A COMPREHENSIVE DATASET OF GENES WITH LOSS-OF-FUNCTION MUTANT PHENOTYPES IN *ARABIDOPSIS THALIANA*

By

JOHN PAUL LLOYD

Bachelor of Science in Microbiology

Oklahoma State University

Stillwater, OK

2009

Submitted to the Faculty of the
Graduate College of the
Oklahoma State University
in partial fulfillment of
the requirements for
the Degree of
MASTER OF SCIENCE
July, 2012

A COMPREHENSIVE DATASET OF GENES WITH LOSS-OF-FUNCTION MUTANT PHENOTYPES IN *ARABIDOPSIS THALIANA*

Thesis Approved:

David Meinke

Thesis Adviser

Andrew Doust

Gerald Schoenknecht

Ming Yang

Sheryl Tucker

Dean of the Graduate College

TABLE OF CONTENTS

LIST OF TABLES

Table Page

LIST OF FIGURES

CHAPTER I

INTRODUCTION

Nature of Phenotype Data

Mutant phenotypes, both dominant and recessive, are an important tool in the understanding of gene function. Dominant phenotypes usually result from a gain-of-function mutation. Examples include disruptions of promoter regions that cause overexpression or inappropriate expression of a gene product, and changes to protein domains or active sites that create a novel gene function not masked by a wild type allele. In some cases, dominant phenotypes result from dominant negative mutations that produce a defective protein product with an antagonistic effect on other proteins in the cell. Because of the diversity of these defects, it can be difficult to interpret the biological significance of a dominant phenotype. By comparison, recessive phenotypes, which result from the loss of gene function, are more straightforward to interpret. Recessive phenotypes result from either complete abolition or varying degrees of reduction in gene function. Less frequently, semi-dominant phenotypes observed in heterozygotes are produced by the loss of gene function. These are often the result of haploinsufficiency; a single functional allele does not generate enough gene product to meet the needs of a cell. The focus of my Master's research is genes with recessive, loss-of-function mutant phenotypes in *Arabidopsis thaliana*.

Well-curated and reliable datasets of mutant phenotype information are an important component of model genetic systems. Ideally, these datasets should provide a direct connection between a mutant gene and the resulting phenotype and should include the full range of phenotypes identified in an organism through genetic analysis. Phenotype datasets allow for convenient access to mutant phenotype information in an organism, but they function as more than simple repositories of data. Studying comprehensive mutant phenotype information can offer insights into the biological consequences resulting from disruption of a protein family, metabolic network, or organelle function. They can also be utilized to evaluate the selective pressure exerted to maintain particular morphologies and the role phenotype plays in gene evolution (Hurst and Smith, 1999; Hirsh and Fraser, 2001; Jordan et al., 2002). Phenotype datasets therefore facilitate the investigation of a wide range of important biological questions.

Availability of Phenotype Data

The importance of collections of phenotype information associated with specific gene disruptions is reflected in the presence of widely-used phenotype datasets in a variety of eukaryotic model systems. The Online Mendelian Inheritance in Man database (McKusick, 2007) and Mouse Genome Database (Blake et al., 2011) are important phenotype datasets in mammals. These two collections represent an important integration between basic research and clinical care. Flybase, Wormbase, and the *Saccharomyces* Genome Database keep phenotype datasets for the classic model systems of *Drosophila*, *C. elegans*, and yeast, respectively (Drysdale and FlyBase Consortium, 2008; Engel et al., 2010; Harris et al., 2010). The emerging model fish system, *D. rerio*, also has a phenotype database at the Zebrafish Information Network (Bradford et al., 2011). PhenomicDB serves as a single location that synthesizes and houses phenotype data from these databases, as well as information from a variety of other sources and organisms (Kahraman et al., 2005).

By contrast, genome-wide genotype-to-phenotype data in plants are difficult to obtain. The primary resource for data concerning Arabidopsis, TAIR (www.arabidopsis.org), contains some phenotype information, but it cannot be easily queried or compiled. The Maize Genome Database (Lawrence et al., 2004) has information on classical maize mutants and their phenotypes, but the data are difficult to access and are not necessarily associated with the gene responsible for the mutant phenotype. Gramene, a database of genome information for grasses (Ware et al., 2002), can be queried for protein-coding genes associated with a phenotype in rice. However, it returns information for very few genes, and the phenotype data are difficult to interpret and cannot always be readily associated with a specific locus. Tomato phenotype information found at the Sol Genomics Network (Mueller et al., 2005) shares similar issues. In general, phenotype data for plants are either difficult to access, not well-curated, or not clearly associated with a malfunctioning gene.

Some strides have been made in the curation of phenotype data in Arabidopsis. The first attempt at a broad phenotype dataset in Arabidopsis was published nine years ago by Meinke et al. (2003). This work established a collection of 620 genes with either loss- or gain-of-function mutant phenotypes. This dataset falls short of the comprehensive one desired, however, because the phenotype information was incomplete at the time it was published and is now out of date. Additional small datasets of information geared toward specific phenotypes have been produced; examples include defects in gametophyte development (Johnson et al., 2004; Boavida et al., 2009; Pagnussat et al., 2005) and seedling photomorphogenesis (Khanna et al., 2006). A comprehensive dataset of genes in Arabidopsis with a published mutant phenotype has remained elusive.

Outline and Scope of Thesis

This thesis describes the construction of a comprehensive dataset of loss-of-function mutant phenotype information in Arabidopsis. The phenotype data are limited primarily to recessive phenotypes, but include a small number of semi-dominant, loss-of-function phenotypes observed in heterozygotes. The dataset is gene-based; all phenotype information is associated with a disrupted gene. Phenotypes captured in the dataset are observed in mutants harboring alleles that eliminate gene function (null or knockout alleles) and those resulting from incomplete disruption of gene function (knockdown alleles and some RNA interference lines). A complementary dataset was also produced to catalogue phenotypes resulting from the disruption of multiple, redundant genes.

The Arabidopsis phenotype dataset presented here has already contributed to three peer-reviewed journal publications. One paper that resembles this thesis describes the construction of the single and multiple mutant phenotype datasets, and the analysis of relationships between mutant phenotype and protein function, subcellular localization, number of protein interactors, and genetic redundancy (Lloyd and Meinke, 2012). The supplementary datasets provided with this publication represent the first comprehensive source of gene-based phenotype information in plants. Discrete portions of the dataset contributed to two additional publications. One paper utilized a list of genes whose protein products are localized to the chloroplast and display a knockout phenotype, including embryo lethality (Bryant et al., 2011). This allowed for a comparison of the types phenotypes (embryo lethality, altered pigmentation, or other defects) that result from inhibiting chloroplast functions. Another paper investigated the basis of reproductive lethality in Arabidopsis (Muralla et al., 2011). Comparisons were made between genes whose disruption results in either gametophyte or embryo lethality. While a collection of embryo-defective genes has long been available through the SeedGenes database (www.seedgenes.org), a compilation of genes whose disruption results in gametophyte defects needed to be produced. The Arabidopsis phenotype dataset described here contributed to the production of this dataset of genes with gametophyte defects. This thesis will highlight the primary conclusions and my contributions to these three publications while including some additional details and analysis. I have also included figures and tables from these publications. Please refer to the original papers for more detailed discussion of the concepts, scope, and conclusions of these publications.

Looking ahead, the second chapter of this thesis describes the construction of a single-gene mutant phenotype dataset composed of 2,400 genes (Lloyd and Meinke, 2012). The third chapter discusses the construction and analysis of a dataset of Arabidopsis genes with gametophyte defects. These genes with gametophyte phenotypes represent a subset of the genes included in the complete single-gene dataset. The fourth chapter focuses on the organization and production of a dataset that catalogs phenotypes resulting from the disruption of multiple redundant genes. This dataset includes phenotypes that were not observed in single gene disruptions due to genetic redundancy. The fifth and final chapter describes the variety of biological questions that the Arabidopsis phenotype dataset has been used to address. In addition to the primary text, supplemental tables displaying the bulk of the data curated for these phenotype datasets are appended to this thesis. Three additional appendices describing the controlled but non-binding vocabulary used to describe mutant phenotypes, the complete phenotype classification system, and the protein function classification system used throughout this project are also included.

CHAPTER II

SINGLE GENE MUTANT PHENOTYPE DATASET

Definition and Classification of Mutant Phenotypes

A clear, precise definition of what changes resulting from gene disruption constitute a mutant phenotype in *Arabidopsis thaliana* must be established before building a phenotype dataset. For this project, phenotypes are defined as heritable changes in plant viability, morphology, physiology, or cellular ultrastructure. Changes in the structure or levels of plant hormones, storage products, or other biochemicals are considered phenotypes. Defects observed only under specialized growth conditions or in specific genetic backgrounds are also included. The dataset includes phenotypes of knockout and knockdown alleles, as well as semi-dominant features resulting from loss of gene function that are observed in heterozygotes. Distinct phenotypes resulting from the disruption of more than one genetically redundant gene were catalogued in a complementary multiple mutant dataset (see Chapter 4). Gain-of-function mutant phenotypes were excluded.

In order to differentiate between molecular changes that qualify as phenotypes and those that do not, a prioritized hierarchy was developed for biochemical and physiological defects (Table 1). The most subtle defect expected from a recessive mutant is the production of an abnormal, nonfunctional protein product or the production of no gene product at all. Slightly more noticeable defects include changes in gene expression profiles, RNA editing, or the accumulation of protein complexes. These subtle genetic defects (Table 1; Levels 0, 1, and 2) likely result from many or all gene disruption events, and, thus, are not considered phenotypes. More striking biochemical defects involve changes in the accumulation of metabolites and alterations in molecular processes. These changes can often be detected through biophysical assays or observation of the levels and structures of the chemicals involved. Molecular defects are perhaps more notable when they involve plant storage products (e.g. starch and lipids) or plant hormones. This is reflected in a higher priority for alteration of these particular chemicals in the biochemical defect hierarchy. Changes in cellular products and processes beyond the DNA, RNA, or protein level (Table 1; Levels 3, 4, and 5) represent the lower boundary of defects that are considered phenotypes for the Arabidopsis phenotype dataset.

The phenotype classification system produced for the dataset centers around a brief, curated phenotype description. This description is a plainly-written phrase condensed from discussion in the scientific literature of changes observed in homozygous mutant plants compared to their wild-type counterparts. For example, a report of the differences in response to the hormone auxin between a mutant and wild-type plant may be condensed to the phrase “Sensitive to auxin.” These phenotype descriptions use controlled but non-binding vocabulary, and, as much as possible, similar phenotypes are

Table 1. Biochemical Defect Hierarchy

Level	Description of Biochemical Defect
0	Disrupted gene produces no protein product or produces a defective protein product
1	Defects in the editing and modification of other mRNA
2[a]	Disruption of the expression, structure, or modification of another protein or protein complex
3[a,b]	Change in physiological or biochemical process
3.1	Detected by use of instrumentation or biophysical assay
3.2	Detected chemically through a change in the accumulation, profile, or structure of a metabolite or biochemical
4	Changes in the accumulation, structure, or transport of a storage product
5	Changes in the accumulation, structure, or transport of a hormone

[a] The "phenotype boundary" exists between levels two and three of this classification system. This boundary separates defects considered phenotypes from those that are not considered phenotypes.

[b] The most subtle biochemical defect considered a phenotype for this project.

described using similar terminology. See Appendix A for the full list of controlled vocabulary utilized in the dataset. Some consideration was given to the flow of a description, and if alterations to phrasing produced a cleaner or easier to understand description, alternate vocabulary was used. For example, a mutant with both dark green leaves and serrated leaf margins might have the phenotype description “Dark green leaves with serrated margins,” as opposed to two separate descriptions for each defect. Care was also taken to maintain the original words used to describe a phenotype, provided the author’s words could be integrated into the existing vocabulary structure. Because of the above considerations, a single phrase cannot be used to query the dataset and retrieve all associated phenotypes. This underscores the utility of developing a robust ontology system to classify mutant phenotypes in Arabidopsis and other plants. Such a system would be a useful update to this dataset in the future.

The phenotype description was then used to place the corresponding gene into a three-tiered classification system (Figure 1). The broadest tier consists of four prioritized, exclusive phenotype groups: essential, morphological, cellular-biochemical, and conditional. These groups are further divided into eleven prioritized, exclusive phenotype classes: gametophyte, embryo-seed, lethal, vegetative, reproductive, timing, cellular, biochemical, and three conditional classes. The conditional classes are based on abnormal responses to non-standard physical, chemical, or biological growth conditions. Here, biological refers to pathogens, herbivores, or other biological interactors. Phenotypes resulting from the strongest documented allele are used in class and group designations. The prioritization of the phenotype groups and classes is designed to reflect the stage in the life cycle when a phenotype is first observed, and, to some extent, the

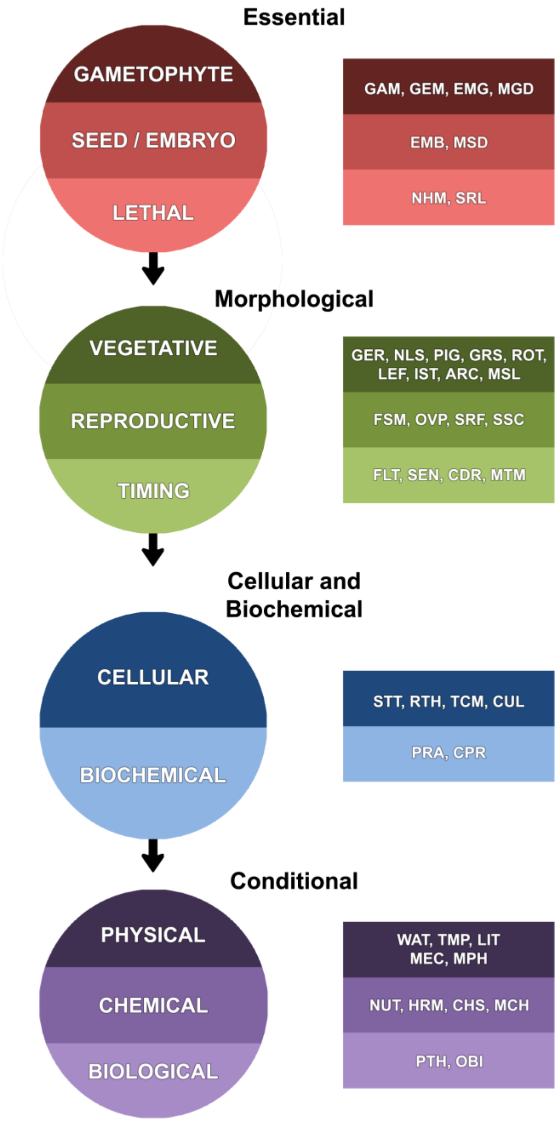

Figure 1. Overview of the Phenotype Classification System. Classification system for Arabidopsis genes with mutant phenotypes based on a series of unique, prioritized phenotype groups (black headings; complete circles) and classes (circle segments), along with nonexclusive phenotype subsets (abbreviated in rectangles). Phenotype subsets are described in more detail in Appendix B.

difficulty required to detect a phenotype. Exclusive group and class assignments are useful in comparing phenotype genes in Arabidopsis with one another and with those in other model organisms. Forty-two non-exclusive phenotype subsets that are associated with a phenotype class are also outlined. For example, the four subsets in the reproductive class are abnormal floral and silique morphology, sporophytic defects in ovules or pollen, sterility and reduced fertility, and sporophytic defects in seeds or seed coats. See Appendix B for an overview of the complete phenotype classification system and a detailed description of all phenotype subsets. Phenotypes resulting from weak alleles (W) or observed in heterozygotes (S) are associated with a subset through use of unique symbols [phenotype subsets associated with putative knockout alleles are denoted by an ‘X’]. Affiliating a gene with all appropriate subsets allows for easy extraction of all genes associated with a particular phenotype of interest.

In order to illustrate the placement of a gene within the three tiers of the phenotype classification system, I will use as an example, *MRE11* (At5g54260), which has the following phenotype description: dwarf; sterile; long telomeres; sensitive to genotoxic stress. This mutant displays phenotypes that fall into the morphological (dwarfing and sterility), cellular-biochemical (long telomeres), and conditional (sensitivity to genotoxic stress) phenotype groups. Due to priority, however, *MRE11* is assigned to the morphological group. Within the morphological group, *MRE11* has defects that could be classified as both vegetative and reproductive. Again, priority indicates this gene should be placed in the vegetative class. Unlike the groups and classes, the phenotype subsets are non-exclusive. As a result, *MRE11* is associated in the dataset with all appropriate subsets: growth rate and size, sterility and reduced fertility, cellular ultrastructure, and chemical stress

Some counterintuitive phenotype classifications are included in this system. For example, defects in stomata, trichomes, or root hairs are classified in the cellular phenotype group, instead of the morphological. This reflects the subtlety of defects in these small epidermal structures. Sporophytic defects in ovule and pollen development, however, are considered reproductive defects, despite the effort required to characterize these phenotypes. This classification most readily associates these defects with the process that they are involved in. The difference between the two biochemical subsets, product accumulation and cellular process, can be somewhat unclear, as defects in a metabolic process can interfere with the accumulation of a downstream chemical. As a result, assignment to either subset may depend on how the phenotype was initially described. The subsets within the conditional-chemical class assign non-hormone compounds as nutrients, stressors, or miscellaneous chemicals. Sugars, nontoxic atmospheric gases, and elements and compounds required for plant development are considered nutrients. This classification is maintained regardless of toxicity at high concentrations. Unlike nutrients, stressors serve only to impede plant development. Salts such as sodium chloride are included as stressors because of their longstanding role as a source of osmotic stress. A miscellaneous subset was also included for chemicals that cannot be clearly labeled as either nutrient or stressor. Aluminum and cadmium, for example, fall into this category.

