SUPPLEMENTARY INFORMATION

**SUPPLEMENTARY FILE 1. Subtree-prune-and-regraft distances (SPR) calculated using rSPR software for the ML trees generated with IQ-Tree 1.5.5 for the alignments produced by GBlocks 0.91b with different values of the parameter “Minimum Number Of Sequences For A Flank Position”.**

The lowest value for which the tree topology was the most stable (marked with black dot) was considered optimal.

**SUPPLEMENTARY FILE 2. Alignment of 145 complete or almost complete sequences of the 18S rRNA gene of Myxomycetes (139) and dictyostelids as an outgroup (6) in FASTA format.**

Conservative positions (1105) selected with GBlocks for phylogeny construction for Fig 2 are shown in a mask in the first line.

**SUPPLEMENTARY FILE 3. List of GenBank accessions used for supplementary alignment (supplementary file 1).**

**SUPPLEMENTARY FILE 4. Sources of information for the revised hierarchical classification.**

For the following studies contributing information to the phylogeny of Myxomycetes, the group of interest, the used marker and outgroup of a phylogenetic tree is listed.