

Supplementary Materials

Figure supplementary legends

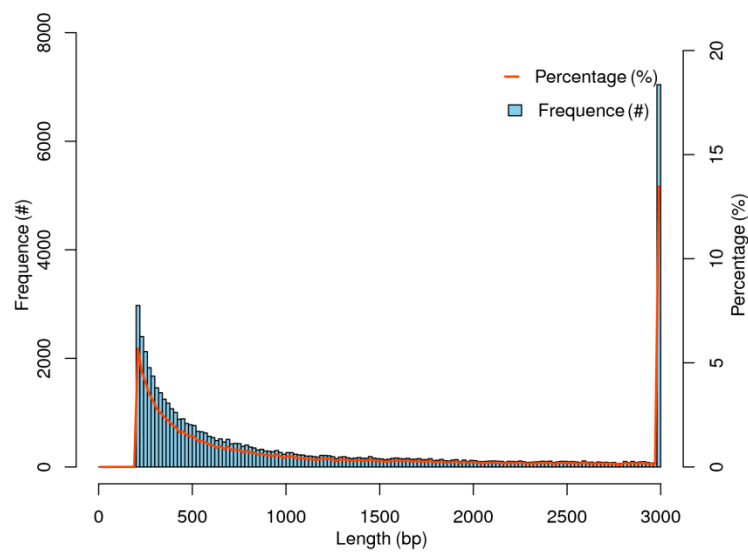


Figure S1. Length distribution of assembled unigenes.

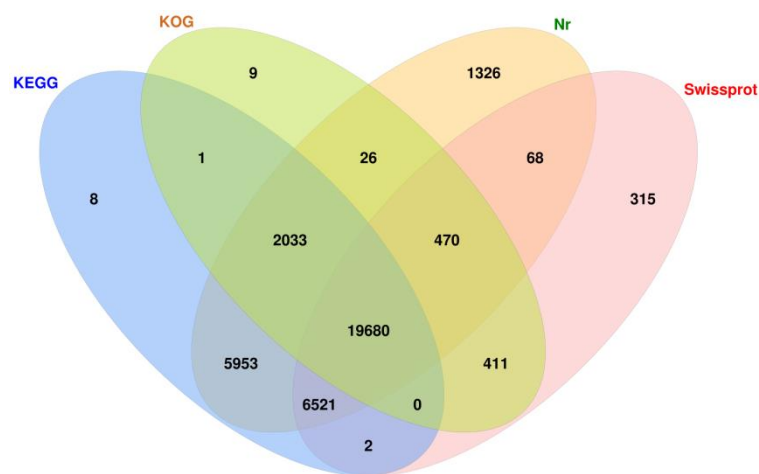


Figure S2. Basic annotation for all unigenes in *A. venetum* on KEGG, KOG, Nr, and Swissprot databases.

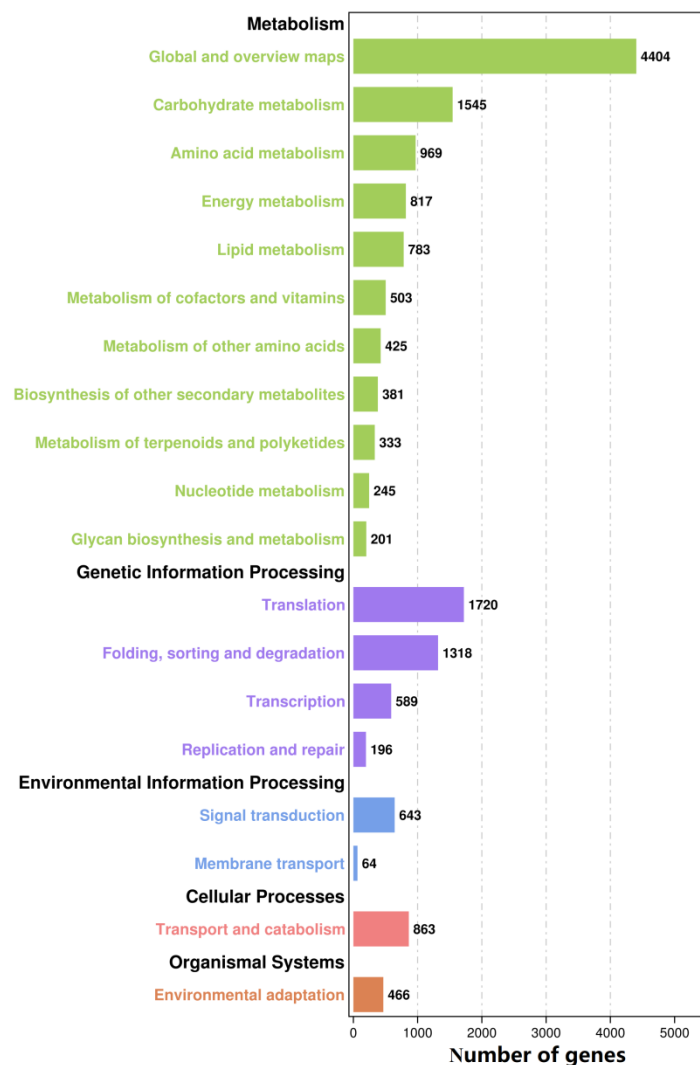


Figure S3. KEGG enrichment of DEGs at NaCl (300 mmol/L) vs. CK.

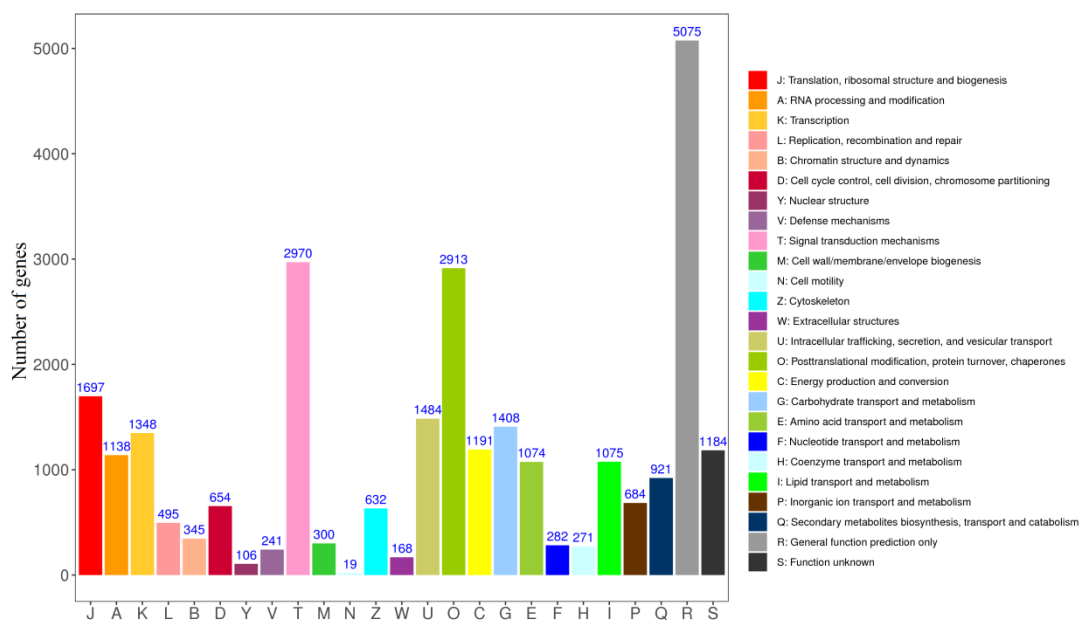


Figure S4. Distribution of unigenes in the transcriptome with KOG functional classification.

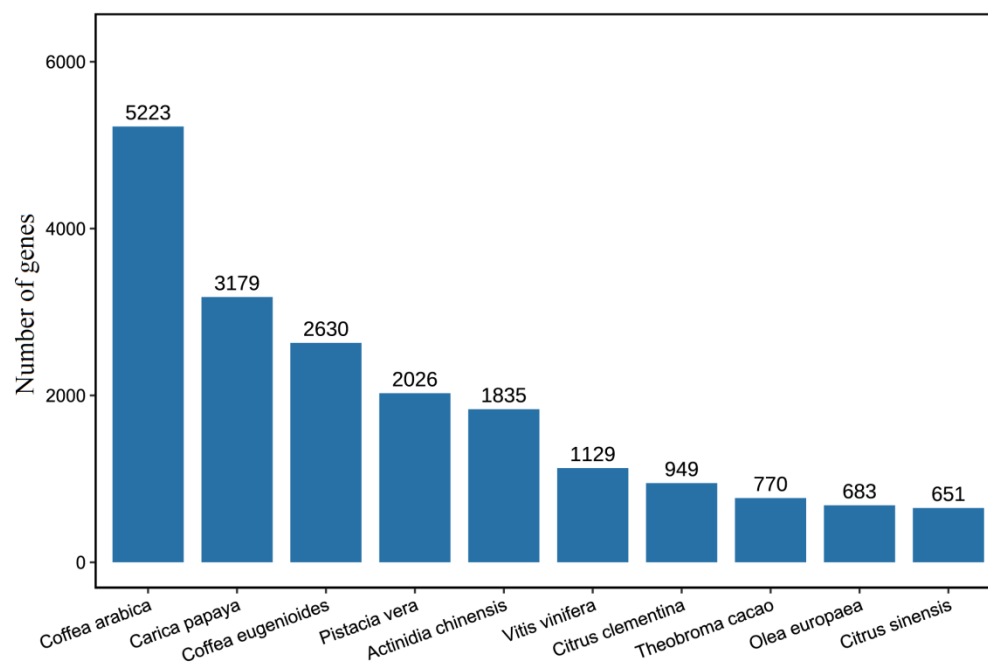


Figure S5. Annotation of unigenes on NR database and distribution of the top 10 species.

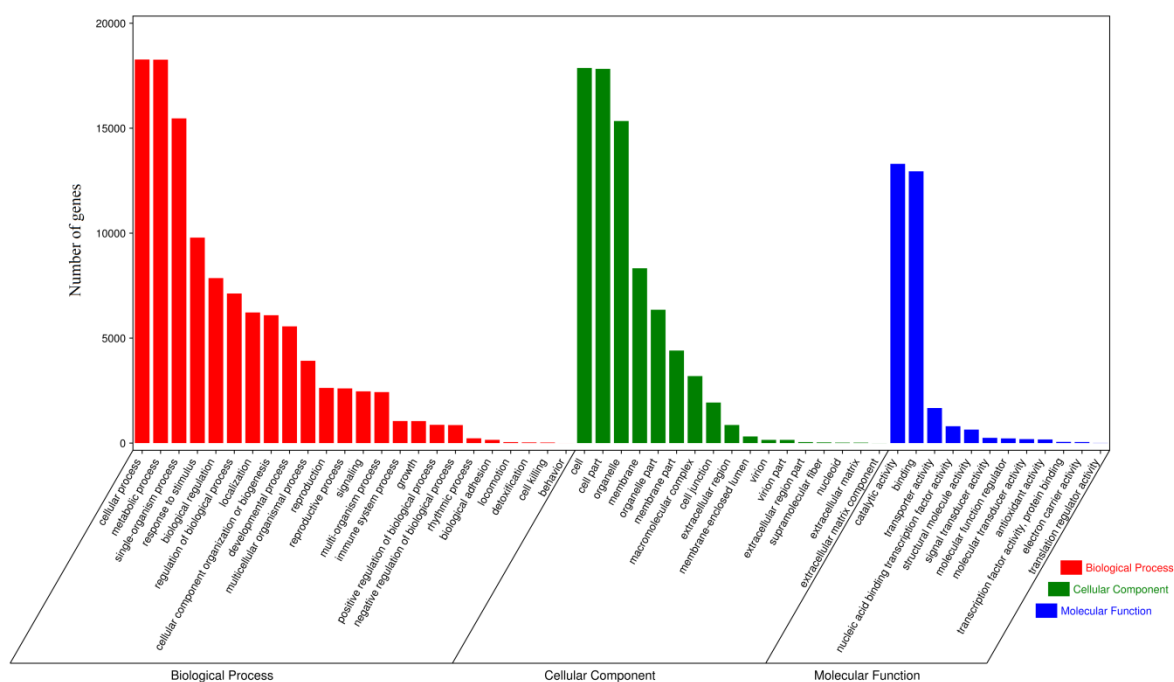


Figure S6. Annotation of unigenes on GO database and biological classification.

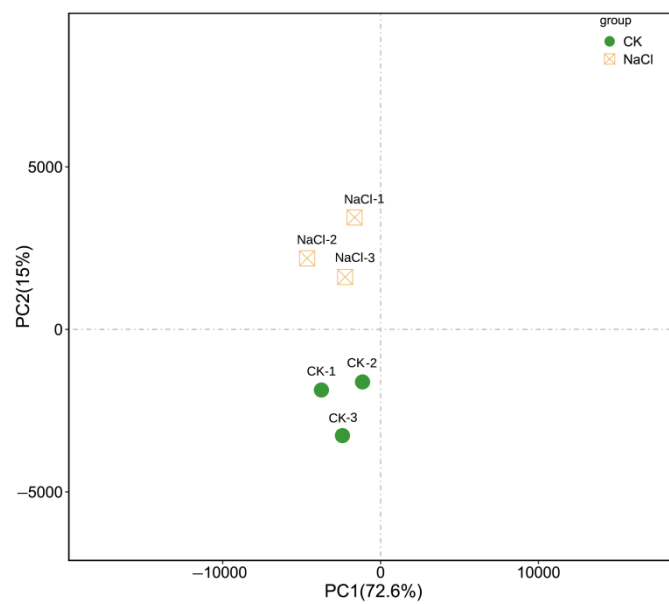


Figure S7. Principal component analysis (PCA) of CK and NaCl (300 mmol/L).

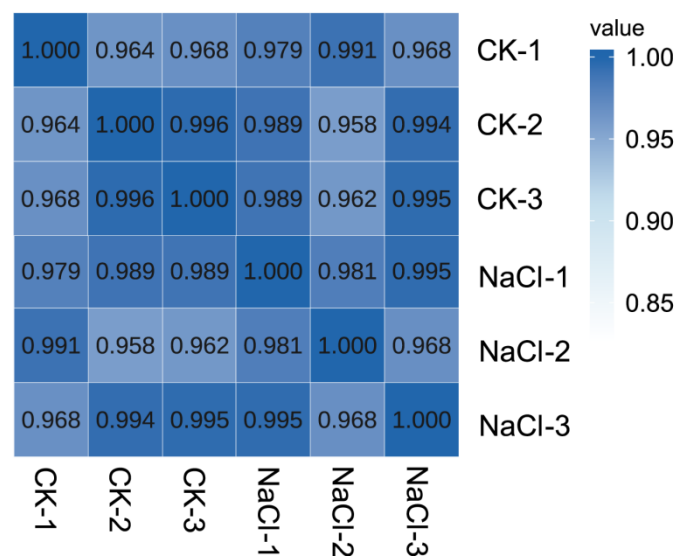


Figure S8. Pearson correlation analysis of CK and NaCl (300 mmol/L).

Table supplementary legends

Table S1. One hundred and twenty-three genes associated with other stress response at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Response to heat and cold			
<i>HSP18.5-C</i>	P05478	18.5 kDa class I heat shock protein	-1.40
<i>HSPD1</i>	P10809	60 kDa heat shock protein, mitochondrial	8.44
<i>COR413PM2</i>	Q9SVL6	Cold-regulated 413 plasma membrane protein 2	3.85
<i>HSP70-4</i>	Q9LHA8	Heat shock 70 kDa protein 4	9.70
<i>HSP70-14</i>	Q9S7C0	Heat shock 70 kDa protein 14	4.23
<i>HSC-2</i>	P27322	Heat shock cognate 70 kDa protein 2	4.26
<i>HSPA8</i>	A2Q0Z1	Heat shock cognate 71 kDa protein	3.68
<i>HSC80</i>	P36181	Heat shock cognate protein 80	1.30
<i>HSP81-2</i>	Q69QQ6	Heat shock protein 81-2	-9.91
<i>HSP83A</i>	P51819	Heat shock protein 83	-1.02
<i>HSP90-5</i>	Q9SIF2	Heat shock protein 90-5, chloroplastic	3.80
<i>HSP90-6</i>	F4JFN3	Heat shock protein 90-6, mitochondrial	8.42
<i>HSP90AB1</i>	P08238	Heat shock protein HSP 90-beta	5.70
<i>HSEAB2</i>	Q6VBB2	Heat stress transcription factor A-2b	1.86
<i>HSFB3</i>	O22230	Heat stress transcription factor B-3	2.73
<i>HOP2</i>	Q5XEP2	Hsp70-Hsp90 organizing protein 2	4.31
<i>LTI65</i>	Q04980	Low-temperature-induced 65 kDa protein	3.24
<i>HSP70</i>	Q02028	Stromal 70 kDa heat shock-related protein, chloroplastic	4.17
Others			
<i>At1g06620</i>	Q84MB3	1-aminocyclopropane-1-carboxylate oxidase homolog 1	-2.37
<i>At1g06650</i>	Q8H1S4	1-aminocyclopropane-1-carboxylate oxidase homolog 3	3.03
<i>At1g03400</i>	Q94A78	1-aminocyclopropane-1-carboxylate oxidase homolog 4	-1.91
<i>At1g43910</i>	Q9LP11	AAA-ATPase At1g43910	8.89
<i>ABRA</i>	P11140	Abrin-a	8.82
<i>AAG</i>	Q9M6E9	Agglutinin-1	5.47
<i>ALDH2B4</i>	Q9SU63	Aldehyde dehydrogenase family 2 member B4, mitochondrial	4.12
<i>ALD1</i>	Q9ZQI7	Aminotransferase ALD1, chloroplastic	8.89
<i>PRB1</i>	P11670	Basic form of pathogenesis-related protein 1	-1.06
<i>FOX2</i>	Q9FZC5	Berberine bridge enzyme-like 4	-4.01
<i>At1g30700</i>	Q9SA85	Berberine bridge enzyme-like 8	-3.38
<i>MEE23</i>	O64743	Berberine bridge enzyme-like 15	-1.04
<i>CATHB2</i>	Q93VC9	Cathepsin B-like protease 2	4.83
<i>CBSX2</i>	Q9C5D0	CBS domain-containing protein CBSX2, chloroplastic	8.80
<i>DJA6</i>	Q0JB88	Chaperone protein dnaJ A6	4.00
<i>Chga</i>	P26339	Chromogranin-A	6.05
<i>CRY1</i>	Q43125	Cryptochrome-1	4.63
<i>XCP1</i>	O65493	Cysteine protease XCP1	-10.84
<i>XCP2</i>	Q9LM66	Cysteine protease XCP2	4.98
<i>CYTI</i>	Q06445	Cysteine proteinase inhibitor	10.19
<i>CYS6</i>	Q8H0X6	Cysteine proteinase inhibitor 6	9.09
<i>CYS7</i>	Q8LC76	Cysteine proteinase inhibitor 7	9.96
<i>DEF</i>	A3FPF2	Defensin-like protein	4.81
<i>DHN1</i>	P12950	Dehydrin DHN1	3.25
<i>LPD1</i>	Q9M5K3	Dihydrolipoyl dehydrogenase 1, mitochondrial	4.45
<i>CjBAp12</i>	Q9ZP41	EG45-like domain containing protein	11.34
<i>GUN</i>	P22503	Endoglucanase	-6.57
<i>CHI1</i>	Q39799	Endochitinase 1	8.62
<i>ENDO4</i>	F4JJL0	Endonuclease 4	3.49
<i>KOR</i>	Q38890	Endoglucanase 25	2.96
<i>EP3</i>	Q9M2U5	Endochitinase EP3	7.32
<i>At1g78830</i>	Q9ZVA2	EP1-like glycoprotein 2	-2.05
<i>At1g78850</i>	Q9ZVA4H	EP1-like glycoprotein 3	3.32
<i>ephA</i>	I6YGS0	Epoxide hydrolase A	-4.41
<i>FLZ14</i>	Q8GYX2	FCS-Like Zinc finger 14	3.56
<i>hmp</i>	Q7WHW5	Flavohemoprotein	-9.78
<i>At3g05950</i>	Q9SFF9	Germin-like protein subfamily 1 member 7	-3.22
<i>GLP10</i>	Q9M263	Germin-like protein subfamily 2 member 4	4.60
<i>GLYR1</i>	Q9LSV0	Glyoxylate/succinic semialdehyde reductase 1	4.15
<i>GLYR2</i>	F4I907	Glyoxylate/succinic semialdehyde reductase 2, chloroplastic	4.96

