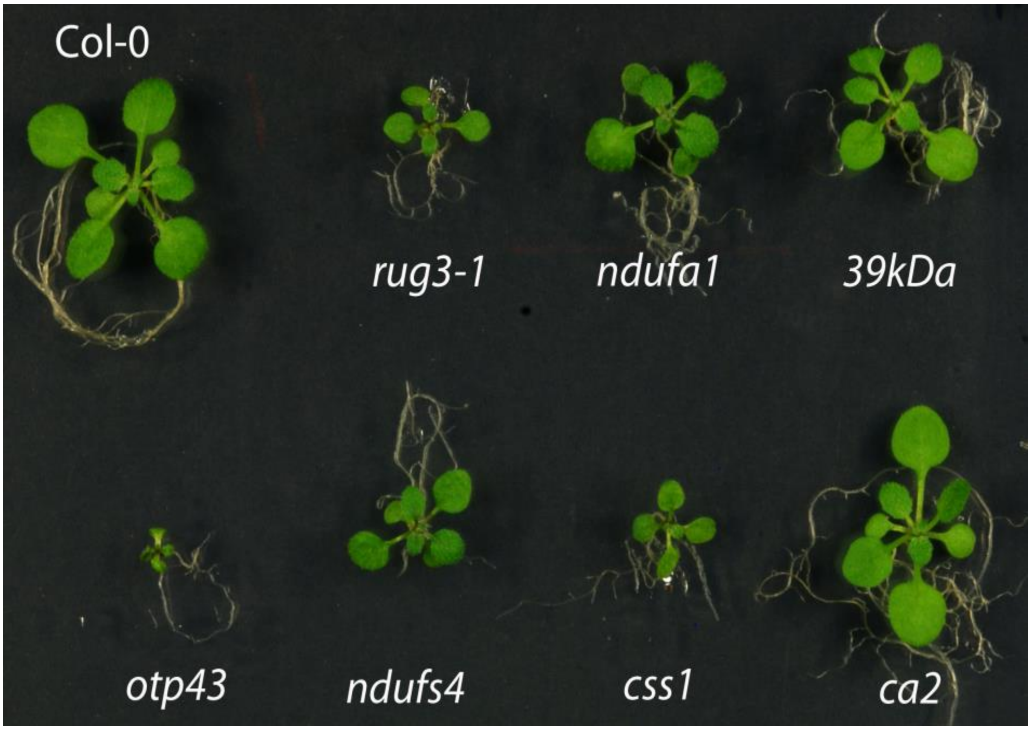

Supplemental Figure 1: Growth phenotypes of complex I mutants.
Previously published complex I mutants were collected. Seeds were plated on 0.5X MS medium with 1% sucrose and stratified for 2 days. The plates were incubated under long day conditions in a growth chamber for 3 weeks. Mutants used: *rug3-1* (Kühn et al., 2011), *ndufa1*, *ndufs4* (Meyer et al., 2009), *39kDa* (Meyer et al., 2011), *otp43* (Falcon de Longevialle et al., 2007), *css1* (Nakagawa and Sakurai, 2006), *ca2* (Perales et al., 2005).

