

Table of Genes

Where duplicate names or alleles exist they are listed in the gene name column. Note that abbreviations in different species are sometimes totally different genes. For compactness, numbers at the end of a gene name are sometimes omitted unless the gene is known to encode a protein of different function from the other numbers. In general the genes as listed as the wild-types in capital letters; mutants would be in lower case letters. In the species column will be found the main species of reference; if several the one in which it was found first is usually also listed, though some derive from e.g., yeast. For the sake of avoiding duplication the initials of the species name are omitted before the gene name in the table below, though sometimes included they are within the gene name. The species are listed in the species column:

A, animals; *Ac*, *Actinidia chinensis* (Kiwifruit); *Agt*, *Agrobacterium tumefaciens*; *Ar*, *A. rhizogenes*; *At*, *Arabidopsis thaliana*; *Bsp*, *Brassica* species; *Bo*, *B. oleracea* (Broccoli); *Cr*, *Catharanthus rosea* (Madagascar periwinkle); *Cm*, *Cucurbita maxima* (pumpkin); *Cme*, *Cucumis melo* (melon); *Cs*, *Cucumis sativus* (cucumber); *Cp*, *Cucurbita pepo* (zucchini); *Dc*, *Dianthus caryophyllus* (carnation); *Dm*, *Drosophila melanogaster*; *Ec*, *E. coli*; *Fa*, *Fragaria ananassa* (strawberry); *Gm*, *Glycine max* (soybean); *H*, human; *Hv*, *Hordeum vulgare* (barley); *Le*, *Lycopersicon esculentum* (tomato); *M*, Mammals; *Md*, *Malus domestica* (apple); *mi*, microbial; *Mt*, *Medicago truncatula* (alfalfa); *Np*, *Nicotiana plumbaginifolia*; *Nt*, *N. tabacum* (tobacco); *Os*, *Oryza sativa* (rice); *Pd*, *Prunus domestica* (plum); *Ph*, *Petunia hybrida*; *Pi*, *P. inflata*; *Ph*, *Phalenopsis* sp.; *Pa*, *Phaseolus aureus* (mung bean); *Pc*, *P. coccineus* (runner bean); *Pv*, *P. vulgaris* (bush bean); *Pl*, *P. lunatus* (lima bean); *Ps*, *Pisum sativum* (pea); *Pp*, *Pseudomonas putida*; *Psa*, *P. savastanoi*; *Psp*, *Pseudomonas* sp.; *Sc*, *Saccharomyces cerevisiae* (yeast); *Sp*, *Schizosaccharomyces pombe*; *Ssp*, *Solanum* sp.; *St*, *Solanum tuberosum* (potato); *So*, *Spinacia oleracea* (spinach); *Ta*, *Triticum aestivum* (wheat); *Vf*, *Vicia faba* (faba bean); *Vv*, *Vitis vinifera* (grape); *Zm*, *Zea mays* (maize); *Ze*, *Zinnia elegans*.

Other abbreviations: eh, eukaryotic homologues; plh, plant homologues S, several.

| Gene symbol | Gene name meaning | Species | Function | Chap. |
|----------------------|--|------------------------------|--|-------------|
| AAO3 | Abscisic Aldehyde Oxidase | <i>At</i> | Oxidation of abscisic aldehyde to abscisic acid | B5 |
| AAPK | ABA-Activated Protein Kinase | <i>Vf</i> | Serine threonine protein kinase activated by ABA | D6 |
| ABA1 | Abscisic Acid Deficient 1 | <i>At</i> ; <i>Np</i> | Zeaxanthin epoxidase; epoxidation of zeaxanthin to violaxanthin; the first step of ABA synthesis | B5,D6 E4 |
| ABA2 | Abscisic Acid-Deficient | <i>At</i> ; <i>Np</i> | Oxidation of xanthoxin to abscisic aldehyde | B5 |
| ABA3 | Abscisic Acid-Deficient | <i>At</i> | Sulfurylation of molybdenum cofactor | B5 |
| ABAP1 | ABA Binding Protein 1 | <i>Vf</i> | Proposed ABA receptor | D6 |
| ABAR CHLH GUN5 | ABA Receptor Chlorophyll H Genes Uncoupled 5 | <i>At</i> | H subunit of chloroplast Mg ²⁺ chelatase; implicated as ABA receptor | D6 |
| ABC | ATP-Binding Cassette | <i>A</i> plants yeasts | Large family of membrane transporters possessing wide substrate specificity | E1 |

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| <i>ABH1</i> | <i>ABA Hypersensitive 1</i> | <i>At</i> | RNA cap-binding protein; mutation of which confers an ABA hypersensitive phenotype | D6,E4 |
| <i>ABI1,2</i> | <i>ABA-insensitive</i> | <i>At</i> | Protein phosphatases (PP2Cs); dominant mutations confer ABA-insensitivity | D6,E4 E7 |
| <i>ABI3</i> | <i>ABA-insensitive</i> | <i>At</i> | Promotes embryonic development; B3 domain transcription factor; orthologous to maize Vp1 | D6,E4 E7 |
| <i>ABI4</i> | <i>ABA-insensitive</i> | <i>At</i> | Promotes embryo maturation and seedling stress response; AP2 domain transcription factor | D6,E4 E7 |
| <i>ABI5</i> | <i>ABA-insensitive</i> | <i>At</i> | Promotes embryo maturation and seedling stress response; bZIP domain transcription | D6,E4 E7 |
| <i>ABP1</i> | <i>Auxin Binding Protein 1</i> | many | Binds auxins; putative auxin receptor | D1 |
| <i>ABRK</i> | <i>ABA-Related Kinase</i> | <i>Vf</i> | Serine threonine protein kinase activated by ABA, probably identical to AAPK | D6 |
| <i>ACC deaminase</i> | <i>ACC deaminase</i> | <i>Psp</i> | Conversion of ACC into α -ketoglutaric acid | B4 |
| <i>ACO</i> | <i>ACC Oxidase</i> | <i>Le; Cme; Pi; M; Dc;Bo; Ph; many</i> | Oxidation of ACC to ethylene | B4,E7 D4,D5 |
| <i>ACS</i> | <i>ACC Synthase</i> | <i>Le; Cp; Ph;Md Pd;At; many</i> | Conversion of S-adenosyl methionine to ACC in ethylene biosynthesis | D4,B4 D5,E7 D3 |
| <i>AFB</i> | <i>Auxin signaling F-box</i> | <i>At</i> | TIR1-like F-box protein involved in auxin signaling | D1 |
| <i>AGL20</i> <i>SOC1</i> | <i>Agamous-Like20/Suppressor of Overexpression of Constans 1</i> | <i>At</i> | Flowering time genes | E5 E3A |
| <i>AGL24</i> | <i>Agamous-Like 24</i> | <i>At</i> | Flowering time genes | E3A |
| <i>AGPase</i> | <i>ADP-Glucose Pyrophosphorylase</i> | many | Starch synthesis | E5 |
| <i>AGR1</i> | <i>Agravitropic1</i> | <i>At</i> | Identical to <i>EIR1</i> and <i>PIN2</i> auxin efflux regulators | E1 |
| <i>AHK1</i> | <i>At Histidine Kinase</i> | <i>At</i> | Putative osmosensing histidine kinase | D3 |
| <i>AHK2,3,4</i> | <i>At Histidine Kinase 2/3/4</i> | <i>At</i> | Membrane-bound histidine kinases; putative cytokinin receptors, <i>ahk4</i> is allelic to <i>cre1-1</i> and <i>wol</i> | C3,D3 |
| <i>AHK5</i> | <i>At Histidine Kinase 5</i> | <i>At</i> | Unknown | D3 |

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|----------------------|---|------------------------------|--|--------------|
| <i>AHP</i> | <i>At Histidine Phosphotransfer Protein</i> | <i>At</i> | Phosphorelay from AHKS to ARRS | D3 |
| <i>AIR3</i> | <i>Auxin Induced Root3</i> | <i>At</i> | Putative subtilisin-like protease | D1 |
| <i>AKIP1</i> | <i>AAPK-Interacting Protein 1</i> | <i>Vf</i> | Single-stranded RNA binding protein that is a substrate for AAPK | D6 |
| <i>AKT1</i> | <i>At K⁺ Transporter 1</i> | <i>At</i> | Shaker-like inwardly rectifying K ⁺ channel | D6 |
| <i>AKT2/3</i> | <i>At K⁺ Transporter 2</i> | <i>At</i> | K ⁺ channel | D6 |
| <i>ALH1</i> | <i>ACC-Related Long Hypocotyl 1</i> | <i>At</i> | Ethylene and auxin crosstalk | D4 |
| <i>AMP</i> | <i>Altered Meristem Program</i> | <i>At</i> | Regulates number of cotyledons formed; similar to glutamate carboxypeptidases | E4 |
| <i>ANT</i> | <i>Aintegumenta</i> | <i>At</i> | Transcription factor modulating ovule and lateral organ development and embryogenesis | C4 |
| <i>AOC</i> | <i>Allene Oxide Cyclase</i> | many | Conversion of 12,13-EOT to 12-OPDA in JA biosynthesis | F1 |
| <i>AOS</i> | <i>Allene Oxide Synthase</i> | <i>At</i> ; flax; many | Conversion of 13-hydroperoxylinolenic acid to 12,13-epoxy-octadecatrienoic acid, the first step specific to the octadecanoid pathway; JA biosynthesis | E5,E6 G1 |
| <i>AOX</i> | <i>Amine Oxidase</i> | <i>mi</i> | Conversion of tryptamine to indole-3-acetaldehyde | B1 |
| <i>API,2</i> | <i>Apetala 1,2</i> | <i>At</i> | Floral homeotic gene, specifies floral meristem and sepal identity; transcription factor; activated by FT/FD complex | B2,D3 E3A |
| <i>APRR 3,4,5</i> | <i>At Pseudo-Response Regulator 3,4,5</i> | <i>At</i> | Circadianly regulated putative transcription factors | D3 |
| <i>APRR1/TOC1</i> | <i>At Pseudo-Response Regulator/Timing of CAB 1</i> | <i>At</i> | Regulator of circadian rhythm timing | D3 |
| <i>APRR2</i> | <i>At Pseudo-Response Regulator 2</i> | <i>At</i> | Putative MYB transcription factor | D3 |
| <i>APT</i> | <i>Adenine Phosphoribosyltransferase</i> | <i>At</i> | Cytokinin nucleotide formation via salvage pathway | B3 |
| <i>ARATH CDKA;1</i> | <i>At Cyclin-Dependent Protein Kinase A;1</i> | <i>At</i> , plh | Cell cycle regulator, interacts with cyclin in cell cycle dependent manner to form serine/threonine specific protein kinase complex | C3 |
| <i>ARATH CYCD3;1</i> | <i>At Cyclin D3;1</i> | <i>At</i> , plh | Cell cycle regulator, interacts with cyclin-dependent protein kinase in a cell cycle-dependent manner to form a serine/threonine specific protein kinase complex | C3 |

