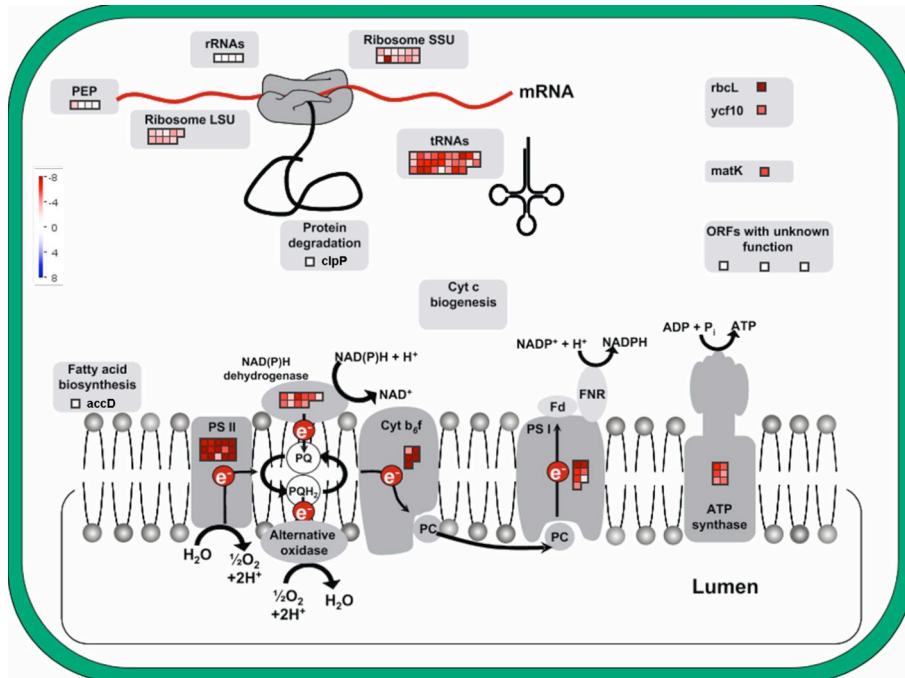


A



B

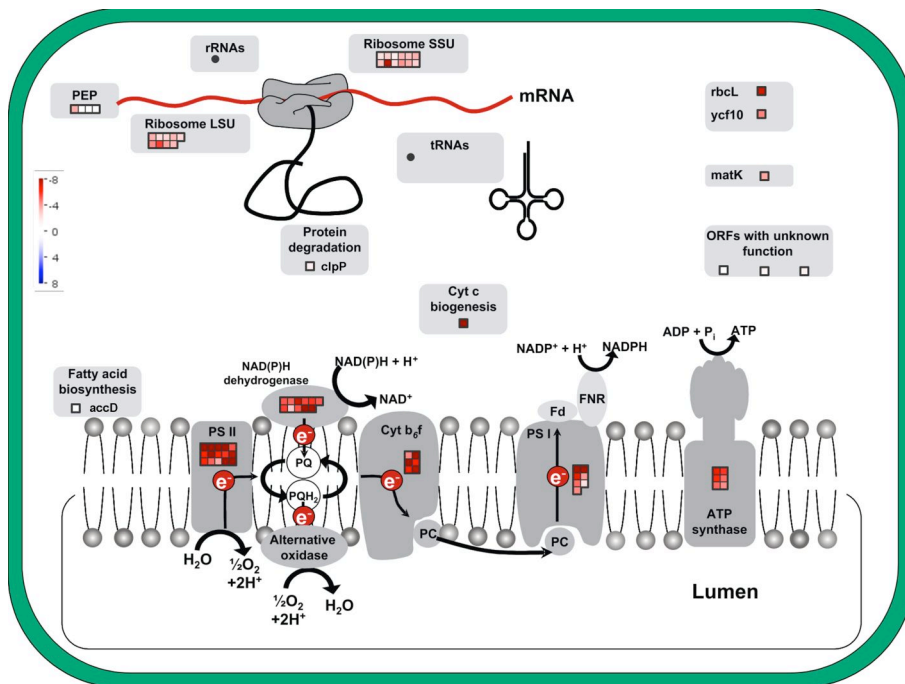


Figure S1. Graphical presentation of results from array experiments using the MapMan software (Thimm et al., 2004). Red and blue colors indicate down- and up-regulation of gene expression. For each gene, expression is displayed in log₂ tuber/leaf signal ratio. A, Oligo array hybridizations with Cy3-labeled total RNA from potato tubers and leaves. B, Oligo array hybridizations with Cy3-labeled polysome-associated mRNA from potato tubers and leaves.

Table S1. Data from microarray analysis with total RNA. Results are ranked according to gene function and decreasing log₂ Tuber/Leaf value.