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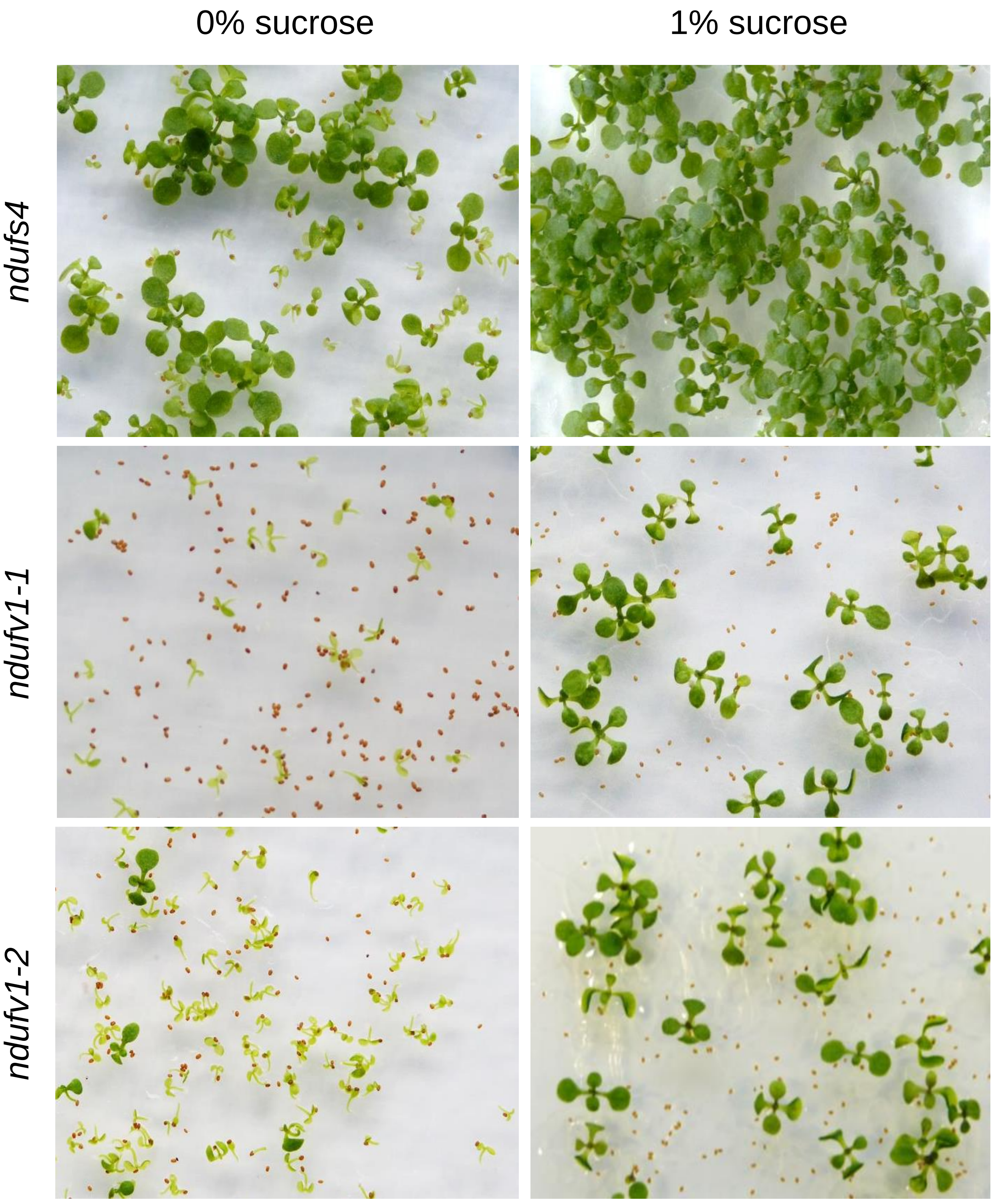
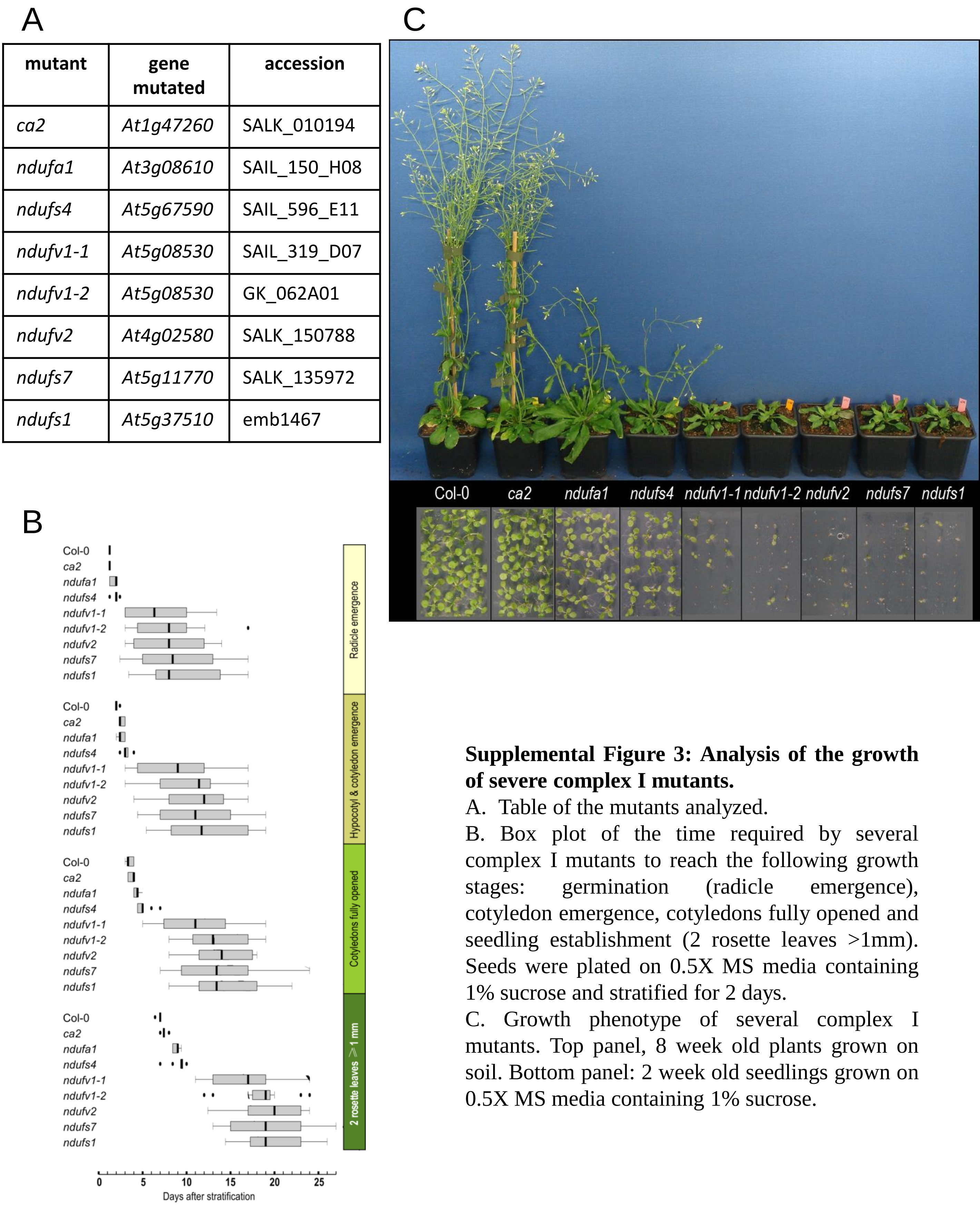


Supplemental Figure 2: Growth phenotypes of complex I mutants in the absence or presence of sucrose.

Seeds were surface sterilized and plated on 0.5X MS medium containing the sucrose concentrations indicated above the photos and stratified for 2 days. The plates were transferred to a growth chamber and incubated in a 12 h light/12 h dark regime. The photo was taken 3 weeks after sowing. Small yellow seedlings are aborted whereas green seedlings are established.



