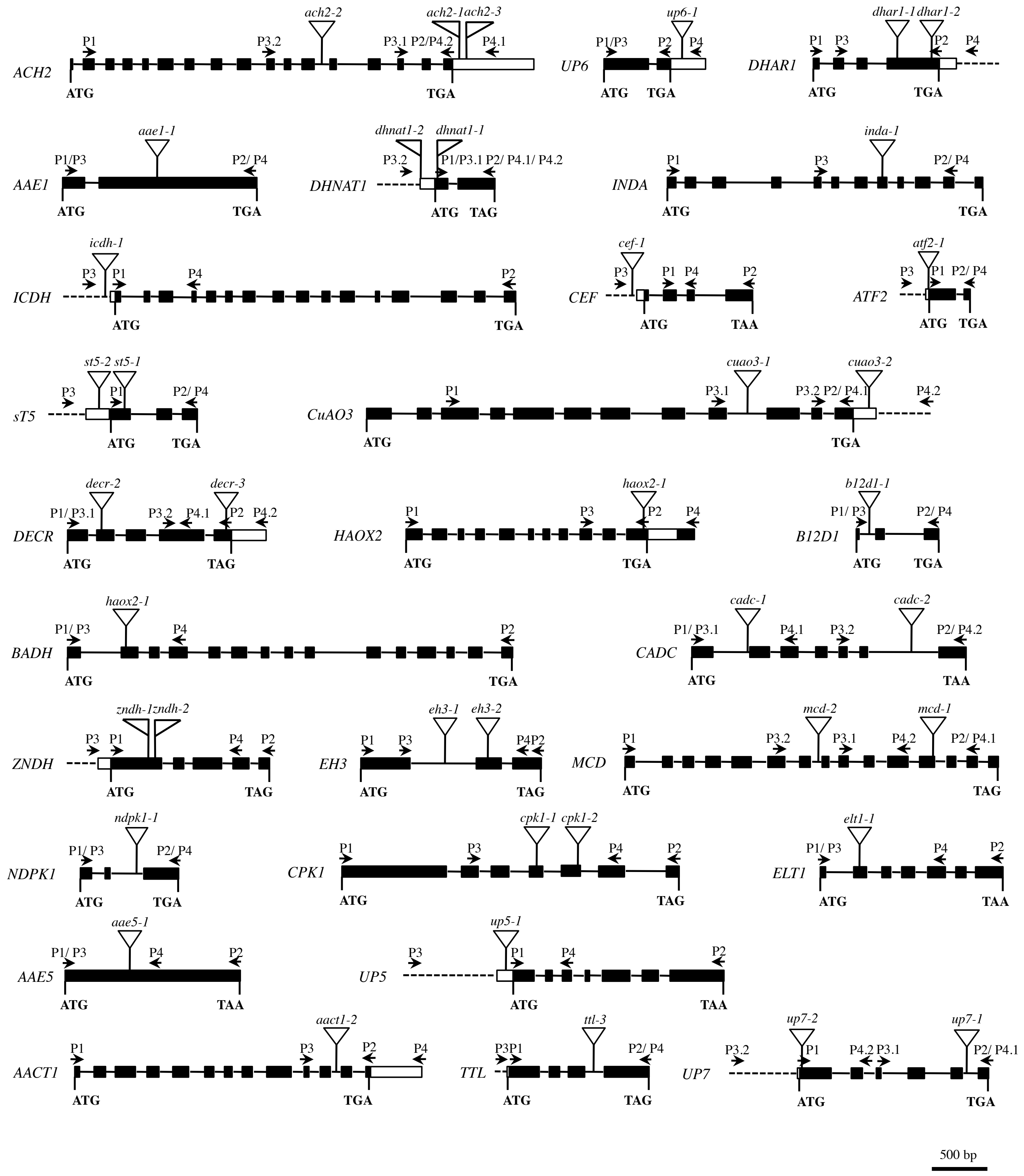
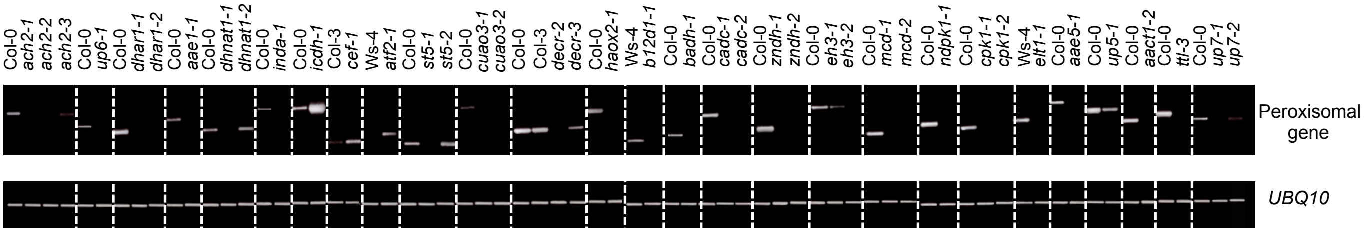
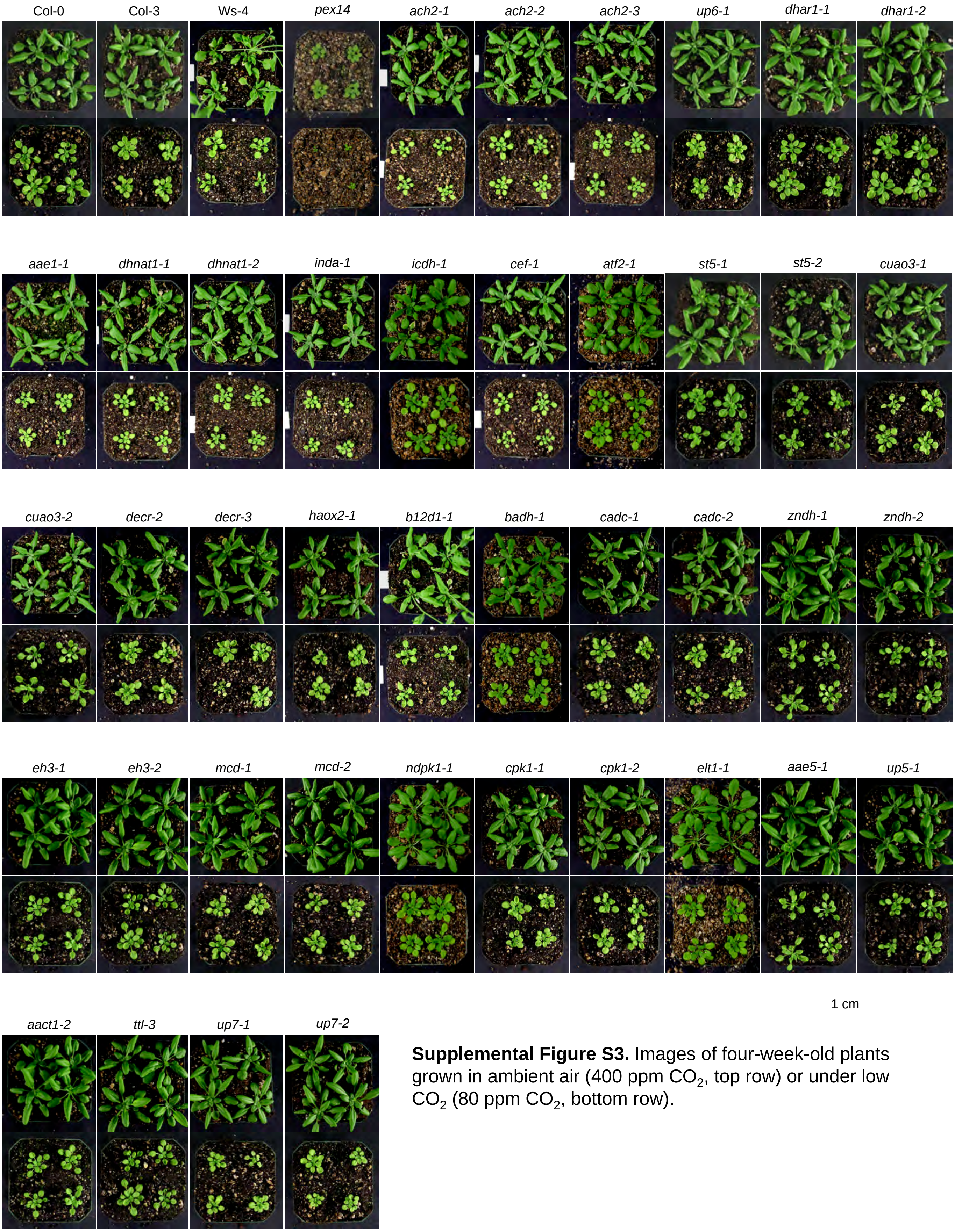


