

SUPPLEMENTARY FIGURE LEGENDS

Fig S1. Schematic illustration of the radial pattern and the position of the middle cortex in the Arabidopsis root.

Fig S2. Gene-ontology analysis of genes altered in *spy-3* root. Functional categorization was based on annotation for GO Biological Process.

Fig S3. GO enrichment analysis of genes altered by the *spy* mutation. The AmiGO program was used for this analysis. Shown: biological processes, molecular functions, and cellular compartments represented by the genes down-regulated (A–C) and up-regulated (D) in *spy-3* root.

Fig S4. The *MLI*, *IRX3* and *SUC2* promoters confer expression in the epidermis, xylem, and phloem, respectively in the Arabidopsis root. Shown: the GUS staining pattern in the roots of one-week-old transgenic plants expressing the GUS reporter gene under the control of these promoter sequences.

Fig S5. Confocal-microscopy images showing middle cortex in the roots of one-week-old root of *spy-12*, *spy-13*, *spy-15*, and *spy-17* seedlings. Framed areas are shown at the right at a higher magnification.

mc, middle cortex; c, cortex; e, endodermis. Bars = 20 μ m.

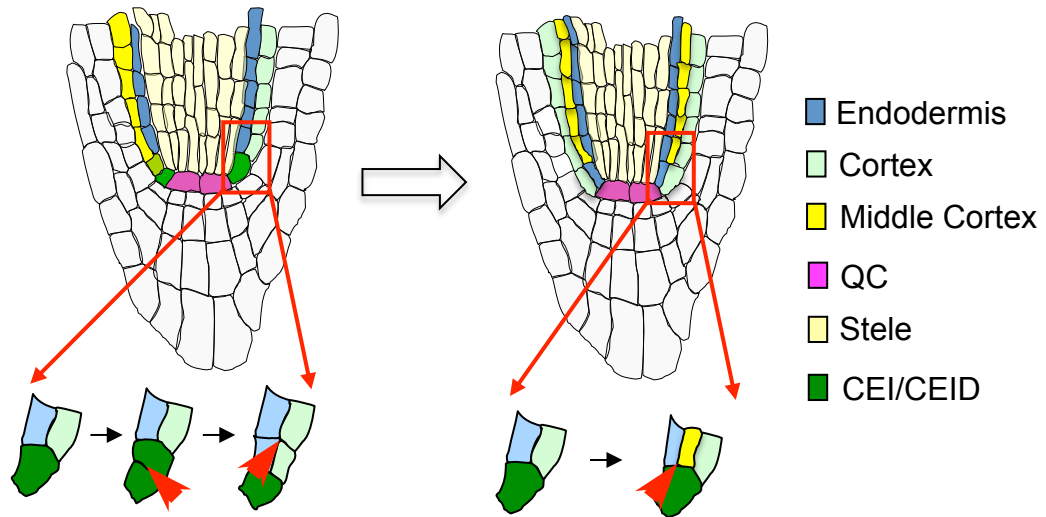


Fig S1. Schematic illustration of the radial pattern and the position of the middle cortex in the Arabidopsis root.

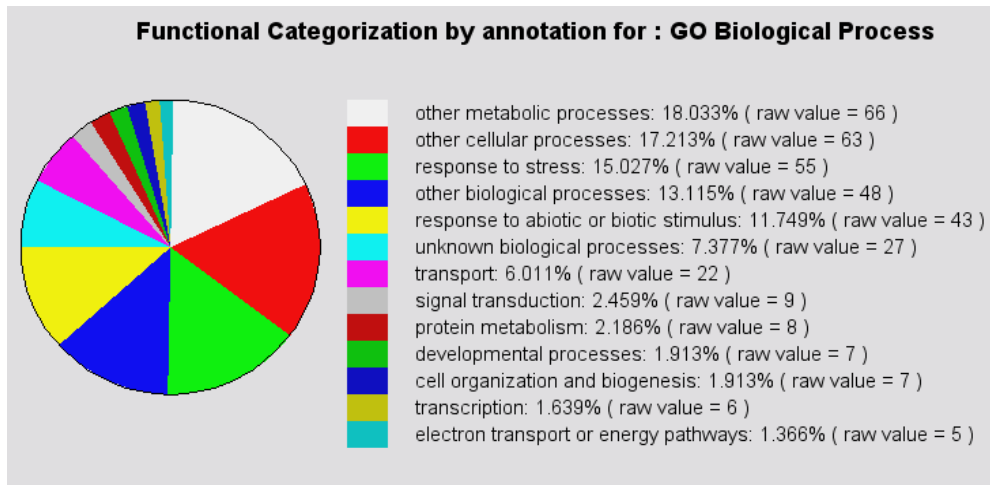


Fig S2. Gene-ontology analysis of genes altered in *spy-3* root. Functional categorization was based on annotation for GO Biological Process.