<i>HEL</i>	P43082	Hevein-like preproprotein	-2.27
<i>RCD1</i>	Q8RY59	Inactive poly [ADP-ribose] polymerase RCD1	5.11
<i>PPF-1</i>	Q9FY06	Inner membrane protein PPF-1, chloroplastic	3.41
<i>KTI5</i>	Q9LMU2	Kunitz trypsin inhibitor 5	10.79
<i>Bp10</i>	Q00624	L-ascorbate oxidase homolog	3.11
<i>LRR1</i>	Q9FPJ5	Leucine-rich repeat protein 1	4.97
<i>LRR2</i>	Q6NQP4	Leucine-rich repeat protein 2	5.61
<i>MIF</i>	P14174	Macrophage migration inhibitory factor	9.74
<i>PRU1</i>	O50001	Major allergen Pru ar 1	7.56
<i>Mup1</i>	P11588	Major urinary protein 1	-12.22
<i>MLO1</i>	O49621	MLO-like protein 1	1.96
<i>MLP28</i>	Q9SSK9	MLP-like protein 28	4.00
<i>MLP328</i>	Q9ZVF3	MLP-like protein 328	3.99
<i>MLP423</i>	Q93VR4	MLP-like protein 423	2.71
<i>HSPRO2</i>	O04203	Nematode resistance protein-like HSPRO2	4.24
<i>NHL1</i>	Q9SRN0	NDR1/HIN1-like protein 1	-2.84
<i>NHL6</i>	Q8LD98	NDR1/HIN1-like protein 6	3.32
<i>NHL10</i>	Q9SJ52	NDR1/HIN1-like protein 10	4.38
<i>NHL13</i>	Q9ZVD2	NDR1/HIN1-like protein 13	-1.15
<i>AGP31</i>	Q9FZA2	Non-classical arabinogalactan protein 31	4.70
<i>NUDT8</i>	Q8L7W2	Nudix hydrolase 8	-1.08
<i>NUDT17</i>	Q9ZU95	Nudix hydrolase 17, mitochondrial	4.69
<i>OSM34</i>	P50700	Osmotin-like protein OSM34	4.35
<i>AAE3</i>	Q9SMT7	Oxalate--CoA ligase	9.37
<i>PCO2</i>	Q8LGJ5	Plant cysteine oxidase 2	-4.29
<i>PLAT2</i>	Q9SIE7	PLAT domain-containing protein 2	3.99
<i>CEP14</i>	Q52K95	Precursor of CEP14	-1.23
<i>GIP2</i>	P0DO21	Probable aspartic proteinase GIP2	7.13
<i>CSA</i>	Q06652	Probable phospholipid hydroperoxide glutathione peroxidase	4.37
<i>HEV1</i>	P02877	Pro-hevein	12.11
<i>ASPG1</i>	Q9LS40	Protein ASPARTIC PROTEASE IN GUARD CELL 1	3.73
<i>DJ1D</i>	Q9M8R4	Protein DJ-1 homolog D	4.17
<i>EXL2</i>	Q9FE06	Protein EXORDIUM-like 2	3.53
<i>EXL3</i>	Q9FHM9	Protein EXORDIUM-like 3	4.44
<i>EXL5</i>	Q9SII5	Protein EXORDIUM-like 5	3.22
<i>JOKA2</i>	M1BJF6	Protein JOKA2	5.93
<i>SRC2</i>	O04023	Protein SRC2 homolog	4.54
<i>At5g40382</i>	Q9FNE0	Putative cytochrome c oxidase subunit 5C-4	1.07
<i>RGA3</i>	Q7XA40	Putative disease resistance protein RGA3	1.67
<i>PDC2</i>	Q9FFT4	Pyruvate decarboxylase 2	-2.18
<i>rcf2</i>	Q9P3B2	Respiratory supercomplex factor 2 homolog C1565.01	-9.04
<i>PO21</i>	Q03278	Retrovirus-related Pol polyprotein from type-1 retrotransposable element R2	4.32
<i>RggA</i>	Q9SQ56	RGG repeats nuclear RNA binding protein A	3.84
<i>RGGB</i>	O23593	RGG repeats nuclear RNA binding protein B	4.26
<i>DFC</i>	Q9LX15	Protein DOWNSTREAM OF FLC	5.05
<i>SAG20</i>	Q94AK6	Senescence associated gene 20	-2.64
<i>SERINC3</i>	Q5R533	Serine incorporator 3	5.25
<i>SN1</i>	Q948Z4	Snakin-1	-1.01
<i>Sst</i>	P60041	Somatostatin	5.34
<i>At5g22580</i>	Q9FK81	Stress-response A/B barrel domain-containing protein At5g22580	10.14
<i>ICIS</i>	P08820	Subtilisin inhibitor	10.17
<i>TLP</i>	P83958	Thaumatococcus-like protein	-2.17
<i>At5g16400</i>	Q9XFH9	Thioredoxin F2, chloroplastic	5.63
<i>TRXH</i>	Q43636	Thioredoxin H-type	3.37
<i>At3g15360</i>	Q9SEU6	Thioredoxin M4, chloroplastic	3.61
<i>ATHX</i>	Q8LD49	Thioredoxin X, chloroplastic	9.30
<i>At1g08570</i>	O64654	Thioredoxin-like 1-1, chloroplastic	3.90
<i>CDSP32</i>	Q9SGS4	Thioredoxin-like protein CDSP32, chloroplastic	2.89
<i>TL17</i>	P81760	Thylakoid lumenal 17.4 kDa protein, chloroplastic	5.14
<i>CLEB3J9</i>	Q9THX6	Thylakoid lumenal 29 kDa protein, chloroplastic	5.61
<i>PHOS34</i>	Q8L4N1	Universal stress protein PHOS34	4.18
<i>At3g17800</i>	Q9LVJ0	UV-B-induced protein At3g17800, chloroplastic	4.21
<i>WIN2</i>	P09762	Wound-induced protein WIN2	-1.40
<i>SAP4</i>	Q9SJM6	Zinc finger A20 and AN1 domain-containing stress-associated protein 4	5.06
<i>SAP8</i>	A2YEZ6	Zinc finger A20 and AN1 domain-containing stress-associated protein 8	4.67

Table S2. Two hundred and eight genes associated with other primary metabolism at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Carbohydrate metabolism			
<i>SMT2</i>	Q39227	24-methylenesterol C-methyltransferase 2	3.04
<i>HMG1</i>	P14891	3-hydroxy-3-methylglutaryl-coenzyme A reductase 1	3.84
<i>ISPG</i>	F4K0E8	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase (ferredoxin)	0.72
<i>ISPH</i>	Q94B35	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	4.84
<i>ACO1</i>	Q42560	Aconitate hydratase 1	4.31
<i>ACOC</i>	P49608	Aconitate hydratase, cytoplasmic	3.48
<i>ACA7</i>	Q8L817	Alpha carbonic anhydrase 7	-3.10
<i>PHSL1</i>	P04045	Alpha-1,4 glucan phosphorylase L-1 isozyme	4.75
<i>STP-1</i>	P53535	Alpha-1,4 glucan phosphorylase L-2 isozyme	4.56
<i>AMY1.1</i>	P17859	Alpha-amylase	-3.91
<i>PHSH</i>	P53537	Alpha-glucan phosphorylase, H isozyme	3.92
<i>AGL2</i>	Q9F234	Alpha-glucosidase 2	8.62
<i>BCA4</i>	Q94CE4	Beta carbonic anhydrase 4	3.44
<i>BMY1</i>	O64407	Beta-amylase	5.83
<i>BXL1</i>	Q9FGY1	Beta-D-xylosidase 1	8.20
<i>BFRUCT1</i>	Q43089	Beta-fructofuranosidase, cell wall isozyme	9.83
<i>BGAL</i>	P48980	Beta-galactosidase	4.25
<i>BGAL3</i>	Q9SCV9	Beta-galactosidase 3	3.94
<i>CP12-2</i>	Q9LZP9	Calvin cycle protein CP12-2, chloroplastic	4.10
<i>Os05g0361200</i>	Q0DIV0	Ferrochelataase-2, chloroplastic	3.30
<i>FTHS</i>	P28723	Formate--tetrahydrofolate ligase	4.79
<i>E13A</i>	Q03773	Glucan endo-1,3-beta-glucosidase	-2.25
<i>At4g34480</i>	Q9M069	Glucan endo-1,3-beta-glucosidase 7	4.20
<i>HGN1</i>	P52407	Glucan endo-1,3-beta-glucosidase, basic vacuolar isoform	7.78
<i>CHLY</i>	P23472	Hevamine-A	-5.25
<i>AS</i>	Q9AR73	Hydroquinone glucosyltransferase	8.59
<i>BAM9</i>	Q8VYW2	Inactive beta-amylase 9	4.94
<i>Ins2</i>	P01326	Insulin-2	8.50
<i>IDH5</i>	Q945K7	Isocitrate dehydrogenase [NAD] catalytic subunit 5, mitochondrial	4.66
<i>IDHC</i>	P50218	Isocitrate dehydrogenase [NADP]	4.24
<i>ACEA</i>	P17069	Isocitrate lyase	4.92
<i>ARA1</i>	O23461	L-arabinokinase	3.81
<i>LDHB</i>	P07195	L-lactate dehydrogenase B chain	9.22
<i>MD1</i>	Q9FSF0	Malate dehydrogenase	3.65
<i>MDH1</i>	O48902	Malate dehydrogenase [NADP], chloroplastic	4.38
<i>MDHG</i>	P19446	Malate dehydrogenase, glyoxysomal	4.11
<i>MMDH</i>	P17783	Malate dehydrogenase, mitochondrial	3.60
<i>MASY</i>	P17815	Malate synthase, glyoxysomal	4.40
<i>GANAB</i>	Q14697	Neutral alpha-glucosidase AB	8.37
<i>NIA</i>	P17569	Nitrate reductase [NADH]	3.39
<i>Gba2</i>	Q69ZF3	Non-lysosomal glucosylceramidase	3.57
<i>PPCC</i>	Q9FV65	Phosphoenolpyruvate carboxylase 2	3.73
<i>PPC4</i>	Q8GVE8	Phosphoenolpyruvate carboxylase 4	3.56
<i>At1g56190</i>	P50318	Phosphoglycerate kinase 2, chloroplastic	3.77
<i>PGKY</i>	Q42962	Phosphoglycerate kinase, cytosolic	3.16
<i>At5g64460</i>	Q9FGF0	Phosphoglycerate mutase-like protein 1	4.80
<i>PDAT1</i>	Q9FNA9	Phospholipid:diacylglycerol acyltransferase 1	4.57
<i>algC</i>	Q88BD4	Phosphomannomutase/phosphoglucomutase	2.99
<i>KPPR</i>	P27774	Phosphoribulokinase, chloroplastic	3.59
<i>At1g48100</i>	Q949Z1	Polygalacturonase At1g48100	1.62
<i>At5g22620</i>	Q9FNJ9	Probable 2-carboxy-D-arabinitol-1-phosphatase	3.03
<i>OsI_031067</i>	A2Z3C4	Probable 6-phosphogluconolactonase 4, chloroplastic	8.78
<i>CXE7</i>	Q9ZQ91	Probable carboxylesterase 7	-3.85
<i>RFS2</i>	Q94A08	Probable galactinol--sucrose galactosyltransferase 2	8.81
<i>RFS6</i>	Q8RX87	Probable galactinol--sucrose galactosyltransferase 6	3.07
<i>GSVIVT00026920001</i>	A7PZL3	Probable polygalacturonase	4.74
<i>RPI3</i>	Q9S726	Probable ribose-5-phosphate isomerase 3, chloroplastic	3.99
<i>BGLU41</i>	Q9FIU7	Putative beta-glucosidase 41	-1.62
<i>AAPC</i>	Q40784	Putative glucose-6-phosphate 1-epimerase	5.47
<i>pdca</i>	Q4WXX9	Pyruvate decarboxylase	-9.54
<i>At3g55800</i>	P46283	Sedoheptulose-1,7-bisphosphatase, chloroplastic	3.66
<i>SHM4</i>	O23254	Serine hydroxymethyltransferase 4	3.92

GLYM	P50433	Serine hydroxymethyltransferase, mitochondrial	3.70
SDH	Q9FJ95	Sorbitol dehydrogenase	9.41
STS1	Q93XK2	Stachyose synthase	1.15
N/A	Q6DQL1	Succinate--CoA ligase [ADP-forming] subunit alpha-2	5.29
TALDO1	P37837	Transaldolase	4.75
TKT	P29401	Transketolase	4.81
TKTC	Q43848	Transketolase, chloroplastic	3.48
GAE1	Q9M0B6	UDP-glucuronate 4-epimerase 1	3.57
GAE6	Q9LIS3	UDP-glucuronate 4-epimerase 6	3.25
UXS5	Q9SN95	UDP-glucuronic acid decarboxylase 5	3.70
XYLA	Q9FKK7	Xylose isomerase	-2.81
Glycolytic			
PMGI	P35493	2,3-bisphosphoglycerate-independent phosphoglycerate mutase	3.72
ogdh	Q54JE4	2-oxoglutarate dehydrogenase, mitochondrial	3.14
ENOA	P06733	Alpha-enolase	4.14
PFKP	Q01813	ATP-dependent 6-phosphofructokinase, platelet type	8.61
ENO2	P25696	Bifunctional enolase 2/transcriptional activator	9.09
ENO	P42896	Enolase	4.13
ENO1	Q9LEJ0	Enolase 1	-1.86
GAPDH	P04406	Glyceraldehyde-3-phosphate dehydrogenase	4.84
PGK1	P00558	Phosphoglycerate kinase 1	9.42
PGAM1	P18669	Phosphoglycerate mutase 1	4.04
ODPA	P52902	Pyruvate dehydrogenase E1 component subunit alpha	4.43
PDH-E1 ALPHA	Q24457	Pyruvate dehydrogenase E1 component subunit alpha-3	3.23
Os08g0536000	Q6Z1G7	Pyruvate dehydrogenase E1 component subunit beta-1	4.92
OsL_35105	B8BJ39	Pyruvate kinase 1, cytosolic	4.51
Pkm	P52480	Pyruvate kinase PKM	-1.98
KPYC	P22200	Pyruvate kinase, cytosolic isozyme	3.77
TPI1	P60174	Triosephosphate isomerase	3.25
TPIC	P48496	Triosephosphate isomerase, chloroplastic	3.17
TPIP1	P48495	Triosephosphate isomerase, cytosolic	3.33
Amino metaolism			
IPMS2	Q9C550	2-isopropylmalate synthase 2, chloroplastic	8.62
ILL1	Q94AR8	3-isopropylmalate dehydratase large subunit, chloroplastic	5.36
At2g45300	P05466	3-phosphoshikimate 1-carboxyvinyltransferase, chloroplastic	3.34
HPD	P93836	4-hydroxyphenylpyruvate dioxygenase	1.05
DHDPS2	Q9FVC8	4-hydroxy-tetrahydrodipicolinate synthase 2, chloroplastic	4.38
MS1	O50008	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase 1	3.54
ILVB3	P27819	Acetolactate synthase 3, chloroplastic	4.52
AG118	O04866	Acetylornithine aminotransferase, mitochondrial	8.97
VIT_05s0020g04080	F6HDT7	Acireductone dioxygenase 2	3.92
ACR12	Q9LZ23	ACT domain-containing protein ACR12	9.35
SAHH	P50246	Adenosylhomocysteinase	3.59
AIH	Q8GWW7	Agmatine deiminase	3.89
GDCST	O65396	Aminomethyltransferase, mitochondrial	4.28
ASA1	P32068	Anthranilate synthase alpha subunit 1, chloroplastic	8.69
SPE1	Q39827	Arginine decarboxylase	3.19
AS	O24661	Asparagine synthetase [glutamine-hydrolyzing]	4.49
ASP3	P46644	Aspartate aminotransferase 3, chloroplastic	4.27
ASP5	P46248	Aspartate aminotransferase, chloroplastic	8.32
AKHSDH2	O81852	Bifunctional aspartokinase/homoserine dehydrogenase 2, chloroplastic	2.56
PCAS-1	Q76MX2	Bifunctional L-3-cyanoalanine synthase/cysteine synthase 1	3.95
ctps	Q54V77	CTP synthase	4.29
CGS1	P55217	Cystathionine gamma-synthase 1, chloroplastic	4.38
CYSK	Q43317	Cysteine synthase	4.14
CYSKP	O81155	Cysteine synthase, chloroplastic/chromoplastic	3.72
HEMB1	Q9SFH9	Delta-aminolevulinic acid dehydratase 1, chloroplastic	3.96
LYSA1	Q949X7	Diaminopimelate decarboxylase 1, chloroplastic	3.90
DAPF	Q9LFG2	Diaminopimelate epimerase, chloroplastic	3.76
PYD1	Q9LVI9	Dihydropyrimidine dehydrogenase (NADP(+)), chloroplastic	3.26
PECT1	Q9ZVI9	Ethanolamine-phosphate cytidyltransferase	5.18
GAD	Q07346	Glutamate decarboxylase	5.58
GAD5	Q9LSH2	Glutamate decarboxylase 5	4.05
EMB2360	P42770	Glutathione reductase, chloroplastic	3.90
GLSN	Q03460	Glutamate synthase [NADH], amyloplastic	9.12
GSA	Q85WB7	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic	3.58