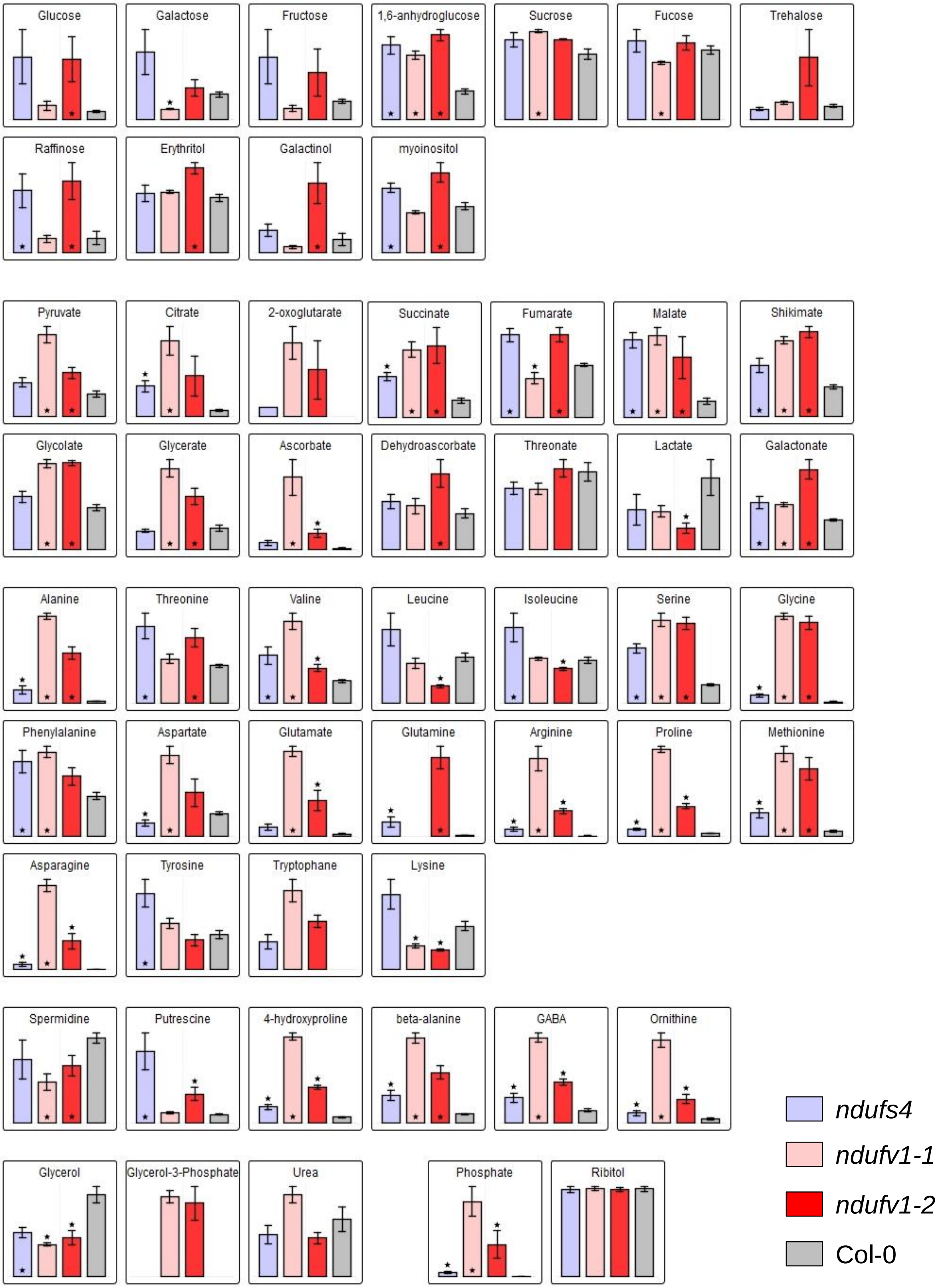
mutant	gene mutated	accession
ca2	*At1g47260*	SALK_010194
ndufa1	*At3g08610*	SAIL_150_H08
ndufs4	*At5g67590*	SAIL_596_E11
ndufv1-1	*At5g08530*	SAIL_319_D07
ndufv1-2	*At5g08530*	GK_062A01
ndufv2	*At4g02580*	SALK_150788
ndufs7	*At5g11770*	SALK_135972
ndufs1	*At5g37510*	emb1467

Supplemental Figure 3: Analysis of the growth of severe complex I mutants.

A. Table of the mutants analyzed.

B. Box plot of the time required by several complex I mutants to reach the following growth stages: germination (radicle emergence), cotyledon emergence, cotyledons fully opened and seedling establishment (2 rosette leaves >1mm). Seeds were plated on 0.5X MS media containing 1% sucrose and stratified for 2 days.

C. Growth phenotype of several complex I mutants. Top panel, 8 week old plants grown on soil. Bottom panel: 2 week old seedlings grown on 0.5X MS media containing 1% sucrose.

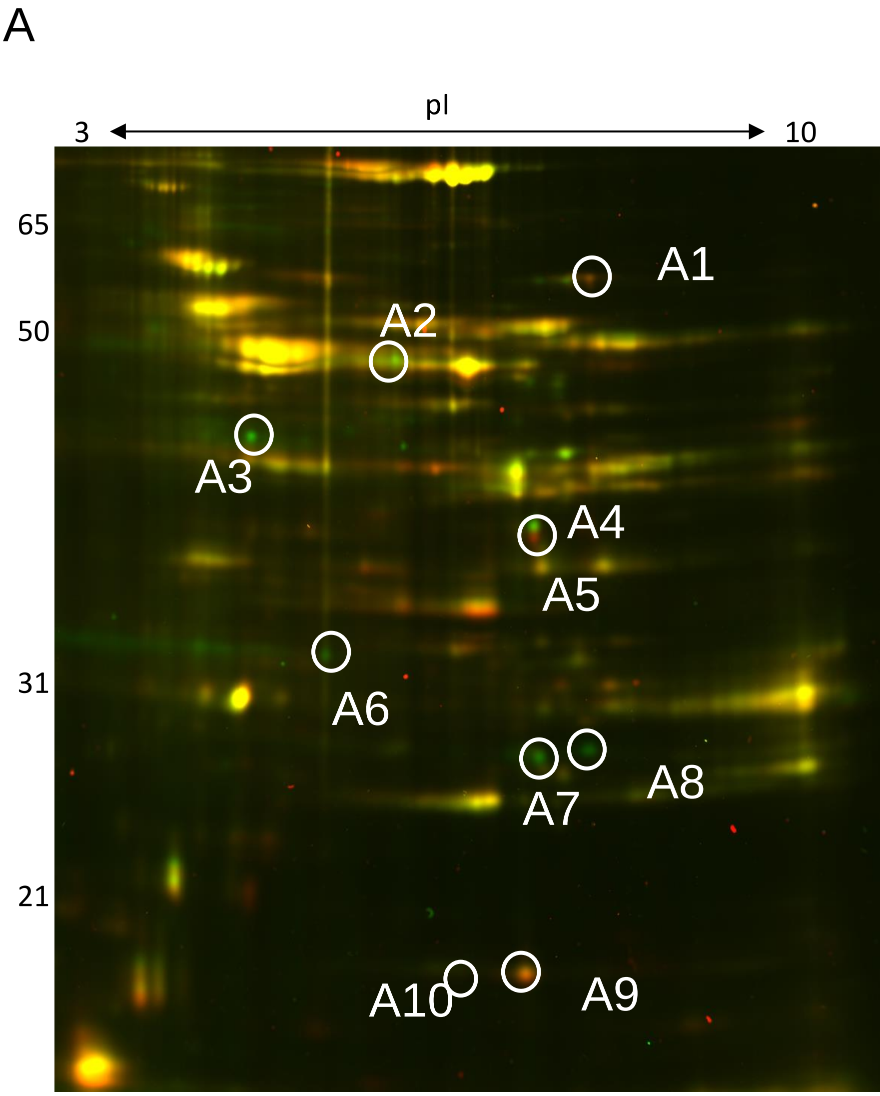


Supplemental Figure 4: Metabolite profiles of complex I mutants.
Rosette leaves of plants at the same physiological stage were harvested. Metabolites were extracted and analysed using GC-MS. For each metabolite, the bar of Col-0 represents a normalised abundance of 1. Bars represent means +/- SE (n=6)

Supplemental Figure 5: Comparison of the mitochondrial proteomes of *ndufv1-1* and *ndufs4* using DIGE.