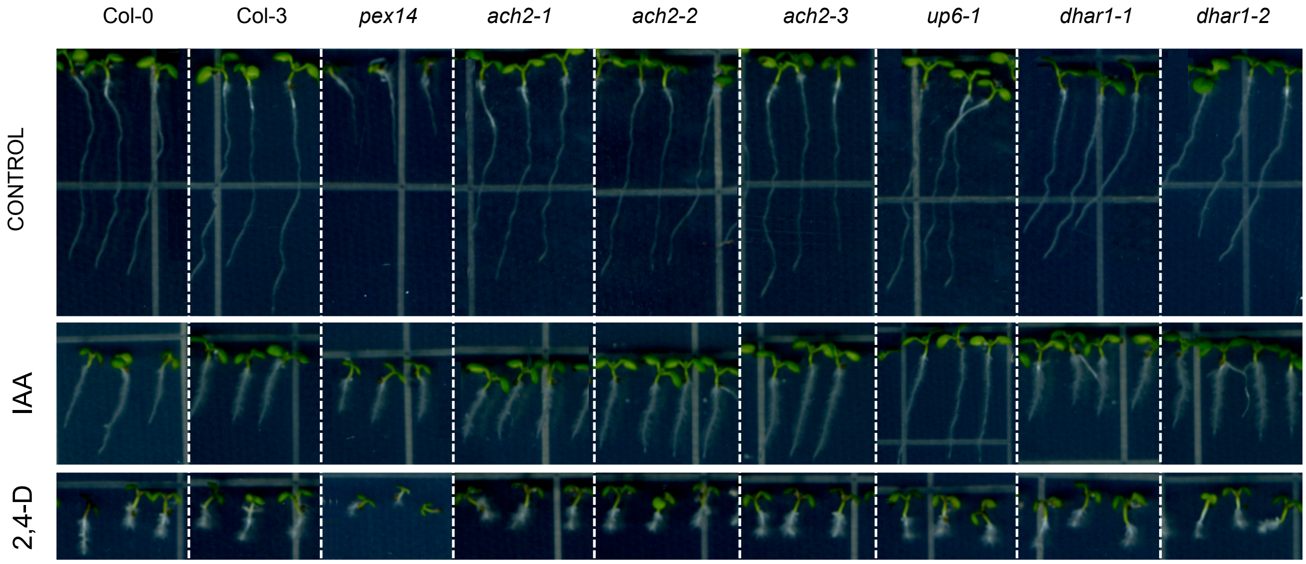
**Supplemental Figure S1.** Schematics of peroxisomal genes analyzed in this study. Black boxes, coding regions; open boxes, untranslated regions; solid lines, introns; dashed lines, intergenic regions. Positions of the T-DNA insertions are indicated. Primers used for genotyping (P3 and P4) and RT-PCR (P1 and P2) are also indicated.

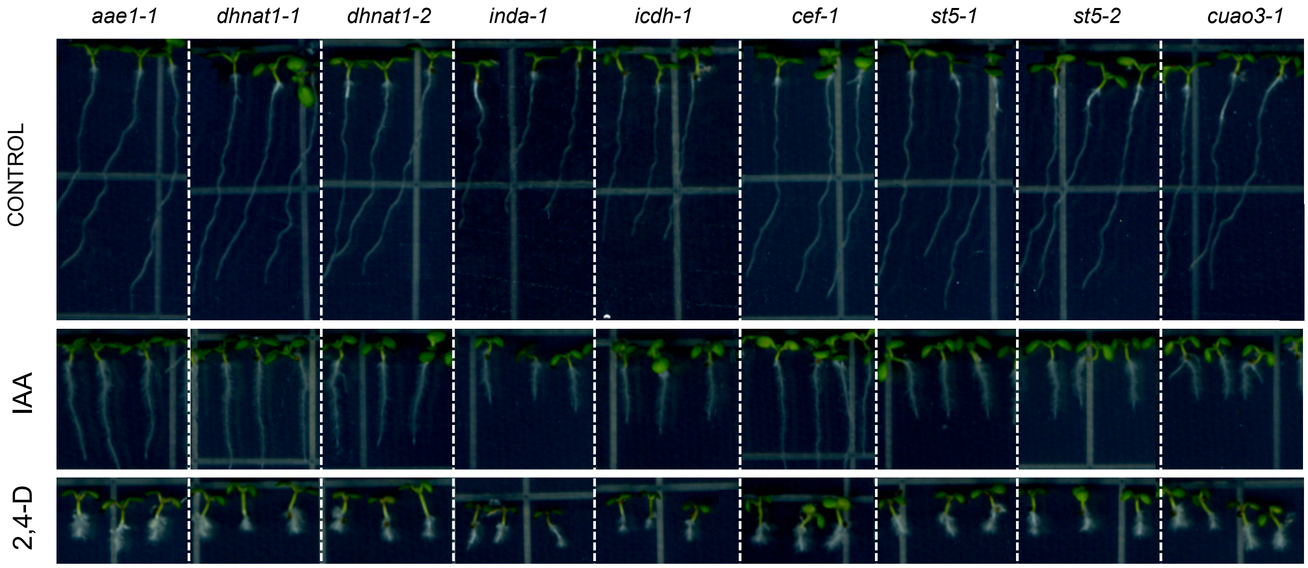


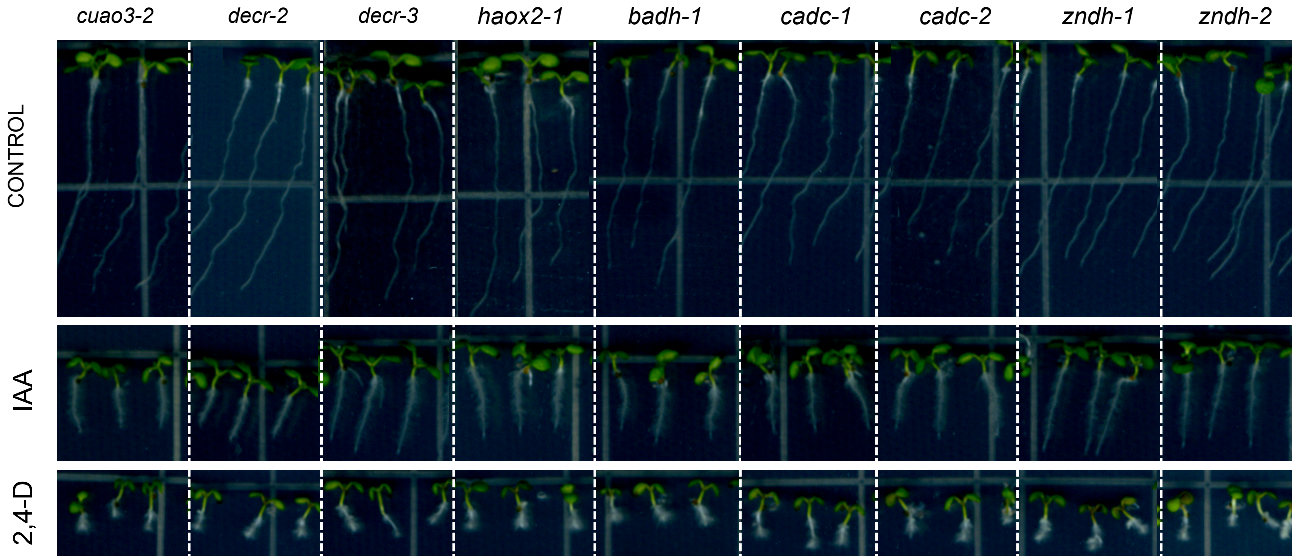
**Supplemental Figure S2**. RT-PCR analysis of 7d mutant seedlings.
Gene-specific primers used for each pair of PCR reaction (35 cycles) are listed in the Supplemental Table S5. *UBQ10* was used to normalize the expression level (25 cycles).