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| <i>ArcB</i> | <i>Aerobic Respiration Control B</i> | <i>Ec</i> | Response regulator; negative transcriptional regulator of genes in aerobic pathways | D3 |
| <i>ARF</i> | <i>Auxin Response Factor</i> | <i>At</i> ; many | Transcription factor for auxin-dependent gene expression that binds to Auxin Response Elements | D1,E1 E4 |
| <i>ARF-GEF</i> | <i>Guanine Nucleotide Exchange Factor for GTPases of the ARF Type</i> | many | Guanine nucleotide exchange factor for small ADP-ribosylation factor-type (ARF-type); GTPases involved in the regulation of intracellular vesicle trafficking | E1 |
| <i>ARR (other)</i> | <i>At Response Regulator</i> | <i>At</i> | Type-As are negative regulators of cytokinin signaling; type-Bs are putative transcriptional activators | D3 |
| <i>ARR 1,2,11,10</i> | <i>At Response Regulator 1, 2, 11, 10</i> | <i>At</i> | Transcription factor type response regulators | D3 |
| <i>ARR2</i> | <i>At Response Regulator 2</i> | <i>At</i> | A type-B response regulator mediating cytokinin-induced expression of type-A ARRs | E6 |
| <i>ARR4</i> | <i>At Response Regulator 4</i> | <i>At</i> | Response regulator; stabilizes PHYB-fr and negatively regulates cytokinin signaling | C3,D3 |
| <i>ARR7</i> | <i>At Response Regulator 7</i> | <i>At</i> | Response regulator; negatively regulates cytokinin signaling | C3 |
| <i>ASK1</i> | <i>At SKP1-Like 1</i> | <i>Sc</i> | Subunit of SCF (E3 ligase) | D1,F1 |
| <i>ATR1</i> | <i>Altered Tryptophan Regulation</i> | <i>At</i> | Myb transcription factor | B1 |
| <i>ATS</i> | <i>Aberrant Testa Shape</i> | <i>At</i> | Maternally inherited effects on seed shape | E4 |
| <i>AUX/IAA</i> | <i>Auxin/Indole Acetic Acid</i> | many | Transcription factor involved in auxin signaling | D1,E4 |
| <i>AUX1</i> | <i>Auxin-Resistant 1</i> | <i>At</i> | Similar to amino acid permeases; putative auxin influx carrier | D4,E1 E2 |
| <i>AXR1</i> | <i>Auxin Resistant 1</i> | <i>At</i> | Subunit of the RUB activating enzyme Similar to the ubiquitin-activating enzyme E1 Involved in auxin action | D1,D4 E2A |
| <i>AXR 2 IAA7</i> | <i>Auxin Resistant 2,</i> | <i>At</i> | See <i>AUX/IAA</i> | D1 |
| <i>AXR 4</i> | <i>Auxin Resistant 4</i> | <i>At</i> | Unknown | D1 |
| <i>AXR 6 CUL1</i> | <i>Auxin Resistant 6</i> | <i>At</i> | Cullin subunit of SCF ubiquitin ligase complex | D1,E1 E4 |
| <i>AZ34 NAR2A</i> | | <i>Hv</i> | Conversion of ABA aldehyde to ABA | E3 |
| <i>BAK1</i> | <i>Bri1-Associated Receptor Kinase</i> | <i>At</i> | Brassinosteroid signal transduction | D7 |

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|-----------------------------|--|---------------------|---|---------------|
| <i>BASI-D</i> | <i>PhyB Activation-Tagged Suppressor 1 – Dominant</i> | <i>At</i> | Brassinosteroid-26-hydroxylase | B6 |
| <i>b-CHI, ATHCHIB</i> | <i>At Basic Chitinase</i> | <i>At</i> | Class1 chitinase involved in ethylene and jasmonic acid signaling during systemic acquired resistance | D4 |
| <i>CHLH GUN5 ABAR</i> | <i>Chlorophyll H Genes Uncoupled 5 ABA Receptor</i> | <i>At</i> | H subunit of chloroplast Mg ²⁺ chelatase; implicated as ABA receptor | D6 |
| <i>BDL BODENLOS IAA12</i> | <i>Bodenlos (Bottomless)</i> | <i>At</i> | AUX/IAA-class transcriptional repressor (<i>IAA12</i>) for <i>ARF5</i> ; involved in regulation of embryo patterning | D1,E4 E1, E2A |
| <i>BES1</i> | <i>bri1-EMS-Suppressor 1</i> | <i>At</i> | Brassinosteroid signal transduction; can be nuclear localized | D7 |
| <i>BIG</i> | <i>Big</i> | plants <i>A</i> | Identical to <i>DOC1</i> and <i>TIR3</i> , homologous to the <i>Drosophila</i> Calossin (calO)/Pushover protein. Involved in vesicle trafficking | E1 |
| <i>BIN2</i> | <i>Brassinosteroid-Insensitive 2</i> | <i>At</i> | Shaggy-like kinase A negative regulator of brassinosteroid signaling | D7 |
| <i>BR22ox CYP90B1 DWF4</i> | <i>Brassinosteroid 22-Oxidase</i> | <i>At</i> | C22 hydroxylation of campestanol | B7 |
| <i>BR23ox CYP90A1 CPD</i> | <i>Brassinosteroid 23-Oxidase</i> | <i>At</i> | C23 α -hydroxylation of cathasterone and 6-deoxocathasterone | B7 |
| <i>BR24red DIM/DWF1 LKB</i> | <i>Brassinosteroid 24-reductase</i> | <i>At; Ps</i> | Isomerization and reduction of the $\Delta^{24(28)}$ bond of 24-methylenecholesterol during BR biosynthesis | B7 |
| <i>BR5red DET2; LK</i> | <i>Brassinosteroid 5-Reductase</i> | <i>At Ps</i> | C5 α -reduction of (24R)-ergost-4-en-3-one during BR biosynthesis | B7 |
| <i>BR6ox CYP85A</i> | <i>Brassinosteroid-6-Oxidase</i> | <i>Le; At</i> | C6 oxidation of 6-deoxo intermediates in brassinosteroid biosynthesis | B6,B7 |
| <i>BRC ; TB1 ; FCI</i> | <i>Branched</i> | <i>At, Zm Os</i> | TCP transcription factor in shoot branching | E2A |
| <i>BRI1 LKA(in Ps)</i> | <i>Brassinosteroid Insensitive</i> | <i>At; Ps; many</i> | Brassinosteroid receptor kinase involved in the perception of brassinosteroids; the <i>bri1</i> null mutants are extreme dwarfs with multiple developmental defects | B7,D7 E6,E4 |
| <i>BRS1</i> | <i>Bri1-5 Suppressor 1</i> | <i>At</i> | Carboxypeptidase putatively involved in brassinosteroid signaling | D7 |
| <i>BRZ1</i> | <i>Brassinazole Resistant 1</i> | <i>At</i> | Brassinosteroid signal transduction; can be nuclear localized | D7 |
| <i>BSAS</i> | <i>β-Substituted Alanine Synthase</i> | <i>At; So</i> | A family of genes with some of them capable of encoding β -cyanoalanine synthase | B4 |

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| <i>BTB</i> | <i>Broad-Complex, Trimtrack And Bric-A-Brac</i> | <i>A</i> | Transcription factor | C2 |
| <i>BX1</i> | <i>Benzoxazineless</i> | <i>Zm</i> | Indole synthase, tryptophan synthase alpha paralog | B1 |
| <i>CAB</i> | <i>Chlorophyll a/b Binding Protein</i> | many | Platform of light-harvesting chlorophyll <i>a/b</i> | E6 |
| <i>CAS</i> | <i>β-Cyanoalanine Synthase</i> | <i>At; So</i> | See <i>BSAS</i> | B4 |
| <i>CBP</i> | <i>Cytokinin Binding Protein</i> | <i>At</i> | Unknown | D3 |
| <i>CCA1</i> | <i>Circadian Clock Associated1</i> | <i>At</i> | MYB transcription factor; negative regulator of TOC1 | D3 |
| <i>CCD</i> | <i>Carotenoid Cleavage Dioxygenase</i> | <i>At</i> | Oxidative cleavage of carotenoids | B5, E2A |
| <i>CDC2</i> | <i>Cell Division Cycle 2</i> | <i>Sp, eh</i> | Mitotic cyclin dependent protein kinase | C3 |
| <i>CDC25</i> | <i>Cell Division Cycle 25</i> | <i>Sp, eh</i> | Protein phosphatase | C3 |
| <i>CEV1</i> | <i>Constitutive Expression of VSP1</i> | <i>At</i> | Cellulose synthase A3 (CESA3) | F1 |
| <i>CheY</i> | <i>Chemotaxis Y</i> | <i>Ec</i> | Response regulator; regulates direction of flagellar rotation | D3 |
| <i>CHK</i> | <i>Cytokinin Hypersensitive</i> | <i>At</i> | Unknown | D3 |
| <i>CHL1</i> | <i>Chlorate Resistant 1</i> | <i>At</i> | Mutant of <i>atnrt1</i> ; confers a chlorate-resistant phenotype | D6 |
| <i>CIMI</i> | <i>Cytokinin-Induced Message1, B-Expansin</i> | <i>Gm</i> | Cell-wall loosening | C4 |
| <i>CIN</i> | <i>Cytokinin Insensitive</i> | <i>At</i> | Unknown | D3 |
| <i>cisZOG1,2</i> | <i>Cis-Zeatin O-Glucosyltransferase</i> | <i>Zm</i> | <i>O</i> -glucosylation of <i>cis</i> -zeatin | B3 |
| <i>CKI</i> | <i>Cytokinin independent 1-2 (gain of function mutants)</i> | <i>At</i> | Histidine protein kinase required for female gametophyte development | D3,E6 |
| <i>CKX</i> | <i>Cytokinin Oxidase/ Dehydrogenase</i> | many | Cytokinin degradation | B3 |
| <i>CLA1</i> | <i>Cloroplastos Alterados (Altered Chloroplasts)</i> | <i>At</i> | 1-deoxy-D-xylulose 5-phosphate synthase (DXS) | B2 |
| <i>CLV1</i> | <i>Clavata Receptor Kinase</i> | <i>At</i> | CLV3 receptor; helps determine apical meristem cell fate | F3 |
| <i>CLV2</i> | <i>Clavata Receptor-Like Protein</i> | <i>At</i> | Associates with CLV1 to produce an active receptor | F3 |