Gene	Group	Complexes (code) ^a	Operons (code) ^b	Average Leaf ^c	Average Tuber ^c	Log ₂ T/L	Significance FDR Test ^d
<i>psbN</i>	Photosynthesis	PSII (1)	-	1323,65	127,61	-3,37	*
<i>psbJ</i>	Photosynthesis	PSII (1)	2	1040,57	25,78	-5,34	*
<i>psbH</i>	Photosynthesis	PSII (1)	3	3360,02	20,76	-7,34	*
<i>psbB</i>	Photosynthesis	PSII (1)	3	3324,20	19,53	-7,41	*
<i>psbL</i>	Photosynthesis	PSII (1)	2	3473,34	19,54	-7,47	*
<i>psbA</i>	Photosynthesis	PSII (1)	-	26943,89	146,18	-7,53	*
<i>psbZ</i>	Photosynthesis	PSII (1)	1	5742,05	23,57	-7,93	*
<i>psbK</i>	Photosynthesis	PSII (1)	7	4463,10	16,66	-8,07	*
<i>psbI</i>	Photosynthesis	PSII (1)	7	2661,86	8,45	-8,30	*
<i>psbC</i>	Photosynthesis	PSII (1)	1	9349,12	18,23	-9,00	*
<i>psbF</i>	Photosynthesis	PSII (1)	2	3456,84	5,62	-9,27	*
<i>psbT</i>	Photosynthesis	PSII (1)	3	3404,68	4,79	-9,47	*
<i>psbD</i>	Photosynthesis	PSII (1)	1	8586,41	11,75	-9,51	*
<i>psbM</i>	Photosynthesis	PSII (1)	-	2546,98	3,31	-9,59	*
<i>psbE</i>	Photosynthesis	PSII (1)	2	1632,90	1,36	-10,23	*
<i>ycf3</i>	Photosynthesis	PSI (2)	-	1191,01	274,48	-2,12	*
<i>ycf4</i>	Photosynthesis	PSI (2)	-	654,62	27,68	-4,56	*
<i>psaI</i>	Photosynthesis	PSI (2)	-	1906,80	47,32	-5,33	*
<i>psaJ</i>	Photosynthesis	PSI (2)	-	1483,35	20,28	-6,19	*
<i>psaC</i>	Photosynthesis	PSI (2)	5	4090,50	51,86	-6,30	*
<i>psaB</i>	Photosynthesis	PSI (2)	8	5012,74	24,48	-7,68	*
<i>psaA</i>	Photosynthesis	PSI (2)	8	3419,98	14,38	-7,89	*
<i>petA</i>	Photosynthesis	Cytb ₆ f (3)	-	615,66	34,63	-4,15	*
<i>petN</i>	Photosynthesis	Cytb ₆ f (3)	-	857,87	2,98	-8,17	*
<i>petG</i>	Photosynthesis	Cytb ₆ f (3)	-	4912,08	12,90	-8,57	*
<i>petD</i>	Photosynthesis	Cytb ₆ f (3)	3	5498,95	11,24	-8,93	*
<i>petB</i>	Photosynthesis	Cytb ₆ f (3)	3	6695,76	11,61	-9,17	*
<i>atpF</i>	Photosynthesis	ATPase (4)	9	1528,47	88,85	-4,10	*
<i>atpH</i>	Photosynthesis	ATPase (4)	9	2110,63	105,63	-4,32	*
<i>atpI</i>	Photosynthesis	ATPase (4)	9	1517,74	49,60	-4,94	*
<i>atpB</i>	Photosynthesis	ATPase (4)	4	454,87	11,51	-5,30	*
<i>atpE</i>	Photosynthesis	ATPase (4)	4	968,47	17,59	-5,78	*
<i>atpA</i>	Photosynthesis	ATPase (4)	9	864,48	9,98	-6,44	*
<i>ndhF</i>	Photosynthesis	NAD(P)H DH (5)	-	52,63	8,48	-2,63	*
<i>ndhH</i>	Photosynthesis	NAD(P)H DH (5)	5	257,98	31,57	-3,03	*
<i>ndhB</i>	Photosynthesis	NAD(P)H DH (5)	-	366,95	43,96	-3,06	*
<i>ndhK</i>	Photosynthesis	NAD(P)H DH (5)	6	331,86	16,28	-4,35	*
<i>ndhG</i>	Photosynthesis	NAD(P)H DH (5)	5	352,47	10,40	-5,08	*
<i>ndhA</i>	Photosynthesis	NAD(P)H DH (5)	5	1220,83	26,44	-5,53	*
<i>ndhE</i>	Photosynthesis	NAD(P)H DH (5)	5	1523,54	32,16	-5,57	*
<i>ndhD</i>	Photosynthesis	NAD(P)H DH (5)	5	512,14	10,55	-5,60	*
<i>ndhI</i>	Photosynthesis	NAD(P)H DH (5)	5	1895,56	37,68	-5,65	*
<i>ndhC</i>	Photosynthesis	NAD(P)H DH (5)	6	455,09	2,91	-7,29	*
<i>rbcL</i>	Photosynthesis	Rubisco (6)	-	22038,00	72,48	-8,25	*
<i>cemA</i>	Photosynthesis	Others (7)	-	476,46	13,92	-5,10	*
Average				3435.05	35.04	-6,46	
<i>trnV-GAC</i>	Genetic system	tRNA (9)	-	128,26	37,50	-1,77	*
<i>trnR-ACG</i>	Genetic system	tRNA (9)	-	515,12	92,23	-2,48	*
<i>trnI-CAU</i>	Genetic system	tRNA (9)	-	58,81	9,67	-2,61	*
<i>trnI-GAU</i>	Genetic system	tRNA (9)	13	1816,07	204,07	-3,15	*