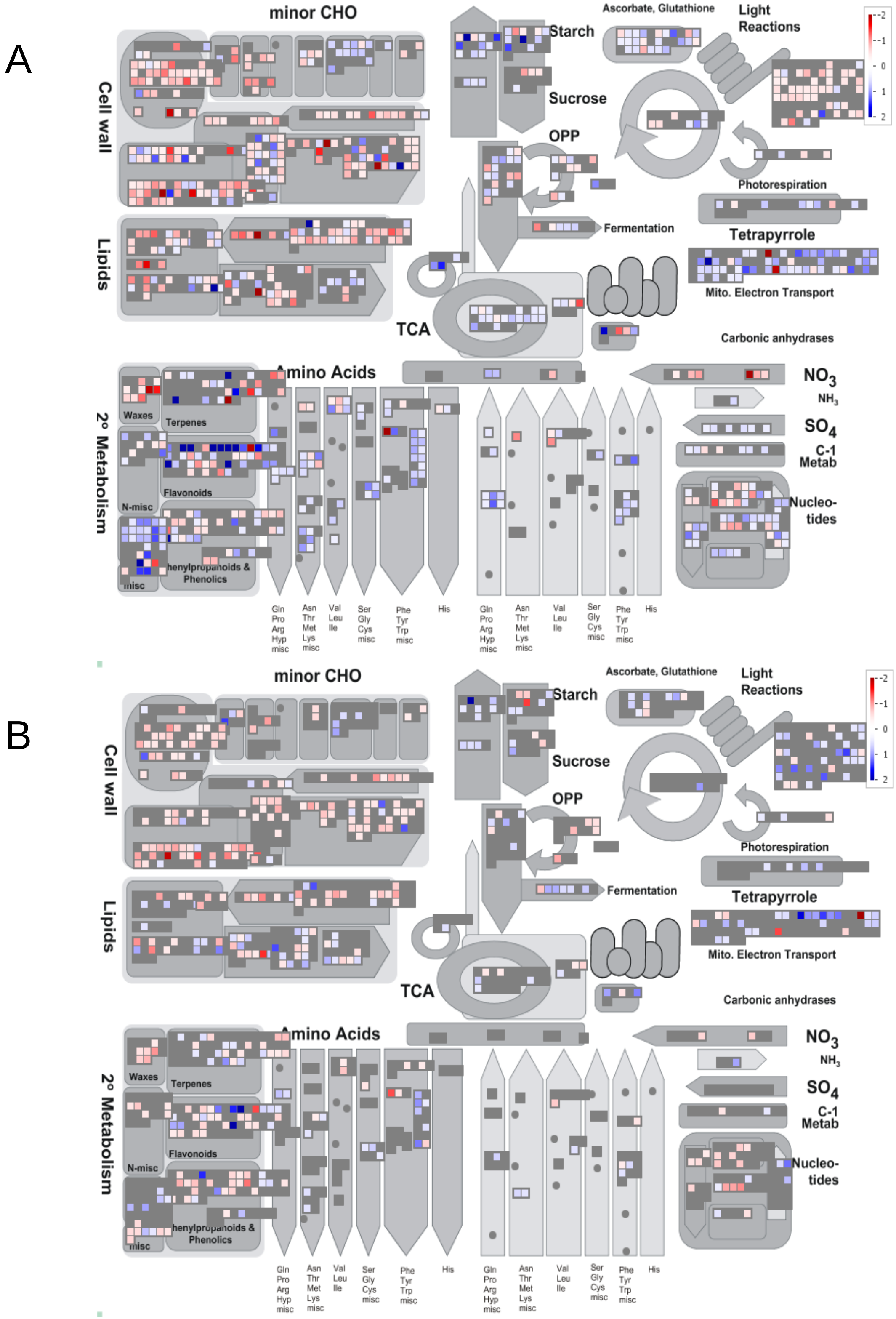
A. Representative gel with the proteins spots shown in false colors, *ndufv1-1* in red and *ndufs4* in green. Yellow indicates protein spots having the same intensity in both samples. The 10 spots that show a statistically significant differential abundance (more than 1.5 fold, n=3, $p<0.05$) are surrounded and labeled A1 to A10. The pI range is indicated on top of the gel and the molecular weight (in kD) marker in indicated on the left of the gel.

B. Table showing the results of the mass spectrometric analysis of the 10 spots, only identified proteins with a calculated pI and MW corresponding to the position of the spot are shown. Score : protein identification score given by MASCOT, pept : number of peptides identified, AGI : Arabidopsis Gene identifier. Proteins showing a higher abundance in *ndufv1-1* are highlighted in red, the other show a lower abundance in *ndufv1-1* compared to *ndufs4*.



B

spot	score	pept	AGI	annotation
A1	137	10	At3g47930	L-galactono-1,4-lactone dehydrogenase (GLDH)
A2	2785	91	At1g79440	Aldehyde dehydrogenase
	901	45	At3g48000	Aldehyde dehydrogenase
	737	23	At1g23310	Glutamate:glyoxylate aminotransferase
	661	19	At1g70580	Alanine-2-oxoglutarate aminotransferase
A3	291	13	At5g08270	Unknown protein
A4	2721	113	At3g20000	TOM40
A5	701	31	At1g13440	Glyceraldehyde-3-phosphate dehydrogenase
A6	162	6	At1g18490	Unknown protein
A7	1036	39	At1g15390	Peptide deformylase
A8	599	23	At5g63510	Carbonic anhydrase like
A9	1258	47	At3g06050	Peroxiredoxin IIF
A10	1077	43	At3g06050	Peroxiredoxin IIF



Supplemental Figure 6: Mapman metabolism maps

These maps represent the expression changes measured by our microarray analysis. Genes are grouped according to the Mapman categories. Only categories related to primary and secondary metabolism are shown. Each square represents one gene, only genes for which a significant expression value was measured (Holm-Bonferroni method, p-val < 0.05) are represented. Genes down regulated are indicated in red and genes upregulated are indicated in blue, the darkest the color is, the strongest the change is, see scale on the top right of each panel. A. Map of *ndufv1-1*. B. Map of *ndufs4*.