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| <i>CLV3</i> | <i>Clavata (club-like)</i> | <i>At</i> | Signaling peptide; 96AA ligand for CLV1/CLV2 receptor kinase; restricts SAM size | D3,F3 |
| <i>CO</i> <i>Hd1</i> | <i>Constans</i> <i>Heading date 1</i> | <i>At</i> <i>Os</i> | Transcription factor; B-box type zinc finger protein; serves as link between the clock oscillator and flowering time genes; required for flowering in response to long days | B2,E5 E3A |
| <i>COI1</i> | <i>Coronatine</i> <i>Insensitive 1</i> <i>(Phytotoxin)</i> | <i>At</i> | Required for response to jasmonates; protein contains 16 leucine-rich repeats and an F-box motif; component of E3 ubiquitin ligase; involved in wounding and parthenogenesis | D4,E6 F1 |
| <i>COL</i> | <i>Constans-Like</i> | <i>St</i> | Unknown | E5 |
| <i>COP1</i> | <i>Constitutive Photomorphogenesis 1</i> | <i>At</i> | Light-dependent regulator of HY5 protein stability; repressor of photomorphogenic development | D1,D3 E3A |
| <i>COP9</i> | <i>Constitutive Photomorphogenesis 9</i> | <i>At</i> | Subunit of the signalosome; regulates the 26S proteasome | D3 |
| <i>CPI</i> | <i>Cysteine Proteinase1</i> | <i>At</i> | Protein turnover | B2 |
| <i>CPD</i> <i>BR23ox</i> <i>CYP90A1</i> | <i>Constitutive Photomorphogenesis and Dwarfism</i> | <i>At</i> | C-23 α -steroid hydroxylase of cathasterone and 6 deoxocathasterone involved in brassinosteroid biosynthesis | B7,D7 B6 |
| <i>CPH, ORC; SMT</i> | <i>Cephalopod</i> | <i>At</i> | Sterol methyltransferase; plant sterol biosynthesis | E1 |
| <i>CPR5,6</i> | <i>Constitutive Expression of Pr Genes5,6</i> | <i>At</i> | Regulator of expression of pathogenesis-related (PR) genes | D4 |
| <i>CPS</i> <i>GAI(in At)</i> <i>LS (in Ps)</i> | <i>ent-Copalyl Diphosphate Synthase</i> | <i>At; Ps</i> <i>S</i> | Converts geranylgeranyl diphosphate to <i>ent</i> -copalyl diphosphate | B2,B7 |
| <i>CRE1</i> | <i>Cytokinin Response (resistant) 1</i> | <i>At</i> | Membrane-bound histidine kinase cytokinin receptor; <i>cre1-1</i> is allelic to <i>ahk4</i> and <i>wol</i> | C3,D3 |
| <i>CSBP</i> | <i>Cytokinin Specific Binding Protein</i> | <i>Pa</i> | Unknown | D3 |
| <i>CTR1</i> | <i>Constitutive Triple Response 1</i> | <i>At; Le</i> | Mitogen-activated protein kinase | D4,D5 E6,E4 |
| <i>CTS</i> | <i>Comatose</i> | <i>At</i> | ATP binding cassette (ABC) transporter regulating transport of acyl-coAs into the peroxisome; promotes germination and represses embryo dormancy | E4 |
| <i>CU3</i> | <i>Curl 3</i> | <i>Le sp</i> | Encodes tomato BRI1 | D7 |
| <i>CUC1</i> | <i>Cup-Shaped Cotyledon 1</i> | <i>At</i> | No apical meristem (NAM) domain protein; functions redundantly with <i>CUC2</i> to promote embryonic apical meristem formation, cotyledon separation and expression of <i>STM</i> | E4 |

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| <i>CUC2</i> | <i>Cup-Shaped Cotyledon 2</i> | <i>At</i> | Transcriptional activator of the NAC gene family modulating shoot apical meristem and cotyledon; see <i>CUC1</i> | C4,E4 |
| <i>CUL1</i> | <i>Cullin</i> | <i>Sc</i> | Subunit of SCF E3 ligase; <i>At</i> Cdc53/cullin homolog | D1 |
| <i>CVP1</i> | <i>Cotyledon Vascular Pattern 1</i> | many | Transferring a methyl group to C-24 ¹ position to form C29 sterols | B6 |
| <i>CYCD3</i> | <i>Cyclin D3</i> | gene family many | Control of the cell cycle at the G1 to S transition; however tobacco <i>CycD3;1</i> (<i>Nicta CycD3;1</i>) may have a role at mitosis; interacts with cyclin-dependent protein kinase in cell cycle dependent manner to form serine/ threonine specific protein kinase complex | C3,D3 |
| <i>CYP79B2,3</i> | <i>Cytochrome P450</i> | <i>At</i> | Conversion of tryptophan to indole-3-acetaldoxime | B1 |
| <i>CYP79F1</i> | <i>Cytochrome P450</i> | <i>At</i> | Synthesis of short-chain methionine-derived aliphatic glucosinolates abolished in mutant allele | B1 |
| <i>CYP83B1</i> | <i>Cytochrome P450</i> | <i>At</i> | Synthesis of indole glucosinolates; N-hydroxylation of indole-3-acetaldoxime in vitro | B1 |
| <i>CYR1</i> | <i>Cytokinin Resistant1</i> | <i>At</i> | Unknown | D3 |
| <i>D1</i> | <i>Dwarf1</i> | <i>Os</i> | Putative α subunit of heterotrimeric G protein | D2 |
| <i>D3, MAX2, RMS4</i> | <i>Dwarf3</i> | <i>Os, At, Ps</i> | F-box protein involved in shoot branching | E2A |
| <i>D8</i> | <i>Dwarf8</i> | <i>Zm</i> | DELLA-class repressor of GA-inducible gene expression | D2,E4 |
| <i>D10, MAX4, RMS1, DAD1</i> | <i>Dwarf10</i> | <i>Os, At, Ps, Ph</i> | Carotenoid Cleavage Dioxygenase 8 | E2A |
| <i>D17, MAX3, RMS5</i> | <i>Dwarf17</i> | <i>Os, At, Ps</i> | Carotenoid Cleavage Dioxygenase 7 | E2A |
| <i>DAD1</i> | <i>Delayed Anther Dehiscence1</i> | <i>At</i> | Phospholipase A1 involved in JA biosynthesis in Arabidopsis anthers | F1 |
| <i>DAD1, MAX4, RMS1, D10</i> | <i>Decreased Apical Domiance1</i> | <i>Ph, At, Ps, Os</i> | Carotenoid Cleavage Dioxygenase 8 | E2A |
| <i>DAG1,2</i> | <i>DOF Affecting Germination</i> (see <i>DOF</i>) | <i>At</i> | Highly homologous zinc finger transcription factors with opposing effects on germination | E4 |
| <i>DBP</i> | <i>At DNA Binding Protein</i> | <i>At</i> | Auxin-inducible DNA binding protein | D3 |
| <i>DCT1</i> | <i>Divalent Cation Transporter 1</i> | <i>M</i> | Metal ion transporter, NRAMP2, similar to <i>Smf1</i> and <i>MVL</i> | D4 |

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|--|---|-------------------------|--|----------------------|
| <i>DDE1</i> | <i>Delayed Dehiscence1</i> | <i>At</i> | 12-OPDA reductase in JA biosynthesis; see OPR | F1 |
| <i>DDE2</i> | <i>Delayed Dehiscence2</i> | <i>At</i> | Allene oxide synthase See AOS | F1 |
| <i>DEF1</i> | <i>Defenseless 1</i> | <i>Le</i> | Unidentified gene involved in wound-inducible JA synthesis | F1 |
| <i>DET2</i> <i>BR5red</i> | <i>De-Etiolated</i> | <i>At, Ps</i> | A steroid 5 α -reductase involved in the formation of campestanol from campesterol in BR biosynthesis | B7,D7 E6,E4 B6 |
| <i>DFL1</i> <i>GH3-6</i> | <i>Dwarf in Light</i> | <i>At</i> | Adenylate-forming enzyme | D1 |
| <i>DIM/DWF1</i> <i>BR24red</i> | <i>Diminutive/ Dwarf</i> | <i>At</i> | Isomerization and reduction of the $\Delta^{24(28)}$ bond of 24-methylenecholesterol | B7 |
| <i>DIR1</i> | <i>Defective In Induced Resistance</i> | <i>At</i> | Putative lipid transport protein involved in SAR signaling | F2 |
| <i>DOC1</i> | <i>Dark Overexpression of CAB</i> | plants <i>A</i> | Identical to <i>TIR3 (BIG)</i> | E1 |
| <i>DOF</i> | <i>DNA-Binding with One Finger</i> | many | Transcription factor | C2 |
| <i>DVL1</i> | <i>Devil 1</i> | <i>At</i> | Unknown | F3 |
| <i>DWF1</i> <i>BR24red</i> <i>LKB</i> | <i>Dwarf 1</i> | <i>At, Ps</i> | Δ^5 -sterol- Δ^{24} -oxidoreductase involved in sterol biosynthesis | B6,D7 |
| <i>DWF4</i> <i>BR22ox</i> <i>CYP90B1</i> | <i>Dwarf 4</i> | <i>At</i> | C-22 α -steroid hydroxylation of campestanol in brassinosteroid biosynthesis | B6,B7 D7 |
| <i>DWF5</i> | <i>Dwarf 5</i> | <i>Sc, At, H</i> | $\Delta^{5,7}$ -sterol- Δ^7 -reductase involved in sterol biosynthesis | B6,D7 |
| <i>DWF7</i> | <i>Dwarf 7</i> | <i>At</i> | Desaturase involved in sterol biosynthesis | B6,D7 |
| <i>E2F</i> | <i>E2 Promoter Binding Factor</i> | HeLa cells- H; eh | Transcription factor; originally isolated in human HeLa cells as binding promoter of adenovirus E2 protein | C3 |
| <i>E8</i> | <i>Ethylene induced 8</i> | <i>Le</i> | Unknown; Fe(II) dioxygenase family Negative feedback regulation of ethylene biosynthesis | B4 |
| <i>EBF1,2</i> | <i>Ein3-Binding F Box Protein 1,2</i> | <i>At</i> | F box proteins that interact with EIN3 | D4 |
| <i>ECR1</i> | <i>E1 C-Terminal Related 1</i> | <i>At</i> | Subunit of the RUB activating enzyme | D1 |
| <i>EDS1</i> | <i>Enhanced Disease Susceptibility 1</i> | <i>At</i> | Lipase-like protein involved in race-specific resistance | F2 |
| <i>EDS16</i> | <i>Enhanced Disease Susceptibility 16</i> | <i>At</i> | See <i>SID2</i> Also known as <i>SID2</i> | F2 |
| <i>EEL</i> | <i>Elevated Em Levels</i> | <i>At</i> | bZIP class transcription factor; same clade as ABI5 | E4 |
| <i>EER1</i> | <i>Enhanced Ethylene Response 1</i> | <i>At</i> | See <i>RCN1</i> | D4 |