Gene	Group	Complexes (code) ^a	Operons (code) ^b	Average Leaf ^c	Average Tuber ^c	Log ₂ T/L	Significance FDR Test ^d
<i>trnA-UGC</i>	Genetic system	tRNA (9)	13	1152,00	124,92	-3,21	*
<i>trnM-CAU</i>	Genetic system	tRNA (9)	-	219,30	16,31	-3,75	*
<i>trnV-UAC</i>	Genetic system	tRNA (9)	-	918,10	59,78	-3,94	*
<i>trnQ-UGG</i>	Genetic system	tRNA (9)	-	2615,63	122,28	-4,42	*
<i>trnD-GUC</i>	Genetic system	tRNA (9)	10	7111,00	318,43	-4,48	*
<i>trnG-GCC</i>	Genetic system	tRNA (9)	-	663,47	26,40	-4,65	*
<i>trnfM-CAU</i>	Genetic system	tRNA (9)	-	549,52	18,57	-4,89	*
<i>trnP-UGG</i>	Genetic system	tRNA (9)	-	996,36	31,54	-4,98	*
<i>trnS-GCU</i>	Genetic system	tRNA (9)	-	165,06	5,07	-5,02	*
<i>trnT-UGU</i>	Genetic system	tRNA (9)	-	208,89	6,42	-5,02	*
<i>trnS-GGA</i>	Genetic system	tRNA (9)	-	287,97	8,66	-5,05	*
<i>trnN-GUU</i>	Genetic system	tRNA (9)	-	3224,20	92,82	-5,12	*
<i>trnE-UUC</i>	Genetic system	tRNA (9)	10	2818,17	64,45	-5,45	*
<i>trnY-GUA</i>	Genetic system	tRNA (9)	10	1917,63	36,00	-5,74	*
<i>trnC-GCA</i>	Genetic system	tRNA (9)	-	805,37	14,37	-5,81	*
<i>trnK-UUU</i>	Genetic system	tRNA (9)	-	600,11	7,89	-6,25	*
<i>trnL-UAG</i>	Genetic system	tRNA (9)	-	34,68	0,42	-6,37	*
<i>trnF-GAA</i>	Genetic system	tRNA (9)	-	1726,73	19,79	-6,45	*
<i>trnH-GUG</i>	Genetic system	tRNA (9)	-	6557,67	72,87	-6,49	*
<i>trnL-CAA</i>	Genetic system	tRNA (9)	-	2653,32	28,06	-6,56	*
<i>trnL-UAA</i>	Genetic system	tRNA (9)	-	6981,68	62,73	-6,80	*
<i>trnW-CCA</i>	Genetic system	tRNA (9)	-	316,82	2,47	-7,00	*
<i>trnT-GGU</i>	Genetic system	tRNA (9)	-	2203,85	16,23	-7,09	*
<i>trnS-UGA</i>	Genetic system	tRNA (9)	-	217,58	1,33	-7,35	*
<i>trnG-UCC</i>	Genetic system	tRNA (9)	7	1013,12	5,72	-7,47	*
<i>rrn23</i>	Genetic system	rRNA (10)	13	47145,69	24261,17	-0,96	NS
<i>rrn16</i>	Genetic system	rRNA (10)	13	52077,14	25282,83	-1,04	NS
<i>rrn5</i>	Genetic system	rRNA (10)	13	40814,72	16139,08	-1,34	*
<i>rrn4.5</i>	Genetic system	rRNA (10)	13	48356,24	18222,87	-1,41	*
<i>rpl16</i>	Genetic system	Rpl (11)	11	219,83	58,68	-1,91	*
<i>rpl14</i>	Genetic system	Rpl (11)	11	125,30	20,89	-2,58	*
<i>rpl36</i>	Genetic system	Rpl (11)	-	342,48	47,42	-2,85	*
<i>rpl22</i>	Genetic system	Rpl (11)	11	188,79	23,99	-2,98	*
<i>rpl2</i>	Genetic system	Rpl (11)	11	476,00	54,74	-3,12	*
<i>rpl23</i>	Genetic system	Rpl (11)	11	135,35	12,21	-3,47	*
<i>rpl33</i>	Genetic system	Rpl (11)	-	204,54	17,11	-3,58	*
<i>rpl32</i>	Genetic system	Rpl (11)	-	297,34	20,96	-3,83	*
<i>rpl20</i>	Genetic system	Rpl (11)	-	135,21	8,30	-4,03	*
<i>rps3</i>	Genetic system	Rps (12)	11	171,21	39,68	-2,11	*
<i>rps12</i>	Genetic system	Rps (12)	-	477,47	107,42	-2,15	*
<i>rps4</i>	Genetic system	Rps (12)	-	104,25	23,23	-2,17	*
<i>rps7</i>	Genetic system	Rps (12)	-	350,20	68,67	-2,35	*
<i>rps15</i>	Genetic system	Rps (12)	-	118,26	13,68	-3,11	*
<i>rps19</i>	Genetic system	Rps (12)	11	199,88	22,56	-3,15	*
<i>rps8</i>	Genetic system	Rps (12)	11	156,90	15,92	-3,30	*
<i>rps11</i>	Genetic system	Rps (12)	11	193,87	18,13	-3,42	*
<i>rps2</i>	Genetic system	Rps (12)	9	251,85	21,15	-3,57	*
<i>rps16</i>	Genetic system	Rps (12)	-	889,86	63,33	-3,81	*
<i>rps18</i>	Genetic system	Rps (12)	-	250,27	11,54	-4,44	*
<i>rps14</i>	Genetic system	Rps (12)	8	3094,02	8,23	-8,55	*
<i>rpoB</i>	Genetic system	Rpo (13)	12	214,60	244,29	0,19	NS
<i>rpoC2</i>	Genetic system	Rpo (13)	12	25,89	11,66	-1,15	NS
<i>rpoC1</i>	Genetic system	Rpo (13)	12	64,84	20,39	-1,67	*