<i>GGAT2</i>	Q9S7E9	Glutamate--glyoxylate aminotransferase 2	3.10
<i>GLNA</i>	P32289	Glutamine synthetase nodule isozyme	5.74
<i>GLN2</i>	O22506	Glutamine synthetase, chloroplastic	4.22
<i>At3g24170</i>	P48641	Glutathione reductase, cytosolic	3.23
<i>GST</i>	Q04522	Glutathione S-transferase	3.46
<i>GSTP1</i>	P09211	Glutathione S-transferase P	9.62
<i>GSTZ</i>	P57108	Glutathione S-transferase zeta class	-2.54
<i>GDCSH</i>	Q39732	Glycine cleavage system H protein, mitochondrial	3.61
<i>HMT3</i>	Q8LAX0	Homocysteine S-methyltransferase 3	-2.33
<i>HGO</i>	Q9ZRA2	Homogentisate 1,2-dioxygenase	-2.58
<i>IGPS</i>	P49572	Indole-3-glycerol phosphate synthase, chloroplastic	3.71
<i>At3g58610</i>	Q05758	Ketol-acid reductoisomerase, chloroplastic	3.72
<i>LDHA</i>	P00338	L-lactate dehydrogenase A chain	10.53
<i>MGL</i>	Q9SGU9	Methionine gamma-lyase	8.44
<i>MTHFR2</i>	O80585	Methylenetetrahydrofolate reductase 2	4.19
<i>NNMT</i>	P40261	Nicotinamide N-methyltransferase	9.12
<i>ODC</i>	O22616	Ornithine decarboxylase	4.23
<i>MSRA</i>	Q9SEC2	Peptide methionine sulfoxide reductase	4.04
<i>MSRB2</i>	Q9C5C8	Peptide methionine sulfoxide reductase B2, chloroplastic	9.39
<i>SHKB</i>	P37822	Phospho-2-dehydro-3-deoxyheptonate aldolase 2, chloroplastic	5.38
<i>GSTX4</i>	Q03666	Probable glutathione S-transferase	5.08
<i>PAO4</i>	Q8H191	Probable polyamine oxidase 4	4.91
<i>POX1</i>	P92983	Proline dehydrogenase 1, mitochondrial	6.07
<i>WAT1</i>	Q94AP3	Protein WALLS ARE THIN 1	5.29
<i>Os02g0773300</i>	Q6ZHE5	Putative D-cysteine desulphydrase 1, mitochondrial	4.70
<i>RIDA</i>	Q94JQ4	Reactive Intermediate Deaminase A, chloroplastic	9.05
<i>SAMDC</i>	Q96555	S-adenosylmethionine decarboxylase proenzyme	9.59
<i>SAMS</i>	Q8GTL5	S-adenosylmethionine synthase	4.13
<i>METK1</i>	A9P822	S-adenosylmethionine synthase 1	4.17
<i>SAMS2</i>	Q96552	S-adenosylmethionine synthase 2	9.25
<i>AGT1</i>	Q56YA5	Serine--glyoxylate aminotransferase	3.90
<i>TSB</i>	O50046	Tryptophan synthase beta chain 2, chloroplastic	-1.08
Lipid metabolism			
<i>PLSC</i>	Q42670	1-acyl-sn-glycerol-3-phosphate acyltransferase	1.15
<i>DWF5</i>	Q9LDU6	7-dehydrocholesterol reductase	5.38
<i>AKR1B1</i>	P15121	Aldo-keto reductase family 1 member B1	4.06
<i>ASPR</i>	O04057	Aspartic proteinase	3.64
<i>EPHX2</i>	Q6Q2C2	Bifunctional epoxide hydrolase 2	1.09
<i>APG</i>	Q9LU14	GDSL esterase/lipase APG	3.77
<i>At2g04570</i>	Q9SJB4	GDSL esterase/lipase At2g04570	8.96
<i>At4g01130</i>	Q9M153	GDSL esterase/lipase At4g01130	3.61
<i>At5g45670</i>	Q9FK75	GDSL esterase/lipase At5g45670	3.93
<i>INO1</i>	Q9LW96	Inositol-3-phosphate synthase	1.86
<i>PLC2</i>	Q39033	Phosphoinositide phospholipase C 2	3.94
<i>DALL3</i>	Q3EBR6	Phospholipase A1-Igamm2, chloroplastic	-3.25
<i>PLD1</i>	Q41142	Phospholipase D alpha 1	3.68
<i>pldY</i>	Q54K50	Phospholipase D Y	3.29
<i>CK1</i>	Q9M9H6	Probable choline kinase 1	4.82
<i>GPAT3</i>	Q9SYJ2	Probable glycerol-3-phosphate acyltransferase 3	5.16
<i>GPAT8</i>	Q5XF03	Probable glycerol-3-phosphate acyltransferase 8	3.42
<i>PDX1</i>	Q39963	Probable pyridoxal 5'-phosphate synthase subunit PDX1	4.22
<i>SQD2</i>	Q8S4F6	Sulfoquinovosyl transferase SQD2	3.78
Fatty acid metabolism			
<i>KCS1</i>	Q9MAM3	3-ketoacyl-CoA synthase 1	2.98
<i>CUT1</i>	Q9XF43	3-ketoacyl-CoA synthase 6	4.54
<i>FDH</i>	Q570B4	3-ketoacyl-CoA synthase 10	4.21
<i>KCS19</i>	Q9LZ72	3-ketoacyl-CoA synthase 19	3.19
<i>KCS20</i>	Q9FG87	3-ketoacyl-CoA synthase 20	3.23
<i>PED1</i>	Q56WD9	3-ketoacyl-CoA thiolase 2, peroxisomal	5.19
<i>fabG</i>	Q9X248	3-oxoacyl-[acyl-carrier-protein] reductase FabG	1.51
<i>ACP1</i>	P93092	Acyl carrier protein 1, chloroplastic	-2.70
<i>ACBP</i>	Q39779	Acyl-CoA-binding protein	4.54
<i>ACX4</i>	Q96329	Acyl-coenzyme A oxidase 4, peroxisomal	9.47
<i>AOS3</i>	Q8GZP5	Allene oxide synthase 3	-3.70
<i>MOD1</i>	Q9SLA8	Enoyl-[acyl-carrier-protein] reductase [NADH], chloroplastic	3.52
<i>HPL</i>	K4CF70	Fatty acid hydroperoxide lyase, chloroplastic	6.42
<i>FACT</i>	Q9FFQ7	Fatty alcohol:caffeoyle-CoA acyltransferase	-2.33

<i>LOX2.1</i>	O24370	Linoleate 13S-lipoxygenase 2-1, chloroplastic	4.84
<i>LOX3.1</i>	O24371	Linoleate 13S-lipoxygenase 3-1, chloroplastic	3.34
<i>LACS6</i>	Q8LPS1	Long chain acyl-CoA synthetase 6, peroxisomal	5.16
<i>LACS8</i>	Q9SJD4	Long chain acyl-CoA synthetase 8	4.26
<i>SMO1-2</i>	Q1EC69	Methylsterol monooxygenase 1-2	8.67
<i>FAD7</i>	P48620	Omega-3 fatty acid desaturase, chloroplastic	4.74
<i>FAD6C</i>	P48627	Omega-6 fatty acid desaturase, chloroplastic	3.77
<i>FATB1</i>	Q9SQI3	Palmitoyl-acyl carrier protein thioesterase, chloroplastic	8.61
<i>ADS3</i>	Q949X0	Palmitoyl-monogalactosyldiacylglycerol delta-7 desaturase, chloroplastic	-2.33
<i>ACX1</i>	O65202	Peroxisomal acyl-coenzyme A oxidase 1	3.64
<i>MFP2</i>	Q9ZPI5	Peroxisomal fatty acid beta-oxidation multifunctional protein MFP2	3.38
<i>Os02g0639600</i>	Q6H5U3	Sphingolipid delta(4)-desaturase DES1-like	8.90
<i>S-ACP-DES6</i>	Q84VY3	Stearoyl-[acyl-carrier-protein] 9-desaturase 6, chloroplastic	-1.09
<i>STAD</i>	P22337	Stearoyl-[acyl-carrier-protein] 9-desaturase, chloroplastic	4.01
Sulfur metabolism			
<i>AKN</i>	O49204	Adenylyl-sulfate kinase, chloroplastic	3.69
<i>APS1</i>	Q9LIK9	ATP sulfurylase 1, chloroplastic	4.50
<i>APS2</i>	Q43870	ATP sulfurylase 2	4.35

Table S3. One hundred and fifty genes associated with other cell morphogenesis at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Growth and development			
<i>AGRN</i>	O00468	Agrin	8.86
<i>AKR2A</i>	Q9SAR5	Ankyrin repeat domain-containing protein 2A	3.55
<i>AGP20</i>	Q9M373	Arabinogalactan protein 20	3.35
<i>CLPP4</i>	Q94B60	ATP-dependent Clp protease proteolytic subunit 4, chloroplastic	4.54
<i>CLPP6</i>	Q9SAA2	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic	4.84
<i>CLPR1</i>	Q9XJ35	ATP-dependent Clp protease proteolytic subunit-related protein 1	4.93
<i>CNN3</i>	Q15417	Calponin-3	8.54
<i>MEE14</i>	Q9XIM0	CCG-binding protein 1	3.37
<i>CCN1</i>	O00622	CCN family member 1	9.69
<i>CCN2</i>	P29279	CCN family member 2	4.75
<i>CDC48</i>	P54774	Cell division cycle protein 48 homolog	5.66
<i>CPFTSY</i>	O80842	Cell division protein FtsY homolog, chloroplastic	4.38
<i>FTSZ2-1</i>	O82533	Cell division protein FtsZ homolog 2-1, chloroplastic	4.80
<i>CLPC</i>	P35100	Chaperone protein ClpC, chloroplastic	3.86
<i>CLPD</i>	P42762	Chaperone protein ClpD, chloroplastic	5.36
<i>ATJ8</i>	Q9SAG8	Chaperone protein dnaJ 8, chloroplastic	4.25
<i>ATJ11</i>	Q9FYB5	Chaperone protein dnaJ 11, chloroplastic	4.07
<i>COL1A1</i>	P02452	Collagen alpha-1(I) chain	6.45
<i>COL4A1</i>	P02462	Collagen alpha-1(IV) chain	9.87
<i>COL4A2</i>	P08572	Collagen alpha-2(IV) chain	9.81
<i>COL6A2</i>	P12110	Collagen alpha-2(VI) chain	8.26
<i>CYCD3-3</i>	Q9SN11	Cyclin-D3-3	4.25
<i>DUSP1</i>	P28562	Dual specificity protein phosphatase 1	8.06
<i>E134</i>	Q9ZT66	Endo-1,3;1,4-beta-D-glucanase	-3.20
<i>EBP1</i>	M1CZC0	ERBB-3 BINDING PROTEIN 1	4.50
<i>FLA1</i>	Q9FM65	Fasciclin-like arabinogalactan protein 1	3.73
<i>FLA7</i>	Q9SJ81	Fasciclin-like arabinogalactan protein 7	9.41
<i>FLA10</i>	Q9LZX4	Fasciclin-like arabinogalactan protein 10	4.07
<i>FLA11</i>	Q8LEJ6	Fasciclin-like arabinogalactan protein 11	-1.19
<i>FLA12</i>	Q8LEE9	Fasciclin-like arabinogalactan protein 12	-1.05
<i>FLA17</i>	Q66GR0	Fasciclin-like arabinogalactan protein 17	4.14
<i>FSTL1</i>	Q12841	Follistatin-related protein 1	8.41
<i>FRL4A</i>	Q9LUV4	FRIGIDA-like protein 4a	4.09
<i>SERPINE2</i>	P07093	Glia-derived nexin	7.82
<i>At5g07830</i>	Q9FF10	Heparanase-like protein 1	8.74
<i>IFRD1</i>	Q5S1U6	Interferon-related developmental regulator 1	8.45
<i>KRT19</i>	P08727	Keratin, type I cytoskeletal 19	6.19
<i>KRT8</i>	P05787	Keratin, type II cytoskeletal 8	8.48
<i>MMP14</i>	P50281	Matrix metalloproteinase-14	4.54
<i>VIPP1</i>	O80796	Membrane-associated protein VIPP1, chloroplastic	9.87
<i>2MMP</i>	O04529	Metalloendoproteinase 2-MMP	-1.44
<i>SKU5</i>	Q9SU40	Monocopper oxidase-like protein SKU5	3.32

<i>MYH9</i>	P35579	Myosin-9	5.69
<i>MYL12A</i>	P19105	Myosin regulatory light chain 12A	4.87
<i>AHNAK</i>	Q09666	Neuroblast differentiation-associated protein AHNAK	4.98
<i>SMG7</i>	A9QM73	Nonsense-mediated mRNA decay factor SMG7	4.83
<i>NPM1</i>	P06748	Nucleophosmin	3.79
<i>PATL3</i>	Q56Z59	Patellin-3	3.03
<i>At1g60420</i>	O80763	Probable nucleoredoxin 1	10.27
<i>Os01g0794400</i>	Q0JIL1	Probable nucleoredoxin 2	4.24
<i>CDI</i>	Q9XIP8	Protein CDI	4.21
<i>CHUP1</i>	Q9LI74	Protein CHUP1, chloroplastic	3.79
<i>CRWN1</i>	F4HRT5	Protein CROWDED NUCLEI 1	3.40
<i>CURT1A</i>	O04616	Protein CURVATURE THYLAKOID 1A, chloroplastic	3.68
<i>CURT1B</i>	Q8LCA1	Protein CURVATURE THYLAKOID 1B, chloroplastic	3.52
<i>HTH</i>	Q9S746	Protein HOTHEAD	8.63
<i>kra</i>	Q9VNE2	Protein krasavietz	4.46
<i>PHI-1</i>	O82161	Protein PHOSPHATE-INDUCED 1	0.00
<i>PTAC16</i>	Q9STF2	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 16, chloroplastic	3.88
<i>REC2</i>	F4JKH6	Protein REDUCED CHLOROPLAST COVERAGE 2	5.02
<i>SEOB</i>	Q9SS87	Protein SIEVE ELEMENT OCCLUSION B	8.35
<i>SMXL7</i>	O80875	Protein SMAX1-LIKE 7	4.43
<i>At3g05500</i>	Q9MA63	REF/SRPP-like protein At3g05500	9.29
<i>RTN4</i>	Q9NQC3	Reticulon-4	8.37
<i>RTNLB2</i>	Q9SUT9	Reticulon-like protein B2	5.93
<i>SEPTIN2</i>	Q15019	Septin-2	8.78
<i>SPARC</i>	P09486	SPARC	6.96
<i>SIR1</i>	O82802	Sulfite reductase 1 [ferredoxin], chloroplastic	3.36
<i>TOM2A</i>	Q9C5W7	Tobamovirus multiplication protein 2A	8.77
<i>TAGLN</i>	Q01995	Transgelin	9.16
<i>TAGLN2</i>	P37802	Transgelin-2	3.58
<i>VCAN</i>	P13611	Versican core protein	8.38
<i>CER1</i>	F4HVV0	Very-long-chain aldehyde decarboxylase CER1	-5.55
Microtubule cytoskeleton organization			
<i>MAP65-1</i>	Q9FLP0	65-kDa microtubule-associated protein 1	4.05
<i>MAP65-6</i>	Q9SIS3	65-kDa microtubule-associated protein 6	5.11
<i>ACT</i>	O81221	Actin	4.12
<i>AC97</i>	P30171	Actin-97	3.81
<i>ADF1</i>	Q9FVI2	Actin-depolymerizing factor 1	5.29
<i>ADF2</i>	Q9FVI1	Actin-depolymerizing factor 2	5.87
<i>CAP1</i>	Q01518	Adenylyl cyclase-associated protein 1	3.63
<i>ACTN1</i>	P12814	Alpha-actinin-1	5.29
<i>ACTN4</i>	O43707	Alpha-actinin-4	9.44
<i>CFL1</i>	P23528	Cofilin-1	3.71
<i>CAP1</i>	O65902	Cyclase-associated protein 1	8.73
<i>FPP4</i>	Q0WSY2	Filament-like plant protein 4	8.31
<i>WLIM1</i>	Q94JX5	LIM domain-containing protein WLIM1	9.33
<i>MSN</i>	P26038	Moesin	4.34
<i>MYL6</i>	P60661	Myosin light polypeptide 6	3.54
<i>Pyy</i>	Q9EPS2	Peptide YY	10.20
<i>PRO1</i>	O82572	Profilin-1	3.72
<i>SP1L1</i>	B3H4F1	Protein SPIRAL1-like 1	9.47
<i>TMSB10</i>	P63314	Thymosin beta-10	11.83
<i>TPM4</i>	P02561	Tropomyosin alpha-4 chain	9.89
<i>TUBA</i>	P33629	Tubulin alpha chain	6.31
<i>TUBA1</i>	P28752	Tubulin alpha-1 chain	3.60
<i>TUBA1A</i>	P68362	Tubulin alpha-1A chain	3.72
<i>TUBA2</i>	Q40832	Tubulin alpha-2 chain	-10.23
<i>TUBA3</i>	Q56WH1	Tubulin alpha-3 chain	3.69
<i>TUBB1</i>	P37392	Tubulin beta-1 chain	4.13
<i>TUBB4B</i>	Q3MHM5	Tubulin beta-4B chain	8.62
<i>TUBB5</i>	P46265	Tubulin beta-5 chain	3.47
<i>VLN2</i>	O81644	Villin-2	3.62
<i>WDR1</i>	O75083	WD repeat-containing protein 1	3.54
Cell wall			
<i>ASD1</i>	Q9SG80	Alpha-L-arabinofuranosidase 1	4.64
<i>UGE1</i>	Q42605	Bifunctional UDP-glucose 4-epimerase and UDP-xylose 4-epimerase 1	4.28
<i>CALS3</i>	Q9LXT9	Callose synthase 3	4.55
<i>phiA</i>	A2R2S8	Cell wall protein phiA	-9.90

