



Fig. S7. | Consistency of RAD-seq and gene-based phylogenies. To check whether our RAD-seq based phylogeny was consistent with previous analyses, we compared the topology of subtrees of overlapping taxa between the current analysis (i.e. as seen in Fig. S4) and a previous analyses based on different molecular data (tree from a family wide diversification analysis in Economato et al. 2018, most of the data from Ward et al. 2015 which also inferred a nearly identical topology). In some cases, where the same species was not sequenced, a closely related species from the same species group was substituted for the comparison (*S. atopogenys* for *S. ocypete*, *S. sistrura* for *S. olsoni*, *S. simoni* for *S. ludovici*, *S. hubbewatyorum* for *S. nitens*), these are denoted with parentheses. Numbers indicate bootstrap support for nodes that disagreed between the two trees. Note the 11-gene phylogeny recovered the ambatrix group in the “root 1” position, sister to the rest of *Strumigenys* (although *capitata* group was not included).