Gene	Group	Complexes (code) ^a	Operons (code) ^b	Average Leaf ^c	Average Tuber ^c	Log ₂ T/L	Significance FDR Test ^d
<i>rpoA</i>	Genetic system	Rpo (13)	11	100,49	13,20	-2,93	*
<i>clpP</i>	Genetic system	Clp (14)	-	709,75	356,83	-0,99	*
<i>matK</i>	Genetic system	MatK (15)	-	419,82	8,61	-5,61	*
Average				4113.14	1445.76	-3,95	
<i>accD</i>	Others	ACCCase (16)	-	118,86	38,40	-1,63	NS
<i>ycf2</i>	Others	<i>ycf (18)</i>	-	45,86	28,54	-0,68	NS
<i>ycf1</i>	Others	<i>ycf (17)</i>	-	31,37	17,73	-0,82	NS
<i>ycf15</i>	Others	<i>ycf (19)</i>	-	87,60	43,56	-1,01	*
Average				70.92	32.06	-1,04	
Average all genes				3684.86	811.48	-4.88	

^a PSII, photosystem II; PSI, photosystem I; Cytb₆f, cytochrome b₆f complex; ATPase, H⁺-ATP synthase; NAD(P)H DH, NADH dehydrogenase; Rubisco, Ribulose-1,5-bisphosphate carboxylase/oxygenase (Large subunit); Rpl, ribosomal proteins (large subunit); Rps, ribosomal proteins (small subunit); Rpo, plastid encoded polymerase (PEP) subunits; Clp, ATP-dependent protease (proteolytic subunit); MatK, MatK maturase; ACCCase, acetyl-CoA carboxylase (β subunit); *ycf*, hypothetical chloroplast reading frame. Codes as in Fig. 1b.

^b Operons deduced from tobacco data (Wakasugi et al. 1998). Codes as in Fig. 1c.

^c Normalized fluorescence units

^d *, significant with $\alpha=0.05$; NS, not significant (Benjamini and Hochberg 1995, Reiner et al. 2003)

Table S2. Data from microarray analysis with RNA from potato polysomes. Results are ranked according to gene function and decreasing log₂ Tuber/Leaf value.