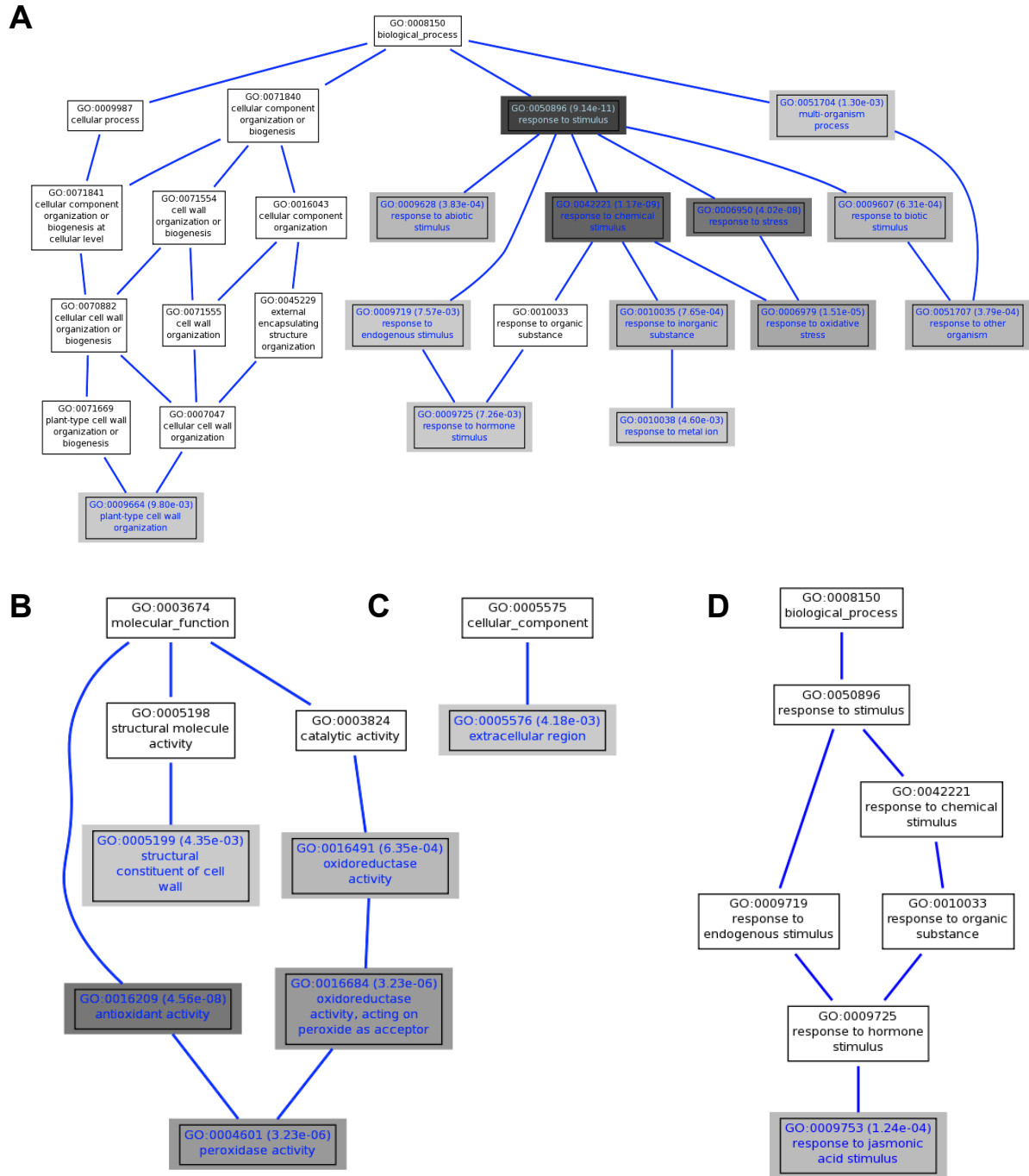


Fig S3. GO enrichment analysis of genes altered by the *spy* mutation. The AmiGO program was used for this analysis. Shown: biological processes, molecular functions, and cellular compartments represented by the genes down-regulated (A–C) and up-regulated (D) in *spy-3* root.