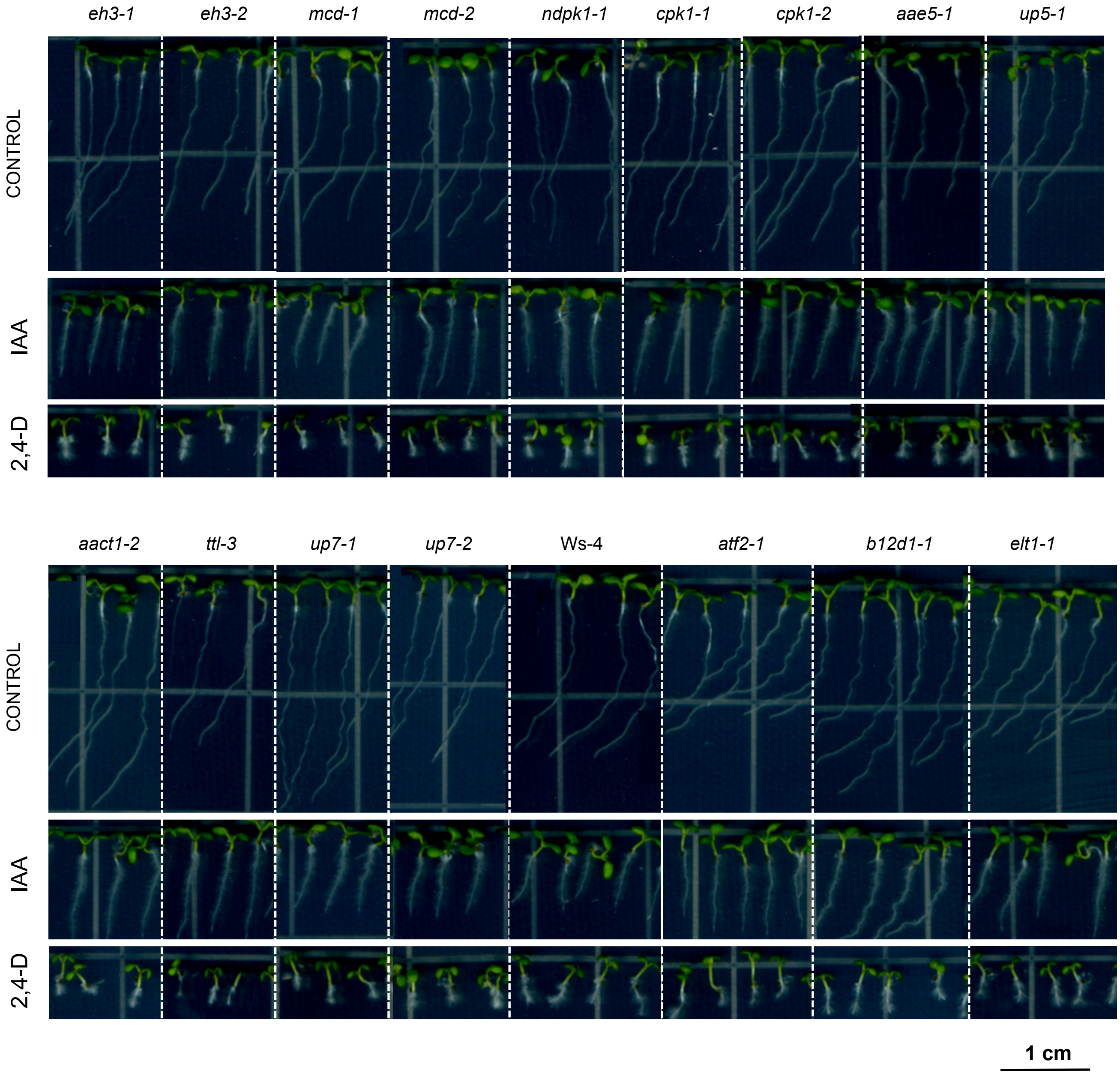


**Supplemental Figure S3.** Images of four-week-old plants grown in ambient air (400 ppm $CO_2$, top row) or under low $CO_2$ (80 ppm $CO_2$, bottom row).

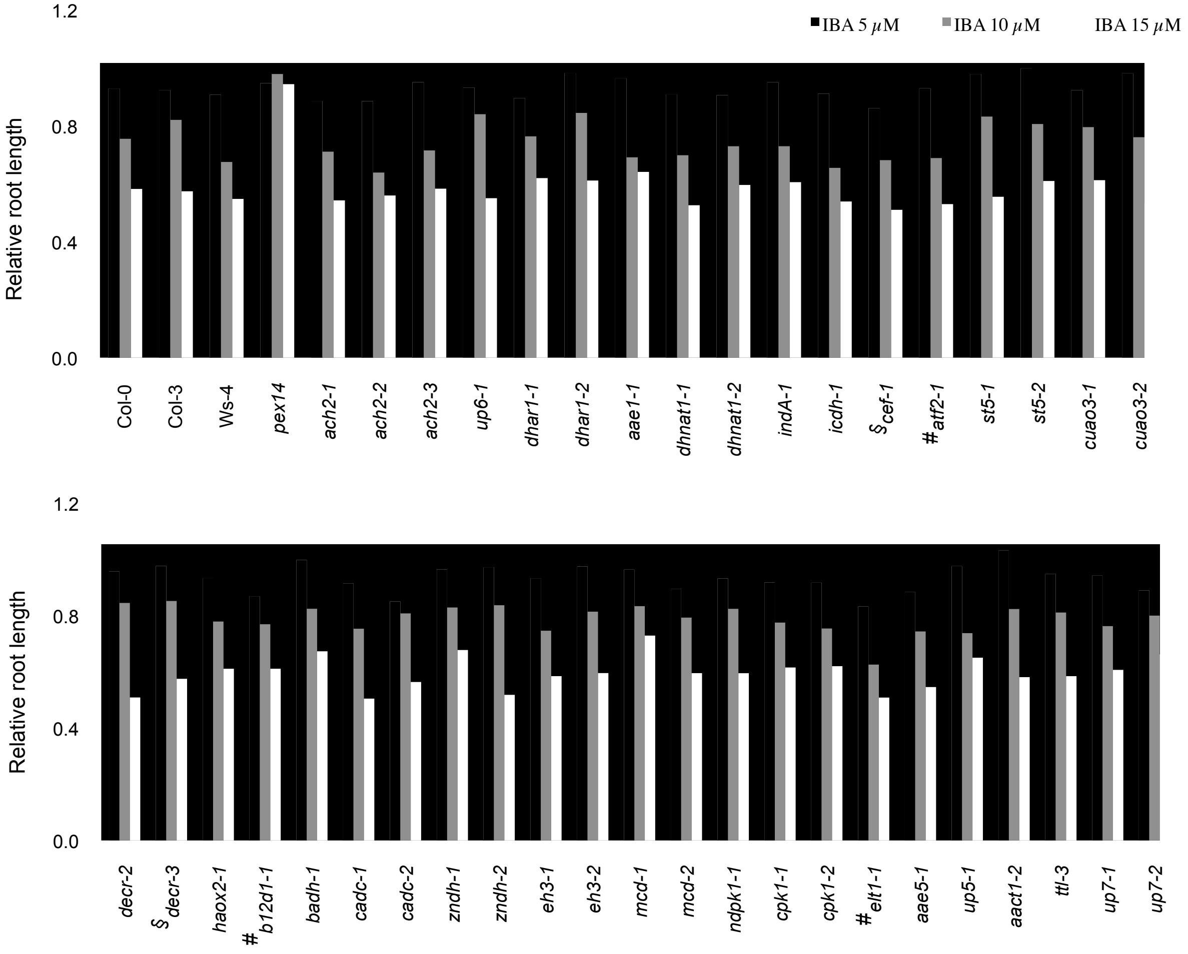

Col-0
Col-3
pex14
ach2-1
ach2-2
ach2-3
up6-1
dhar1-1
dhar1-2
CONTROL
IAA
2,4-D


aae1-1
dhnat1-1
dhnat1-2
inda-1
icdh-1
cef-1
st5-1
st5-2
cuao3-1
CONTROL
IAA
2,4-D


cuao3-2
decr-2
decr-3
haox2-1
badh-1
cadc-1
cadc-2
zndh-1
zndh-2
CONTROL
IAA
2,4-D

