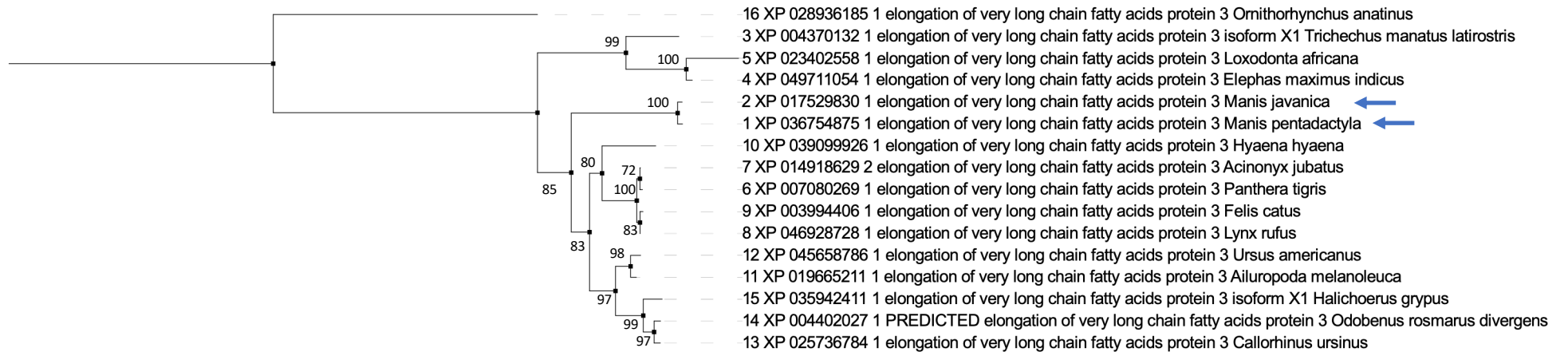


Tree scale: 0.1



Online Resource 6. Neighbor-joining phylogenetic tree (amino acid sequence alignment produced with Mafft (defaults), JTT substitution model; numbers at nodes represent percentage of 1000 bootstraps).