Table of Genes

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|----------------------|--|-----------------------------|--|----------------------|
| <i>EFR1</i> | <i>Ethylene Response Factor 1</i> | <i>At</i> | AP2-domain transcription factor | F1 |
| <i>EIL1,2</i> | <i>Ethylene-Insensitive 3-Like 1,2</i> | <i>At</i> | Ethylene signal transduction | D4 |
| <i>EIN2</i> | <i>Ethylene Insensitive 2</i> | <i>At; Le</i> | Ethylene signal transduction; allelic to <i>ERA3</i> | E4,D4 D5,E6 |
| <i>EIN3</i> | <i>Ethylene Insensitive 3</i> | <i>At</i> | Transcription factor involved in ethylene signal transduction | D4,D5 |
| <i>EIN4</i> | <i>Ethylene Insensitive4</i> | <i>At</i> | Ethylene receptor | D4,D5 |
| <i>EIN5,7</i> | <i>Ethylene Insensitive 5,7</i> | <i>At</i> | Ethylene signal transduction | D4 |
| <i>EIN6/EEN</i> | <i>Ethylene Insensitive 6/Enhancer of Ethylene Insensitivity</i> | <i>At</i> | Ethylene insensitive double mutant associated with mechanical stimuli pathway and ethylene signal transduction | D4 |
| <i>EIR1 PIN2</i> | <i>Ethylene Insensitive Root 1</i> | <i>At</i> | Identical to <i>AGR1</i> and <i>PIN2</i> auxin efflux regulators | E1 |
| <i>EKO</i> | <i>See KO</i> | | | |
| <i>ENOD40</i> | <i>ENOD40 Nod Factor Precursor</i> | Leg-umes | Role in establishing symbiotic N-fixation | F3 |
| <i>ERA1</i> | <i>Enhanced Response to ABA 1</i> | <i>At</i> | β subunit of farnesyl transferase; ABA-hypersensitive phenotype | D6,E4 |
| <i>ERA3</i> | <i>Enhanced Response To ABA</i> | <i>At</i> | Signal transduction for multiple hormones; allelic to <i>EIN2</i> | E4 |
| <i>ERF1</i> | <i>Ethylene Response Factor 1</i> | <i>At</i> | Transcription factor mediating expression of ethylene-inducible genes; EREBP like protein that binds CGG box of ethylene regulated promoters | D4,D5 F1 |
| <i>ERS1, 2</i> | <i>Ethylene Response Sensor</i> | <i>At</i> | Ethylene receptors | D4,D5 |
| <i>ETO1</i> | <i>Ethylene Overproducing</i> | <i>At</i> | A protein that interacts with the C-terminal end of <i>AtACS5</i> and increases its stability | B4,D4 |
| <i>ETO2/3</i> | <i>Ethylene Overproducing 2/3</i> | <i>At</i> | Forms of <i>AtACS5/9</i> (respectively) mutated within the C-terminal domain | B4,D4 |
| <i>ETR1,2</i> | <i>Ethylene Response 1,2</i> | <i>At; Cme; Le</i> | Ethylene receptor histidine kinase; mutant form confers dominant ethylene insensitivity | D3,D4 D5,E6 E7 |
| <i>EXP</i> | α -Expansin | <i>Cs; At, Le, Os; many</i> | Cell-wall loosening | C4 |
| <i>EXPB</i> | β -Expansin | many | Cell-wall loosening | C4 |
| <i>EXPL</i> | <i>Expansin-Like</i> | many | Unknown | C4 |
| <i>EXPR</i> | <i>Expansin-Related</i> | many | Unknown | C4 |

Table of Genes

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|---|--|---------------------------|---|----------------------|
| <i>FAD</i> | <i>Fatty Acid Desaturase</i> | <i>At</i> ; many | Introduction of double bonds into fatty acyl chain; the triple mutant (genes 3, 7 & 8 produces little linolenic acid (thus is unable to accumulate jasmonates) | F1,E6 |
| <i>FC1 ; BRC ; TB1</i> | <i>Fine culm</i> | <i>Os, At, Zm</i> | TCP transcription factor in shoot branching | E2A |
| <i>FK</i> | <i>Fackel (torch, flare)</i> | many | $\Delta^{8,14}$ -sterol- Δ^{14} -reductase | B6 |
| <i>FCA</i> | <i>Flowering Control A</i> | <i>At</i> | RNA-binding protein; flowering regulator; interacts with FY to repress <i>FLC</i> | D6 |
| <i>FLC</i> | <i>Flowering Locus C</i> | <i>At</i> | Repressor of flowering prior to vernalization | D6 E3A |
| <i>FLC</i> | <i>Flacca</i> | <i>Le</i> | Sulfurylation of molybdenum cofactor; conversion of ABA aldehyde to ABA | B5,E3 |
| <i>FliM</i> | <i>Flagella M</i> | <i>Ec</i> | Subunit of the flagellar motor complex | D3 |
| <i>FRY1</i> | <i>Fiery</i> | <i>At</i> | Phosphoinositide catabolism | E4 |
| <i>FT Hd3a SFT</i> | <i>Flowering Locus T, Heading date 3a, Single Flower Truss</i> | <i>At Os Le</i> | Control of floral transition; encoded protein is florigen | E5, E3A |
| <i>FUL</i> | <i>Fruitful</i> | <i>At</i> | Flower timing gene | E3A |
| <i>FUS3</i> | <i>Fusca (brown, dusky)</i> | <i>At</i> | Promotes embryonic development; B3 domain transcription factor | E4 |
| <i>FUS9 COP10</i> | <i>Fusca9/Constitutive Photomorphogenic10</i> | <i>At</i> | Similar to E2 ubiquitin-conjugating enzyme; interacts with COP1 and COP9 | D3 |
| <i>FY</i> | <i>Flowering locus Y</i> | <i>At</i> | mRNA 3' end processing factor; flowering regulator; interacts with FCA to repress <i>FLC</i> | D6 |
| <i>FZY</i> | <i>Floozy</i> | <i>Ph</i> | Flavin monooxygenase, overexpression results in IAA accumulation | B1 |
| <i>GAI; CPS</i> | <i>GA-Deficient-1</i> | <i>At</i> | GA biosynthesis (<i>ent</i> -CPP synthase) | E7 |
| <i>GA20ox GA5 (in At)</i> | <i>Gibberellin 20-Oxidase</i> | <i>Cm;At St; Ps; many</i> | Converts GA ₁₂ to GA ₉ and GA ₅₃ to GA ₂₀ Converts GA ₁₂ to GA ₂₅ (in <i>Cm</i>) | B2,B7 E5,E7 |
| <i>GA2ox GA 2β-Hydroxylase SLN (in Ps)</i> | <i>Gibberellin 2-Oxidase</i> | <i>Pc; Ps; At; many</i> | GA catabolism; converts C19-GAs to biologically inactive 2 β -hydroxy analogs and to 2-oxo analogs (GA-catabolites); converts C20-GAs to 2 β -hydroxy analogs | B2,B7 E7 |
| <i>GA3ox GA 3β-hydroxylase GA4; GA4H (in At); Le (in Ps)</i> | <i>Gibberellin 3-Oxidase GA 3-hydroxylase</i> | many <i>At</i> | Converts GA ₉ to GA ₄ and GA ₂₀ to GA ₁ | A2,B1 B2,B7 E7 |
| <i>GAI</i> | <i>GA-Insensitive</i> | <i>At; Vv</i> | DELLA protein, a negative regulator of GA signaling | C2,D2 E4,E7 |
| <i>GAMYB</i> | <i>GA Regulated MYB</i> | <i>Hv</i> | MYB transcription factor | C2,E4 |

Table of Genes

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|---|---|--------------------|--|-------------|
| <i>GAS1</i> | <i>Galactinol Synthase</i> | <i>Cm</i> | Galactinol synthesis; promoter is used for minor-vein-specific expression | E3A |
| <i>GCA2</i> | <i>Growth Controlled By ABA 2</i> | <i>At</i> | Unknown, but <i>gca2</i> mutant has an ABA-insensitive phenotype | D6 |
| <i>GCR1</i> | <i>G-Protein Coupled Receptor1</i> | <i>At</i> | Promotes germination | E4 |
| <i>GCR2</i> | <i>G-Protein Coupled Receptor 2</i> | <i>At</i> | Proposed ABA receptor and G-protein-coupled receptor | D6 |
| <i>GH3</i> | (Isolated by) <i>Gretchen Hagen 3</i> | <i>Gm</i> many | Auxin-responsive gene, <i>JAR1</i> -like; adenylate-forming enzyme | B1,D1 E2 |
| <i>GH45</i> | <i>Glycosyl Hydrolase Family-45</i> | many fungi | Hydrolysis of glycosidic bond | C4 |
| <i>GID1</i> | <i>Gibberellin Insensitive1</i> | <i>Os; At</i> | GA receptor | D2 |
| <i>GID2</i> | <i>GA-Insensitive Dwarf 2</i> | <i>Os</i> | F-box factor that targets DELLA proteins for proteasomal degradation; a positive regulator of GA signaling; orthologous to <i>SLY</i> | C2,D2 E4 |
| <i>GIN1,5</i> | <i>Glucose Insensitive</i> | <i>At</i> | See <i>ABA2/3</i> respectively | A2,B5 |
| <i>GL2</i> | <i>Glabra2</i> | <i>At</i> | Homeodomain transcription factor modulating hair formation | C4 |
| <i>GLUT4</i> | <i>Glucose Transporter4</i> | <i>M</i> | Insulin-regulated glucose transporter | E1 |
| <i>GMPOZ</i> | <i>GAMYB Associated POZ</i> | <i>Hv</i> | Transcription factor | C2 |
| <i>GN</i> | <i>Gnom</i> | many | ARF-GEF | E1 |
| <i>GORK1</i> | <i>Guard cell Outwardly Rectifying K⁺ Channel 1</i> | <i>At</i> | Outwardly rectifying K ⁺ channel | D6 |
| <i>GPA1</i> | <i>G Protein Subunit 1</i> | <i>At;</i> many | α subunit of heterotrimeric G protein; <i>gpa1</i> mutants show ABA-insensitivity in certain guard cell responses; promotes germination | D6,E4 |
| <i>GRD2</i> | <i>GA-Responsive Dwarf 2</i> | <i>Hv</i> | Putative GA3ox, a GA biosynthetic enzyme | D2 |
| <i>GSE</i> | <i>GA-Sensitivity</i> | <i>Hv</i> | A positive regulator of GA signaling | D2 |
| <i>GTG1,2</i> | <i>GPCR Type G protein</i> | <i>At</i> | Membrane-localized protein with GTPase activity involved in ABA sensing | D6 |
| <i>GUN5</i> <i>ABAR</i> <i>CHLH</i> | <i>Genes Uncoupled 5</i> <i>ABA Receptor</i> <i>Chlorophyll H</i> | <i>At</i> | H subunit of chloroplast Mg ²⁺ chelatase; implicated as ABA receptor | D6 |
| <i>Ga</i> | <i>Ga - A Subunit of Heterotrimeric G Proteins</i> | many | Signal transduction | B2 |