Standard laboratory conditions need to be defined in order to determine what phenotypes are conditional. Standard conditions are considered plant growth under long days at room temperature and ambient atmospheric gas levels. The inclusion of long days as part of standard conditions classifies phenotypes observed only under short days or continuous light as conditional. Plants may be grown in soil, agar, or a hydroponic system. Growth conditions were assumed to be standard if no specifications were provided in a publication.

Confidence Status of Gene-to-Phenotype Associations

It is important to be certain that a phenotype is due to the disruption of a known gene. Because most mutant plants are the result of random mutagenesis, which can disrupt multiple genes and cause other chromosomal aberrations, close linkage of a phenotype and disrupted gene is not sufficient to confirm the association. Gene-to-phenotype associations in the dataset were considered confirmed if molecular complementation with a wild-type copy of the gene resulted in a wild-type appearance, or if additional mutants disrupted in same gene showed similar phenotypes. Reversion of a phenotype following transposon excision or other biochemical analysis could also confirm an association. For example, if a disrupted gene was known to encode a nitrogen transporter and the mutant plant showed the expected nitrogen-related phenotype, the association was classified as confirmed. Genes with associations that were not confirmed are included in the dataset when supported by other genetic data because most will likely turn out to be correct. Deletions of large chromosomal regions often result in gametophyte lethality. Because of this, genes with gametophyte phenotypes that could not be verified to result from disruption of a single gene were excluded from the dataset.

Dataset Construction

Four approaches were utilized in the production of the Arabidopsis phenotype dataset: (1) updates to phenotype information contained in the original list of 620 genes with mutant phenotypes (620 list) published nine years ago (Meinke et al., 2003), (2) inclusion of information on embryo-defective phenotypes from the SeedGenes database, (3) evaluation of a list of candidate genes furnished by TAIR; and (4) PubMed searches for papers describing Arabidopsis phenotype information, followed by direct literature curation. These approaches allowed for the location and curation of thousands of abstracts and papers describing gene-based Arabidopsis mutant phenotypes. This resulted in a comprehensive collection of Arabidopsis phenotype data that is current through 2010.

The 620 list served as a foundation for this study, though updates to this phenotype information were required. Many phenotype descriptions were out-of-date or inconsistent with the terminology of the current dataset. Additionally, the 620 list contained dominant mutants and both enhancer and suppressor phenotypes associated with multiple mutants. For the current dataset, the multiple mutant phenotypes involving the disruption of genetically redundant genes (typically enhancer phenotypes) were reassigned to the multiple mutant dataset described in Chapter 4. Dominant phenotypes and non-redundant multiple mutant phenotypes (typically suppressor phenotypes) were removed entirely from the dataset. Work on removing inappropriate phenotypes and updating the confirmation status of genes in this list was directed and performed by Dr. David Meinke with the help of an undergraduate research assistant, Krista McGuire.

The embryo-defective phenotype information stored in the SeedGenes database was also included in the current dataset. The description of “embryo defective,” along with the stage at which defective embryos were observed was carried over for many of the genes included in SeedGenes. However, some genes were reclassified as having a mixture of both gametophyte and embryo defects by utilizing data such as low percentage of mutant seeds or the biased appearance of mutant seeds toward the distal end of a silique. Several datasets of gametophyte-defective genes provided with publications describing these phenotypes were included in the dataset (Johnson et al., 2004; Pagnussat et al., 2005; Boavida et al., 2009) due to interest in producing a robust dataset of gametophyte-defective genes. See Chapter 3 for detailed discussion of the construction and contents of the dataset of genes with gametophyte defects, and Muralla et al. (2011) for updated information on genes with embryo and gametophyte phenotypes. Dr. David Meinke was primarily responsible for the curation of phenotype genes from SeedGenes.

Direct literature curation was also employed to identify mutant phenotypes observed in Arabidopsis. Two strategies were used to streamline this effort: curation of a list of candidate phenotype genes provided by TAIR, and PubMed literature searches involving appropriate keywords. The TAIR list included over 1,300 genes associated in some way with phenotype data in their database. Gene names, symbols, and locus numbers for each gene were included, but potential mutant phenotypes were not noted. The first year of my work on this project was focused almost entirely on searching for relevant publications describing a loss-of-function phenotype for each gene in this list. I also received help from several undergraduate research assistants and other Meinke laboratory staff. When curation of this list was complete, over 400 genes were removed for having no documented phenotype, not coding for protein, displaying only a multiple mutant phenotype, or some other reason. The TAIR list of candidate genes was produced early in 2009, and as a result, it only reliably directed us toward phenotype data published through 2008. To help capture phenotype data beyond this date, two separate PubMed keyword searches were employed: one performed at the beginning of 2010 to identify phenotypes published in 2009, and another in mid-2011 to identify those from 2010. The exact keyword string used in the search for phenotype data published in 2009 was: ("2009/01/01"[Publication Date]: "2009/12/31"[Publication Date]) AND (Arabidopsis AND (Mutant OR Mutants OR Mutation OR Mutations OR Knockout OR Null)). The search for data published in 2010 utilized a similar format. These two searches together resulted in over 3,000 promising abstracts that were subsequently evaluated to assess whether an associated paper described a gene-based loss-of-function phenotype in Arabidopsis.

Phenotype descriptions, along with group, class, and subset assignments, were included in the final phenotype dataset. Additional information (e.g. protein function and level of genetic redundancy) was also catalogued (Table 2). Gene identifiers, such as locus numbers, names, symbols, and aliases, were collected primarily from TAIR, but literature curation occasionally revealed additional aliases or updated locus numbers. The confirmation status of a gene-to-phenotype association was noted as either confirmed or not confirmed. For the purposes of data tracking, the last author and year of publication from a paper describing a mutant phenotype were included. This information is not meant to reflect a definitive date of gene identification or the laboratory that should in each case be given credit, but instead simply reflects a source of phenotype

Table 2. Information Included in the Dataset

Number of Dataset Columns[a]	Nature of Information
4	Locus number; gene name, symbol, aliases
1	Confirmation Status of gene-to-phenotype associtaion
3	Phenotype group, class, and subset assignments
1	Brief, curated description of mutant phenotype
1	Method of gene identification
2	Reference laboratory and year of publication
3	Closest BLASTP match within Arabidopsis
2	Limited protein function information, classification
2	Mitochondrial and plastid localization information

[a] In the complete Arabidopsis phenotype dataset (Lloyd and Meinke, 2012; Table S2).

information used in the compilation of this dataset. The method used to identify a disrupted gene, either forward or reverse genetics, was included. Forward genetic methods were further noted as map-based cloning or T-DNA / transposon insertion. Brief descriptions of putative protein functions were collected from publications. BLASTP analyses were performed and the locus number of the top Arabidopsis hit and the e-value of this match were included. Plastid or mitochondrial localization was predicted using a variety of public sources. This was coupled with manual curation of publications to determine a probable subcellular localization. More detailed discussion of protein function curation, genetic redundancy status, and mitochondrial or plastid localization prediction are found within the corresponding sections discussing these analyses in Chapter 5.

The complete Arabidopsis phenotype dataset is available as a spreadsheet in the supplementary data of a *Plant Physiology* publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S2). This spreadsheet features 19 columns of phenotype, gene, and data tracking information (Table 2) for the 2,400 genes in the dataset; a total of over 45,000 cells of data. Truncated forms of the single gene phenotype dataset lacking a reference lab, year of publication, protein function classification, and BLASTP e-value and locus number of top match for each gene can be found appended to this thesis. Appendix C contains the phenotype and mutant information for genes included in the dataset. Appendix D describes other data collected, such as encoded protein function, genetic redundancy status, and subcellular localization of gene products.

Dataset Overview

The phenotype dataset includes information on the biological consequences resulting from the disruption of 2,400 genes in Arabidopsis. The relative abundance of any given phenotype in the dataset reflects the total number of target genes involved and difficulty required to observe a particular defect, as well as general community interest in a research area. The prioritized nature of the phenotype groups and classes also tends to favor categories of higher priority. The most abundant categories in the dataset are the morphological group (36% of genes) and vegetative class (26%). These defects are not only common and easily identifiable, but they have long been the focus of plant scientists interested in plant growth and development. The essential group and embryo-seed class represent the next most common categories, containing 30% and 15% of genes in the dataset, respectively. Inclusion of the information on embryo and gametophyte defects from SeedGenes and other sources bolstered the numbers of genes included in these categories. But early developmental defects are also quite common; approximately 1,000 embryo-defective genes alone are expected in the Arabidopsis genome (Muralla et al., 2011).

The least common phenotype group is cellular-biochemical (13% of genes). This is most likely due to the priority hierarchy of the phenotype classification system. Disruption of almost any gene results in a biochemical or molecular defect, but the chemical change will often be overlooked if it leads to a more severe phenotype. In addition, cellular phenotypes can be difficult to characterize, as identifying these defects often require specialized knowledge, equipment, and skill. Despite much community interest in the molecular mechanisms controlling the timing of plant growth, the timing class (3% of genes) is the least represented in the dataset. This could be a genuine reflection of the low number of genes involved in the process. However, timing defects can be difficult to characterize, and it may be that many mutants display a timing phenotype that goes unnoticed. A full outline of the distributions of all phenotype groups and classes is available in Table 3.

The distribution of the 42 phenotype subsets shows similar trends as the groups and classes. The five highest represented subsets are found within the two most common phenotype classes in the dataset. Four of these (EMB, GRS, PIG, and LEF) are associated with at least 10% of the genes in the dataset. Likewise, the least frequent subsets tend to be constituents of the two least common phenotype classes. They are also often categories designed to include miscellaneous, uncommon phenotypes. Six of the seven subsets that represent at most 1% of genes in the dataset correspond to one of these issues, and the two smallest subsets (OBI and MTM) correspond to both. See Figure 2 for the distribution of all phenotype subsets in the dataset.

Eighty-four percent of all gene-to-phenotype associations cataloged in this dataset are confirmed (Table 3). The most frequent methods of confirmation are molecular complementation and the use of multiple alleles. One or both of these were employed to confirm 76% of associations in the dataset. Using multiple alleles was more common, however, as these confirmed 55% of associations, compared with 38% for molecular complementation. Only 10% of phenotypes were confirmed by some other method. Essential phenotypes are less likely to be confirmed than other phenotypes in the dataset. This is probably due to the inclusion of many essential embryo and gametophyte phenotypes from large-scale studies and unpublished public databases. These types of

Table 3. Phenotype Group and Class Distributions

Phenotype Category		Genes in Dataset		Gene Identity Confirmed	
Group[a]	Class	Number	Percentage	Number	Percentage
ESN		719	29.9	540	75.1
	Gametophyte	197	8.2	136	69.0
	Embryo-Seed	370	15.4	281	75.9
	Lethal	152	6.3	123	80.9
MRP		862	35.9	775	89.9
	Vegetative	640	26.7	572	89.2
	Reproductive	152	6.3	141	92.8
	Timing	70	2.9	62	88.6
CLB		297	12.4	261	87.9
	Cellular	124	5.2	111	89.5
	Biochemical	173	7.2	150	86.7
CND		522	21.8	445	85.2
	Physical	157	6.6	126	80.3
	Chemical	257	10.7	229	89.1
	Biological	108	4.5	90	83.3
Total		2,400	100.0	2,021	84.2

[a] ESN, essential; MRP, morphological; CLB, cellular and biochemical; CND, conditional.

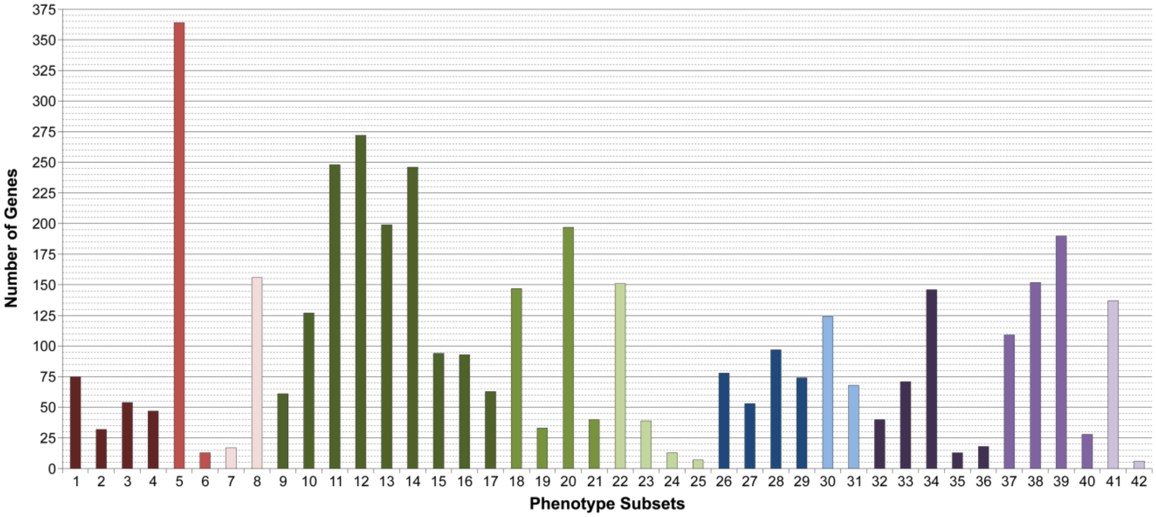

Figure 2. Distribution of Phenotype Subsets. Distribution of phenotype subset assignments for Arabidopsis genes with a loss-of-function mutant phenotype. Subsets are colored according to phenotype class (Figure 1) and numbered as described in Appendix B. Most essential genes are assigned to a single phenotype subset. Many other genes have more than one subset assignment. Phenotypes of weak alleles and semi-dominant features observed in heterozygotes are included.

sources tend to include a larger number of unconfirmed phenotypes compared with more focused studies, as confirmation of a gene-to-phenotype association is often a requirement for publication.

Genes identified through forward genetics may be expected to display essential or morphological phenotypes more often than cellular, biochemical, or conditional phenotypes because they are readily identified when screening a large mutagenized population. To test this assertion, the number of genes that display essential and morphological phenotypes and those associated with cellular, biochemical, and conditional defects were compared based on forward or reverse genetic identification methods. Genes associated with both methods were considered part of the forward genetic category for this investigation. In these cases, the mutant phenotype was often first identified through a large-scale genetic screen and reverse genetic methods were employed to clone a gene or confirm a gene-to-phenotype association. This comparison indicated that essential and morphological phenotypes were more commonly associated with forward genetic methods (χ^2 test, $p < 0.001$). This suggests that subtle biochemical defects or those identified under specialized growth conditions are more frequently identified through reverse genetic approaches, and conversely, that obvious loss-of-function phenotypes can be efficiently identified through forward genetic screens.

The number of genes with a published mutant phenotype in Arabidopsis has been increasing steadily since 2001 (Figure 3A). Around 200 new genes have been identified each year from this point forward. One reason for the stable increase of new phenotype information is the availability of powerful reverse genetics tools. Figure 3B shows the shift from forward to reverse genetic methods, particularly over the three-year span from

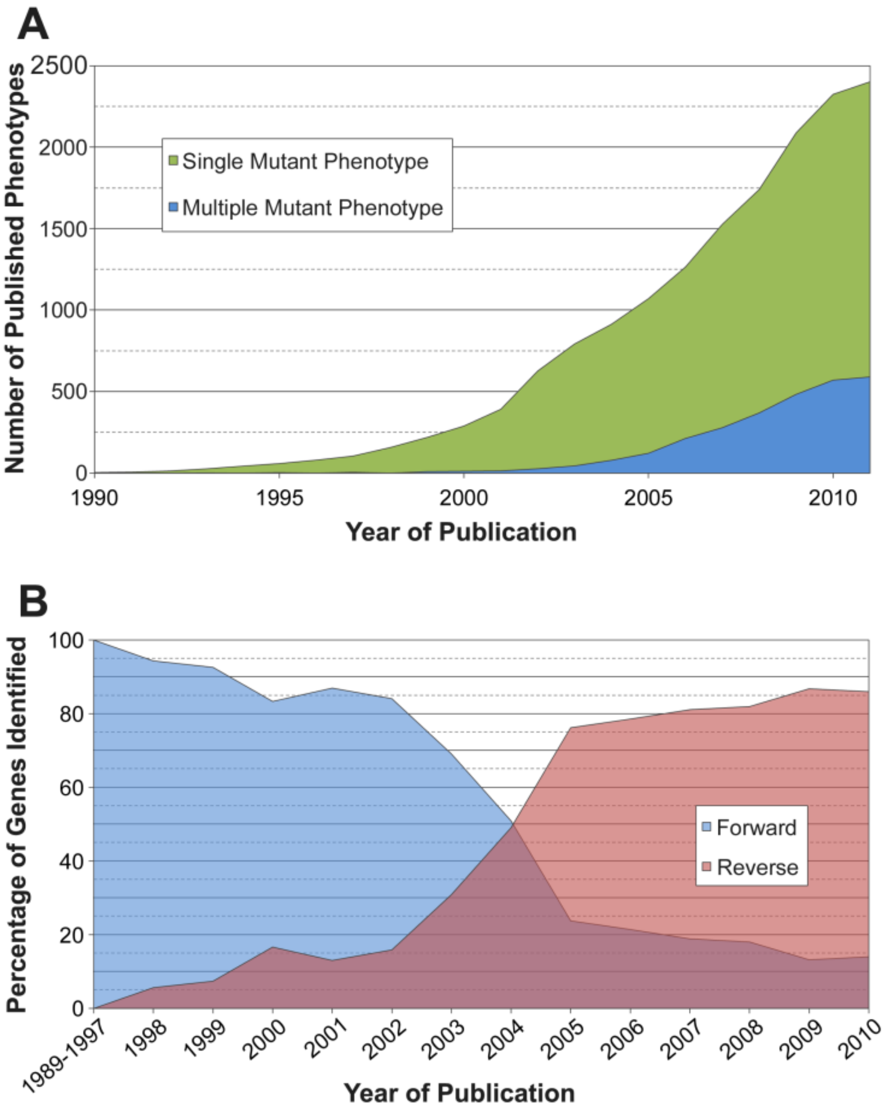

Figure 3. Historical Perspective on Genes with Mutant Phenotypes. Historical perspective on the identification of Arabidopsis genes with a loss-of-function mutant phenotype through forward and reverse genetics. The year of publication in some cases refers to the date of inclusion in a public database. Additional details on gene identification methods are presented in Appendix C.

