

## Dataset brief Supplemental Information

### Supplemental Methods.

#### **Cultivation of *Phaeodactylum tricornutum***

Cells of *Phaeodactylum tricornutum* (Pt1) Bohlin Strain 8.6 CCMP2561 (Culture Collection of Marine Phytoplankton, now known as NCMA: National Center for Marine Algae and Microbiota) were maintained and grown in a volume of 1 L in 2-L flasks at 20°C, in a modified ESAW (Enriched Seawater, Artificial Water) medium (NaCl 362.7 mM; Na<sub>2</sub>SO<sub>4</sub> 25 mM; KCl 8.03 mM; NaHCO<sub>3</sub> 2.067 mM; KBr 0.725 mM; H<sub>3</sub>BO<sub>3</sub> 0.372 mM; NaF 0.0657 mM; MgCl<sub>2</sub> 47.18 mM; CaCl<sub>2</sub> 9.134 mM; SrCl<sub>2</sub> 0.082 mM; Na<sub>2</sub>-glycerophosphate 21.8 μM; Na<sub>2</sub>SiO<sub>3</sub> 105.6 μM; disodium ethylenediaminetetraacetate dehydrate (Na<sub>2</sub>EDTA) 14.86 μM; Fe(NH<sub>4</sub>)<sub>2</sub>(SO<sub>4</sub>)<sub>2</sub> 5.97 μM; FeCl<sub>3</sub> 0.592 μM; MnSO<sub>4</sub> 2.42 μM; ZnSO<sub>4</sub> 0.254 μM; CoSO<sub>4</sub> 0.0569 μM; Na<sub>2</sub>MoO<sub>4</sub> 0.52 μM; H<sub>3</sub>BO<sub>3</sub> 61.46 μM; Na<sub>2</sub>SeO<sub>3</sub> 10 nM; biotin (vitamin H) 8.18 nM; cobalamin (vitamin B<sub>12</sub>) 2.94 nM; thiamine (vitamin B<sub>1</sub>) 0.594 μM) [1] using ten times enriched nitrogen and phosphate sources (10N10P containing 5.49 mM NaNO<sub>3</sub> and 0.224 mM NaH<sub>2</sub>PO<sub>4</sub>) [2]. Cultivation was performed by gentle agitation, without bubbling air. Nitrogen starvation was performed by transferring cells to the same medium without any addition of NaNO<sub>3</sub> (00N10P medium). Cells were grown on a 12:12 light (50 μE m<sup>-2</sup>.sec<sup>-1</sup>) / dark cycle. Growth was evaluated by cell counting using a TECAN infinite M1000Pro plate reader and determined following the equation  $y=1.834 \cdot 10^{-08} x + 0.03758$  with x= the absorbance at 730 nm and y= the number of cells [3].

#### **Sample preparation for mass spectrometry (MS)-based proteomic analyses**

After cultivation of *Phaeodactylum tricornutum* cell in 10N10P or 00N10P for 7 days, in biological triplicate, protein fractions were prepared as described previously [4]. Following a protein quantification with a Bradford assay, 20 μg of proteins were solubilized in Laemmli buffer and stacked in the top of a 4-12% NuPAGE gel (Invitrogen). After staining with R-250 Coomassie Blue (Biorad), proteins were digested in-gel using trypsin (modified, sequencing purity, Promega), as previously described [5]. Resulting peptides were fractionated by tip-based strong cation exchange (3M Empore). For this, dried peptides were dissolved in 5% acetonitrile, 1% TFA and eluted in 4 fractions (F1: 100 mM ammonium acetate, 20% ACN, 0.5 % formic acid; F2: 175 mM ammonium acetate, 20% ACN, 0.5 % formic acid; F3: 375

mM ammonium acetate, 20% ACN, 0.5 % formic acid; F4: 80% acetonitrile, 5% ammonium hydroxide) before desalting using C18 reverse phase chromatography (Ultra-Micro SpinColumns, Harvard Apparatus).