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|-------------------|--|---------------|---|-------|
| <i>HB</i> | <i>Homeobox HD-ZIP gene</i> | <i>At</i> | Encoding transcriptional regulator expressed early in procambial (or provascular) cells | E2 |
| <i>HBT</i> | <i>Hobbit</i> | <i>At</i> | Homolog of the CDC27 subunit of the anaphase-promoting complex (APC); required for cell division and cell differentiation in meristems | E4 |
| <i>Hd1</i> | <i>Heading date 1</i> | <i>Os</i> | Rice ortholog of AtCO; promotes flowering in short days | E3A |
| <i>Hd3a</i> | <i>Heading date 3a</i> | <i>Os</i> | Rice ortholog of AtFT; expressed in short days | E3A |
| <i>HK1</i> | <i>Histidine Kinase 1</i> | <i>Zm</i> | Cytokinin receptor | B3 |
| <i>HLS1</i> | <i>Hookless 1</i> | <i>At</i> | Ethylene regulated apical hook development, putative N-acetyltransferase | D4 |
| <i>HOG1</i> | <i>High Osmolarity Glycerol Response 1</i> | <i>Sc</i> | MAP kinase central to the high-osmolarity signaling pathway | D3 |
| <i>HRT</i> | <i>Hordeum Repressor of Transcription</i> | <i>Hv</i> | Transcription factor | C2 |
| <i>HXK1</i> | <i>Hexokinase 1</i> | <i>At</i> | Conversion of glucose to glucose-6-phosphate and sense of sugar level | E6 |
| <i>HYD1</i> | <i>Hydra 1</i> | <i>Sc, At</i> | Sterol Δ^8 - Δ^7 isomerase | B6 |
| <i>HYL1</i> | <i>HYponastic Leaves 1</i> | <i>At</i> | Double-stranded RNA binding protein; <i>hyl1</i> mutant shows reduced sensitivity to auxin and cytokinin and ABA hypersensitivity (although guard cell ABA responses are wild-type) | D6,E4 |
| <i>IAA1-3</i> | <i>Indole Acetic Acid 1-3</i> | <i>At</i> | Auxin-inducible nuclear-localized proteins | D3 |
| <i>IAA17 AXR3</i> | <i>Indole Acetic Acid 17/Auxin Resistant 3</i> | <i>At</i> | Auxin-inducible nuclear-localized protein | D3 |
| <i>IAA3 SHY2</i> | <i>Indole Acetic Acid 3/Short Hypocotyl</i> | <i>At</i> | Auxin-inducible nuclear-localized protein (suppressor of <i>HY2</i>) | D3 |
| <i>iaaL</i> | <i>IAA-lysine synthetase</i> | <i>Psa</i> | over-expression results in extremely low IAA concentrations | E2 |
| <i>iaaM</i> | <i>tryptophan mono-oxygenase</i> | <i>Agt</i> | Produces indoleacetamide from tryptophan; over-expression results in high IAA concentrations | E2 |
| <i>JaaspH</i> | <i>IAA-Aspartic Acid Hydrolase</i> | <i>mi</i> | Hydrolysis of IAA-Asp | B1 |
| <i>IAGLU</i> | <i>IAA-Glucose Synthase</i> | <i>Zm</i> | UDP-glucosyl transferase specific to IAA-Glucose formation | B1 |
| <i>IAH</i> | <i>IndoleAcetamide Hydrolase</i> | <i>mi</i> | Conversion of indole-3-acetamide to IAA | B1 |
| <i>IAO</i> | <i>Indole-3-Acetaldehyde Oxidase</i> | <i>mi</i> | Conversion of indole-3-acetaldehyde to IAA | B1 |

Table of Genes

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|--|---|---|--|-----------------------|
| <i>IAP1</i> | <i>IAA-Modified Protein</i> | Pv | IAA-modified protein | B1 |
| <i>IBC6</i> | <i>Induced By Cytokinin 6 (Same as ARR5)</i> | <i>At</i> | Negative regulator of cytokinin signaling | D3 |
| <i>IBC7</i> | <i>Induced By Cytokinin 7 (Same as ARR4)</i> | <i>At</i> | See <i>ARR4</i> above | D3 |
| <i>ICK1</i> | <i>Cyclin-Dependent Kinase Inhibitor</i> | <i>At</i> | Suppress cell division | E4 |
| <i>IGL</i> | <i>Indole-3-Glycerol Phosphate Lyase</i> | <i>Zm</i> | Indole synthase, tryptophan synthase alpha paralog | B1 |
| <i>IPDC</i> | <i>Indole Pyruvate Decarboxylase</i> | <i>mi</i> | Conversion of indole-3-pyruvic acid to indole-3-acetaldehyde | B1 |
| <i>IPT1,3-8</i> | <i>Isopentenyl Transferase 1,3-8</i> | <i>Agt;</i> <i>At;</i> many | Cytokinin biosynthesis; catalyses the rate-limiting step of cytokinin biosynthesis: the condensation of 2- Δ -isopentenyl PPi with AMP to form isopentenylAMP | B3,C3 E3,E5, E6 |
| <i>IPT2,9</i> | <i>Isopentenyl-transferase 2,9</i> | <i>At</i> | Isopentenylation of tRNA | B3 |
| <i>ISI4</i> | <i>Impaired Sucrose Induction</i> | <i>At</i> | See <i>ABA2</i> | B5 |
| <i>JAI1</i> <i>COI1</i> | <i>Jasmonate-Insensitive 1</i> | <i>Le</i> | Regulator of JA signaling; see <i>COI1</i> | F1 |
| <i>JAR1</i> <i>FIN219</i> <i>GH3-11</i> | <i>Jasmonic Acid Resistant 1; Far Red Insensitive 219</i> | <i>At</i> | Adenylate-forming enzyme; acyl adenylate-forming firefly luciferase superfamily; adenylation of JA | B1,D1 F1 |
| <i>JAS1</i> <i>JAZ10</i> | <i>Jasmonate Associated 1</i> | <i>At</i> | Repressor of jasmonate signaling and substrate for COI1 | F1 |
| <i>JAZ,1-12</i> | <i>Jasmonate ZIM-Domain</i> | <i>At;</i> many | Repressors of jasmonate signaling and substrates for COI1 | F1 |
| <i>JIN1</i> <i>MYC2</i> | <i>Jasmonate Insensitive 1</i> | <i>At;</i> <i>Le</i> | bHLH transcription factor involved in Jasmonate signaling | F1 |
| <i>JMT</i> | <i>Jasmonate Methyl Transferase</i> | <i>At</i> | Conversion of JA to methyl-JA | F1 |
| <i>KAO1,2</i> <i>NA (in Ps)</i> <i>CYP88A6,7</i> | <i>Ent-Kaurenoic Acid Oxidase</i> | <i>Hv;</i> <i>Cm;</i> <i>Ps;</i> <i>At;</i> many | GA biosynthesis; oxidation of <i>ent</i> -kaurenoic acid to GA ₁₂ | B2,E7 B7 |
| <i>KAT1,2</i> | <i>Voltage-Gated K⁺ Channel of At1/2</i> | <i>At</i> | Inwardly rectifying K ⁺ channel | D6 |
| <i>KGM</i> | <i>Kinase Associated With GAMYB</i> | <i>Hv</i> | Protein kinase | C2 |
| <i>KIP</i> | <i>Kinase Inhibitory Protein</i> | <i>H;</i> eh | Inhibition of cyclin/CDK complexes, homologs in plants known as Kip-related proteins (KRP) | C3 |
| <i>kn1</i> | <i>Knotted 1</i> | <i>Zm</i> | Homeobox transcription factor | D3 |

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|---|--|----------------------------|--|--------------|
| <i>KNAT1-2</i> | <i>Knotted-Like From At 1-2</i> | <i>At</i> | Homeobox transcription factor; class I <i>KNOX</i> gene | D3,E5 |
| <i>KNOX</i> | <i>Knotted1-Like Homeobox</i> | many | Transcription factors involved in establishing organ identity | B2 |
| <i>KO</i> <i>GA3 (inAt)</i> <i>LH (in Ps)</i> <i>CYP701A10</i> | <i>ent-Kaurene Oxidase</i> | <i>S</i> <i>At; Ps</i> | Oxidizes <i>ent</i> -kaurene to <i>ent</i> -kaurenoic acid | B2,B7 E7 |
| <i>KS</i> <i>GA2(inAt)</i> | <i>ent-Kaurene Synthase</i> | <i>Cm;At</i> <i>S</i> | Converts <i>ent</i> -copalyl diphosphate to <i>ent</i> -kaurene | B2,E7 |
| <i>LAX</i> | <i>Like AUX1</i> | <i>At</i> | Homologue of <i>AUX1</i> ; putative auxin uptake carrier | E1 |
| <i>LE</i> <i>GA3ox1</i> | <i>Length. Pea length genes (L-) are named in alphabetical order</i> | <i>Ps</i> | GA ₂₀ 3-oxidation | B7,E5 E7 |
| <i>LEC1</i> | <i>Leafy Cotyledon</i> | <i>At</i> | Promotes embryonic development; CCAAT-box binding factor | E4 |
| <i>LEC2</i> | <i>Leafy Cotyledon</i> | <i>At</i> | Promotes embryonic development; B3 domain transcription factor | E4 |
| <i>LFY</i> | <i>Leafy</i> | <i>At</i> | Transcription factor modulating floral organs; promotes transition from inflorescence to floral meristem | B2,C4 E3A |
| <i>LH; KO1</i> <i>CYP701A10</i> | <i>See LE</i> | <i>Ps</i> | <i>Ent</i> -kaurene oxidation | B7 |
| <i>LHY</i> | <i>Late Elongated Hypocotyl</i> | <i>At</i> | MYB transcription factor; negative regulator of TOC1 | D3 |
| <i>LK</i> <i>BR5red</i> | <i>See LE</i> | <i>Ps</i> | C5 α -duction during BR biosynthesis (see <i>DET2</i> below) | B7 |
| <i>LKA; BRI1</i> | <i>See LE</i> | <i>Ps</i> | BR receptor | B7 |
| <i>LKB</i> <i>BR24red</i> | <i>See LE</i> | <i>Ps</i> | C24 reduction during BR biosynthesis (see <i>DIM/DWF1</i>) | B7 |
| <i>LKC</i> | <i>See LE</i> | <i>Ps</i> | Unknown BR mutant | B7 |
| <i>LKD</i> | <i>See LE</i> | <i>Ps</i> | Unknown BR mutant | B7 |
| <i>LOS5,6</i> | <i>Low Expression of Osmotic Stress-Responsive Genes</i> | <i>At</i> | See <i>ABA3,1</i> respectively | B5 |
| <i>LOX</i> | <i>Lipoxygenase</i> | <i>St;</i> many | Oxygenation of polyunsaturated fatty acids | E5,F1 |
| <i>LS; CPS</i> | <i>See LE</i> | <i>Ps</i> | Synthesis of copalyl diphosphate | B7 |
| <i>LUC</i> | <i>Luciferase</i> | Firefly | Catalyzes the oxidation of luciferin producing light | D3 |
| <i>MAN2</i> | <i>Endo-B-Mannanase</i> | <i>Le</i> | Hydrolysis of mannan | C3 |
| <i>MAX1</i> | <i>More Axillary Growth1</i> | <i>At</i> | Cytochrome p450 | E2A |
| <i>MAX2,</i> <i>RMS4, D3,</i> | <i>More Axillary Growth2</i> | <i>At,Ps,</i> <i>Os</i> | F-box protein involved in shoot branching | E2A |

