**Table S1**. Number of contigs containing rRNAs and tRNAs in each transcriptome.

|  |  |  |
| --- | --- | --- |
| Species | rRNAs | tRNAs |
| *P. parvum* | 2 | 3 |
| *C. brevifilum* | 8 | 0 |
| *C. ericina* | 17 | 13 |
| *P. antarctica* | 7 | 1 |

|  |  |  |  |
| --- | --- | --- | --- |
|  |  |  |  |

**Table S2. Predicted proteins related to cobalamin biosynthesis.** METH: B12-dependent methionine synthase; MCM: methylmalonyl-CoA mutase; CobB: cobyrinic acid a,c-diamine synthase; CobNST: CobN subunit of cobaltochelatase; CobW: protein putatively involved in cobalamin biosynthesis but its specific catalytic role is unclear.

|  |  |
| --- | --- |
| **ORF** | **Annotation** |
| ***P. parvum***  6621\_1  5553\_1  19779\_1, 17579\_1 | METH  MCM  CobW |
| ***C. brevifilum***  63818\_1  109570\_1  26401\_1, 110009\_1, 78490\_1  13986\_1 | METH  MCM  CobW  CobB |
| ***C. ericina***  13279\_1, 32542\_1  29808\_1  35493\_1, 40785\_1, 50658\_1, 16219\_1, 10713\_1, 45973\_1, 26167\_1, 3438\_1, 2169\_1, 38987\_1  39377\_1 | METH  MCM  CobW  CobNST |
| ***P. antarctica***  27826\_1, 46214\_1, 11053\_1  38804\_1, 38597\_1, 46771\_1  24567\_1, 7519\_1, 17091\_1, 24039\_1, 41170\_1, 28986\_1  35735\_1 | METH  MCM  CobW  CobNST |

**Table S3. Proteins containing polyketide synthase ketosynthase (KS) domains.**

|  |  |  |
| --- | --- | --- |
| **Protein ID** | **Species** | **PKS domains** |
| 18839 | *P. parvum* | KS |
| 2015 | *P. parvum* | KS |
| 26981 | *P. parvum* | KS |
| 30494 | *P. parvum* | KS |
| 7797 | *P. parvum* | KS |
| 106225 | *C. brevifilum* | KS, KR, PP |
| 106729 | *C. brevifilum* | KS, DH, KR, PP |
| 107078 | *C. brevifilum* | KS, PP, KR |
| 107100 | *C. brevifilum* | KS, PP |
| 4093 | *P. antarctica* | KS, PP |
| 15245 | *P. antarctica* | KS |
| 23625 | *P. antarctica* | KS |
| 4182 | *P. antarctica* | KS |
| 49699 | *P. antarctica* | KS |
| 54160 | *P. antarctica* | KS |

**Table S4. Results of the non-parametric Krustal-Wallis tests for each KOG function.** The influence of phylogeny and trophic mode was tested independently with a non-parametric Krustal-Walis test followed by a Steel-Fligner test if significant differences were observed. All calculations done with XLSTAT (v.2013.06.04, Adinsoft TM) with an alpha of 0.01. Two data sets were used in this statistical analysis: (1) a dataset with most of the species present in Figure 4 but for the Mycetozoa *D. purpureaum*, the Choanoflagellate *M. brevicollis* and the Rhodophyte *C. merolae* due to statistical reasons; and (2) a reduced dataset considering only the Stramenopiles and Prymnesiophyta. Abreviations as follows: NS, not significant; YES, significant difference detected.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Original dataset | | | Reduced dataset | | | |
| KOG | Phyla | Type | KOG | Phyla | Type |
| A | NS | NS | A | NS | NS |
| **B** | **YES** | NS | B | NS | NS |
| **C** | **YES** | NS | C | NS | NS |
| **D** | NS | **YES** | D | NS | **YES** |
| E | NS | NS | E | NS | NS |
| F | NS | NS | F | NS | NS |
| **G** | NS | **YES** | G | NS | **YES** |
| **H** | NS | **YES** | H | NS | **YES** |
| **I** | **YES** | NS | I | NS | NS |
| J | NS | NS | J | NS | NS |
| **K** | **YES** | **YES** | K | NS | **YES** |
| **L** | **YES** | **YES** | L | NS | NS |
| **M** | **YES** | NS | M | NS | NS |
| N | NS | NS | N | NS | NS |
| **O** | **YES** | NS | O | NS | NS |
| P | NS | NS | P | NS | NS |
| Q | NS | NS | Q | NS | NS |
| R | NS | NS | R | NS | NS |
| T | NS | NS | T | NS | NS |
| **U** | **YES** | NS | U | NS | NS |
| V | NS | NS | V | NS | NS |
| W | NS | NS | W | NS | NS |
| **Y** | **YES** | NS | Y | NS | NS |
| **Z** | **NS** | **YES** | **Z** | **NS** | **NS** |

****

**Figure A. Key components of the thiamine biosynthesis pathway.** Colored squares represent presence in *Prymnesium parvum* (brown), *Chrysochromulina brevifilum* (red), *Chrysochromulina ericina* (blue), and *Phaeocystis antarctica* (green). In some organisms, the functionalities of THID and ThiE are combined into a single enzyme, such as ThiDE. Abbreviations: HMP-P, 4-amino-2-methyl-5-hydroxymethylpyrimidine phosphate; HMP-PP, 4-amino-2-methyl-5-hydroxymethylpyrimidine pyrophosphate; HET-P, hydroxyethylthiazole phosphate; DXP, 1-deoxy-D-xylulose 5-phosphate.