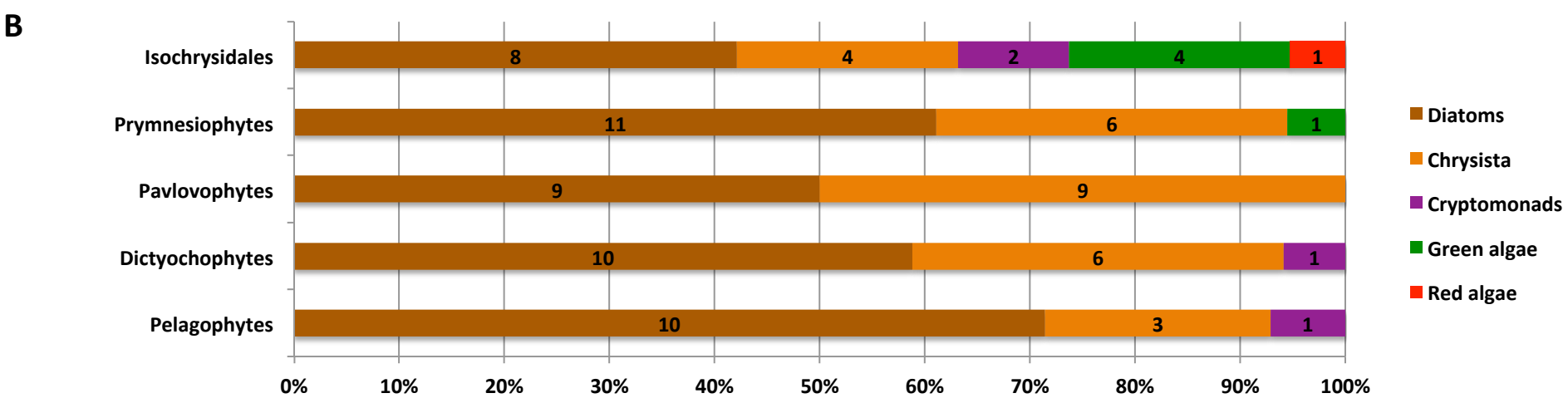Fig. 8- figure supplement 4. Evidence for gene transfer from pelagophytes and dictyochyophytes into haptophytes. Panel A shows the next deepest sister groups identified for haptophyte proteins of hypogyristean origin in single-gene trees. The pie chart **(i)** compares the number of single-gene trees in which the combined clade of hatpohyte and hypogyristean proteins resolves within a larger clade comprising the ochrophyte HPPG, compared to the number that resolves in external positions, either with other lineages or as a sister-group to all other sequences within the HPPG clade. Sequences for which no clear next deepest sister group affinity could be identified are listed as "not determined". The heatmap (**ii**) shows the specific sister-group sequences associated with 65 HPPGs in which the haptophyte sequences specifically resolve with the pelagophyte/ dictyochophyte clade and for which a clear internal or external position for the haptophyte/ hypogyristean group relative to the remaining ochrophyte HPPG clade could be identified. Both analyses indicate a clear bias for haptophyte sequences branching within a deeper ochrophyte clade, not just restricted to the immediate sister-groups. **Panel B** tabulates the BLAST next best hits for haptophyte sequences for which a phylogenetically consistent (>3 consecutive top hits) top hit to hypogyristea could be identified, and pelagophyte/ dictyochophyte sequences for which a phylogenetically consistent top hit to haptophytes could be identified. In each case either the largest number of sequences, or (in the case of pavlovophytes) the joint largest number of sequences for which a phylogenetically consistent next best hit could be identified resolved with diatoms, indicating that these sequences were probably present in a common ancestor of diatoms and hypogyristea, and subsequently transferred to haptophytes.