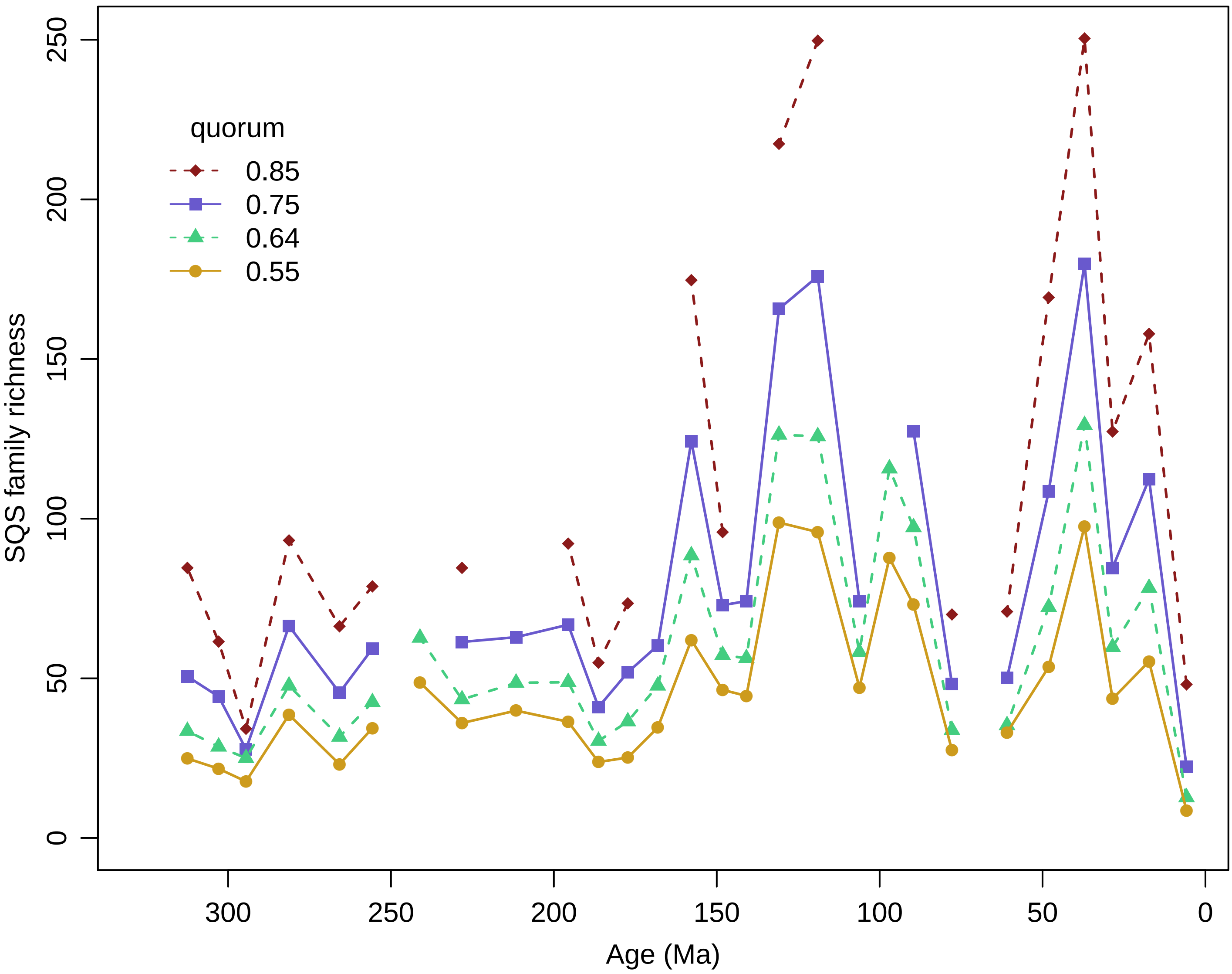
Fig. S7. Comparison of rarefied diversity curves constructed from different subsets of the published literature. (A) Bars indicate the proportion of occurrences published after 1900 (red) and 1950 (blue) in each time interval. (B) Rarefied diversity curves from all publications (gray curve with one standard deviation error bars), only papers published after 1900 (red curve), and only papers published after 1950. Diversity trends are not significantly changed when older literature, which may contain less reliable identifications, is excluded.

