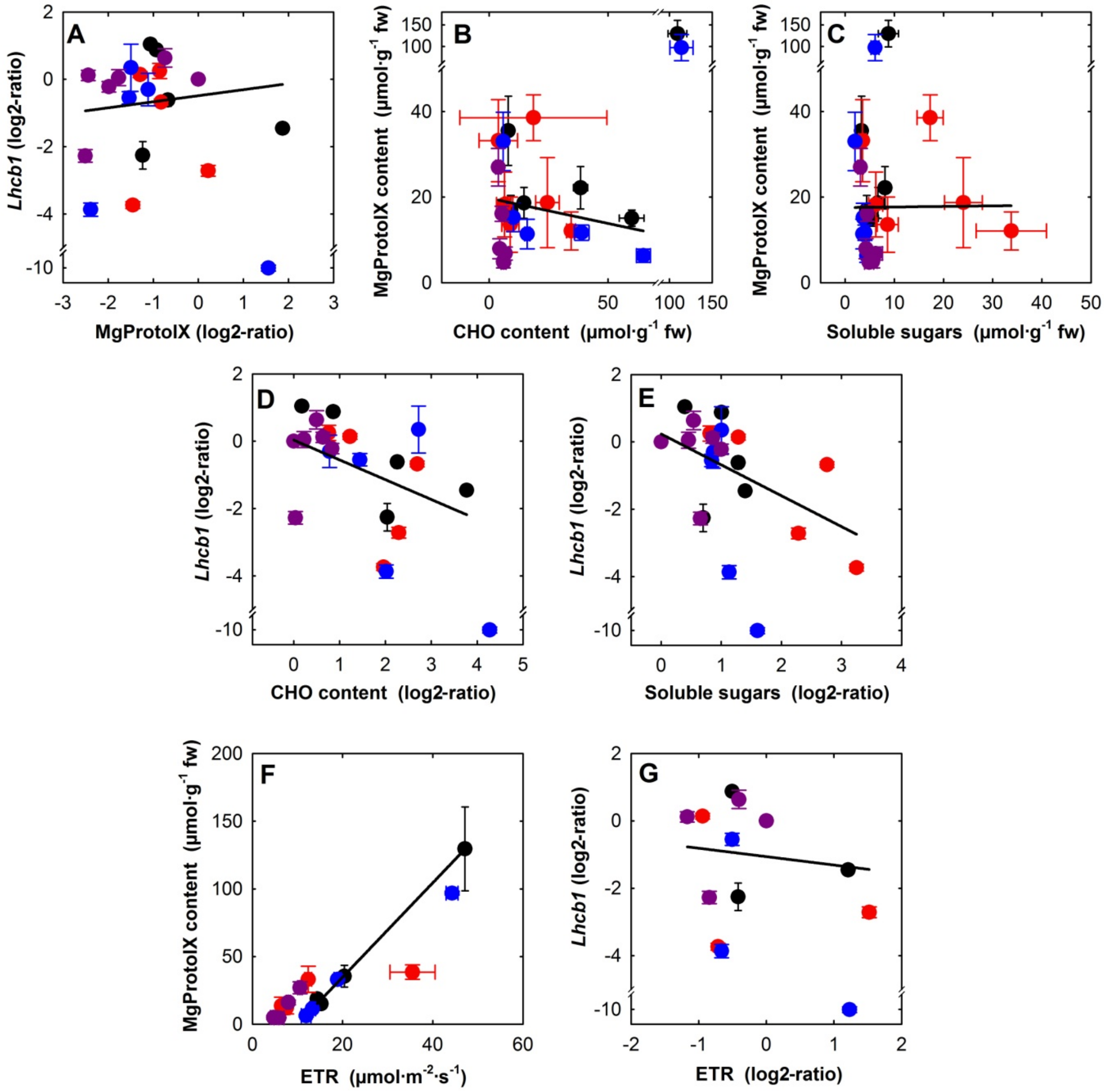
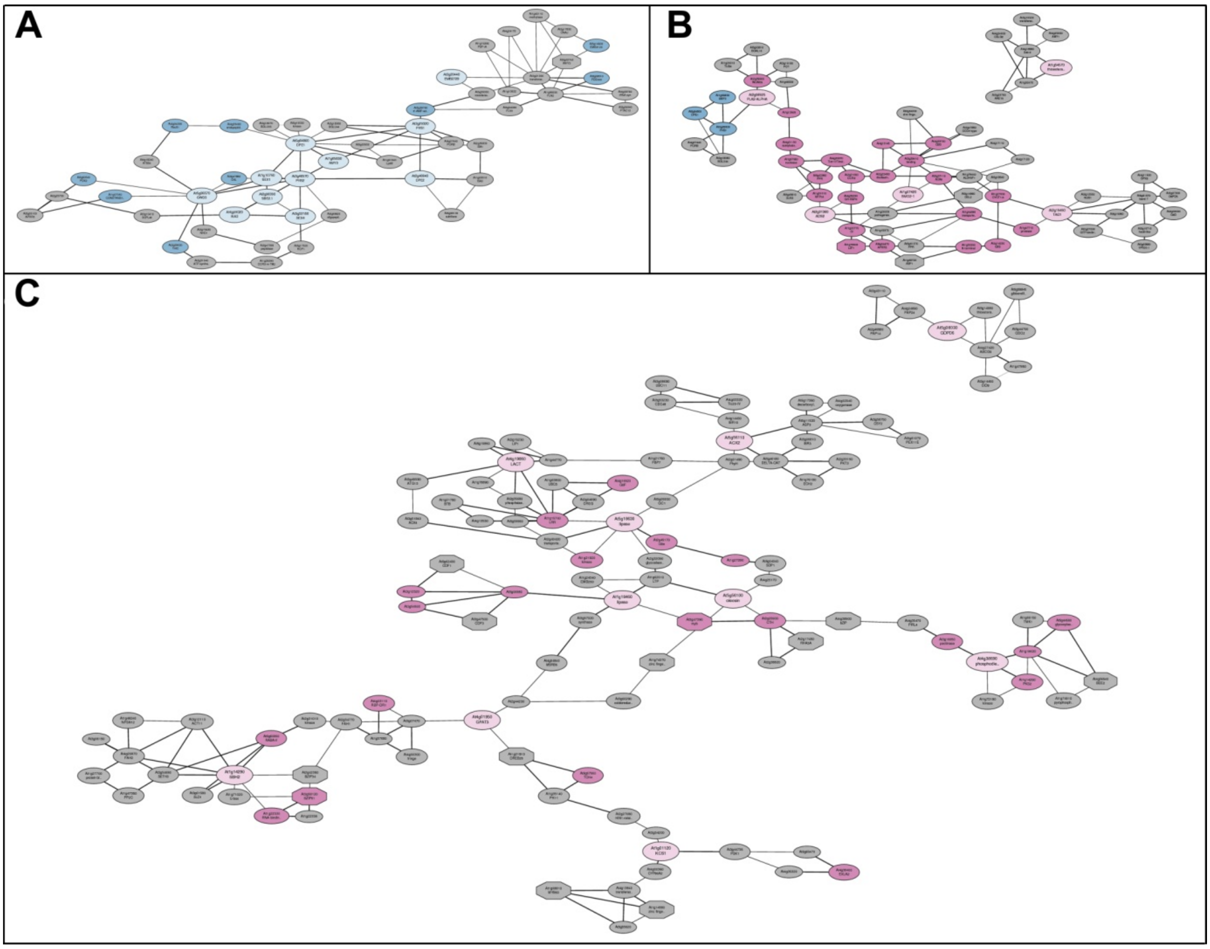
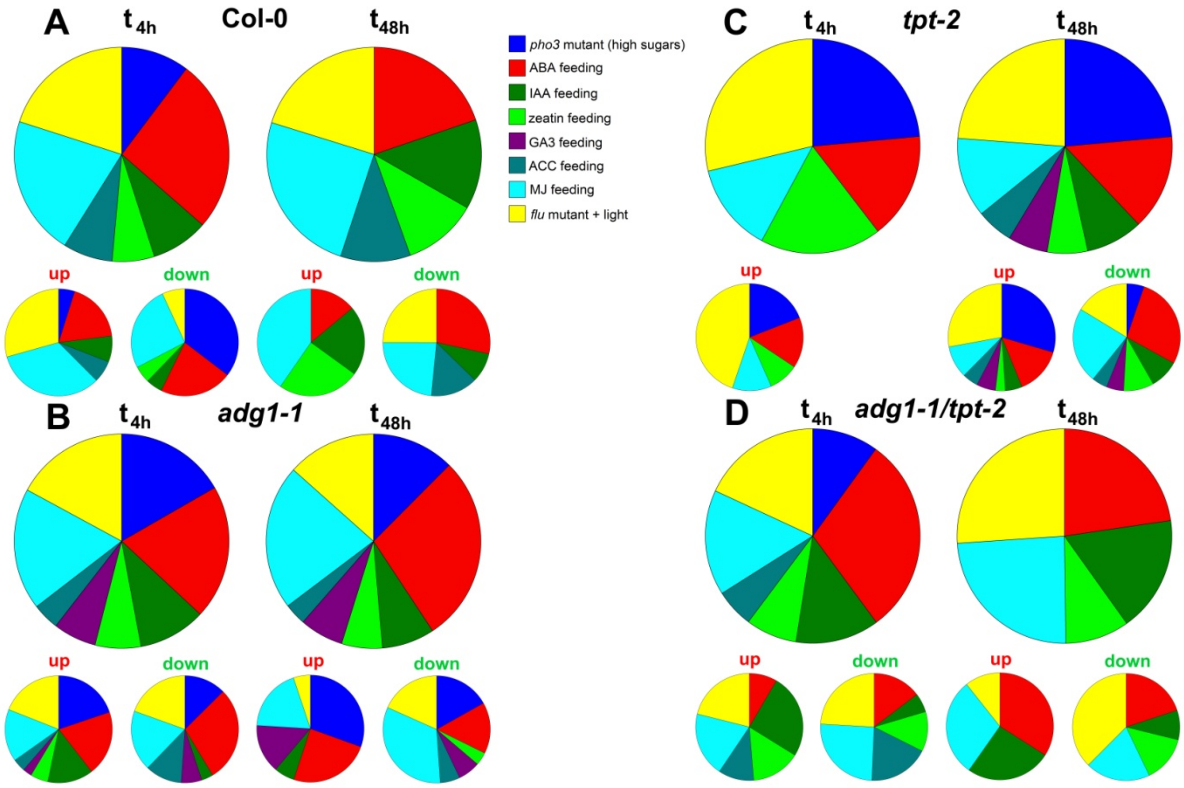