Table of Genes

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|------------------------------|---|-----------------------|--|------------------|
| <i>MAX3, RMS5, D17</i> | <i>More Axillary Growth3</i> | <i>At, Ps, Os</i> | Carotenoid Cleavage Dioxygenase 7 | E2A |
| <i>MAX4, RMS1, D10, DAD1</i> | <i>More Axillary Growth4</i> | <i>At, Ps, Os, Ph</i> | Carotenoid Cleavage Dioxygenase 8 | E2A |
| <i>MDR1</i> | <i>Multidrug Resistance 1</i> | many | Multi-drug resistance sub-family of ABC transporters. Some members involved in auxin transport | E1 |
| <i>MNK</i> | <i>Menkes Copper-Transporting ATPase</i> | <i>M</i> | Substrate-regulated efflux transporter for Cu ions | E1 |
| <i>MP ARF5</i> | <i>Monopteros</i> | <i>At</i> | Auxin response factor (ARF) transcription factor; regulator of embryo patterning; putative interactor with BDL | D1, E1 E2, E4 |
| <i>MPK4, 6, 13</i> | <i>Mitogen Activated Protein Kinase 4, 6, 13</i> | <i>At</i> | Protein kinase (note: kinases of kinases repeat the K in the abbreviation) | D4, F1 |
| <i>MRP5</i> | <i>Multidrug Resistance-Related Protein 5</i> | <i>At</i> | Closely related to <i>MDRS</i> | E1 |
| <i>MSG2 IAA19</i> | <i>Massugu</i> | <i>At</i> | See <i>AUX/IAA</i> | D1 |
| <i>MSR1</i> | <i>Mitochondrial-Specific Arginyl-tRNA Synthetase 1</i> | <i>Sc</i> | Arginyl-tRNA synthetase | D3 |
| <i>MVL MALVOLIO</i> | <i>Malvolio</i> | <i>Dm</i> | NRAMP Metal-ion transporter similar to <i>Smf1</i> and <i>DCT1</i> | D4 |
| <i>NA; KAO1 CYP88A6</i> | <i>Nana</i> | <i>Ps</i> | <i>Ent</i> -kaurenoic acid oxidase | A2, B7 E5 |
| <i>NAC1</i> | <i>NAM, ATAF1, CUC2</i> | <i>Ph</i> | Transcription factor | D1 |
| <i>NAHG</i> | <i>Salicylate Hydroxylase</i> | <i>Pp</i> | Converts salicylic acid to catechol | E6, F2 |
| <i>NAR2A</i> | <i>Molybdenum Cofactor</i> | <i>Hv</i> | Molybdenum cofactor synthesis | B5 |
| <i>NCED</i> | <i>Nine-Cis-Epoxy-Carotenoid Dioxygenase</i> | <i>Zm; Le; many</i> | Cleavage of 9- <i>cis</i> -epoxy-carotenoids to xanthoxin in ABA biosynthesis | B5, E7 |
| <i>NIA1, 2</i> | <i>Nitrate Assimilation 1, 2</i> | <i>At</i> | Cytokinin-inducible nitrate reductase | C3, D6 |
| <i>NIM1</i> | <i>Non-Inducible Immunity 1</i> | <i>At</i> | Ankyrin repeat protein that transduces the SA signal that activates SAR Also known as <i>NPRI, SAIL</i> | F2 |
| <i>NIT1-, 4</i> | <i>Nitrilase 1-4</i> | <i>At</i> | Conversion of IAN (indole-3-acetonitrile) to IAA in vitro, null allele is resistant to inhibitory effects of IAN | B1, E6 |
| <i>NOT NCED</i> | <i>Notabilis</i> | <i>Le</i> | See <i>NCED</i> | B5 |

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| <i>NPH4</i> <i>MSG1</i> <i>ARF7</i> | <i>Non-Phototropic Hypocotyl 4</i> <i>Massugu 1</i> | <i>At</i> | Affects blue light and gravitropic and auxin mediated growth responses; see <i>ARF</i> | D1,D4 |
| <i>NPQ2</i> | <i>Non-Photochemical Quenching</i> | <i>At</i> | See <i>ABA1</i> | B5 |
| <i>NPR1</i> <i>NIM1</i> , <i>SAIL</i> | <i>Nonexpresser of Pr Genes 1</i> <i>SA Insensitive</i> | <i>At</i> | Controls systemic acquired resistance (SAR) Confers resistance to pathogens; see <i>NIM1</i> | D4,F2 |
| <i>NR</i> | <i>Never-Ripe</i> | <i>Le</i> | Ethylene receptor | D4,D5 E7 |
| <i>NRT1</i> | <i>Nitrate/Chlorate Transporter 1</i> | <i>At</i> | Dual affinity nitrate transporter | D6 |
| <i>ODC</i> | <i>Ornithine Decarboxylase</i> | many | Polyamine biosynthesis | E5 |
| <i>OPR</i> | <i>12-Oxo-Phytodienoic Acid Reductase</i> | <i>At</i> ; many | Conversion of 12-oxo-PDA to 3-oxo-2-(2'(Z)-pentenyl)-cyclopentane-1-octanoic acid (OPC-8:0) in JA biosynthesis | E6;F1 |
| <i>ORCA3</i> | <i>Octadecanoid-Responsive AP2-Domain Protein</i> | <i>Cr</i> | ERF/AP2-domain transcription factor | F1 |
| <i>ORE12</i> | <i>Oresara 12 (delayed senescence)</i> | <i>At</i> | Gain of function mutation in AHK3 | D3 |
| <i>ORP</i> | <i>Orange Pericarp</i> | <i>Zm</i> | Tryptophan synthase beta | B1 |
| <i>OST1</i> | <i>Open Stomata 1</i> | <i>At</i> | ABA-activated serine-threonine protein kinase; probably ortholog of <i>AAPK ost1</i> mutants show guard cell insensitivity to ABA | D6 |
| <i>PAD4</i> | <i>Phytoalexin Deficient 4</i> | <i>At</i> | Lipase-like protein involved in race-specific resistance | F2 |
| <i>PAS</i> | <i>Pasticcino (tartlet)</i> | <i>At</i> | Mutants show uncontrolled cell division | D3 |
| <i>PAT</i> | <i>Parthenocarpic</i> | <i>Le</i> | Unknown; mutation promotes parthenocarpy | E7 |
| <i>PBF</i> | <i>Prolamin Box Binding Factor</i> | Cereals | Transcription factor | C2 |
| <i>PDF1</i> | <i>Protodermal Factor 1</i> | <i>At</i> | Encodes a putative extracellular proline-rich protein | B2 |
| <i>PDF1.2</i> | <i>Plant Defensin 1.2</i> | <i>At</i> | Encodes an ethylene- and jasmonate-responsive plant defensin | D4 |
| <i>PEP</i> | <i>Pepino (Same as Pasticcino 2)</i> | <i>At</i> | Unknown | D3 |
| <i>PGP1</i> | <i>P-Glycoprotein 1</i> | <i>At</i> | Member of a sub-group of MDR proteins | E1 |
| <i>PHOR1</i> | <i>Photoperiod Responsive 1</i> | <i>St</i> | U-box arm-repeat protein, a positive regulator of GA signaling | D2 |
| <i>PHYA</i> | <i>Phytochrome A</i> | <i>At</i> ; many | Light labile red/far-red absorbing photoreceptor; serine-threonine kinase | D3,E5 |

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|-----------------------------|--|--------------------|--|----------------|
| <i>PHYB</i> | <i>Phytochrome B</i> | At; many | Light stable red/far-red absorbing photoreceptor; putative histidine kinase | D3,E5 |
| <i>PID</i> | <i>Pinoid</i> | <i>At</i> | Serine/threonine protein kinase involved in auxin transport and/or signaling | D1,E1 |
| <i>PIF3</i> | <i>Phytochrome Interacting Factor 3</i> | <i>At</i> | Putative helix-loop-helix transcription factor | D3 |
| <i>PIN</i> | <i>Pin-Formed</i> | <i>At</i> | Family of auxin efflux regulators | A2,E1 E2,E4 |
| <i>PIN2</i> | <i>Proteinase Inhibitor II</i> | <i>Le</i> | Defense-related | E5,G1 |
| <i>PIRIN1</i> | <i>Pirin1</i> | <i>At</i> | Interacts with α subunit of G-protein; promotes germination | E4 |
| <i>PIS1</i> | <i>Polar Auxin Transport Inhibitor Sensitive 1</i> | <i>At</i> | Putative negative regulator of polar auxin transport | E1 |
| <i>PKABA1</i> | <i>Protein Kinase Responsive To ABA 1</i> | <i>Hv</i> | Protein kinase; suppresses GA-inducible gene expression in aleurone | C2,E4 |
| <i>PKL</i> | <i>Pickle</i> | <i>At</i> | Chromatin remodeling factor; suppresses embryonic development; a positive regulator of GA signaling? | D2,E4 |
| <i>PLD</i> | <i>Phospholipase D</i> | <i>At</i> | Catalyzes hydrolysis of phosphatidylcholine to phosphatidic acid and choline | D3 |
| <i>PLS</i> | <i>Polaris</i> | <i>At</i> | 36AA peptide of unknown function | D3 |
| <i>POTH1</i> | <i>Potato Homeodomain 1</i> | <i>St</i> | KNOX gene | E5 |
| <i>POZ</i> | <i>Poxvirus Zinc Finger</i> | Virus; <i>A</i> | Transcription factor | C2 |
| <i>PPD,1-2</i> | <i>Peapod</i> | <i>At</i> | Members of the TIFY protein family, involved in leaf development | F1 |
| <i>PRO-SYSTEMIN</i> | <i>Systemin Precursor</i> | <i>Ssp</i> | Systemic wound signaling | F1,F3 |
| <i>ProTomHys Sys</i> | <i>Hydroxyproline-Rich Glycopeptide Precursor</i> | <i>Nt; Le</i> | Precursor of two hydroxyproline-rich peptide defense signals | F3 |
| <i>Ps-IAA4/5</i> | <i>Ps Indole Acetic Acid 4/5</i> | <i>Ps</i> | See <i>AUX/IAA</i> | D1,C4 |
| <i>PSKa precursor</i> | <i>Phytosulfokine-α Precursor</i> | many | Regulates cellular de-differentiation and proliferation | F3 |
| <i>PSY</i> | <i>Phytoene Synthase</i> | many | Converts geranylgeranyl diphosphate to phytoene | B2 |
| <i>PYR PYL RCAR</i> | <i>Pyrabactin Resistance; Pyrabactin Resistance-Like; Regulatory Component of ABA Receptor</i> | <i>At</i> | Soluble family of proteins involved in ABA sensing | D6 |