### MS-based proteomic analyses

The dried extracted peptides of each SCX fraction were resuspended in 5% acetonitrile, 0.1% trifluoroacetic acid, and analyzed by online nanoliquid chromatography coupled to MS/MS (Ultimate 3000 RSLCnano and Q-Exactive HF, Thermo Fisher Scientific) using a 140 min gradient. For this purpose, the peptides were sampled on a precolumn (300 µm x 5 mm PepMap C18, Thermo Scientific) and separated in a 75 µm x 250 mm C18 column (Reprosil-Pur 120 C18-AQ, 1.9 µm, Dr. Maisch). The MS and MS/MS data were acquired by Xcalibur.

### Protein identification and quantification

Raw files were processed using MaxQuant (version 1.5.8.3) <sup>[6]</sup>. Spectra were searched against a compilation of the *P. tricornutum* protein database from the Ensembl Protists portal (Phaeodactylum\_tricornutum.ASM15095v2.pep.all.fasta, 12,178 entries), the organellar-encoded proteins downloaded from NCBI (165 entries) and the frequently observed contaminant database embedded in MaxQuant. Trypsin/P was chosen as the enzyme and 2 missed cleavages were allowed. Precursor and fragment mass error tolerances were set at their default values (i.e. 20 ppm and 4.5 ppm for precursors for first and main searches, and 20 ppm for fragments). Peptide modifications allowed during the search were: carbamidomethylation (C, fixed), acetyl (Protein N-ter, variable), and oxidation (M, variable). Minimum peptide length was set to 7 amino acids. Minimum number of peptides, razor + unique peptides and unique peptides were all set to 1. Maximum false discovery rates, calculated by employing a reverse database strategy, were set to 0.01 at peptide-spectrum match and protein levels. For label-free quantification, the “Match between runs” option was activated and used with default parameters. Intensity-based absolute quantification (iBAQ, <sup>[7]</sup>) values were calculated from MS1 intensities of razor and unique peptides. The MS proteomic data have been deposited to the ProteomeXchange Consortium via the PRIDE <sup>[8]</sup> partner repository with the dataset identifier PXD033328.

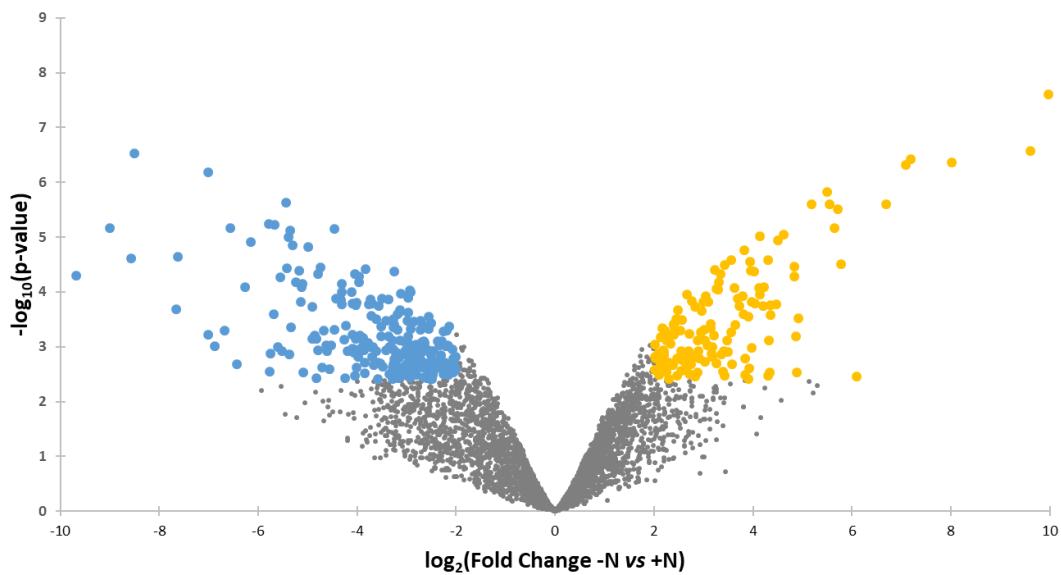
### Statistical analysis and Bioanalysis