Supplementary Fig. S1. Correlation analyses of *Lhcb1* expression levels, ETR, as well as contents of MgProtoIX, soluble sugars and total carbohydrates. (**A**) *Lhcb1* expression *vs* MgProtoIX contents. MgProtoIX *vs* total carbohydrates (**B**), soluble sugars (**C**), or ETR (**F**). *Lhcb1* expression *vs s* total carbohydrates (**D**), soluble sugars (**E**), or ETR (**G**). The data were obtained from Figs. 1 to 3. Where necessary log2-ratios instead of absolute values were used. The colours represent Col-0 (black), *tpt-2* (blue), *adg1-1* (red) and *adg1-1/tpt-2* (dark purple).



Supplementary Fig. S2. Graphviz presentation of co-expression networks obtained with ATTEDII for data shown in Supplementary Table S7A and Supplementarty Document S3. The query genes were found amongst the commonly regulated genes 4h after LL/HL-transfer. `Query genes´ related to major CHO metabolism (up-regulated) (**A**), lipid metabolism up- (**B**) or down-regulated (**C**), are marked in light blue or purple colour, respectively. Co-expressed genes indentified as differentially regulated in the array experiment are marked in dark-blue or purple colour. All other genes within the co-expression network are marked in grey. The dark blue-coloured genes marked in (**B**) are associated with major CHO metabolism and were co-expressed with `query genes´ for lipid metabolism.



Supplementary Figure S3. Relative distribution of differentially regulated genes in publicly available microarray experiments compared to in-house expression data for Col-0 (**A**), *tpt-2* (**B**), *adg1-1* (**C**) and *adg1-1/tpt-2* at t_{4h} and t_{48h} after LL/HL-transfer.

Supplementary Table S11. Contents of metabolites determined by GC/MS in leaves of **(A)** Col-0, **(B)** *adg1-1*, **(C)** *tpt-2* and **(D)** *adg1-1/tpt-2* grown either continuously in LL or HL or after a LL/HL-transfer at t_{4h} or t_{48h}. The data represent the mean of five independent samples ± SE.

A

Metabolites	**Relative metabolite content (arbitrary units·g^{-1} fw)**			
Sugars	**Col-0 t_0 (LL)**	**Col-0 t_{4h}**	**Col-0 t_{48h}**	**Col-0 (HL)**
D-Sucrose	3.255 ± 0.062	6.083 ± 0.101	7.325 ± 0.124	6.776 ± 0.190
D-Glucose	0.532 ± 0.039	21.348 ± 0.680	12.206 ± 1.136	13.711± 1.251
D-Fructose	0.737 ± 0.042	16.803 ± 0.449	9.683 ± 1.846	12.775 ± 0.897
D-Mannose	0.146 ± 0.012	0.496 ± 0.044	0.967 ± 0.572	1.215 ± 0.104
D-Maltose	0.122 ± 0.007	0.250 ± 0.020	1.871 ± 0.255	0.519 ± 0.027
α,α'- D-Trehalose	0.247 ± 0.026	0.476 ± 0.030	4.097 ± 0.431	2.844 ± 0.169
Raffinose	0.073 ± 0.015	0.369 ± 0.061	0.197 ± 0.027	2.117 ± 0.527
1,6-anhydro, β-D-Glucose	6.101 ± 0.939	8.124 ± 1.125	14.672 ± 1.616	10.773 ± 1.493
1-O-methyl-, α-D-Mannopyranoside	3.525 ± 0.158	3.642 ± 0.375	9.498 ± 0.492	6.665 ± 0.309
DL-Fucose	0.815 ± 0.025	2.280 ± 0.199	3.359 ± 0.314	3.463 ± 0.180
D-Arabinose	0.852 ± 0.054	0.609 ± 0.026	1.350 ± 0.066	1.502 ± 0.113
Glucoheptose	0.105 ± 0.012	0.331 ± 0.031	0.518 ± 0.062	0.400 ± 0.011
Amino acids	**Col-0 t_0 (LL)**	**Col-0 t_{4h}**	**Col-0 t_{48h}**	**Col-0 (HL)**
DL-Glutamic acid	32.455 ± 1.864	124.727 ± 2.566	165.011 ± 2.397	39.409 ± 3.015
L-Aspartic acid	9.675 ± 0.164	9.138 ± 0.408	18.602 ± 1.704	6.243 ± 0.738
DL-Asparagine	n.d.	0.439 ± 0.167	3.457 ± 1.799	0.063 ± 0.007
DL-Alanine	1.700 ± 0.084	3.270 ± 0.615	5.075 ± 1.160	0.286 ± 0.039
Glycine	3.515 ± 0.228	144.514 ± 2.407	115.600 ± 1.315	14.483 ± 0.327
DL-Serine	10.116 ± 0.358	28.045 ± 0.745	54.533 ± 1.411	38.380 ± 0.840
DL-Threonine	12.512 ± 0.546	19.471 ± 0.774	31.469 ± 0.879	10.606 ±0.532
DL-Cysteine	0.611 ± 0.041	1.021 ± 0.138	2.313 ± 0.511	1.789 ± 0.212
DL-Methionine	0.168 ± 0.012	0.852 ± 0.077	0.823 ± 0.174	0.069 ± 0.014
L-Isoleucine	0.803 ± 0.014	3.146 ± 0.190	3.806 ± 0.259	3.342 ± 0.077
DL-Valine	3.195 ± 0.098	14.803 ± 0.463	16.162 ± 0.968	10.188 ± 0.458
L-Lysine	0.195 ± 0.009	0.509 ± 0.037	0.649 ± 0.082	0.361 ± 0.031
DL-Arginine, -NH3	0.082 ± 0.013	0.339 ± 0.022	0.826 ± 0.394	0.094 ± 0.008
DL-Phenylalanine	0.723 ± 0.042	9.609 ± 0.630	5.678 ± 1.749	2.007 ± 0.095
DL-Tyrosine	n.d.	0.430 ± 0.042	0.443 ± 0.123	0.151 ± 0.020
L-Tryptophan	0.440 ± 0.016	0.662 ± 0.052	0.778 ± 0.038	0.722 ± 0.027
L-Proline	7.164 ± 0.833	35.885 ± 1.733	60.061 ± 3.783	14.332 ± 2.103
β-Alanine	0.159 ± 0.011	0.785 ± 0.065	1.383 ± 0.121	0.704 ± 0.051

A (continued)

Organic acids	**Col-0 t_0 (LL)**	**Col-0 t_{4h}**	**Col-0 t_{48h}**	**Col-0 (HL)**
Pyruvic acid	0.610 ± 0.034	0.667 ± 0.061	0.967 ± 0.067	0.841 ± 0.048
2-methyl-DL-Malic acid	0.094 ± 0.007	0.338 ± 0.029	1.023 ± 0.028	0.516 ± 0.025
Glutaric acid	0.846 ± 0.058	1.611 ± 0.235	5.958 ± 0.397	4.389 ± 0.098
Succinic acid	0.667 ± 0.029	1.350 ± 0.114	6.427 ± 0.975	3.803 ± 0.257
Fumaric acid	106.355 ± 3.898	125.302 ± 1.852	111.554 ± 2.943	133.314 ± 2.247
Malonic acid	n.d.	0.197 ± 0.022	0.193 ± 0.022	0.124 ± 0.018
DL-Glyceric acid	0.581 ± 0.016	2.972 ± 0.359	3.602 ± 0.100	6.238 ± 0.211
3-hydroxy-Butyric acid	0.299 ± 0.017	0.399 ± 0.051	0.733 ± 0.069	0.436 ± 0.025
D-Gluconic acid or D-Galactonic acid	7.233 ± 0.486	11.108 ± 1.195	15.170 ± 1.927	20.526 ± 0.506
Benzoic acid	5.339 ± 0.149	6.958 ± 0.712	7.477 ± 0.391	6.589 ± 0.154