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|--------------------------------------|--|-------------------------|---|-------------|
| <i>RAC1</i> | ras-related C3 botulinum toxin substrate | <i>At</i> | RHO-like small GTPase; synonymous with <i>ROP6</i> ; negative regulator of guard cell ABA response | D6 |
| <i>RALF precursor</i> | <i>Rapid Alkalinization Peptide Precursor</i> | many | Unknown | F3 |
| <i>RANI</i> | <i>Responsive-To-Antagonist 1</i> | <i>At</i> | ATP dependent copper transporter vital for ethylene response pathway | D4 |
| <i>RB1</i> | <i>Retinoblastoma-Like Protein 1</i> | <i>Nt, eh</i> | Cell cycle regulator, hyperphosphorylated by cyclin-dependent protein kinase complex | C3 |
| <i>RBX1</i> | <i>Ring Box 1</i> | <i>Sc</i> | SCF subunit | D1 |
| <i>RCAR PYR PYL</i> | <i>Regulatory Component of ABA Receptor Pyrabactin Resistance; Pyrabactin Resistance-Like;</i> | <i>At</i> | Soluble family of proteins involved in ABA sensing | D6 |
| <i>RCE1</i> | <i>Rub Conjugating Enzyme 1</i> | <i>At</i> | Conjugation of RUB to substrates | D1 |
| <i>RCN1</i> | <i>Roots Curl In NPA 1</i> | <i>At</i> | Serine/Threonine protein phosphatase type 2A regulatory subunit; <i>rcn1</i> mutant shows impaired guard cell response to ABA | D4,D6 E1 |
| <i>RcsC</i> | <i>Regulator of capsule synthesis C</i> | <i>Ec</i> | Sensor histidine kinase; regulates genes encoding envelope proteins | D3 |
| <i>RDO</i> | <i>Reduced Dormancy</i> | <i>At</i> | Four loci of unknown cellular/molecular function | E4 |
| <i>RGA</i> | <i>Repressor of gal-3</i> | <i>At</i> | DELLA protein, a negative regulator of GA signaling | C2,D2 E4 |
| <i>RGL1,2,3</i> | <i>RGA-LIKE 1-3</i> | <i>At</i> | DELLA proteins, negative regulators of GA signaling | D2,E4 |
| <i>RHD6</i> | <i>Root Hair Defective6</i> | <i>At</i> | Unknown | C4 |
| <i>RHT1</i> | <i>Reduced Height 1</i> | <i>Ta</i> | DELLA-class repressor of GA-inducible gene expression | D2,E4 E7 |
| <i>RIN</i> | <i>Ripening Inhibited</i> | <i>Le</i> | MADS box transcription factor Loss-of-function mutant fruits fail to ripen | E7,D4 D5 |
| <i>RMS1, MAX4, D10, DAD1</i> | <i>Ramosus1</i> | <i>Ps,At, Os,Ph</i> | Carotenoid Cleavage Dioxygenase 8 | E2A |
| <i>RMS4, MAX2, D3,</i> | <i>Ramosus4</i> | <i>Ps,At, Os</i> | F-box protein involved in shoot branching | E2A |
| <i>RMS5, MAX3, D17,</i> | <i>Ramosus5</i> | <i>Ps,At, Os</i> | Carotenoid Cleavage Dioxygenase 7 | E2A |
| <i>ROLC</i> | | <i>Ar</i> | Hydrolysis of CK conjugates | E5 |
| <i>ROP6,10 RAC1</i> | <i>RHO of Plants 6,10</i> | <i>At</i> | RHO-like small GTPase; <i>rop10</i> null mutants are ABA hypersensitive | D6 |

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|------------------------|--|-------------------|---|-------|
| <i>RPN12</i> | <i>Regulatory Particle Non-ATPase 12</i> | <i>Sc; At; eh</i> | Regulatory component of the 26S proteasome complex | C3,D3 |
| <i>RSP1,2 RAS</i> | <i>Raspberry</i> | <i>At</i> | Promote embryonic morphogenesis; suppress embryonic development of suspensor | E4 |
| <i>RUB1 NEDD8</i> | <i>Related to Ubiquitin</i> | <i>Sc</i> | Modifier of CUL1; regulates SCF activity | D1 |
| <i>SABP1</i> | <i>SA Binding Protein 1</i> | <i>Nt</i> | SA-sensitive catalase | F2 |
| <i>SABP2</i> | <i>SA Binding Protein 2</i> | <i>Nt</i> | SA-stimulated lipase and putative SA receptor | F2 |
| <i>SAD</i> | <i>Scutellum and Aleurone Expressed DOF</i> | <i>Hv</i> | Transcription factor | C2 |
| <i>SAD1</i> | <i>Supersensitive To ABA And Drought 1</i> | <i>At</i> | Sm-like small nuclear ribonucleoprotein; <i>sad1</i> mutants are ABA and drought hypersensitive | D6,E4 |
| <i>SAG12</i> | <i>Leaf Senescence-Specific Gene 12</i> | <i>At</i> | Vacuole-targeted cysteine proteinase | E6 |
| <i>SAG13</i> | <i>Leaf Senescence-Specific Gene 13</i> | <i>At</i> | Short-chain alcohol dehydrogenase | E6 |
| <i>SAI1;NIM1, NPR1</i> | <i>SA Insensitive</i> | <i>At</i> | See <i>NIM</i> | F2 |
| <i>SAMase</i> | <i>S-Adenosyl Methionine Hydrolase</i> | T3 bacteriophage | Conversion of S-adenosyl methionine into methylthioadenosine | B4 |
| <i>SAMS</i> | <i>SAM Synthase</i> | <i>At; Le; Ac</i> | ATP:L-methionine S-adenosyltransferase involved in the transfer of the adenosyl moiety from ATP to methionine | B4 |
| <i>SAUR</i> | <i>Small Auxin-Up RNA</i> | <i>Gm;At</i> | Unknown | D1 |
| <i>SAUR-AC1</i> | <i>Small Auxin-Up RNA-Arabidopsis Columbia 1</i> | <i>At</i> | Unknown | D3 |
| <i>SCR precursor</i> | <i>Brassica S-Locus Cysteine- Rich Peptide Precursor</i> | <i>Bsp</i> | Produces S-locus peptide signal for self incompatibility | F3 |
| <i>SD1</i> | <i>Semidwarf-1</i> | <i>Os</i> | GA biosynthesis (GA 20-oxidase) | E7 |
| <i>SDGs</i> | <i>Senescence-Down-Regulated Genes</i> | <i>At</i> | Expression is down-regulated during leaf senescence | E6 |
| <i>SENs</i> | <i>Senescence-Associated Genes</i> | <i>At</i> | Expressed during leaf senescence in <i>At</i> | E6 |
| <i>SEP3</i> | <i>Sepallata</i> | <i>At</i> | Floral development gene | E3A |
| <i>SHI</i> | <i>Short Internodes</i> | <i>At</i> | Zinc finger protein, a negative regulator of GA signaling? | D2 |
| <i>SHO</i> | <i>Shooting</i> | <i>Ph</i> | See <i>IPT1</i> | B3 |

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|--------------------------------|--|---------------------|---|-------------|
| <i>SHY1,6</i> <i>IAA6,3</i> | <i>Short Hypocotyl</i> | <i>At</i> | See <i>AUX/IAA</i> | D1 |
| <i>SID2</i> | <i>SA-Deficient 2</i> | <i>At</i> | Encodes isochorismate synthase involved in SA synthesis Also known as <i>EDS16</i> | F2 |
| <i>SIMKK</i> | <i>Salt Stress-Induced MAPKK</i> | <i>Mt</i> | Salt stress- and pathogen-induced <i>Medicago</i> MAPKK | D4 |
| <i>SIS4</i> | <i>Sugar Insensitive 4</i> | <i>At</i> | See <i>ABA1</i> | B5 |
| <i>SIT</i> | <i>Sitiens</i> | <i>Le</i> | Conversion of ABA-aldehyde to ABA | B5,E3 |
| <i>SLG</i> | <i>Brassica S-Locus Glycoprotein</i> | <i>Bsp</i> | Activates SRK to trigger an incompatibility signaling cascade | F3 |
| <i>SLN</i> <i>GA2ox1</i> | <i>Slender</i> | <i>Ps</i> | GA ₂₀ 2-oxidation, GA ₁ 2-oxidation | B7 |
| <i>SLN1</i> | <i>Synthetic Lethal of N-End Rule 1</i> | <i>Sc</i> | Two-component histidine kinase involved in osmosensing | D3,D4 D5 |
| <i>SLN</i> | <i>Slender</i> | <i>Hv</i> | DELLA protein, a negative regulator of GA signaling | C2,D2 E4 |
| <i>SLR1</i> | <i>Slender Rice 1</i> | <i>Os</i> | DELLA protein, a negative regulator of GA signaling | B2,C2 D2 |
| <i>SLR1;IAA14</i> | <i>Solitary Root 1</i> | <i>At</i> | See <i>AUX/IAA</i> | D1 |
| <i>SLY1</i> | <i>Sleepy 1</i> | <i>At</i> | F-box factor that targets DELLA proteins for proteasomal degradation; a positive regulator of GA signaling orthologous to <i>GID2</i> | D2,E4 |
| <i>SMF1</i> | <i>Suppressor of MIF 1</i> | <i>Sc</i> | NRAMP Metal-ion transporter similar to <i>MVL</i> and <i>DCT1</i> | D4 |
| <i>SMT1</i> | <i>Sterol C-24 Methyl Transferase 1</i> | <i>At</i> ; many | Synthesis of membrane sterols; transferring a methyl group to C-24 position of sterols, allelic to <i>ORC</i> , <i>CPH</i> | B6,E1 |
| <i>SnRK2</i> | <i>Snf1 Related Protein Kinase</i> | <i>At</i> | Family of kinases involved in ABA, drought, and osmotic stress response | D6 |
| <i>SPR2</i> <i>FAD7</i> | <i>Suppressor of Prosystemin-Mediated Responses2</i> | many | Omega-3 Fatty acid desaturase involved in the production of linolenic acid for JA biosynthesis | F1 |
| <i>SPY</i> | <i>Spindly</i> | <i>At</i> | O-linked GlcNAc transferase; a negative regulator of GA signaling | C2,D2 E4 |
| <i>SR 160</i> | <i>Tomato Systemin Receptor</i> | <i>Le</i> | Interacts with systemin to initiate defense signaling | F3 |
| <i>SRK</i> | <i>Brassica S-Locus Receptor Kinase</i> | <i>Bsp</i> | Interacts with <i>SLG</i> and <i>SCR</i> to initiate self incompatibility | F3 |
| <i>SRK2E</i> | <i>SNF1-Related Protein Kinase 2E</i> | <i>At</i> | Snrk2-type protein kinase; synonymous with <i>OST1</i> | D6 |
| <i>SSI1</i> | <i>Suppressor of Salicylic Acid Insensitive 1</i> | <i>At</i> | Activator of defense response gene expression and lesion formation | D4 |
| <i>SSK1</i> | <i>Suppressor of Sensor Kinase 1</i> | <i>Sc</i> | Response regulator; negatively regulates the HOG1 pathway | D3 |