Supplemental Table 1: Analysis of the gene categories showing differential response in *ndufv1-1* and *ndufs4*

			ndufv1-1		***ndufs4***	
	MapMan bin	direction	proportion	pval	proportion	pval
PS	lightreaction	down	0.50	0.033	0.24	0.739
major CHO metabolism	raffinose family	down	0.55	0.007	0.45	0.849
major CHO metabolism	myo-inositol	up	0.50	0.009	0.36	0.3
OPP	non-reductive PP	down	0.44	0.178	0.33	0.001
mitochondrial electron transport / ATP synthe	NADH-DH	up	0.60	0.001	0.29	0.544
mitochondrial electron transport / ATP synthe	cytochrome c reductase	up	0.78	0.001	0.22	0.364
cell wall	pectin synthesis	down	0.57	0.001	0.29	0.839
amino acid metabolism	amino acid synthesis	up	0.59	0.001	0.36	0.172
metal handling	NA	down	0.40	0.008	0.50	0.073
metal handling	binding, chelation and storage	down	0.38	0.263	0.45	0.008
secondary metabolism	phenylpropanoids	down	0.43	0.055	0.51	0.003
secondary metabolism	N misc	down	0.43	0.259	0.57	0.001
secondary metabolism	sulfur-containing	up	0.56	0.001	0.35	0.239
secondary metabolism	flavonoids	down	0.34	0.992	0.50	0.005
hormone metabolism	abscisic acid	up	0.40	0.916	0.43	0.018
hormone metabolism	cytokinin	down	0.42	0.884	0.47	0.001
hormone metabolism	jasmonate	down	0.42	0.128	0.64	0.004
stress	biotic	up	0.36	0.591	0.43	0.006
stress	thioredoxin	down	0.45	0.006	0.34	0.055
stress	ascorbate and glutathione	up	0.50	0.002	0.45	0.062
nucleotide metabolism	synthesis	down	0.19	1	0.37	0.008
nucleotide metabolism	synthesis	up	0.67	0.001	0.22	0.993
nucleotide metabolism	phosphotransfer and pyrophosphatases	up	0.55	0.001	0.41	0.101
misc	cytochrome P450	down	0.41	0.399	0.45	0.036
misc	alcohol dehydrogenases	up	0.33	0.272	0.56	0.007
misc	peroxidases	down	0.53	0.004	0.26	0.831
misc	acid and other phosphatases	down	0.45	0.004	0.31	0.374
misc	myrosinases-lectin-jacalin	down	0.46	0.194	0.35	0.014
misc	dynamin	up	0.33	0.543	0.50	0.026

misc	short chain dehydrogenase/reductase (SDR)	up	0.50	0.001	0.38	0.459
misc	GCN5-related N-acetyltransferase	down	0.38	0.579	0.44	0.008
RNA	regulation of transcription	up	0.41	0.105	0.41	0.037
DNA	synthesis/chromatin structure	down	0.38	0.901	0.36	0.026
protein	synthesis	up	0.62	0.001	0.27	0.857
protein	postranslational modification	down	0.39	0.033	0.32	0.998
protein	postranslational modification	up	0.37	0.968	0.45	0.003
protein	degradation	down	0.44	0.001	0.36	0.132
signalling	in sugar and nutrient physiology	up	0.46	0.093	0.46	0.001
signalling	receptor kinases	down	0.49	0.002	0.38	0.45
signalling	phosphinositides	down	0.43	0.018	0.24	0.985
signalling	phosphinositides	up	0.24	0.983	0.40	0.016
signalling	MAP kinases	down	0.46	0.003	0.40	0.445
signalling	light	up	0.39	0.129	0.56	0.001
development	late embryogenesis abundant	up	0.59	0.006	0.36	0.537
development	squamosa promoter binding like (SPL)	up	0.38	0.824	0.54	0.033
transport	potassium	down	0.62	0.002	0.35	0.185
transport	unspecified anions	down	0.55	0.022	0.36	0.246

Supplemental Table 2. Overview of the metabolite reporting list.

GC-TOF-MS metabolites

	A	B	C	D	E	F	G	H	I
1									
2	**Experiment title:**		Metabolite profiling of Arabidopsis complex I mutatnts						
3	**Organism/Plant specie**		*Arabidopsis thaliana*						
4	**Organ/tissue:**		Leaf						
5	**Analytical tool:**		GC-TOF-MS						
6									
7	Peak/compound no.- number referenced back to the main text								
8	Ret . Time- Time expected, Tag Time Index and Time deviation								
9	Putative Name- putative identification of the metabolite/derivative								
10	Corresponding metabolite name in literature								
11	Mol. Formula- molecular formula of the metabolite or its FA adduct;								
12	Mass to charge ratio (m/z)								
13	(S)- identification confirmed by a standard compound								
14	I, II, III- different isomers								
15	Identification level (A; B; C; D)- (A) standard or NMR; (B) MS/MS; (C) MS^E; (D) MS only								
16									
17	**Peak/Compound no.**	**Time Expected**	**Tag Time Index**	**Time Deviation**	**Putative metabolite name (Derivative)**	**Corresponding Metabolite in Literature**	**Metabolite Class**	**Mol formula**	**Mass to charge ratio (m/z)**
18	1	190250	190298	-0.08	M000100_A105001-101_CONT-METB_190250_TOF_Lactic acid, DL- (2TMS)	Lactate	Acid (Hydroxy)	C3H6O3	117
19	2	206867	206910	0.01	M000517_A106002-101_CONT-MST_206867_TOF_Glycolic acid (2TMS)	Glycolate	Acid (Hydroxy)	C2H4O3	177
20	3	208565	208986	0.29	M000026_A110001-101_METB_208565_TOF_Alanine, DL- (2TMS)	Alanine	Amino acids	$C_3H_7NO_2$	116
21	4	222650	222654	-0.01	M000071_A104002-101_METB_222650_TOF_Pyruvic acid (1MEOX) (1TMS)	Pyruvate	Acid (Oxo)	C3H4O3	174
22	5	271580	271581	0	M000030_A122001-101_METB_271580_TOF_Valine, DL- (2TMS)	Valine	Amino acids	$C_5H_{11}NO_2$	144
23	6	291783	291650	-0.05	M000053_A129003-101_METB_291783_TOF_Glycerol (3TMS)	Glycerol	Polyol (Triol)	C3H8O3	103
24	7	305020	304900	-0.01	M000025_A129002-101_METB_301020_TOF_Leucine, DL- (2TMS)	Leucine	Acid (Amino)	C6H13NO2	158
25	8	319193	318906	-0.05	M000017_A132002-101_METB_319193_TOF_Isoleucine, L- (2TMS)	Isoleucine	Amino acids	$C_6H_{13}NO_2$	158
26	9	325180	325031	0.02	M000031_A133001-101_METB_325180_TOF_Glycine (3TMS)	Glycine	Acid (Amino)	C2H5NO2	174
27	10	327380	326918	-0.12	M000015_A128001-101_METB_327380_TOF_Serine, DL- (2TMS)	Serine	Acid (Amino)	C3H7NO3	116
28	11	333520	332458	-0.29	M000075_A129001-101_METB_333520_TOF_Phosphoric acid (3TMS)	Phosphate	Inorganic acid	H3O4P	299
29	12	338693	338470	-0.01	M000029_A132003-101_METB_338693_TOF_Proline, L- (2TMS)	Proline	Amino acids	$C_5H_9NO_2$	142
30	13	340357	339685	-0.21	M000364_A127002-101_METB_340357_TOF_Urea (2TMS)	Urea	Amide	CH4N2O	189
31	14	345050	344408	-0.18	M000073_A135003-101_METB_345050_TOF_Glyceric acid, DL- (3TMS)	Glycerate	Acid (Hydroxy)	C3H6O4	189
32	15	365427	365088	-0.09	M000074_A134001-101_METB_365427_TOF_Succinic acid (2TMS)	Succinate	Organic acids	$C_4H_6O_4$	247

