Additional file 3. Phylogenies inferred from 47 individual proteins

Consensus alignments of orthologous sequences of 47 proteins retrieved from 14 amoebozoan genomes were determined using M-coffee (Wallace et al., 2006), with 8 alignment algorithms. Regions with poor consensus alignment or with long insertions in only few proteins were deleted. Phylogenies were inferred by Bayesian inference (Ronquist and Huelsenbeck, 2003) using a mixed amino-acid substitution models with rate variation between sites estimated by a gamma distribution with a proportion of invariable sites. Analysis were run for 1 million generations. Trees were rooted at midpoint using Figtree (http://tree.bio.ed.ac.uk/software/figtree/), with posterior probabilities shown at the nodes. Panel A: proteins a-h; Panel B: proteins m-x. The consensus phylogeny of all 47 concatenated proteins (see also figure 2) is shown top left in Panel A.