<i>CESA1</i>	O48946	Cellulose synthase A catalytic subunit 1 [UDP-forming]	3.66
<i>CESA2</i>	O48947	Cellulose synthase A catalytic subunit 2 [UDP-forming]	3.84
<i>CESA3</i>	Q941L0	Cellulose synthase A catalytic subunit 3 [UDP-forming]	4.10
<i>CSLG2</i>	Q8VYR4	Cellulose synthase-like protein G2	2.88
<i>EXPA1</i>	Q9C554	Expansin-A1	4.90
<i>EXPA4</i>	O48818	Expansin-A4	3.77
<i>EXPA8</i>	O22874	Expansin-A8	-2.95
<i>EXLA1</i>	Q9LZT4	Expansin-like A1	4.02
<i>GALS3</i>	O65431	Galactan beta-1,4-galactosyltransferase GALS3	5.61
<i>GDPDL3</i>	Q9SZ11	Glycerophosphodiester phosphodiesterase GDPDL3	3.29
<i>GDPDL4</i>	Q9FJ62	Glycerophosphodiester phosphodiesterase GDPDL4	-1.16
<i>LRX5</i>	Q9SN46	Leucine-rich repeat extensin-like protein 5	3.06
<i>MAN4</i>	Q8L5J1	Mannan endo-1,4-beta-mannosidase 4	3.18
<i>HHT1</i>	Q94CD1	Omega-hydroxypalmitate O-feruloyl transferase	3.68
<i>PAE8</i>	Q6DBP4	Pectin acetylesterase 8	3.89
<i>PECS-1.1</i>	O04886	Pectinesterase 1	4.74
<i>PECS-2.1</i>	O04887	Pectinesterase 2	-1.39
<i>MPE3</i>	Q43111	Pectinesterase 3	-1.03
<i>BXL2</i>	Q94KD8	Probable beta-D-xylosidase 2	4.13
<i>GATL1</i>	Q9LN68	Probable galacturonosyltransferase-like 1	-1.05
<i>GATL10</i>	Q9LHD2	Probable galacturonosyltransferase-like 10	-1.76
<i>GATL3</i>	Q0V7R1	Probable galacturonosyltransferase-like 3	1.39
<i>GATL7</i>	Q8VYF4	Probable galacturonosyltransferase-like 7	5.23
<i>XTH28</i>	Q38909	Probable xyloglucan endotransglucosylase/hydrolase protein 28	3.57
<i>XTH33</i>	Q8LC45	Probable xyloglucan endotransglucosylase/hydrolase protein 33	-1.58
<i>XTH6</i>	Q8LF99	Probable xyloglucan endotransglucosylase/hydrolase protein 6	2.98
<i>XTHB</i>	Q8LNZ5	Probable xyloglucan endotransglucosylase/hydrolase protein B	3.61
<i>IQD1</i>	Q9SF32	Protein IQ-DOMAIN 1	4.40
<i>IQD14</i>	Q8LPG9	Protein IQ-DOMAIN 14	1.54
<i>IPP</i>	A2X8Q3	Soluble inorganic pyrophosphatase	6.10
<i>PPA4</i>	Q9LFF9	Soluble inorganic pyrophosphatase 4	4.54
<i>PPA6</i>	Q9LXC9	Soluble inorganic pyrophosphatase 6, chloroplastic	2.89
<i>AXS2</i>	Q9SGE0	UDP-D-apiose/UDP-D-xylose synthase 2	3.85
<i>XTH22</i>	Q38857	Xyloglucan endotransglucosylase/hydrolase protein 22	-1.22
<i>XTH31</i>	P93046	Xyloglucan endotransglucosylase/hydrolase protein 31	-3.75
<i>XTH9</i>	Q8LDW9	Xyloglucan endotransglucosylase/hydrolase protein 9	5.39
Cell death			
<i>LGALS1</i>	P09382	Galectin-1	10.68
<i>GAS6</i>	Q14393	Growth arrest-specific protein 6	5.53
<i>MT-RNR2</i>	Q8IVG9	Humanin	8.21
<i>IGFBP3</i>	P17936	Insulin-like growth factor-binding protein 3	8.58
<i>IGFBP4</i>	P22692	Insulin-like growth factor-binding protein 4	6.91
<i>IGFBP7</i>	Q16270	Insulin-like growth factor-binding protein 7	10.58
<i>MAGED1</i>	Q9Y5V3	Melanoma-associated antigen D1	8.21

Table S4. Other forty six TFs at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
<i>COL4</i>	Q940T9	Zinc finger protein CONSTANS-LIKE 4	2.76
<i>COL9</i>	Q9SSE5	Zinc finger protein CONSTANS-LIKE 9	3.40
<i>COL15</i>	Q9C7E8	Zinc finger protein CONSTANS-LIKE 15	3.63
<i>COL16</i>	Q8RWD0	Zinc finger protein CONSTANS-LIKE 16	3.98
<i>Os01g0871200</i>	Q943I6	Zinc finger protein STOP1 homolog	8.92
<i>ZFP6</i>	Q39265	Zinc finger protein 6	-4.21
<i>ZAT6</i>	O22533	Zinc finger protein ZAT6	-1.51
<i>ZAT10</i>	Q96289	Zinc finger protein ZAT10	5.60
<i>MIF2</i>	Q9LJW5	Mini zinc finger protein 2	-1.01
<i>MIP1B</i>	Q9LRM4	B-box domain protein 31	1.94
<i>BBX19</i>	C0SVM5	B-box zinc finger protein 19	1.25
<i>BLH1</i>	Q9SJ56	BEL1-like homeodomain protein 1	4.15
<i>BLH7</i>	Q9SIW1	BEL1-like homeodomain protein 7	9.02
<i>CIP7</i>	O80386	COP1-interacting protein 7	3.28
<i>DCN</i>	P07585	Decorin	8.51
<i>GATA8</i>	Q9SV30	GATA transcription factor 8	3.18
<i>GBF1</i>	P42774	G-box-binding factor 1	4.49
<i>HMGAI</i>	Q6URC2	High mobility group protein HMG-	5.81

<i>KNAP3</i>	O04136	I/HMG-Y	
<i>ATHB-7</i>	P46897	Homeobox protein knotted-1-like 3	3.78
<i>ATHB-12</i>	Q9M276	Homeobox-leucine zipper protein ATHB-7	2.23
		Homeobox-leucine zipper protein ATHB-12	1.23
<i>ATHB-16</i>	Q940J1	Homeobox-leucine zipper protein ATHB-16	3.40
<i>HAT22</i>	P46604	Homeobox-leucine zipper protein HAT22	1.36
<i>HOX16</i>	A2X980	Homeobox-leucine zipper protein HOX16	4.45
<i>HIF1A</i>	Q16665	Hypoxia-inducible factor 1-alpha	9.20
<i>LBD4</i>	Q9SHE9	LOB domain-containing protein 4	1.20
<i>LBD15</i>	Q8L5T5	LOB domain-containing protein 15	-3.06
<i>LBD18</i>	O22131	LOB domain-containing protein 18	-2.08
<i>LOXL2</i>	Q9Y4K0	Lysyl oxidase homolog 2	9.91
<i>MBF1A</i>	Q9SJI8	Multiprotein-bridging factor 1a	3.33
<i>AFP3</i>	Q94F39	Ninja-family protein AFP3	1.33
<i>NFYA4</i>	Q8VY64	Nuclear transcription factor Y subunit A-4	1.93
<i>PAX8</i>	Q06710	Paired box protein Pax-8	8.42
<i>CAF1-9</i>	Q9LXM2	Probable CCR4-associated factor 1 homolog 9	9.59
<i>CAF1-11</i>	Q9FMS6	Probable CCR4-associated factor 1 homolog 11	-1.50
<i>GLK1</i>	Q5Z5I4	Probable transcription factor GLK1	3.82
<i>LHY</i>	Q6R0H1	Protein LHY	1.07
<i>PTMA</i>	P06454	Prothymosin alpha	8.86
<i>SCL13</i>	Q9M0M5	Scarecrow-like protein 13	3.82
<i>TPR1</i>	Q0WV90	Topless-related protein 1	3.99
<i>Os07g0631100</i>	Q8LHP0	Transcription elongation factor 1 homolog	10.12
<i>CSA</i>	Q5NBM8	Transcription factor CSA	3.36
<i>DIVARICATA</i>	Q8S9H7	Transcription factor DIVARICATA	9.63
<i>GTE7</i>	Q7Y214	Transcription factor GTE7	4.35
<i>MYC2</i>	A0A3Q7HRZ6	Transcription factor MYC2	3.81
<i>GT-2</i>	Q39117	Trihelix transcription factor GT-2	4.70

Table S5. One hundred and thirty-seven genes associated with other bio-signaling at NaCl (300 mmol/L) vs.CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Calcium ion			
<i>RCAN2</i>	Q14206	Calciopressin-2	-9.14
<i>CBP</i>	Q2QY10	Calcium-binding protein CBP	9.34
<i>KRP1</i>	O81831	Calcium-binding protein KRP1	-1.63
<i>cam</i>	A8CEP3	Calmodulin	-10.18
<i>CALM1</i>	P0DP23	Calmodulin-1	5.14
<i>CAM-1</i>	P62200	Calmodulin-1/11/16	4.80
<i>CBP60A</i>	C0SVV6	Calmodulin-binding protein 60 A	3.28
<i>CBP60B</i>	Q9FKL6	Calmodulin-binding protein 60 B	2.98
<i>CANX</i>	P27824	Calnexin	8.62
<i>CALX</i>	Q39817	Calnexin homolog	3.24
<i>CAPN2</i>	P17655	Calpain-2 catalytic subunit	5.17
<i>CALU</i>	O43852	Calumenin	8.69
<i>CML13</i>	Q94AZ4	Probable calcium-binding protein CML13	5.09
<i>CML16</i>	Q9LI84	Probable calcium-binding protein CML16	1.30
<i>CML18</i>	Q0DJV6	Probable calcium-binding protein CML18	-1.13
<i>CML27</i>	Q9LE22	Probable calcium-binding protein CML27	10.02
<i>S100A6</i>	P06703	Protein S100-A6	3.33
<i>S100A16</i>	Q96FQ6	Protein S100-A16	8.91
Protein kinase			
<i>CPK6</i>	Q38872	Calcium-dependent protein kinase 6	3.97
<i>CPK19</i>	P53683	Calcium-dependent protein kinase 19	9.29
<i>CPK28</i>	Q9FKW4	Calcium-dependent protein kinase 28	4.19
<i>CPK32</i>	Q6NLQ6	Calcium-dependent protein kinase 32	3.23
<i>CIPK6</i>	O65554	CBL-interacting serine/threonine-protein kinase 6	4.52
<i>CIPK25</i>	Q8W1D5	CBL-interacting serine/threonine-protein kinase 25	4.86
<i>CDKF-4</i>	Q6Z8C8	Cyclin-dependent kinase F-4	3.87
<i>CDKG-2</i>	A2XUW1	Cyclin-dependent kinase G-2	6.65

CRK8	O65468	Cysteine-rich receptor-like protein kinase 8	5.39
CRK26	Q9T0J1	Cysteine-rich receptor-like protein kinase 26	4.87
MPK3	Q39023	Mitogen-activated protein kinase 3	-1.67
MPK17	Q84M93	Mitogen-activated protein kinase 17	9.31
MAPKKK3	F4HRJ4	Mitogen-activated protein kinase kinase 3	8.64
At5g24010	Q9FLW0	Probable receptor-like protein kinase At5g24010	3.24
At1g01540	Q3EDL4	Probable serine/threonine-protein kinase At1g01540	3.10
At1g54610	Q9ZVM9	Probable serine/threonine-protein kinase At1g54610	8.29
SIS8	Q9C9U5	Probable serine/threonine-protein kinase SIS8	3.54
At5g49770	Q9LT96	Probable leucine-rich repeat receptor-like protein kinase At5g49770	3.91
PTI11	Q8H1G6	PTI1-like tyrosine-protein kinase 1	3.32
RLK7	F4I2N7	Receptor-like protein kinase 7	8.52
FER	Q9SCZ4	Receptor-like protein kinase FERONIA	6.05
THE1	Q9LK35	Receptor-like protein kinase THESEUS 1	1.10
BSK1	Q944A7	Serine/threonine-protein kinase BSK1	3.60
CTR1	Q05609	Serine/threonine-protein kinase CTR1	-2.32
MHK	P43294	Serine/threonine-protein kinase MHK	8.59
PBL35	Q9SRH7	Serine/threonine-protein kinase PBL35	8.52
PLK2	Q9NYY3	Serine/threonine-protein kinase PLK2	8.72
SAPK10	Q75H77	Serine/threonine-protein kinase SAPK10	8.37
SRK2A	P43291	Serine/threonine-protein kinase SRK2A	4.38
STY13	Q9ZQ31	Serine/threonine-protein kinase STY13	3.30
STY46	F4JTP5	Serine/threonine-protein kinase STY46	3.30
CCR4	Q9FIJ6	Serine/threonine-protein kinase-like protein CCR4	-1.43
ASK1	P43288	Shaggy-related protein kinase alpha	3.81
ASK10	Q39019	Shaggy-related protein kinase kappa	4.58
KIN10	Q38997	SNF1-related protein kinase catalytic subunit alpha KIN10	4.11
KING1	Q8LBB2	SNF1-related protein kinase regulatory subunit gamma-1	3.29
Protein phosphatase			
At2g29380	Q9ZW21	Probable protein phosphatase 2C 24	1.50
Os04g0609600	Q0JAA0	Probable protein phosphatase 2C 44	8.69
Os06g0717800	Q5Z8P0	Probable protein phosphatase 2C 60	3.90
At5g53140	Q94AT1	Probable protein phosphatase 2C 76	5.08
SRF6	Q9C8M9	Protein STRUBBELIG-RECEPTOR FAMILY 6	8.68
PAP2	Q9SDZ9	Purple acid phosphatase 2	5.06
PAP18	Q9LJU7	Purple acid phosphatase 18	4.89
PPP2R1A	Q32PI5	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	4.91
PP2AA2	Q38950	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	3.24
PPP6R3	Q5F471	Serine/threonine-protein phosphatase 6 regulatory subunit 3	3.78
Others			
TFT7	P93212	14-3-3 protein 7	3.77
YWHAE	P62261	14-3-3 protein epsilon	9.13
YWHAQ	Q3SZI4	14-3-3 protein theta	4.32
YWHAZ	P63103	14-3-3 protein zeta/delta	4.06
GF14	P46266	14-3-3-like protein	3.63
GF14A	Q96450	14-3-3-like protein A	2.60
GF14D	Q96453	14-3-3-like protein D	4.01
21KD	P17407	21 kDa protein	-1.32
ASP	P32765	21 kDa seed protein	4.06
CPN20	O65282	20 kDa chaperonin, chloroplastic	3.19
Alb	P07724	Albumin	-6.57
Serpina1c	Q00896	Alpha-1-antitrypsin 1-3	-12.26
APLP2	Q06481	Amyloid beta precursor like protein 2	5.13
APP	P05067	Amyloid-beta precursor protein	9.34
ANXA2	P07355	Annexin A2	7.20
ANXA5	P08758	Annexin A5	4.01
psl1	P08594	Aqualysin-1	-10.86
CKL1	P42158	Casein kinase 1-like protein 1	4.17
CKL2	Q9CAI5	Casein kinase 1-like protein 2	4.21
HD16	Q852L0	Casein kinase 1-like protein HD16	4.33
CBBY	Q94K71	CBBY-like protein	4.59
CD81	P60033	CD81 antigen	5.05
CD59	P13987	CD59 glycoprotein	5.12
CD151	P48509	CD151 antigen	9.74
DKK3	Q9UBP4	Dickkopf-related protein 3	8.44

