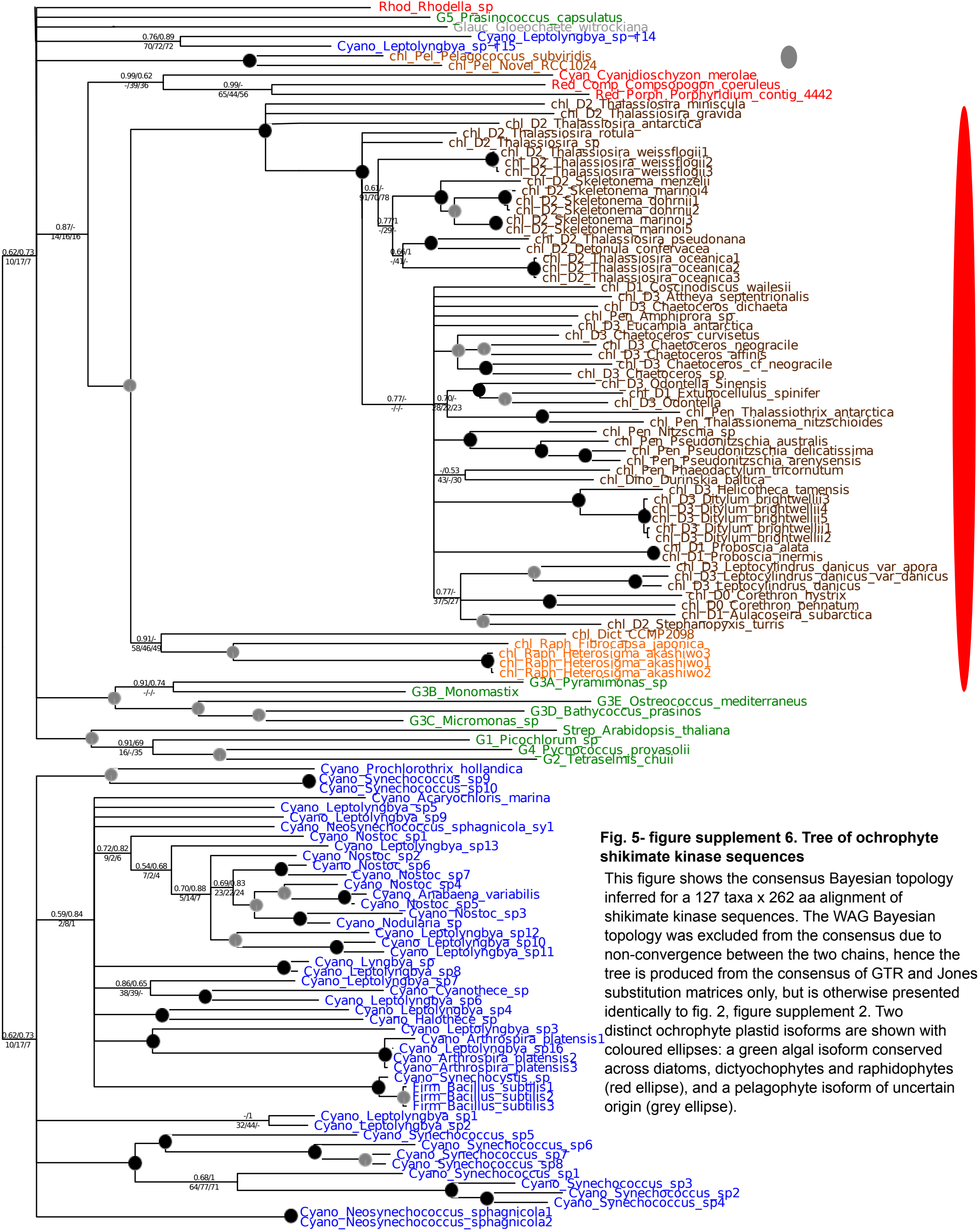

Fig. 5- figure supplement 6. Tree of ochrophyte shikimate kinase sequences

This figure shows the consensus Bayesian topology inferred for a 127 taxa x 262 aa alignment of shikimate kinase sequences. The WAG Bayesian topology was excluded from the consensus due to non-convergence between the two chains, hence the tree is produced from the consensus of GTR and Jones substitution matrices only, but is otherwise presented identically to fig. 2, figure supplement 2. Two distinct ochrophyte plastid isoforms are shown with coloured ellipses: a green algal isoform conserved across diatoms, dictyochophytes and raphidophytes (red ellipse), and a pelagophyte isoform of uncertain origin (grey ellipse).