Figure S2. Midpoint-rooted Maximum-Likelihood trees with topologies different from the phylotranscriptomic tree topology (Fig. 1B in the main text), divergent branch topology is in red. The trees were constructed based on alignments with 10 randomly picked amino acid sequences and 100 rounds of rapid bootstrap analysis. Trees in panel A and B were the most common among such variants. With increasing number of randomly selected proteins, the topologies converge towards the fully resolved 792-amino acid sequences phylogeny (see Fig. 2 in the main text).