Supplementary Figure S1. Maximum likelihood tree for ATP5FA1 proteins obtained using the MamXB+FO+G4 model of sequence evolution in IQ-TREE. Rate matrices for the MamXB model are available in a nexus file from https://github.com/ebraun68/clade_specific_prot_models (last accessed 24 November 2021). (**a**) Topology with branch lengths. (**b**) Topology with ultrafast bootstrap values. Note that the topologies in parts **a** and **b** are identical, part **b** is presented as a cladogram to make it easier to read the support values. The position of the root is arbitrary.