Miscellaneous	**Col-0 t_0 (LL)**	**Col-0 t_{4h}**	**Col-0 t_{48h}**	**Col-0 (HL)**
Glycerol	1.502 ± 0.067	2.968 ± 0.304	2.913 ± 0.140	3.985 ± 0.468
myo-Inositol	12.818 ± 0.580	19.915 ± 0.402	23.725 ± 1.369	26.920 ± 0.374
Galactinol	0.091 ± 0.012	0.571 ± 0.062	0.970 ± 0.174	4.876 ± 0.910
Erythritol	0.272 ± 0.012	0.730 ± 0.088	1.060 ± 0.073	0.821 ± 0.049
Tyramine	0.408 ± 0.013	0.797 ± 0.073	0.991 ± 0.154	1.452 ± 0.036
DL-Ornithine	0.601 ± 0.021	2.979 ± 0.132	5.020 ± 1.605	0.569 ± 0.098
Putrescine	1.086 ± 0.073	7.529 ± 0.641	10.936 ± 0.941	3.108 ± 0.486

B

Metabolites	**Relative metabolite content (arbitrary units·g^{-1} fw)**			
Sugars	***adg1-1* t_0 (LL)**	***adg1-1* t_{4h}**	***adg1-1* t_{48h}**	***adg1-1* (HL)**
D-Sucrose	5.662 ± 0.184	6.691 ± 0.061	7.080 ± 0.047	7.897 ± 0.118
D-Glucose	6.765 ± 0.528	25.970 ± 0.174	24.411 ± 0.440	26.822 ± 0.368
D-Fructose	10.905 ± 0.632	20.173 ± 0.213	19.711 ± 0.366	20.947 ± 0.336
D-Mannose	0.486 ± 0.017	1.116 ± 0.115	3.837 ± 0.181	1.859 ± 0.126
D-Maltose	n.d.	0.545 ± 0.030	0.517 ± 0.044	0.142 ± 0.012
α,α'- D-Trehalose	0.162 ± 0.013	0.437 ± 0.034	3.334 ± 0.229	1.476 ± 0.066
Raffinose	n.d.	0.168 ± 0.019	0.074 ± 0.007	0.111 ± 0.015
1,6-anhydro, β-D-Glucose	7.350 ± 0.730	16.062 ± 0.622	18.570 ± 1.735	22.615 ± 3.391
1-O-methyl-, α-D-Mannopyranoside	3.547 ± 0.333	1.722 ± 0.139	1.457 ± 0.031	2.071 ± 0.223
DL-Fucose	1.303 ± 0.034	2.939 ± 0.289	4.932 ± 0.199	4.252 ± 0.280
D-Arabinose	1.070 ± 0.032	0.654 ± 0.043	2.080 ± 0.205	2.795 ± 2.265
Glucoheptose	0.167 ± 0.010	0.444 ± 0.018	0.781 ± 0.033	0.529 ± 0.035
Amino acids	***adg1-1* t_0 (LL)**	***adg1-1* t_{4h}**	***adg1-1* t_{48h}**	***adg1-1* (HL)**
DL-Glutamic acid	29.829 ± 1.808	65.857 ± 5.493	176.494 ± 1.888	37.772 ± 1.714
L-Aspartic acid	7.341 ± 0.280	8.407 ± 0.426	13.491 ± 0.952	5.025 ± 0.400
DL-Asparagine	0.193 ± 0.056	0.062 ± 0.013	12.021 ± 1.145	0.273 ± 0.065
DL-Alanine	1.778 ± 0.095	2.735 ± 0.452	10.569 ± 1.408	1.272 ± 0.161
Glycine	4.776 ± 0.235	84.629 ± 3.231	116.061 ± 1.686	22.941 ± 1.590
DL-Serine	6.097 ± 0.222	23.157 ± 1.375	49.678 ± 1.476	25.879 ± 1.761
DL-Threonine	16.884 ± 0.636	21.588 ± 1.051	33.180 ± 1.800	20.370 ± 1.934
DL-Cysteine	0.941 ± 0.035	1.374 ± 0.136	4.577 ± 0.420	3.200 ± 0.250
DL-Methionine	0.137 ± 0.016	0.485 ± 0.058	0.532 ± 0.066	0.106 ± 0.011
L-Isoleucine	0.925 ± 0.025	2.984 ± 0.338	3.552 ± 0.203	2.962 ± 0.256
DL-Valine	3.308 ± 0.092	12.348 ± 0.903	19.391 ± 1.093	12.170 ± 0.954
L-Lysine	0.284 ± 0.011	0.635 ± 0.038	0.961 ± 0.082	0.534 ± 0.049
DL-Arginine, -NH3	0.074 ± 0.007	0.335 ± 0.037	2.837 ± 0.324	0.221 ± 0.023
DL-Phenylalanine	1.869 ± 0.039	12.419 ± 1.041	14.334 ± 0.922	3.100 ± 0.172
DL-Tyrosine	0.060 ± 0.003	0.428 ± 0.031	1.004 ± 0.085	0.250 ± 0.040
L-Tryptophan	0.334 ± 0.016	0.564 ± 0.018	0.638 ± 0.018	0.581 ± 0.029
L-Proline	4.014 ± 0.293	30.162 ± 2.257	67.997 ± 7.015	18.805 ± 2.639
β-Alanine	0.353 ± 0.022	0.585 ± 0.078	2.124 ± 0.108	0.855 ± 0.057

B (continued)

Organic acids	***adg1-1* t_0 (LL)**	***adg1-1* t_{4h}**	***adg1-1* t_{48h}**	***adg1-1* (HL)**
Pyruvic acid	0.527 ± 0.043	0.525 ± 0.043	0.870 ± 0.050	1.086 ± 0.061
2-Methyl-DL-malic acid	0.121 ± 0.009	0.357 ± 0.033	1.132 ± 0.064	0.616 ± 0.023
Glutaric acid	1.075 ± 0.026	1.827 ± 0.183	5.075 ± 0.333	3.033 ± 0.141
Succinic acid	1.045 ± 0.040	3.746 ± 0.427	13.658 ± 0.547	4.391 ± 0.164
Fumaric acid	136.964 ± 4.410	115.525 ± 1.695	98.817 ± 3.491	116.770 ± 2.312
Malonic acid	n.d.	0.105 ± 0.018	0.176 ± 0.034	0.069 ± 0.012
DL-Glyceric acid	0.395 ± 0.008	2.993 ± 0.358	4.656 ± 0.256	3.977 ± 0.216
3-hydroxy-Butyric acid	0.210 ± 0.015	0.335 ± 0.039	0.589 ± 0.067	0.331 ± 0.051
D-Gluconic acid or D-Galactonic acid	10.026 ± 0.467	12.481 ± 1.317	14.139 ± 2.164	14.509 ± 1.642
Benzoic acid	4.206 ± 0.339	6.773 ± 0.685	6.524 ± 0.305	7.034 ± 0.272
Miscellaneous	***adg1-1* t_0 (LL)**	***adg1-1* t_{4h}**	***adg1-1* t_{48h}**	***adg1-1* (HL)**
Glycerol	1.243 ± 0.024	2.197 ± 0.245	2.552 ± 0.047	4.424 ± 1.145
myo-Inositol	6.351 ± 0.345	13.788 ± 0.778	18.833 ± 0.741	16.165 ± 0.538
Galactinol	n.d.	0.310 ± 0.034	0.170 ± 0.015	0.473 ± 0.077
Tyramine	0.444 ± 0.020	0.938 ± 0.084	0.643 ± 0.111	0.877 ± 0.086
Erythritol	0.527 ± 0.039	1.070 ± 0.125	4.685 ± 0.379	1.436 ± 0.093
DL-Ornithine	1.059 ± 0.047	2.072 ± 0.244	11.812 ± 1.380	1.245 ± 0.135
Putrescine	2.931 ± 0.101	9.603 ± 1.257	36.145 ± 2.688	11.367 ± 1.118