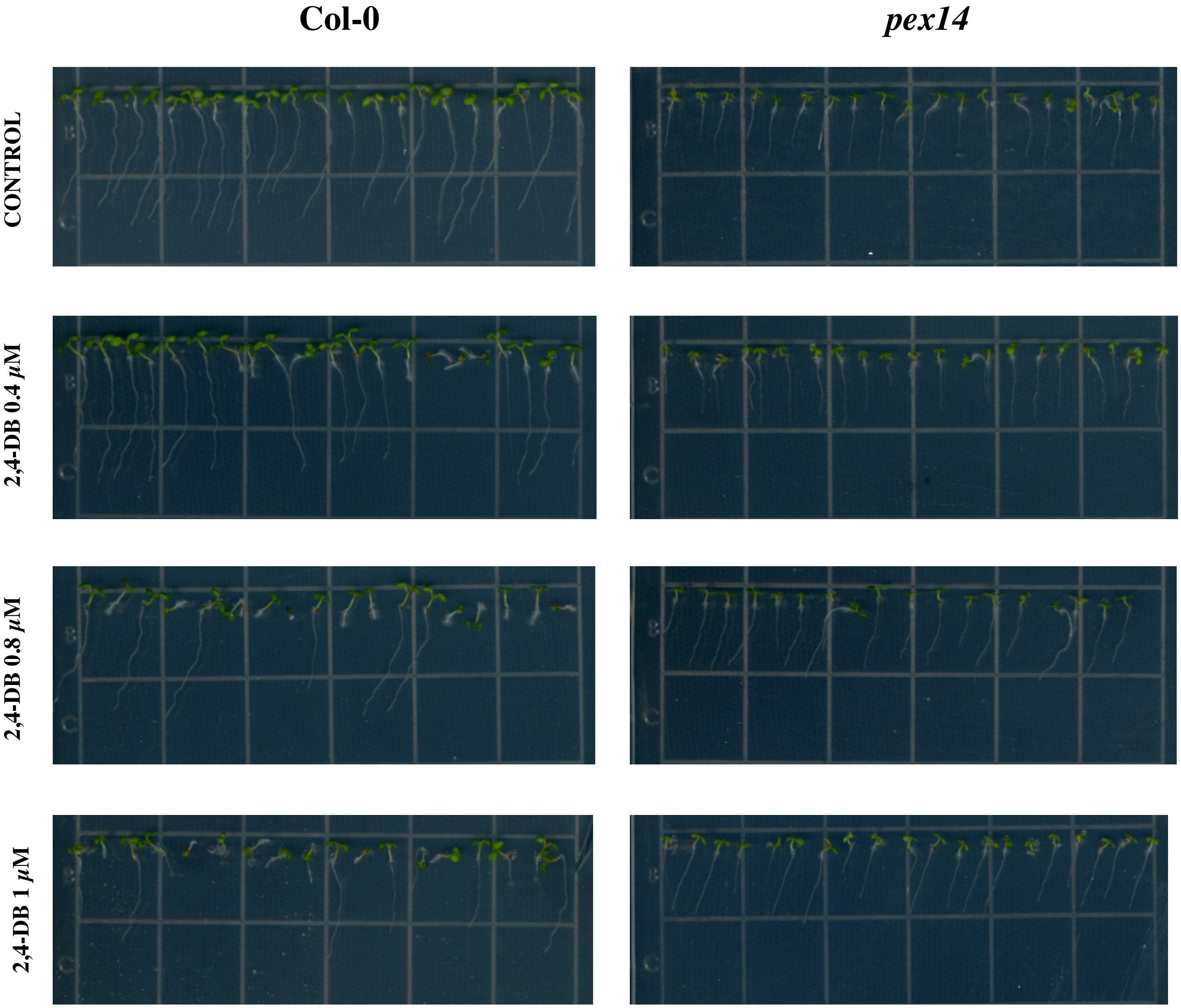


**Supplemental Figure S4.** IAA and 2,4-D responses.
Seven-day-old seedlings grown on 1/2 LS medium supplemented with 0.5% Suc and 100 nM IAA or 2,4-D.

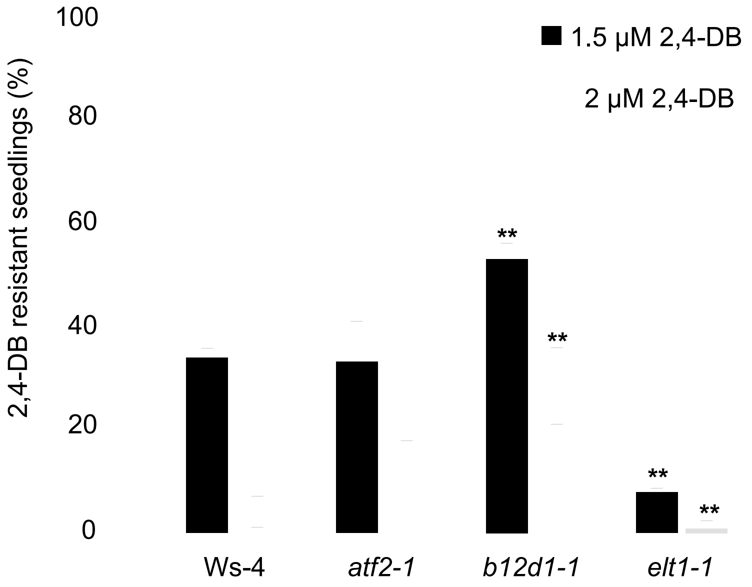


**Supplemental Figure S5.** IBA response of peroxisomal mutants.

Relative root lengths (ratio between root length on IBA vs. without IBA) of 7d seedlings grown on 1/2 LS medium supplemented with 0.5% Suc and 5 µM (black bars), 10 µM (grey bars) or 15 µM (white bars) of IBA are shown. Data represent means ± se of three independent experiments. For each experiment, n≥30. Section and hashtag signs indicate mutants in Col-3 and Ws-4 backgrounds respectively. Except for the control mutant *pex14*, none of the mutants display statistically significant reduction in the response to IBA.

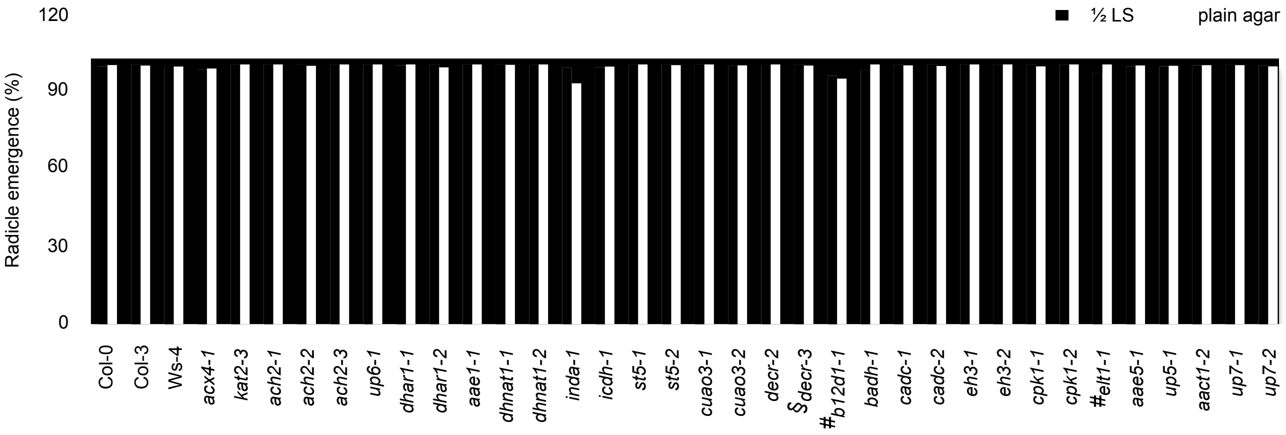


**Supplemental Figure S6.** Responsiveness of Col-0 and *pex14* to 2,4-DB.
Images show 7d seedlings grown on 1/2 LS medium supplemented with 0.5% Suc and 0.4 µM, 0.8 µM or 1 µM 2,4-DB. Scale bar = 1 cm.



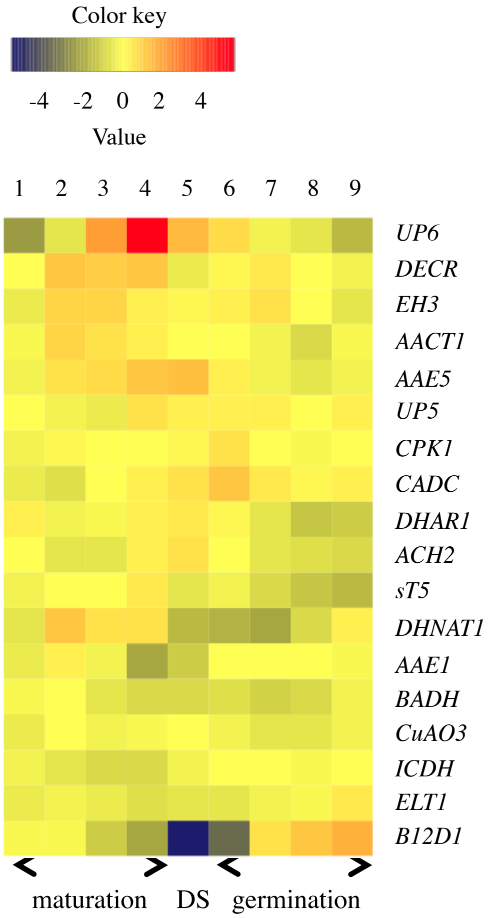
**Supplemental Figure S7.** Responsiveness of mutants in Ws-4 background to 2,4-DB.

Percentage of 7d seedlings with long (resistant) root after growing on 1/2 LS medium supplemented with 0.5% Suc and 1.5 or 2.0 µM of 2,4-DB. Data represent means ± se of three independent experiments. For each experiment, $n \geq 30$. Asterisks indicate changes significantly different from that in the wild type Ws-4. Student's *t* test, *$p<0.01$, ** $p<0.001$.