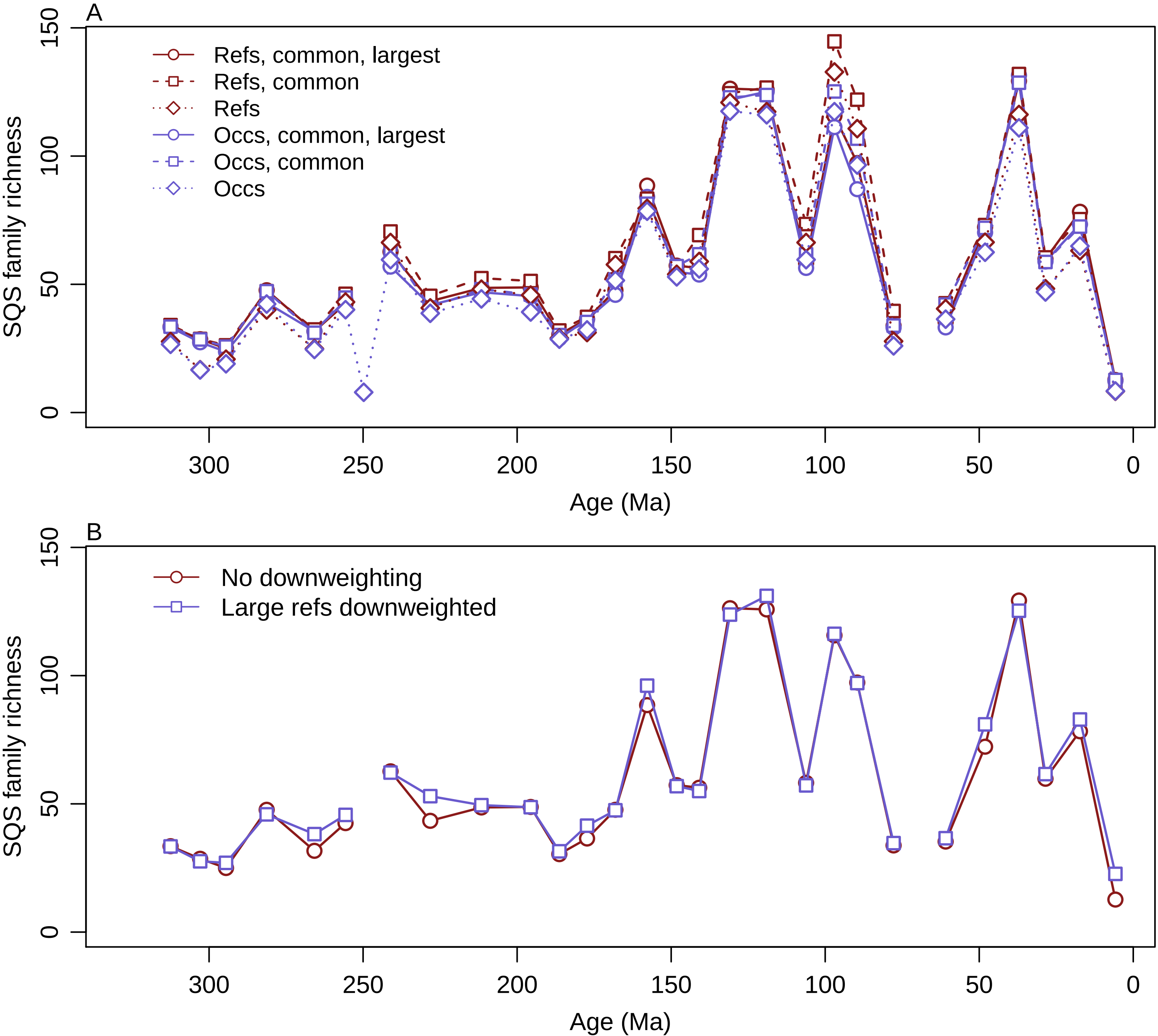
1. Alroy, J. 2010 Fair sampling of taxonomic richness and unbiased estimation of origination and extinction rates. In *Quantitative Methods in Paleobiology. The Paleontological Society Papers, Vol 16* (eds J. Alroy & G. Hunt), pp. 55–80.