C

Metabolites	**Relative metabolite content (arbitrary units·g^{-1} fw)**			
Sugars	***tpt-2*** **t_0 (LL)**	***tpt-2*** **t_{4h}**	***tpt-2*** **t_{48h}**	***tpt-2*** **(HL)**
D-Sucrose	3.386 ± 0.063	4.175 ± 0.157	7.152 ± 0.127	8.134 ± 0.248
D-Glucose	0.666 ± 0.044	3.189 ± 0.224	22.965 ± 0.685	16.006 ± 0.748
D-Fructose	0.913 ± 0.032	3.376 ± 0.236	17.424 ± 0.464	8.609 ± 0.564
D-Mannose	0.191 ± 0.017	0.462 ± 0.041	0.769 ± 0.030	0.562 ± 0.059
D-Maltose	0.886 ± 0.045	0.509 ± 0.055	10.976 ± 0.813	6.708 ± 0.954
α,α'- D-Trehalose	0.248 ± 0.016	0.314 ± 0.029	1.223 ± 0.126	0.838 ± 0.080
Raffinose	0.104 ± 0.010	0.350 ± 0.057	0.250 ± 0.022	0.139 ± 0.023
1,6-anhydro, β-D-Glucose	3.593 ± 0.493	9.476 ± 1.402	10.553 ± 0.445	14.375 ± 2.019
1-O-methyl-, α-D-Mannopyranoside	6.533 ± 0.223	7.662 ± 0.506	2.200 ± 0.164	5.778 ± 0.810
DL-Fucose	0.920 ± 0.054	1.963 ± 0.130	3.657 ± 0.173	2.427 ± 0.341
D-Arabinose	0.815 ± 0.096	0.723 ± 0.060	1.221 ± 0.092	2.577 ± 0.249
Glucoheptose	0.096 ± 0.022	0.325 ± 0.043	0.374 ± 0.056	0.222 ± 0.021
Amino acids	***tpt-2*** **t_0 (LL)**	***tpt-2*** **t_{4h}**	***tpt-2*** **t_{48h}**	***tpt-2*** **(HL)**
DL-Glutamic acid	53.294 ± 2.592	98.735 ± 6.497	169.430 ± 3.908	87.257 ± 9.739
L-Aspartic acid	12.935 ± 0.680	18.301 ± 1.220	19.163 ± 1.581	13.648 ± 1.869
DL-Asparagine	n.d.	0.045 ± 0.009	2.847 ± 0.382	0.820 ± 0.381
DL-Alanine	2.357 ± 0.057	3.526 ± 0.258	10.505 ± 0.598	3.275 ± 0.229
Glycine	4.407 ± 0.258	107.478 ± 1.701	109.623 ± 2.306	80.016 ± 3.368
DL-Serine	15.969 ± 0.706	65.008 ± 0.910	66.137 ± 1.239	63.031 ± 1.454
DL-Threonine	15.830 ± 0.973	42.280 ± 1.347	39.311 ± 1.212	44.857 ± 1.726
DL-Cysteine	0.558 ± 0.064	1.255 ± 0.155	2.019 ± 0.116	2.007 ± 0.316
DL-Methionine	0.238 ± 0.023	1.074 ± 0.155	0.782 ± 0.117	0.328 ± 0.061
L-Isoleucine	1.038 ± 0.041	3.647 ± 0.383	4.447 ± 0.150	3.851 ± 0.326
DL-Valine	4.621 ± 0.156	15.562 ± 1.432	24.076 ± 1.064	17.124 ± 1.605
L-Lysine	0.242 ± 0.017	0.488 ± 0.071	0.617 ± 0.033	0.637 ± 0.063
DL-Arginine, -NH3	0.128 ± 0.019	0.256 ± 0.039	0.677 ± 0.032	0.286 ± 0.055
DL-Phenylalanine	0.911 ± 0.037	3.588 ± 0.331	5.816 ± 0.289	3.486 ± 0.489
DL-Tyrosine	n.d.	0.102 ± 0.024	0.493 ± 0.021	0.229 ± 0.028
L-Tryptophan	0.492 ± 0.030	0.644 ± 0.044	0.731 ± 0.029	0.554 ± 0.033
L-Proline	6.839 ± 0.425	70.172 ± 4.469	42.499 ± 4.535	70.521 ± 5.587
β-Alanine	0.187 ± 0.008	0.862 ± 0.083	1.800 ± 0.092	1.360 ± 0.134

C (continued)

Organic acids	***tpt-2*** **t_0 (LL)**	***tpt-2*** **t_{4h}**	***tpt-2*** **t_{48h}**	***tpt-2*** **(HL)**
Pyruvic acid	0.794 ± 0.059	1.637 ± 0.176	1.069 ± 0.037	1.612 ± 0.190
2-Methyl-DL-malic acid	0.166 ± 0.007	0.416 ± 0.017	1.213 ± 0.043	0.557 ±0.050
Glutaric acid	0.947 ± 0.045	1.632 ± 0.126	5.024 ± 0.269	2.771 ± 0.353
Succinic acid	1.447 ± 0.058	3.816 ± 0.270	10.514 ± 0.443	8.221 ± 0.919
Fumaric acid	117.778 ± 3.673	101.630 ± 2.485	91.506 ± 2.352	112.648 ± 3.501
Malonic acid	n.d.	0.207 ± 0.020	0.204 ± 0.015	0.247 ± 0.153
DL-Glyceric acid	0.804 ± 0.038	7.920 ± 0.485	8.878 ± 0.388	7.281 ± 0.698
3-hydroxy-Butyric acid	0.408 ± 0.018	0.560 ± 0.037	0.794 ± 0.042	0.524 ± 0.069
D-Gluconic acid or D-Galactonic acid	7.160 ± 0.460	11.984 ± 1.322	14.063 ± 1.256	25.587 ±3.280
Benzoic acid	5.736 ± 0.143	7.487 ± 0.184	7.347 ± 0.295	8.712 ± 0.887

Miscellaneous	***tpt-2*** **t_0 (LL)**	***tpt-2*** **t_4**	***tpt-2*** **t_{48}**	***tpt-2*** **(HL)**
Glycerol	1.415 ± 0.048	2.790 ± 0.236	2.413 ± 0.127	3.547 ± 0.182
myo-Inositol	11.443 ± 0.722	18.019 ± 0.436	23.179 ± 0.533	15.782 ± 0.559
Galactinol	0.127 ± 0.013	1.549 ± 0.204	1.312 ± 0.123	0.413 ± 0.047
Tyramine	0.422 ± 0.032	0.679 ± 0.048	0.854 ± 0.086	1.120 ± 0.134
Erythritol	0.352 ± 0.031	0.779 ± 0.062	1.283 ± 0.067	1.287 ± 0.161
DL-Ornithine	0.708 ± 0.047	1.835 ± 0.304	4.192 ± 0.348	1.745 ± 0.218
Putrescine	1.140 ± 0.054	3.902 ± 0.345	16.551 ± 0.999	14.764 ± 1.628

D

Metabolites	**Relative metabolite content (arbitrary units·g^{-1} fw)**			
Sugars	***adg1-1/tpt-2*** **t_0 (LL)**	***adg1-1/tpt-2*** **t_{4h}**	***adg1-1/tpt-2*** **t_{48h}**	***adg1-1/tpt-2*** **(HL)**
D-Sucrose	3.790 ± 0.149	5.294 ± 0.073	5.928 ± 0.082	4.770 ± 0.186
D-Glucose	2.923 ± 0.439	13.410 ± 1.300	10.768± 0.736	5.729 ± 0.771
D-Fructose	3.924 ± 0.476	5.836 ± 0.473	8.440 ± 0.537	3.758 ± 0.287
D-Mannose	0.300 ± 0.017	0.737 ± 0.085	0.582 ± 0.012	0.353 ± 0.022
D-Maltose	n.d.	0.379 ± 0.043	0.205 ± 0.017	0.141 ± 0.034
α,α'- D-Trehalose	0.152 ± 0.019	0.178 ± 0.019	0.250 ± 0.026	0.759 ± 0.098
Raffinose	n.d.	0.137 ± 0.016	0.032 ± 0.003	n.d.
1,6-anhydro, β-D-Glucose	5.285 ± 1.062	14.692 ± 1.139	16.991 ± 1.032	6.848 ± 1.479
1-O-methyl-, α-D-Mannopyranoside	4.754 ± 0.185	4.072 ± 0.258	5.782 ± 0.318	3.755 ± 0.359
DL-Fucose	1.145 ± 0.042	2.504 ± 0.330	1.623 ± 0.038	1.152 ± 0.102
D-Arabinose	1.283 ± 0.081	0.891 ± 0.104	1.871 ± 0.101	1.404 ± 0.109
Glucoheptose	0.152 ± 0.014	0.314 ± 0.042	0.378 ± 0.019	0.137 ± 0.010
Amino acids	***adg1-1/tpt-2*** **t_0 (LL)**	***adg1-1/tpt-2*** **t_{4h}**	***adg1-1/tpt-2*** **t_{48h}**	***adg1-1/tpt-2*** **(HL)**
DL-Glutamic acid	35.303 ± 1.804	73.146 ± 5.631	70.013 ± 4.776	37.772 ± 4.500
L-Aspartic acid	10.986 ± 0.890	13.559 ± 0.590	15.069 ± 1.222	11.318 ± 1.376
DL-Asparagine	n.d.	0.030 ± 0.003	0.125 ± 0.032	0.505 ± 0.174
DL-Alanine	2.148 ± 0.188	5.947 ± 0.495	6.390 ± 0.614	0.950 ± 0.080
Glycine	2.523 ± 0.148	20.289 ± 1.631	7.615 ± 0.377	4.302 ± 0.255
DL-Serine	7.704 ± 0.517	19.015 ± 1.191	16.563 ± 0.494	14.933 ± 0.676
DL-Threonine	49.848 ± 0.911	68.305 ± 4.333	51.722 ± 2.373	72.887 ± 4.955
DL-Cysteine	0.791 ± 0.105	1.359 ± 0.183	2.691 ± 0.209	1.060 ± 0.156
DL-Methionine	0.125 ± 0.029	0.387 ± 0.070	0.269 ± 0.037	0.118 ± 0.018
L-Isoleucine	1.233 ± 0.052	3.347 ± 0.234	3.065 ± 0.178	2.165 ± 0.114
DL-Valine	4.867 ± 0.303	13.861 ± 0.900	12.719 ± 0.614	6.813 ± 0.446
L-Lysine	0.369 ± 0.019	0.604 ± 0.086	0.657 ± 0.029	0.523 ± 0.052
DL-Arginine, -NH3	0.092 ± 0.011	0.219 ± 0.026	0.194 ± 0.011	0.097 ± 0.010
DL-Phenylalanine	1.341 ± 0.115	3.051 ± 0.259	2.354 ± 0.112	1.095 ± 0.104
DL-Tyrosine	n.d.	0.092 ± 0.027	0.167 ± 0.018	0.121 ± 0.021
L-Tryptophan	0.482 ± 0.015	0.561 ± 0.041	0.632 ± 0.009	0.514 ± 0.037
L-Proline	6.943 ± 1.310	26.598 ± 1.854	22.410 ± 4.796	9.856 ± 1.323
β-Alanine	0.435 ± 0.016	0.614 ± 0.048	1.475 ± 0.046	1.003 ± 0.073