Statistical analysis was performed using ProStaR <sup>[9]</sup>. At first, proteins identified in the reverse and contaminant databases and proteins quantified in less than three replicates of one

condition were discarded. After log<sub>2</sub> transformation, iBAQ values were normalized by median centering over the six samples. Missing values imputation was then performed within each sample using the 2.5% quantile value. Statistical testing was conducted using limma. The final set of differentially expressed proteins were sorted out using a log<sub>2</sub> (fold change) cut-off of 2 (i.e. fold change  $\geq 4$ ) and a  $-\log_{10}(p\text{-value})$  cut-off of 2.4 (i.e. p-value  $< 0.004$ ), leading to a FDR  $< 1\%$  according to the Benjamini-Hochberg estimator.

For annotations: descriptions of the proteins were obtained from the Ensembl fasta file. Correspondence with the gene version at Joint Genome Institute (JGI) (<https://genome.jgi.doe.gov/Phatr2> and [https://genome.jgi.doe.gov/Phatr2\\_bd](https://genome.jgi.doe.gov/Phatr2_bd)) is indicated whenever possible. Prediction of transmembrane helices in proteins was performed at the TMHMM Server v.2.0 (<https://services.healthtech.dtu.dk/service.php?TMHMM-2.0>) [10] and isoelectric point (IP) values were predicted using the Avg\_Pi output of the standalone IPC Isoelectric Point Calculator program (<http://isoelectric.org>) [11]. Enrichment analysis of functional annotation terms was performed using DAVID Functional Annotation Tool [12,13] with default settings. Category enrichment was measured using Expression Analysis Systematic Explorer (EASE) scores computed based on a one-tailed jackknifed Fisher exact test [12,13]. The gene ontology (GO) terms [14] and functional keywords from Uniprot [15], INTERPRO [16], COG [17] and KEGG [18] databases were clustered and the statistical significance of each cluster was assessed using an Enrichment Score (-log<sub>10</sub> geometric mean of the cluster members EASE scores). Functional annotation clusters were considered significant at Enrichment Score  $> 1$  using the *Phaeodactylum tricornutum* proteome in UniprotKB as background.

## Supplemental Figures



**Supplemental Figure 1S.** MS-based quantitative proteomic analysis of *P. tricornutum* grown with or without nitrogen. Volcano plot displaying the differential abundance of proteins reliably identified and quantified in three biological replicates of *P. tricornutum* cells grown in nitrogen-poor versus nitrogen-rich medium. The volcano plot represents the  $-\log_{10}$  (limma p-value) on y axis plotted against the  $\log_2(\text{Fold Change } -\text{N}/+\text{N})$  on x axis. Orange dots represent proteins found more abundant in cells grown in nitrogen-poor medium, whereas blue dots correspond to proteins found more abundant in cells grown in nitrogen-rich medium (Fold change  $\geq 4$  and p-value  $< 0.004$ , leading to a Benjamini-Hochberg FDR  $< 1\%$ ).

## Supplemental Tables

**Table 1S.** List of 3,768 *P. tricornutum* proteins identified and quantified by MS-based proteomics and analyzed by differential abundance analysis. A total of 384 proteins were selected as differentially abundant between the -N and +N conditions, with 242 proteins significantly decreased (blue) and 142 proteins significantly increased in the nitrogen-depleted condition (yellow). "Protein(s) Group" indicates the set of proteins that share the same peptides (or a subset). "First ID" indicates the representative proteins of the Protein groups as output by MaxQuant. "Unique + razor peptides", peptides specific to the protein group + those shared by other protein group(s) and that were assigned to this protein group. "FC", Fold Change -N/+N. "Chromosome Contig", "GeneSymbol", "Description", "Uniprot.Accession" are all fields parsed from the Ensembl fasta headers. "Mapping to JGI identifiers (Phatr2)" was based on blast and identity of the chromosome. "Average pI" (Isoelectric Point) was output by the standalone IPC tool and number of "Predicted Transmembrane Domains" was computed with the TMHMM-2.0 server algorithm. "Log2(iBAQ)" are the log-intensities in each replicate after normalisation and (in grey) imputation of missing values.

