



**Fig. 1 | Evolutionary relationships and diversification patterns of butterflies.** Time-calibrated tree of 2,244 butterfly species based on 391 loci and 150 amino acid partitions. Branches show distinct changes in diversification (circles) as estimated by clade-specific models. Letters at nodes refer to clades with significant rate shifts (see section 6 of Supplementary Results). Coloured lines

in the outer ring beside tips indicate association with one of the 13 host modules (see section 17 of Extended Online Methods). Black lines in the host association ring indicate species without data, and asterisks denote non-monophyletic subfamilies. Supplementary Fig. 1 shows this tree with visible species names and ages for all nodes.

## Results and discussion

To elucidate patterns of global butterfly diversification in space and time, we used targeted exon capture<sup>8</sup> to assemble a dataset of 391 gene regions (161,166 nucleotides and 53,722 amino acids) from 2,244 butterfly species (Supplementary Table 1). The majority (1,914 specimens) of butterflies sampled were newly sequenced for this study, representing all families, subfamilies and tribes, and 92% of recognized genera, from 90 countries. These were obtained from 28 specimen collections across the world (see section 2 of the Extended Online Methods). Phylogenomic trees were inferred with nucleotides

or translated amino acids with nine different subsets and partitioning schemes. Our trees were highly congruent, with strong support for the monophyly of all families and nearly all subfamilies with branch support metrics (SH-aLRT, ultrafast bootstrap) and multispecies coalescent species tree analyses (Supplementary Table 2). We also conducted four-cluster likelihood mapping to identify potentially conflicting signals in our datasets (Supplementary Table 3). Our results strongly support the need for revision of the classification of at least 36 butterfly tribes (27% of total) as currently circumscribed (Supplementary Table 2).