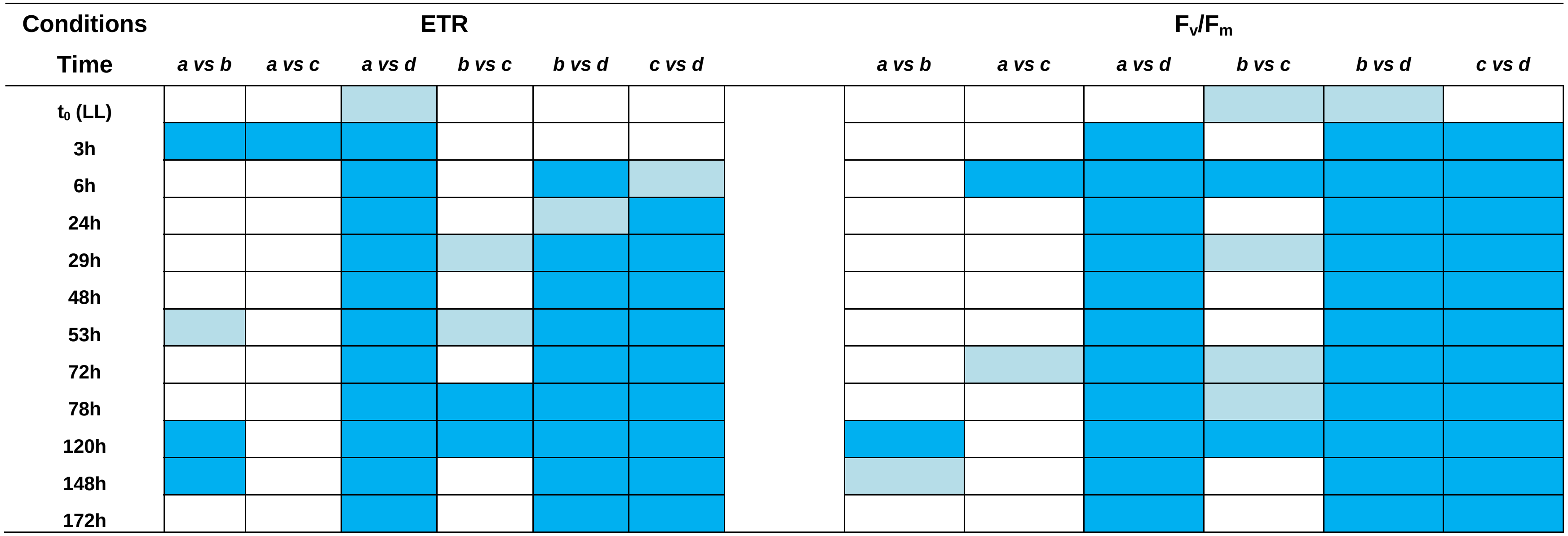
D (continued)

Organic acids	***adg1-1/tpt-2*** **t_0 (LL)**	***adg1-1/tpt-2*** **t_{4h}**	***adg1-1/tpt-2*** **t_{48h}**	***adg1-1/tpt-2*** **(HL)**
Pyruvic acid	0.623 ± 0.032	1.098 ± 0.066	1.085 ± 0.119	0.624 ± 0.024
2-Methyl-DL-malic acid	0.163 ± 0.017	0.380 ± 0.013	0.615 ± 0.021	0.164 ± 0.019
Glutaric acid	1.089 ± 0.039	1.516 ± 0.179	2.077 ± 0.054	1.113 ± 0.051
Succinic acid	1.055 ± 0.070	3.552 ± 0.184	2.543 ± 0.075	0.707 ± 0.050
Fumaric acid	96.776 ± 1.606	91.044 ± 1.664	85.786 ± 1.356	82.427 ± 10.166
Malonic acid	n.d.	0.141 ± 0.022	0.141 ± 0.008	0.077 ± 0.008
DL-Glyceric acid	0.401 ± 0.012	0.957 ± 0.103	0.897 ± 0.038	0.784 ± 0.056
3-hydroxy-Butyric acid	0.381 ± 0.024	0.502 ± 0.056	0.513 ± 0.020	0.308 ± 0.044
D-Gluconic acid or D-Galactonic acid	9.217 ± 0.680	15.217 ± 1.815	17.174 ± 0.751	11.413 ± 1.477
Benzoic acid	5.675 ± 0.215	5.329 ± 0.288	5.027 ± 0.070	5.944 ± 0.278

Miscellaneous	***adg1-1/tpt-2*** **t_0 (LL)**	***adg1-1/tpt-2*** **t_{4h}**	***adg1-1/tpt-2*** **t_{48h}**	***adg1-1/tpt-2*** **(HL)**
Glycerol	1.222 ± 0.125	2.269 ± 0.164	2.330 ± 0.194	10.105 ± 3.539
myo-Inositol	7.066 ± 0.155	13.693 ± 0.513	16.346 ± 0.444	6.161 ± 0.348
Galactinol	0.127 ± 0.028	0.459 ±0.059	0.166 ± 0.010	0.073 ± 0.013
Erythritol	0.886 ± 0.019	1.572 ± 0.086	1.794 ± 0.036	1.962 ± 0.211
Tyramine	0.527 ± 0.013	0.810 ± 0.116	0.688 ± 0.016	0.588 ± 0.034
DL-Ornithine	0.712 ± 0.057	0.945 ± 0.108	1.308 ± 0.085	1.252 ± 0.116
Putrescine	1.919 ± 0.123	6.920 ± 0.981	5.177 ± 0.385	5.953 ± 0.883

Supplementary Document S1

Document S1 (Table 1). Statistical analysis (ANOVA/Tukey-Kramer) of photosynthetic electron transport (ETR) and F_v/F_m ratios of wild-type and mutant plants in a time series after transfer from LL conditions (*i.e.* a PFD of 30 µmol·m^{-2}·s^{-1}) to HL (*i.e.* a PFD of 300 µmol·m^{-2}·s^{-1}) within 172 h. The plant lines are denoted, *a* = Col-0, *b* = *tpt-2*, *c* = *adg1-1*, *d* = *adg1-1/tpt-2.* Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.

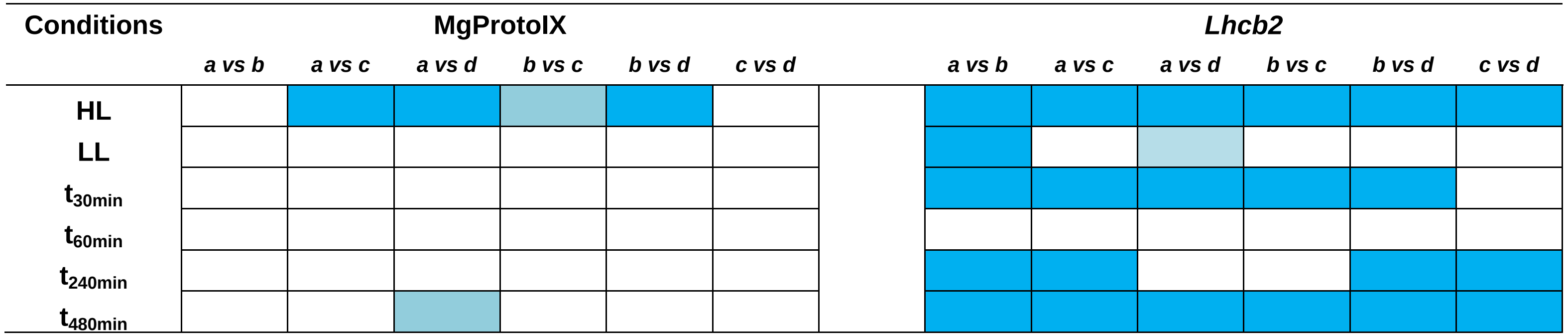


Conditions	**ETR**						**F_v/F_m**					
Time	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
t_0 (LL)			▨							▨	▨	
3h	■	■	■						■		■	■
6h			■		■	▨		■	■	■	■	■
24h			■		▨	■			■		■	■
29h			■	▨	■	■			■	▨	■	■
48h			■		■	■			■		■	■
53h	▨		■	▨	■	■			■		■	■
72h			■		■	■		▨	■	▨	■	■
78h			■	■	■	■			■	▨	■	■
120h	■		■	■	■	■	■		■	■	■	■
148h	■		■		■	■	▨		■		■	■
172h			■		■	■			■		■	■

Document S1 (Table 2). Statistical analysis (ANOVA/Tukey-Kramer) of starch, soluble sugar, and anthocyanin levels of wild-type and mutant plants in a time series after tansfer from LL conditions (*i.e.* a PFD of 30 μmol·m^{-2}·s^{-1}) to HL (*i.e.* a PFD of 300 μmol·m^{-2}·s^{-1}) within 148 min. The plant lines are denoted, *a* = Col-0, *b* = *tpt-2, c* = *adg1-1*, *d* = *adg1-1/tpt-2.* Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.

Condition	**Starch**						**Sucrose**						**Glucose**						**Fructose**						**Condition**	**Anthocyanin**					
Time	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	**Time**	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
t$_0$ (LL)		■	■	■	■																				**t$_0$ (LL)**						
30 min	■	■	■	■	■											▨				▨		■			**4 h**						
60 min	■	■	■	■	■		▨		▨							▨						■			**8 h**						
120 min	■	■	■	■	■		■		■	■		■		■		■		■		■		■		■	**24 h**	■		■	▨		■
240 min		■	■	■	■			▨		■		■		■		■		■		■		■		■	**32 h**	▨		■	▨		■
480 min		■	■	■	■			■		■		■		■		■		■		■		■		■							
HL		■	■	■	■					■		■		■		■		■		▨		■		■	**HL**		■		■		■

Document S1 (Table 3). Statistical analysis (ANOVA/Tukey-Kramer) of MgProtoIX contents and Lhcb1 transcript abundance of wild-type and mutant plants in a time series after transfer from LL conditions (*i.e*. a PFD of 30 μmol·m^{-2}·s^{-1}) to HL (*i.e.* a PFD of 300 μmol·m^{-2}·s^{-1}) within 480 min. The plant lines are denoted, *a* = Col-0; *b* = *tpt-2, c* = *adg1-1*, *d* = *adg1-1/tpt-2.* Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.



