components	concentration (g/L)
KNO <sub>3</sub>	1
NaCl	32
$KH_2PO_4 \cdot 2H_2O$	0.07
NaHCO <sub>3</sub>	0.04
$MgCl_2 \cdot 7H_2O$	6.7
MgSO <sub>4</sub> ·7H <sub>2</sub> O	5.5
$CaCl_2 \cdot 2H_2O$	1.1
$VB_1$	$7.5 \times 10^{-6}$
$VB_{12}$	10×10 <sup>-6</sup>
Biotin	50×10 <sup>-6</sup>
$Na_2EDTA \cdot 2H_2O$	9×10 <sup>-3</sup>
FeCl <sub>3</sub> ·6H <sub>2</sub> O	$1.164 \times 10^{-3}$
$MnCl_2 \cdot 4H_2O$	$0.492 \times 10^{-3}$
ZnCl <sub>2</sub>	$0.06 \times 10^{-3}$
CoCl <sub>2</sub> .6H <sub>2</sub> O	$0.024 \times 10^{-3}$
NaMoO <sub>4</sub> ·2H <sub>2</sub> O	$0.048 \times 10^{-3}$
HEPES	$1.19 \times 10^{-2}$
<b>VB</b> <sub>12</sub>	$0.0135 \times 10^{-2}$
H <sub>3</sub> BO <sub>3</sub>	$2.86 \times 10^{-3}$
MnSO <sub>4</sub> ·H <sub>2</sub> O	$1.86 \times 10^{-3}$
$ZnSO_4 \cdot 7H_2O$	$0.22 \times 10^{-3}$
$CuSO_4 \cdot 7H_2O$	$0.08 \times 10^{-3}$
$(NH_4) \in MO_2O_2 4 \cdot 7H_2O$	$0.05 \times 10^{-3}$

 Table S1
 Chemical composition of Erdschreiber's medium.

 Table S2. Sequences of the primer pairs of different genes of Phaeodactylum

Gene	Orientation	Sequence (5'-3')
psbO	Forward	CGGTGATGGGGTGTGTATG
	Reverse	ACTCGCTTTGGGGGATGGA
ATPeF00	Forward	GATAATTCTTCCATTTCGTGC
	Reverse	AGGTCGCTACATCAGTGCC
PRDX5	Forward	GCATCCCAGTGGCGATAAAC
	Reverse	CGGGCAACGTAGAGGAGAAC
SARS	Forward	GAATGGCTGGCAAATCAAAGG
	Reverse	TGGCGTGGAAACCACTAAACG
RP-L8e	Forward	GTTCACTCCAAGCCGATTACG
	Reverse	GCGAGGATCACCATTTATGC
Acting	Forward	GCCGCRGGTGAAAMCTAA
	Reverse	AATCCAAARACCTTCCTCCC

tricornutum amplified by quantitative real-time PCR.

**Table S3.** Differentially expressed proteins (with a functional annotation) in *Phaeodactylum tricornutum* exposed to 200  $\mu$ M total Al for 4 h (68 annotated proteins are listed out of 165 differentially expressed proteins). The column ratio is the mean protein expression level of the Al-exposed cells divided by that of the control. The protein expression was up- and down-regulated when the ratio was >1.3 and <0.77 respectively and when the differences between the treatment and the control was

•		1 1		< A	05
C10	miticant	IV d	itterent	(n/1)	(15)
312	mincant	iyu	morun	v > v	.0.57.
	,	2		<b>N</b>	

Protein	Protein description	Patio	D voluo
number	Protein description		r value
Photosynthesi	S		
B7FYL0	Protein fucoxanthin chlorophyll a/c protein	1.8	5.43E-04
B7G6S9	Protein fucoxanthin chlorophyll a/c protein	1.3	6.60E-03
B7FSI1	Protein fucoxanthin chlorophyll a/c protein	2.4	3.48E-02
B7G871	Protein fucoxanthin chlorophyll a/c protein	1.6	6.80E-03
B7FR60	Protein fucoxanthin chlorophyll a/c protein	2.2	3.28E-02
Q9TK52	Ribulose bisphosphate carboxylase large	0.7	1.33E-03
	chain	0.7	
B7FZ96	Oxygen-evolving enhancer protein 1	0.7	2.40E-03
A0T0A2	Photosystem I assembly protein Ycf4	0.6	0.56
B7FVX0	Ubiquinol-cytochrome c reductase subunit	0.5	1.37E-05
B7FYG2	SUF system FeS cluster assembly	0.8	5.44E-03
A0T0C8	Ferredoxin	0.7	1.10E-09