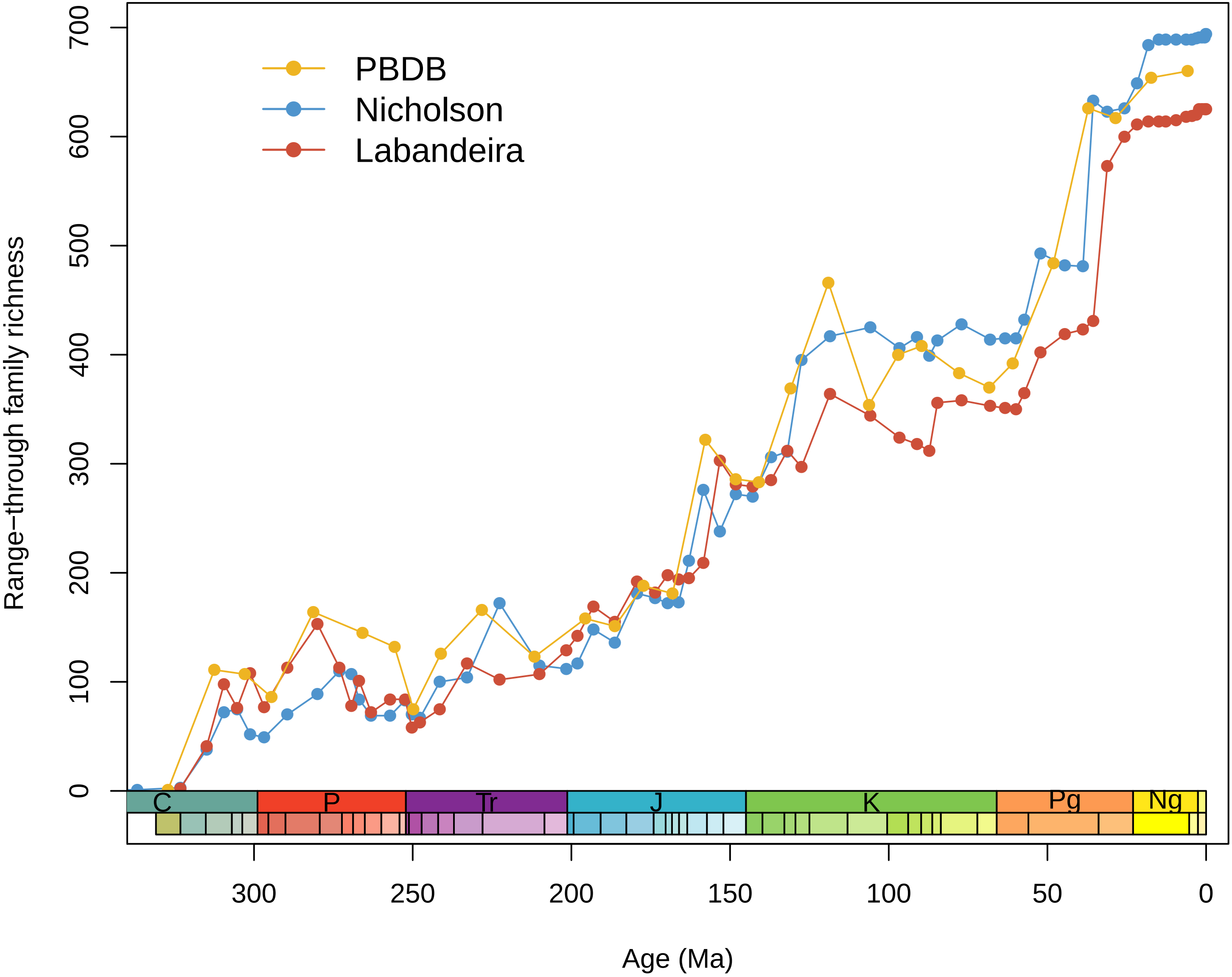
2. Labandeira, C. C. & Sepkoski, J. J. 1993 Insect diversity in the fossil record. *Science.* **261**, 310–315.

