## Phylogenomics indicates Amazonia as the major source of Neotropical swarm-

## founding social wasps diversity

Appendix 3. Supplementary tree figures.

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Figure S1. ML tree from unpartitioned RAxML analysis of the Epiponini-129T-F0 data set.



Figure S2. ML tree from unpartitioned RAxML analysis of the Epiponini-129T-F50 data set.



Figure S3. ML tree from unpartitioned RAxML analysis of the Epiponini-112T-F50 data set.



Figure S4. ML tree from unpartitioned RAxML analysis of the Epiponini-78T-F70 data set.



**Figure S5.** ML tree from the by-locus partitioned RAxML analysis of the Epiponini-112T-F50 data set.



**Figure S6.** ML tree from the hcluster partitioned RAxML analysis of the Epiponini-112T-F50 data set.



**Figure S7.** ML tree from the reluster partitioned RAxML analysis of the Epiponini-112T-F50 data set.



**Figure S8.** Bayesian tree from unpartitioned ExaBayes analysis of the Epiponini-112T-F50 data set.



**Figure S9.** Species tree from ASTRAL analysis of the 950 UCE loci of the Epiponini-112T data set. Support values form 100 multi-locus bootstrap replicates.



**Figure S10.** Species tree from ASTRAL analysis of the 500 best UCE loci (best = lowest clocklikeness value) of the Epiponini-112T data set. Support values form 100 multi-locus bootstrap replicates.



**Figure S11.** Time-calibrated tree from BEAST analysis using a constraint topology, a set of 100 best (best = lowest clocklikeness value) selected loci, and four fossil calibrations. Node labels are ages in millions of years ago and node bars indicate 95% highest posterior densities.



**Figure S12.** Ancestral areas estimated with BioGeoBEARS using the DEC model. Node labels indicate the most likely ancestral area.



**Figure S13.** Ancestral areas estimated with BioGeoBEARS using the DEC model. Pie charts on nodes indicate the relative probabilities of ancestral areas.



**Figure S14.** Ancestral areas estimated with RASP using the DEC model. Pie charts on nodes indicate the most likely state of ancestral areas.