Gene	Group	Complexes (code) ^a	Operons (code) ^b	Average Leaf ^c	Average Tuber ^c	Log ₂ T/L	Significance FDR Test ^d
<i>psbN</i>	Photosynthesis	PSII (1)	-	454,39	34,41	-3,72	NS
<i>psbM</i>	Photosynthesis	PSII (1)	-	657,58	18,73	-5,13	NS
<i>psbE</i>	Photosynthesis	PSII (1)	2	2789,68	66,18	-5,40	*
<i>psbJ</i>	Photosynthesis	PSII (1)	2	1178,37	19,26	-5,93	*
<i>psbL</i>	Photosynthesis	PSII (1)	2	7200,14	98,02	-6,20	*
<i>psbI</i>	Photosynthesis	PSII (1)	7	4100,30	49,64	-6,37	*
<i>psbF</i>	Photosynthesis	PSII (1)	2	5867,05	66,90	-6,45	*
<i>psbK</i>	Photosynthesis	PSII (1)	7	4277,04	21,09	-7,66	*
<i>psbA</i>	Photosynthesis	PSII (1)	-	61759,10	91,93	-9,39	*
<i>psbB</i>	Photosynthesis	PSII (1)	3	37675,27	54,60	-9,43	*
<i>psbH</i>	Photosynthesis	PSII (1)	3	28765,53	40,65	-9,47	*
<i>psbD</i>	Photosynthesis	PSII (1)	1	26373,45	27,25	-9,92	*
<i>psbC</i>	Photosynthesis	PSII (1)	1	17658,39	18,15	-9,93	*
<i>psbT</i>	Photosynthesis	PSII (1)	3	20043,97	17,93	-10,13	*
<i>psbZ</i>	Photosynthesis	PSII (1)	1	21047,87	7,05	-11,54	*
<i>ycf3</i>	Photosynthesis	PSI (2)	-	2237,32	490,60	-2,19	NS
<i>psaI</i>	Photosynthesis	PSI (2)	-	6914,70	413,78	-4,06	*
<i>ycf4</i>	Photosynthesis	PSI (2)	-	3350,36	159,77	-4,39	*
<i>psaJ</i>	Photosynthesis	PSI (2)	-	2359,78	74,89	-4,98	*
<i>psaC</i>	Photosynthesis	PSI (2)	5	3847,30	31,98	-6,91	*
<i>psaB</i>	Photosynthesis	PSI (2)	8	31763,63	127,72	-7,96	*
<i>psaA</i>	Photosynthesis	PSI (2)	8	39672,25	159,27	-7,96	*
<i>petA</i>	Photosynthesis	Cytb ₆ f (3)	-	5267,76	232,00	-4,50	*
<i>petG</i>	Photosynthesis	Cytb ₆ f (3)	-	15034,25	162,61	-6,53	*
<i>petL</i>	Photosynthesis	Cytb ₆ f (3)	-	4866,09	50,24	-6,60	*
<i>petN</i>	Photosynthesis	Cytb ₆ f (3)	-	588,81	2,75	-7,74	*
<i>petB</i>	Photosynthesis	Cytb ₆ f (3)	3	35038,34	141,02	-7,96	*
<i>petD</i>	Photosynthesis	Cytb ₆ f (3)	3	19428,00	56,36	-8,43	*
<i>atpI</i>	Photosynthesis	ATPase (4)	9	5954,79	295,74	-4,33	*
<i>atpF</i>	Photosynthesis	ATPase (4)	9	9254,09	295,26	-4,97	*
<i>atpH</i>	Photosynthesis	ATPase (4)	9	17446,69	515,74	-5,08	*
<i>atpB</i>	Photosynthesis	ATPase (4)	4	5404,69	90,63	-5,90	*
<i>atpE</i>	Photosynthesis	ATPase (4)	4	5041,46	69,94	-6,17	*
<i>atpA</i>	Photosynthesis	ATPase (4)	9	11890,75	109,16	-6,77	*
<i>ndhH</i>	Photosynthesis	NAD(P)H DH (5)	5	1867,11	235,38	-2,99	*
<i>ndhB</i>	Photosynthesis	NAD(P)H DH (5)	-	1059,28	32,06	-5,05	*
<i>ndhF</i>	Photosynthesis	NAD(P)H DH (5)	-	232,66	6,12	-5,25	*
<i>ndhA</i>	Photosynthesis	NAD(P)H DH (5)	5	5402,86	131,26	-5,36	*
<i>ndhI</i>	Photosynthesis	NAD(P)H DH (5)	5	6459,35	149,45	-5,43	*
<i>ndhD</i>	Photosynthesis	NAD(P)H DH (5)	5	937,36	19,60	-5,58	*
<i>ndhG</i>	Photosynthesis	NAD(P)H DH (5)	5	1743,73	32,36	-5,75	*
<i>ndhE</i>	Photosynthesis	NAD(P)H DH (5)	5	2819,21	46,95	-5,91	*
<i>ndhC</i>	Photosynthesis	NAD(P)H DH (5)	6	3541,01	19,77	-7,48	*
<i>ndhJ</i>	Photosynthesis	NAD(P)H DH (5)	6	1500,97	4,50	-8,38	*
<i>ndhK</i>	Photosynthesis	NAD(P)H DH (5)	6	1527,14	0,68	-11,13	*
<i>rbcL</i>	Photosynthesis	Rubisco (6)	-	64120,67	387,62	-7,37	*
<i>cemA</i>	Photosynthesis	Others (7)	-	3436,97	145,91	-4,56	NS
<i>ccsA</i>	Photosynthesis	Others (8)	-	466,86	0,61	-9,58	*
Average				11673,42	110,91	-6,67	
<i>rpl14</i>	Genetic system	Rpl (11)	11	1313,26	260,98	-2,33	*