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|---------------------|--|----------------------|--|--------------------|
| <i>SSU</i> | <i>Small Subunit Gene</i> | many | Component of ribulose-1,6-bisphosphate carboxylase/oxygenase (rubisco) | E6 |
| <i>ST2A</i> | <i>Sulfotransferase</i> | <i>At</i> | Hydroxyjasmonate sulfotransferase | F1 |
| <i>STE,DWF7</i> | <i>Sterol/Dwarf 7</i> | <i>At</i> | Steroid C-5 desaturase | B6 |
| <i>STM</i> | <i>Shoot Meristemless</i> | <i>At</i> | KNOX homeobox transcription factor; regulator of shoot meristem formation and maintenance | B2,D3 E4,E5 |
| <i>STP1</i> | <i>Stunted Plant 1</i> | <i>At</i> | Monosaccharide/H ⁺ symporter | D3 |
| <i>SUC2</i> | <i>Suc/H⁺ symporter 2</i> | <i>At</i> | Suc/H ⁺ symporter; promoter is commonly used for phloem-specific expression | E3A |
| <i>SUS1</i> | <i>Abnormal Suspensor 1</i> | <i>At</i> | MicroRNA processing; allelic to Short integuments1 and Carpel factory | E4 |
| <i>SUS2</i> | <i>Abnormal Suspensor</i> | <i>At</i> | Putative pre-mRNA splicing factor | E4 |
| <i>SUSY</i> | <i>Sucrose Synthase</i> | many | Sucrose breakdown | E5 |
| <i>SYR1</i> | <i>Syntaxin-Related 1</i> | <i>Nt</i> | Syntaxin | D6 |
| <i>TAT</i> | <i>Tryptophan Aminotransferase</i> | <i>mi</i> | Conversion of tryptophan to indole-3-pyruvic acid | B1 |
| <i>TBI; BRC, FC</i> | <i>Teosinte Branched</i> | <i>Zm, At Os</i> | TCP transcription factor in shoot branching | E2A |
| <i>TCH3</i> | <i>Touch 3</i> | <i>At</i> | Calmodulin-like protein, expression induced by touch and darkness | D4 |
| <i>TCH4</i> | <i>Touch 4</i> | <i>At</i> | Xyloglucan endotransglucosylase/hydrolase | D7 |
| <i>TCP10</i> | <i>TBI/CYC/PCF10</i> | <i>At</i> | Putative transcription factor | D3, E2A |
| <i>TDC</i> | <i>Tryptophan Decarboxylase</i> | <i>mi, Cr</i> | Conversion of tryptophan to tryptamine | B1 |
| <i>TED</i> | <i>Tracheary Element Differentiation</i> | <i>Ze</i> | Expressed during early stages of vessel element differentiation | E2 |
| <i>TFL SP</i> | <i>Terminal Flower, Self Pruning</i> | <i>At Le</i> | Phosphatidylethanolamine-binding protein; delays flowering; regulates flower position | E3A |
| <i>THI2.1</i> | <i>Thionin</i> | <i>At</i> | Defense-related | E5 |
| <i>TIR1</i> | <i>Transport Inhibitor Response 1</i> | <i>At</i> | F-box protein; related to yeast GRR1P and human SKP2 proteins, involved in ubiquitin-mediated processes; interacts with ASK1 and Aux/IAAs; an auxin receptor | D1,D4 E2A F1 |
| <i>TIR3</i> | <i>Transport Inhibitor Response 3</i> | <i>At</i> | Identical to <i>BIG</i> and <i>DOCI</i> . Putative NPA-binding protein | E1 |
| <i>TMO</i> | <i>Tryptophan Monoxygenase</i> | <i>mi</i> | Conversion of tryptophan to indole-3-acetamide | B1 |
| <i>TMR</i> | <i>Tumor Morphology of Roots</i> | <i>Agt</i> | See <i>IPT</i> | B3 |

| | | | | |
|----------------------|---|---------------|---|-------------|
| <i>TRAB1</i> | <i>Transcription Factor Responsible for ABA Regulation 1</i> | <i>Os</i> | bZIP domain transcription factor; likely <i>ABI5</i> ortholog | E4 |
| <i>TRIP1</i> | <i>Transforming Growth Factor-Beta Receptor Interacting Protein 1</i> | <i>At, Pv</i> | WD-domain protein, subunit of eif3 translation initiation factor Homolog of mammalian signaling protein | D7 |
| <i>TT4</i> | <i>Transparent Testa 4</i> | <i>At</i> | Chalcone synthase, a key enzyme in flavonoid biosynthesis | E1 |
| <i>TTG</i> | <i>Transparent Testa Glabrous</i> | <i>At</i> | WD40 repeat protein, binds transcription factors modulating the fate of root epidermal cells and testa structure | C4,E4 |
| <i>TWN1</i> | <i>Twin 1</i> | <i>At</i> | Required for suppressing embryogenic development in suspensor cells | E4 |
| <i>TWN2</i> | <i>Twin 2</i> | <i>At</i> | Valyl-tRNA synthetase; required for proper proliferation of basal cells | E4 |
| <i>TZS</i> | <i>Trans-Zeatin Secretion</i> | <i>Agt</i> | See <i>IPT</i> | B3 |
| <i>UBA2a</i> | <i>UBP1-Associated Protein 2a</i> | <i>At</i> | Single-stranded RNA binding protein | D6 |
| <i>UCUI</i> | <i>Ultracurvata 1</i> | <i>At</i> | Allelic to <i>BIN2</i> | D7 |
| <i>UGT84B1</i> | <i>UDP-Glucosyltransferase</i> | <i>At</i> | UDP-glucosyl transferase specific to IAA-Glucose formation | B1 |
| <i>VH</i> | <i>Vascular highway</i> | <i>At</i> | A leucine-rich receptor kinase, expressed in provascular/procambium cells | E2 |
| <i>VP1</i> | <i>Viviparous</i> | <i>Zm</i> | B3 domain transcription factor; <i>ABI3</i> ortholog, Embryo maturation | E4,E7 |
| <i>VP14 NCEDI</i> | <i>Viviparous</i> | <i>Zm</i> | See <i>NCED</i> | B5 |
| <i>Vp2,7,8 and 9</i> | <i>Viviparous</i> | <i>Zm</i> | ABA biosynthesis | E4 |
| <i>VP5</i> | <i>Viviparous</i> | <i>Zm</i> | Defect in carotenoid biosynthesis; causing phytoene accumulation and ABA deficiency | E3,E4 E7 |
| <i>WEE1</i> | <i>Wee 1 (i.e., small)</i> | <i>Sp, eh</i> | Protein kinase, cell cycle regulator active at G ₂ /M transition | C3 |
| <i>WEI2,3,4</i> | <i>Weak Ethylene Insensitive</i> | <i>At</i> | Ethylene signal transduction | D4 |
| <i>WOL</i> | <i>Wooden Leg</i> | <i>At</i> | Membrane-bound histidine kinase, cytokinin receptor, wol mutant allele is impaired in cytokinin binding, see also <i>AHK4</i> and <i>CRE1</i> | C3,D3 E4 |
| <i>WUS</i> | <i>Wuschel (ruffled, disheveled)</i> | <i>At</i> | Homeobox transcription factor for stem cell identity; shoot and floral meristem organization | D3,F3 |
| <i>XanF</i> | <i>Xantha F</i> | <i>Hv</i> | Barley Mg ²⁺ chelatase subunit; homolog of CHLH | D6 |

Table of Genes

| | | | | |
|----------------------|--|-----------|--|-------|
| <i>XET4</i> | <i>Xyloglucan Endo-transglycosylase</i> | <i>Le</i> | Endotransglycosylation of xyloglucan | C4 |
| <i>XTH5</i> | <i>Xyloglucan Endo-transglycosylase/Hydrolase</i> | <i>At</i> | Cell wall modification | B2 |
| <i>YojN</i> | <i>Regulator of Capsule Synthesis (Same as RCSD)</i> | <i>Ec</i> | Sensor histidine kinase; regulates colanic capsule synthesis | D3 |
| <i>YPD1</i> | <i>Tyrosine Phosphatase Dependent 1</i> | <i>Sc</i> | His-phosphotransfer protein in the HOG1 pathway | D3 |
| <i>YUCCA</i> | <i>Yucca</i> | <i>At</i> | Flavin monooxygenase, conversion of tryptamine to N-hydroxyl tryptamine in vitro, overexpression results in IAA accumulation | B1 |
| <i>ZE3</i> | <i>Zeatin Resistant 3</i> | <i>At</i> | Unknown | D3 |
| <i>ZIM</i> | <i>Zinc-finger Inflorescence Meristem</i> | <i>At</i> | Zinc-finger protein expressed in inflorescence meristem; member of TIFY family | F1 |
| <i>ZML</i> | <i>ZIM-like</i> | <i>At</i> | ZIM-like protein; member of TIFY protein family | F1 |
| <i>ZmHP2</i> | <i>Zm Histidine Phosphotransfer Protein 2</i> | <i>Zm</i> | His-phosphotransfer protein | D3 |
| <i>Zmp Zm -p60.1</i> | | <i>Zm</i> | Cytokinin-glucoside specific β -glucosidase; releasing free cytokinins from cytokinin-O-glucosides | C3,E3 |
| <i>ZmRR1,2</i> | <i>Zm Response Regulator 1,2</i> | <i>Zm</i> | Response regulator involved in nitrogen signaling | D3 |
| <i>ZOG1</i> | <i>Trans-Zeatin O-Glucosyltransferase1</i> | <i>Pl</i> | O-glucosylation of <i>trans</i> -zeatin | B3 |
| <i>ZOX1</i> | <i>Trans-Zeatin O-Xylosyltransferase 1</i> | <i>Pv</i> | O-xylosylation of <i>trans</i> -zeatin | B3 |

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