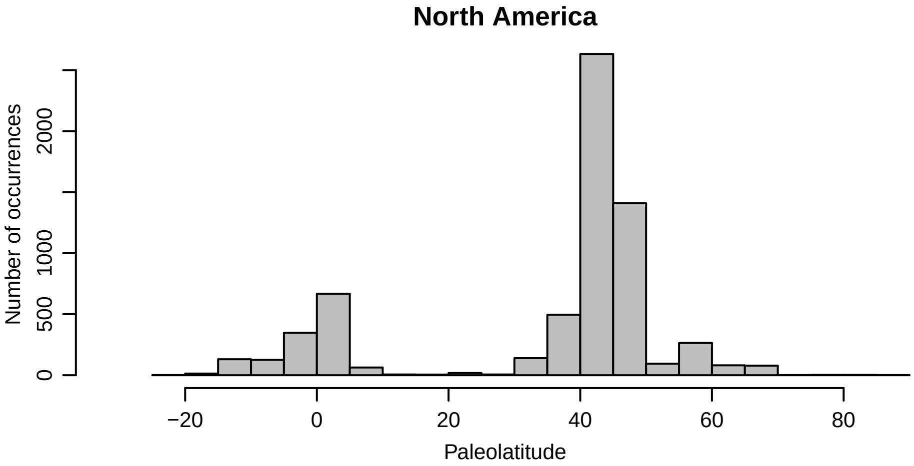
3. Nicholson, D. B., Mayhew, P. J. & Ross, A. J. 2015 Changes to the fossil record of insects through fifteen years of discovery. *PLoS One* **10**, e0128554.

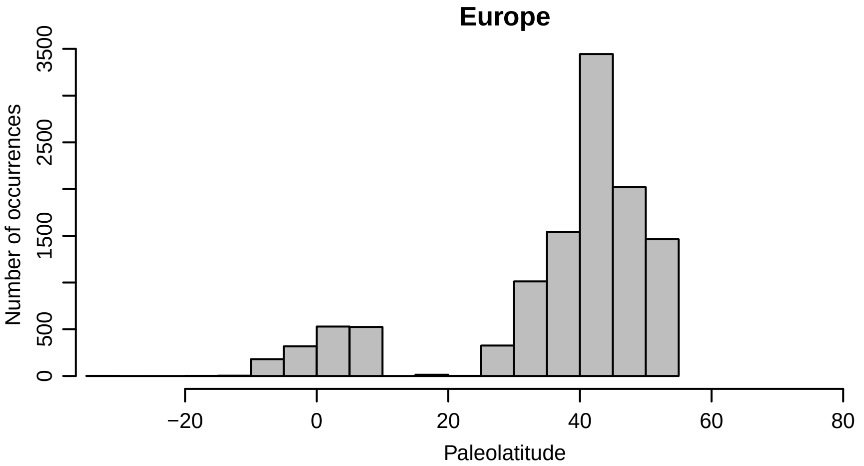
4. Kampstra, P. 2008 Beanplot: a boxplot alternative for visual comparison of distributions. *J. Stat. Software, Code Snippets* **28**, 1–9.