33	16	368365	367370	-0.27	M000016_A140001-101_METB_368365_TOF_Threonine, DL- (3TMS)	Threonine	Amino acids	$C_4H_9NO_3$	291
34	17	371255	371391	0.04	M000067_A137001-101_METB_371255_TOF_Fumaric acid (2TMS)	Fumarate	Organic acids	$C_4H_4O_4$	245
35	18	394250	393926	-0.08	M000027_A144001-101_METB_394250_TOF_Alanine, beta- (3TMS)	beta-alanine	Amino acids	$C_3H_7NO_2$	174
36	19	408455	408460	0.01	M000054_A150002-101_METB_408455_TOF_Erythritol (4TMS)	Erythritol	Polyol (Tetraol)	C4H10O4	217
37	20	440995	440812	-0.03	M000065_A149001-101_METB_440995_TOF_Malic acid, DL- (3TMS)	Malate	Organic acids	$C_4H_6O_5$	245
38	21	448453	448236	-0.02	M000034_A153001-101_METB_448453_TOF_Proline, 4-hydroxy-, DL-, trans- (3T	4-hydroxyproline	Acid (Amino)	C5H9NO3	140
39	22	452200	452146	0.02	M000114_A153003-101_METB_452200_TOF_Butyric acid, 4-amino- (3TMS)	GABA	Amino acids	$C_4H_9NO_2$	174
40	23	457283	457044	-0.05	M000033_A152002-101_METB_457283_TOF_Aspartic acid, L- (3TMS)	Aspartate	Amino acids	$C_4H_7NO_4$	232
41	24	458330	457912	-0.13	M000078_A156001-101_METB_458330_TOF_Threonic acid (4TMS)	Threonate	Acid (Hydroxy)	C4H8O5	292
42	25	474325	474088	-0.06	M000018_A152001-101_METB_474325_TOF_Methionine, DL- (2TMS)	Methionine	Acid (Amino)	C5H11NO2S	128
43	26	507780	507893	0.01	M000036_A163001-101_METB_507780_TOF_Glutamic acid, DL- (3TMS)	Glutamate	Amino acids	$C_5H_9NO_5$	348
44	27	517180	517401	0.05	M000186_A175002-101_METB-METB_517180_TOF_Putrescine (4TMS)	Putrescine	Polyamine	$C_4H_{12}N_2$	214
45	28	522140	521998	0.03	M000591_A173002-101_METB_522140_TOF_Fucose, DL- (1MEOX) (4TMS)	Fucose	Sugar (Hexose, de	C6H12O5	117
46	29	523847	523650	0.03	M000571_A158004-101_METB_523847_TOF_Glutaric acid, 2-oxo- (1MEOX) (2TM	2-oxoglutarate	Acid (Oxo)	C5H6O5	198
47	30	531145	530862	-0.13	M000011_A164001-101_METB_531145_TOF_Phenylalanine, DL- (2TMS)	Phenylalanine	Amino acids	$C_9H_{11}NO_2$	192
48	31	550100	549922	-0.01	M000013_A168001-101_METB_550100_TOF_Asparagine, DL- (3TMS)	Asparagine	Amino acids	$C_4H_8N_2O_3$	116
49	32	557320	556396	-0.13	M000248_A172001-101_METB_557320_TOF_Glucose, 1,6-anhydro, beta-D- (3TM	1,6-anhydroglucose	Sugar (Hexose, al	C6H10O5	204
50	33	570427	570358	-0.01	M000028_A182002-101_METB-METB_570427_TOF_Ornithine, DL- (4TMS)	Ornithine	Acid (Amino)	C5H12N2O2	142
51	34	574230	573794	-0.08	M000328_A177002-101_METB_574230_TOF_Glycerol-3-phosphate, DL- (4TMS)	Glycerol-3-Phosphate	Triol phosphate	C3H9O6P	357
52	35	579380	578894	-0.08	M000606_A187002-101_METB_579380_TOF_Fructose, D- (1MEOX) (5TMS)	Fructose	Sugar (Hexose)	C6H12O6	307
53	36	585405	585031	-0.09	M000607_A181002-101_METB_585405_TOF_Shikimic acid (4TMS)	Shikimate	Acid (Hydroxy)	C7H10O5	204
54	37	587270	586972	-0.05	M000043_A191002-101_METB-METB_587270_TOF_Galactose, D- (1MEOX) (5T	Galactose	Sugar (Hexose, al	C6H12O6	160
55	38	592883	592536	-0.06	M000069_A182004-101_METB-METB_592883_TOF_Citric acid (4TMS)	Citrate	Organic acid	$C_6H_8O_7$	273
56	39	598300	598120	0.05	M000032_A178001-101_METB_598300_TOF_Glutamine, DL- (3TMS)	Glutamine	Acid (Amino)	C5H10N2O3	245
57	40	598880	598513	-0.04	M000040_A191001-101_METB-METB_598880_TOF_Glucose, D- (1MEOX) (5TM	Glucose	Sugar (Hexose, al	C6H12O6	160
58	41	605940	605763	-0.02	M000038_A183001-101_METB-METB_605940_TOF_Arginine, DL-, -NH3 (3TMS)	Arginine	Acid (Amino)	C6H11N3O2	157
59	42	615467	615058	-0.08	M000014_A192003-101_METB_615467_TOF_Lysine, L- (4TMS)	Lysine	Amino acids	$C_6H_{14}N_2O_2$	174
60	43	624990	624668	0	M000082_A185002-101_METB-METB_624990_TOF_Dehydroascorbic acid dimer	Dehydroascorbate	Hydroxy acid	$C_6H_6O_6$	173
61	44	626890	626336	-0.1	M000596_A199002-101_METB_626890_TOF_Galactonic acid (6TMS)	Galactonate	Acid (Hexonic)	C6H12O7	292
62	45	651990	650829	-0.17	M000001_A195002-101_METB_651990_TOF_Ascorbic acid, L(+)- (4TMS)	Ascorbate	Acid (Hydroxy)	C6H8O6	117
63	46	653910	654002	0.02	M000060_A209002-101_METB_653910_TOF_Inositol, myo- (6TMS)	myoinositol	Polyol	$C_6H_{14}O_6$	191
64	47	658337	658004	-0.06	M000035_A194002-101_METB_658337_TOF_Tyrosine, DL- (3TMS)	Tyrosine	Amino acids	$C_9H_{11}NO_3$	218
65	48	723585	723554	-0.03	M000106_A226002-101_METB_723585_TOF_Spermidine (5TMS)	Spermidine	Amine (Poly)	C7H19N3	144
66	49	790560	789999	-0.08	M000012_A223001-101_METB_790560_TOF_Tryptophan, L- (3TMS)	Tryptophane	Amino acids	$C_{11}H_{12}N_2O_2$	202
67	50	840783	841026	0.04	M000044_A264001-101_METB_840783_TOF_Sucrose, D- (8TMS)	Sucrose	Sugar (disacchari	$C_{12}H_{22}O_{11}$	451
68	51	876240	875263	-0.11	M000671_A274002-101_METB_876240_TOF_Trehalose, alpha,alpha'-, D- (8TMS	Trehalose	Sugar (disacchari	$C_{12}H_{22}O_{11}$	191
69	52	940280	938950	-0.14	M000673_A299002-101_METB_940280_EIROE_Galactinol (9TMS)	Galactinol	Conjugate (Hexos	C12H22O11	204
70	53	1033367	1032568	-0.08	M000049_A337002-101_METB_1033367_TOF_Raffinose (11TMS)	Raffinose	Sugar (trisacchari	$C_{18}H_{32}O_{16}$	204