<i>DCBLD2</i>	Q96PD2	Discoidin, CUB and LCCL domain-containing protein 2	9.74
<i>ERG3</i>	Q25AG5	Elicitor-responsive protein 3	-1.37
<i>FN1</i>	P02751	Fibronectin	11.00
<i>FHL2</i>	Q14192	Four and a half LIM domains protein 2	5.15
<i>LGALS3BP</i>	Q08380	Galectin-3-binding protein	5.45
<i>Gnat1</i>	P20612	Guanine nucleotide-binding protein G(t) subunit alpha-1	-11.53
<i>GNB1</i>	P62871	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1	0.89
<i>GNB2L1</i>	Q4R7Y4	Guanine nucleotide-binding protein subunit beta-2-like 1	4.86
<i>GNBL</i>	Q39836	Guanine nucleotide-binding protein subunit beta-like protein	4.16
<i>NSN1</i>	Q9M8Z5	Guanine nucleotide-binding protein-like NSN1	8.68
<i>GDI1</i>	Q96254	Guanosine nucleotide diphosphate dissociation inhibitor 1	4.38
<i>ITM2B</i>	Q9Y287	Integral membrane protein 2B	9.73
<i>ITGA3</i>	P26006	Integrin alpha-3	9.81
<i>ITGB1</i>	P05556	Integrin beta-1	7.79
<i>lapp</i>	P12968	Islet amyloid polypeptide	13.78
<i>pKIWI504</i>	P43390	Metallothionein-like protein type 2	3.58
<i>MIP1</i>	Q8RX22	MND1-interacting protein 1	-2.95
<i>NRG2</i>	Q93YU8	Nitrate regulatory gene2 protein	9.06
<i>Ppy</i>	P10601	Pancreatic prohormone	11.60
<i>Prph2</i>	P15499	Peripherin-2	-7.68
<i>PI4KG7</i>	Q9SI52	Phosphatidylinositol 4-kinase gamma 7	2.96
<i>PHOT1</i>	O48963	Phototropin-1	2.87
<i>PHOT2</i>	P93025	Phototropin-2	3.84
<i>PMP3</i>	Q4HXT6	Plasma membrane proteolipid 3	-9.84
<i>PCAP1</i>	Q96262	Plasma membrane-associated cation-binding protein 1	4.31
<i>SERPINE1</i>	P05121	Plasminogen activator inhibitor 1	11.40
<i>AGD8</i>	Q8H100	Probable ADP-ribosylation factor GTPase-activating protein AGD8	3.93
<i>PAP27</i>	Q5MAU8	Probable inactive purple acid phosphatase 27	5.36
<i>PDIA6</i>	P38661	Probable protein disulfide-isomerase A6	3.75
<i>At3g55350</i>	Q9M2U3	Protein ALP1-like	3.76
<i>TIC</i>	Q94KE2	Protein TIME FOR COFFEE	4.52
<i>At5g47540</i>	Q9FGK3	Putative MO25-like protein At5g47540	3.26
<i>REN1</i>	F4JQZ3	Rho GTPase-activating protein REN1	-1.19
<i>Rho</i>	P15409	Rhodopsin	-9.76
<i>Rom1</i>	P32958	Rod outer segment membrane protein 1	-9.73
<i>Sag</i>	P20443	S-arrestin	-9.73
<i>SPP</i>	O81062	Signal peptide peptidase	5.08
<i>SPPL2</i>	Q8W469	Signal peptide peptidase-like 2	4.36
<i>D14</i>	Q95QR3	Strigolactone esterase D14	5.00
<i>BRI1</i>	Q8L899	Systemin receptor SR160	5.12
<i>THBS1</i>	P07996	Thrombospondin-1	8.22
<i>THY1</i>	P04216	Thy-1 membrane glycoprotein	9.18
<i>TGFB1</i>	Q15582	Transforming growth factor-beta-induced protein ig-h3	5.50
<i>RHOA</i>	P61585	Transforming protein RhoA	3.89
<i>TPT1</i>	P13693	Translationally-controlled tumor protein	5.79
<i>TCTP</i>	Q5J907	Translationally-controlled tumor protein homolog	4.68
<i>APRR1</i>	Q9LKL2	Two-component response regulator-like APRR1	3.64
<i>PLAU</i>	P00749	Urokinase-type plasminogen activator	9.82

Table S6. One hundred and ten genes associated with transport at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Sugar			
<i>At5g17010</i>	Q6AWX0	D-xylose-proton symporter-like 2	5.29
<i>At5g59250</i>	Q0WWW9	D-xylose-proton symporter-like 3, chloroplastic	8.93
<i>At5g16150</i>	Q56ZZ7	Plastidic glucose transporter 4	5.80
<i>SUC2</i>	Q39231	Sucrose transport protein SUC2	3.12
<i>STP13</i>	Q94AZ2	Sugar transport protein 13	9.64
<i>At5g18840</i>	Q8LB19	Sugar transporter ERD6-like 16	-3.19
Protein			
<i>aac</i>	P02723	ADP,ATP carrier protein	-9.69
<i>ANT1</i>	O22342	ADP,ATP carrier protein 1, mitochondrial	3.60
<i>AAC3</i>	O49447	ADP,ATP carrier protein 3, mitochondrial	4.94
<i>ARF</i>	O48920	ADP-ribosylation factor	4.31
<i>arf1</i>	P36579	ADP-ribosylation factor 1	-10.21
<i>ARF2</i>	P51823	ADP-ribosylation factor 2	3.85

<i>AGD5</i>	Q9FL69	ADP-ribosylation factor GTPase-activating protein AGD5	4.69
<i>SNAA</i>	P93798	Alpha-soluble NSF attachment protein	4.72
<i>AP2M1</i>	Q3ZC13	AP-2 complex subunit mu	5.08
<i>RAN3</i>	Q8H156	GTP-binding nuclear protein Ran-3	5.12
<i>EMB2001</i>	O81004	GTP-binding protein At2g22870	8.62
<i>SAR1B</i>	Q01474	GTP-binding protein SAR1B	4.38
<i>YPTM2</i>	Q05737	GTP-binding protein YPTM2	4.21
<i>IMPA1</i>	Q96321	Importin subunit alpha-1	3.55
<i>NACA</i>	Q13765	Nascent polypeptide-associated complex subunit alpha	9.42
<i>NACA1</i>	Q9M612	Nascent polypeptide-associated complex subunit alpha-like protein	-10.00
<i>At1g73230</i>	Q9CAT7	Nascent polypeptide-associated complex subunit beta	3.39
<i>OPT3</i>	O23482	Oligopeptide transporter 3	1.03
<i>SFH8</i>	F4IHJ0	Phosphatidylinositol/phosphatidylcholine transfer protein SFH8	6.71
<i>TIC55</i>	O49931	Protein TIC 55, chloroplastic	4.92
<i>TIC62</i>	Q8H0U5	Protein TIC 62, chloroplastic	3.20
<i>TIC110</i>	Q8LPR9	Protein TIC110, chloroplastic	4.52
<i>SecA</i>	Q41062	Protein translocase subunit SecA, chloroplastic	2.71
<i>sec61a</i>	Q54XK2	Protein transport protein Sec61 subunit alpha	4.01
<i>SCAMP1</i>	A2YMP7	Putative secretory carrier-associated membrane protein 1	3.56
<i>RAB7</i>	P31022	Ras-related protein Rab7	9.54
<i>RABC2A</i>	O49841	Ras-related protein RABC2a	1.38
<i>RABE1C</i>	P28186	Ras-related protein RABE1c	3.68
<i>RABH1B</i>	O80501	Ras-related protein RABH1b	5.33
<i>SYP121</i>	Q9ZSD4	Syntaxin-121	-1.18
<i>SYP51</i>	Q9SA23	Syntaxin-51	5.58
<i>TOC120</i>	Q9LUS2	Translocase of chloroplast 120, chloroplastic	8.63
<i>VAMP725</i>	O48850	Vesicle-associated membrane protein 725	3.83
Amino acid			
<i>AVT3C</i>	Q9SVG0	Amino acid transporter AVT3C	3.18
<i>AVT6A</i>	Q9LI61	Amino acid transporter AVT6A	3.44
<i>BAT1</i>	Q9ZU50	Amino-acid permease BAT1	2.96
<i>CAT2</i>	Q9ASS7	Cationic amino acid transporter 2, vacuolar	4.24
<i>CAT7</i>	Q9SQZ0	Cationic amino acid transporter 7, chloroplastic	4.68
<i>LHT1</i>	Q9FKS8	Lysine histidine transporter 1	9.46
<i>YPQ1</i>	Q12010	Probable vacuolar amino acid transporter YPQ1	-1.98
lipid			
<i>MALD3</i>	Q9M5X7	Non-specific lipid-transfer protein	3.69
<i>LTP1</i>	O24037	Non-specific lipid-transfer protein 1	1.07
<i>LTPG1</i>	Q9C7F7	Non-specific lipid transfer protein GPI-anchored 1	10.13
<i>LSAT_1X82001</i>	A0A2J6KL39	Non-specific lipid-transfer protein Lac s 1	3.50
<i>SYT1</i>	Q9SKR2	Synaptotagmin-1	3.52
<i>SYT4</i>	A0JJX5	Synaptotagmin-4	5.85
ABC			
<i>ABCB4</i>	O80725	ABC transporter B family member 4	9.11
<i>ABCB11</i>	Q9FWX7	ABC transporter B family member 11	-1.42
<i>ABCC1</i>	Q9C8G9	ABC transporter C family member 1	4.33
<i>ABCC2</i>	Q42093	ABC transporter C family member 2	5.06
<i>ABCC5</i>	Q7GB25	ABC transporter C family member 5	-2.29
<i>ABCF1</i>	Q9FJH6	ABC transporter F family member 1	4.65
<i>ABCF5</i>	Q9LV93	ABC transporter F family member 5	3.36
<i>ABCG7</i>	Q9ZU35	ABC transporter G family member 7	2.87
<i>ABCG20</i>	Q9LFG8	ABC transporter G family member 20	2.36
<i>ABCG36</i>	Q9XIE2	ABC transporter G family member 36	3.40
Others			
<i>Apoa1</i>	Q00623	Apolipoprotein A-I	-7.20
<i>PIP1-5</i>	Q9AR14	Aquaporin PIP1-5	3.66
<i>TIP1-1</i>	P25818	Aquaporin TIP1-1	1.27
<i>TIP2-1</i>	Q41951	Aquaporin TIP2-1	4.40
<i>SWEET16</i>	Q10LN5	Bidirectional sugar transporter SWEET16	1.50
<i>CHC1</i>	Q0WNJ6	Clathrin heavy chain 1	4.00
<i>At1g62020</i>	Q94A40	Coatomer subunit alpha-1	3.56
<i>At1g52360</i>	Q9C827	Coatomer subunit beta'-2	3.00
<i>DIT1</i>	Q9LXV3	Dicarboxylate transporter 1, chloroplastic	5.01
<i>EP1</i>	Q39688	Epidermis-specific secreted glycoprotein EP1	-0.88
<i>CHMP1A</i>	Q8LE58	ESCRT-related protein CHMP1A	5.55
<i>EXO70A1</i>	Q9LZD3	Exocyst complex component EXO70A1	-1.65
<i>EXO70A3</i>	F4KG58	Exocyst complex component EXO70A3	-1.97

<i>KHSRP</i>	Q8UVD9	Far upstream element-binding protein 2	3.23
<i>FUBP3</i>	Q96I24	Far upstream element-binding protein 3	3.25
<i>HIPP26</i>	Q9SZN7	Heavy metal-associated isoprenylated plant protein 26	2.95
<i>Hgsnat</i>	Q3UDW8	Heparan-alpha-glucosaminide N-acetyltransferase	4.21
<i>Ipo5</i>	Q8BKC5	Importin-5	8.97
<i>INT1</i>	Q8VZR6	Inositol transporter 1	1.19
<i>NAT6</i>	Q27GI3	Nucleobase-ascorbate transporter 6	3.84
<i>ATAD1</i>	F6QV99	Outer mitochondrial transmembrane helix translocase	3.96
<i>AZI1</i>	Q9SU35	pEARLI1-like lipid transfer protein 1	3.67
<i>PMA4</i>	Q03194	Plasma membrane ATPase 4	3.45
<i>PLGG1</i>	Q9FVQ4	Plastidal glycolate/glycerate translocator 1, chloroplastic	5.77
<i>TLC1</i>	Q24381	Plastidic ATP/ADP-transporter	3.20
<i>SCY1</i>	Q38885	Preprotein translocase subunit SCY1, chloroplastic	4.11
<i>PIP1-2</i>	Q7XSQ9	Probable aquaporin PIP1-2	3.92
<i>PIP2-5</i>	Q9SV31	Probable aquaporin PIP2-5	3.81
<i>INT2</i>	Q9C757	Probable inositol transporter 2	1.23
<i>SULTR4;2</i>	Q8GYH8	Probable sulfate transporter 4.2	3.87
<i>DTX51</i>	Q9SZE2	Protein DETOXIFICATION 51	-2.31
<i>DTX54</i>	Q9LE20	Protein DETOXIFICATION 54	1.32
<i>NPF1.2</i>	Q9M817	Protein NRT1/ PTR FAMILY 1.2	3.71
<i>NPF2.10</i>	Q944G5	Protein NRT1/ PTR FAMILY 2.10	1.32
<i>NPF6.4</i>	Q9LVE0	Protein NRT1/ PTR FAMILY 6.4	4.75
<i>NPF7.3</i>	Q9LQL2	Protein NRT1/ PTR FAMILY 7.3	1.19
<i>NPF8.3</i>	P46032	Protein NRT1/ PTR FAMILY 8.3	4.27
<i>SKD1</i>	Q9ZNT0	Protein SUPPRESSOR OF K(+) TRANSPORT GROWTH DEFECT 1	4.26
<i>TIC100</i>	Q8LPR8	Protein TIC 100	3.83
<i>ALY1</i>	Q8L773	THO complex subunit 4A	5.83
<i>TMN2</i>	Q940S0	Transmembrane 9 superfamily member 2	9.34
<i>TMN4</i>	Q9FHT4	Transmembrane 9 superfamily member 4	3.77
<i>TMN7</i>	Q9LIC2	Transmembrane 9 superfamily member 7	4.59
<i>TMN8</i>	F4KIB2	Transmembrane 9 superfamily member 8	3.49
<i>TMN12</i>	F4JRE0	Transmembrane 9 superfamily member 12	4.32
<i>TMED9</i>	Q9BVK6	Transmembrane emp24 domain-containing protein 9	8.59
<i>tmem184C</i>	Q54WM0	Transmembrane protein 184 homolog DDB_G0279555	8.41
<i>TPT</i>	Q9ZSR7	Triose phosphate/phosphate translocator TPT, chloroplastic	3.97

Table S7. One hundred and twenty-five genes associated with photosynthesis and energy at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
Photosynthesis			
<i>PHR2</i>	Q8LB72	Blue-light photoreceptor PHR2	3.13
<i>CAB12</i>	P13869	Chlorophyll a-b binding protein, chloroplastic	4.08
<i>CAB13</i>	P27489	Chlorophyll a-b binding protein 13, chloroplastic	3.39
<i>CAB21</i>	P27493	Chlorophyll a-b binding protein 21, chloroplastic	3.72
<i>CAB-151</i>	P27518	Chlorophyll a-b binding protein 151, chloroplastic	3.16
<i>CAP10A</i>	P27524	Chlorophyll a-b binding protein CP24 10A, chloroplastic	2.84
<i>LHCA1</i>	Q01667	Chlorophyll a-b binding protein 6, chloroplastic	3.75
<i>LHCB5</i>	Q9XF89	Chlorophyll a-b binding protein CP26, chloroplastic	4.12
<i>LHCB4.1</i>	Q07473	Chlorophyll a-b binding protein CP29.1, chloroplastic	4.36
<i>LHCB4.3</i>	Q9S7W1	Chlorophyll a-b binding protein CP29.3, chloroplastic	4.14
<i>lhca-P4</i>	Q9SQL2	Chlorophyll a-b binding protein P4, chloroplastic	4.12
<i>ELI</i>	P11432	Early light-induced protein, chloroplastic	1.11
<i>CHLP</i>	Q9ZS34	Geranylgeranyl diphosphate reductase, chloroplastic	4.11
<i>GGPS</i>	Q94ID7	Geranylgeranyl pyrophosphate synthase, chloroplastic	3.45
<i>HEMA1</i>	P93111	Glutamyl-tRNA reductase 1, chloroplastic	5.00
<i>HPR-A</i>	P13443	Glycerate dehydrogenase	3.88
<i>GOX</i>	P05414	Glycolate oxidase	3.77
<i>LIL3.1</i>	Q9SYX1	Light-harvesting complex-like protein 3 isotype 1, chloroplastic	3.93
<i>LIPC</i>	P80471	Light-induced protein, chloroplastic	3.94
<i>LIR1</i>	Q96500	Light-regulated protein 1, chloroplastic	3.72
<i>CRTL-E-1</i>	O65837	Lycopene epsilon cyclase, chloroplastic	3.36
<i>CHLM</i>	Q9SW18	Magnesium protoporphyrin IX methyltransferase, chloroplastic	4.39
<i>CHLD</i>	Q24133	Magnesium-chelatase subunit ChlD, chloroplastic	3.55
<i>CHLH</i>	Q9FNB0	Magnesium-chelatase subunit ChlH, chloroplastic	3.46

