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<sub>4h</sub> and t<sub>48h</sub> 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 t4h or t48h. The data represent the mean of five independent samples ± SE.

| Metabolites                                      | Col-0 t0 (LL) | Col-0 t4h | Col-0 t48h | Col-0 (HL) |
|--------------------------------------------------|---------------|-----------|------------|------------|
| Sugars                                           |               |           |            |            |
| D-Sucrose                                        | 3.255 ± 0.062 | 6.063 ± 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,β-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                                      |               |           |            |            |
| 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 |
| Organic acids | Col-0 t₀ (LL) | Col-0 t₄h | Col-0 t₄₈h | 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 | 111.564 ± 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 t₀ (LL) | Col-0 t₄h | Col-0 t₄₈h | 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 |
### Metabolites

| Sugars                              | Relative metabolite content (arbitrary units·g⁻¹ fw) |
|-------------------------------------|------------------------------------------------------|
|                                     | adjg1-1 t₀ (LL) | adjg1-1 t₄h | adjg1-1 t₄8h | adjg1-1 (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-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 | 0.237 ± 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 ± 1.886 | 22.941 ± 1.590 |
| DL-Serine                           | 6.097 ± 0.222   | 23.157 ± 1.375 | 49.678 ± 1.478 | 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 ± 0.922   | 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 | 14.324 ± 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   | 0.636 ± 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 |
| Organic acids                                      | adg1-1 t₀ (LL)       | adg1-1 t₄h | adg1-1 t₄₈h | 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 | 4.666 ± 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 t₀ (LL)       | adg1-1 t₄h | adg1-1 t₄₈h | 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 |
| Metabolites                                      | Relative metabolite content (arbitrary units·g⁻¹ fw) |
|-------------------------------------------------|------------------------------------------------------|
|                                                 | tpt-2  t₀ (LL)  | tpt-2  t₄h  | tpt-2  t₄₈h  | tpt-2  (HL)  |
| **Sugars**                                      |             |             |             |             |
| 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| 22.065 ± 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|
| a,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**                                 |             |             |             |             |
| 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 ± 3.388|
| 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 ± 1.604| 17.124 ± 1.605|
| L-Lysine                                        | 0.242 ± 0.017| 0.488 ± 0.071| 0.817 ± 0.033| 0.637 ± 0.063|
| DL-Arginine, -NH3                               | 0.128 ± 0.019| 0.256 ± 0.039| 0.877 ± 0.032| 0.286 ± 0.055|
| DL-Phenylalanine                                | 0.911 ± 0.037| 3.388 ± 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 ± 0.082| 1.360 ± 0.134|
| Organic acids                                      | tpt-2  t₀ (LL) | tpt-2  t₄ | tpt-2  t₄₈ | 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**                                 |                |            |            |            |
| 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 |
| Galactitol                                        | 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 |
| Metabolites                        | Relative metabolite content (arbitrary units·g\(^{-1}\) fw) |
|-----------------------------------|----------------------------------------------------------|
|                                   | adg1-1/tpt-2 (LL) | adg1-1/tpt-2 t<sub>n</sub> | adg1-1/tpt-2 t<sub>48h</sub> | 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     |
| α,α'-D-Trehalose                  | 0.152 ± 0.019     | 0.178 ± 0.019              | 0.250 ± 0.026               | 0.759 ± 0.098     |
| D-Galactose                       | 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-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 ± 4.956    |
| DL-Cysteine                       | 0.791 ± 0.105     | 1.359 ± 0.183              | 2.661 ± 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 t₀ (LL) | adg1-1/tpt-2 t₄h | adg1-1/tpt-2 t₄₈h | 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**                                  |                      |                  |                   |                  |
| 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    |
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/$F_m$ |
|------------|-----|---------|
| 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 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 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   | a vs b    | a vs c      | a vs d   | b vs c   | b vs d   | c vs d   |
| t₀ (LL)   |        |         |         |          |           |             |         |          |          |         |
| 30 min    |        |         |         |          |           |             |         |          |          |         |
| 60 min    |        |         |         |          |           |             |         |          |          |         |
| 120 min   |        |         |         |          |           |             |         |          |          |         |
| 240 min   |        |         |         |          |           |             |         |          |          |         |
| 480 min   |        |         |         |          |           |             |         |          |          |         |
| HL        |        |         |         |          |           |             |         |          |          |         |
| t₀ (LL)   |        |         |         |          |           |             |         |          |          |         |
| 4 h       |        |         |         |          |           |             |         |          |          |         |
| 8 h       |        |         |         |          |           |             |         |          |          |         |
| 24 h      |        |         |         |          |           |             |         |          |          |         |
| 32 h      |        |         |         |          |           |             |         |          |          |         |
| 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         |          |        |        |        |        |        |          |        |        |        |        |        |
| \(t_{30}\)min |          |        |        |        |        |        |          |        |        |        |        |        |
| \(t_{60}\)min |          |        |        |        |        |        |          |        |        |        |        |        |
| \(t_{240}\)min |          |        |        |        |        |        |          |        |        |        |        |        |
| \(t_{480}\)min |          |        |        |        |        |        |          |        |        |        |        |        |
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 µmol·m⁻²·s⁻¹) to HL (i.e. a PFD of 300 µmol·m⁻²·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      | t₀         |        |        |        |        |        |        |
|          | t₄         |        |        |        |        |        |        |
|          | HL         |        |        |        |        |        |        |
| Asc      | t₀         |        |        |        |        |        |        |
|          | t₄₉       |        |        |        |        |        |        |
|          | HL         |        |        |        |        |        |        |
| DHA + ASC| t₀        |        |        |        |        |        |        |
|          | t₄         |        |        |        |        |        |        |
|          | HL         |        |        |        |        |        |        |
| GSSG     | t₀         |        |        |        |        |        |        |
|          | t₄₉       |        |        |        |        |        |        |
|          | HL         |        |        |        |        |        |        |
| GSH      | t₀         |        |        |        |        |        |        |
|          | t₄₉       |        |        |        |        |        |        |
|          | HL         |        |        |        |        |        |        |
| GSSG+GSH | t₀        |        |        |        |        |        |        |
|          | t₄₉       |        |        |        |        |        |        |
|          | 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**                       |       |       |        |             |
| 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)      |       |       |        |             |
### Amino acids