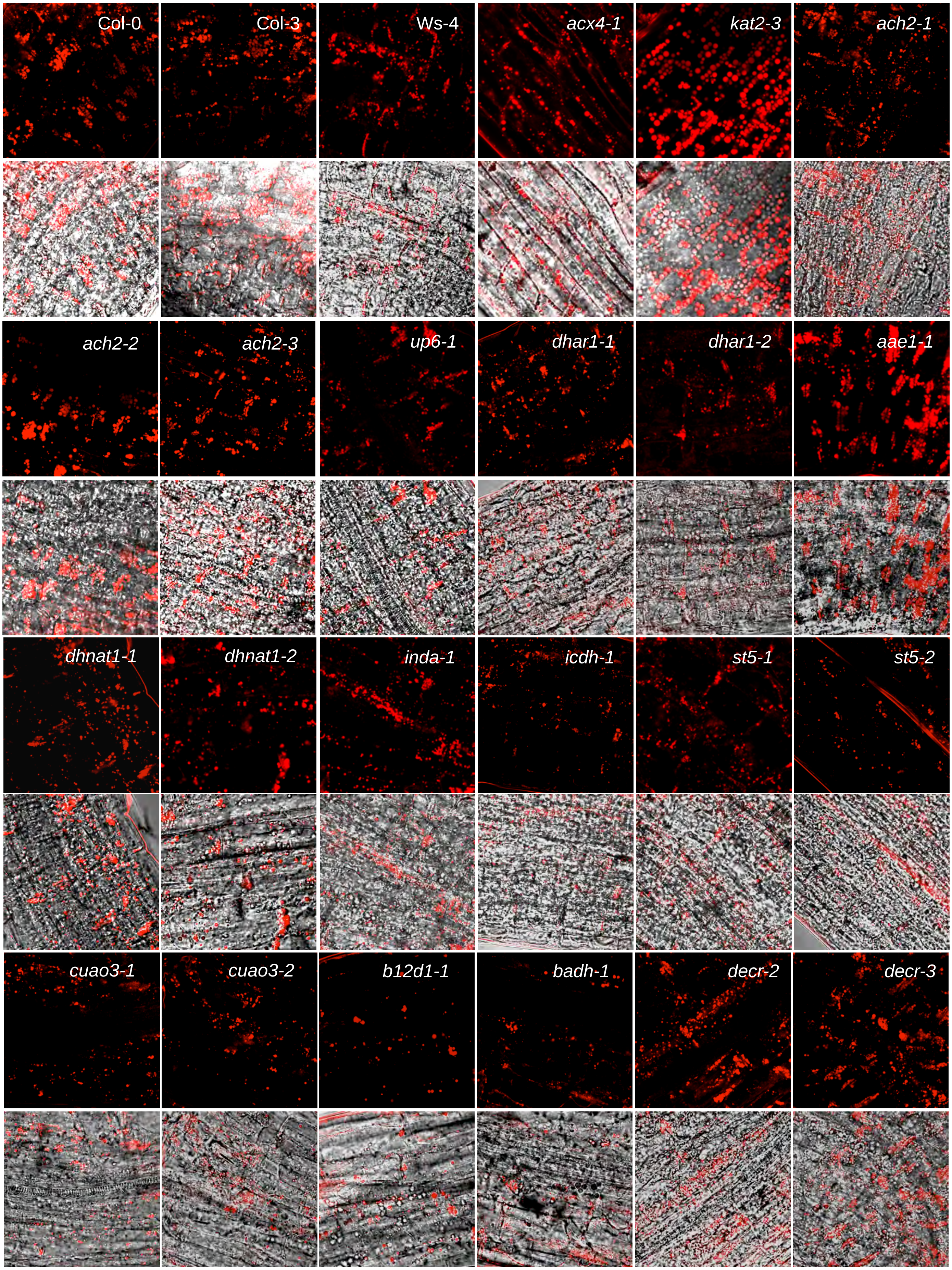
**Supplemental Figure S8**. Seed germination potential of peroxisomal mutants.

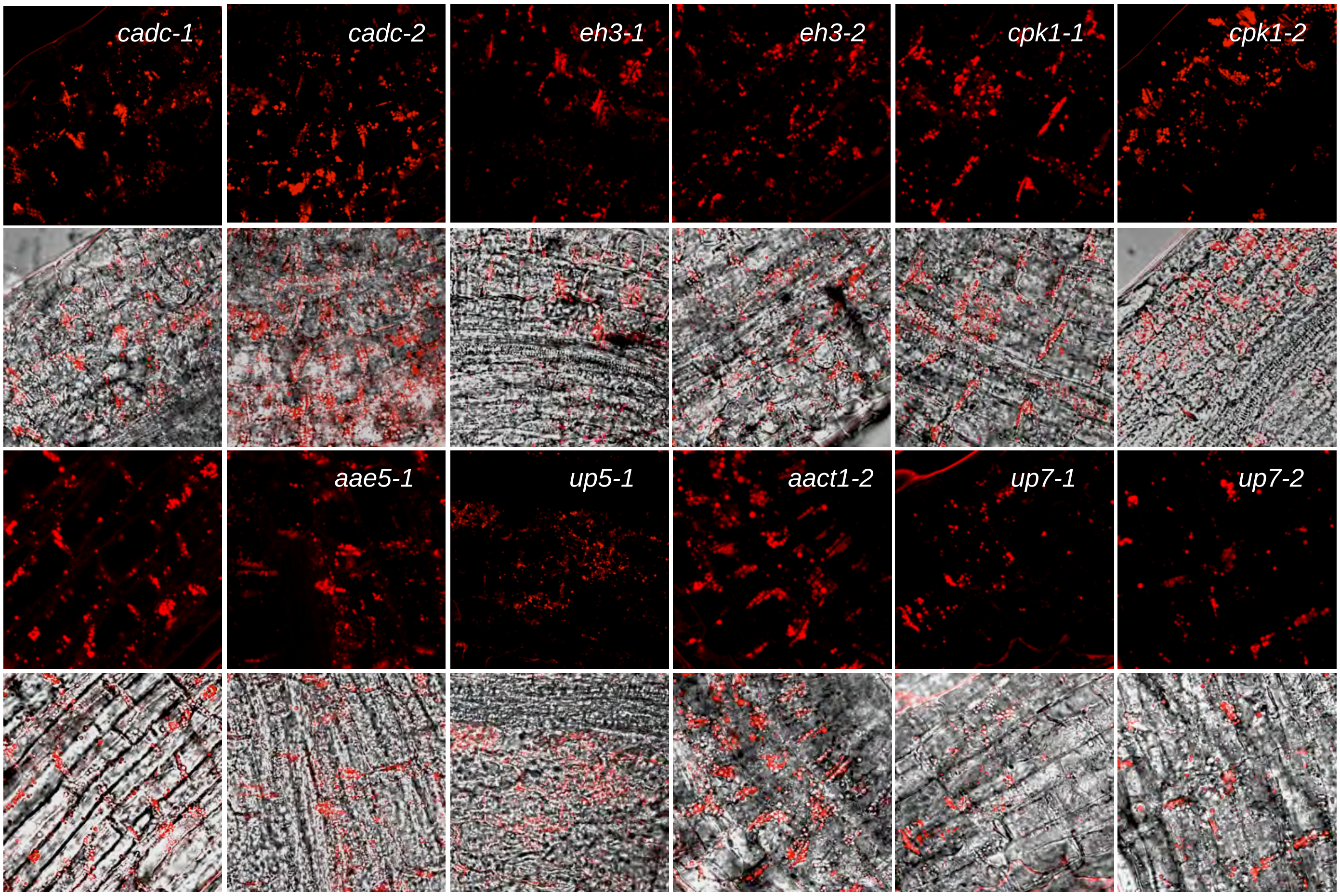
Percentage of radicle emergence from seeds grown on plain agar (0.8% agar) or 1/2 LS medium is presented. Data represent means ± SE of three independent experiments. For each experiment, n = 50. Section and hashtag signs indicate mutants in Col-3 and Ws-4 backgrounds respectively.



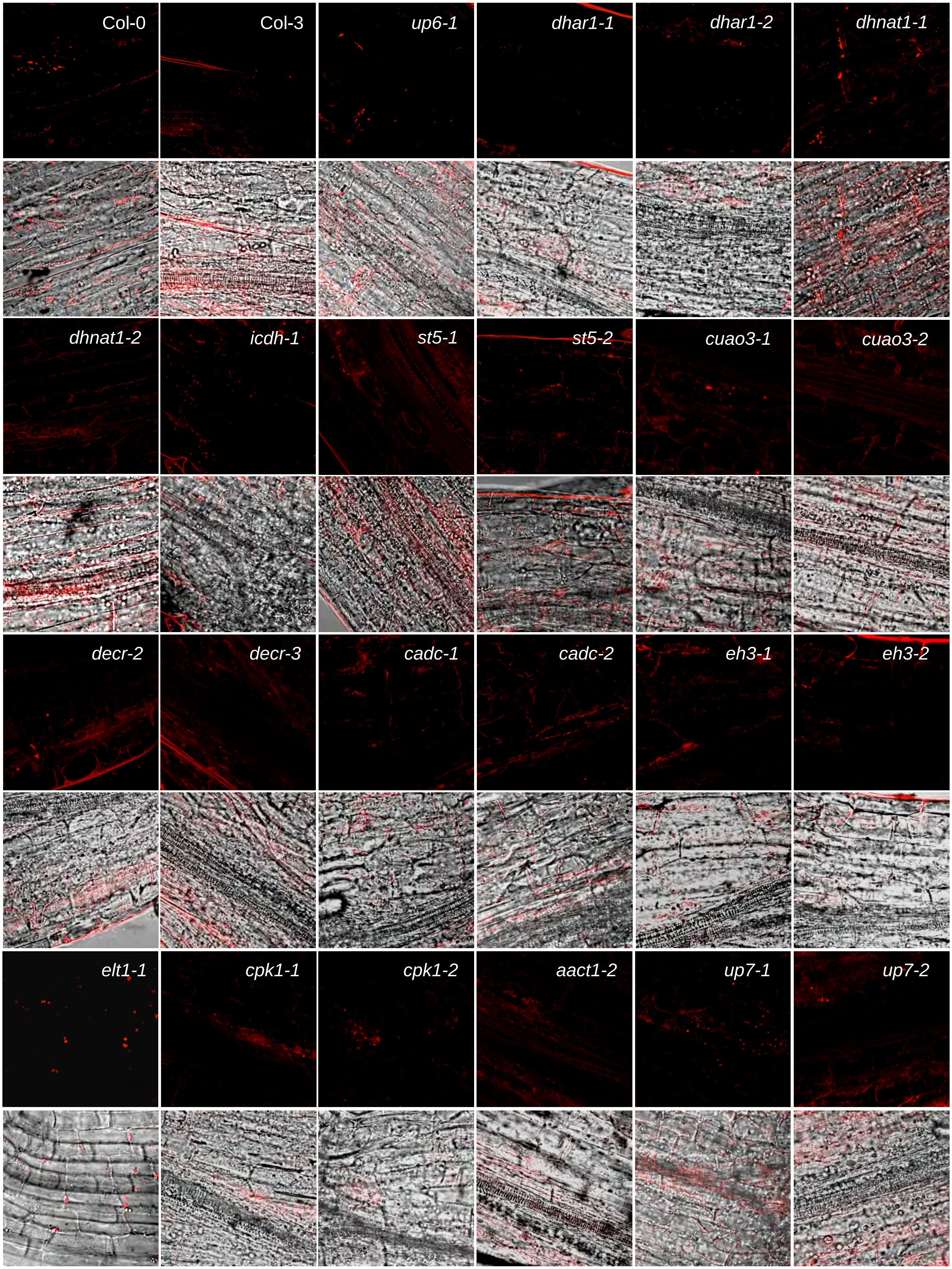
**Supplemental Figure S9**. Heatmap showing relative expression levels of candidate genes in seed maturation and germination.

