



**Fig. 9- figure supplement 3. Single-gene tree topologies associated with individual plastid-encoded genes.** These heatmaps show the first sister-groups identified to haptophytes, and members of the pelagophyte/ dictyochophyte clade, in single-gene trees of component genes included in concatenated trees of plastid-encoded proteins using both the gene-rich (i) and taxon-rich (ii) alignments. Topologies are given for trees inferred with MrBayes using the Jones substitution matrix, and RAxML trees inferred using JTT, under the same conditions as the multigene trees. The identity of the first sister-group is shaded according to the legend given below. Only three single-gene trees (labelled with black arrows) support any sister-group relationship between haptophytes and the pelagophyte/ dictyochophyte clade; however, in each case (explained beneath the legend) this topology is not robustly supported, either due to polyphyly of one of the constituent lineages, or conflicting topologies identified via alternative methods.

ii) Taxon-rich dataset