Conditions	**MgProtoIX**							***Lhcb2***					
	a vs b	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***		***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
HL		■	■	▒	■			■	■	■	■	■	■
LL								■		▒			
t_{30min}								■	■	■	■	■	
t_{60min}													
t_{240min}								■	■			■	■
t_{480min}			▒					■	■	■	■	■	■

Document S1 (Table 4). Statistical analysis (ANOVA/Tukey-Kramer) of contents of redox components of wild-type and mutant plants in a time series after transfer from LL conditions (*i.e.* a PFD of 30 $\mu mol \cdot m^{-2} \cdot s^{-1}$) to HL (*i.e.* a PFD of 300 $\mu mol \cdot m^{-2} \cdot s^{-1}$) within 4h compared to HL grown plants. The biotypes are denoted, *a* = Col-0; *b* = *tpt-2*, *c* = *adg1-1*, *d* = *adg1-1/tpt-2.* Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.

Compound	**Conditions**	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
DHA	**t_0**						
	t_4	■			■	■	
	HL	■			▨	■	
Asc	**t_0**						
	t_{4h}	■			■	■	
	HL						
DHA + ASC	**t_0**						
	t_4						
	HL						
GSSG	**t_0**						
	t_{4h}						
	HL						
GSH	**t_0**						
	t_{4h}						
	HL						
GSSG+GSH	**t_0**						
	t_{4h}						
	HL				▨		

Document S1 (Table 5). Statistical analysis (ANOVA/Tukey-Kramer) of metabolite contents of wild-type and mutant plants in a time series after transfer from LL conditions (*i.e.* a PFD of 30 µmol·m^{-2}·s^{-1}) to HL (*i.e.* a PFD of 300 µmol·m^{-2}·s^{-1}) within 4h and 48h compared to HL- or LL-grown plants. The conditions are denoted, *a* = t_0 (LL); *b* = t_{4h} (HL), *c* = t_{48h} (HL), *d* = HL. Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.

Metabolites	**Col-0**						***tpt-2***						***adg1-1***						***adg1-1/tpt-2***					
Sugars	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
Sucrose, D- (8TMS)	■	■	■	■	■	▨	▨	■	■	■	■	■	■	■	■		■	■	■	■	■	▨		■
Glucose, D- (1MEOX) (5TMS)	■	■	■	■	■		▨	■	■	■	■	■	■	■	■			■	■	■			■	■
Fructose, D- (1MEOX) (5TMS)	■	■	■	■			■	■	■	■	■	■	■	■	■				▨	■		■	▨	■
Mannose, D- (1MEOX) (5TMS)							■	■	■	■		▨	▨	■	■	■	■	■	■	■			■	▨
Maltose, D- (1MEOX) (8TMS)		■		■		■		■	■	■	■	■	■	■	■		■	■	■	■	▨	■	■	
Trehalose, alpha,alpha'-, D- (8TMS)		■	■	■	■	■		■	■	■	■	▨		■	■	■	■	■			■		■	■
Raffinose (11TMS)			■		■	■	■	▨			■		■	■	■	■	▨		■			■	■	
Glucose, 1,6-anhydro, beta-D- (3TMS)		■		▨			▨	■	■				▨	■	■				■	■			■	■
Mannopyranoside, 1-O-methyl-, alpha-D- (4TMS)		■	■	■	■	■		■	■	▨				■	■	■	■	■		■		▨		▨
Fucose, DL- (1MEOX) (4TMS)	■	■	■	■	■		▨	■	■	■		■	■	■	■	■	■		■			▨	■	
Arabinose, D- (1MEOX) (4TMS)	■	▨	■	■	■				■		■	■								■		■	▨	▨
Glucoheptose (1MEOX) (6TMS)	■	■	■	■			■	■					■	■	■	■	■	■	■	■			■	■

Document S1 (Table 5), continued

Amino acids																								
Pyroglutamic acid / Glutamic acid	■	■		■	■	■	■	■	■	■		■	■	■		■	■	■	■	■			■	■
Aspartic acid, L- (3TMS)		■		■		■		▨						■		■	■	■						
Asparagine, DL- (3TMS)								■		■		■		■		■		■			■		■	▨
Alanine, DL- (3TMS)		▨			▨	■		■		■		■		■		■		■	■	■			■	■
Glycine (3TMS)	■	■	■	■	■	■	■	■	■		■	■	■	■	■	■	■	■	■	■		■	■	
Serine, DL- (3TMS)	■	■	■	■	■	■	■	■	■				■	■	■	■		■	■	■	■		■	
Threonine, DL- (3TMS)	■	■		■	■	■	■	■	■			▨		■		■		■	■		■	▨		■
Cysteine, DL- (3TMS)		■	▨	▨				■	■	▨				■	■	■	■	■		■		■		■
Methionine, DL- (2TMS)							■	■			■	▨	■	■			■	■	■				■	
Isoleucine, L- (2TMS)	■	■	■				■	■	■				■	■	■				■	■	■		■	■
Valine, DL- (2TMS)	■	■	■		■	■	■	■	■	■		■	■	■	■	■		■	■	■			■	■
Lysine, L- (4TMS)	■	■				■	▨	■	■				■	■	▨	■		■	▨	■				
Arginine, DL-, -NH3 (3TMS)								■	▨	■		■		■		■		■	■	■			■	■
Phenylalanine, DL- (2TMS)	■	■		▨	■		■	■	■	■		■	■	■			■	■	■	■		▨	■	■
Tyrosine, DL- (3TMS)	■	■			▨	▨	▨	■	■	■	■	■	■	■		■		■	▨	■	■			
Tryptophan, L- (2TMS)	■	■	■				▨	■				▨	■	■	■					■				▨
Proline, L- (2TMS)	■	■		■	■	■	■	■	■	■		■	■	■		■		■	■	■			■	▨
Alanine, beta- (3TMS)	■	■	■	■		■	■	■	■	■		▨		■	■	■		■		■	■	■	■	■

Document S1 (Table 5), continued

Organic acids																											
Pyruvic acid (1MEOX) (1TMS)		■	▨	■				■		■	▨					■	■	■	■	▨		■	■			■	■
Malic acid, 2-methyl-, DL- (3TMS)	■	■	■	■	■	■		■	■	■	■	▨	■		■	■	■	■	■	■		■	■		■	■	■
Glutaric acid (2TMS)		■	■	■	■	■			■	■	■	▨	■			■	■	■	■	■		▨	■		■	▨	■
Succinic acid (2TMS)		■	■	■	▨	▨		▨	■	■	■	■	▨		■	■	■	■		■		■	■		■	■	■
Fumaric acid (2TMS)	■		■	■		■		■	■				■		■	■	■	■		■							
Malonic acid (2TMS)	■	■	■												▨	■				■		■	■	■		■	■
Glyceric acid, DL- (3TMS)	■	■	■		■	■		■	■	■					■	■	■	■				■	■	■			
Butyric acid, 3-hydroxy- (2TMS)		■		■		■			■		▨		■			■		■								▨	■
Gluconic/Galactonic acid (6TMS)		■	■		■	■				■		■	■									▨	■				▨
Benzoic acid (1TMS)		▨								■					■	■	■	■									

Document S1 (Table 5), continued.

Others																											
Glycerol (3TMS)	▨	▨	■					■	■	■		▨	■				■							▨		▨	▨
Inositol, myo- (6TMS)	■	■	■	▨	■			■	■	■	■		■		■	■	■	■		▨		■	■		■	■	■
Galactinol (9TMS)			■		■	■		■	■			■	■		■		■			■		■			■	■	
Erythritol (4TMS)								▨	■	■	■	■				■	▨	■		■		■	■	■			
Tyramine (3TMS)	▨	■	■		■	■			▨	■		■			■		■					▨					
Ornithine, DL- (4TMS)		■				■		▨	■		■		■			■		■		■			■	■			
Putrescine (4TMS)	■	■		■	■	■			■	■	■	■			▨	■	■	■		■		■	▨	■			

Document S1 (Table 6). Statistical analysis (ANOVA/Tukey-Kramer) of metabolite contents of wild-type and mutant plants in a time series after transfer from LL conditions (*i.e.* a PFD of 30 µmol·m^{-2}·s^{-1}) to HL (*i.e.* a PFD of 300 µmol·m^{-2}·s^{-1}) within 4h and 48h compared to HL- or LL-grown plants. The plant lines are denoted, *a* = Col-0; *b* = *tpt-2*, *c* = *adg1-1*, *d* = *adg1-1/tpt-2.* Significance levels of P < 0.05 or P < 0.01 are indicated by light or dark blue colours.