<i>CHLI</i>	P93162	Magnesium-chelatase subunit ChlI, chloroplastic	2.70
<i>CRD1</i>	Q6SJV8	Magnesium-protoporphyrin IX monomethyl ester [oxidative] cyclase	3.78
<i>PSBO</i>	Q40459	Oxygen-evolving enhancer protein 1, chloroplastic	3.89
<i>PSBP</i>	P93566	Oxygen-evolving enhancer protein 2, chloroplastic	4.07
<i>PSBQ</i>	P12301	Oxygen-evolving enhancer protein 3, chloroplastic	3.33
<i>PGRL1A</i>	Q8H112	PGR5-like protein 1A, chloroplastic	3.85
<i>PGLP1A</i>	P0DKC3	Phosphoglycolate phosphatase 1A, chloroplastic	3.85
<i>LHCA3</i>	Q9SY97	Photosystem I chlorophyll a/b-binding protein 3-1, chloroplastic	3.51
<i>LHCA5</i>	Q9C639	Photosystem I chlorophyll a/b-binding protein 5, chloroplastic	3.18
<i>LHCA6</i>	Q8LCQ4	Photosystem I chlorophyll a/b-binding protein 6, chloroplastic	3.99
<i>psaD</i>	P32869	Photosystem I reaction center subunit II, chloroplastic	3.95
<i>PSAF</i>	Q9SHE8	Photosystem I reaction center subunit III, chloroplastic	3.55
<i>PSAEA</i>	Q41228	Photosystem I reaction center subunit IV A, chloroplastic	3.25
<i>PSAN</i>	P49107	Photosystem I reaction center subunit N, chloroplastic	4.54
<i>PSAK</i>	Q9SUI5	Photosystem I reaction center subunit psaK, chloroplastic	3.80
<i>PSAG</i>	Q9S7N7	Photosystem I reaction center subunit V, chloroplastic	3.22
<i>PSAH2</i>	Q9SUI6	Photosystem I reaction center subunit VI-2, chloroplastic	3.86
<i>PSAL</i>	Q9SUI4	Photosystem I reaction center subunit XI, chloroplastic	4.02
<i>PSAO</i>	Q949Q5	Photosystem I subunit O	3.64
<i>PSBR</i>	P10690	Photosystem II 10 kDa polypeptide, chloroplastic	4.11
<i>PSBS</i>	Q02060	Photosystem II 22 kDa protein, chloroplastic	3.43
<i>PSBT</i>	P31336	Photosystem II 5 kDa protein, chloroplastic	3.22
<i>PSBY</i>	P80470	Photosystem II core complex proteins psbY, chloroplastic	3.90
<i>PSBW</i>	Q39194	Photosystem II reaction center W protein, chloroplastic	3.50
<i>PSB27-1</i>	Q9LR64	Photosystem II repair protein PSB27-H1, chloroplastic	4.00
<i>PSY</i>	P49293	Phytoene synthase, chloroplastic	4.29
<i>CCD4</i>	Q49675	Probable carotenoid cleavage dioxygenase 4, chloroplastic	2.93
<i>NYC1</i>	Q5N800	Probable chlorophyll(ide) b reductase NYC1, chloroplastic	4.49
<i>ABC1K1</i>	Q8RWG1	Protein ACTIVITY OF BC1 COMPLEX KINASE 1, chloroplastic	4.27
<i>ABC1K3</i>	Q9MA15	Protein ACTIVITY OF BC1 COMPLEX KINASE 3, chloroplastic	3.41
<i>ABC1K8</i>	Q93Y08	Protein ACTIVITY OF BC1 COMPLEX KINASE 8, chloroplastic	4.08
<i>CYP97A3</i>	Q93VK5	Protein LUTEIN DEFICIENT 5, chloroplastic	5.90
<i>SGR</i>	A9YF60	Protein STAY-GREEN homolog, chloroplastic	-2.32
<i>THF1</i>	Q7XAB8	Protein THYLAKOID FORMATION1, chloroplastic	4.26
<i>PORA</i>	Q41249	Protochlorophyllide reductase, chloroplastic	3.76
<i>PPD3</i>	Q9S720	PsbP domain-containing protein 3, chloroplastic	9.12
<i>PYG7</i>	B9DHG0	Tetratricopeptide repeat domain-containing protein PYG7, chloroplastic	8.75
<i>At1g54780</i>	Q9ZVL6	UPF0603 protein At1g54780, chloroplastic	4.27
<i>VDE1</i>	Q9SM43	Violaxanthin de-epoxidase, chloroplastic	3.89
<i>ZDS</i>	Q9FV46	Zeta-carotene desaturase, chloroplastic/chromoplastic	4.15
Energy			
<i>DBR</i>	Q9SLN8	2-alkenal reductase (NADP(+)-dependent)	8.73
<i>adh-1</i>	Q9P6C8	Alcohol dehydrogenase 1	-9.86
<i>FTSH</i>	Q9BAE0	ATP-dependent zinc metalloprotease FTSH, chloroplastic	3.26
<i>FTSH2</i>	O80860	ATP-dependent zinc metalloprotease FTSH 2, chloroplastic	4.22
<i>FTSH6</i>	Q1PDW5	ATP-dependent zinc metalloprotease FTSH 6, chloroplastic	1.39
<i>FTSH11</i>	Q9FGM0	ATP-dependent zinc metalloprotease FTSH 11, chloroplastic/mitochondrial	3.81
<i>ATPD</i>	P32980	ATP synthase delta chain, chloroplastic	3.65
<i>ATP5F1A</i>	P25705	ATP synthase subunit alpha, mitochondrial	4.32
<i>ATPF2</i>	P31853	ATP synthase subunit b', chloroplastic	4.62
<i>ATPB</i>	P29685	ATP synthase subunit beta, mitochondrial	3.88
<i>At3g52300</i>	Q9FT52	ATP synthase subunit d, mitochondrial	4.11
<i>ATP4</i>	Q40089	ATP synthase subunit delta', mitochondrial	4.58
<i>Atp5f1e</i>	P56382	ATP synthase subunit epsilon, mitochondrial	-10.09
<i>Atp5mf</i>	P56135	ATP synthase subunit f, mitochondrial	-3.56
<i>ATPC</i>	P26360	ATP synthase subunit gamma, mitochondrial	4.32
<i>CEQORH</i>	Q9SV68	Chloroplast envelope quinone oxidoreductase homolog	9.51
<i>MT-CYB</i>	P00156	Cytochrome b	12.19
<i>CYTb5-E</i>	Q42342	Cytochrome b5 isoform E	9.19
<i>petC</i>	P08980	Cytochrome b6-f complex iron-sulfur subunit, chloroplastic	3.77
<i>petM</i>	P80883	Cytochrome b6-f complex subunit 7	3.36
<i>QCR7-2</i>	F4JWS8	Cytochrome b-c1 complex subunit 7-2, mitochondrial	4.82
<i>MT-CO1</i>	P00395	Cytochrome c oxidase subunit 1	7.30
<i>MT-CO2</i>	P00403	Cytochrome c oxidase subunit 2	13.22
<i>MT-CO3</i>	P00414	Cytochrome c oxidase subunit 3	8.37
<i>COX5B-1</i>	Q9LW15	Cytochrome c oxidase subunit 5b-1, mitochondrial	5.57

<i>At4g27520</i>	Q9T076	Early nodulin-like protein 2	4.35
<i>FDC2</i>	Q9C7Y4	Ferredoxin C 2, chloroplastic	9.52
<i>FD1</i>	O04090	Ferredoxin-1, chloroplastic	3.93
<i>GLU1</i>	Q9ZNZ7	Ferredoxin-dependent glutamate synthase 1, chloroplastic/mitochondrial	3.74
<i>LFNR1</i>	Q9FKW6	Ferredoxin--NADP reductase, leaf isozyme 1, chloroplastic	4.09
<i>FENR2</i>	O04397	Ferredoxin--NADP reductase, root-type isozyme, chloroplastic	4.10
<i>NIR1</i>	P38500	Ferredoxin--nitrite reductase, chloroplastic	3.48
<i>FTRV</i>	P80680	Ferredoxin-thioredoxin reductase, variable chain	3.14
<i>FRO7</i>	Q3KTM0	Ferric reduction oxidase 7, chloroplastic	2.38
<i>FR13</i>	Q948P6	Ferritin-3, chloroplastic	4.29
<i>ADNT1</i>	O04619	Mitochondrial adenine nucleotide transporter ADNT1	4.94
<i>VDAC2</i>	P42056	Mitochondrial outer membrane protein porin of 36 kDa	4.18
<i>PUMP5</i>	Q9SJY5	Mitochondrial uncoupling protein 5	2.84
<i>MPP</i>	P29677	Mitochondrial-processing peptidase subunit alpha	3.70
<i>ndhM</i>	A9PJQ8	NAD(P)H-quinone oxidoreductase subunit M, chloroplastic	4.40
<i>At3g08610</i>	Q9C9Z5	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 1	5.14
<i>At2g20360</i>	Q9SK66	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 9	5.80
<i>At5g08530</i>	Q9FNN5	NADH dehydrogenase [ubiquinone] flavoprotein 1, mitochondrial	3.68
<i>N/A</i>	Q43644	NADH dehydrogenase [ubiquinone] iron-sulfur protein 1, mitochondrial	4.23
<i>MT-ND1</i>	P03886	NADH-ubiquinone oxidoreductase chain 1	12.21
<i>MT-ND2</i>	P03891	NADH-ubiquinone oxidoreductase chain 2	7.93
<i>MT-ND4</i>	P03905	NADH-ubiquinone oxidoreductase chain 4	9.39
<i>MT-ND5</i>	P03915	NADH-ubiquinone oxidoreductase chain 5	9.11
<i>GAPN</i>	P93338	NADP-dependent glyceraldehyde-3-phosphate dehydrogenase	4.57
<i>NADP-ME4</i>	Q9CA83	NADP-dependent malic enzyme 4, chloroplastic	3.46
<i>PNSL5</i>	Q9ASS6	Photosynthetic NDH subunit of lumenal location 5, chloroplastic	4.39
<i>PNSB1</i>	Q9S9N6	Photosynthetic NDH subunit of subcomplex B 1, chloroplastic	4.43
<i>PNSB2</i>	Q94AQ8	Photosynthetic NDH subunit of subcomplex B 2, chloroplastic	5.11
<i>PNSB3</i>	Q9LU21	Photosynthetic NDH subunit of subcomplex B 3, chloroplastic	3.64
<i>PNSB4</i>	Q8RXS1	Photosynthetic NDH subunit of subcomplex B 4, chloroplastic	3.62
<i>PNSB5</i>	Q9FG89	Photosynthetic NDH subunit of subcomplex B 5, chloroplastic	4.93
<i>PETE</i>	P00299	Plastocyanin A, chloroplastic	3.40
<i>At2g21870</i>	Q9SJ12	Probable ATP synthase 24 kDa subunit, mitochondrial	2.77
<i>At4g27270</i>	Q6NQE2	Probable NAD(P)H dehydrogenase (quinone) FQR1-like 1	6.99
<i>STR4</i>	Q9M158	Rhodanese-like domain-containing protein 4, chloroplastic	4.61
<i>STR9</i>	O48529	Rhodanese-like domain-containing protein 9, chloroplastic	8.75

Table S8. Fifty-eight genes associated with secondary metabolism at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
<i>MENB</i>	Q8GYN9	1,4-dihydroxy-2-naphthoyl-CoA synthase, peroxisomal	4.58
<i>ACO1</i>	Q9MB94	1-aminocyclopropane-1-carboxylate oxidase	3.67
<i>ACO3</i>	Q08507	1-aminocyclopropane-1-carboxylate oxidase 3	9.11
<i>IN37</i>	P23525	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase, chloroplastic	4.36
<i>2ODD19</i>	Q6Z244	2-oxoglutarate-dependent dioxygenase 19	4.35
<i>AOP2</i>	Q945B5	2-oxoglutarate-dependent dioxygenase AOP2	-1.11
<i>UGT85A23</i>	F8WLS6	7-deoxyloganetin glucosyltransferase	3.88
<i>ADH2</i>	Q96533	Alcohol dehydrogenase class-3	3.45
<i>CYP707A2</i>	O81077	Abscisic acid 8'-hydroxylase 2	2.35
<i>CYP707A2</i>	K4CI52	Abscisic acid 8'-hydroxylase CYP707A2	4.05
<i>AAO3</i>	Q7G9P4	Abscisic-aldehyde oxidase	-2.50
<i>RhGT1</i>	Q4R119	Anthocyanidin 5,3-O-glucosyltransferase	3.19
<i>COMT1</i>	Q43609	Caffeic acid 3-O-methyltransferase	4.61
<i>CAMT</i>	Q43095	Caffeoyl-CoA O-methyltransferase	9.14
<i>CCD1</i>	Q8LP17	Carotenoid 9,10(9',10')-cleavage dioxygenase 1	3.60
<i>CHS2</i>	P48387	Chalcone synthase 2	-1.31
<i>CCR1</i>	Q9S9N9	Cinnamoyl-CoA reductase 1	3.91
<i>CAD1</i>	Q2KNL5	Cinnamyl alcohol dehydrogenase 1	8.90
<i>SMT1</i>	Q9LM02	Cycloartenol-C-24-methyltransferase	-9.90
<i>CYP72A15</i>	Q9LUC5	Cytochrome P450 72A15	-2.81
<i>CYP72A225</i>	W8JWW3	Cytochrome P450 72A225	-1.23
<i>CYP736A117</i>	A0A068Q6L2	Cytochrome P450 736A117	1.75
<i>CYP76C1</i>	O64636	Cytochrome P450 76C1	4.90
<i>CYP81Q32</i>	W8JMU7	Cytochrome P450 81Q32	-4.07
<i>CYP82A3</i>	O49858	Cytochrome P450 82A3	3.31
<i>CYP84A1</i>	Q42600	Cytochrome P450 84A1	-2.19
<i>CKX6</i>	Q9LY71	Cytokinin dehydrogenase 6	1.13
<i>SOT15</i>	Q8L5A7	Cytosolic sulfotransferase 15	4.27
<i>SC5D</i>	Q9ZT29	Delta(7)-sterol-C5(6)-desaturase	8.81
<i>DHCR24</i>	Q15392	Delta(24)-sterol reductase	5.01
<i>GALUR</i>	O49133	D-galacturonate reductase	2.10
<i>FDH1</i>	Q07511	Formate dehydrogenase, mitochondrial	9.66
<i>VTC2</i>	Q8RWE8	GDP-L-galactose phosphorylase 1	4.17
<i>MIOX4</i>	Q8H1S0	Inositol oxygenase 4	-1.55
<i>LAC14</i>	Q9FY79	Laccase-14	10.59
<i>TT10</i>	Q84J37	Laccase-15	-1.08
<i>GULLO3</i>	Q9LYD8	L-gulonolactone oxidase 3	-1.25
<i>MSBP2</i>	Q9M2Z4	Membrane steroid-binding protein 2	3.49
<i>MYRS</i>	Q93X23	Myrcene synthase, chloroplastic	8.62
<i>PAL1</i>	O64963	Phenylalanine ammonia-lyase 1	4.95
<i>BETV6</i>	Q9FUW6	Phenylcoumaran benzylic ether reductase Betv6	4.70
<i>THIC</i>	O82392	Phosphomethylpyrimidine synthase, chloroplastic	3.71
<i>YUC10</i>	Q9FVQ0	Probable indole-3-pyruvate monooxygenase YUCCA10	1.66
<i>At1g67280</i>	Q8W593	Probable lactoylglutathione lyase, chloroplastic	2.95
<i>PAP3</i>	O82291	Probable plastid-lipid-associated protein 3, chloroplastic	9.24
<i>LGU</i>	Q39366	Putative lactoylglutathione lyase	3.56
<i>SILD</i>	Q94KL7	Secoisolariciresinol dehydrogenase	10.63
<i>SFGH</i>	Q8LAS8	S-formylglutathione hydrolase	2.78
<i>SQE3</i>	Q8VYH2	Squalene epoxidase 3	5.82
<i>THI1-2</i>	F6H7K5	Thiamine thiazole synthase 2, chloroplastic	-1.02
<i>THI1</i>	O23787	Thiamine thiazole synthase, chloroplastic	3.66
<i>CYP73A16</i>	Q43054	Trans-cinnamate 4-monooxygenase	5.77
<i>RHM1</i>	Q9SYM5	Trifunctional UDP-glucose 4,6-dehydratase/UDP-4-keto-6-deoxy-D-glucose 3,5-epimerase/UDP-4-keto-L-rhamnose-reductase RHM1	5.82
<i>CYP92C6</i>	A0A1D6F9Y9	Trimethyltridecatetraene synthase	1.07
<i>UGT89B2</i>	Q6VAA5	UDP-glycosyltransferase 89B2	-2.25
<i>HDLBP</i>	Q00341	Vigilin	8.57
<i>CYP82C4</i>	Q9SZ46	Xanthotoxin 5-hydroxylase CYP82C4	10.38
<i>ABA2</i>	O81360	Zeaxanthin epoxidase, chloroplastic	4.08

Table S9. Twenty-one genes associated with polynucleotide metabolism at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
<i>ACIN1</i>	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus	3.62
<i>FAS2</i>	Q6ZD63	Chromatin assembly factor 1 subunit FAS2 homolog	-1.07
<i>DRT100</i>	Q00874	DNA damage-repair/toleration protein DRT100	4.25
<i>SSRP1</i>	O04235	FACT complex subunit SSRP1	5.37
<i>At5g07800</i>	Q9FF12	Flavin-containing monooxygenase FMO GS-OX-like 9	-1.36
<i>GRP1A</i>	P49310	Glycine-rich RNA-binding protein GRP1A	4.09
<i>HDT2</i>	Q9M4U5	Histone deacetylase HDT2	4.98
<i>H1</i>	P40267	Histone H1	4.52
<i>H2A</i>	P19177	Histone H2A	9.40
<i>H2B-3</i>	O65819	Histone H2B.3	4.74
<i>HTR4</i>	P59169	Histone H3.3	4.67
<i>HMG1</i>	P26585	HMG1/2-like protein	4.18
<i>LARP6A</i>	Q94A38	La-related protein 6A	0.98
<i>LARP6B</i>	O80567	La-related protein 6B	3.57
<i>NDK1</i>	P39207	Nucleoside diphosphate kinase 1	3.82
<i>NAP1;2</i>	Q9ZUP3	Nucleosome assembly protein 1;2	4.71
<i>MRL1</i>	Q0WLC6	Pentatricopeptide repeat-containing protein MRL1, chloroplastic	3.91
<i>PTAC10</i>	F4JF21	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10	5.45
<i>R3HDM2</i>	A0JNC2	R3H domain-containing protein 2	4.01
<i>ECT2</i>	Q9LJE5	YTH domain-containing protein ECT2	4.48
<i>ECT4</i>	A0A1P8AS03	YTH domain-containing protein ECT4	5.54

Table S10. Two hundred and eighty-six genes associated with translation at NaCl (300 mmol/L) vs. CK.

