New Phytologist Supporting Information

The genome of a nonphotosynthetic diatom provides insights into the metabolic shift to heterotrophy and constraints on the loss of photosynthesis

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Supporting Information Figure S1. Contrasting inferences of gene family expansion and contraction in nonphotosynthetic diatoms (Nitzschia Nitz4 and NIES-3581) based on analyses of protein-coding genes from genomes only (a) or genomes and transcriptomes (b). Transcriptome data include Bolidomonas pacifica, Nitzschia CCMP2144, and Nitzschia NIES-3581. The number of gene family expansions and contractions are labeled on each branch with “+” and “–”, respectively, followed in parentheses by the number of significantly rapidly evolving families identified by CAFE. Redundancy in the transcriptome assembly of Nitzschia NIES-3581 resulted in an overestimate of the number of genes in NIES-3581 and, consequently, artifactual overestimates of both gene family expansions in that species as well as contractions in Nitzschia Nitz4.
Supporting Information Figure S2. Light and scanning electron micrographs of *Nitzschia* sp. strain Nitz4. Scale bar = 1 micrometer.