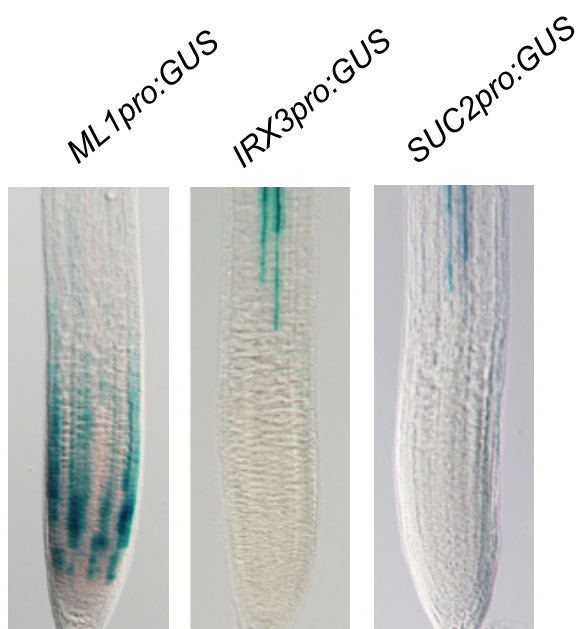


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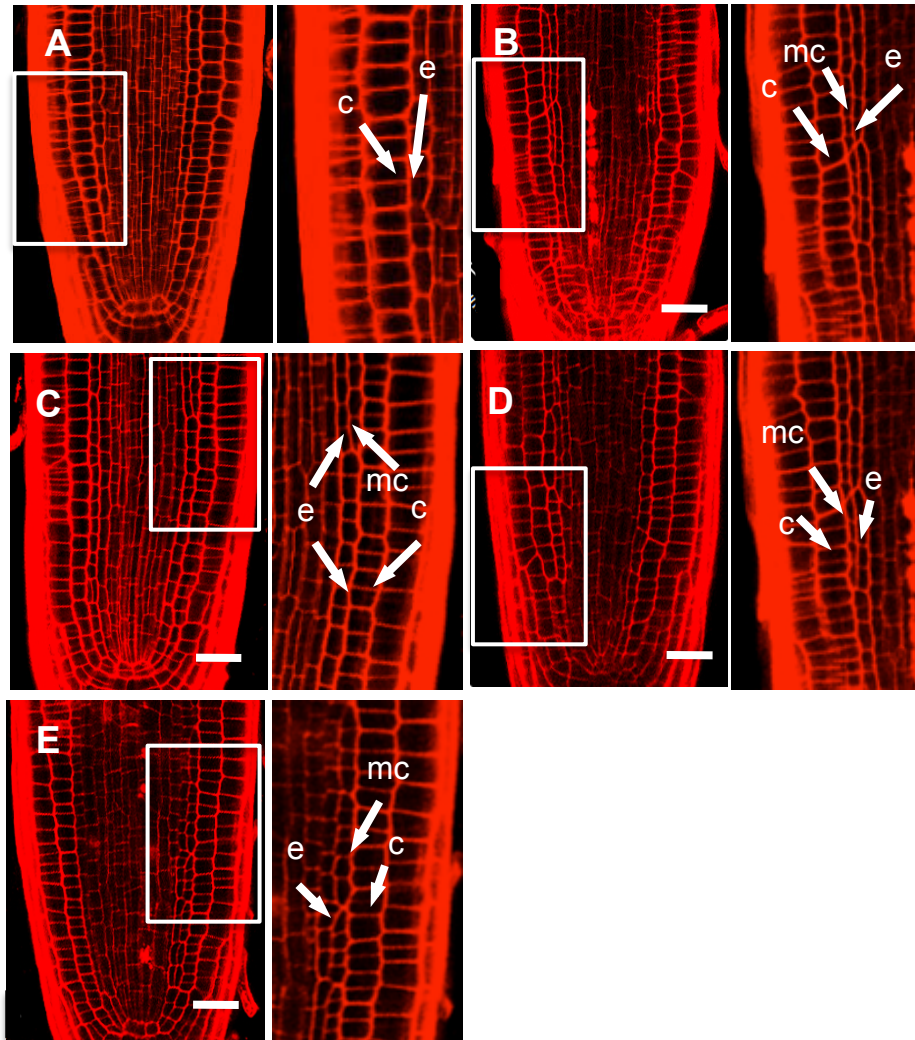


Fig S5. Confocal-microscopy images showing middle cortex in the roots of one-week-old root of Ler (A), *spy-12* (B), *spy-13* (C), *spy-15* (C), and *spy-17* (E) seedlings. Framed areas are shown at the right at a higher magnification.

mc, middle cortex; c, cortex; e, endodermis. Bars = 20 μ m.