Gene	Group	Complexes (code) ^a	Operons (code) ^b	Average Leaf ^c	Average Tuber ^c	Log ₂ T/L	Significance FDR Test ^d
<i>rpl22</i>	Genetic system	Rpl (11)	11	1012,03	167,96	-2,59	*
<i>rpl16</i>	Genetic system	Rpl (11)	11	3362,80	552,21	-2,61	NS
<i>rpl36</i>	Genetic system	Rpl (11)	-	2987,15	289,76	-3,37	*
<i>rpl20</i>	Genetic system	Rpl (11)	-	1335,90	122,87	-3,44	*
<i>rpl2</i>	Genetic system	Rpl (11)	11	4841,60	397,70	-3,61	*
<i>rpl33</i>	Genetic system	Rpl (11)	-	1259,89	86,22	-3,87	NS
<i>rpl23</i>	Genetic system	Rpl (11)	11	1580,93	74,75	-4,40	*
<i>rpl32</i>	Genetic system	Rpl (11)	-	246,71	4,66	-5,73	*
<i>rps4</i>	Genetic system	Rps (12)	-	525,02	153,33	-1,78	NS
<i>rps2</i>	Genetic system	Rps (12)	9	2415,72	531,89	-2,18	NS
<i>rps15</i>	Genetic system	Rps (12)	-	1111,98	197,89	-2,49	NS
<i>rps19</i>	Genetic system	Rps (12)	11	2789,34	409,05	-2,77	*
<i>rps3</i>	Genetic system	Rps (12)	11	2842,96	409,08	-2,80	*
<i>rps12</i>	Genetic system	Rps (12)	-	2967,59	348,05	-3,09	*
<i>rps8</i>	Genetic system	Rps (12)	11	1924,71	214,54	-3,17	*
<i>rps7</i>	Genetic system	Rps (12)	-	1316,83	123,48	-3,41	*
<i>rps11</i>	Genetic system	Rps (12)	11	1372,87	114,89	-3,58	*
<i>rps18</i>	Genetic system	Rps (12)	-	549,61	44,95	-3,61	*
<i>rps16</i>	Genetic system	Rps (12)	-	329,40	18,19	-4,18	*
<i>rps14</i>	Genetic system	Rps (12)	8	5934,88	27,28	-7,76	*
<i>rpoC2</i>	Genetic system	Rpo (13)	12	149,56	267,38	0,84	NS
<i>rpoC1</i>	Genetic system	Rpo (13)	12	318,23	372,45	0,23	NS
<i>rpoB</i>	Genetic system	Rpo (13)	12	404,89	454,15	0,17	NS
<i>rpoA</i>	Genetic system	Rpo (13)	11	741,03	58,16	-3,67	*
<i>clpP</i>	Genetic system	Clp (14)	-	1501,68	452,82	-1,73	NS
<i>matK</i>	Genetic system	MatK (15)	-	717,20	50,07	-3,84	NS
Average				1698,29	229,81	-2,99	
<i>accD</i>	Others	ACCCase (16)	-	1292,08	862,64	-0,58	NS
<i>ycf1</i>	Others	<i>ycf (17)</i>	-	126,48	132,96	0,07	NS
<i>ycf2</i>	Others	<i>ycf (18)</i>	-	273,81	114,09	-1,26	NS
<i>ycf15</i>	Others	<i>ycf (19)</i>	-	147,58	51,59	-1,52	NS
Average				459,99	290,32	-0,82	
Average all genes				7696,43	160,63	-5,11	

^a PSII, photosystem II; PSI, photosystem I; Cytb₆f, cytochrome b₆f complex; ATPase, H⁺-ATP synthase; NAD(P)H DH, NAD(P)H dehydrogenase; Rubisco, Ribulose-1,5-bisphosphate carboxylase/oxygenase (Large subunit); Rpl, ribosomal proteins (large subunit); Rps, ribosomal proteins (small subunit); Rpo, plastid encoded polymerase (PEP) subunits; Clp, ATP-dependent protease (proteolytic subunit); MatK, MatK maturase; ACCCase, acetyl-CoA carboxylase (β subunit); *ycf*, hypothetical chloroplast reading frame. Codes as in Fig. 7b.

^b Operons deduced from tobacco data (Wakasugi et al. 1998). Codes as in Fig. 7c.

^c Normalized fluorescence units

^d *, significant with α=0.05; NS, not significant (Bejamini and Hochberg 1995, Reiner et al. 2003)

Table S3. List of primers used for different analyses.