The corresponding table is provided as an independent Excel file.

**Table 2S.** 3,226 protein sequences with a Uniprot ID out of the 3,768 proteins identified in the whole proteome analysis of *Phaeodactylum tricornutum*. Sequences with protein domains and/or gene ontology terms recorded with the UniprotKB standards [15] where used for functional annotation enrichment analyses. Sequences without any Uniprot ID were discarded from such analyses.

A0A024QYS3; B1PJ31; B1PJ47; B5Y3A6; B5Y3B1; B5Y3B2; B5Y3B4; B5Y3B5; B5Y3B7; B5Y3B9; B5Y3C0; B5Y3C2; B5Y3C3; B5Y3C7; B5Y3C9; B5Y3D3; B5Y3D6; B5Y3E3; B5Y3E4; B5Y3E5; B5Y3E8; B5Y3E9; B5Y3F0; B5Y3F4; B5Y3F5; B5Y3F9; B5Y3G0; B5Y3G3; B5Y3G4; B5Y3G5; B5Y3G7; B5Y3G8; B5Y3G9; B5Y3H0; B5Y3H2; B5Y3H3; B5Y3H5; B5Y3H6; B5Y3H8; B5Y3H9; B5Y3J1; B5Y3J3; B5Y3J4; B5Y3J5; B5Y3J9; B5Y3K5; B5Y3K6; B5Y3K8; B5Y3L0; B5Y3L1; B5Y3L2; B5Y3L3; B5Y3L4; B5Y3L9; B5Y3M3; B5Y3M6; B5Y3M8; B5Y3N7; B5Y3N8; B5Y3P1; B5Y3P3; B5Y3P4; B5Y3P7; B5Y3Q3; B5Y3Q5; B5Y3Q6; B5Y3Q7; B5Y3R0; B5Y3R1; B5Y3R6; B5Y3R9; B5Y3S0; B5Y3S3; B5Y3S6; B5Y3S8; B5Y3S9; B5Y3T0; B5Y3T1; B5Y3T5; B5Y3T7; B5Y3T8; B5Y3T9; B5Y3U2; B5Y3U4; B5Y3U6; B5Y3U9; B5Y3V0; B5Y3V3; B5Y3W1; B5Y3W5; B5Y3W6; B5Y3W7; B5Y3X1; B5Y3X3; B5Y3X4; B5Y3X6; B5Y3Y0; B5Y3Y1; B5Y3Y2; B5Y3Y9; B5Y3Z0; B5Y400; B5Y404; B5Y405; B5Y407; B5Y408; B5Y410; B5Y414; B5Y416; B5Y418; B5Y422; B5Y424; B5Y426; B5Y428; B5Y429; B5Y432; B5Y433; B5Y436; B5Y437; B5Y440; B5Y444; B5Y446; B5Y447; B5Y453; B5Y454; B5Y455; B5Y458; B5Y460; B5Y470; B5Y471; B5Y475; B5Y477; B5Y488; B5Y490; B5Y493; B5Y495; B5Y4A1; B5Y4A7; B5Y4A9; B5Y4B1; B5Y4C1; B5Y4D9; B5Y4E2; B5Y4E3; B5Y4G0; B5Y4G5; B5Y4G7; B