Down regulated in *spy-3* root

| PROBESET | QVALUE | Foldchange | WT_MEAN | SPY3_MEAN | GeneName |
|------------|------------|------------|------------|-------------|--------------------|
| 261567_at | 6.2565E-19 | 5.21074422 | 4.48618229 | 0.860948474 | AT1G33055 |
| 258487_at | 2.0556E-18 | 3.14056473 | 3.31518071 | 1.055600186 | AT3G02550 |
| 249675_at | 5.6651E-20 | 3.07435263 | 4.96642246 | 1.615436827 | AT5G35940 |
| 246114_at | 4.6693E-18 | 2.84694016 | 18.167635 | 6.381460093 | AT5G20250 |
| 250682_x_a | 0.00043164 | 2.50589037 | 6.80653593 | 2.716214571 | AT5G06630 |
| 251629_at | 2.9279E-21 | 2.46214453 | 2.15705643 | 0.87608847 | AT3G57410 |
| 253161_at | 3.2001E-20 | 2.24675678 | 1.32038615 | 0.587685398 | AT4G35770 |
| 254644_at | 4.2591E-14 | 2.2066556 | 1.45350933 | 0.658693334 | AT4G18510 |
| 254818_at | 1.4356E-15 | 2.18447878 | 6.02344764 | 2.757384366 | AT4G12470 |
| 252291_s_a | 9.8869E-11 | 2.12291259 | 6.73392791 | 3.172023165 | AT3G49120 |
| 258402_at | 1.5808E-15 | 2.10848518 | 19.9610562 | 9.467012814 | AT3G15450 |
| 249862_at | 3.2719E-17 | 2.0435918 | 10.2065799 | 4.994431814 | AT5G22920 |
| 258939_at | 4.2244E-15 | 2.03082938 | 2.54940148 | 1.255349913 | AT3G10020 |
| 246238_at | 7.6778E-16 | 2.01657768 | 2.3538376 | 1.1672437 | AT4G36670 |
| 260549_at | 2.1526E-13 | 2.00977124 | 9.58533029 | 4.769363853 | AT2G43535 |
| 246601_at | 3.0297E-13 | 1.96182486 | 5.4959786 | 2.801462406 | AT1G31710 |
| 260547_at | 4.0044E-15 | 1.94173037 | 1.10900948 | 0.57114494 | AT2G43550 |
| 258984_at | 3.219E-18 | 1.9327736 | 1.63082477 | 0.843774339 | AT3G08970 |
| 247540_at | 2.5588E-17 | 1.91885546 | 3.86418822 | 2.01379849 | AT5G61590 |
| 247327_at | 2.0135E-11 | 1.9178884 | 16.2160562 | 8.45516151 | AT5G64120 |
| 246195_at | 1.1723E-17 | 1.9139341 | 1.47655563 | 0.771476735 | AT4G36410 |
| 259264_at | 1.0265E-12 | 1.90501216 | 2.09917078 | 1.101919887 | AT3G01260 |
| 249337_at | 8.2597E-06 | 1.87618477 | 3.97632054 | 2.119365108 | AT5G41080 |
| 261157_at | 1.317E-12 | 1.87009024 | 4.98429873 | 2.665271766 | AT1G34510 |
| 252834_at | 1.5666E-13 | 1.84806837 | 1.33297914 | 0.721282375 | AT4G40070 |
| 252882_at | 3.544E-07 | 1.84340925 | 4.90884345 | 2.662915707 | AT4G39675 |
| 247293_at | 2.1284E-19 | 1.83490179 | 1.16232131 | 0.633451507 | AT5G64510 |
| 259544_at | 1.8932E-19 | 1.81763864 | 2.32234049 | 1.277668966 | AT1G20620 |
| 253332_at | 3.1634E-10 | 1.81698386 | 2.99705807 | 1.649468735 | AT4G33420 |
| 245668_at | 8.707E-12 | 1.81297598 | 3.94194063 | 2.174292801 | AT1G28330 |
| 257823_at | 1.604E-11 | 1.81111933 | 3.88384875 | 2.144446627 | AT3G25190 |
| 258225_at | 2.7135E-08 | 1.80081842 | 6.15537358 | 3.418097849 | AT3G15630 |
| 250868_at | 1.9899E-21 | 1.79805486 | 1.70985127 | 0.95094499 | AT5G03860 |
| 251109_at | 1.6541E-14 | 1.79134026 | 8.23858243 | 4.599116423 | AT5G01600 |
| 250683_x_a | 1.5285E-06 | 1.7905013 | 4.84876373 | 2.708048151 | AT5G06640 |
| 258256_at | 0.00051441 | 1.75824569 | 2.57545081 | 1.464784375 | AT3G26890 |
| 259181_at | 2.4789E-15 | 1.75741706 | 3.94499272 | 2.244767518 | AT3G01690 |
| 258930_at | 3.3131E-08 | 1.74377431 | 0.85967222 | 0.492995117 | AT3G10040 |
| 251438_s_a | 6.6871E-11 | 1.73968508 | 15.3003795 | 8.794913341 | AT3G59930;AT5G3335 |
| 255516_at | 1.9571E-09 | 1.73451076 | 15.2905805 | 8.815500511 | AT4G02270 |
| 259454_at | 9.8339E-19 | 1.73359609 | 0.98843793 | 0.57016622 | AT1G44050 |
| 249742_at | 3.5384E-18 | 1.72615944 | 1.82909418 | 1.059632229 | AT5G24490 |
| 261149_s_a | 1.1198E-12 | 1.7240656 | 9.23322604 | 5.355495774 | AT1G19570;AT1G1955 |
| 253666_at | 3.6087E-11 | 1.71827354 | 3.61647235 | 2.104712821 | AT4G30270 |
| 246375_at | 5.1218E-12 | 1.71441709 | 2.83795838 | 1.655348862 | AT1G51830 |
| 247871_at | 9.1537E-13 | 1.70817576 | 5.04229049 | 2.951856953 | AT5G57530 |
| 254225_at | 0.00015222 | 1.70795463 | 11.1732393 | 6.541882967 | AT4G23670 |
| 259076_at | 3.4731E-09 | 1.70154189 | 1.64040966 | 0.96407245 | AT3G02140 |
| 256255_at | 6.2425E-13 | 1.70151645 | 3.77411059 | 2.21808645 | AT3G11280 |
| 258421_at | 5.5558E-07 | 1.69808685 | 2.76851005 | 1.630370113 | AT3G16690 |
| 255886_at | 4.6462E-13 | 1.69571255 | 1.99361939 | 1.175682393 | AT1G20340 |
| 254092_at | 4.3578E-22 | 1.69147073 | 1.63405976 | 0.966058551 | AT4G25090 |
| 254534_at | 8.9558E-15 | 1.68850893 | 2.54349606 | 1.506356296 | AT4G19680 |
| 257924_at | 1.1088E-13 | 1.68643335 | 3.74959542 | 2.223387848 | AT3G23190 |
| 254907_at | 1.9093E-09 | 1.6829452 | 6.27580076 | 3.729058304 | AT4G11190 |