2002 to 2005. The timing for this shift logically follows the sequencing and publication of the Arabidopsis genome (Arabidopsis Genome Initiative, 2000), and the development of widely-used collections of public insertion lines (Sessions et al., 2002; Alonso et al., 2003; Rosso et al., 2003). Forward genetics continues to play an important role in the landscape of Arabidopsis mutants, however, as an average of 60 phenotype genes identified through these methods have been published each year since 2005.

Phenotype genes in Arabidopsis are dispersed widely throughout the genome, with the exception of centromeric regions (Figure 4). The number of phenotype genes (χ^2 test, P = 0.81) and the distribution of phenotype groups (P = 0.59) are similar for each Arabidopsis chromosome (five in total). The ends of chromosomes are also well represented. The first and last 25 locus numbers of each chromosome average 3.4 phenotype genes, slightly higher than the genome-wide average of 2.2 (χ^2 test, P = 0.02). There are 191 cases of two physically adjacent phenotype genes (within 10 locus numbers), and 34 cases of three adjacent phenotype genes. The largest congregation of phenotype genes is a group of four adjacent essential genes on chromosome three. These four genes show no sequence similarity to one another and, as a result, their close proximity and related phenotypes are probably due to chance.

Future Updates to the Arabidopsis Phenotype Dataset

This project was designed to catalogue all published, gene-based phenotype information in Arabidopsis. While the phenotype data collected are robust enough to produce meaningful results for the analyses described in this thesis, some published mutant phenotypes have likely escaped our detection. Phenotype descriptions in the

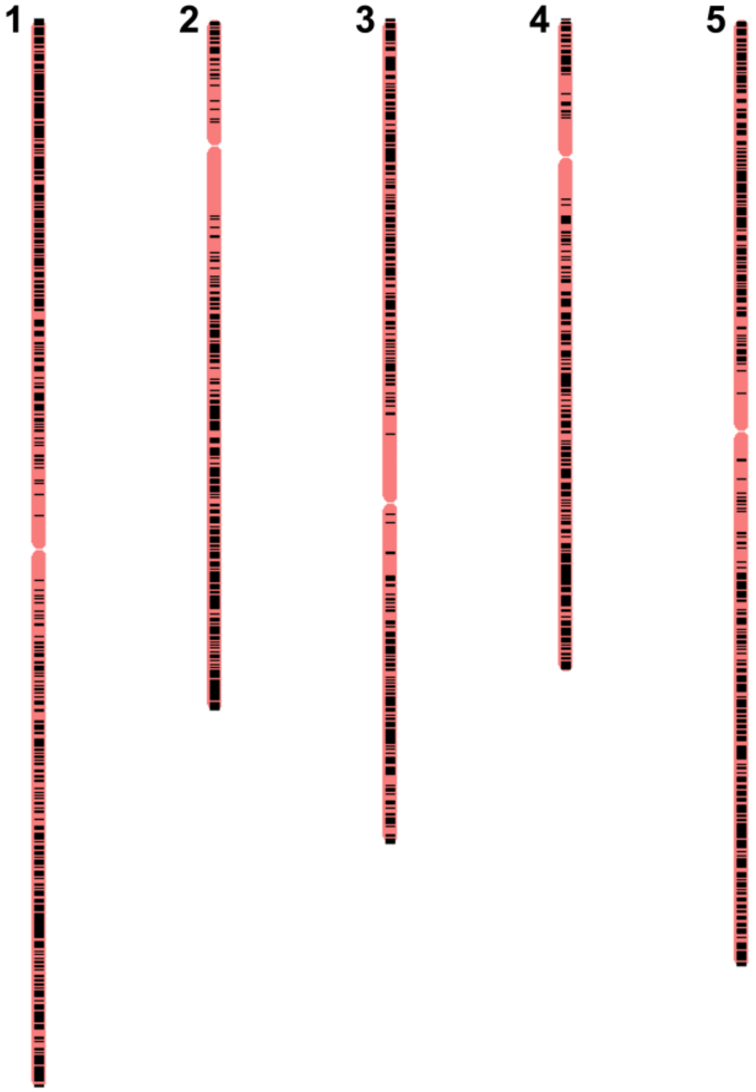

Figure 4. Chromosomal Distribution of Arabidopsis Phenotype Genes. Chromosomal locations of 2,400 phenotype genes of Arabidopsis (black lines) placed on a sequence-based physical map of the genome. This figure was generated using the map visualization tool available through TAIR (www.arabidopsis.org/jsp/ChromosomeMap/tool.jsp).

dataset may also be incomplete or inaccurate. Work by Dr. David Meinke on an upcoming review of dominant mutants in Arabidopsis identified nine genes in this dataset (*AHA4*, *AXR3*, *EIN4*, *MTO1*, *OLD3*, *TUA4*, *TUA6*, *VEN3*, and *VEN6*) which should not have been included because they result from dominant, gain-of-function mutations. This work also identified nine other genes (*AXR6*, *CH42*, *CSA1*, *ETO2*, *GPRAT2*, *IXR2*, *PPD1*, *PUR4*, and *SHY2*) in the dataset with inaccurate phenotype descriptions in need of updates. If this dataset is to be the foundation of a comprehensive database of genome-wide phenotype information in Arabidopsis, missing data will need to be located, and all inaccurate records identified and corrected. In addition to improving the saturation and accuracy of current mutant phenotype information, the dataset will need to be periodically updated. Because of the continued expansion of mutant phenotype information, with over 600 genes added to the dataset from papers published in 2009 and 2010 alone, indefinite manual curation by a single individual is not feasible. Instead, we hope to draw upon the Arabidopsis community for input and help with curating this potentially valuable resource.

I do not intend to be involved principally in the future direction of the phenotype dataset, but I have identified several paths that can help streamline future updates and curation of Arabidopsis mutant phenotype data. Corrections to the existing information could come from researchers whose data we used while producing the dataset, provided they are willing to access the dataset and notify us of the required updates. It would also be beneficial to have the controlled vocabulary used in describing phenotypes vetted by experts in a related field. This would ensure that phenotypes are being correctly catalogued and communicated. A promising avenue for collecting phenotype data published in the future is through collaborations with scientific journals. Systems for collecting gene information at the point of publication are already in place for other types of data, such as encoded protein function or subcellular localization of a gene product. Including phenotype data in the information requested from authors could prove to be a simple but effective method for identifying basic phenotype information. Data mining approaches should also be explored. The manually-curated dataset we produced could serve as a benchmark or gold standard for programs written to automatically identify and curate phenotype data in the scientific literature. A robust set of ontology terms would be a useful update to the dataset. Such a system would make it more efficient to manipulate the data through computational approaches. Preliminary work is already moving forward to bring this idea to fruition (see Chapter 5; Phenotypes of Putative Orthologs). Large-scale phenotyping centers for Arabidopsis that are capable of growing mutant plants under standardized conditions and noting all aberrant features of a mutant are another potentially important resource. Data from these centers can not only provide vast phenotype information but they are also useful in combating the bias that often occurs when an author focuses on his or her phenotype of interest and ignores other phenotypes of a mutant plant. Such centers are currently in use in Australia (www.plantphenomics.org.au) and Germany (http://www.fz-juelich.de/ibg/ibg-2/de/home/home_node.html).

It may be necessary to enlist a wide range of volunteer curators from the Arabidopsis community in this effort. The primary function of these curators would be to edit the phenotype data uncovered through journal collaborations, data mining, or other approaches. They would also serve to ensure that all new phenotype data are compliant with defined standards for phenotype curation in Arabidopsis. If the system of phenotype data submission is well constructed, minimal time would be required for this service, as many phenotypes could simply be approved or quickly curated before moving on to the next. I would be willing to serve as an oversight curator, provided that the position was not too time consuming. The potential role of volunteer curators, journal collaborators, and original authors willing to examine and correct our data illustrates the importance of Arabidopsis researchers in the future of phenotype curation in the model plant. Ultimately, the Arabidopsis community will be vital to the prolonged relevance of this phenotype dataset.

CHAPTER III

ARABIDOPSIS GENES WITH GAMETOPHYTE PHENOTYPES

Phenotypes of Mutant Gametophytes

The haploid gametophyte represents the first stage in the life cycle of *Arabidopsis thaliana*. Defective embryo sac (megagametophyte) or pollen development is therefore the earliest detectable phenotype of a gene disruption in Arabidopsis. Phenotypes of mutant gametophytes can take the form of abnormal morphology, altered pollen germination or tube growth, loss of pollen tube attraction, or failure of fertilization. These changes often result in lower transmission of a mutant allele, as mutant gametophytes participate in fertilization at a lower rate compared to wild type. This can be observed when homozygous mutant phenotypes segregate from heterozygous plants in a proportion lower than the expected 25%. The most severe transmission defect is the failure of both male and female gametophytes to participate in fertilization. Mutant alleles that result in this level of disruption cannot be maintained because they are not passed on to the next generation. Haploid embryo sacs and pollen have a complex relationship with their surrounding parental tissue, and as a result, some phenotypes observed in gametophytes are due to sporophytic defects. For example, the outer exine layer of pollen is deposited by the paternal tapetum, and ovule integuments represent surrounding maternal tissue. Defects in sporophytic structures can be distinguished from defects in the haploid gametophyte by observing a mutant gametophytic phenotype segregate alongside wild type from heterozygous plants or by performing reciprocal crosses between heterozygous and wild-type plants.

Meinke laboratory interest in gametophyte phenotypes grew out of a longstanding focus on genes with embryo defects. Many embryo-defective (*EMB*) genes display a mixture of both embryo and gametophyte defects. In addition, there are *EMB* genes that display no evidence of a gametophyte defect but encode proteins that function in basic cellular processes. It is curious that a gene whose protein product is required for a fundamental process, such as DNA replication or protein synthesis, could be disrupted in a functional gametophyte. How do these gametophytes survive? To investigate this, robust datasets of genes with both embryo and gametophyte phenotypes are required. SeedGenes has long provided a well-curated database with information on hundreds of genes that display embryo-defective phenotypes, but a corresponding dataset of genes exhibiting gametophyte phenotypes has been lacking. To help address this question, a thorough dataset of gametophyte-defective genes in Arabidopsis was produced with contributions from the primary phenotype dataset, reclassification of some genes in the SeedGenes database, and additional literature searches and curation. This dataset was published alongside updates to the SeedGenes database in Muralla et al. (2011).

Construction and Organization of the Gametophyte Dataset

Genes with gametophyte phenotypes were identified primarily through the same four approaches used to establish the main phenotype dataset (see Chapter 2; Dataset

Construction). Specific PubMed searches were also performed to identify additional genes required for gametophyte function. The exact keyword string for this search was: Arabidopsis AND (Gametophyte OR Gametophytic) AND (Mutation OR Mutant OR Knockout OR Null). Papers identified with this search were subsequently examined, gametophyte phenotypes curated, and associated genes included in the dataset. Many genes in the SeedGenes database display evidence of gametophyte defects in addition to their embryo phenotypes. Genes with a low percentage of mutant seeds (indicating reduced transmission of a mutant gamete) and those with a non-random distribution of mutant seeds (typically toward the distal end of a silique, indicating a pollen tube defect), were included in this dataset because of inferred gametophyte defects.

A number of genes described in three published datasets cataloguing gametophyte defects were also included. These datasets were focused primarily on male gametophytes (Boavida et al., 2009), female gametophytes (Pagnussat et al., 2005) or a mixture of both (Johnson et al., 2004). Because gametophyte defects often arise from large deletions and other chromosomal aberrations that are common in insertion mutagenesis populations, genes from these datasets were subjected to additional criteria before they were included. These genes had to be represented by more than one distinct mutant allele or have flanking sequences recovered from both sides of an insertion. These guidelines excluded many genes from the final dataset, but they also helped to ensure that gametophyte phenotypes catalogued in these publications were due to the disruption of a single gene.

In order to facilitate more detailed analyses of gametophyte-defective genes, additional information specific to gametophyte phenotypes was collected. Subclasses of defects were outlined for both male and female gametophytes. Pollen phenotypes were classified by abnormal development, loss of germination, altered tube growth, or the failure to fertilize an ovule. Embryo sac phenotypes were assigned as abnormal development, impaired pollen tube attraction, failure of fertilization, or very early embryo arrest. The transmission efficiency (TE) of a mutant allele could be quantified through reciprocal crosses of heterozygous and wild-type plants (Howden et al., 1998). Following a reciprocal cross, the TE for either the male or female gamete was calculated as: [number of heterozygous plants] / [number of wild type plants]. Full transmission of a mutant allele is expected to result in a TE of 1. Reduced transmission can range as low as 0 (no transmission). If TE data were available for both male and female gametophytes, the expected percentage of homozygous mutant individuals following self-fertilization of heterozygotes was calculated with the following formula: (TE male / (TE male + 1)) × (TE female / (TE female + 1)) × 100. The '1' in this equation is equivalent to full (normal) transmission. As an example, if the male TE is 0.2 and female TE is 0.5, 5.6% homozygous mutant individuals are expected. A set of symbols was developed to serve as general indicators of transmission (Table 4). Using this system, a mutant allele with a pollen TE of 0.6 and no transmission through the embryo sac would be represented by the symbol M / 0 ♀. As another example, if the male gametophyte was not studied and the female gametophyte was noted to have decreased transmission but detailed reciprocal cross data were not provided, the symbol assigned was X / (F).

If available, homozygous mutant phenotypes were catalogued separate from the haploid gametophyte defect. For cases where no homozygous mutant plants were recovered, but male or female gametophytes showed incomplete transmission defects, an embryo lethal phenotype was inferred, EMBi. This designation was modified to [EMBi]

Table 4. Gametophyte Transmission Defect Symbols

Male Symbol	Female Symbol	Description of Transmission Defect
+	+	TE above 0.8
M	F	TE between 0.4 and 0.8
MM	FF	TE between 0.1 and 0.4
MMM	FFF	TE greater than 0 and less than 0.1
0 ♂	0 ♀	No transmission
(M)	(F)	Decrease in transmission noted; Detailed TE information not available
X	X	Transmission not discussed

Symbols representing male and female transmission efficiencies (TE) were brought together with a forward slash (e.g. M / FF) to indicate overall gametophyte transmission for a given mutant. See text for more examples.

when the percentage of homozygous mutant seeds was predicted to be below 2%. If transmission through either the male or female side is zero, no homozygous plants are expected and a homozygous phenotype is therefore not applicable. Other homozygous phenotypes observed at the seedling or adult stage were classified using the same categories and priority applied to the phenotype dataset as a whole.

It is common for mutants with gametophyte defects to also show some combination of embryo defects. To accommodate this, a system was devised to classify mutants as displaying gametophyte defects alone, embryo defects alone, or a mixture of both. Integral to this determination was the expected or observed percentage of homozygous mutant seeds following self-fertilization of heterozygotes. Genes were defined as showing only gametophyte defects (GAM) if they were predicted to produce 2% or fewer mutant seeds. This percentage correlates to one mutant seed per silique and is roughly equivalent to the background rate of seed abortion (Meinke and Sussex, 1979). Genes were defined as displaying mostly gametophyte defects with some embryo defects (GEM) if they were predicted to produce between 2% and 10% mutant seeds. Genes predicted to have greater than 10% mutant seeds as well as some gametophyte defects were considered to have primarily embryo defects (EMG). Most genes reclassified from SeedGenes to the gametophyte dataset were assigned to this EMG category.

Overview of the Gametophyte Dataset

The complete gametophyte phenotype dataset contains 173 genes with defects in the development of haploid embryo sacs or pollen. In addition to data provided for all genes with mutant phenotypes, these genes were associated with symbols representing transmission efficiency, distinct homozygous mutant phenotype assignments, specific male and female gametophyte defects, and a gametophyte subclass: GAM, GEM, EMG, Viable, or Uncertain. Eighty-nine of the genes in the dataset (51%) show a mixture both embryo and gametophyte defects. In this group, 25 show primarily gametophyte phenotypes (GEM), 44 show primarily embryo phenotypes (EMG), and 20 cannot be definitively classified due to incomplete TE data. The other 84 genes (49%) show no evidence of embryo defects. For 14 of these, homozygous plants are viable and display some other mutant phenotype. The other 70 gametophyte-defective genes with no embryo defects exhibit zero or very low transmission through one or both gametes (GAM). Fourteen of these show severe defects in both male and female transmission, but 44 are primarily male and 12 are primarily female. The full gametophyte dataset can be found in Table S2 of Muralla et al. (2011). In addition, a modified version of the dataset lacking a reference laboratory, year of publication, and predicted protein function and class can be found appended to this thesis (Appendix E).