B5Y509	Phytoene desaturase-like protein	0.8	4.27E-02	
B7FNY6	Early light induced protein	0.6	2.19E-11	
Energy				
B7GEA5	F-type H+-transporting ATPase subunit epsilon	1.6	3.01E-03	
B7FRC1	Fructose-bisphosphate aldolase	1.7	3.87E-03	
B7G9G7	Pyruvate kinase	1.3	4.61E-02	
B7G5R3	Transketolase	1.4	7.60E-03	
B7GAR0	Fructose-1,6-bisphosphatase	1.3	7.15E-03	
B7FV38	F-type H+-transporting ATPase subunit O	0.7	3.58E-03	
Stress and defe	ense			
B7GDY5	Glutaredoxin	1.6	1.36E-03	
B5Y3H3	D-galacturonate reductase	1.6	2.29E-03	
B7G9U5	Thioredoxin-like	0.7	1.35E-02	
B7G7V1	Peroxiredoxin 5	0.7	4.06E-02	
B7G0V9	Glutathione peroxidase (Fragment)	0.7	2.47E-02	
Membrane transporters				
B7FWX0	ABC-2 type transporter	1.9	2.09E-03	
B7FT94	Vacuolar protein sorting-associated protein	1.4	6.51E-03	
	Vacuolar protein sorting-associated protein			
B5Y4G7	35	1.5	3.71E-02	

B7GCD8	Cation-transporting P-type ATPase	0.7	5.87E-12		
Protein homeostasis					
B7G256	DNA/RNA helicase	0.7	2.67E-03		
D70144	Ttranscription initiation factor TFIIF subunit	1 7	4 715 02		
B/G166	beta	1./	4./1E-03		
B7G4R8	Spliceosome	1.3	4.48E-02		
B7FP73	Splicing factor 3B subunit 3	1.4	1.45E-02		
B7GB16	Translation initiation factor 2 subunit 3	1.4	1.34E-02		
B5Y531	Translation initiation factor 4A	1.6	8.90E-03		
B5Y3P7	Small subunit ribosomal protein S25e	1.9	2.47E-02		
B7FXJ2	Small subunit ribosomal protein S9	1.4	4.24E-02		
B7G5I7	Large subunit ribosomal protein L17e	1.4	8.90E-02		
B7FP80	40S ribosomal protein S8	1.5	3.36E-03		
B7FPQ0	Large subunit ribosomal protein L5e	1.3	2.24E-04		
B7FTL4	Large subunit ribosomal protein L34e	1.5	2.21E-02		
B7G0R5	60S ribosomal protein L18a	1.5	5.37E-05		
B5Y4I0	Large subunit ribosomal protein L30e	2.7	1.93E-03		
A0T0D4	30S ribosomal protein S18	1.5	1.40E-03		
B7G672	Ribosomal protein L10	1.5	1.96E-03		
B5Y3U9	Large subunit ribosomal protein L8e	1.4	2.87E-02		
B7FQD6	Large subunit ribosomal protein LP0	0.7	7.78E-06		
B7G4H1	Translation initiation factor 3 subunit D	0.5	0.01		

D7EDV2	Translation elongation factor	0.7	5.80E-02
B/FKA3	EF1B/ribosomal protein S6	0.7	
B7G8H9	Translation elongation factor EF1B	0.5	2.59E-08
B7GBW8	Seryl-tRNA synthetase	1.4	5.11E-02
B7G0F8	Tryptophanyl-tRNA synthetase	1.4	2.44E-03
B7FPF4	HSP20-like chaperone	1.4	4.68E-02
B7FRV0	Heat shock protein DnaJ	1.4	4.90E-03
B7G391	Cold-shock protein	0.6	8.79E-03
B7G7H8	DnaJ-containing protein	1.3	1.45E-03
Signal transdu	action		
B7FYW7	Calcium ion binding	0.7	4.24E-02
B7FYN9	Calcium ion binding	0.6	4.48E-02
B7G0P9	cAMP/cGMP-dependent protein kinase	1.4	3.89E-02
D7E000	Serine/threonine/dual specificity protein	1.2	4 505 02
B/FQ88	kinase	1.5	4.52E-03
B7FV98	Protein kinase-like	0.7	3.07E-02
B7G1H7	Protein kinase-like	0.7	6.36E-03
B7G8W0	5-methylthioribose kinase	0.5	4.93E-04
B7FUD8	Lactoylglutathione lyase	0.7	2.13E-02
B7S419	3'5'-cyclic nucleotide phosphodiesterase	1.3	3.66E-02
B7GBQ5	GTP-binding protein TypA	1.4	2.15E-02
B7G5Z2	Small GTP-binding protein	1.3	2.66E-02

B7G858 Rab GDI p	rotein	1.6	1.56E-02
Cytoskeleton			
B7G878 Actin/actin	like protein	1.4	3.13E-02

**Figure S1.** Quality control validation of mass spectrometry data (A) Mass error distribution and (B) peptide length of all identified peptides by iTRAQ.



**Figure S2:** (A) Effect of different total initial nominal Al concentrations on the cell yield (×  $10^5$  cells mL<sup>-1</sup>) of *Phaeodactylum tricornutum* as a function of exposure time. (B) F<sub>v</sub>/F<sub>m</sub>: maximum quantum yield of PSII, (C)  $\Phi$ II: effective photochemical efficiency of PSII, and (D) relative electron transport rate (rETR) are also shown for each Al concentrations and time points.



Time (d)

**Figure S3.** The effects of a 4-h exposure of *Phaeodactylum tricornutum* to 200  $\mu$ M total Al on the transcription of several genes. (\*) and (\*\*) represent statistically significant differences when compared with the control at *p* < 0.05 and at *p* < 0.01 levels, respectively.