| | | | | | |
|------------|------------|------------|------------|-------------|-----------|
| 258434_at | 6.8384E-14 | 1.68085198 | 1.31189569 | 0.780494477 | AT3G16770 |
| 256774_at | 2.7139E-08 | 1.66886528 | 2.22359979 | 1.332402216 | AT3G13760 |
| 245637_at | 6.5059E-05 | 1.66666155 | 4.01605044 | 2.409637655 | AT1G25230 |
| 255127_at | 2.2353E-16 | 1.65837171 | 2.50496198 | 1.510494883 | AT4G08300 |
| 245136_at | 8.6236E-14 | 1.65503129 | 1.5648362 | 0.945502486 | AT2G45210 |
| 259980_at | 4.8798E-19 | 1.65281436 | 1.98949729 | 1.203702815 | AT1G76520 |
| 259383_at | 1.165E-08 | 1.65140197 | 9.93438486 | 6.015727875 | AT3G16470 |
| 255648_at | 5.4272E-10 | 1.64922346 | 0.90077849 | 0.546183409 | AT4G00910 |
| 259478_at | 3.621E-05 | 1.64889245 | 6.31904978 | 3.832299538 | AT1G18980 |
| 245925_at | 1.4704E-16 | 1.63068416 | 1.94349792 | 1.19182976 | AT5G28770 |
| 260693_at | 1.4003E-09 | 1.62861841 | 11.2678609 | 6.918662373 | AT1G32450 |
| 259982_at | 1.3255E-14 | 1.628231 | 1.2234572 | 0.751402723 | AT1G76410 |
| 255435_at | 3.4009E-21 | 1.627958 | 1.22305219 | 0.751279939 | AT4G03280 |
| 254805_at | 6.5049E-09 | 1.62605899 | 1.22770633 | 0.755019549 | AT4G12480 |
| 251842_at | 4.4002E-11 | 1.6138777 | 3.008347 | 1.864048925 | AT3G54580 |
| 260236_at | 1.7209E-17 | 1.61256393 | 2.32214287 | 1.440031515 | AT1G74470 |
| 251356_at | 1.7319E-07 | 1.61046386 | 3.61772621 | 2.246387706 | AT3G61060 |
| 254025_at | 7.9287E-08 | 1.6071162 | 3.15980119 | 1.966131138 | AT4G25790 |
| 259846_at | 5.9763E-13 | 1.60386607 | 1.77160408 | 1.104583549 | AT1G72140 |
| 260287_at | 2.1906E-08 | 1.6022095 | 4.90836871 | 3.063499954 | AT1G80440 |
| 252367_at | 2.2119E-07 | 1.59977473 | 4.21770547 | 2.636437119 | AT3G48360 |
| 253613_at | 7.4748E-10 | 1.59570189 | 3.35262224 | 2.10103294 | AT4G30320 |
| 252872_at | 3.3772E-17 | 1.59569818 | 2.46502053 | 1.544791216 | AT4G40010 |
| 257504_at | 5.9292E-16 | 1.59466166 | 1.61500977 | 1.012760145 | AT1G52250 |
| 254107_at | 1.5792E-11 | 1.59418336 | 1.68679322 | 1.058092352 | AT4G25220 |
| 251249_at | 1.2641E-17 | 1.59364605 | 1.24868328 | 0.783538657 | AT3G62160 |
| 260741_at | 1.1799E-07 | 1.59326487 | 5.06637651 | 3.179870844 | AT1G15040 |
| 247280_at | 1.0015E-07 | 1.57904353 | 13.9960425 | 8.863620443 | AT5G64260 |
| 253687_at | 5.9592E-06 | 1.57755103 | 4.04876448 | 2.566487177 | AT4G29520 |
| 257315_at | 1.0684E-12 | 1.57734717 | 9.67034954 | 6.130767983 | AT3G30775 |
| 254550_at | 1.1861E-05 | 1.57011039 | 6.86360095 | 4.371412983 | AT4G19690 |
| 250474_at | 3.983E-09 | 1.5639956 | 2.42509007 | 1.55057346 | AT5G10230 |
| 260284_at | 5.5665E-06 | 1.56300545 | 5.96903438 | 3.818946617 | AT1G80380 |
| 246991_at | 3.5892E-10 | 1.55602332 | 13.0480213 | 8.385492153 | AT5G67400 |
| 248828_at | 1.2452E-11 | 1.55596796 | 2.287607 | 1.470214721 | AT5G47110 |
| 251443_at | 6.9806E-16 | 1.55230379 | 1.53351895 | 0.98789874 | AT3G59940 |
| 259609_at | 4.3605E-09 | 1.55209054 | 0.80898513 | 0.521222897 | AT1G52410 |
| 246595_at | 1.4485E-14 | 1.55014004 | 1.59309634 | 1.027711239 | AT5G14780 |
| 253163_at | 9.9113E-07 | 1.54534798 | 9.4803271 | 6.134752314 | AT4G35750 |
| 248050_at | 1.5348E-13 | 1.54079135 | 1.18367709 | 0.768226724 | AT5G56100 |
| 247333_at | 2.0431E-05 | 1.53286411 | 10.3594584 | 6.758236626 | AT5G63600 |
| 259841_at | 5.383E-05 | 1.52937817 | 12.0340031 | 7.868559481 | AT1G52200 |
| 259757_at | 0.00013168 | 1.52618728 | 7.04960232 | 4.619093881 | AT1G77510 |
| 255290_at | 1.2058E-08 | 1.52313807 | 2.3685209 | 1.555027049 | AT4G04640 |
| 258527_at | 5.1756E-09 | 1.51271457 | 2.88141581 | 1.904798084 | AT3G06850 |
| 247813_at | 1.2867E-13 | 1.50974787 | 1.19213788 | 0.789627136 | AT5G58330 |
| 253228_at | 8.1575E-07 | 1.50918768 | 4.91112513 | 3.254151344 | AT4G34630 |
| 248371_at | 1.0563E-11 | 1.50706731 | 0.86751592 | 0.575631834 | AT5G51810 |
| 256302_at | 6.3472E-14 | 1.50678271 | 3.89709591 | 2.586368879 | AT1G69526 |
| 249800_at | 1.3153E-13 | 1.50273849 | 2.2214007 | 1.478235043 | AT5G23660 |
| 255140_x_a | 0.00024917 | 1.50136937 | 4.31864959 | 2.876473753 | AT4G08410 |