Species detected before	**Identification level (A-D)**	Time Expected	Tag_Time _Index	Time Deviation	Name Analyte		Tag_Mass
Arabidopsis	A	190250	190298	-0.08	M000100_	Lactate	117
Arabidopsis	A	206867	206910	0.01	M000517_	Glycolate	177
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	208565	208986	0.29	M000026_	Alanine	116
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	222650	222654	-0.01	M000071_	Pyruvate	174
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	271580	271581	0	M000030_	Valine	144
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	291783	291650	-0.05	M000053_	Glycerol	103
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	305020	304900	-0.01	M000025_	Leucine	158
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	319193	318906	-0.05	M000017_	Isoleucine	158
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	325180	325031	0.02	M000031_	Glycine	174
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	327380	326918	-0.12	M000015_	Serine	116
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	333520	332458	-0.29	M000075_	Phosphate	299
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	338693	338470	-0.01	M000029_	Proline	142
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	340357	339685	-0.21	M000364_	Urea	189
Tomato, Arabidopsis	A	345050	344408	-0.18	M000073_	Glycerate	189
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	365427	365088	-0.09	M000074_	Succinate	247

Tomato, Arabidopsis, potato	A	368365	367370	-0.27	M000016_	Threonine	291
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	371255	371391	0.04	M000067_	Fumarate	245
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	394250	393926	-0.08	M000027_	beta-alanine	174
Tomato, Arabidopsis, potato	A	408455	408460	0.01	M000054_	Erythritol	217
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	440995	440812	-0.03	M000065_	Malate	245
Tomato, Arabidopsis, potato	A	448453	448236	-0.02	M000034_	4-hydroxyproline	140
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	452200	452146	0.02	M000114_	GABA	174
Tomato, Arabidopsis, potato	A	457283	457044	-0.05	M000033_	Aspartate	232
Tomato, Arabidopsis, potato	A	458330	457912	-0.13	M000078_	Threonate	292
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	474325	474088	-0.06	M000018_	Methionine	128
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	507780	507893	0.01	M000036_	Glutamate	348
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	517180	517401	0.05	M000186_	Putrescine	214
Tomato, Arabidopsis, potato	A	522140	521998	0.03	M000591_	Fucose	117
Tomato, Arabidopsis, potato	A	523847	523650	0.03	M000571_	2-oxoglutarate	198
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	531145	530862	-0.13	M000011_	Phenylalanine	192
Tomato, Arabidopsis, potato	A	550100	549922	-0.01	M000013_	Asparagine	116
Tomato, Arabidopsis, potato	A	557320	556396	-0.13	M000248_	1,6-anhydroglucose	204
Arabidopsis	A	570427	570358	-0.01	M000028_	Ornithine	142
Tomato, Arabidopsis, potato	A	574230	573794	-0.08	M000328_	Glycerol-3-Phospha	357
Tomato, Arabidopsis, potato, Lotus japonicus	A	579380	578894	-0.08	M000606_	Fructose	307
Tomato, Arabidopsis	A	585405	585031	-0.09	M000607_	Shikimate	204
Tomato, Arabidopsis, potato, Lotus japonicus	A	587270	586972	-0.05	M000043_	Galactose	160
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	592883	592536	-0.06	M000069_	Citrate	273
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	598300	598120	0.05	M000032_	Glutamine	245
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	598880	598513	-0.04	M000040_	Glucose	160
Tomato, Arabidopsis, potato	A	605940	605763	-0.02	M000038_	Arginine	157
Tomato, Arabidopsis, potato	A	615467	615058	-0.08	M000014_	Lysine	174
Tomato, Arabidopsis, potato	A	624990	624668	0	M000082_	Dehydroascorbate	173
Tomato, Arabidopsis, potato	A	626890	626336	-0.1	M000596_	Galactonate	292
Tomato, Arabidopsis, potato	A	651990	650829	-0.17	M000001_	Ascorbate	117
Tomato, Arabidopsis, potato	A	653910	654002	0.02	M000060_	myoinositol	191
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	658337	658004	-0.06	M000035_	Tyrosine	218
Arabidopsis	A	723585	723554	-0.03	M000106_	Spermidine	144
Tomato, Arabidopsis, potato	A	790560	789999	-0.08	M000012_	Tryptophane	202
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	840783	841026	0.04	M000044_	Sucrose	451
Tomato, Arabidopsis, potato	A	876240	875263	-0.11	M000671_	Trehalose	191
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	940280	938950	-0.14	M000673_	Galactinol	204
Tomato, Arabidopsis, potato, *Lotus japonicus*	A	1033367	1032568	-0.08	M000049_	Raffinose	204