| 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)                |  |  |  |  |
| 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)               |
| 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                        | t₀ (LL) | t₄h (HL) | t₄₈h (HL) | HL       |
|------------------------------------|---------|----------|-----------|----------|
| **Sugars**                         | a vs b  | a vs c   | a vs d    | b vs c   |
| 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)        |         |          |           |          |
| 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)             |       |       |       |       |
### 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) |
| 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 \textit{adg1-1} 48h after LL/HL-transfer (Supplementary Table S4A). Moreover, the gene coding for the glucose 6-phosphate/phosphate translocator 2 (\textit{GPT2}; At1g61800) was highly up-regulated in \textit{adg1-1}.

\textbf{(B) \textit{tpt-2} vs \textit{Col-0}}

Under LL-conditions, a limitation in the day-path of photoassimilate export from the chloroplast in the \textit{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 \textit{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, \textit{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).

\textbf{(c) \textit{adg1-1/tpt-2} vs \textit{Col-0}}

Despite the relative high number of specifically altered genes in the \textit{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 \textit{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 \textit{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 \textit{adg1-1/tpt-2} and \textit{tpt-2} was, as expected, the \textit{TPT} gene (Supplementary Table S2D). In the overlapping region between \textit{adg1-1/tpt-2} and \textit{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 t48h 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.
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 t₄h vs t₀ (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 t₄h vs t₀ and t₄₈h vs t₀, respectively, with an overlap of five genes. The ten down-regulated genes at t₄h vs t₀ 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 t₄₈h vs t₀ (not shown).

In the category `major CHO metabolism´, the 11 up-regulated genes at t₄h vs t₀ 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 amyllopectin at C₆ and C₃ (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. disproportionate enzyme 2 [At2g40840; Lu & Sharkey, 2004] and glucan phosphorylase 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 t4h vs t0 and t48h vs t0, 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 t4h vs t0, only two genes were also found at t48h vs t0. Likewise, of the 18 down-regulated transport associated genes at t4h vs t0, only six were also found at t48h vs t0 (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 t4h vs t0 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).