| description |
|---|
| Expressed protein |
| LOB domain protein 41 / lateral organ boundaries domain protein 41 (LBD41), Jacalin lectin family protein, similar to myrosinase-binding protein homolog Similar to alkaline alpha galactosidase, putative [Arabidopsis thaliana] Proline-rich extensin-like family protein, contains proline-rich extensin domains, Villin 3 (VLN3), nearly identical to villin 3 (VLN3) (Arabidopsis thaliana) GI:3415117 Senescence associated protein (SEN1), Dark inducible 1 (DIN1). Pi-deficiency Clavata3 / ESR-Related-2 (CLE2), CLAVATA3/ESR-Related-2 (CLE2) Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar AT3G49120, peroxidase 34; AT3G49110, Perx33 Expressed protein, similar to auxin down-regulated protein ARG10 (Vigna radiata) Zinc finger (C3HC4-type RING finger) family protein, contains Pfam |
| Expressed protein |
| Mannitol transporter, putative, similar to mannitol transporter (Apium graveolens Encodes a defensin-like (DEFL) family protein. Copper amine oxidase, putative, similar to copper amine oxidase (Lens culinaris) Encodes a defensin-like (DEFL) family protein. DNAJ heat shock N-terminal domain-containing protein, low similarity to Encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 Peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) Ubiquitin-conjugating enzyme 17 (UBC17), E2; identical to gi:2801446 Aldose 1-epimerase family protein, similar to non-cell-autonomous protein Glycerophosphoryl diester phosphodiesterase family protein, weak similarity to Peroxidase, putative, similar to peroxidase ATP13a GB:CAA67312 from Similar to zinc finger (C3HC4-type RING finger) family protein (ATL6) [Arabidopsis |
| Expressed protein |
| Expressed protein |
| Catalase 3 (SEN2), almost identical to catalase 3 SP:Q42547, GI:3123188 from Peroxidase, putative, identical to class III peroxidase ATP32 (Arabidopsis thaliana) Dormancy-associated protein, putative (DRM1), identical to dormancy-associated Nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313 |
| Expressed protein |
| Malate synthase, putative, strong similarity to glyoxysomal malate synthase from Ferritin 1 (FER1), identical to ferritin (Arabidopsis thaliana) GI:1246401, Proline-rich extensin-like family protein, contains proline-rich extensin domains, |
| Expressed protein |
| Expressed protein |
| Expressed protein, est match [AT3G59930, Encodes a defensin-like (DEFL) family protein.];[AT5G33355, Pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain 30S ribosomal protein, putative, similar to SP:P19954 Plastid-specific 30S Both genes encodes dehydroascorbate reductase MERI-5 protein (MERI-5) (MERI5B) / endo-xyloglucan transferase / xyloglucan Leucine-rich repeat protein kinase, putative, similar to light repressible receptor Xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, Major latex protein-related / MLP-related, low similarity to major latex protein |
| Expressed protein |
| Myb family transcription factor, contains Pfam profile: PF00249 Myb-like DNA- Nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family Plastocyanin, similar to plastocyanin GI:1865683 from (Arabidopsis thaliana) RBOHD, respiratory burst oxidase, putative / NADPH oxidase Iron-responsive transporter (IRT2), member of the Zinc (Zn ²⁺)-Iron (Fe ²⁺) Lesion inducing protein-related, similar to ORF, able to induce HR-like lesions Disease resistance-responsive family protein / dirigent family protein, similar to |