5Y4G8; B5Y4G9; B5Y4H0; B5Y4H3; B5Y4H4; B5Y4H6; B5Y4I0; B5Y4I1; B5Y4I2; B5Y4I5; B5Y4J7; B5Y4J8; B5Y4K3; B5Y4K4; B5Y4L1; B5Y4L5; B5Y4L9; B5Y4N5; B5Y4N8; B5Y4P2; B5Y4Q1; B5Y4Q5; B5Y4R5; B5Y4R8; B5Y4S0; B5Y4S3; B5Y4S4; B5Y4T0; B5Y4T2; B5Y4T6; B5Y4U3; B5Y4U4; B5Y4U7; B5Y4V1; B5Y4V2; B5Y4V9; B5Y4W1; B5Y4W2; B5Y4W6; B5Y4X4; B5Y4X5; B5Y4Y5; B5Y4Y7; B5Y4Z0; B5Y4Z2; B5Y4Z4; B5Y4Z5; B5Y4Z7; B5Y4Z8; B5Y4Z9; B5Y501; B5Y502; B5Y503; B5Y507; B5Y509; B5Y510; B5Y512; B5Y516; B5Y522; B5Y523; B5Y525; B5Y531; B5Y533; B5Y536; B5Y541; B5Y542; B5Y554; B5Y555; B5Y557; B5Y558; B5Y560; B5Y563; B5Y565; B5Y573; B5Y576; B5Y578; B5Y581; B5Y582; B5Y589; B5Y593; B5Y594; B5Y5A4; B5Y5A5; B5Y5A7; B5Y5A9; B5Y5B0; B5Y5B2; B5Y5B4; B5Y5B6; B5Y5C0; B5Y5C6; B5Y5C8; B5Y5D0; B5Y5D2; B5Y5D4; B5Y5E1; B5Y5E9; B5Y5F0; B5Y5F3; B5Y5F4; B5Y5F7; B5Y5F8; B5Y5G4; B5Y5G7; B5Y5I1; B5Y5I4; B5Y5I5; B5Y5I6; B5Y5I8; B5Y5J0; B5Y5J4; B5Y5J5; B5Y5J6; B5Y5J9; B5Y5K0; B5Y5K7; B5Y5K8; B5Y5K9; B5Y5L0; B5Y5L3; B5Y5L4; B5Y5L9; B5Y5M0; B5Y5M2; B5Y5N6; B5Y5P1; B5Y5P6; B5Y5Q0; B5Y5Q5; B5Y5Q7; B5Y5R0; B5Y5R2; B5Y5R5; B5Y5R6; B5Y5R8; B5Y5S1; B5Y5S5; B5Y5S6; B5Y5T2; B5Y5T3; B5Y5T6; B5Y5U1; B5Y5U5; B5Y5U7; B5Y5V7; B5Y5W1; B5Y5W2; B5Y5W3; B5Y5W9; B7FNR9; B7FNS4; B7FNS5; B7FNS6; B7FNT2; B7FNT4; B7FNT6; B7FNT8; B7FNT9; B7FNU0; B7FNU7; B7FNU8; B7FNU0; B7FNV6; B7FNW0; B7FNW3; B7FNW4; B7FNW8; B7FNX0; B7FNX3; B7FNX5; B7FNX7; B7FNY2; B7FNY3; B7FNY4; B7FNY5; B7FNY6; B7FNY9; B7FNZ1; B7FNZ4; B7FNZ9; B7FP03; B7FP04; B7FP05; B7FP06; B7FP10; B7FP17; B7FP19; B7FP20; B7FP22; B7FP23; B7FP24; B7FP26; B7FP30; B7FP32; B7FP34; B7FP35; B7FP39; B7FP42; B7FP44; B7FP48; B7FP52; B7FP55; B7FP57; B7FP61; B