Additional References (Supplementary Document S3)

Dumez S, Wattebled F, Dauvillee D, Delvalle D, Planchot V, Ball SG, D'Hulst C. 2006. Mutants of Arabidopsis lacking starch branching enzyme II substitute plastidial starch synthesis by cytoplasmic maltose accumulation. The Plant Cell 18, 2694-2709. [http://www.ncbi.nlm.nih.gov/pubmed/17028209]

Heazlewood JL, Verboom RE, Tonti-Filippini J, Small I and Millar AH. 2007. SUBA: the Arabidopsis Subcellular Database. Nucleic Acids Research. 35(D), 213-218. [http://www.ncbi.nlm.nih.gov/pubmed/17071959]

Hejazi M, Fettke J, Köttting O, Zeeman SC, Steup M. 2010. The Laforin-like dual-specificity phosphatase SEX4 from Arabidopsis hydrolyzes both C6- and C3-phosphate esters introduced by starch-related dikinases and thereby affects phase transition of alpha-glucans. Plant Physiology 152, 711-722. [http://www.ncbi.nlm.nih.gov/pubmed/20018599]

Kötting O, Pusch K, Tiessen A, Geigenberger P, Steup M, Ritte G. 2005. Identification of a novel enzyme required for starch metabolism in Arabidopsis leaves. The phosphorylation of C6- and C3-positions of glucosyl residues in starch is catalysed by distinct dikinases. FEBS Letters 580, 4872-4876. [http://www.ncbi.nlm.nih.gov/pubmed/16914145]

Kötting O, Pusch K, Tiessen A, Geigenberger P, Steup M, Ritte G. 2005. Identification of a novel enzyme required for starch metabolism in Arabidopsis leaves. The phosphorylation of C6- and C3-positions of glucosyl residues in starch is catalysed by distinct dikinases. FEBS Letters 580, 4872-4876. [http://www.ncbi.nlm.nih.gov/pubmed/16914145]
Stettler M, Eicke S, Mettler T, Messerli G, Hortensteiner S, Zeeman SC. 2009. Blocking the metabolism of starch breakdown products in Arabidopsis leaves triggers chloroplast degradation. *Molecular Plant*, 2, 1233-1246. [http://www.ncbi.nlm.nih.gov/pubmed/19946617](http://www.ncbi.nlm.nih.gov/pubmed/19946617)

Streb S, Delatte T, Umhang M, Eicke S, Schorderet M, Reinhardt D, Zeeman SC. 2008. Starch granule biosynthesis in Arabidopsis is abolished by removal of all debranching enzymes but restored by the subsequent removal of an endoamylase. *The Plant Cell*. 20, 3448-3466. [http://www.ncbi.nlm.nih.gov/pubmed/19074683](http://www.ncbi.nlm.nih.gov/pubmed/19074683)

Tanz SK, Castleden I, Hooper CM, Vacher M, Small I; Millar, AH. 2013. SUBA3: a database for integrating experimentation and prediction to define the SUBcellular location of proteins in Arabidopsis. *Nucleic Acids Research*. 41(D), 1185-1191. [http://www.ncbi.nlm.nih.gov/pubmed/23180787](http://www.ncbi.nlm.nih.gov/pubmed/23180787)

Wattebled F, Planchot V, Dong Y, Szydlowski N, Pontoire B, Devin A, Ball S, D'Hulst C. 2008. Further evidence for the mandatory nature of polysaccharide debranching for the aggregation of semicrystalline starch and for overlapping functions of debranching enzymes in Arabidopsis leaves. *Plant Physiology* 148, 1309-1323. [http://www.ncbi.nlm.nih.gov/pubmed/18815382](http://www.ncbi.nlm.nih.gov/pubmed/18815382)

Yu T-S, Kofler H, Häusler RE, Hille D, Flügge UI, Zeeman SC, Smith AM, Kossmann J, Lloyd J, Ritte G, Steup M, Lue W-L, Weber A. 2001. The Arabidopsis sex1 mutant is defective in the R1 protein, a general regulator of starch degradation in plants, and not the chloroplast hexose transporter. *The Plant Cell* 13, 1907-1918. [http://www.ncbi.nlm.nih.gov/pubmed/11487701](http://www.ncbi.nlm.nih.gov/pubmed/11487701)