ERF72, the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain

Purple acid phosphatase family protein, contains Pfam profile: PF00149 calcineurin

Nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule

Auxin-responsive protein-related, weakly similar to small auxin up RNA

Auxin efflux carrier family protein, contains auxin efflux carrier domain,

Jacalin lectin family protein, contains Pfam profile: PF01419 jacalin-like lectin

Expressed protein, contains Pfam profile PF01027: Uncharacterized protein family

Germin-like protein, putative, similar to germin-like protein subfamily T member 1

bZIP transcription factor family protein, similar to seed storage protein opaque-

Proton-dependent oligopeptide transport (POT) family protein, contains Pfam

Zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain,

Cytochrome B6-F complex iron-sulfur subunit, chloroplast / Rieske iron-sulfur

Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein,

Proline-rich extensin-like family protein, contains proline-rich extensin domains,

Geranylgeranyl reductase, identical to geranylgeranyl reductase GB:Y14044

F-box family protein / lectin-related, low similarity to PP2 lectin polypeptide

Allergen V5/Tpx-1-related family protein, similar to SP:Q40374 Pathogenesis-

Proton-dependent oligopeptide transport (POT) family protein, contains Pfam

Kelch repeat-containing F-box family protein, similar to SP:Q9ER30 Kelch-related

Speckle-type POZ protein-related, contains Pfam PF00651 : BTB/POZ domain;

Allergen V5/Tpx-1-related family protein, similar to SP:Q40374 Pathogenesis-

Serine/threonine protein kinase, putative, similar to serine-threonine protein

Dynein light chain type 1 family protein, similar to SP:O02414 Dynein light chain

Transporter, putative, similar to glycerol-3-phosphate transporter (glycerol 3-

Transferase family protein, low similarity to *Taxus cuspidata* transferases: 10-

Glutamine amidotransferase-related

Phosphate-responsive protein, putative, similar to phi-1 (phosphate-induced gene)

Expressed protein

Proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase

Iron-responsive transporter (IRT1), identical to Fe(II) transport protein

Annexin 7 (ANN7), nearly identical to calcium-binding protein annexin 7

Phosphoribulokinase/uridine kinase-related

Peroxidase 73 (PER73) (P73) (PRXR11), identical to SP:Q43873 Peroxidase 73

Lil3 protein, putative, similar to Lil3 protein (*Arabidopsis thaliana*)

Kelch repeat-containing F-box family protein, contains Pfam profiles PF01344:

Caldesmon-related, weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957)

Formate dehydrogenase (FDH), identical to GI:7677266

Rho-GTPase-activating protein-related, contains weak similarity to Rho-GTPase-

Glycine-rich protein / oleosin, contains Pfam PF01277: Oleosin domain

Flavonol synthase, putative, similar to SP:Q96330; contains Pfam profile PF03171:

Expressed protein, similar to PGPS/D12 (*Petunia x hybrida*) GI:4105794; contains

Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene

ATP synthase gamma chain 1, chloroplast (ATPC1), identical to SP:Q01908 ATP

Branched chain alpha-keto acid dehydrogenase E2 subunit (din3), identical to

Malate dehydrogenase (NADP), chloroplast, putative, strong similarity to

Expressed protein

Encodes gibberellin 20-oxidase. Involved in gibberellin biosynthesis. Up-regulated

UbiE/COQ5 methyltransferase family protein, low similarity to SP:Q05197

Nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule

Proline-rich extensin-like family protein, contains proline-rich extensin domains,