Supplemental table 3: list of primers used in this study

genotyping of *ndufv1-1*

LP	ACGGCCATCAGAAACTTTAGG
RP	GTTGGATCGTCTTACGGGAAC
LB	TAGCATCTGAATTTCATAACCAATCTCGATACAC

genotyping of *ndufv1-2*

LP	CGATCTGTTTGGTTACCTCCTG
RP	CATGTGGTTCTGGTTATGATTTTG
LB	ATATTGACCATCATACTCATTGC

genotyping of *ndufv2*

LP	TGTGATTCATTAAATCATTCTGCC
RP	GAGACATCGAATCAGCTTTGC
LB	TGGTTCACGTAGTGGGCCATCG

genotyping of *ndufS7*

LP	TCAACTGGTAAACAACGGGAG
RP	TTTGATTGTGGTTGTATGACTCG
LB	TGGTTCACGTAGTGGGCCATCG

genotyping of *ndufS1*

LP	TGAAAACCCAAGTTAAAGCTCTC
RP	GCAAACACCTCGGGACTG
LB	TAGCATCTGAATTTCATAACCAATCTCGATACAC

Supplemental Experimental procedures

Metabolite profiling

GC-TOF-MS based metabolite profiling was performed basically as described by Lisec et al. (Lisec et al., 2006). Polar metabolites were extracted from 50 mg of frozen leaf material and 150 µl of each extract was used for the analysis. TagFinder (Luedemann et al., 2012) was used for peak annotation and quantification with Golm Metabolome Database (http://gmd.mpimp-golm.mpg.de; (Kopka et al., 2005) as a reference library. The parameters used for the peak annotation are listed in Supplemental Table 2 according to (Fernie et al., 2011). The intensity of each fragment was normalized by that of ribitol which was added into the extraction solution as an internal standard.

Differential Gel Electrophoresis (DIGE)

Mitochondrial proteins from *ndufv1*-1 and *ndufs4* plants were precipitated overnight at -20°C in 100% (v/v) acetone. After centrifugation at 20,000g and 4°C for 20 min, pellets were resuspended in 10 mL of DIGE lysis buffer (8 M urea, 4% (w/v) CHAPS, and 40 mM Tris, pH 8.5) and centrifuged again at 12,000g and 4°C for 10 min in order to remove insoluble material. Fifty micrograms of proteins from each sample was labeled with a different Cy dye (Cy-3 or Cy-5) by addition of 400 pmol of dye (freshly prepared in dimethylformamide according to the manufacturer's instructions) on ice in the dark for 30 min. The reaction was stopped by addition of 10 mM lysine for 10 min on ice in the dark. An equal volume of DIGE lysis buffer with 22 mM DTT was added to each sample. Each of the labeled protein samples were mixed, and rehydration buffer (8 M urea, 4% (w/v), CHAPS, 0.5% (v/v), 3–10 nonlinear immobilized pH gradient buffer, 18 mM DTT, and 0.001% (w/v) bromophenol blue) was added to give a final volume of 450 µL. The mix was loaded onto a 24-cm-long strip with immobilized nonlinear pH gradient of 3 to 10 (Immobiline DryStrip; GE Healthcare). Rehydration of the strips and the first IEF dimension electrophoresis were performed on an IPGphor unit (GE Healthcare) using the following settings: 12 h at 30 V (rehydration step), 1 h at 500 V, 1 h gradient from 500 V to 1,000 V, 1 h gradient from 1,000 V to 3,000 V, 2 h gradient from 3,000 V to 8,000 V, and 5 h at 8,000 V. After IEF, strips were incubated for 15 min in an equilibration buffer (6 M urea, 2% (w/v) SDS, 26% (v/v) glycerol, 65 mM DTT, 0.001% (w/v) bromophenol blue, and 50 mM Tris-HCl, pH 8.8) and then for 15 min in an equilibration buffer containing iodoacetamide (6 M urea, 2% (w/v) SDS, 26% (v/v) glycerol, 135 mM DTT, 0.001% (w/v) bromophenol blue, and 50mM Tris-HCl, pH8.8). The equilibrated strips were then loaded on top of a 12% (w/v) acrylamide gel. Following separation, gels were scanned using the Typhoon Trio Variable Mode Imager at a resolution of 100 (pixel size) with the photomultiplier tube set to 500 V. Proteins were processed (quantification) using the DeCyder 2-D Differential Analysis software version 6.5 (GE Healthcare). In order to get statistical significance from these experiments, three sets of proteins from three independent experiments were labeled and submitted to electrophoresis. Standard gels were also performed, and precipitation, IEF, and SDS-PAGE were run in parallel with labeled samples. These standard gels were loaded with a mix of 150 mg of each protein sample. After electrophoresis, proteins were visualized by colloidal Coomassie Brilliant Blue (G250) staining. The aim of the standard gel is to allow identification of proteins by excision gel spots followed by mass spectrometry.

Identification of Proteins by Liquid Chromatography-Tandem Mass Spectrometry

Protein spots were excised from the gel and subjected to tryptic digestion following the standard protocol from (Shevchenko et al., 1996). Prior LC MS/MS analysis the samples were desalted with C_{18} ZipTips (Millipore, Bedford, MA) following the manufacturer's instructions. The desalted samples were resuspended in 10 µl 2.5% acetonitrile and 0.5% TFA. The reversed phase separation of the peptides was performed on a nanoflow HPLC (Proxeon Biosystems, Odense, Denmark) using a Chromolith® CapRod® RP-18e 150-0.2 (Millipore, Darmstadt, Germany) column. A binary solvent system (solution A: 0.5% acetic acid, 5% isopropanol, solution B: 0.5% acetic acid, 5% isopropanol, 80% acetonitrile) was used for separation of the peptides in a 30 min linear gradient (95–40% A, followed by a final peptide elution step for 5 min at 20% A). The HPLC was coupled via a nano ESI ion source to a high resolution Orbitrap hybrid mass spectrometer (LTQ-Orbitrap, Thermo Fisher Scientific, San Jose, CA). The spectral acquisition for the full scan MS spectra was performed at a full-width half-maximum resolution of 30,000 in the Orbitrap section of the MS, while the data dependent MS/MS, with up to five spectra per preceding full scan, were obtained in the linear ion trap of the LTQ. Database search was performed by Mascot 2.4 (Matrix Science Ltd., London, UK) with the criteria as follows: *Arabidopsis* protein database (TAIR10 protein DB, version September 2012); proteolytic enzyme: trypsin allowing up to one missed cleavage; maximal precursor and fragment ion errors: 10 ppm and 0.8 Da. As modifications: fixed: Carbamidomethylation of cysteine; variable: oxidation of methionine. We set the threshold for identification to three different peptides and a score for the protein above 100.

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