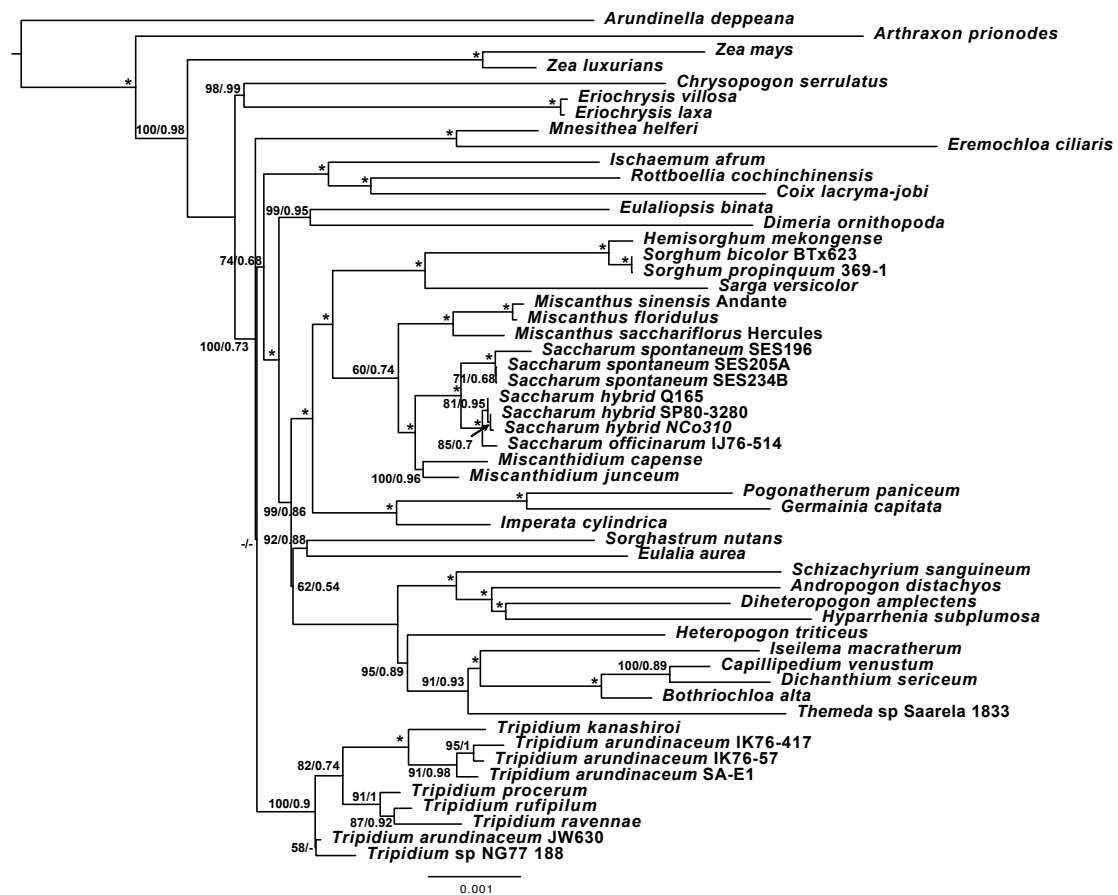


Additional file 4



Phylogeny generated from a standard alignment, after Prank optimization, using LSC, IR_A and SSC partitions only. Topological changes and generally poorer branch supports are shown so that this phylogeny can be compared with Figure 3 of the main manuscript. Branch supports are given as non-parametric bootstrap values/Bayesian inference values. The scale bar at the bottom represents the number of substitutions per site. The phylogeny was rooted on *Arundinella deppeana*.