Upregulated in *spy-3* root

| PROBESET | QVALUE | Foldchange | WT_MEAN | SPY3_MEAN | GeneName |
|-----------|-----------|------------|-----------|------------|--------------|
| 258321_at | 1.576E-16 | 2.2894982 | 1.2692223 | 2.90588233 | AT3G22840 |
| 247463_at | 9.073E-13 | 2.1936634 | 1.7469028 | 3.83211676 | AT5G62210 |
| 245928_s_ | 4.139E-18 | 2.0299978 | 0.7396035 | 1.50139345 | AT5G24770;AT |
| 253259_at | 1.605E-18 | 2.0141501 | 0.6991625 | 1.40821826 | AT4G34410 |
| 261443_at | 3.935E-12 | 1.9784271 | 1.1412976 | 2.25797419 | AT1G28480 |
| 258217_at | 4.732E-14 | 1.9688663 | 3.6920107 | 7.26907537 | AT3G18000 |
| 245341_at | 2.235E-16 | 1.9373447 | 1.0377818 | 2.01054112 | AT4G16447 |
| 248794_at | 1.886E-19 | 1.8972664 | 0.5366021 | 1.0180771 | AT5G47220 |
| 245306_at | 4.88E-19 | 1.8789241 | 1.5446547 | 2.90228894 | AT4G14690 |
| 249894_at | 1.091E-15 | 1.8665719 | 0.5937052 | 1.10819338 | AT5G22580 |
| 246888_at | 1.625E-09 | 1.8537551 | 2.05847 | 3.81589916 | AT5G26270 |
| 246814_at | 1.481E-17 | 1.8507825 | 0.6185703 | 1.14483901 | AT5G27200 |
| 258145_at | 3.49E-10 | 1.6821494 | 3.3032814 | 5.55661302 | AT3G18200 |
| 260067_at | 5.227E-16 | 1.6737381 | 1.2876934 | 2.15526148 | AT1G73780 |
| 258218_at | 2.1E-07 | 1.6681322 | 5.0205699 | 8.37497415 | AT3G18000 |
| 248048_at | 1.471E-11 | 1.6450317 | 1.1479185 | 1.88836222 | AT5G56080 |
| 254158_at | 2.161E-05 | 1.631901 | 1.8252195 | 2.97857758 | AT4G24380 |
| 252988_at | 1.057E-20 | 1.6253982 | 1.196362 | 1.94456466 | AT4G38410 |
| 245041_at | 3.291E-05 | 1.6108129 | 3.0616733 | 4.93178279 | AT2G26530 |
| 260429_at | 2.428E-10 | 1.5590744 | 1.4134724 | 2.20370868 | AT1G72450 |
| 254524_at | 8.666E-14 | 1.5407044 | 0.8959236 | 1.38035342 | AT4G20000 |
| 247625_at | 2.629E-09 | 1.5386136 | 1.2171215 | 1.87267976 | AT5G60200 |
| 245560_at | 5.917E-16 | 1.5383141 | 0.7442175 | 1.14484029 | AT4G15480 |
| 245185_at | 8.401E-15 | 1.5302292 | 0.933897 | 1.42907639 | AT1G67760 |
| 252327_at | 6.563E-08 | 1.5259786 | 2.4429465 | 3.72788391 | AT3G48740 |
| 257536_at | 1.721E-17 | 1.5072734 | 0.8948766 | 1.34882369 | AT3G02800 |

| description |
|---|
| Chlorophyll A-B binding family protein / early light-induced protein (ELIP), Embryo-specific protein-related, contains weak similarity to embryo-specific [AT5G24770, vegetative storage protein 2 (VSP2), identical to SP:O82122 |
| RRTF1, ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription |
| Glutaredoxin family protein, contains INTERPRO Domain IPR002109, |
| Phosphoethanolamine N-methyltransferase 1 / PEAMT 1 (NMT1), identical to Expressed protein |
| Encodes a member of the ERF (ethylene response factor) subfamily B-3 of Chlorophyll A-B binding family protein / early light-induced protein, putative, Expressed protein |
| Expressed protein, ; expression supported by MPSS |
| Acyl carrier protein, chloroplast, putative / ACP, putative, similar to Acyl carrier |
| Nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule |
| Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, |
| Phosphoethanolamine N-methyltransferase 1 / PEAMT 1 (NMT1), identical to Nicotianamine synthase, putative, similar to nicotianamine synthase |
| Expressed protein, contains Pfam profile: PF03959 domain of unknown function |
| Dehydrin, putative, similar to dehydrin ERD10 (Low-temperature-induced protein |
| Expressed protein |
| Expressed protein |
| VQ motif-containing protein, contains PF05678: VQ motif |
| Dof-type zinc finger domain-containing protein, similar to dof6 zinc finger protein |
| UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam |
| Similar to T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative |
| Nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule |
| Similar to tyrosine specific protein phosphatase family protein [Arabidopsis |