Analysis of the Gametophyte Dataset

With the gametophyte dataset constructed, we began to address how mutant gametophytes lacking basic cellular processes are able to survive and participate in fertilization. One possibility explored was whether the protein functions encoded by GAM, GEM / EMG, or EMB genes could explain the survival of these mutant gametes. Protein functions were collected from the literature and placed into a classification system produced by the Meinke laboratory (Appendix F). When protein classifications were compared, it was found that similar protein functions are encoded by genes displaying both embryo and gametophyte defects (Figure 5). Therefore the survival of mutant gametophytes cannot be explained by protein function alone. Some trends can be identified, however. For example, genes with only gametophyte defects are overrepresented by membrane trafficking and mitochondrial electron transport functions. Disruption of membrane trafficking often interrupts cellular tip growth and results in severe defects in pollen tube development. Interfering with mitochondrial electron transport, however, causes disruption of both male and female gametophytes. This indicates that energy products from this organelle are vital to gametophyte development. True embryo defects, on the other hand, often result from disruption of DNA synthesis and RNA modification. Genes displaying a mixture of embryo and gametophyte defects tend to encode gene products involved in protein synthesis, modification or degradation. The phenotypic consequences of disrupting protein synthesis vary depending on the location in the cell where translation is abolished. Complete disruption of cytosolic translation results in absolute lethality of both male and female gametophytes (Berg et al., 2005), loss of mitochondrial translation produces severe male and female gametophyte defects (Muralla et al., 2011), and interrupting chloroplast translation causes only embryo defects (Bryant et al., 2011). The relationship between plastid genome expression and mutant phenotype is discussed in more detail in Chapter 5.

Further analysis of genes with embryo and gametophyte defects revealed no correlation between genetic redundancy or strength of mutant allele and a specific early lethality phenotype (Muralla et al., 2011). Instead, the current hypothesis explaining the survival of mutant gametophytes is that functional gene products produced in the heterozygous, diploid sporocyte are often retained in haploid gametophytes and allow for

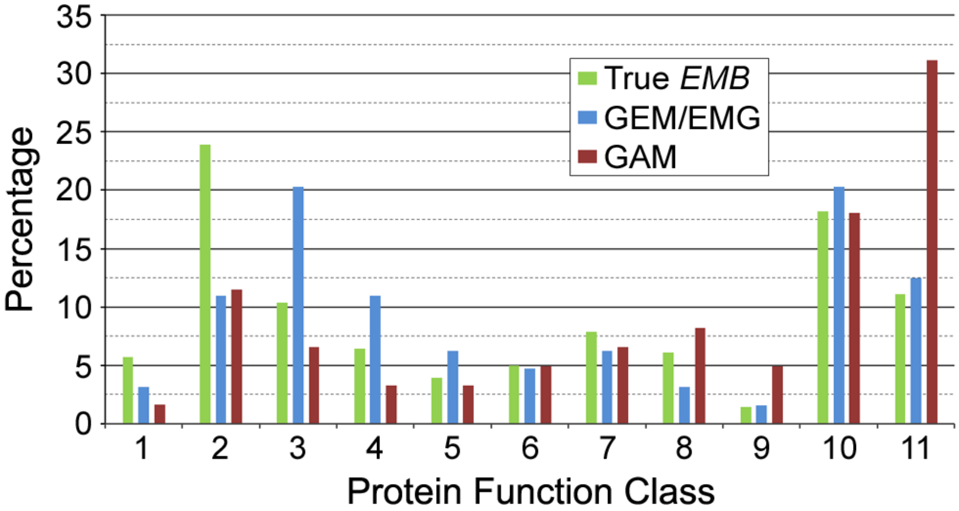

Figure 5. Protein Functions of Genes with Embryo and Gametophyte Phenotypes. True *EMB* genes are those with no observed or inferred gametophyte defects. (1) DNA synthesis; repair; (2) RNA synthesis; modification; (3) protein synthesis; (4) Protein modification; transport; (5) protein degradation; (6) chromosome dynamics; (7) transcriptional regulation; (8) signaling pathways; (9) energy; electron transport; (10) metabolism; (11) cell structure; membrane function; trafficking. Significant differences are observed for function classes 2 ($\chi 2$ test, $p<0.05$), 3 ($p<0.05$), and 11 ($p<0.001$).

normal development. In order to provide evidence for this assertion, transcript levels in the microsporocyte were compared for selected genes with either gametophyte or embryo defects. While I did not contribute directly to the analysis, the dataset of gametophyte genes I helped to produce was utilized. Microsporocyte transcription was analyzed for 107 gametophyte-defective genes with either severe or moderate pollen transmission phenotypes and 75 single copy embryo-defective genes displaying either preglobular or globular phenotypes. Data describing transcription during these periods of development are available in several publications (Honys and Twell, 2004; Pina et al., 2005; Wang et al., 2008). In general, genes displaying early embryo defects when disrupted are either not transcribed or transcribed at a low level during late stages of pollen development. Genes with male gametophyte defects, however, tend to show higher levels of transcription during this period. This preliminary analysis is consistent with the stored gene product hypothesis. An overview of pollen transcript accumulation profiles for genes with male gametophyte and early embryo defects is available in Table 5. See Muralla et al. (2011) for a more detailed discussion of this investigation.

Table 5. Transcription of Genes with Embryo and Gametophyte Defects during Pollen Development[a]

Transcript Accumulation Pattern	Single-Copy *EMB* Genes[b]		Male Gametophyte Defective[c]	
	Preglobular[d]	Globular[d]	Moderate[d]	Severe[d]
Transcript detected early in pollen development, but not in mature pollen	70%	64%	55%	27%
Transcript detected throughout pollen development	17%	29%	43%	61%
Transcript detected throughout pollen development; ≥2X higher at later stages	0%	2%	2%	26%
Transcript detected throughout pollen development; ≥2X higher at early stages	4%	10%	12%	13%
Other patterns of transcript accumulation	13%	7%	2%	12%

[a] Based on published, large-scale microarray datasets for wild-type plants (Honys and Twell, 2004; Pina et al., 2005; Wang et al., 2008).

[b] Non-redundant genes with embryo arrest stage shown; no gametophyte defects observed.

[c] Moderate (EMG and GEM) and severe (GAM) classes are described in the text.

[d] Percentages of essential genes with transcript detected are noted. Total number of genes analyzed: preglobular (23/25); globular (42/50); moderate (42/48); severe (51/59). Excluded genes were not part of the microarray dataset or had no transcript detected during pollen development.

CHAPTER IV

MULTIPLE MUTANT PHENOTYPE DATASET

Phenotypes Resulting from Mutations in Multiple Genes

Redundancy plays a complex role in an observed loss-of-function mutant phenotype and can influence or completely mask the consequence of abolishing a gene function. There are two common types of redundancy: genetic and functional. Genetic redundancy, also referred to as structural redundancy (Bouché and Bouchez, 2001), arises most commonly through the retention of ancestral gene duplications. In order to evaluate the full consequence of eliminating an associated gene function, the disruption of multiple genes is required. Functional redundancy, on the other hand, often results from the presence of alternative metabolic pathways or cellular processes. Genes displaying functional redundancy do not share sequence similarity or recent ancestry. For example, *CRC,* a YABBY transcription factor, has a loss-of-function abnormal carpel morphology phenotype (Bowman and Smyth, 1999). When *CRC* is disrupted alongside *PKL,* a CHD3 chromatin remodeling factor, the phenotype is exacerbated and appears as ectopic ovules.

Partial loss of carpel polarity is also observed in the double mutant (Eshed et al., 1999). These two genes do not share sequence similarity, but both function in the maintenance of carpel polarity. While interesting and useful, functional redundancy is not a focus of this project. Genes displaying genetic redundancy, however, can complement research on single mutant phenotypes, particularly with regard to investigation of the relationship between phenotype and protein function or subcellular localization. In the interest of capturing these loss-of-function phenotypes, I constructed an additional dataset of mutant phenotypes resulting from the disruption of multiple genetically redundant genes.

Early methods for constructing multiple mutant plants and circumventing redundancy included crossing non-allelic single mutant plants with similar phenotypes or subjecting a known mutant plant to further mutagenesis. Redundancy could then be identified by exacerbation of the original phenotype. Forward genetic enhancer screens have been occasionally successful in this goal, but they often uncover functional redundancy, rather than genetic. These screens may also uncover loci whose disruption suppresses the initial phenotype. Suppression of a mutant phenotype is most often due to functional similarity and is therefore not of interest to this project. Compared to these methods, however, reverse genetic approaches are much more efficient and straightforward. Genes with similar sequences and expression patterns can be readily identified through publically-available tools (BLAST searches; Genevestigator), and putative knockout lines for candidate genes can be acquired and crossed to produce a desired multiple mutant. The ease of these reverse genetic methods is reflected in the increased number of genes with published multiple mutant phenotypes in recent years (see Chapter 2; Figure 3A).

In addition to serving as a repository for information on the biological consequences of disrupting more than one gene, the multiple mutant phenotype dataset has many possible applications. Gene redundancy is frequently predicted based on general sequence and expression similarity, but the criteria used to define redundancy in these terms are often inconsistent and somewhat arbitrary. Genes in this dataset, however, are experimentally confirmed to be redundant. This provides a tractable collection that can help improve the criteria used to predict genetic redundancy. In addition, genes in the single and multiple mutant phenotype datasets display disparate levels of redundancy: there are unique genes in the single gene dataset, as well as partially-redundant genes displaying both single and multiple mutant phenotypes, and fully-redundant genes that show no observable phenotype when disrupted alone. Investigating the modulation of sequence evolution or selective pressure as it relates to degree of redundancy is another potential application of the multiple mutant dataset.

Construction and Organization of the Multiple Mutant Dataset

Multiple mutant phenotypes were identified primarily through the four methods used to produce the main phenotype dataset (see Chapter 2; Dataset Construction). Several enhancer phenotypes in the 620 list (Meinke et al., 2003) that involved the disruption of multiple genetically-redundant genes were reclassified and included in the multiple mutant phenotype dataset. In addition, the Meinke laboratory has published a small collection of double mutants with embryo phenotypes (Tzafrir et al., 2004). These double mutants and associated genes were curated and included. While focused primarily on uncovering single mutant phenotypes, literature curation of the TAIR list of candidate phenotype genes and PubMed searches for phenotype data published in 2009 and 2010 also identified many genes associated with multiple mutant phenotypes. Multiple mutant phenotypes uncovered through these methods were considered to result from genetic redundancy if all genes involved matched one another with a significance of at least e-30 following BLASTP analysis. Sets of genes that did not meet this standard were excluded. Both the terminology utilized for phenotype descriptions (see Appendix A) and the phenotype classification system (see Appendix B or Chapter 2; Figure 1) developed for the primary phenotype dataset were also applied to the multiple mutant phenotype dataset.

Sets of similar genes associated with a multiple mutant phenotype were classified as clusters. These clusters are characterized in two distinct manners, as complete or incomplete, and simple or complex. Complete clusters include all potential paralogs within the Arabidopsis genome. Phenotypes observed following the disruption of a complete cluster are therefore analogous to those resulting from the disruption of one single copy gene, as genetic redundancy is no longer a factor when interpreting the significance of the phenotype. Incomplete clusters are clusters involving genes that identify additional potential paralogs that are not included in the cluster. The number of other similar genes remaining in the genome for an incomplete cluster can range from one to well over fifty.

Clusters were also classified as simple or complex. Simple clusters are defined by association with only one documented multiple mutant phenotype. Each distinct multiple mutant phenotype in a cluster is referred to as a grouping. As an example of a simple cluster, three genes - *CathB1*, *CathB2*, and *CathB3* - are disrupted together in a triple mutant with documented senescence and disease susceptibility phenotypes (McLellan et al., 2009). None of these three genes is further involved in any higher order (e.g. quadruple or pentuple) or lower order (e.g. double) multiple mutants. The cluster formed by these genes is therefore considered simple. Complex clusters, on the other hand, are associated with more than one grouping. For example, three other genes – *BON1*, *BON2*, and *BON3* – are associated in a triple mutant with a documented seedling lethal phenotype (Yang et al., 2006). While none of these genes is present in higher order multiple mutants, some are included in two separate double mutants: one involving *BON1* and *BON2* and another involving *BON1* and *BON3*. Because more than one grouping (one triple mutant phenotype and two double mutant phenotypes) is associated with the genes in this cluster, it is considered complex. Eight additional examples of complex clusters are illustrated in Figure 6.

Simple gene clusters are further characterized by the presence or absence of single mutant phenotypes of the genes involved. Simple clusters were defined as exclusive if none of the genes involved displayed a single mutant phenotype. All documented phenotype data for loci in exclusive clusters are noted in one multiple mutant phenotype grouping. These genes can be considered fully redundant to one another. Simple clusters were considered asymmetric if at least one gene in the cluster displayed a single mutant phenotype, while at least one other did not. For example, in a simple cluster of five genes, *NPY1-5*, four of the genes show only an associated pentuple mutant phenotype (loss of root gravitropism; Li et al., 2011). However, one of the genes, *NPY1*, also shows a distinct single mutant phenotype. The cluster is therefore considered asymmetric.

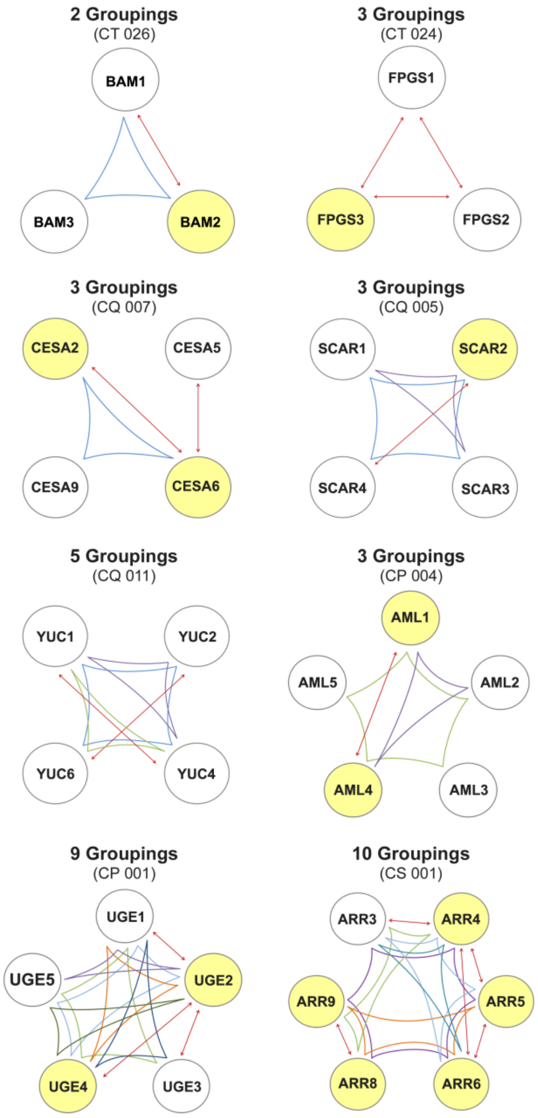

Figure 6. Complex Multiple Mutant Clusters. Examples of complex clusters of three or more redundant genes with two or more groupings of genes associated with a multiple mutant phenotype. Genes with a single mutant phenotype are highlighted in yellow. Lines indicate groupings that produce a documented phenotype more severe than that of the corresponding single mutants or multiple mutants with fewer members. Cluster identification numbers are noted in parentheses. Appendices G and H present additional information on the genes and phenotypes involved.

Simple clusters can also be described as symmetric if all associated genes display a single mutant phenotype. Genes with a documented single mutant phenotype in both asymmetric and symmetric clusters can be considered partially redundant to their partners.

Only distinct multiple mutant phenotypes are catalogued in this dataset. For example, if a double mutant had a dwarf phenotype and disruption of a third redundant gene did not exacerbate the effect or otherwise result in a different phenotype, this triple mutant phenotype was not included. This also means that if a higher order and lower order multiple mutant grouping within one complex cluster share the same phenotype description, the phenotype must be more severe in the higher order multiple mutant. For example, in one complex cluster of four genes – *TOE1*, *TOE2*, *SMZ*, and *SNZ* – there is a double mutant and a quadruple mutant with the same phenotype description: early flowering. Because these groupings are both included in the dataset, this means the higher order mutant shows a more severe early flowering defect compared to the double mutant.

