Supplementary Fig. 1. ML phylogenetic tree based on concatenated datasheet, see text for details. Numbers indicate bootstrap values for Maximum Likelihood. The tree was prepared for publication using EasyTreeEditor[1] software (see brief description under the tree).

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[1] **EasyTreeEditor** is available from https://sanamyan.com/easytreeeditor

- It supports standard tree file formats (Newick or Nexus) and displays them as rectangular cladograms.
- All labels (taxa, clades) can be edited directly on the tree as plain text (including italic and bold formatting).
- Line colors, thickness, collapsing/expanding clades, and color highlighting - all these can be easily modified without navigating through menus.
- The topology comparison between two trees is particularly convenient.
- ML support values and Bayesian probabilities from two trees can be automatically combined ("95/0.99") into a single tree - the program will automatically match corresponding branches and copy values where needed.
- Tree export for publication in PDF. You can specify the page width in millimeters to match journal requirements - extremely useful in some cases.