Log2-normalized expression values during seed maturation and germination were downloaded from BAR expression browser. 1, Seed stage 3 with siliques; 2, Seed stage 5 with siliques; 3, Seed stage 7 without silique; 4, Seed stage 9 without silique; 5, Dry seed (DS); 6, 3-h imbibed seed ; 7, 6-h imbibed seed; 8, 12-h imbibed seed ; 9, 24-h imbibed seed.


Col-0
Col-3
Ws-4
acx4-1
kat2-3
ach2-1
ach2-2
ach2-3
up6-1
dhar1-1
dhar1-2
aae1-1
dhnat1-1
dhnat1-2
inda-1
icdh-1
st5-1
st5-2
cuao3-1
cuao3-2
b12d1-1
badh-1
decr-2
decr-3



**Supplemental Figure S10.** Visualization of hypocotyl oil bodies in 5d etiolated seedlings. Confocal images are from representative 5d mutant or wild-type (Col-0, Col-3, or Ws-4) seedlings grown on 0.8% agar plates. Top row, nile red fluorescence; bottom row, bright-field images. Scale bar = 10 μm.


Col-0
Col-3
up6-1
dhar1-1
dhar1-2
dhnat1-1
dhnat1-2
icdh-1
st5-1
st5-2
cuao3-1
cuao3-2
decr-2
decr-3
cadc-1
cadc-2
eh3-1
eh3-2
elt1-1
cpk1-1
cpk1-2
aact1-2
up7-1
up7-2

**Supplemental Figure S11.** Visualization of hypocotyl oil bodies in 7d etiolated seedlings.
Confocal images of representative seedlings grown on 0.8% agar plates are shown. Top row, nile red fluorescence; bottom row, merge of nile red images with bright-field images. Scale bar, 10 μM.

**Supplemental Table S1.** Lines without T-DNA insertion and lines for which homozygotes could not be identified.

***Mutants without T-DNA insertion:***

| Gene Locus | Acronym | Annotation | PTS | Line | Ecotype |
|---|---|---|---|---|---|
| At1g20560 | AAE1 | Acyl-activating enzyme isoform 1 | SKL | SALK_082448 | Col-0 |
| | | | | SALK_082430 | Col-0 |
| | | | | SALK_082437 | Col-0 |
| At2g26230 | Uri | Uricase | SKL | CS812424 | Col-3 |
| | | | | SALK_131436 | Col-0 |
| At5g58220 | TTL1/ ALNS | Transthyretin-like protein 1/ Allantoin synthase | RLx$_5$HL | CS875458 | Col-0 |

***List of heterozygous mutants:***

| Gene Locus | Acronym | Annotation | PTS | Line | Ecotype |
|---|---|---|---|---|---|
| At1g54340 | ICDH / IDHP1 | NADP-dependent isocitrate deshydrogenase | SRL | SALK_039193C | Col-0 |
| At2g26230 | Uri | Uricase | SKL | SALK_131438 | Col-0 |
| At3g02360 | 6PGDH | Phosphogluconate dehydrogenase | SKI | SALK_071687 | Col-0 |
| | | | | GK_692E09 | Col-0 |
| At3g48140 | B12D1 | Senescence-associated protein/ B12D-related protein | | SALK_006284C | Col-0 |
| At4g39660 | AGT2 | Alanine: glyoxylate aminotransferase 2 | SRL | SALK_003381 | Col-0 |
| | | | | GK_325A04 | Col-0 |

**Supplemental Table S2.** Identification of peroxisomal proteins analyzed in this study from previous proteomic studies.

| | | | Etiolated seedlings | | Greenings cotyledons | Cell culture | Green Leaves |
|---|---|---|---|---|---|---|---|
| **Gene Locus** | **Acronym** | **Annotation** | **Fukao et al, 2003** | **Quan et al, 2013** | **Fukao et al., 2002** | **Eubel et al, 2008** | **Reumann et al, 2009** |
| At1g01710 | ACH2 | Acyl-CoA thioesterase 2 | | X | | X | X |
| At1g16730 | UP6 | Unknown protein 6 | | X | | | X |
| At1g19570 | DHAR1 | Dehydroascorbate reductase | | | | | X |
| At1g20560 | AAE1 | Acyl-activating enzyme isoform 1 | | | X | X | X |
| At1g48320 | DHNAT1/sT1 | DHNA-CoA thioesterase 1/ Small thioesterase 1 | | X | | | X |
| At1g50510 | INDA | Indigoidine synthase A | | X | | X | X |
| At1g54340 | ICDH | NADP-dependent isocitrate deshydrogenase | X | X | | X | X |
| At1g64850 | CEF | Calcium binding EF-hand | | | | | X |
| At1g77540 | ATF2 | Acetyltransferase 2 | | X | | | X |
| At2g29590 | sT5 | Small thioesterase 5 | | | | | X |
| At2g42490 | CuAO3 | Copper amine oxidase 3 | | X | | X | X |
| At3g12800 | SDRb / DECR | Short-chain dehydrogenase/ reductase isoform b/ 2,4-dienoyl-CoA reductase | | X | | X | X |
| At3g14150 | HAOX2 | Hydroxy-acid oxidase isoform 2 | | | | | X |
| At3g48140 | B12D1 | B12D-related protein | | | | | X |
| At3g48170 | BADH | Aldehyde deshydrogenase | | X | | X | X |
| At3g55640 | CADC | $Ca^{2+}$-dependent carrier | | X | | X | X |
| At3g56460 | ZnDH | Zinc-binding dehydrogenase | | X | | X | X |
| At4g02340 | EH3 | Epoxide hydrolase isoform 3 | | | | X | X |
| At4g04320 | MCD | Malonyl-CoA decarboxylase | | | | X | X |
| At4g09320 | NDPK1 | Nucleoside diphosphate kinase type 1 | | X | | | X |
| At5g04870 | CPK1 | Calcium dependent protein kinase 1 | | | | | |
| At5g11910 | ELT1 | Esterase/ lipase/ thioesterase family isoform 1 | | | | | X |
| At5g16370 | AAE5 | Acyl-activating enzyme 5 | | X | X | X | X |
| At5g44250 | UP5 | Unknown protein 5 | | | | | X |
| At5g47720 | AACT1 | Acetoacetyl-CoA thiolase 1.3 | | X | | | |
| At5g58220 | TTL | Transthyretin-like protein | | | | X | X |
| At5g65400 | UP7 | Serine Hydrolase 1 | | | | | X |

**Supplemental Table S3.** Measurements for the sucrose dependence assays.

Relative hypocotyl (dark) and root (light) lengths (-Suc versus +Suc) of 7d seedlings grown on 1/2 LS medium supplemented with or without Suc. Data represent means ± SE of three independent experiments. For each experiment, n = 50.