Overview of the Multiple Mutant Dataset

The final multiple mutant dataset contains 591 genes associated with a mutant phenotype resulting from the disruption of more than one redundant gene. Of these, 401 (68%) have no documented single mutant phenotype. These genes are widely dispersed in the genome (Figure 7). A total of 248 clusters are defined in the dataset. Of the 203 simple clusters, 96 are exclusive (87 doubles, seven triples, and two quadruples), 76 are asymmetric (70 doubles, five triples, and one pentuple), and 31 are symmetric (all

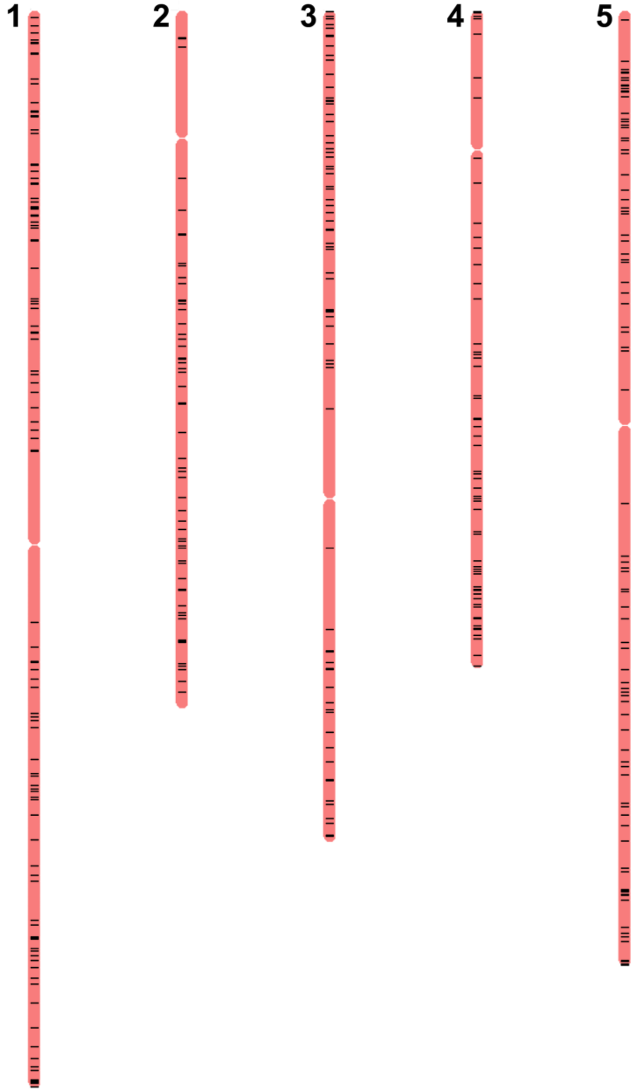

Figure 7. Chromosomal Distribution of Fully Redundant Arabidopsis Genes. Chromosomal locations of 401 Arabidopsis genes (black lines) that lack a single mutant phenotype but are associated with one or more multiple mutant phenotypes when combined with mutations in potential paralogs. Figure generated using the map visualization tool available through TAIR (www.arabidopsis.org/jsp/ChromosomeMap/tool.jsp).

Table 6. Features and Phenotypes of Multiple Mutant Clusters

Genes in Cluster	Cluster Features			Cluster Phenotype Groups[a]			
	Type[b]	Number	Complete[c] (%)	ESN	MRP	CLB	CND
2	EXC	87	33	35	34	8	10
	ASY	70	39	30	27	6	7
	SYM	31	10	17	9	2	3
3	EXC	7	43	0	2	0	5
	ASY	5	20	0	3	0	2
	CPX	26	8	6	13	4	3
4+	EXC	2	100	0	2	0	0
	ASY	1	0	0	1	0	0
	CPX	19	0	8	8	2	1

[a] ESN, Essential; MRP, morphological; CLB, cellular and biochemical; CND, conditional.

[b] EXC, Exclusive, both single mutants have no phenotype; ASY, asymmetric, one single mutant has a phenotype but the multiple mutant is more severe; SYM, symmetric, both single mutants have a phenotype but the multiple mutant is more severe; CPX, complex, phenotype information available for two or more combinations of genes within a cluster.

[c] Complete clusters disrupt all potential paralogs in Arabidopsis.

doubles). The 45 complex clusters include 144 groupings and 166 genes. Sixty-seven of the clusters (27%) are complete, and most of these are simple (97%). See Table 6 for a breakdown of features and phenotypes identified for multiple mutant clusters. The complete multiple mutant dataset can be found as a supplementary table to the *Plant Physiology* publication describing the Arabidopsis phenotype dataset (Lloyd and Meinke, 2012; Table S6). The dataset takes the form of a spreadsheet with four tabs containing information on the genes, clusters, and groupings that make up the multiple mutant dataset. A truncated version of the multiple mutant dataset emphasizing the genes and groupings involved can be found appended to this thesis (Appendices G and H).

The most severe phenotypes documented for multiple mutant gene clusters were more often assigned to the essential and morphological phenotype groups than the phenotypes in the single mutant dataset (χ^2 test, $p<0.001$; Figure 8A). This observation raises several potential conclusions: (1) elimination of genetic redundancy through multiple gene knockouts will lead toward more severe phenotypes; (2) single gene knockouts are more likely to be used when studying cellular, biochemical and conditional phenotypes, or perhaps most intriguing; (3) genes with severe phenotypes are preferentially maintained as duplicates to protect against particularly deleterious gene loss. The correlation between more severe phenotypes and multiple gene knockouts fails to hold, however, when comparing only the phenotypes resulting from the disruption of complete clusters and single copy genes (Figure 8B). This provides some evidence that essential genes are not duplicated to prevent loss.

The oldest phenotype information catalogued in this dataset, a nitrogen-related conditional phenotype involving the disruption of *NIA1* and *NIA2*, was published in 1993

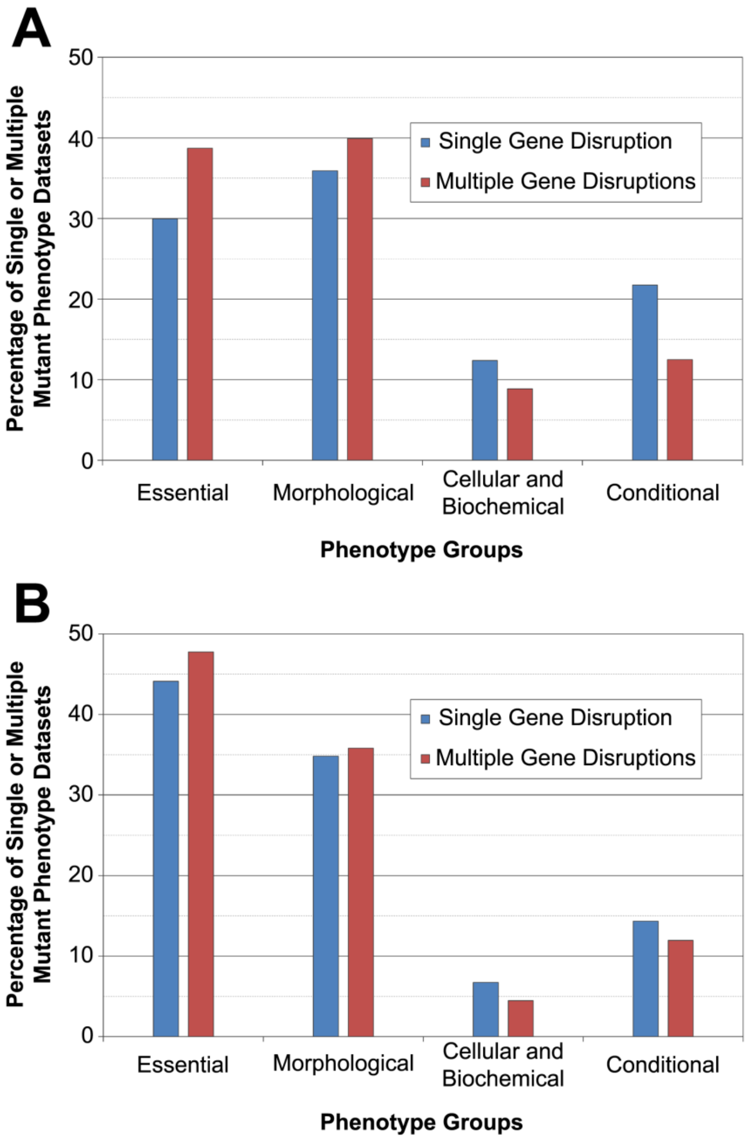

Figure 8. Phenotype Group Distributions of Single and Multiple Mutants. Phenotypes observed following the disruption of a single gene or multiple genes. (A) Phenotypes of all single mutants and the highest priority phenotype of multiple mutant clusters. (B) Phenotypes of only single-copy genes and complete multiple mutant clusters.

(Wilkinson and Crawford). However, 86% of multiple mutant clusters were not published until at least 2005. This year was also when reverse genetics first became the most common method used to identify genes with loss-of-function phenotypes (Chapter 2; Figure 3B). It is fitting, then, that most genes with a multiple mutant phenotype were discovered through reverse genetic methods. Eighty-eight percent of all genes included in this dataset, and 98% of those with no documented single mutant phenotype were discovered through these methods. It is logical that genes with no single mutant phenotype are discovered overwhelmingly through reverse genetics, as they are unlikely to be uncovered through forward genetic screens.

The complexity referred to in complex clusters extends beyond cataloguing more than one phenotype grouping for a set of genes. As an example, a complex cluster may not document the phenotype resulting from disruption of all genes associated with the cluster. Only 26 of the 45 complex clusters (64%) have a phenotype documented for the disruption of all constituents. For specific cases, see clusters CT 024, CQ 007, and CP 001 illustrated in Figure 6. In addition, the highest order mutant in a complex cluster may not show the most severe phenotype. One such five-gene cluster documented in this dataset - identified as CP 005 and involving *PHV*, *CNA*, *PHB, AtHB8*, and *REV* - demonstrates this unusual situation. In this cluster, two triple mutant combinations involving *REV*, *PHB* and either *CNA* or *PHV* result in seedling lethality due to apical polarity defects. However, quadruple mutants involving *PHV*, *CNA*, *PHB*, and *AtHB8*, but not *REV*, display only dwarfing phenotypes (Prigge et al., 2005). This is a case where triple mutants show a phenotype of higher priority (essential; lethal) than a quadruple mutant (morphological; vegetative) in the same cluster.

Sequence and Expression Similarity of Redundant Genes

Two sets of double mutants – fully-redundant pairs with no documented single mutant phenotypes and partially-redundant pairs where one or both genes display a single mutant phenotype – represent an interesting collection of genes that show varying degrees of genetic redundancy. We were interested if fully-redundant pairs showed greater similarity in protein sequence and expression pattern compared to the partially-redundant pairs. In order to determine the degree of sequence similarity, BLASTP e-values and scores between gene partners in fully- and partially-redundant double mutants were recorded. These metrics were also documented for all protein-coding genes in the genome to their most similar Arabidopsis match. Genes with no significant match (BLASTP e-30 cutoff) were excluded from this analysis. The percentage of genes in each category that displayed an unusually high degree of sequence similarity (e-value more significant than e-100 over at least 95% of protein length) was assessed: 65% of fully-redundant genes show this high level of sequence similarity, compared to only 49% and 40% for genes in partially-redundant pairs and the whole genome, respectively. In addition, fully-redundant genes displayed a higher average BLASTP score compared to partially-redundant genes (Student's T-test; $P = 0.01$). The average BLASTP score of fully-redundant genes was also higher than the genome as a whole ($P < 0.001$). These analyses demonstrate that fully-redundant genes display an especially high level of sequence similarity.

We also expected that fully-redundant gene pairs would show more similar levels and patterns of expression compared to partially-redundant pairs. Further, we expected that a gene in a partially-redundant pair with a documented single mutant phenotype would display a higher level or broader pattern of expression than a partner with only a multiple mutant phenotype. To test these assertions, expression data from public microarray datasets available through Genevestigator (www.genevestigator.com) were collected for 23 exclusive and 21 asymmetric double mutants. This investigation excluded gene pairs whose disruption resulted in cellular, biochemical, or conditional phenotypes in order to streamline analysis and avoid subtle phenotypes or genes whose expression patterns would not be expected to be captured through a general analysis of transcriptomes. Expression similarity within gene pairs was assigned to one of three categories: (1) transcript abundance differs by less than 2-fold, (2) transcript abundance differs between 2- and 3-fold, and (3) transcript abundance differs by greater than 3 fold. Using this system, asymmetric pairs displayed a slightly higher divergence of expression compared to exclusive pairs (χ^2 test, $P = 0.024$). Additionally, in 18 of the 21 asymmetric pairs, the gene with the documented single mutant phenotype also displayed a higher overall level of expression compared to its counterpart. Analysis of expression data between these two groups was performed by Dr. David Meinke. This investigation indicates that fully redundant gene pairs show greater similarity in expression levels compared to those that are partially redundant. Because genetic redundancy correlates with both similarity in encoded protein sequence and expression levels, more sophisticated analysis of these metrics for the fully- and partially-redundant genes in this dataset could help to advance the criteria used to predict this factor.

CHAPTER V

ANALYSIS OF THE ARABIDOPSIS PHENOTYPE DATASET

This chapter highlights the analysis and future applications of the dataset of mutant phenotypes in *Arabidopsis thaliana*. Emphasis was placed on the relationship between mutant phenotype and protein function, subcellular protein localization, protein connectivity, and genetic redundancy. I also present a preliminary analysis of the similarity between mutant phenotypes of putatively orthologous gene pairs of Arabidopsis and several important crop plants (tomato, rice, and maize). I then conclude with a discussion of genes that display no apparent loss-of-function phenotype.

Protein Function and Mutant Phenotype

Do proteins with similar functions exhibit similar loss-of-function phenotypes? In order to investigate this question, descriptions of the protein functions encoded by Arabidopsis phenotype genes were curated from the primary literature. These were then assigned to a protein function class in a system devised by the Meinke laboratory (see

Appendix F). This analysis included only single-copy genes (BLASTP e-30 cutoff). Excluding genes with potential paralogs minimizes the effect genetic redundancy has on an observed phenotype. The distributions of phenotype groups within the eleven defined protein functions in our classification system were then compared (Figure 9). A wide range of phenotypes arise when disrupting particular protein functions, and conversely, many cellular processes are represented for each phenotype group.

However, some trends within the phenotype groups can be identified. The essential group is enriched in genes that encode protein and RNA synthesis functions. Essential genes are also underrepresented by transcriptional and signaling regulators. Genes with morphological phenotypes, however, show opposite patterns. This group is overrepresented by genes that encode transcriptional regulation and signaling functions but is deficient in protein synthesis functions. The enrichment of regulatory roles in the morphological group indicates that a mutant plant that has normal cellular machinery but cannot appropriately signal for a function at the correct time will often result in unusual development of plant organs. Genes encoding proteins with energy and electron transport functions are most common in the cellular and biochemical group. This is due primarily to an abundance of chlorophyll fluorescence and non-photochemical quenching phenotypes in the literature. Absent from this phenotype group are genes responsible for DNA, RNA, or protein synthesis. Unsurprisingly, the prevalence of these basic functions in essential genes and their scarcity in genes with subtle cellular defects serves to reinforce the importance of these roles in plant development. Common functions encoded by genes in the conditional group are signaling and DNA repair. The high frequency of signaling functions in this group is to be expected, as a mutant plant that

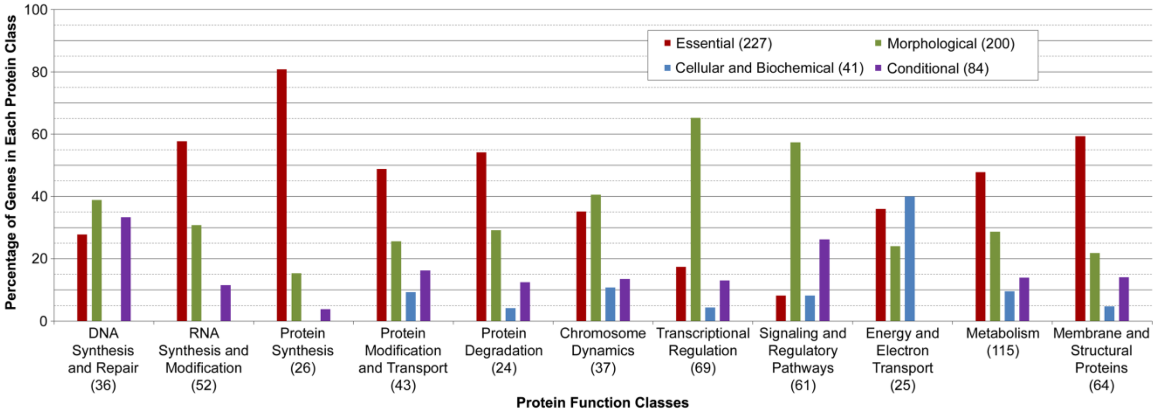

Figure 9. Protein Functions of Phenotype Genes. Distribution of phenotype groups among single-copy Arabidopsis phenotype genes with different protein functions. The total numbers of genes analyzed are noted in parentheses.

cannot sense or respond to changing environmental stimuli may only deviate from wild-type development under those conditions. In addition, defects in DNA repair are often identified through exposure of mutant plants to non-standard genotoxic stress conditions.

Subcellular Localization and Mutant Phenotype

In addition to the protein function encoded by a gene, the subcellular compartment where this product functions could also influence an observed mutant phenotype. To evaluate this possibility, we determined whether gene products in our dataset were localized to the mitochondrion or chloroplast. These two compartments were chosen because prediction data were more robust for them in comparison with other cellular locations. In order to determine likely mitochondrial or plastid localization, literature curation was coupled with a point system involving experimental results and prediction program data from SUBA (suba.plantenergy.uwa.edu.au), as well as two compilations of proteins expected to function in the chloroplast.