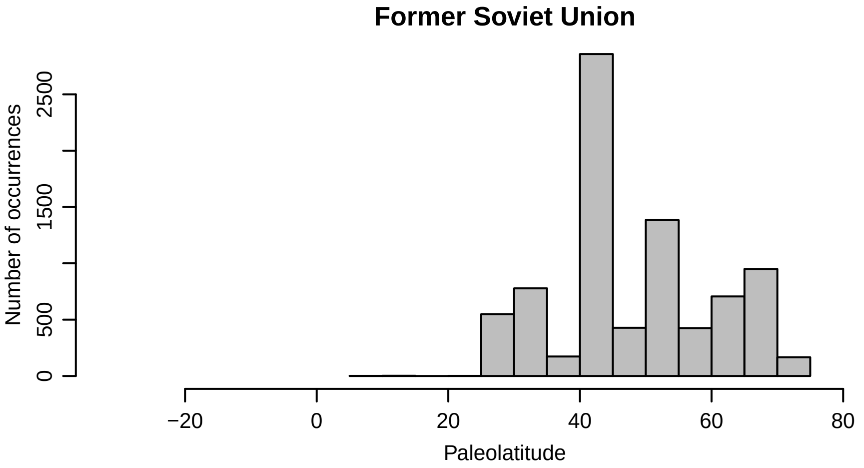

quorum
0.85
0.75
0.64
0.55
SQS family richness
0
50
100
150
200
250
Age (Ma)
300
250
200
150
100
50
0