| | | DARK | | | LIGHT | | |
|---|---|---|---|---|---|---|---|
| | | mean | SE | Student test | mean | SE | Student test |
| | Col0 | 0.85 | 0.027 | - | 0.84 | 0.056 | - |
| | Col3 | 0.90 | 0.045 | - | 0.88 | 0.038 | - |
| | Ws4 | 0.80 | 0.024 | - | 0.94 | 0.039 | - |
| | *pex14* | 0.22 | 0.030 | 2.70113E-21 | 0.14 | 0.019 | 5.06518E-28 |
| **At1g01710** | *ach2-1* | 0.81 | 0.046 | 0.099780022 | 0.85 | 0.054 | 0.781488227 |
| | *ach2-2* | 0.88 | 0.066 | 0.14394992 | 0.95 | 0.036 | 0.000733983 |
| | *ach2-3* | 0.91 | 0.034 | 0.000904445 | 0.83 | 0.042 | 0.628189991 |
| **At1g16730** | *up6-1* | 0.94 | 0.078 | 0.004495419 | 0.89 | 0.039 | 0.163499548 |
| **At1g19570** | *dhar1-1* | 0.87 | 0.014 | 0.088216133 | 0.88 | 0.021 | 0.232105387 |
| | *dhar1-2* | 0.88 | 0.017 | 0.06028705 | 0.80 | 0.049 | 0.267459055 |
| **At1g20560** | *aae1-1* | 0.97 | 0.056 | 6.87515E-05 | 0.85 | 0.052 | 0.791591679 |
| **At1g48320** | *dhnat1-1* | 0.81 | 0.060 | 0.121543694 | 0.82 | 0.060 | 0.538924628 |
| | *dhnat1-2* | 0.81 | 0.039 | 0.327294242 | 0.82 | 0.029 | 0.438858416 |
| **At1g50510** | *inda-1* | 0.83 | 0.027 | 0.184775749 | 0.76 | 0.010 | 0.0139893 |
| **At1g54340** | *icdh-1* | 0.74 | 0.037 | 0.000153897 | 0.85 | 0.045 | 0.941075033 |
| **At1g64850** | *cef-1* | 0.83 | 0.028 | 0.152712563 | 0.83 | 0.077 | 0.33154256 |
| **At1g77540** | *atf2-1* | 0.84 | 0.013 | 0.223973757 | 0.78 | 0.069 | 0.010691507 |
| **At2g29590** | *st5-1* | 0.98 | 0.063 | 5.76434E-05 | 0.80 | 0.096 | 0.260361059 |
| | *st5-2* | 0.94 | 0.025 | 3.03002E-05 | 0.96 | 0.086 | 0.003391833 |
| **At2g42490** | *cuao-1* | 0.86 | 0.037 | 0.415983857 | 0.90 | 0.041 | 0.146159872 |
| | *cuao-2* | 0.92 | 0.034 | 0.009217858 | 0.82 | 0.017 | 0.595812737 |
| **At3g12800** | *decr-2* | 1.02 | 0.017 | 1.65719E-07 | 0.86 | 0.117 | 0.672608646 |
| | *decr-3* | 1.04 | 0.022 | 0.013135616 | 0.90 | 0.065 | 0.672542951 |
| **At3g14150** | *haox1-1* | 0.95 | 0.030 | 2.211E-05 | 0.91 | 0.057 | 0.03432197 |
| **At3g48140** | *b12d1-1* | 0.79 | 0.014 | 0.737902312 | 0.89 | 0.065 | 0.252919227 |
| **At3g48170** | *badh-1* | 0.86 | 0.116 | 0.692022112 | 0.79 | 0.058 | 0.086638398 |
| **At3g55640** | *cadc-1* | 1.00 | 0.021 | 1.6556E-07 | 0.90 | 0.034 | 0.064334466 |
| | *cadc-2* | 0.80 | 0.066 | 0.0520033 | 1.05 | 0.033 | 3.16612E-07 |
| **At3g56460** | *zndh-1* | 0.97 | 0.027 | 3.21522E-06 | 0.90 | 0.066 | 0.09468511 |
| | *zndh-2* | 0.99 | 0.050 | 6.47175E-06 | 0.89 | 0.012 | 0.309884302 |
| **At4g02340** | *eh3-1* | 0.92 | 0.037 | 0.00082387 | 0.89 | 0.107 | 0.175933598 |
| | *eh3-2* | 0.96 | 0.054 | 0.000134123 | 0.89 | 0.087 | 0.198442622 |
| **At4g04320** | *mcd-1* | 1.01 | 0.168 | 0.009532992 | 0.90 | 0.160 | 0.236621439 |
| | *mcd-2* | 0.86 | 0.111 | 0.797343451 | 0.90 | 0.091 | 0.10510667 |
| **At4g09320** | *ndpk-1* | 0.81 | 0.057 | 0.150957756 | 0.89 | 0.028 | 0.287200891 |
| **At5g04870** | *cpk1-1* | 0.94 | 0.076 | 0.005890754 | 0.85 | 0.073 | 0.784468002 |
| | *cpk1-2* | 0.98 | 0.063 | 8.16885E-05 | 0.83 | 0.071 | 0.693940174 |
| **At5g11910** | *elt1-1* | 0.89 | 0.053 | 0.067961956 | 0.91 | 0.039 | 0.324510445 |
| **At5g16370** | *aae5-1* | 0.95 | 0.067 | 0.003761092 | 0.88 | 0.024 | 0.290013306 |
| **At5g44250** | *up5-1* | 0.79 | 0.047 | 0.00818022 | 0.86 | 0.054 | 0.49299674 |
| **At5g47720** | *aact1-2* | 0.81 | 0.099 | 0.355669223 | 0.89 | 0.052 | 0.233434107 |
| **At5g58220** | *ttl-3* | 0.99 | 0.028 | 5.63043E-07 | 0.94 | 0.038 | 0.009693737 |
| **At5g65400** | *up7-1* | 0.89 | 0.103 | 0.266844759 | 0.76 | 0.024 | 0.013005102 |
| | *up7-2* | 0.86 | 0.092 | 0.671106101 | 0.86 | 0.040 | 0.713764227 |

**Supplemental Table S4**. Log2 expression values downloaded from BAR expression browser to generate heatmap shown in Supplemental Figure S8

| Locus | Annotation | Acronym | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 |
|---|---|---|---|---|---|---|---|---|---|---|---|
| At1g16730 | Unknown protein 6 | UP6 | -2.3 | -0.4 | 2.3 | 5.9 | 1.7 | 0.9 | -0.2 | -0.5 | -1.6 |
| At3g12800 | Short-chain dehydrogenase/ reductase isoform b | DECR | 0.1 | 1.4 | 1.2 | 1.3 | -0.3 | 0.3 | 0.6 | 0.2 | -0.1 |
| At4g02340 | Epoxide hydrolase isoform 3 | EH3 | -0.3 | 1 | 1.1 | 0.5 | 0.3 | 0.5 | 0.7 | 0.1 | -0.4 |
| At5g47720 | Acetoacetyl-CoA thiolase 1.3 | AACT1 | 0 | 1.1 | 0.8 | 0.4 | 0.2 | 0.1 | -0.1 | -0.7 | 0 |
| At5g16370 | Acyl-activating enzyme 5 | AAE5 | -0.1 | 0.8 | 0.9 | 1.4 | 1.6 | 0.5 | -0.1 | -0.4 | -0.2 |
| At5g44250 | Unknown protein 5 | UP5 | 0.2 | -0.2 | -0.3 | 0.7 | 0.5 | 0.5 | 0.5 | 0.2 | 0.5 |
| At5g04870 | Calcium dependent protein kinase 1 | CPK1 | -0.1 | 0.3 | 0.1 | 0.1 | 0.3 | 0.7 | 0.1 | 0 | 0.2 |
| At3g55640 | Ca2+-dependent carrier | CADC | -0.3 | -0.6 | 0.2 | 0.5 | 0.7 | 1.4 | 0.6 | 0.3 | 0.4 |
| At1g19570 | Dehydroascorbate reductase | DHAR1 | 0.4 | -0.1 | 0 | 0.4 | 0.6 | 0.3 | -0.5 | -1.2 | -1.1 |
| At1g01710 | Acyl-CoA thioesterase 2 | ACH2 | 0.1 | -0.4 | -0.5 | 0.4 | 0.7 | 0.2 | -0.4 | -0.6 | -0.8 |
| At2g29590 | Small thioesterase 5 | sT5 | -0.1 | 0.1 | 0.2 | 0.6 | -0.4 | -0.1 | -0.7 | -1.2 | -1.6 |
| At1g48320 | DHNA-CoA thioesterase 1/ Small thioesterase 1 | DHNAT1 | -0.5 | 1.3 | 0.8 | 0.7 | -1.5 | -1.7 | -2 | -0.8 | 0.4 |
| At1g20560 | Acyl-activating enzyme isoform 1 | AAE1 | -0.3 | 0.5 | -0.1 | -2 | -1 | 0.1 | 0.2 | 0.1 | 0 |
| At3g48170 | Aldehyde deshydrogenase | BADH | 0 | 0.2 | -0.4 | -0.7 | -0.7 | -0.6 | -0.9 | -0.7 | -0.1 |
| At2g42490 | Copper amine oxidase 3 | CuAO3 | -0.3 | 0.1 | -0.1 | 0 | 0.2 | -0.2 | -0.4 | -0.4 | -0.1 |
| At1g54340 | NADP-dependent isocitrate deshydrogenase | ICDH | -0.1 | -0.4 | -0.7 | -0.7 | -0.1 | 0.2 | 0.1 | 0 | 0.1 |
| At5g11910 | Esterase/ lipase/ thioesterase family isoform 1 | ELT1 | -0.3 | -0.2 | -0.3 | -0.6 | -0.5 | -0.5 | -0.1 | 0 | 0.6 |
| At3g48140 | B12D-related protein | B12D1 | 0 | 0 | -1 | -2 | -5.6 | -3.6 | 0.7 | 1.4 | 1.8 |

| Number as | Developmental stage |
|---|---|
| 1 | Seed stage 3 with siliques |
| 2 | Seed stage 5 with siliques |
| 3 | Seed stage 7 without silique |
| 4 | Seed stage 9 without silique |
| 5 | Dry seed |
| 6 | 3-h imbibed seed |
| 7 | 6-h imbibed seed |
| 8 | 12-h imbibed seed |
| 9 | 24-h imbibed seed |

