**Supplemental Table 1**

Full results from targeted metabolomics analysis.  Treatments are noted as RCobSL (replete cobalamin, saturating light); RCobLL (replete cobalamin, low light); LCobSL (low cobalamin, saturating light); and LCobLL (low cobalamin, low light), each has three replicates (AB, CD, and EF).  Reported peak areas are adjusted (via B-MIS normalization (Boysen *et. al.* (2018)) and then normalized to biomass. FDR-adjusted p values are given for both saturating light (SL) and low light (LL) univariate comparisons between cobalamin treatments (*n* = 3 per treatment), and for combined (pooled light treatments, *n* = 6 per treatment). We only performed univariate comparisons if the compound was detected in at least 2 treatments. Average peak size, Log2(Limited/Replete Cobalamin), and color correspond to Figure 3. Compounds marked as “Light Blue” are significantly different between cobalamin treatments in either saturating or low light conditions, compounds marked at “Dark Blue” are significantly different under both light conditions or when light treatments are pooled (*p* < 0.05 for all).

**Supplemental Table 2**

Compounds that significantly contributed (*p* < 0.05) to the NMDS analysis.

**Supplemental Table 3**

Full results from untargeted metabolomics analysis.  Treatments and values are the same as in Supplemental Table 1.  MF = mass feature, fraction is chromatographic conditions that gave observed mass feature, mz = *m/z*, rt = retention time (in seconds).

**Supplemental Table 4**

Complete results from gene search in *T. pseudonana* and other publicly available diatom genomes for processes discussed in the text. Maximum-likelihood trees for these genes are found in Supplemental Figures 1-3.

**Supplemental Table 5**

Isotope-labeled standards used for extraction standards and injection standards. The fraction, column, and ion mode (z) used for analysis for each standard are displayed as well as the injection concentration and extracted *m/z.* Extraction standards were spiked during extraction, injection standards were spiked just before analysis by LC-MS

**Supplemental Table 6**

Experimental parameters and basic results of untargeted analysis.  Retention time (RT) range and resolution for the different chromatography and ion mode configurations.  Parameters used for XCMS. Results include the peak picking score (PPS) from IPO, initial number of mass features (MFs), number of MFs after filtering out peaks with CV > 30% after B-MIS normalization and likely isotopologues as described in text (Quality MFs).

**Supplementary Figure 1**

Maximum-likelihood tree of adenosylmethionine decarboxylase (AdoMetDC). Numbers beside branches represent support values from 1,000 bootstrap trees. The query sequence used to construct this tree was taken from *A. thaliana*. Branches colored by taxonomy: diatoms, orange; rhodophytes, red; viridiplantae, green; haptophytes, dark purple; cryptophytes, light purple; non-diatom stramenopiles, magenta; non-diatom alveolates, blue; opisthokonts and amoebozoa, maroon; excavates, pale blue; rhizaria, dark purple; dinophyceae, dark blue; glaucophyta, teal; bacteria and archaea, yellow; virus, gray.  The tree was rooted with a bacterial adenosylmethionine decarboxylase and based on 436 amino acids; scale bar represents the proportion of amino acid substitutions per site along each branch.

**Supplementary Figure 2**

Maximum-likelihood tree of propionyl-CoA carboxylase (PCC). Numbers beside branches represent support values from 1,000 bootstrap trees. The query sequences used to construct this tree were taken from *H. sapiens*. Branches colored by taxonomy: diatoms, orange; rhodophytes, red; viridiplantae, green; haptophytes, dark purple; cryptophytes, light purple; non-diatom stramenopiles, magenta; non-diatom alveolates, blue; opisthokonts and amoebozoa, maroon; excavates, pale blue; rhizaria, dark purple; dinophyceae, dark blue; glaucophyta, teal; bacteria and archaea, yellow; virus, gray.  The tree was rooted with methylcrotonyl-CoA carboxylase and based on 404 amino acids; scale bar represents the proportion of amino acid substitutions per site along each branch.

**Supplementary Figure 3**

Maximum-likelihood tree of carnitine palmitoyltransferase (CPT2). The query sequences used to construct this tree were taken from *H. sapiens*. Numbers beside branches represent support values from 1,000 bootstrap trees. Branches colored by taxonomy: diatoms, orange; rhodophytes, red; viridiplantae, green; haptophytes, dark purple; cryptophytes, light purple; non-diatom stramenopiles, magenta; non-diatom alveolates, blue; opisthokonts and amoebozoa, maroon; excavates, pale blue; rhizaria, dark purple; dinophyceae, dark blue; glaucophyta, teal; bacteria and archaea, yellow; virus, gray.  The tree was rooted with carnitine acetyltransferase and choline acetyltransferase and based on 438 amino acids; scale bar represents the proportion of amino acid substitutions per site along each branch.