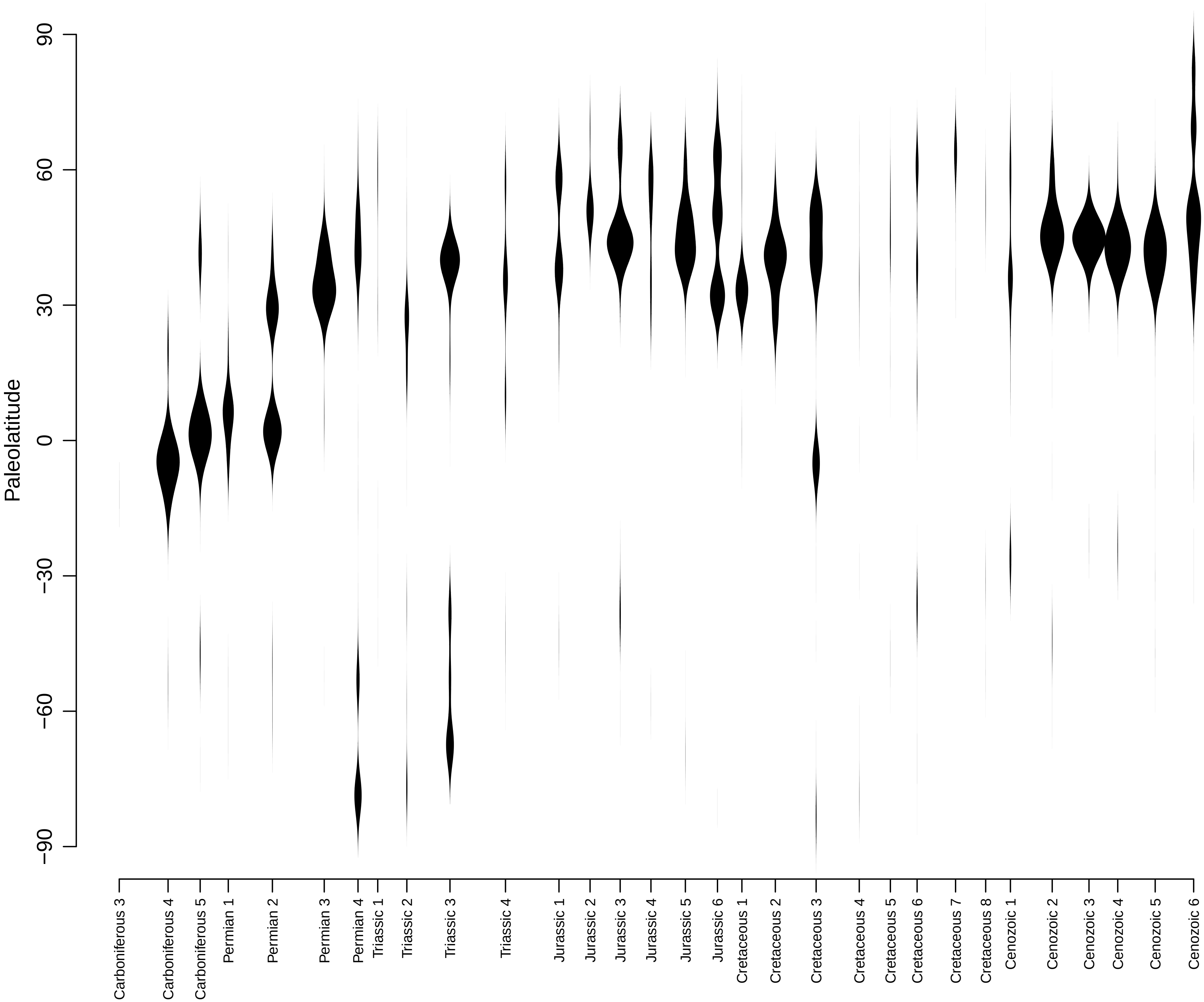

A
Refs, common, largest
Refs, common
Refs
Occs, common, largest
Occs, common
Occs
SQS family richness
0
50
100
150
300
250
200
150
100
50
0
Age (Ma)
B
No downweighting
Large refs downweighted
SQS family richness
0
50
100
150
300
250
200
150
100
50
0
Age (Ma)

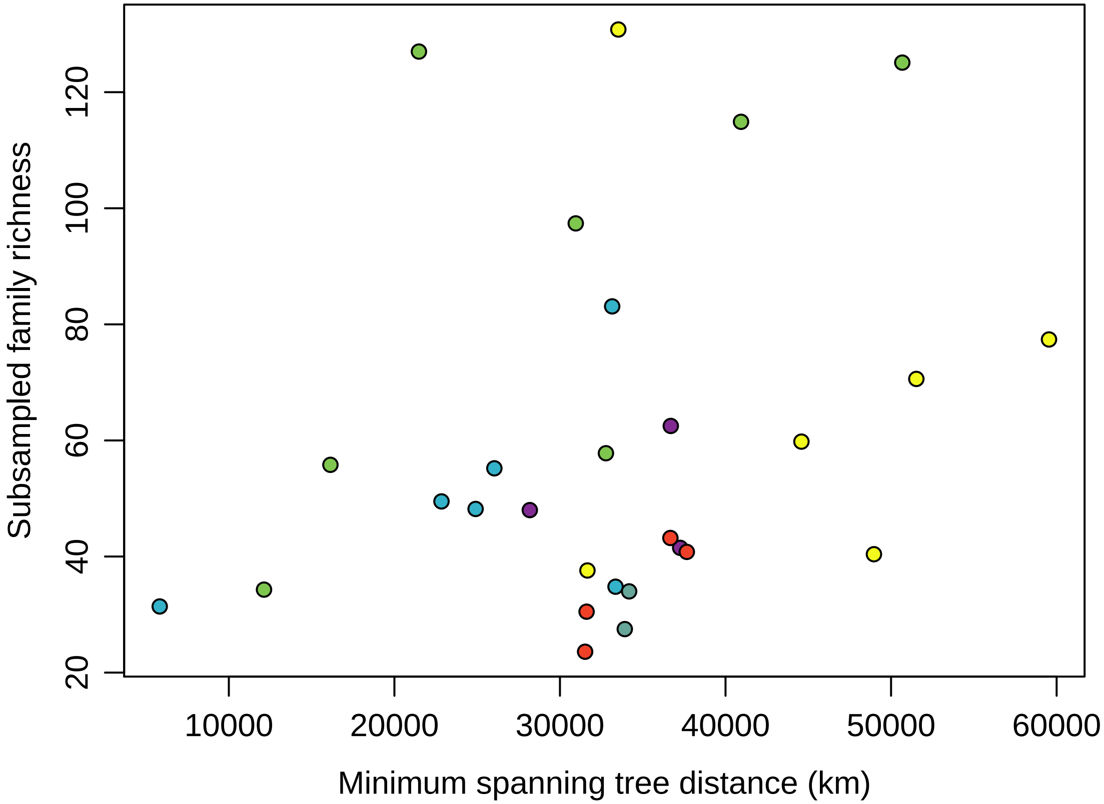

PBDB
Nicholson
Labandeira
Range−through family richness
0
100
200
300
400
500
600
700
C
P
Tr
J
K
Pg
Ng
300
250
200
150
100
50
0
Age (Ma)