Gene name	SwissProt ID	Protein name	log ₂ FC (NaCl vs. CK)
<i>CPN10-1</i>	Q9M1C2	10 kDa chaperonin 1, chloroplastic	5.56
<i>PSRP2</i>	P82277	30S ribosomal protein 2, chloroplastic	5.69
<i>At1g68590</i>	Q9SX22	30S ribosomal protein 3-1, chloroplastic	4.26
<i>RPS1</i>	P29344	30S ribosomal protein S1, chloroplastic	4.00
<i>RPS10</i>	Q9LK61	30S ribosomal protein S10, chloroplastic	3.96
<i>RPS13</i>	P42732	30S ribosomal protein S13, chloroplastic	4.64
<i>RPS17</i>	P16180	30S ribosomal protein S17, chloroplastic	5.60
<i>rps21</i>	P82024	30S ribosomal protein S21, chloroplastic	4.55
<i>RPS31</i>	O80439	30S ribosomal protein S31, chloroplastic	5.16
<i>rps5</i>	P93014	30S ribosomal protein S5, chloroplastic	4.81
<i>RPS6</i>	Q8VY91	30S ribosomal protein S6 alpha, chloroplastic	3.51
<i>RPS9</i>	Q9XJ27	30S ribosomal protein S9, chloroplastic	3.61
<i>ROC4</i>	P19683	31 kDa ribonucleoprotein, chloroplastic	3.29
<i>RPS0</i>	B2B1Z3	40S ribosomal protein S0	-11.08
<i>rps10</i>	O77082	40S ribosomal protein S10	-10.49
<i>RPS11</i>	Q3T0V4	40S ribosomal protein S11	-0.21
<i>RPS12</i>	Q9SMI3	40S ribosomal protein S12	-4.32
<i>RPS13</i>	P62302	40S ribosomal protein S13	-3.38
<i>RS142</i>	P19951	40S ribosomal protein S14	-11.12
<i>RPS14C</i>	P42036	40S ribosomal protein S14-3	3.87
<i>RPS15</i>	P34737	40S ribosomal protein S15	-10.94
<i>RPS15A</i>	Q08112	40S ribosomal protein S15-1	5.48
<i>RPS15A</i>	Q76182	40S ribosomal protein S15a	-10.78
<i>RPS16</i>	P46293	40S ribosomal protein S16	3.85
<i>RPS17</i>	P08708	40S ribosomal protein S17	4.75
<i>RPS18</i>	Q3T0R1	40S ribosomal protein S18	4.26
<i>RPS19A</i>	Q9SGA6	40S ribosomal protein S19-1	3.34
<i>rps1901</i>	P58234	40S ribosomal protein S19-A	-10.84
<i>RPS2</i>	P15880	40S ribosomal protein S2	4.22
<i>rps20</i>	P23403	40S ribosomal protein S20	-11.30
<i>RPS20B</i>	Q9STY6	40S ribosomal protein S20-2	5.24
<i>RPS23</i>	Q3T199	40S ribosomal protein S23	9.80
<i>RPS23A</i>	P0CY39	40S ribosomal protein S23-A	-10.57
<i>RPS2D</i>	Q9SCM3	40S ribosomal protein S2-4	4.64
<i>RPS24A</i>	Q9SS17	40S ribosomal protein S24-1	-2.56
<i>rps25</i>	Q6PBI5	40S ribosomal protein S25	-11.32
<i>rps2602</i>	Q9UTG4	40S ribosomal protein S26-B	-10.88

<i>RPS27B</i>	Q9M2F1	40S ribosomal protein S27-2	10.41
<i>RPS3</i>	Q3T169	40S ribosomal protein S3	3.22
<i>RPS3B</i>	Q9M339	40S ribosomal protein S3-2	-11.08
<i>RPS3C</i>	Q9FJA6	40S ribosomal protein S3-3	3.02
<i>RS3A</i>	Q8GTE3	40S ribosomal protein S3a	4.58
<i>RPS4</i>	O22424	40S ribosomal protein S4	3.87
<i>RPS4X</i>	Q76N24	40S ribosomal protein S4, X isoform	3.79
<i>RPS5</i>	O65731	40S ribosomal protein S5	-11.00
<i>RPS6</i>	P62753	40S ribosomal protein S6	5.89
<i>RPS6B</i>	P51430	40S ribosomal protein S6-2	3.97
<i>RPS7</i>	Q8LJU5	40S ribosomal protein S7	3.17
<i>RPS8</i>	P49199	40S ribosomal protein S8	9.15
<i>RPS9B</i>	Q9LXG1	40S ribosomal protein S9-1	-11.08
<i>RPS9C</i>	Q9FLF0	40S ribosomal protein S9-2	10.03
<i>RAP40</i>	O65751	40S ribosomal protein SA	4.41
<i>RPL1</i>	Q9LY66	50S ribosomal protein L1, chloroplastic	2.86
<i>RPL10</i>	Q9FY50	50S ribosomal protein L10, chloroplastic	3.86
<i>RPL11</i>	Q9MAP3	50S ribosomal protein L11, chloroplastic	4.48
<i>RK12</i>	P36688	50S ribosomal protein L12, chloroplastic	4.06
<i>RPL13</i>	Q9SYL9	50S ribosomal protein L13, chloroplastic	3.19
<i>RPL15</i>	P25873	50S ribosomal protein L15, chloroplastic	4.30
<i>RPL17</i>	O80363	50S ribosomal protein L17, chloroplastic	3.35
<i>RPL18</i>	Q9SX68	50S ribosomal protein L18, chloroplastic	4.61
<i>At4g17560</i>	Q8W463	50S ribosomal protein L19-1, chloroplastic	3.93
<i>RPL21</i>	P51412	50S ribosomal protein L21, chloroplastic	3.39
<i>RPL24</i>	P92959	50S ribosomal protein L24, chloroplastic	4.40
<i>RPL27</i>	P82190	50S ribosomal protein L27, chloroplastic	3.39
<i>RPL3</i>	O80360	50S ribosomal protein L3, chloroplastic	3.86
<i>RPL31</i>	Q9FWS4	50S ribosomal protein L31, chloroplastic	4.11
<i>RPL35</i>	P23326	50S ribosomal protein L35, chloroplastic	9.63
<i>RPL4</i>	O50061	50S ribosomal protein L4, chloroplastic	4.09
<i>RPL5</i>	O04603	50S ribosomal protein L5, chloroplastic	4.31
<i>RPL6</i>	O23049	50S ribosomal protein L6, chloroplastic	2.96
<i>RPL9</i>	P25864	50S ribosomal protein L9, chloroplastic	4.23
<i>RP-P0</i>	O24573	60S acidic ribosomal protein P0	-11.32
<i>RPP0B</i>	Q42112	60S acidic ribosomal protein P0-2	4.65
<i>RPP1B</i>	O23095	60S acidic ribosomal protein P1-2	5.30
<i>RPL10</i>	P27635	60S ribosomal protein L10	4.25
<i>SC34</i>	A2ZCQ7	60S ribosomal protein L10-1	-11.03
<i>rpl10a</i>	Q6PC69	60S ribosomal protein L10a	-11.08
<i>RPL11</i>	P46287	60S ribosomal protein L11	3.73
<i>RPL11A</i>	P42795	60S ribosomal protein L11-1	-10.29
<i>RPL12</i>	P61284	60S ribosomal protein L12	10.54
<i>rpl1201</i>	P0CT83	60S ribosomal protein L12-A	-10.27
<i>RPL13</i>	P26373	60S ribosomal protein L13	4.00
<i>RL13A</i>	P93099	60S ribosomal protein L13a	-10.98
<i>RPL14</i>	Q3T0U2	60S ribosomal protein L14	-9.93
<i>RPL14A</i>	Q9SIM4	60S ribosomal protein L14-1	5.46
<i>RPL15</i>	O82528	60S ribosomal protein L15	3.17
<i>SB62</i>	O65082	60S ribosomal protein L15-2	-10.26
<i>RPL17B</i>	P51413	60S ribosomal protein L17-2	-3.27
<i>RPL18B</i>	P42791	60S ribosomal protein L18-2	-3.68
<i>RPL18A</i>	Q9ATF5	60S ribosomal protein L18a	1.27
<i>RPL18AA</i>	Q8L7K0	60S ribosomal protein L18a-1	-11.08
<i>RPL19C</i>	P49693	60S ribosomal protein L19-3	4.29
<i>RPL21</i>	O82574	60S ribosomal protein L21	-10.64
<i>RPL21E</i>	Q9FDZ9	60S ribosomal protein L21-2	3.43
<i>Rpl221l</i>	Q9D7S7	60S ribosomal protein L22-like 1	-5.12
<i>RPL23A</i>	P49690	60S ribosomal protein L23	3.10
<i>RPL23A</i>	O22644	60S ribosomal protein L23A	9.63
<i>RPL24</i>	Q862I1	60S ribosomal protein L24	9.54
<i>RPL24A</i>	Q42347	60S ribosomal protein L24-1	4.07
<i>RPL26</i>	P61257	60S ribosomal protein L26	10.64
<i>RPL26A</i>	P51414	60S ribosomal protein L26-1	4.36
<i>RPL27</i>	P0DJ19	60S ribosomal protein L27	-10.54
<i>RPL27A</i>	P46776	60S ribosomal protein L27a	10.85
<i>RPL27AC</i>	P49637	60S ribosomal protein L27a-3	9.98

<i>RPL28A</i>	O82204	60S ribosomal protein L28-1	3.81
<i>RPL28C</i>	Q9M0E2	60S ribosomal protein L28-2	-9.75
<i>RPL29</i>	P47914	60S ribosomal protein L29	3.71
<i>RPL3</i>	P39023	60S ribosomal protein L3	5.24
<i>RPL31</i>	Q9M573	60S ribosomal protein L31	4.17
<i>RPL32</i>	E2RKA8	60S ribosomal protein L32	-10.34
<i>ARP2</i>	P22738	60S ribosomal protein L3-2	3.64
<i>RPL32A</i>	P49211	60S ribosomal protein L32-1	3.88
<i>RPL34</i>	P40590	60S ribosomal protein L34	3.23
<i>Rpl35</i>	Q6ZWV7	60S ribosomal protein L35	-10.81
<i>RPL35AC</i>	Q9C912	60S ribosomal protein L35a-3	-10.64
<i>RPL36C</i>	Q9LZ57	60S ribosomal protein L36-3	-10.25
<i>rpl3702</i>	P05733	60S ribosomal protein L37-B	-10.44
<i>RPL4</i>	P36578	60S ribosomal protein L4	6.51
<i>RPL5</i>	Q6UNT2	60S ribosomal protein L5	5.24
<i>RPL5B</i>	P49227	60S ribosomal protein L5-2	3.11
<i>RPL6</i>	Q02878	60S ribosomal protein L6	6.03
<i>RPL7</i>	P18124	60S ribosomal protein L7	4.83
<i>RPL7D</i>	Q9LHP1	60S ribosomal protein L7-4	6.03
<i>RPL7A</i>	P62424	60S ribosomal protein L7a	5.24
<i>RPL7A-1</i>	P35685	60S ribosomal protein L7a-1	4.04
<i>RPL8</i>	Q3T0S6	60S ribosomal protein L8	4.92
<i>RPL8C</i>	Q42064	60S ribosomal protein L8-3	3.53
<i>RPL9</i>	P30707	60S ribosomal protein L9	3.46
<i>POPTRDRAFT_821063</i>	B9HQZ6	Alanine--tRNA ligase, chloroplastic/mitochondrial	7.16
<i>EMB1027</i>	O23247	Arginine--tRNA ligase, chloroplastic/mitochondrial	3.18
<i>IBI1</i>	Q9M084	Aspartate--tRNA ligase 2, cytoplasmic	8.64
<i>BAG5</i>	O65373	BAG family molecular chaperone regulator 5, mitochondrial	-1.38
<i>BBD2</i>	Q93VH2	Bifunctional nuclease 2	3.72
<i>BT1</i>	Q9FMK7	BTB/POZ and TAZ domain-containing protein 1	2.56
<i>At1g63850</i>	Q9CAJ9	BTB/POZ domain-containing protein At1g63850	8.68
<i>CALR</i>	O81919	Calreticulin	3.91
<i>Cpe</i>	Q00493	Carboxypeptidase E	2.13
<i>CPN60B2</i>	Q9LJE4	Chaperonin 60 subunit beta 2, chloroplastic	3.92
<i>CSP41A</i>	Q9LYA9	Chloroplast stem-loop binding protein of 41 kDa a, chloroplastic	4.82
<i>CSP41B</i>	Q9SA52	Chloroplast stem-loop binding protein of 41 kDa b, chloroplastic	4.08
<i>CUL1</i>	Q5ZC88	Cullin-1	8.86
<i>RH15</i>	Q56XG6	DEAD-box ATP-dependent RNA helicase 15	4.13
<i>RH3</i>	Q8L7S8	DEAD-box ATP-dependent RNA helicase 3, chloroplastic	3.60
<i>Os01g0911100</i>	Q5N7W4	DEAD-box ATP-dependent RNA helicase 30	5.64
<i>RH31</i>	Q9FFQ1	DEAD-box ATP-dependent RNA helicase 31	3.17
<i>RH50</i>	Q8GUG7	DEAD-box ATP-dependent RNA helicase 50	8.71
<i>RH53</i>	Q9LUW5	DEAD-box ATP-dependent RNA helicase 53, mitochondrial	2.94
<i>RH7</i>	Q39189	DEAD-box ATP-dependent RNA helicase 7	4.38
<i>DESI1</i>	Q6ICB0	Desumoylating isopeptidase 1	3.53
<i>dnaJb6</i>	Q6P642	DnaJ homolog subfamily B member 6	4.70
<i>OST48</i>	Q944K2	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit	4.87
<i>STT3B</i>	Q9FX21	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit STT3B	4.27
<i>RZPF34</i>	Q9FFB6	E3 ubiquitin-protein ligase RZFP34	1.72
<i>UPL1</i>	Q8GY23	E3 ubiquitin-protein ligase UPL1	3.80
<i>REFA1</i>	O64937	Elongation factor 1-alpha	6.74
<i>EEF1A1</i>	P68103	Elongation factor 1-alpha 1	5.29
<i>At5g12110</i>	Q84WM9	Elongation factor 1-beta 1	4.86
<i>EEF1G</i>	P26641	Elongation factor 1-gamma	4.56
<i>Os02g0220500</i>	Q6YW46	Elongation factor 1-gamma 2	4.02
<i>EEF2</i>	P13639	Elongation factor 2	5.31
<i>fusA1</i>	P34811	Elongation factor G-1, chloroplastic	3.75
<i>TUFB1</i>	P46280	Elongation factor Tu, chloroplastic	4.35
<i>HSPA5</i>	P11021	Endoplasmic reticulum chaperone BiP	5.73
<i>HSP90B1</i>	P14625	Endoplasmin	4.82
<i>HSP90</i>	P35016	Endoplasmin homolog	4.08
<i>IF4A8</i>	P41381	Eukaryotic initiation factor 4A-8	3.78
<i>EIF4A1</i>	Q3SZ54	Eukaryotic initiation factor 4A-I	3.91
<i>EIF4A3A</i>	Q5VNM3	Eukaryotic initiation factor 4A-III homolog A	4.87
<i>Gsp1</i>	Q8R050	Eukaryotic peptide chain release factor GTP-binding subunit ERF3A	8.53

<i>ERF1-3</i>	P35614	Eukaryotic peptide chain release factor subunit 1-3	3.93
<i>IF1A</i>	P56331	Eukaryotic translation initiation factor 1A	4.65
<i>TIF3B1</i>	P56821	Eukaryotic translation initiation factor 3 subunit B	7.26
<i>TIF3C1</i>	Q9XHM1	Eukaryotic translation initiation factor 3 subunit C	3.81
<i>TIF3E1</i>	Q9C5Z3	Eukaryotic translation initiation factor 3 subunit E	4.94
<i>TIF3F1</i>	O04202	Eukaryotic translation initiation factor 3 subunit F	8.75
<i>EIF4G2</i>	Q95L46	Eukaryotic translation initiation factor 4 gamma 2	3.29
<i>EIF4B</i>	P23588	Eukaryotic translation initiation factor 4B	4.91
<i>EIF4B1</i>	Q9LIN5	Eukaryotic translation initiation factor 4B1	8.76
<i>IF5A</i>	Q9AXJ4	Eukaryotic translation initiation factor 5A	4.58
<i>EIF-5A2</i>	P24922	Eukaryotic translation initiation factor 5A-2	3.23
<i>EIF(ISO)4G1</i>	Q93ZT6	Eukaryotic translation initiation factor isoform 4G-1	4.52
<i>At1g29880</i>	O23627	Glycine--tRNA ligase, mitochondrial 1	4.91
<i>RNP1</i>	Q8W034	Heterogeneous nuclear ribonucleoprotein 1	3.72
<i>HNRNPA1</i>	P09867	Heterogeneous nuclear ribonucleoprotein A1	4.23
<i>LONP2</i>	O04979	Lon protease homolog 2, peroxisomal	3.82
<i>BIP4</i>	Q03684	Luminal-binding protein 4	5.23
<i>BIP5</i>	Q03685	Luminal-binding protein 5	-1.17
<i>MRF1</i>	Q94BR1	MA3 DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR 1	4.32
<i>MORF5</i>	Q9C7Y2	Multiple organellar RNA editing factor 5, chloroplastic/mitochondrial	3.14
<i>MORF8</i>	Q9LKA5	Multiple organellar RNA editing factor 8, chloroplastic/mitochondrial	4.33
<i>MORF9</i>	Q9LPZ1	Multiple organellar RNA editing factor 9, chloroplastic	3.21
<i>RCE1</i>	Q9SDY5	NEDD8-conjugating enzyme Ubc12	4.08
<i>PAPS2</i>	O82312	Nuclear poly(A) polymerase 2	8.89
<i>PAPS4</i>	Q8VYW1	Nuclear poly(A) polymerase 4	8.77
<i>Os04g0620700</i>	Q7XTT4	Nucleolin 2	3.13
<i>UBP1</i>	Q9M427	Oligouridylate-binding protein 1	4.32
<i>At5g46580</i>	Q9LS25	Pentatricopeptide repeat-containing protein At5g46580, chloroplastic	3.51
<i>PNAA</i>	P81898	Peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A	3.39
<i>PCKR1</i>	Q39613	Peptidyl-prolyl cis-trans isomerase	3.74
<i>PPIA</i>	P62938	Peptidyl-prolyl cis-trans isomerase A	3.83
<i>PPIB</i>	P23284	Peptidyl-prolyl cis-trans isomerase B	9.52
<i>CYP20-3</i>	P34791	Peptidyl-prolyl cis-trans isomerase CYP20-3, chloroplastic	4.88
<i>CYP28</i>	O65220	Peptidyl-prolyl cis-trans isomerase CYP28, chloroplastic	9.02
<i>CYP40</i>	Q9C566	Peptidyl-prolyl cis-trans isomerase CYP40	1.12
<i>CYP95</i>	Q8RWY7	Peptidyl-prolyl cis-trans isomerase CYP95	3.55
<i>FKBP18</i>	Q9LM71	Peptidyl-prolyl cis-trans isomerase FKBP18, chloroplastic	8.68
<i>FKBP65</i>	Q9FJL3	Peptidyl-prolyl cis-trans isomerase FKBP65	3.55
<i>PABPC1</i>	P61286	Polyadenylate-binding protein 1	3.38
<i>pabpc1a</i>	F1QB54	Polyadenylate-binding protein 1A	-9.88
<i>PAB2</i>	P42731	Polyadenylate-binding protein 2	4.99
<i>PAB8</i>	Q9FXA2	Polyadenylate-binding protein 8	3.44
<i>RBP45</i>	Q9LEB4	Polyadenylate-binding protein RBP45	4.53
<i>RBP47</i>	Q9LEB3	Polyadenylate-binding protein RBP47	3.95
<i>CID7</i>	O64843	Polyadenylate-binding protein-interacting protein 7	4.25
<i>PETs</i>	Q9SZD6	Polyprotein of EF-Ts, chloroplastic	3.90
<i>PCUBI4-1</i>	P0CH04	Polyubiquitin	5.18
<i>UBB</i>	P0CG55	Polyubiquitin-B	9.29
<i>UBC</i>	P0CG68	Polyubiquitin-C	3.56
<i>ubqD</i>	P0CG77	Polyubiquitin-D	4.11
<i>PRP8A</i>	Q9SSD2	Pre-mRNA-processing-splicing factor 8A	8.86
<i>At1g65660</i>	Q9SHY8	Pre-mRNA-splicing factor SLU7-A	4.75
<i>PREP2</i>	Q8VY06	Presequence protease 2, chloroplastic/mitochondrial	4.89
<i>RZFP34</i>	Q5JL96	Probable E3 ubiquitin-protein ligase RZFP34	5.16
<i>At4g00750</i>	Q9ZPH9	Probable methyltransferase PMT15	-4.60
<i>At1g26850</i>	B9DFI7	Probable methyltransferase PMT2	5.51
<i>At1g31850</i>	Q9C6S7	Probable methyltransferase PMT20	4.34
<i>At1g04430</i>	Q940J9	Probable methyltransferase PMT8	3.97
<i>UBC24</i>	Q8VY10	Probable ubiquitin-conjugating enzyme E2 24	5.37
<i>SEC</i>	Q9M8Y0	Probable UDP-N-acetylglucosamine--peptide acetylglucosaminyltransferase SEC	4.23
<i>AGO1</i>	O04379	Protein argonaute 1	3.81
<i>AGO2</i>	Q9SHF3	Protein argonaute 2	4.67
<i>AGO4</i>	Q9ZVD5	Protein argonaute 4	3.79
<i>BSD2</i>	Q9SN73	Protein BUNDLE SHEATH DEFECTIVE 2, chloroplastic	3.97
<i>DCP5</i>	Q9C658	Protein decapping 5	4.42