7FP70; B7FP71; B7FP73; B7FP76; B7FP79; B7FP80; B7FP88; B7FP91; B7FP94; B7FP95; B7FP98; B7FP99; B7FPA1; B7FPA2; B7FPA4; B7FPA6; B7FPA7; B7FPB0; B7FPB3; B7FPB5; B7FPB9; B7FPC4; B7FPC8; B7FPD1; B7FPD3; B7FPD7; B7FPD9; B7FPE1; B7FPE7; B7FPE8; B7FPE9; B7FPE4; B7FPE5; B7FPF5; B7FPF9; B7FPG1; B7FPG5; B7FPG7; B7FPG9; B7FPH1; B7FPH4; B7FPH5; B7FPH8; B7FPI0; B7FPI1; B7FPI2; B7FPI3; B7FPI4; B7FPI7; B7FPJ0; B7FPJ1; B7FPJ4; B7FPJ6; B7FPJ8; B7FPK1; B7FPK3; B7FPL1; B7FPL4; B7FPL5; B7FPL6; B7FPL8; B7FPL9; B7FPM2; B7FPM3; B7FPN7; B7FPN9; B7FPP1; B7FPP2; B7FPP7; B7FPP8; B7FPQ0; B7FPQ3; B7FPQ7; B7FPQ9; B7FPR0; B7FPR1; B7FPR2; B7FPR6; B7FPS3; B7FPS6; B7FPS7; B7FPT3; B7FPT6; B7FPT8; B7FPU2; B7FPU3; B7FPU9; B7FPV1; B7FPV2; B7FPV3; B7FPV7; B7FWP7; B7FWP8; B7FPX0; B7FPX1; B7FPX3; B7FPY0; B7FPY6; B7FPY8; B7FPZ1; B7FPZ6; B7FPZ7; B7FPZ8; B7FQ00; B7FQ09; B7FQ11; B7FQ13; B7FQ24; B7FQ26; B7FQ31; B7FQ32; B7FQ44; B7FQ47; B7FQ48; B7FQ50; B7FQ57; B7FQ66; B7FQ72; B7FQ74; B7FQ80; B7FQ81; B7FQ83; B7FQ84; B7FQ88; B7FQ89; B7FQ90; B7FQ91; B7FQ92; B7FQ93; B7FQ97; B7FQA4; B7FQA6; B7FQA9; B7FQB0; B7FQB2; B7FQB5; B7FQB9; B7FQC2; B7FQC3; B7FQC5; B7FQC6; B7FQD4; B7FQD6; B7FQD8; B7FQD9; B7FQE0; B7FQE1; B7FQE3; B7FQE5; B7FQE6; B7FQE7; B7FQE8; B7FQF2; B7FQF4; B7FQF6; B7FQF7; B7FQG1; B7FQG6; B7FQG7; B7FQG8; B7FQG9; B7FQH4; B7FQH8; B7FQH9; B7FQI0; B7FQI2; B7FQI3; B7FQJ4; B7FQJ5; B7FQJ6; B7FQJ9; B7FQK0; B7FQK1; B7FQK5; B7FQL3; B7FQL4; B7FQL7; B7FQL9; B7FQM0; B7FQM8; B7FQN0; B7FQN1; B7FQN4; B7FQN7; B7FQN8; B7FQP0; B7FQP6; B7FQQ2; B7FQQ3; B7FQQ4; B7FQQ6; B7FQQ8; B7FQQ9; B7FQR0; B7FQR3; B7FQR7; B7FQR8; B7FQR9; B7FQS2; B7FQS4; B7FQS7; B7FQS8; B7FQT0; B7FQT3;