North America
Number of occurrences
0
500
1000
2000
−20
0
20
40
60
80
Paleolatitude

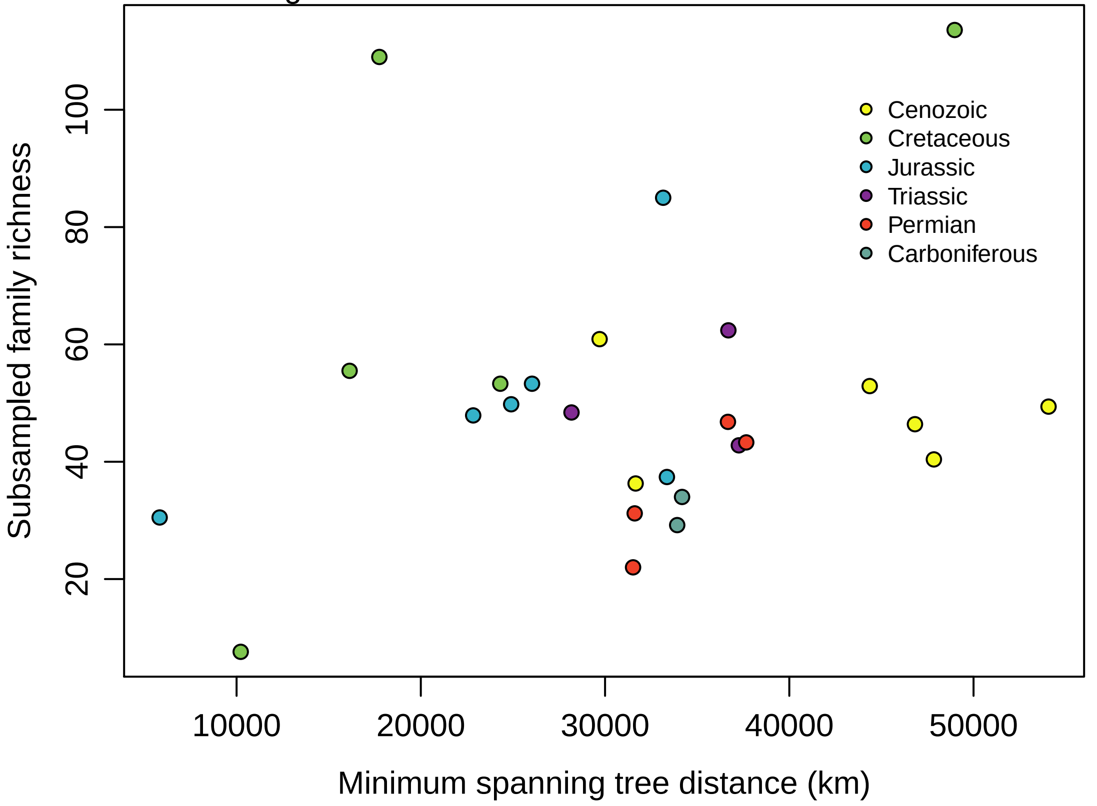

Europe
Number of occurrences
0
500
1500
2500
3500
−20
0
20
40
60
80
Paleolatitude


Former Soviet Union
Number of occurrences
0
500
1500
2500
−20
0
20
40
60
80
Paleolatitude