Sequence ^a	Forward primer	Reverse primer	Use
<i>ndhB-A</i>	5'-TTGGCCTAATTCTTCTTCTG	5'-GCTTGAACCCAATTCTACG	northern
<i>psbD</i>	5'-GTAGGCTGGTCCGGTCTATTGC	5'-AGGTTTTTCATGAGGCTGATCT	northern
<i>rps16-A</i>	5'-AGCCGTCTATCGAATCGTTGCA	5'-TTAATTGAATTTTCGGTTGATTA	northern
<i>accD</i>	5'-TGGATTTAGGGGCGAAGATC	5'-GGGTGATTTTCTCTCCGACT	northern; run-on
<i>clpP-A</i>	5'-AACCGACTTTATCGAGAAAGA	5'-GGGAATGCTATACGTTTGGT	northern; run-on
<i>psbA-A</i>	5'-ACGCGAAAGCGAAAGCCTATG	5'-AGATGGAGCTTCGATAGCAGC	northern; run-on
<i>rbcL-A</i>	5'-GGTAGCTGCGGAATCTTCTACTG	5'-TCCTGAAGCCTCAGGTAGAACAC	northern; run-on
<i>18S-A</i>	5'-TAGATAAAAGGTCGACGCGG	5'-CCCAAAGTCCAACACTACGAGC	northern
<i>Actin</i>	5'-TACAACGAACTTCGTGTTGCG	5'-GCATGTGGCAAAGCATATCC	Southern
<i>atpB</i>	5'-CCAATTAATGTGGCTTGTGAGGT	5'-AGGGCAGTCAAACCAACTCTCAT	run-on
<i>atpH</i>	5'-TTAAACAAAAGGATTTGCAA	5'-ATGAATCCACTGATTTCCGC	run-on
<i>matK</i>	5'-TCCACAGATATTTACAGCCA	5'-TCCGACTTCTATATACTCCC	run-on
<i>ndhG</i>	5'-TATTGACGAGCTACAGCAATTGC	5'-ATGGATTTATCTGAACCAATACA	run-on
<i>ndhI</i>	5'-TGACATTGGTAAGCGACCCA	5'-GTCAACAAAACAATACGAGCC	run-on
<i>petA</i>	5'-GGCTAAAGAAACAGATTACTCGATC	5'-TCGGAAAACAAGAAGTTCTGGTCCGG	run-on
<i>petN</i>	5'-CGTTCTTTTTGACTCTGCGC	5'-CTAGAGTCCACTCCTTCCCC	run-on
<i>psaA</i>	5'-ACATTTCCGGTCAACTCTCCATCA	5'-CACGAAAAGTAAGAAAGTCCGCA	run-on
<i>psbC</i>	5'-GTGACCAAGAAACCACAGGT	5'-GCTTGAGAAGCTTCTGGTCC	run-on
<i>psbZ</i>	5'-GACTCTTGCTTTCCAATTGG	5'-TCAAGAGATGAGAGAATTAAGG	run-on
<i>rpoB</i>	5'-TGTATCCGCGGGATTAATTTGGA	5'-ATCAAGGTTTCAGTCTTCGGTTCA	run-on
<i>rpoC1-A</i>	5'-TGTATAGCTTCTTCGATTTT	5'-GGATTGCCTCGTGAAATAGC	run-on
<i>rpoC1-B</i>	5'-TCGCAGTATACTAGGCCTTC	5'-ATGAATAATAATTTTCTTC	run-on
<i>rpoC2-A</i>	5'-GTGGTGGAAACAAAATATCTC	5'-GTGATACGATCAGCTAAGCC	run-on
<i>rpoC2-B</i>	5'-CGAATAGAGATTGGTTGTGC	5'-CACAAATAAGCGATAGACGG	run-on
<i>rps14</i>	5'-CGCCCCTCCACCCTATCTGTA	5'-CTTCTATTTCTACATCTAGGATTC	run-on
<i>rps2</i>	5'-GAACGACCCTCACAAATTGC	5'-ATATTGGAACATAAATTTGG	run-on
<i>rps3</i>	5'-ACTTGCTTCAGACTGGGTAC	5'-TGTAGGGGAACCTGCCTTC	run-on
<i>rps4</i>	5'-TTAAGTCTGACGAGAATAAT	5'-ATGTCGCGTTACCGAGGACC	run-on
<i>rrn16-A</i>	5'-GCAATAGCTTACCAAGCGCATGA	5'-TTCATTCTTGCGAACGTACTCCC	run-on
<i>rrn23</i>	5'-ATCCGGAGATTCCCGAATAG	5'-GGTAGTCCGCATCTTCACAG	run-on
<i>ycf1</i>	5'-CTCACCTTACAGAGACAGGC	5'-CCCATTGTTGGTCCAATTCGGTG	run-on
<i>ycf2-A</i>	5'-ACCCAATTC AATTCAGTGGG	5'-TTCGAACCCAGATGAAGTTC	run-on
<i>ycf2-B</i>	5'-TCGACAGGGTACAAATATCT	5'-GGATCGTCCAGTTCCTATAG	run-on
<i>ycf3-A</i>	5'-GGATGTCGGCTCAATCCGAA	5'-GTAATGACAGATCACGGCCA	run-on
<i>ycf3-B</i>	5'-GGATAGATCCATGAGAAATCTG	5'-CGAAACGTCTCGTGATCTTC	run-on
<i>atpF</i>	5'-AGTGTAGTGCTTGGTGTATTG	5'-GTTATTTCTTTTCATTGTTCCC	RT-PCR
<i>rpl16</i>	5'-GATATAATTGCTATGCTTAGT	5'-AGGCATTTTAGATGCTGCTAGTG	RT-PCR
<i>rps16-B</i>	5'-CGTTTGAAACGATGTGGTAG	5'-ACAGTTTCTGTAGGTTGAGCCC	RT-PCR
<i>ndhB-B</i>	5'-TGTACGGTCTAATGAGGCTACT	5'-TGGCCTATGGACGAATATGCAA	RT-PCR; editing
<i>ndhB-C</i>	5'-TGCTTCTCTTCGATGGAAG		editing
<i>ndhB-D</i>	5'-AAGCCTTTCATTTGCTTCTC		editing
<i>ndhB-E</i>	5'-GGCTATCCTGAGCAATTGCA		editing
<i>ndhB-F</i>	5'-CCCTCACGTGCGAAATTATAG		editing
<i>ndhD-A</i>	5'-CATATGGGAGACAGAGGAATAGG		editing
<i>ndhD-B</i>	5'-TACCGACAAACCTGTGCTCGAAA		editing
<i>clpP-B</i>	5'-GAACTTTTGGAACACCAATAGGCAT		primer extension
<i>rbcL-B</i>	5'-ACTTGCTT IAGTCTCTGTTTGTGGTGACAT		primer extension
<i>rrn16-B</i>	5'-AGTTGCATTACTTAGAGC		primer extension
<i>18S-B</i>	5'-GGGCATTCGTATTT CATAGTCAGAG	5'-CGGTTCTTGATTAATGAAAACATCCT	qRT-PCR
<i>caf1</i>	5'-GCGCTTCGATTCTGTCTTA	5'-TGAAGGAGTGCCAACGGATT	qRT-PCR
<i>caf2</i>	5'-GGCCTGGGAAGTTGGATAGAG	5'-CTTCCGGTGACCCCACTTTT	qRT-PCR
<i>crr2</i>	5'-GATCGAACCAACTCAAGAGCATT	5'-CCAGACAGATGCATTAGCTTCAA	qRT-PCR
<i>crs1</i>	5'-GCAGACAAGTTGCTGGAAGGA	5'-TCGATAGGCAGTGGCTCACA	qRT-PCR
<i>crs2</i>	5'-TTATTGCCAAAAGGTGGTCATG	5'-TGGAAAATCACGGTTCCTTTA	qRT-PCR
<i>ef1</i>	5'-ATTGGAAACGGATATGCTCCA	5'-TCCTTACCTGAACGCCTGTCA	qRT-PCR
<i>EF-Tu</i>	5'-TGCCCTGGTCACGCTGATT	5'-TCTGCGGCATTGGACCAT	qRT-PCR
<i>GLK</i>	5'-GGCACCTCCAATGCCTCAT	5'-AGGAGCCCATGCTGGTGAT	qRT-PCR
<i>hcf152</i>	5'-TAAACAGAGGTGCGGAATGG	5'-TCCTTCATCAGGTTCCAATGG	qRT-PCR
<i>IF3</i>	5'-CTTCCATTTTGGGCTTCGA	5'-CGTATCGGGCGGAGATAGTG	qRT-PCR
<i>ndhH</i>	5'-CCCTTCTCGTTGCCATTGAA	5'-AATGCTACGAGCTTCCGGAAT	qRT-PCR
<i>pgr3</i>	5'-CGGGCGATTGATTTATTGGA	5'-CAGAATGCATGAAGCAATGGA	qRT-PCR
<i>ppr2</i>	5'-TGCAGGTGAGGCAAAGCATA	5'-CCCCTGATGAGACAGCAAAG	qRT-PCR
<i>psbA-B</i>	5'-AGAGACGCGAAAGCGAAAG	5'-CTGGAGGAGCAGCAATGAA	qRT-PCR