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B7GDA6; B7GDA8; B7GDB8; B7GDD5; B7GDD7; B7GDD8; B7GDD9; B7GDE0; B7GDE2; B7GDE3; B7GDE4; B7GDE5; B7GDE6; B7GDE8; B7GDF0; B7GDF6; B7GDF8; B7GDG0; B7GDG1; B7GDG2; B7GDG7; B7GDH0; B7GDH1; B7GDH3; B7GDH4; B7GDH8; B7GDH9; B7GDI1; B7GDI2; B7GDI5; B7GDI7; B7GDI8; B7GDJ5; B7GDJ7; B7GDJ9; B7GDK2; B7GDK8; B7GDK9; B7GDL0; B7GDL3; B7GDL6; B7GDL8; B7GDL9; B7GDM1; B7GDM2; B7GDM3; B7GDM5; B7GDM6; B7GDN1; B7GDN2; B7GDN3; B7GDN5; B7GDN8; B7GDN9; B7GDP1; B7GDP2; B7GDP7; B7GDP8; B7GDQ6; B7GDR4; B7GDR8; B7GDS2; B7GDS3; B7GDS5; B7GDT2; B7GDT4; B7GDU0; B7GDU1; B7GDU6; B7GDU9; B7GDV6; B7GDV8; B7GDW4; B7GDW6; B7GDX3; B7GDX5; B7GDX6; B7GDX7; B7GDY0; B7GDY1; B7GDY2; B7GDY5; B7GDY6; B7GDY7; B7GDZ2; B7GDZ3; B7GDZ4; B7GDZ6; B7GDZ7; B7GE01; B7GE02; B7GE24; B7GE26; B7GE29; B7GE42; B7GE44; B7GE46; B7GE47; B7GE48; B7GE51; B7GE52; B7GE53; B7GE54; B7GE55; B7GE59; B7GE60; B7GE61; B7GE66; B7GE67; B7GE68; B7GE70; B7GE71; B7GE72; B7GE75; B7GE76; B7GE80; B7GE81; B7GE84; B7GE85; B7GE87; B7GE88; B7GE96; B7GE97; B7GEA4; B7GEA5; B7GEA6; B7GEA8; B7GEA9; B7GEB0; B7GEB6; B7GEB9; B7GEC0; B7GEC5; B7GED0; B7GED7; B7GED8; B7GEE0; B7GEE8; B7GEF0; B7GEF1; B7GEF2; B7GEF3; B7GEF7; B7GEF8; B7GEF9; B7GEG0; B7GEG1; B7GEG3; B7GEG7; B7GEG8; B7GEG9; B7GEH1; B7GEH2; B7GEH3; B7GEI2; B7GEI3; B7GEI7; B7GEJ3; B7GEJ6; B7GEJ8; B7GEL1; B7GEL7; B7GEL9; B7GEM2; B7GEM5; B7GEM7; B7GEN1; B7GEN5; B7GEN7; B7GEP3; B7GER7; B7GES2; B7GES3; B7GES5; B7GES9; B7S3I6; B7S3I7; B7S3I9; B7S3J3; B7S3J9; B7S3M4; B7S3M9; B7S3N4; B7S3N7; B7S3N8; B7S3P0; B7S3P2; B7S3P3; B7S3P9; B7S3Q2; B7S3R8; B7S3S7; B7S3S9; B7S3T6; B7S3U1; B7S3U7; B7S3W3; B7S3W8; B7S3W9; B7S3X0; B7S3X2; B7S3X4; B7S3Y6; B7S3Y7; B7S401; B7S404; B7S406; B7S413; B7S416; B7S417; B7S419; B7S422; B7S426; B7S432; B7S434; B7S436; B7S443; B7S450; B7S451; B7S452; B7S454; B7S456; B7S458; B7S460; B7S462; B7S466; B7S469; B7S470; B7S471; B7S473; B7S475; B7S480; B7S482; B7S483; B7S487; B7S490; B7S491; B7S492; B7S4A8; B7S4B1; B7S4B2; B7S4B4; B7S4B8; B7S4C6; B7S4C8; B7S4E4; B7S4G6; B7S4G9; B7S4I4; B7S4K1; B7S4L0; C6JVY2; C6JVY4; C6JVY6; C6JVY7; C6JVY9; C6L824; D8FSX5; E2E6S2; F1SXAA1; G0WVT5; L8B080; Q08584; Q08585; Q08586; Q41075; Q41093; Q41094; Q84XB6; U5TRI0