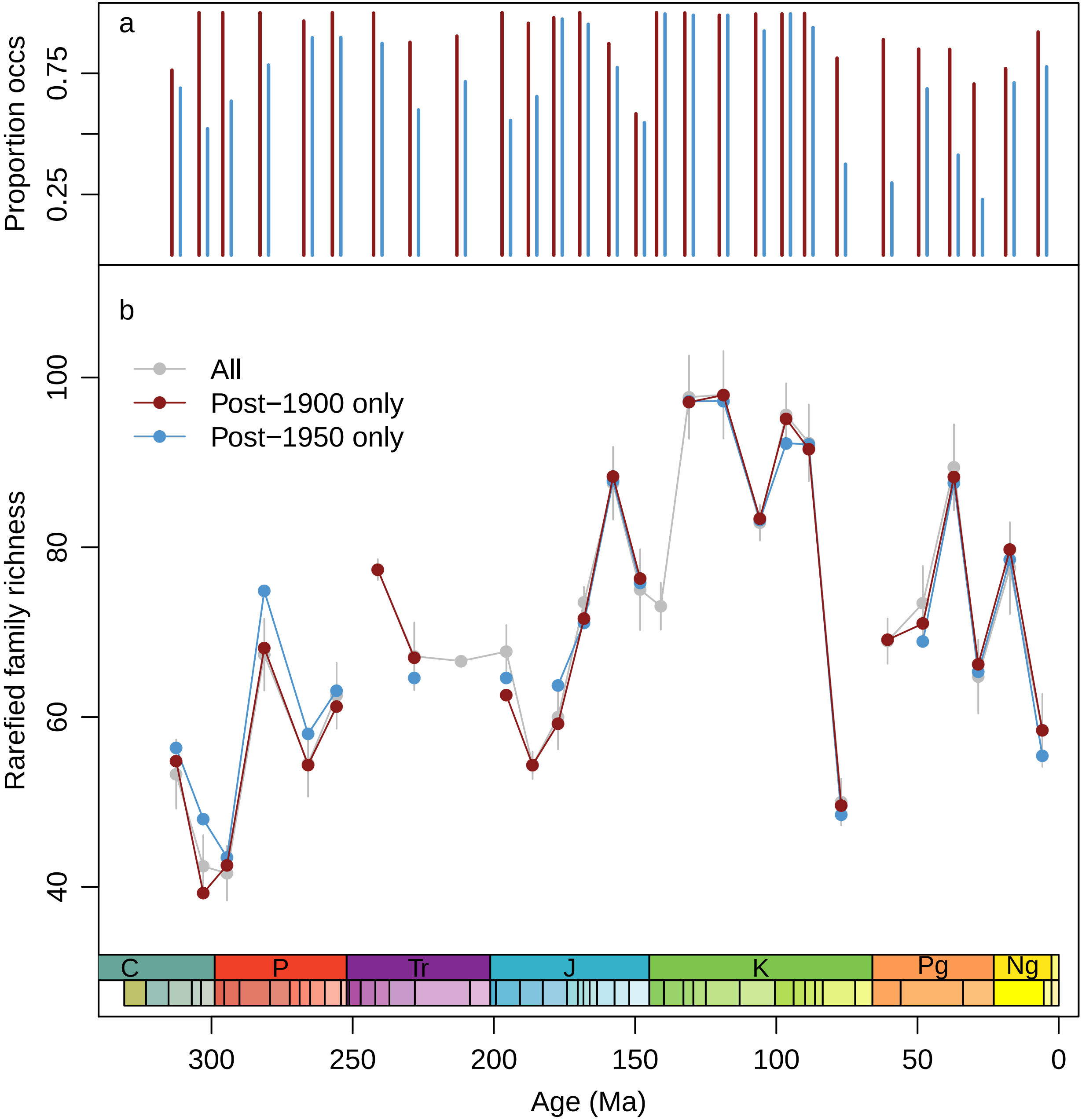

Paleolatitude
90
60
30
0
−30
−60
−90
Carboniferous 3
Carboniferous 4
Carboniferous 5
Permian 1
Permian 2
Permian 3
Permian 4
Triassic 1
Triassic 2
Triassic 3
Triassic 4
Jurassic 1
Jurassic 2
Jurassic 3
Jurassic 4
Jurassic 5
Jurassic 6
Cretaceous 1
Cretaceous 2
Cretaceous 3
Cretaceous 4
Cretaceous 5
Cretaceous 6
Cretaceous 7
Cretaceous 8
Cenozoic 1
Cenozoic 2
Cenozoic 3
Cenozoic 4
Cenozoic 5
Cenozoic 6



A. All insects



B. Excluding amber


a
Proportion occs
0.25
0.75
b
Rarefied family richness
40
60
80
100
All
Post−1900 only
Post−1950 only
C
P
Tr
J
K
Pg
Ng
300
250
200
150
100
50
0
Age (Ma)