Sequence^a	Forward primer	Reverse primer	Use
<i>RF2</i>	5'-CAGGTGGAAAGGGAGGTCAAA	5'-TCTGTACAGCGAACGGCTACA	qRT-PCR
<i>Rpl4</i>	5'-GGGCTCCACCACTCTCAATC	5'-TGGTGAGCCCACGATGAAC	qRT-PCR
<i>RpoTp</i>	5'-TGAGGTCCGGAAGCAGAGA	5'-GCATCCCTGCAAGCAACAG	qRT-PCR
<i>RRF</i>	5'-GCACCCCTGATGCAAGTTCT	5'-TGGCGTCATACCAACATCAGA	qRT-PCR
<i>Sig1</i>	5'-GGGCGCTCAAGGATGAAGTA	5'-CCTCCCAGGTAAGGCACTCA	qRT-PCR
<i>Sig2</i>	5'-CTCCAAGATCACTTGACCAGAA	5'-TTCTCCAGGTCCTGTCTCATGA	qRT-PCR
<i>Sig3</i>	5'-CTGAGAGTCGTTGGTTCAAT	5'-TGTCTTGCCTCATGACAGTT	qRT-PCR
<i>Sig4</i>	5'-AACAACCCGTGGCATGGA	5'-TCGCGTCCCTAAGAGTTGAA	qRT-PCR
<i>Sig5</i>	5'-AGCTACTCAGGCTTGCTCTT	5'-TCATGCTTCCGTACCATCTC	qRT-PCR
<i>Sig6</i>	5'-CCAAGGGAGAAGCAGGTTGTT	5'-ACGCCATTAACCTACCAATCT	qRT-PCR
<i>Why1</i>	5'-GGCACACTGCCGTAAATTCCT	5'-GCACCTGATCTTGGATTAGCAT	qRT-PCR

^a Different letters following the gene's name indicate different uses for the primers or different amplified regions

Table S4. GenBank accession numbers of selected nuclear genes and corresponding potato TIGR TA sequences used for qRT-PCR.

Gene	GenBank accession number	TIGR TA accession number
<i>GLK</i>	AY028368	TA41299_4113
<i>Sig1</i>	AB023572	TC128451
<i>Sig2</i>	At1g08540	TA41296_4113
<i>Sig3</i>	AB019944	TA42763_4113
<i>Sig4</i>	At5g13730	TA35865_4113
<i>Sig5</i>	At5g24120	TA42222_4113
<i>Sig6</i>	At2g36990	BE919893
<i>RpoTp</i>	AJ416570	TA45411_4113
<i>Rpl4</i>	AB010878	TA28304_4113
<i>crr2</i>	At3g46790	TA47528_4113
<i>hcf152</i>	At3g09650	BQ517191
<i>Why1</i>	AF233342	-
<i>crs1</i>	AF290414	BE922744
<i>crs2</i>	AF225708	TA35373_4113
<i>caf1</i>	AY264368	TA48769_4113
<i>caf2</i>	AY264369	CK863778
<i>pgr3</i>	At4g31850	BG594387
<i>ppr2</i>	AY278988	TA28412_4113
<i>IF3</i>	At4g30690	TA28082_4113
<i>EF-Tu</i>	M94204	TA27167_4113
<i>RF2</i>	AJ635428	DN922351
<i>RRF</i>	AJ133751	TA34759_4113

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