**Table 3S.** Functional annotation of differentially abundant proteins. A total of 384 proteins were selected as differentially abundant between the -N and +N conditions, with proteins significantly increased (red) and proteins significantly decreased in the nitrogen-depleted condition (blue). For GO term and functional analyses, proteins recorded with the UniprotKB standards were retained. Amino acid sequences of proteins unrecorded in UniprotKB were indicated. Additional information, including functional domains based on similarity search, or predicted signal peptides and indicated.

The corresponding table is provided as an independent Excel file.

**Table 4S.** Comparison of genes with an upregulated gene expression (transcriptome) with proteins with a higher relative abundance (proteome), upon nitrogen shortage. List of 31 mRNA coding for proteins with a Uniprot ID, out of 78 upregulated genes reported by [19], also identified at the proteomic level in this study. 1 mRNA was common in both transcriptomic and proteomic analysis, but was not functionally annotated. 46 mRNA (=78-32) corresponded to genes coding for proteins undetected in the present proteomic study, possibly with a low relative abundance, or lack of detected peptides.

B5Y3R9; B5Y5S6; B7FP05; B7FP61; B7FQK1; B7FUF2; B7FUR4; B7FVM3; B7FXB5; B7FXR0; B7FYE0; B7FYS6; B7G133; B7G1G6; B7G3J7; B7G4X9; B7G585; B7G5C9; B7G659; B7G6Z9; B7G757; B7G7W5; B7G8B7; B7G8X8; B7GB64; B7GBC3; B7GBG1; B7GBN2; B7GBV8; B7GDM5; B7GE02

**Table 5S.** Comparison of genes with a downregulated expression (transcriptome) with proteins with a lower relative abundance (proteome), upon nitrogen shortage. List of 170 mRNA coding for proteins with a Uniprot ID, out of 248 downregulated genes reported by [19], also identified at the proteomic level in this study. 6 mRNA were common in both transcriptomic and proteomic analysis, but were not functionally annotated. 72 mRNA (=248-176) corresponded to genes coding for proteins undetected in the present proteomic study, possibly with a low relative abundance or lack of detected peptides.

B5Y3B5; B5Y3H6; B5Y3P7; B5Y3U9; B5Y493; B5Y4H0; B5Y4T0; B5Y4U3; B5Y594; B5Y5F0; B5Y5I6; B5Y5L4; B7FNU0; B7FP19; B7FP55; B7FPA1; B7FPC4; B7FPL6; B7FPZ8; B7FQ11; B7FQ93; B7FQE0; B7FQF7; B7FQH9; B7FQI2; B7FQL9; B7FQU7; B7FQZ5; B7FR48; B7FRG3; B7FRZ1; B7FS29; B7FS72; B7FS76; B7FSE5; B7FSI3; B7FSI4; B7FSI8; B7FSN7; B7FSP4; B7FSQ7; B7FSS8; B7FST3; B7FT02; B7FT67; B7FT68; B7FTA2; B7FTQ8; B7FTV7; B7FTW9; B7FU11; B7FU48; B7FU89; B7FU91; B7FUC3; B7FUD3; B7FUG8; B7FUK5; B7FUM7; B7FUR6; B7FUS3; B7FUU0; B7FUV3; B7FUX7; B7FV18; B7FV89; B7FVG2; B7FVH9; B7FVP7; B7FVX9; B7FW77; B7FWQ7; B7FWT4; B7FWY2; B7FWY8; B7FX04; B7FXC9; B7FXP8; B7FXQ2; B7FXR7; B7FXZ0; B7FY07; B7FY54; B7FYF1; B7FYT9; B7FYW4; B7FZ18; B7FZ25; B7FZ92; B7FZ94; B7FZL3; B7FZL9; B7G006; B7G018; B7G0B2; B7G0B7; B7G0I5; B7G0Z0; B7G134; B7G1X7; B7G216; B7G2B6; B7G2W2; B7G3C1; B7G3D4; B7G3S0; B7G3X5; B7G3Y1; B7G4G0; B7G502; B7G503; B7G518; B7G565; B7G593; B7G5G4; B7G5H9; B7G5M3; B7G5Q1; B7G5X2; B7G6V4; B7G6Y1; B7G7B8; B7G955; B7G959; B7G961; B7G9C6; B7G9G2; B7G9G7; B7G9G9; B7G9P2; B7G9R3; B7G9Y7; B7GA11; B7GA98; B7GAC9; B7GAK9; B7GAR9; B7GAS4; B7GB46; B7GB47; B7GBB9; B7GBN9; B7GBR7; B7GC49; B7GCB2; B7GCC1; B7GCG1; B7GCM0; B7GCP7; B7GCT8; B7GCW6; B7GD24; B7GD73; B7GDA8; B7GDE8; B7GDG7; B7GDN8; B7GDT4; B7GDU9; B7GDW4; B7GE80; B7GEF2; B7GEI2; B7GEN5; B7GER7; C6L824; Q08584; Q08585; Q41075; U5TRIO

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