The presence of a phenotype gene in the predicted plastid proteomes of Richly and Leister (2004) or the Plant Proteomics Database (Sun et al., 2009) added one or two points, respectively, to the plastid localization rank for a given locus. An additional point was added if either experimental GFP or mass spectroscopy analysis predicted a gene product was present in the chloroplast. Potential mitochondrial localization was evaluated using a combination of target peptide prediction programs and experimental evidence. A point was added to the mitochondrial localization rank each time the following combinations of prediction programs suggested a gene product was present in mitochondria: (1) TargetP and Predotar; (2) Ipsort and Predotar; (3) TargetP and Ipsort;

and (4) TargetP, Predotar, and Ipsort. Two additional points were assigned if both GFP and mass spectroscopy analysis suggested mitochondrial localization. The highest rank for a gene was five points for plastid localization and six points for mitochondrial localization. Publications describing the subcellular localization for genes recognized through these approaches were then identified. Candidate genes, especially those with low ranks, could be excluded from further analysis if a publication indicated localization elsewhere in the cell. Alternatively, they were included when mitochondrial or plastid localization was confirmed. The 263 genes located through the PubMed search for phenotype information published in 2010 were not subjected to plastid localization analysis, as the manuscript focusing on genes with plastid-localized protein products (Bryant et al., 2011) had been published when the literature search was performed.

Of the 2,400 Arabidopsis phenotype genes, 362 are expected to encode products that localize to chloroplasts and 108 encode products found in the mitochondria. An additional 14 phenotype gene products are predicted to co-localize to both compartments. The distribution of expected subcellular localization for each phenotype group is shown in Figure 10. Genes with protein products that function in the mitochondrion or chloroplast are more likely than others to be essential. Both compartments are frequently associated with embryo defects, but mitochondrial localization is correlated more commonly with gametophyte phenotypes while disruption of chloroplast proteins often results in seedling lethality. Loss of mitochondrial functions does not often result in cellular and biochemical phenotypes. Combined with the high frequency of early lethality resulting from the loss of mitochondrial functions, this indicates a critical role

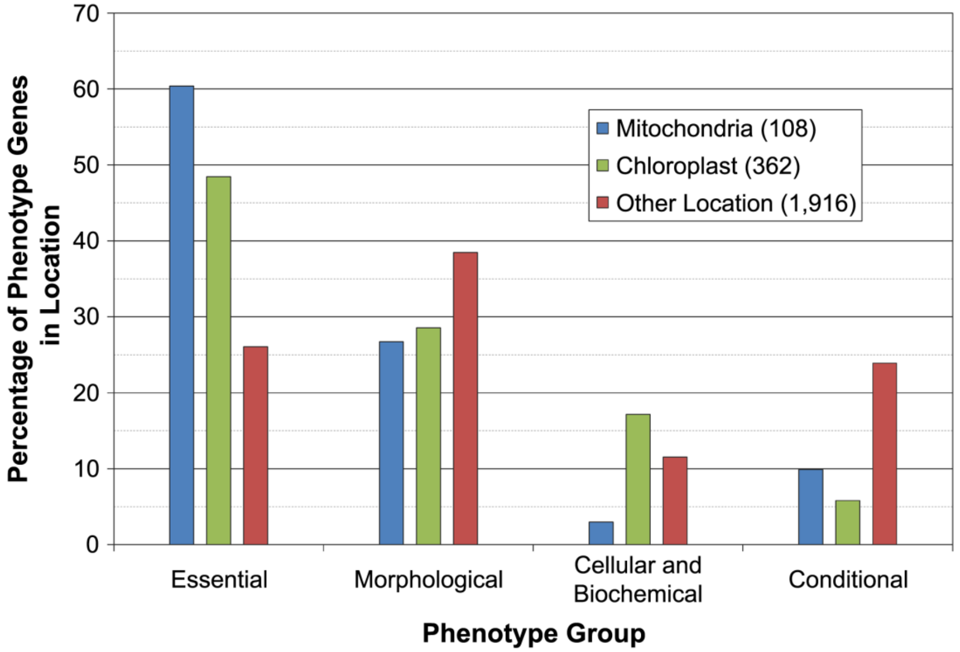

Figure 10. Subcellular Localization of Phenotype Genes. Distribution of predicted subcellular localization among all Arabidopsis phenotype genes. Numbers of genes evaluated are noted in parentheses.

for this compartment over the course of plant development. Mitochondrial and plastid localization are not often associated with conditional phenotypes, especially those observed in response to abnormal physical or biological conditions.

Nuclear genes with chloroplast-localized protein products were the focus of a prior investigation in the Meinke laboratory (Bryant et al., 2011). That project categorized the phenotypes resulting from loss of plastid functions into one of three categories: embryo, pigment or other defects. The Arabidopsis phenotype dataset proved valuable to this study by providing genes with pigment and other seedling or adult phenotypes. Embryo-defective genes were available through the SeedGenes database (www.seedgenes.org). The protein functions underlying these three phenotype categories were then evaluated. Embryo phenotypes arose most frequently following the disruption of amino acid, nucleic acid or vitamin biosynthesis while pigment phenotypes resulted from the disruption of photosynthesis and the production of related chemicals, such as chlorophyll, carotenoids, and terpenoids. Phenotypes observed at the seedling or adult stage typically involve the disruption of other metabolic pathways.

Complete disruption of plastid translation results in embryo lethality in Arabidopsis (Bryant et al., 2011). This is suspected to result from loss of expression of a plastid gene, *accD*, which functions in fatty acid biosynthesis. However, there is natural variation within the Brassicaceae family regarding the consequences of loss of plastid translation. *Brassica napus* seeds germinated on spectinomycin, an inhibitor of chloroplast translation, produce plants with albino leaves (Zubko and Day, 1998). Deviation in the expression of *ACC2*, a duplicated nuclear gene with a plastid-localized protein product that can compensate for loss of plastidial *accD*, is thought to be the basis of this natural variation. Investigating the role of chloroplast translation in early development and potential variation in response to spectinomycin for a range of natural accessions of Arabidopsis has become the basis of another project in the Meinke laboratory and a focus of the graduate work of Nicole Bryant.

Protein Connectivity and Mutant Phenotype

Gene products often interact with one another either transiently or consistently, and as dimers or constituents of large protein complexes. Recently, a preliminary network of binary protein interactions in Arabidopsis was published (Arabidopsis Interactome Mapping Consortium, 2011). With this protein interaction map and our Arabidopsis phenotype dataset, we asked two questions: (1) does the degree of protein connectivity correlate with severity of phenotype; and (2) is the phenotype of one interactor a good predictor of the phenotype of the other? One might expect the loss of a highly-connected protein product will typically result in more severe consequences than the loss of gene product that only interacts with one other protein, as a large number of cellular processes are interfered with through the loss of a single locus. Additionally, if two proteins interact, it might be anticipated that the loss of either would produce a similar phenotype, because the same cellular or metabolic process is disrupted in each case. For this investigation, we produced an edited version of the interactome dataset by removing self-interactors and interactions involving proteins encoded by the mitochondrial or plastid genomes. The edited dataset contains 10,865 binary interactions among 4,785 distinct proteins.

The relationship between degree of protein connectivity and mutant phenotype was investigated by assessing whether the protein products of phenotype genes are more likely than the proteome as a whole to interact with many other proteins, and by comparing the distribution of phenotype groups for genes with many interactors to those with only one interactor. Of the 928 phenotype genes included in the interactome dataset, 4.4% encode a protein product that interacts with at least 20 other proteins. This is marginally higher than the percentage of all proteins in the dataset (3.0%) that interact with this number of proteins (χ^2 test, P = 0.03). However, when only single copy genes are compared, the percentages of gene products that interact with at least 20 other proteins, 1.2% and 1.7% for phenotype genes and the whole dataset, respectively, show no significant difference (P = 0.54). In addition, the distribution of phenotype groups for genes whose products interact with at least 20 other proteins is not different from that of genes encoding a protein with only one interactor (χ^2 test, P = 0.17). Similar results are obtained when comparisons are limited to single copy genes or performed on distributions of phenotype classes.

These analyses indicate that the degree of protein connectivity does not correlate with mutant phenotype. Phenotype genes are not more likely to encode a product that interacts with a large number of other proteins, and gene products with a large number of interactors are not more commonly encoded by genes displaying severe phenotypes. These results contrast with those reported for yeast, where genes encoding highly-connected proteins are more likely to display lethal or pleiotropic phenotypes (Jeong et al., 2001; Yu et al., 2008). Other contradictory results have also suggested that human disease genes tend to encode highly-interacting proteins (Xu and Li, 2006). The reason for this discrepancy may be an incomplete interactome for Arabidopsis; results could change as interaction maps become more populated and accurate.

We also assessed whether the phenotype of one interactor is a good predictor of the phenotype of its partner. Seventy examples of interactions involving paired, single-copy phenotype genes were identified in the interactome dataset. Similarity of phenotype groups and classes was then compared. Phenotype groups matched for 63% of these pairs, while only 39% were expected to be the same by chance, a difference that is statistically significant (χ^2 test, $P < 0.001$). A breakdown of the observed and expected matches for all of these pairs and individual phenotype groups is presented in Table 7. Similar conclusions were reached when the percents of matched phenotype classes were compared. These results indicate that the phenotype of one interactor is a reasonable predictor of the phenotype of the other.

Genetic Redundancy and Mutant Phenotype

In Chapter 4, I discussed the relationship between genetic redundancy and mutant phenotype as it relates to multiple gene disruptions. However, genetic redundancy can also influence the phenotype of a single mutant. To investigate this relationship, we placed phenotype genes into one of three redundancy categories based on BLASTP e-values to their closest Arabidopsis match. Genes were described as unique, or as showing either moderate or high similarity to another Arabidopsis locus. Single-copy genes were defined by a BLASTP e-30 cutoff, moderate similarity was assigned when either a BLASTP e-value was between e-30 and e-80 or more significant than e-80 over less than 80% of protein length, and high similarity was associated with a BLASTP

Table 7. Phenotype Group Similarity of Paired Interactors

Phenotype Group[a]	Percentage of Interactors[b]	Matched Pairs[c]	Expected Matched Pairs[d]	Percentage of Pairs Matched[e]	Expected Percentage of Pairs Matched[d,e]
ESN	45.7	22	14.6	31.4	20.9
MRP	42.1	18	12.4	25.7	17.7
CLB	3.6	1	0.1	1.4	0.1
CND	8.6	3	0.5	4.3	0.7
Total	100	44	27.6	62.9	39.4

[a] ESN, Essential; MRP, morphological; CLB, cellular and biochemical; CND, conditional.

[b] Among 140 total interactors from 70 interacting protein pairs encoded by unique genes in the phenotype dataset.

[c] Paired interactors with the same (matched) group assignment among the 70 pairs.

[d] For each phenotype group, Expected Matched Pairs = Expected Percentage of Pairs Matched [or (Percentage of Total Interactors)^2/100] × 70 total pairs/100.

[e] Paired interactors have matched group assignments more often than expected based on the frequency of each phenotype group.

significance greater than e-80 over at least 80% of protein length. We also characterized all genes in the Arabidopsis genome using these metrics. The distribution of redundancy categories among the phenotype groups, as well as the phenotype dataset as a whole and the entire Arabidopsis genome is presented in Figure 11. In this analysis, genes with trichome, stomata, or root hair defects were assigned to the morphological group, instead of the cellular-biochemical group. This more readily distinguished notable epidermal structure defects from more subtle cellular defects.

Using this system, 31% of all Arabidopsis genes are classified as unique, 27% display moderate similarity and 42% exhibit high similarity to their closest match. Surprisingly, the distribution of redundancy categories for phenotype genes is not significantly different from the genome as a whole (χ^2 test, P = 0.12). Degree of genetic redundancy, then, is a poor predictor of whether a gene will exhibit a mutant phenotype. However, phenotype groups display notable trends in the distribution of genetic redundancy. When compared with the whole genome, the essential phenotype group is enriched for single-copy genes. This observation agrees with previous work on embryo-defective genes in Arabidopsis (Tzafrir et al., 2004). The essential group is also deficient in genes with a highly-similar potential paralog. Conversely, genes with cellular, biochemical, or conditional phenotypes are unlikely to be unique and are more likely to match a highly-similar gene. For biochemical and cellular phenotypes, this potentially indicates that genetic redundancy is masking a more severe phenotype. In the case of conditional phenotypes, it suggests that the extra genetic material produced from gene duplication events is often co-opted to respond to specialized environmental stimuli.

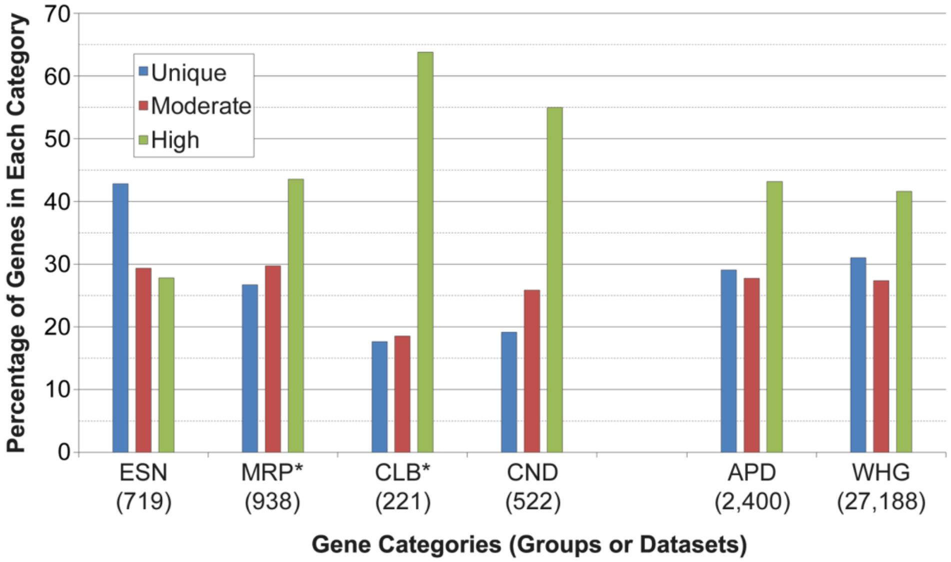

Figure 11. Genetic Redundancy of Phenotype Genes and the Arabidopsis Genome. Levels of protein sequence redundancy (defined in the text) for Arabidopsis genes assigned to different phenotype groups (left side), all genes in the Arabidopsis phenotype dataset (APD), and the whole Arabidopsis genome (WHG). *For this analysis, genes associated with visible defects in epidermal features (trichomes, stomata, root hairs) were moved from the cellular-biochemical (CLB) group to the morphological (MRP) group. The total numbers of genes evaluated are noted in parentheses.

Phenotypes of Putative Orthologs

Does the loss of similar protein functions in different plants produce comparable phenotypes? This question is vital because it assesses whether the research performed with mutants in Arabidopsis can translate to economically-important plants. The most direct and definitive way to address this question is to assemble comprehensive phenotype datasets for other plants, and then compare phenotypes observed following the abolition of similar protein functions. However, large-scale phenotype databases are not available for other plant species. Instead, to investigate this subject we built small, targeted datasets of mutant phenotype information for genes in rice, tomato, and maize and compared the similarities in biological consequence following disruption of genes that putatively encode similar functions in each species.

The identification of phenotype data in other plant species was guided by public databases, PubMed searches, and datasets of phenotype information associated with publications. Candidate phenotype genes in rice were identified through a PubMed search using the keywords rice, Arabidopsis, ortholog, and mutant. Additionally, the Gramene database (www.gramene.org) was queried for protein coding genes in rice with a described phenotype, resulting in a list of 121 genes. For tomato, a collection of 66 genes with mutant phenotypes was provided by the laboratory of Lukas Mueller at Cornell University. Maize genes were located with the help of a recently-published dataset of 112 phenotype genes (Schnable and Freeling, 2011). In total, over 300 candidate phenotype genes in these other species were identified. These loci were considered putatively orthologous to an Arabidopsis phenotype gene if the two genes matched reciprocally with a BLASTP e-40 cutoff. Manual literature curation of mutant phenotypes was then performed for these putatively orthologous genes. Some examples were removed from further analysis because no published phenotype information could be located or because they displayed only dominant or multiple mutant phenotypes.

The final dataset includes 62 pairs of Arabidopsis and either rice, maize, or tomato phenotype genes. Rice genes are most numerous with 30 examples, compared to 17 and 15 examples for tomato and maize, respectively. Six Arabidopsis genes (*ABA1, BRI1, GAI, LAS, SVP*, and *UFO*) were matched to counterparts in both rice and tomato. Morphological defects are more common among the phenotypes we documented in other plant species, indicating a more focused interest on vegetative and reproductive development in crop plants. The complete dataset of these putatively orthologous phenotypes is available as a supplement to the publication describing the Arabidopsis phenotype dataset (Lloyd and Meinke, 2012; Table S7). This version of the ortholog phenotype dataset contains 20 additional gene pairs identified by a forward-only BLASTP match with an Arabidopsis phenotype gene. A truncated version containing only the genes identified by reciprocal BLASTP matches is appended to this thesis (Appendix I).

Paired phenotype descriptions were compared and their similarity was subjectively described as low, moderate, moderate-high, or high. Pairs with low similarity share no phenotypes, while those with high similarity share all, or almost all, phenotypes. For example, the phenotype of the Arabidopsis gene *ASY1*, ‘severely reduced fertility due to defects in meiosis,’ and the rice gene *PAIR2*, ‘sterile; loss of homologous chromosome pairing,’ were considered to be highly similar. Phenotypes described as moderately similar were only tangentially comparable. In one case, the phenotype of the Arabidopsis gene *UFO*, ‘homeotic floral transformations,’ was considered to be moderately similar to the phenotype of the paired tomato gene, *AN1*, ‘leaves are small and highly suppressed with a cauliflower-like appearance; no flowers form; determinate floral meristems replaced by indeterminate proliferous shoot.’ In this example, the two genes show distinct floral phenotypes, but other phenotypes are notably different. Paired phenotypes somewhere between high and moderate similarity were considered moderate-to-highly similar. This category was often invoked when two genes displayed one strikingly similar phenotype alongside many other disparate phenotypes. For example, the phenotype of the Arabidopsis gene *ABA1*, ‘wilty; low ABA levels,’ was categorized as moderate-to-highly similar to the phenotype of the tomato gene *ZEP1*, ‘decreased biomass; wilty; green leaves; beige flowers; intense red fruits; increased carotenoids.’ In this case, the two genes share one specific phenotype, a wilty disposition, while also displaying many other defects that are unique to each putative ortholog.