**Supplemental Table S5.** Primers used for genotyping and RT-PCR analysis.
P1 and P2 were used for RT-PCR; P3 and P4 were used for genotyping.

| Name | | | Sequence |
|---|---|---|---|
| LB_SALK | | | ATTTTGCCGATTTCGGAAC |
| LB_SAIL | | | TAGCATCTGAATTTCATAACCAATCTCGATACAC |
| LB_GABI | | | ATATTGACCATCATACTCATTGC |
| LB_Ws4 | | | CGTGTGCCAGGTGCCCACGGAATAGT |
| At1g01710 | *ACH2* | P1 | CGAGTTCCTTGGAAACGTCC |
| | | P2/ P4.2 | TCAGAGCTTCGACGTGCCGG |
| | | P3.1 | GATGTGGTTTCACCGACCTC |
| | | P3.2 | CACCATTATCTGCTACAGCTTC |
| | | P4.1 | GATCCAAAATGGGTCGTACG |
| At1g16730 | *UP6* | P1/ P3 | CATCACCGAATATCCGCCAC |
| | | P2 | AGGTTTGGCGAGAGAGCTGA |
| | | P4 | ACACATCTCAAGCTCTGATAC |
| At1g19570 | *DHAR1* | P1 | TCCTGATCATCTCGGCGACT |
| | | P2 | TCAAGGGTTAACCTTGGGAG |
| | | P3 | CTCTCTGACAAACCCCAGTG |
| | | P4 | GTCCTTGCGAAGAGCGACT |
| At1g20560 | *AAE1* | P1/ P3 | GCTCCGTCAAGTACACGTG |
| | | P2/ P4 | GCACTGGCCTTACACCCGTC |
| At1g48320 | *DHNAT1* | P1/ P3.1 | GCATCGTCCAACACCAAAGC |
| | | P2/ P4.1/ P4.2 | CTTTGCGACCATTTTGAGCATG |
| | | P3.2 | CTTTGGTCCGAAAGACTCTC |
| At1g50510 | *INDA* | P1 | ATGGCTTCTTCTTTAGCTCAAT |
| | | P2/ P4 | CGTGCAAGTGATGTGCCTCC |
| | | P3 | CGGTGCAACTACAGTCTCTG |
| At1g54340 | *ICDH* | P1 | ATGGAATTCGAGAAGATCAA |
| | | P2 | TGGAGTTGTTGCCTAACAATC |
| | | P3 | TCACTGCGGGGAATTCAAAG |
| | | P4 | CGGACTAATCGTCGCACAC |
| At1g64850 | *CEF* | P1 | GAGTGGAGACATAAGCAGGT |
| | | P2 | CATTACGTATTGACTAGATCC |
| | | P3 | GCTCCATGTTTCTGTGGTATTC |
| | | P4 | GATCGAAATGAGGACCAGGC |
| At1g77540 | *ATF2* | P1 | ATGACGAACACGGCGGCGAC |
| | | P2/ P4 | CGTAGACTTGAATACCTCTG |
| | | P3 | GCTCAATTGGCAGAGAGAAG |
| At2g29590 | *sT5* | P1 | GCAATTGAGCGATGAGGTGG |
| | | P2/ P4 | TCAGAGCTTACTAGCTTGTCT |
| | | P3 | GTGGAGGAATCTGAGGAACA |
| At2g42490 | *CUAO3* | P1 | GCTGTCACTCGGGGTGGACA |
| | | P2/ P4.1 | ACCAGTCTGAAGAGCTTTCG |
| | | P3.1 | GACGAGCGAGGTGAGAACAA |
| | | P3.2 | GATTGGCCGGTTATGCCCGT |
| | | P4.2 | CTGGTTCGTCGGAGTTGGAT |
| At3g12800 | *DECR* | P1/ P3.1 | CTCTCCGTTCAAACCTGATG |
| | | P2 | ACAGCTTGCTGGTTGGGAGAC |
| | | P3.2 | GCATTGGAGTGGGGAACTG |
| | | P4.1 | GGACCTGGAGCAATCCCGT |
| | | P4.2 | ATGAGAAACAGAGAGAGTGAC |
| At3g14150 | *HAOX2* | P1 | GGCTAAACAAGCCCTCCCTA |
| | | P2 | GAAGTCTCTCATTCTCTGTCC |
| | | P3 | GATTGCTTCCAGTTGTAACGC |
| | | P4 | CTCAGGACAAAGGGGAGAGC |
| At3g48140 | *B12D1* | P1/ P3 | ATGGCGAGCCGTTGGTTGAG |
| | | P2/ P4 | CAGTATGTAGGATCAGTGAAG |
| At3g48170 | *BADH* | P1/ P3 | ATGGCGATTACGGTGCCGAGAC |
| | | P2 | CAGAGCTTGGAAGGAGGTTTG |
| | | P4 | ACGCCAATGGGTTCCTTCAG |
| At3g55640 | *CADC* | P1/ P3.1 | GCGTCGCAGCTCTTAGCC |
| | | P2/ P4.2 | GCAAATCCCTACACCAGGTAC |
| | | P3.2 | GGTGTTGGGCCTAGTATTGC |
| | | P4.1 | CTGAGCAGCAAGACGAGTTC |
| At3g56460 | *ZNDH* | P1 | ATGGAGGCTTTGGTTTGCCG |

| | | | |
|---|---|---|---|
| | | P2 | CAGTCTTGTGGTCGAGAGCA |
| | | P3 | TAAACGGCGTCGTATCAAATC |
| | | P4 | TAAAGACCATGAACCGTCCAG |
| At4g02340 | *EH3* | P1 | ATGGAGAAGATAGAGCACAC |
| | | P2 | TGTTCGGCGATGATTACTACA |
| | | P3 | CTACAAGGATGCGGTTTCGC |
| | | P4 | TGTTATGTCTAGATCACCCAC |
| At4g04320 | *MCD* | P1 | GCAAGAAAAATCTAGCGATT |
| | | P2/ P4.1 | TGCCTCCACTTTGACGAATAC |
| | | P3.1 | ACCAGAGAACCAAGCAACATG |
| | | P3.2 | TGAAGGAGAAACTCGGTATGT |
| | | P4.2 | GAGGGCATGTTCCTCTTCTG |
| At4g09320 | *NDPK1* | P1/ P3 | TTGCCTCCTACGAATCACAAG |
| | | P2/ P4 | ATAGACCCAAGGGTGAACGC |
| At5g04870 | *CPK1* | P1 | CAAGCAGAAATGGCTTCTTGC |
| | | P2 | CAGGTCCTCCTGTGATGCTTC |
| | | P3 | AGTTCCTCCATTCTGGGCTG |
| | | P4 | GTGATATAGCCGCTCCCATC |
| At5g11910 | *ELT1* | P1/ P3 | ATGTCAGAGACTCGCCGGAA |
| | | P2 | CGCGATGTAATAGGAACAAC |
| | | P4 | AAGTAGTCCTTACCAAGCCG |
| At5g16370 | *AAE5* | P1/ P3 | GCGCCGCAAACTCGCCGCCG |
| | | P2 | CGACTCAACCTCGTCGTACC |
| | | P4 | CTGAAATTCGTTAGTCGCCG |
| At5g44250 | *UP5* | P1 | CAACGGAGGAGAAAGCGAAGC |
| | | P2 | CTCTTCCCCGGTCTCCGCCT |
| | | P3 | AAAACATCATCAAATAGTTACGGATG |
| | | P4 | AGGAACTGGCTTTGCTTTGAG |
| At5g47720 | *AACT1* | P1 | ATGGCTCCGCCTGTCTCTGA |
| | | P2 | TCAGAGTGCCGAATATCCGA |
| | | P3 | CTACAGGTGGTAGCTCTAGC |
| | | P4 | GCTGTGTCCGCTCCCTAGCC |
| At5g58220 | *TTL* | P1 | GAATGGAAGGTTTGCTGTGG |
| | | P2/ P4 | CTAGCTCCCACGGTATGTGG |
| | | P3 | ACAGCTCTAGCTCTCCT |
| At5g65400 | *UP7* | P1 | ATGTTAGGATACTCCTATCC |
| | | P2/ P4.1 | AGAAAGCATCTGCCTAATGCT |
| | | P3.1 | CTGCAGCTATTCCTGGAATG |
| | | P3.2 | CAGTCAAAATTGCCGAAAGAC |
| | | P4.2 | CGCCAAAGAATCAAAACAAAC |