Metabolites	t_0 **(LL)**						t_{4h} **(HL)**						t_{48h} **(HL)**						**HL**					
Sugars	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***	***a vs b***	***a vs c***	***a vs d***	***b vs c***	***b vs d***	***c vs d***
Sucrose, D- (8TMS)		■	▨	■		■	■	■	■	■	■	■			■		■	■	■	■	■		■	■
Glucose, D- (1MEOX) (5TMS)		■	■	■	■	■	■	▨	■	■	■	■	■	■			■	■		■	■	■	■	■
Fructose, D- (1MEOX) (5TMS)		■	■	■	■	■	■	■	■	■	■	■	■	■			■	■	■	■	■	■	■	■
Mannose, D- (1MEOX) (5TMS)		■	■	■	■	■		■		■		▨		■		■		■	■	■	■	■		■
Maltose, D- (1MEOX) (8TMS)	■	■	■	■	■		■	■				▨	■			■	■		■			■	■	
Trehalose, alpha,alpha'-, D- (8TMS)		▨	▨	▨	▨		■		■	▨	▨	■	■		■	■			■	■	■	■		■
Raffinose (11TMS)		■	■	■	■			▨	■	▨	▨			■	■	■	■		■	■	■			
Glucose, 1,6-anhydro, beta-D- (3TMS)				▨				■	■	■	▨					■	▨			■				■
Mannopyranoside, 1-O-methyl-, alpha-D- (4TMS)													■		■			■			▨		▨	
Fucose, DL- (1MEOX) (4TMS)		■	■	■	■									■	■	■	■	■	▨		■	■	■	■
Arabinose, D- (1MEOX) (4TMS)			■		■									■	▨	■	▨							
Glucoheptose (1MEOX) (6TMS)				▨										■		■		■	■	■	■	■		■

Document S1 (Table 6), continued

Amino acids																								
Pyroglutamic acid / Glutamic acid	■			■	■		▨	■	■	■	▨				■		■	■	■			■	■	
Aspartic acid, L- (3TMS)	■			■		■	■		■	■	■	■				▨			■		▨	■		▨
Asparagine, DL- (3TMS)		■		■		■	▨	▨	▨					■		■		■						
Alanine, DL- (3TMS)	■			▨					■		▨	■	■	■			▨	▨	■	■	▨	■	■	
Glycine (3TMS)		■	▨		■	■	■	■	■	■	■	■			■	▨	■	■	■	▨	■	■	■	■
Serine, DL- (3TMS)	■	■	▨	■	■		■		■	■	■		■		■	■	■	■	■	■	■	■	■	■
Threonine, DL- (3TMS)	▨	■	■		■	■	■		■	■	■	■	▨		■		■	■	■		■	■	■	■
Cysteine, DL- (3TMS)		▨		■										■		■		■		■		▨		■
Methionine, DL- (2TMS)					▨										▨		▨		■			■	■	
Isoleucine, L- (2TMS)	■		■		■	■										▨	■				■	▨	■	
Valine, DL- (2TMS)	■		■	■		■							■			▨	■	■	■				■	■
Lysine, L- (4TMS)		■	■		■	■								▨		■		▨	■					
Arginine, DL-, -NH3 (3TMS)				▨										■		■		■	■	▨			■	▨
Phenylalanine, DL- (2TMS)		■	■	■	■	■	■	▨	■	■		■		■		■		■	■	▨			■	■
Tyrosine, DL- (3TMS)		■		■		■	■		■	■		■		■		■	▨	■						▨
Tryptophan, L- (2TMS)				■		■								■	■				■	▨	■			
Proline, L- (2TMS)							■			■	■				■	▨		■	■			■	■	
Alanine, beta- (3TMS)		■	■	■	■	■							▨					■	■			■	▨	

Document S1 (Table 6), continued

Organic acids																											
Pyruvic acid (1MEOX) (1TMS)	▨			■				■		▨	■	■	■									■			▨	■	▨
Malic acid, 2-methyl-, DL- (3TMS)	■		■	▨											▨		■		■	■				■		■	■
Glutaric acid (2TMS)		■	■														■		■	■		■	■	■		■	■
Succinic acid (2TMS)	■	■	■	■	■			■	■	■					■	■	■	■	■	■		■		■	■	■	■
Fumaric acid (2TMS)		■		■	■	■		■	■	■	■	■	■		■	▨	■			▨				■		■	■
Malonic acid (2TMS)	▒	▒	▒	▒	▒	▒			▨		▨																
Glyceric acid, DL- (3TMS)	■	■	■	■	■			■		■	■	■	■		■	▨	■	■	■	■			■	■	■	■	■
Butyric acid, 3-hydroxy- (2TMS)	■	▨	▨	■		■					▨						▨		■							▨	
Gluconic/Galactonic acid (6TMS)		■	▨	■	▨																			▨	■	■	
Benzoic acid (1TMS)		▨		■		■						▨					■		■	▨		▨				■	

Document S1 (Table 6), continued

Others

Glycerol (3TMS)																	▨										
Inositol, myo- (6TMS)		■	■	■	■				■	■	■	■				■	■	▨	■			■	■	■		■	■
Galactinol (9TMS)		■		■		■		■			■	■				■	■	■	■			■	■	■			
Erythritol (4TMS)	■	■	■	■	■	■										■		■		■			▨	■		▨	
Tyramine (3TMS)			■		▨																		■	■		■	
Ornithine, DL- (4TMS)		■		■		■		■	▨	■		▨	■			■		■		■		■	▨	▨			
Putrescine (4TMS)		■	■	■	■	■		▨			■					■		■	■	■		■	■			■	▨

Supplementary Document S2

Static assessment of global gene expression after LL/HL-transfer

(A) *adg1-1 vs* Col-0

The starch-free *adg1-1* single mutant contained the highest number of significantly altered genes in the static comparison, particularly under LL-conditions (Fig. 6A) or 48h after LL/HL-transfer. Under LL-conditions 16 gens belonging to the category `protein metabolism´ were differentially regulated as a part of the 144 highly altered genes. Interestingly, among these 16 genes, 12 genes related to `protein degradation´ were down-regulated and four genes related to `protein synthesis´ were up-regulated (Tables 1, Supplementary Table S2A), suggesting that in the absence of starch the maintenance of protein abundance is promoted.

The transfer from LL to HL had a profound impact on the functional categories of altered genes in the *adg1-1* single mutant. Although the number of differentially regulated genes dropped 4h after transfer to HL, 30 and 17 genes were up- and down-regulated, respectively, compared to the wild type (Table 1, Supplementary Table S3A). Among the 30 up-regulated genes, there were five genes related to `lipid metabolism´. Four of the five proteins reside in chloroplasts. Furthermore, four genes involved in `secondary metabolism´ (flavonoid biosynthesis) were up-regulated and five genes related to `stress´ were down-regulated (Table 1, Supplementary Table S3A). These data suggest an elevated input into lipid formation and/or secondary metabolism as a consequence of a deficiency in the night-path of photoassimilate export from the chloroplast.

The functional pattern of genes changed appreciably after 48h in HL (Fig. 6, Table 1, Supplementary Table S4A). There were a total of 209 genes specifically altered in *adg1-1* compared to the wild type. Interestingly, although the category `lipid metabolism´ was missing among the 58 highly up-regulated genes, there were seven genes belonging to this category among the 151 highly down-regulated genes, with four of these genes related to `lipid degradation´. Hence, the transient enhancement of lipid synthesis (i.e. 4h after LL/HL-transfer) was replaced by an inhibition of lipid degradation in the long term. Furthermore five genes involved in `major CHO metabolism´, 12 genes related to `proteins´ (including seven genes connected to `protein synthesis´), as well as six genes related to `regulation of transcription (RT)´ were highly up-regulated (Table 1). Moreover, the up-regulation of genes involved in `protein synthesis´ was accompanied by a down-regulation of 13 genes related to `protein degradation´, again suggesting an enhanced production and/or maintenance of proteins. Furthermore 21, 11, and seven genes related to `RT´, `stress´ and `signalling´, respectively, were highly down-regulated in *adg1-1* 48h after LL/HL-transfer (Supplementary Table S4A). Moreover, the gene coding for the glucose 6-phosphate/phosphate translocator 2 (*GPT2*; At1g61800) was highly up-regulated in *adg1-1*.

(B) *tpt-2 vs* Col-0

Under LL-conditions, a limitation in the day-path of photoassimilate export from the chloroplast in the *tpt-2* mutant resulted only in the down-regulation of a single gene encoding a disulfide isomerase-like protein (AtPDIL 5-4, At4g27080; Supplementary Table S2B).

The number of highly altered genes in *tpt-2* was increased to 36, 4h after the plants were transferred to HL. There were only two genes down-regulated, amongst them again AtPDIL 5-4 and a protein of unknown function (At4g27080; Supplementary Table S3B). The 34 highly up-regulated genes comprised three genes related to \`major carbohydrate metabolism´ and seven, significantly over-represented genes involved in \`protein degradation´ (Table 1). After 48h in HL, again, there were more genes highly up-regulated (104) than down-regulated (3) (Supplementary Table S4B). Interestingly, AtPDIL 5-4 still belonged to the down-regulated genes. Within the group of up-regulated genes there were three significantly over-represented functional clusters, *i.e.* \`cell wall´, \`hormone metabolism´ and \`stress´ (Table 1). Furthermore, genes related to \`RT´ and \`development´ were represented with at least five members. Ten genes, including a MAPkinase (At1g01560), were connected to \`signalling´, in particular, \`calcium signalling´ (nine genes).