Phenotypes were considered to display high or moderately high similarity in 29% and 24% of gene pairs, respectively. Phenotypes were designated as moderately similar in 21% of examples and did not match at all in 26% of cases. In addition, phenotype groups and classes of paired genes are frequently the same. Gene pairs were matched in group assignment in 68% of gene pairs and class designation in 57%. This analysis indicates that there is a reasonable amount of conservation in the biological relevance of protein functions among a variety of plant species. With regard to translating Arabidopsis phenotype data into other plants, these preliminary results are especially promising when considering that genetic redundancy, evolutionary distance, and differences in plant morphology or reproductive strategies were not taken into account during this investigation.

This subject is currently under further investigation through a pilot project initiated during the Phenotype Ontology Research Coordination Network meeting at the National Evolutionary Synthesis Center during of February of this year (www. phenotypercn.org). Available phenotype data are being collected and curated in four additional plants species (tomato, maize, rice and legumes) by researchers who are familiar with these plants. In order to efficiently manipulate this information, a set of shared ontology terms capable of capturing the full range of observed phenotype data will then be developed. The Arabidopsis phenotype data described in this thesis, as well as the information collected in other plants, will be translated into this system. Orthologous gene pairs between these species will then be identified and the associated phenotypes compared more directly and accurately than in the analysis described above.

Genes with No Loss-of-Function Phenotype

Complete gene disruptions in Arabidopsis do not always result in an obvious mutant phenotype. Redundancy, either from alternative cellular pathways or the maintenance of ancestral gene duplications, is often invoked to explain the absence of biological consequences following gene loss. This is logical for recently duplicated genes, as they have not existed long enough to accumulate deleterious mutations. But if there is no consequence to their loss, how could they persist in a genome? Following gene duplication, if descendant genes do not evolve new functions (neofunctionalization) or begin to share the function of their ancestral gene (subfunctionalization), it becomes increasingly improbable over geological time that both could escape natural selection and remain functional.

Nevertheless, genes resulting from ancient duplications often appear to be evolutionarily conserved despite displaying no obvious loss-of-function phenotype. For many of these cases, I expect there is a loss-of-function phenotype that is overlooked because it is subtle or only manifests under specialized growth conditions. Such phenotypes may be detrimental to viability and competition in the natural environment, but are often difficult to detect in the laboratory. Subjecting mutant plants to a wide range of growth conditions, such as those described as the Arabidopsis gauntlet (www.gantlet.org) or growing mutants in the natural environment where their wild-type accession evolved could help to identify these elusive phenotypes. The lack of an available null allele is another potential reason that a phenotype may not be observed. Residual protein function produced by a weak allele can be enough to prevent the full range of consequences associated with complete disruption of a gene. These possibilities may help explain some unexpected results from analyses described in this chapter, particularly with regard to the similarity of phenotype genes and the whole genome in degree of genetic redundancy and likelihood of protein products being highly interconnected. This is because we have drawn a false distinction between genes that display phenotypes and the rest of the genome. Instead, I expect that most genes in the Arabidopsis genome should exhibit a loss-of-function phenotype.

I contend that there are only two reasonable explanations for the genuine absence of an observable mutant phenotype (i.e. not due to incomplete phenotyping or lack of knockout alleles) associated with an ancient gene: (1) the function of the gene has recently become obsolete, perhaps due to the extinction of a predator or a change in environment, and it can be considered en route to pseudogene status; or (2) another gene has recently taken on the same function through convergent evolution. Testing such an assertion could prove difficult, however, as there is currently no definitive method available to confirm the lack of a loss-of-function phenotype. Still, a dataset of Arabidopsis genes that putatively lack a mutant phenotype could be an interesting and useful collection to supplement the phenotype analyses described in this thesis. Such a dataset could also be helpful in understanding the evolution, modification, and loss of gene function in a model plant.

REFERENCES

Alonso JM, Stepanova AN, Leisse TJ, Kim CJ, Chen H, Shinn P, Stevenson DK, Zimmerman J, Barajas P, Cheuk R, *et al*. (2003) Genome-wide insertional mutagenesis of *Arabidopsis thaliana*. *Science* **301**: 653-657

Arabidopsis Genome Initiative (2000) Analysis of the genome sequence of the flowering plant *Arabidopsis thaliana*. *Nature* **408**: 796-815

Arabidopsis Interactome Mapping Consortium (2011) Evidence for network evolution in an Arabidopsis interactome map. *Science* **333**: 601–607

Berg M, Rogers R, Muralla R, Meinke D (2005) Requirement of aminoacyl-tRNA synthetases for gametogenesis and embryo development in Arabidopsis. *Plant J* **44**: 866-878.

Blake JA, Bult CJ, Kadin JA, Richardson JE, Eppig JT and the Mouse Genome Database Group (2011) The Mouse Genome Database (MGD): premier model organism resource for mammalian genomics and genetics. *Nucleic Acids Res* **39**: D842-848.

Boavida LC, Shuai B, Yu HJ, Pagnussat GC, Sundaresan V, McCormick S (2009) A collection of Ds insertional mutants associated with defects in male gametophyte development and function in *Arabidopsis thaliana*. *Genetics* **181**: 1369-1385

Bouché N, Bouchez D (2001) Arabidopsis gene knockout: phenotypes wanted. *Curr Opin Plant Biol* **4**: 111-117

Bowman JL, Smyth DR (1999) CRABS CLAW, a gene that regulates carpel and nectary development in Arabidopsis, encodes a novel protein with zinc finger and helix-loop-helix domains. *Development* **126**: 2387-2396

Bradford Y, Conlin T, Dunn N, Fashena D, Frazer K, Howe DG, Knight J, Mani P, Martin R, Moxon SA, *et al*. (2011) ZFIN: enhancements and updates to the Zebrafish Model Organism Database. *Nucleic Acids Res* **39**: D822-829

Bryant N, Lloyd J, Sweeney C, Myouga F, Meinke D (2011) Identification of nuclear genes encoding chloroplast-localized proteins required for embryo development in Arabidopsis. *Plant Physiol* **155**: 1678-1689

Drysdale R, FlyBase Consortium (2008) FlyBase : a database for the Drosophila research community. *Methods Mol Biol* **420**: 45-59

Engel SR, Balakrishnan R, Binkley G, Christie KR, Costanzo MC, Dwight SS, Fisk DG, Hirschman JE, Hitz BC, Hong EL, *et al*. (2010) Saccharomyces Genome Database provides mutant phenotype data. *Nucleic Acids Res* **38**: D433-436

Eshed Y, Baum SF, Bowman JL (1999) Distinct mechanisms promote polarity establishment in carpels of Arabidopsis. *Cell* **99**: 199-209

Harris TW, Antoshechkin I, Bieri T, Blasiar D, Chan J, Chen WJ, De La Cruz N, Davis P, Duesbury M, Fang R, *et al*. (2010) WormBase: a comprehensive resource for nematode research. *Nucleic Acids Res* **38**: D463-467

Hirsh AE, Fraser HB (2001) Protein dispensability and rate of evolution. *Nature* **411**: 1046-1049

Honys D, Twell D (2004) Transcriptome analysis of haploid male gametophyte development in Arabidopsis. *Genome Biol* **5**: R85

Howden R, Park SK, Moore JM, Orme J, Grossniklaus U, Twell D (1998) Selection of T-DNA-tagged male and female gametophytic mutants by segregation distortion in Arabidopsis. *Genetics* **149**: 621-631

Hurst LD, Smith NG (1999) Do essential genes evolve slowly? *Curr Biol* **9**: 747-750

Jeong H, Mason SP, Barabasi AL, Oltvai ZN (2001) Lethality and centrality in protein networks. *Nature* **411**: 41–42

Johnson MA, von Besser K, Zhou Q, Smith E, Aux G, Patton D, Levin JZ, Preuss D (2004) Arabidopsis hapless mutations define essential gametophytic functions. *Genetics* **168**: 971-982.

Jordan IK, Rogozin IB, Wolf YI, Koonin EV (2002) Essential genes are more evolutionarily conserved than are nonessential genes in bacteria. *Genome Res* **12**: 962-968

Kahraman A, Avramov A, Nashev LG, Popov D, Ternes R, Pohlenz HD, Weiss B (2005) PhenomicDB: a multi-species genotype/phenotype database for comparative phenomics. *Bioinformatics* **21**: 418-420

Khanna R, Shen Y, Toledo-Ortiz G, Kikis EA, Johannesson H, Hwang YS, Quail PH (2006) Functional profiling reveals that only a small number of phytochrome-regulated early-response genes in Arabidopsis are necessary for optimal deetiolation. *Plant Cell* **18**: 2157-2171

Lawrence CJ, Dong Q, Polacco ML, Seigfried TE, Brendel V (2004) MaizeGDB, the community database for maize genetics and genomics. *Nucleic Acids Res* **32**: D393-397

Li Y, Dai X, Cheng Y, Zhao Y (2011) NPY genes play an essential role in root gravitropic responses in Arabidopsis. *Mol Plant* **4**: 171-179

Lloyd J, Meinke D (2012) A comprehensive dataset of genes with a loss-of-function mutant phenotype in Arabidopsis. *Plant Physiol* **158**:1115-1129

McKusick VA (2007) *Mendelian Inheritance in Man* and its online version, OMIM. *Am J Hum Genet* **80**: 588–604.

McLellan H, Gilroy EM, Yun BW, Birch PR, Loake GJ (2009) Functional redundancy in the Arabidopsis Cathepsin B gene family contributes to basal defence, the hypersensitive response and senescence. *New Phytol* **183**: 408-418

Meinke DW, Meinke LK, Showalter TC, Schissel AM, Mueller LA, Tzafrir I (2003) A sequence-based map of Arabidopsis genes with mutant phenotypes. *Plant Physiol* **131**: 409-418

Meinke DW, Sussex IM (1979) Embryo-lethal mutants of *Arabidopsis thaliana*: A model system for genetic analysis of plant embryo development. *Devel Biol* **72**: 50-61

Mueller LA, Solow TH, Taylor N, Skwarecki B, Buels R, Binns J, Lin C, Wright MH, Ahrens R, Wang Y, *et al*. (2005) The SOL Genomics Network: a comparative resource for Solanaceae biology and beyond. *Plant Physiol* **138**: 1310-1317

Muralla R, Lloyd J, Meinke D (2011) Molecular foundations of reproductive lethality in *Arabidopsis thaliana*. *PLoS One* **6**: e28398

Pagnussat GC, Yu HJ, Ngo QA, Rajani S, Mayalagu S, Johnson CS, Capron A, Xie LF, Ye D, Sundaresan V (2005) Genetic and molecular identification of genes required for female gametophyte development and function in Arabidopsis. *Development* **132**: 603-614

Pina C, Pinto F, Feijó JA, Becker JD (2005) Gene family analysis of the Arabidopsis pollen transcriptome reveals biological implications for cell growth, division control, and gene expression regulation. *Plant Physiol* **138**: 744-756

Prigge MJ, Otsuga D, Alonso JM, Ecker JR, Drews GN, Clark SE (2005) Class III homeodomain-leucine zipper gene family members have overlapping, antagonistic, and distinct roles in Arabidopsis development. *Plant Cell* **17**: 61-76

Richly E, Leister D (2004) An improved prediction of chloroplast proteins reveals diversities and commonalities in the chloroplast proteomes of Arabidopsis and rice. *Gene* **329**: 11-16

Rosso MG, Li Y, Strizhov N, Reiss B, Dekker K, Weisshaar B (2003) An *Arabidopsis thaliana* T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics. *Plant Mol Biol* **53**: 247-259

Schnable JC, Freeling M (2011) Genes identified by visible mutant phenotypes show increased bias toward one of two subgenomes of maize. *PLoS One* **6**: e17855

Sessions A, Burke E, Presting G, Aux G, McElver J, Patton D, Dietrich B, Ho P, Bacwaden J, Ko C, *et al*. (2002) A high-throughput Arabidopsis reverse genetics system. *Plant Cell* **14**: 2985-2994

Sun Q, Zybailov B, Majeran W, Friso G, Olinares PD, van Wijk KJ (2009) PPDB, the Plant Proteomics Database at Cornell. *Nucleic Acids Res* **37**: D969-974

Tzafrir I, Pena-Muralla R, Dickerman A, Berg M, Rogers R, Hutchens S, Sweeney TC, McElver J, Aux G, Patton D, Meinke D (2004) Identification of genes required for embryo development in Arabidopsis. *Plant Physiol* **135**: 1206-1220

Wang Y, Zhang WZ, Song LF, Zou JJ, Su Z, Wu WH (2008) Transcriptome analyses show changes in gene expression to accompany pollen germination and tube growth in Arabidopsis. *Plant Physiol* **148**: 1201-1211

Ware D, Jaiswal P, Ni J, Pan X, Chang K, Clark K, Teytelman L, Schmidt S, Zhao W, Cartinhour S, McCouch S, Stein L (2002) Gramene: a resource for comparative grass genomics. *Nucleic Acids Res* **30**: 103-105

Wilkinson JQ, Crawford NM (1993) Identification and characterization of a chlorate-resistant mutant of *Arabidopsis thaliana* with mutations in both nitrate reductase structural genes NIA1 and NIA2. *Mol Gen Genet* **239**: 289-297.

Xu J, Li Y (2006) Discovering disease-genes by topological features in human protein-protein interaction network. *Bioinformatics* **22**: 2800–2805

Yang S, Yang H, Grisafi P, Sanchatjate S, Fink GR, Sun Q, Hua J (2006) The BON/CPN gene family represses cell death and promotes cell growth in Arabidopsis. *Plant J* **45**: 166-179

Yu H, Braun P, Yildirim MA, Lemmens I, Venkatesan K, Sahalie J, Hirozane-Kishikawa T, Gebreab F, Li N, Simonis N, *et al*. (2008) High quality binary protein interaction map of the yeast interactome network. *Science* **322**: 104–110

Zubko MK, Day A (1998) Stable albinism induced without mutagenesis: a model for ribosome-free plastid inheritance. *Plant J* **15**: 265–271

APPENDIX A: Controlled Vocabulary for Mutant Phenotype Descriptions

This appendix displays the vocabulary used to describe the mutant phenotypes we have catalogued in the Arabidopsis phenotype dataset. This list does not include unusual, non-standard phenotypes that occasionally appear in the dataset. Instead, these descriptions serve as a standard for describing common phenotypes. Terms are separated by phenotype subset. They are ordered from more general descriptions to more specific, and grouped so that phrases describing similar features, such as length or shape of an organ, are nearby one another. Some bracketed phrases are included, as well. These can either be replaced by terms outlined nearby the phrases or by names of plant organs and structures or general phenotype descriptions. Additional notes and examples are included on the following pages to assist in replacing these bracketed phrases. To save space, lists that do not involve bracketed phrases are separated into two columns.