<i>PDIL1-4</i>	Q9FF55	Protein disulfide isomerase-like 1-4	4.58
<i>P4HB</i>	P07237	Protein disulfide-isomerase	6.06
<i>PDIA3</i>	P30101	Protein disulfide-isomerase A3	4.35
<i>PDIA6</i>	Q15084	Protein disulfide-isomerase A6	4.14
<i>grpE</i>	Q8DJB3	Protein GrpE	8.82
<i>VIP4</i>	Q9FNQ0	Protein LEO1 homolog	8.58
<i>NCA1</i>	Q9M2V1	Protein NCA1	3.63
<i>TAR1-A</i>	Q6CQE5	Protein TAR1	-10.79
<i>GOS2</i>	A6MZM2	Protein translation factor SUI1 homolog	4.50
<i>SVR3</i>	F4K410	Putative elongation factor TypA-like SVR3, chloroplastic	5.38
<i>DDB_G0268948</i>	Q55EX9	Putative methyltransferase DDB_G0268948	9.58
<i>RNC1</i>	Q9SZV0	Ribonuclease III domain-containing protein RNC1, chloroplastic	3.98
<i>PSRP1</i>	P19954	Ribosome-binding factor PSRP1, chloroplastic	3.56
<i>RIPt</i>	Q9M653	Ribosome-inactivating protein PMRIPt	4.73
<i>RRF</i>	P37706	Ribosome-recycling factor, chloroplastic	3.28
<i>RBCS</i>	P24007	Ribulose biphosphate carboxylase small subunit, chloroplastic	3.53
<i>RCA2</i>	Q7X999	Ribulose biphosphate carboxylase/oxygenase activase 2, chloroplastic	3.71
<i>RPE</i>	Q43843	Ribulose-phosphate 3-epimerase, chloroplastic	3.43
<i>ATL2</i>	Q8L9T5	RING-H2 finger protein ATL2	-1.72
<i>ATL32</i>	Q8W571	RING-H2 finger protein ATL32	1.34
<i>RBM39</i>	Q5RC80	RNA-binding protein 39	9.13
<i>CP29B</i>	Q9ZUU4	RNA-binding protein CP29B, chloroplastic	4.59
<i>RUBA</i>	P08926	RuBisCO large subunit-binding protein subunit alpha, chloroplastic	3.88
<i>SAMT</i>	Q9SPV4	Salicylate carboxymethyltransferase	5.94
<i>RS41</i>	P92966	Serine/arginine-rich splicing factor RS41	3.85
<i>SR30</i>	Q9XFR5	Serine/arginine-rich splicing factor SR30	8.96
<i>FFC</i>	P37107	Signal recognition particle 54 kDa protein, chloroplastic	3.16
<i>SKP1A</i>	Q39255	SKP1-like protein 1A	10.09
<i>SUMO1</i>	P55852	Small ubiquitin-related modifier 1	3.45
<i>SPP</i>	Q9FIH8	Stromal processing peptidase, chloroplastic	3.65
<i>At2g25737</i>	Q8L7A0	Sulfite exporter TauE/SafE family protein 3	4.67
<i>CCT3</i>	P49368	T-complex protein 1 subunit gamma	8.34
<i>YLS8</i>	Q9FE62	Thioredoxin-like protein YLS8	3.73
<i>THRRS</i>	O04630	Threonine--tRNA ligase, mitochondrial 1	5.25
<i>At1g17220</i>	Q9SHI1	Translation initiation factor IF-2, chloroplastic	3.48
<i>IF3-2</i>	O82234	Translation initiation factor IF3-2, chloroplastic	4.17
<i>TRAM1</i>	Q15629	Translocating chain-associated membrane protein 1	6.03
<i>TIG</i>	Q8S9L5	Trigger factor-like protein TIG, Chloroplastic	4.83
<i>RNU1</i>	Q42404	U1 small nuclear ribonucleoprotein 70 kDa	9.51
<i>UBP23</i>	Q9FPS4	Ubiquitin carboxyl-terminal hydrolase 23	3.51
<i>UCHL1</i>	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1	4.91
<i>UBP13</i>	Q84WU2	Ubiquitin C-terminal hydrolase 13	4.01
<i>DSK2B</i>	Q9SII8	Ubiquitin domain-containing protein DSK2b	4.26
<i>RL40</i>	P46575	Ubiquitin-60S ribosomal protein L40	-11.41
<i>UBA1</i>	P93028	Ubiquitin-activating enzyme E1 1	5.11
<i>UBC28</i>	Q94F47	Ubiquitin-conjugating enzyme E2 28	3.65
<i>UBC35</i>	Q94A97	Ubiquitin-conjugating enzyme E2 35	4.36
<i>N/A</i>	P35135	Ubiquitin-conjugating enzyme E2-17 kDa	4.63
<i>UBC4</i>	P16577	Ubiquitin-conjugating enzyme E2-23 kDa	8.98
<i>UBL5</i>	Q9FGZ9	Ubiquitin-like protein 5	10.73
<i>XRCC6</i>	P12956	X-ray repair cross-complementing protein 6	8.04
<i>YBX1</i>	P67808	Y-box-binding protein 1	2.46

Table S11. Sequences of primer used in qRT-PCR validation.

Genes	Sequences (5' to 3')	Amplicon size (bp)
ACT	Forward: TGGTGTTAGCCACACAGTCC	159
	Reverse: CTCACAATTTACGCTCGGC	
Salt stress (10)		
ALDH7B4	Forward: ACCAGGTGCGATCTTTACGG	117
	Reverse: ACCATTTGACCCACCTTCGT	
ANN2	Forward: TTGGTTCCCCTTGAGTGC	121
	Reverse: CCTCCTCGTCACTGTAAGCC	
RD22	Forward: CAATATGCAGCAACCGCGAC	153
	Reverse: CGTTTTGGCAACTTTGCGTG	
CAMP25	Forward: CTGAAACGCTACCAAAGCC	117

	Reverse: TCGAAACGGGGTCAGAAAGTG	
<i>PCC13</i>	Forward: GGGAAGAATTTCAGCCTCC Reverse: TCTTGACCGGATTCCACACC	176
<i>RBG7</i>	Forward: TTTAGGTGTTTCGTTGGCGG Reverse: TCATCGACTTCTCATCGCCG	166
<i>IQM4</i>	Forward: GAGGAACGTCCTACAGCGTC Reverse: AAGCATCCCTGTTGTCTGGT	112
<i>NFD4</i>	Forward: GGTGAGTGACCAAACGGAT Reverse: CCGCTTCTCCTCTACCGTC	108
<i>WSD1</i>	Forward: ATGCCACGGATTTGTCTGG Reverse: GTTGTACCCTGACTGGCCG	143
<i>At2g40140</i>	Forward: AGTCACATGGCTCTGATGGC Reverse: TGCTCAAAGACCTCACGCAT	174
Antioxidant enzyme activities (12)		
<i>SODCP</i>	Forward: CTCCTCAACGCCAGAACTT Reverse: CATCGTCCTCTGGGTCAAC	142
<i>FSD2</i>	Forward: TGCACAAAATCCCCTTCCAT Reverse: TGTAATCGGGCCTTCGGTTC	161
<i>SODA</i>	Forward: TCTCGCTCCAGTTCGTGAAG Reverse: CTGCACCTTCCGCATTTCATC	119
<i>At5g06290</i>	Forward: CTTAGTCTCGGGTTCCTCG Reverse: TCGAAAACGGCTTCTGCTTC	137
<i>APX3</i>	Forward: AAGAGATCGACAAGGCTCGC Reverse: TCGCACCATGACTAAGCTCC	171
<i>poxN1</i>	Forward: TCCAACGATTCTTCGCCCTT Reverse: ACGAATTTACCTTGCGTGC	104
<i>PRDX1</i>	Forward: TGTGGGACTGCTGATAGGAAGATG Reverse: GGGGCACACAAAGGTGAAGTC	181
<i>PEX11C</i>	Forward: GCTTGAAGGTCAGGCATCT Reverse: CCAGCTCTCCAAGCTCAACT	119
<i>GPX1</i>	Forward: CCCGCGGTCAAAAACACAC Reverse: AAACACCGAAGGGGAGACCT	179
<i>CATA</i>	Forward: GGAGCCAGTGCTAAGGGTTT Reverse: AGAACCGAACGATGAGAGGC	109
<i>CAT1</i>	Forward: CCAGAACGTGTGTGCCATGC Reverse: AGGATCCCTCAGCGTTTCAG	180
<i>PNC1</i>	Forward: TTGCTGCTCGTGAATCCGTT Reverse: GAAGTCCCAAAACGGGGGAG	128
Soluble sugar and protein metabolism (23)		
<i>G6PDC</i>	Forward: CCGAAGGATAGTCTCACGCC Reverse: AGAGCTTTGCCTGCCTTCAT	101
<i>GAPA1</i>	Forward: CGCTGATGTCAAGCCTGTTG Reverse: CTCCATCCCTGTCCACGAAC	155
<i>PGMP</i>	Forward: GGGAGGTGATGGCCGTTATT Reverse: CCCACCATTGGCCTTCTCT	157
<i>UGPA</i>	Forward: CTTGTGGAGGCTGATGCACT Reverse: TGGGAGAAATCGGGAACGAG	156
<i>INVE</i>	Forward: GCGTGTGACCTGTTGATT Reverse: GTCAAAACCATCAGCGAGGC	151
<i>SUS2</i>	Forward: AGAGAGGTTGGGGAGACACT Reverse: AGAATCCGTGCGGAGACAAG	153
<i>FKFBP</i>	Forward: TTCTCAGCCGAAGCCAGATG Reverse: TGGCGATCCTCTTTGGTCC	198
<i>F16P2</i>	Forward: CCTGCACGCTTGTGTTAAGC Reverse: GGTGTTGGAGCATCCAGT	164
<i>FBA3</i>	Forward: CTGTGGGAAGAGATTGGCGT Reverse: GCGCAAGCAGTCAACAAACT	178
<i>GOLS1</i>	Forward: AAAGGCGTTGTTGGATTGGC Reverse: ACGGGTTCGATTTCCTCAC	143
<i>TPS6</i>	Forward: AGTCGGCAAGGAAACGAGAG Reverse: ACGGGGAGCAACCAATGAAT	103
<i>OFUT39</i>	Forward: GCATTGGGCTTCGACAACAG Reverse: GTCAAGTGCGGCTAGCAAAG	180
<i>DPE2</i>	Forward: AGGTGTGGGTGTAGCAATCC	168

	Reverse: TCCCACCACATCCCATGAAC	
AMY3	Forward: ATATTGGCGGCTGTCGGATT Reverse: TGACCCTGAGTAGAGCCAGT	111
BAM1	Forward: GGGTGAGCTTCGTTACCCCTT Reverse: GTGCTACCCCATCTGGCTT	147
GWD3	Forward: ATAAAGGTGGGGCTCGTTGG Reverse: AAGACCCTTCTCTTGCCACG	176
RPN1A	Forward: TGGAAAAACAAGTGCGGCAG Reverse: GCCAATGCAGGGTCACAATC	177
PCS1	Forward: TAGGCGACATGGTGTGGAG Reverse: CCGATCCCTATGCAGTGGAC	103
Cys	Forward: GTGGATCTGCTACACACGGT Reverse: TGGCAACTTGTGGCATTCTTG	105
DEGP1	Forward: TAGTTCTGCGGCTACTGGTC Reverse: TCCAACACCAGAGGATGCAC	160
PBE2	Forward: CATGGTTGCTGCTGATTCTCG Reverse: AACTGAGATCCTGCGCTTGT	193
SBT2.5	Forward: AGCTGGGCTTGGCTTATCAC Reverse: TCTGGTCTCTGACAGTCCGT	123
ALEU	Forward: CCAACAAAAGGGCCTGTCTG Reverse: AGCAATTCTGTGCAGCTCCT	102
Cell morphogenesis (6)		
F16	Forward: GATGGTTCTGTGTGTGCGG Reverse: AGACATGGTGAAGGGACGAC	184
FIP1	Forward: CTGTCCACATCTGCTGGTCC Reverse: ACTTTGCTCGTGACGGATT	176
At5g13200	Forward: CCCCCGTGGAAAAATCAAGC Reverse: GCTTTTGCCGTCACGTTTCAT	166
At5g23350	Forward: AAGAGGAATCCATGGCGAGAG Reverse: TGCTCCAACACTCAGCTTTCC	137
KAI2	Forward: ACTCGGTTTCCGCCATGATT Reverse: CTCCTGTTCAAATCCCCCGT	131
ROH1	Forward: TTCTGGTTCCGACGAGCTTC Reverse: TCACGAATGGCATTGCACAC	195
Transcription factor (8)		
MYB73	Forward: TTGAACCCGAGTAGCCCATC Reverse: CCGTCGTCCAAGAAGAGGTC	133
WRKY24	Forward: CGAGTAGCGTTGAAATGCCG Reverse: TCAACGTCCTCTCTTTCGCC	145
WRKY71	Forward: TCTACAACACTAGGCGGTGC Reverse: TGCTGAAACGGGGTTAGGTT	152
NAC083	Forward: ACGAATACCGCCTTGTACGC Reverse: GCGGCATAAAACCCAACCTCT	101
JA2L	Forward: TGGGTTCTTCCCAGCAAAGC Reverse: CAACTTTGCGTCCTTCGGTG	166
BZIP44	Forward: GCACTTGGATGATCTGATGGC Reverse: GAGGTTTCATGTAGTCTGGGT	100
TCP14	Forward: TTCGGATGCCTGCTCTATGC Reverse: GGACATACTGGAGCCGGAAC	197
UNE10	Forward: CGAAAACGACGACAACCACC Reverse: AATAGCGGCAGCTCTACTCC	146
Hormone response (12)		
GASA2	Forward: TCTCGTCTCACTTCTGGCTCT Reverse: GCCCTCTTGCATAAGTGTGG	126
ARF2A	Forward: AGTTGGCCTATGATCGCCAC Reverse: TCAACAGATCGTCCAAGGGC	157
IAA9	Forward: GGGCAAGGGAAGTTTTCTGG Reverse: CCGAACGAGACCTTTCCTGT	124
TET4	Forward: GTTTCGTTGGCAGGATTCCGC Reverse: CCGACCCTTTATCCGTCACC	139
CISZOG2	Forward: AAGTGGTTGTGGTCGTCGTG Reverse: TGGCGATTATGGGTTGGAGT	127
AHK3	Forward: ACTGGCATTGGGCTTAGCAT Reverse: ACAAGGAAGAGCTCGGTTGG	175

<i>JOX2</i>	Forward: AGCGTGGAGCATAGGGTAGT Reverse: GTCATGGGTGCGTATTGTGC	143
<i>TIFY6B</i>	Forward: GTGGGTCTTCCATGGCTCTT Reverse: GACCCACTCCCTGACTTTGG	160
<i>PYL3</i>	Forward: GCCGTTTATAAGCAGGTGCG Reverse: AGCCTTCTGTGCTGGTTGT	105
<i>PP2CA</i>	Forward: AATGGACGGAGAACTCCACG Reverse: TCAGGAGTAACAACGGCGAC	103
<i>ETR2</i>	Forward: TGATACTCCGGGTGGCTTCT Reverse: GTGCCTCCTACCCCTAGTT	179
<i>ERF013</i>	Forward: TCCTCGCCTTCGTTGTCTTC Reverse: GCCCATTGAGCATATCGGT	176
Ion transport (10)		
<i>CSC1</i>	Forward: AGGTTTACTACCGGGGCTCT Reverse: TAGCTGGTCCAATGCTGTCC	193
<i>CLC-C</i>	Forward: CAGCAGCAGGGTCTGGTATC Reverse: CCCCTGCCCAAGTAAAGAGG	194
<i>RAN1</i>	Forward: TCCCTGTGCTCTTGGATTGG Reverse: TTGACCCGCTGAGCTCTTTC	117
<i>KEA2</i>	Forward: CTGTGGGTTTGGACGTGTG Reverse: AAGCTCTTCCGCACCAACT	182
<i>OEP16</i>	Forward: GGTTCCTCGTAGCGGTCTGG Reverse: TCTTTGCCATTGTTGCTCGC	198
<i>PPI1</i>	Forward: TGAGTGCTGATGGACGCATT Reverse: GCCAGTTCAAATCCCCTGC	151
<i>NHX2</i>	Forward: ATGGGTCTTGTGATGGTCCG Reverse: TATGCCCGGCCCTTGTAAC	187
<i>CAX1</i>	Forward: CGTGGCGTATGTTGCGTATC Reverse: TACCCACGACGTACTCGGAT	194
<i>VHA-a2</i>	Forward: TCGGTTTCATCGTGGCAATCT Reverse: AACCCCTACCGACAAGACAC	145
<i>ZIP1</i>	Forward: GCTGGTGCTATAGGGGTGAG Reverse: GGATTCTGGCTAAGGCAAGGT	182