(c) *adg1-1/tpt-2 vs* Col-0

Despite the relative high number of specifically altered genes in the *adg1-1* mutant, surprisingly, the combined deficiency in the day- and night-path of photoassimilate export resulted in an appreciable lower number of differentially regulated genes in *adg1-1/tpt-2*. Under LL-conditions there were only 21 genes highly up- or down-regulated in the double mutant (Supplementary Table S2C). Among the nine up-regulated genes in *adg1-1/tpt-2,* remarkably, there were three genes related to \`abiotic stress´, sub-category heat. All three genes belong to the putative HSP20-type protein of unknown function (At1g53540, At3g46230, At5g12020). Of the 12 down-regulated genes one half is related to \`histone proteins´ and \`chromatin structure´, suggesting that parts of the DNA was not associated with proteins and/or the plants contained less DNA. The only gene dramatically down-regulated in the overlapping area of *adg1-1/tpt-2* and *tpt-2* was, as expected, the *TPT* gene (Supplementary Table S2D). In the overlapping region between *adg1-1/tpt-2* and *adg1-1* there were 13 up- and 33 down-regulated genes found. Among the down-regulated genes there were six genes related to `chromatin structure´ as well as five genes involved in `protein degradation´, again suggesting a function of starch and/or soluble sugars in protein maintenance and chromatin structure.

After 4h in HL only 10 genes were highly altered in *adg1-1/tpt-2* (Fig. 6B, Supplementary Table S3C). The three up-regulated genes comprised a stress induced protein (At2g40170) involved in ABA metabolism and a chloroplast localised superoxide dismutase (At2g28190). Both genes were more pronounced up-regulated in *adg1-1/tpt-2* compared to *adg1-1* or *tpt-2*. Amongst the down-regulated genes there was a bHLH-type transcription factor (At4g17880; MYC4), which was highly and specifically down-regulated with a log2-ratio of -5.17 in *adg1-1/tpt-2.* Strikingly the same gene was also highly down-regulated after 48h in HL (log2-ratio = -4.21) and even in LL (log2-ratio = -3.68). A closer inspection of the expression profiles (eFP browser, Winter *et al.*, 2007) revealed that this gene is highly regulated by various stress conditions, like for instance oxidative stress, and it responds to jasmonate (Fernández-Calvo *et al.*, 2011). Moreover, the presence of externally fed Suc induces the expression of At4g17880. Furthermore, MYC4 has been identified to be one of the key players in the regulation of glucosinolate biosynthesis (Schweizer *et al.,* 2013). At t_{48h} there were eight more transcriptional regulators within the group of 112 highly down-regulated genes in *adg1-1/tpt-2*. Moreover, the functional categories `amino acids´, `cell wall´, and `major carbohydrate metabolism´ were significantly over-represented (Table 1). Interestingly, among the 36 highly up-regulated genes, 22 were plastome-encoded and belonged to the categories `PS light reaction´ (16 genes), `protein biosynthesis´ (five genes) and `lipid metabolism´ (one gene). Moreover, there were four nuclear-encoded genes involved in `RT´ up-regulated in *adg1-1/tpt-2*.

Supplementary Document S3

Genes associated with `major carbohydrate´- and `lipid metabolism´ as well as `transport´ were commonly up-regulated 4h after LL/HL-transfer

The group of commonly regulated genes as a response to LL/HL-transfer comprised also metabolic genes. Strikingly, seven and 11 genes associated with `lipid-´ and `major CHO metabolism´, respectively, were up-regulated only transiently at t_{4h} *vs* t_0 (Supplementary Table S7A).

Among the up-regulated genes associated with `lipid metabolism´, there were two genes involved in triacylglycerol (TAG) biosynthesis (At1g54570 and At2g19450), a sterol oxidase (At1g07420), probably anchored at the outer envelope (gene ontology, cellular component), a 16:0 delta9 desaturase (At2g31360) and a phospholipase A2 family protein (At2g06925). As an analysis with ATTED-II (version 6.1) revealed, all genes apart from a plastidial thioesterase (At1g54570) belong to a regulatory network (Supplementary Fig. S3B; Supplementary Table S7A).

Moreover, in the category `lipid metabolism´ there were ten and seven genes down-regulated at t_{4h} *vs* t_0 and t_{48h} *vs* t_0, respectively, with an overlap of five genes. The ten down-regulated genes at t_{4h} *vs* t_0 form, with the exception of At5g08030, a large network (Supplementary Fig. S3C), whereas there is no evidence for any exceptional network formation with the seven down-regulated genes at t_{48h} *vs* t_0 (not shown).

In the category `major CHO metabolism´, the 11 up-regulated genes at t_{4h} *vs* t_0 were - in a broader sense - all involved in either starch synthesis or degradation, despite the fact that the *adg1-1* single mutant and the *adg1-1/tpt-2* double mutant lack starch (Supplementary Table S7A). Furthermore, all 11 genes belong to a single regulatory network (Supplementary Fig. S2A). The list of highly up-regulated genes comprised not only chloroplast-localised metabolic enzymes such as α-amylase (At1g69830), disproportionating enzyme 1 (DPE1, At5g64860; Stettler *et al.,* 2009), isoamylase/debranching enzyme (At4g09020; Streb *et al.,* 2008; Wattebled *et al.,* 2008), branching enzyme 1 and 2 (At3g20440; At2g36390; Walters *et al.,* 2004; Dumez *et al.,* 2006) and glucan phosphorylase (At3g29320), but also regulatory proteins such as glucan water dikinase (GWD; SEX1; At1g10760; Yu *et al.,* 2001) phosphoglucan, water dikinases (PWD; AtGWD3; At5g26570; Kötting *et al.,* 2005), involved in the phosphorylation of glucose residues in amylopectin at C_6 and C_3 (Ritte *et al.,* 2006), respectively, and a protein phosphatase (AtSEX4; At3g52180), involved in the dephosphorylation of the aforementioned glucose residues (Hejazi *et al.,* 2010). Moreover, two genes associated with the cytosolic conversion of maltose to sucrose (*i.e.* disproportionating enzyme 2 [At2g40840; Lu & Sharkey, 2004] and glucan posphorylase 2 [At3g46970]) were highly up-regulated 4h after LL/HL-transfer in both wild-type and mutant plants. Again this regulation of genes involved in carbohydrate metabolism also occurred in the starch-free background (*i.e. adg1-1* and *adg1-1/tpt-2*). Interestingly, three of the starch-related genes belong to the co-expression network of phospholipase A (At2g06925; Supplementary Table S7A). Moreover, within the co-regulation network of genes belonging to the category \`major CHO metabolism´, there was a chloroplast localised AMP activated protein kinase induced 4h and 48h after transfer to HL (Supplementary Table S7, A and B). The respective gene (At5g39790) appears to contain a starch binding domain (SUBA3 database; Heazlewood *et al.,* 2007; Tanz *et al*., 2013) and might hence be involved in carbohydrate metabolism or signalling. Most strikingly, the expression of \`starch related´ genes occurred independently from the presence of starch (*i.e.* in the starch-free background *adg1-1*), suggesting that the resulting proteins might have additional unknown functions.

In the category \`secondary metabolism´ there were five and 11 genes up-regulated, related to \`flavonoids´ in a broader sense at t_{4h} *vs* t_0 and t_{48h} *vs* t_0, respectively (Supplementary Table S7, A and B). Only three of these genes were commonly differently regulated at both time points. In addition, three more up-regulated genes belonged to the sub-category \`isoprenoids´ and \`miscellaneous´.

Genes associated with specific \`transport processes´ were differentially expressed most pronounced 4h after LL/HL-transfer

Genes associated with \`transport processes´ were de-regulated both at 4h and 48h after LL/HL-transfer. Of the 14 up-regulated genes at t_{4h} *vs* t_0, only two genes were also found at t_{48h} *vs* t_0. Likewise, of the 18 down-regulated transport associated genes at t_{4h} *vs* t_0, only six were also found at t_{48h} *vs* t_0 (Supplementary Table S7, A and B). Interestingly two genes belonging to the phosphate translocator family were de-regulated after 4h in HL. The glucose 6-phosphate/phosphate translocator2 (GPT2; At1g61800) and the phosphoenolpyruvate/phosphate translocator2 (PPT2; At3g01550) were up- and down-regulated, respectively. It has been demonstrated that *GPT2*, which is usually only expressed in generative tissue (eFP browser; Winter *et al.,* 2007), strongly responds to elevated soluble sugar levels (Kunz *et al.,* 2010, Schmitz *et al.,* 2012), *e.g.* in starch-free mutants or after feeding of exogenous sugars to the plants (Heinrichs *et al.,* 2012). *GPT2* was highly up-regulated with log2-ratios between 3.7 and 6.7 at t_{4h} *vs* t_0 in all plant lines

(Supplementary Table S7). At 48h after LL-to-HL-transfer, the log2-ratios of *GPT2* expression in the wild-type and the *tpt-2* single mutant dropped to lower levels compared to t_{4h} *vs* t_0. However, in the *adg1-1* mutant the expression of *GPT2* was further increased from 6.7 at t_{4h} *vs* t_0 to 7.2 at t_{48h} *vs* t_0, whereas in the double mutant *GPT2* was not significantly altered. The changes in the *GPT2* expression ratios in the time series correspond well with levels of soluble sugars in wild-type and mutant plants (Compare Fig. 1 and Table 4).

Of the 14 up-regulated transport-related genes, six genes encode proteins with a high probability of a mitochondrial localisation and only two are likely to be localised in the chloroplasts. The portion of organelle-localised gene products was further diminished in the group of down-regulated transport related genes (*i.e.* two mitochondrial and one plastidial).

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