Gametophyte, Gametophyte and Embryo, Embryo and Gametophyte, and Miscellaneous Gametophyte Defective

Gametophyte defective
Gametophyte defective (inferred)
Male gametophyte defective
Complete male gametophyte defective
Female gametophyte defective
Complete female gametophyte defective
Ovule abortion
Abnormal pollen
Twisted pollen tubes
Branched pollen tubes
Altered ovule morphology
Embryo defective (inferred)
Rare embryo defective (inferred)

Above phenotype descriptions can replace [gametophyte defect description]***;***
Descriptions of general mutant phenotypes can replace [phenotype description]

[Gametophyte defect description] (no effect on fertility)
[Gametophyte defect description]; Homozygotes are viable: [Phenotype description]

Examples: Branched pollen tubes (no effect on fertility); Male gametophyte defective; Homozygotes are viable: Dwarf

Embryo Defective and Miscellaneous Seed Defective

Embryo defective
Bumpy embryo
Abnormal embryonic cell patterning
Altered embryo cell specification
Enlarged embryo cells
Enlarged endosperm nuclei
Leafy cotyledons
Wrinkled seeds
Initiation of endosperm development in absence of fertilization
Initiation of seed development in absence of fertilization
Small seeds due to reduced endosperm growth
50% mutant seed

Above phenotype descriptions can replace [Embryo defect description]

[Embryo defect description] (segregates from heterozygotes)

Example: Wrinkled seeds (segregates from heterozygotes)

No Homozygous Mutants

No homozygous mutant plants recovered

Seedling and Rosette Lethal

Seedling lethal
Seedling lethal without exogenous [nutrient / chemical]; ***Example***: Seedling lethal without exogenous sucrose
Seedling lethal on soil
Seedling lethal (inferred from pigment defect)
Rosette lethal

Germination

Abnormal germination
Altered germination rate
Low germination rate
Very low germination rate
Delayed germination
Severely delayed germination
Slightly delayed germination
Complete loss of germination
Early germination
Delayed after-ripening
Complete loss of after-ripening
Reduced seed dormancy
Increased seed dormancy

Non-Lethal Seedling

General seedling phenotype descriptions

Abnormal seedling morphology
Small seedlings
Slightly smaller seedlings
Tall seedlings
Variegated seedlings
Thick seedlings
Slow seedling growth
Slightly slower seedling growth
Very slow seedling growth
Delayed seedling growth
Delayed seedling establishment
Delayed early development
Complete loss of apical hook formation
Exaggerated apical hook

Cotyledon phenotype descriptions

Abnormal cotyledon morphology
Abnormal cotyledon shape
Abnormal cotyledon number
Decreased cotyledon number
Increased cotyledon number
Pleiotropic cotyledon defects
Abnormal cotyledon positioning
Abnormal cotyledon growth

Long cotyledonary petiole

Descriptors outlined after the underlined phrases below can replace [size / shape / miscellaneous descriptor]

[Size / Shape / Miscellaneous descriptor] cotyledons
    Sizes: Large, small, slightly smaller
    Shapes: Narrow, downward-bending, upward-bending, long, wide, heart-shaped, cup-shaped, curled, thick, open, fused, partially fused, lanceolate, linear, lobed, concave
    Miscellaneous descriptors: Rough

Examples: Large cotyledons; Long cotyledons; Rough cotyledons

Hypocotyl phenotype descriptions
Thick hypocotyl
Abnormal hypocotyl gravitropism

Descriptors outlined after the underlined phrase below can replace [size]

[Size] hypocotyl
    Sizes: Short, very short, slightly shorter, long, slightly longer

Examples: Short hypocotyl; Slightly longer hypocotyl

Pigmentation

Pigment defective embryo

Pigment defective seedlings

Descriptors outlined after the underlined phrase below can replace [color]

[Color]
[Color] or [color]
[Color] to [color]
[Color] [plant part]
    Colors: albino, bright green, brown, dark green, pale, pale green, pale yellow, pale, yellow-green, purple, red, slightly darker green, slightly pale green, variegated, yellow, yellow-green

Examples: Pale yellow; Brown or dark green; Albino to pale green; Pale leaves

Plant Growth Rate and Size

Plant size phenotype descriptions

Dwarf
Semi-dwarf
Severe dwarf
Reduced dry weight
Reduced fresh weight
Slightly reduced fresh weight
Increased dry weight
Increased fresh weight
Reduced biomass
Increased biomass
Increased [plant part] biomass

Plant growth rate phenotype descriptions

Slow growth
Slightly slower growth
Very slow growth
Delayed growth
Slightly delayed growth
Increased growth rate

Names of any plant organs or structures can replace [plant part]

Slow [plant part] growth
Slightly slower [plant part] growth
Increased [plant part] growth rate

Examples: Slow leaf growth; Increased inflorescence stem growth rate

Root

General root phenotype descriptions

Abnormal root growth
Abnormal root morphology
Abnormal root architecture
Short roots
Slightly shorter roots
Small root system
Very short roots
Long roots
Thick roots
Wide roots
Slow root growth
Slightly slower root growth
Delayed root growth
Abnormal root gravitropism
Reduced root gravitropism
Slightly reduced root gravitropism
Complete loss of root gravitropism
Twisted root growth
Helical root growth

Primary root phenotype descriptions

Short primary root
Very short primary root
Long primary root

Lateral root phenotype descriptions

Abnormal lateral root formation
Early lateral root formation
Short lateral roots
Thick lateral roots
Few lateral roots
Slightly fewer lateral roots
Increased lateral root number

Leaf

General leaf phenotype descriptions

Abnormal leaf morphology
Abnormal leaf growth
Abnormal leaf shape
Abnormal leaf number
Few leaves
Increased leaf number
Abnormal leaf curvature
Abnormal leaf position
Delayed leaf growth
Slow leaf growth

Descriptors outlined after the underlined phrases below can replace [size / shape / miscellaneous descriptor]

[Size / Shape / Miscellaneous descriptor] leaves

Sizes: Short, slightly shorter, small, slightly smaller, very small, large
Shapes: Narrow, pointed, serrated, slightly serrated, crinkled, rounded, slightly rounded, wavy, scalloped, twisted, slightly twisted, upward-bending, downward-bending, warped, malformed, thick, slightly thicker, thin, pointed, slightly pointed, elongated, crumpled, misshapen, torn, undulated, reticulated, wrinkled, curved, lancet-shaped, asymmetric, rolled, short, stunted, sessile, distorted, linear
Miscellaneous descriptors: Rough, fused

***Examples*:** Small leaves; Slightly serrated leaves; Fused leaves

Rosette leaf phenotype descriptions

Abnormal rosette leaf morphology
Few rosette leaves
Increased rosette leaf number
Delayed rosette growth
Reduced rosette biomass

Descriptors outlined after the underlined phrases below can replace [size / shape]

[Size / Shape] rosette leaves
[Size / Shape] rosette

Sizes: Small, slightly smaller, large, slightly larger
Shapes: Narrow, serrated, rounded, flat, curled, wrinkly

Examples: Large rosette leaves; Small rosette; Narrow rosette leaves

Cauline leaf phenotype descriptions

Abnormal cauline leaf formation
Few cauline leaves
Increased cauline leaf number
Slightly increased cauline leaf number
Small cauline leaves
Wide cauline leaves

Leaf part phenotype descriptions

Long petioles
Short petioles
Complete loss of petiole elongation
Red petioles
Narrow first true leaves
Pointed first true leaves
Cupped first true leaves
Irregular leaf blade surface
Serrated leaf margins
Downward-bending leaf margins
Uneven leaf margins
Bent leaf margins
Short leaf blades

Inflorescence Stem

Slow inflorescence growth
Slightly shorter primary inflorescence stem

Descriptors outlined after the underlined phrases below can replace [height / color / miscellaneous descriptor]

[Height / Color / Miscellaneous descriptor] inflorescence stems
Heights: Short, very short, tall
Colors: Glossy, bright green, dull
Miscellaneous descriptors: Thick, thin, spindly

Examples: Tall inflorescence stems; Glossy inflorescence stems; Thick inflorescence stems

Shoot Architecture

Abnormal inflorescence stem architecture
Increased branching
Decreased branching
Complete loss of branching
Complete loss of auxiliary inflorescences
Abnormal phyllotaxy
Abnormal [leaf or floral] phyllotaxy
Abnormal inflorescence stem gravitropism

Reduced inflorescence stem gravitropism
Helical growth
Increased primary inflorescence number
Corymb-like inflorescences

Both Inflorescence Stem and Shoot Architecture

Fasciated stems and inflorescences
Fasciated adventitious stems and inflorescences
Complete loss of primary inflorescence
Pin-shaped inflorescences
Fused stems and inflorescences
Twisted inflorescence stems
Crooked inflorescence stems
Zig-zag inflorescence stems

Miscellaneous Shoot and Leaf

Necrotic lesions
Necrotic lesions on leaves / rosette / rosette leaves / cauline leaves
Spontaneous lesions
Chlorotic
Chlorotic leaves / rosette / rosette leaves / cauline leaves
Slightly chlorotic
Slightly chlorotic leaves / rosette / rosette leaves / cauline leaves
Severe chlorosis
Bleached leaves
Wilty
Wilty leaves
Severe wilting
Leaves stay green during senescence
Aerial rosettes

Flower and Silique Morphology

Few flowers
Few siliques
Abnormal flower number
Abnormal flower position
Homeotic floral transformations
Increased flower growth rate
Slow flower development
Arrested flower development
Precocious flower development
Delayed flower bud opening
Indehiscent floral organs
Delayed floral organ abscission
Indehiscent siliques
Reduced silique shattering
Abnormal anther dehiscence

Descriptors outlined after the underlined phrase below can replace [flower part]

Decreased [flower part] number
Complete loss of [flower part] formation
Increased [flower part] number
Abnormal [flower part] morphology
Slightly altered [plant part] morphology
Abnormal [flower part] development
Flower parts: Flower, petal, stamen, floral organ, silique, petal margins, pistil, filament, floral bud, stigma, stigma papillae, pedicel

Examples: Decreased petal number; Complete loss of flower formation; Increased stamen number; Abnormal silique morphology; Slightly altered floral bud morphology; Abnormal stigma development

Descriptors outlined after the underlined phrases below can replace [size / shape / miscellaneous descriptor] ***and*** [flower part]

[Size / Shape / Miscellaneous descriptor] [flower part]
Shape: Narrow, elongated, twisted, slightly flattened, severely serrated, bended, fused, distorted, wrinkled, blunt, unfused, downward-curling, thick, club-shaped, radialized
Size: Small, large, short, very short
Miscellaneous descriptors: Sterile, glossy, downward-pointing
Flower parts: Flowers, petals, stamens, floral organs, siliques, sepal margins, petal margins, pistil, filaments, floral buds, stigma, stigma papillae, pedicel

Examples: Large petals; Narrow sepal margins; Glossy siliques

Ovule and Pollen

Ovule phenotype descriptions
Abnormal ovules
Abnormal ovule development
Abnormal integuments
Short integuments
Complete loss of pollen exine layer

Pollen phenotype descriptions
Pollen abortion
Collapsed pollen
Large pollen
Slightly smaller pollen
Dyad pollen
Tetrad pollen
Low pollen germination rate
Decreased pollen number

Abnormal pollen wall development
Abnormal pollen exine layer
Abnormal pollen tetrad formation
Abnormal pollen maturation

Above phenotype descriptions can replace [ovule or pollen defect description]

[Ovule or pollen defect description] (no reduction in fertility)
[Ovule or pollen defect description] (does not segregate in heterozygotes)

Examples: Low pollen germination rate (no reduction in fertility); Abnormal ovules (does not segregate in heterozygotes)

Sterility and Reduced Fertility

Sterile
Completely sterile
Reduced fertility
Severely reduced fertility
Slightly reduced fertility
Partial to complete sterility
Increased seed yield
Male sterile
Reduced male fertility
Completely male sterile
Female sterile
Reduced female fertility

Above phenotype descriptions can replace [fertility phenotype]***; Descriptors outlined after the underlined phrase below can replace*** [defect]

[Fertility phenotype] due to [defect]

Defects: Defects in meiosis, short filaments, short integuments, anther defects, pollen defects, indehiscent anthers, delayed anther dehiscence, abnormal anther dehiscence, abnormal pollen maturation

Examples: Sterile due to defects in meiosis; Reduced fertility due to short integuments

Seed and Seed Coat

Abnormal seeds
Abnormal seed morphology
Abnormal seed shape
Large seeds
Small seeds
Heavy seeds
Slightly reduced seed mass
Shriveled seeds
Wrinkled seeds
Reduced seed mucilage
Abnormal seed mucilage
Dark seeds
Abnormal seed coat
Yellow seed coat
Pale seed coat
Translucent seeds

Abnormal seed coat coloration

Flowering Time

Early flowering
Slightly early flowering
Very early flowering
Late flowering
Slightly late flowering
Very late flowering
Complete loss of flowering

Above phenotype descriptions can replace [flowering time defect]

[Flowering time defect] independent of photoperiod

Example: Very early flowering independent of photoperiod

Senescence

Abnormal senescence
Early senescence
Delayed senescence
Slightly delayed senescence
Severely delayed senescence

Names of any plant organs or structures can replace [plant part]

Early [plant part] senescence
Delayed [plant part] senescence

Examples: Early leaf senescence; Delayed flower senescence

Circadian Rhythms

Abnormal circadian rhythms
Short circadian rhythms
Long circadian rhythms
Complete loss of circadian rhythms

Above phenotype descriptions can replace [circadian rhythm defect]***; Names of any plant organs or structures can replace*** [plant part]

[Circadian rhythm defect] independent of light conditions
[Circadian rhythm defect] in [plant part] movements

Examples: Abnormal circadian rhythms independent of light conditions; Long circadian rhythms in leaf movements

Miscellaneous Timing

Abnormal vegetative phase change
Early vegetative phase change
Abnormal vernalization response
Reduced vernalization response
Altered vernalization response
Reduced vernalization response
Altered vernalization requirement for flowering

Stomata and Trichomes

Stomata phenotype descriptions

Abnormal stomata development
Abnormal stomata morphology
Increased stomatal density
Complete loss of stomata formation
Reduced stomatal width
Increased stomatal width
Increased stomatal opening rate
Abnormal stomatal patterning
Clustered stomata
Abnormal stomatal regulation
Abnormal stomatal response to light
Swollen guard cells

Trichome phenotype descriptions

Abnormal trichomes
Abnormal trichome development
Abnormal trichome morphology
Slightly altered trichome morphology
Abnormal trichome branching
Severely branched trichomes
Unbranched trichomes
Increased trichome branching
Reduced trichome branching
Short trichome branches
Abnormal trichome patterning
Large trichomes
Few trichomes
Very few trichomes
Increased trichome number
Distorted trichomes
Clustered trichomes
Multicellular trichomes

Root Hairs

Abnormal root hair growth
Abnormal root hair development
Root hair defective
Short root hairs
Slightly shorter root hairs
Long roots hairs
Increased root hair density
Decreased root hair density
Complete loss of root hairs
Thick root hairs

Wavy root hairs
Branched root hairs
Straight root hairs

Tissue and Cell Morphology

Venation and vascular tissue phenotype descriptions

Abnormal vein morphology
Abnormal vein patterning
Abnormal vascular patterning
Disorganized vascular patterning
Slightly abnormal vascular development
Severely increased vascular tissue
Abnormal vascularization
Reduced vascularization
Abnormal cotyledon vasculature
Abnormal vascular tissue
Abnormal vascular bundle patterning
Reduced venation
Abnormal xylem
Slightly abnormal xylem
Collapsed xylem
Increased xylem
Collapsed vessel elements
Deformed vessel elements

Names of any plant organs or structures can replace [plant part]

Abnormal [plant part] venation
Abnormal veins in [plant part]
Abnormal vein patterning in [plant part]
Disorganized [plant part] venation
Increased [plant part] vein complexity
Reduced [plant part] venation
Vascular discontinuity in [plant part]
Complete loss of [plant part] venation

Examples: Abnormal cotyledon venation; Abnormal veins in sepals; Abnormal vein patterning in leaves; Disorganized root venation; Reduced cauline leaf venation; Complete loss of flower venation

Meristem phenotype descriptions

Abnormal meristem development
Slightly smaller meristems
Large shoot meristems
Large floral meristems
Disorganized floral meristems
Abnormal SAM morphology
Large SAM
Rounded SAM
Flattened SAM
Disorganized SAM
Complete loss of SAM formation
Abnormal RAM morphology
Large RAM
Disorganized RAM

Cell morphology phenotype descriptions

Names of any plant organs or structures can replace [plant part]

Abnormal [plant part] cell patterning
Abnormal [plant part] cell morphology
Abnormal [plant part] cell division
Abnormal [plant part] cell positioning
Increased [plant part] cell density
Increased [plant part] cell number
Thin [plant part] cells
Large [plant part] cells
Misshapen [plant part] cells

Examples: Abnormal root cell patterning; Abnormal epidermal cell morphology; Abnormal SAM cell division; Increased leaf mesophyll layer cell density; Increased quiescent center cell number; Large floral meristem cells; Misshapen hypocotyl cells

Cellular Ultrastructure

General cellular ultrastructure phenotype descriptions

Names of any organelle of cellular structures can replace [organelle / cell structure]

Abnormal [organelle / cell structure] morphology
Abnormal [organelle / cell structure] development
Slightly altered [organelle / cell structure] morphology
Disorganized [organelle / cell structure] morphology

Examples: Abnormal telomere morphology; Abnormal mitochondria development

Nucleus, chloroplast, and mitochondrion phenotype descriptions

Small nuclei
Multiple nuclei
Large nuclei
Few chloroplasts
Large chloroplasts
Abnormal chloroplast positioning
Severely reduced chloroplast movement
Arrested chloroplast division
Constricted chloroplasts
Elongated mitochondria
Severely elongated mitochondria

Other cellular structure and organelle phenotype descriptions

Short telomeres
Disorganized endomembranes
Disorganized actin filaments
Disorganized microtubules

Abnormal peroxisome division
Complete loss of ER body formation
Large oil bodies
Reduced sister chromatid alignment
Abnormal ploidy levels
Increased ploidy levels
Increased ploidy levels due to endoreduplication
Abnormal mitotic spindle morphogenesis
Abnormal cell plates
Abnormal cell walls
Decreased secondary cell wall thickness
Abnormal microtubule development
Delayed meiotic cell divisions

Product Accumulation

Descriptors outlined after the underlined phrases below can replace [general amount] ***and*** [chemical]***; Names of any plant organs or structures can replace*** [plant part]

[General amount] [chemical] levels
[General amount] [chemical] levels in [plant part]
Abnormal [chemical] levels
Abnormal [chemical] composition
Complete loss of [chemical] production / accumulation

General amounts: Low, very low, elevated, severely elevated, abnormal
Chemicals: Threonine, methionine, 16:0 fatty acid, trienoic fatty acid , monounsaturated fatty acid, starch, xylan, pectin, heme, fatty acid, ABA, glucosinolate, fructose, glucose, sucrose, anthocyanin, chlorophyll, free leucine, carotenoid, phosphatidylmethylethanolamine, secondary alcohol, ketone, terpene, sulfate, fucosylated xyloglucan, sinapoylmalate, sinapoylglucose, suberin, phosphate, arabinose, nectar, cellulose, maltose, maltodextrin, flavonoid, potassium, ascorbate, iron, manganese, zinc, protochlorophyllide, nitrile, sterol, sterol ester, lutein, sulfolipid, aliphatic glucosinolate, triacylglycerol, palmitic acid, phytochelatin

Examples: Low pectin levels; Elevated anthocyanin levels in cotyledons; Abnormal starch levels; Abnormal fucosylated xyloglucan composition; Complete loss of suberin production

[General amount] levels of [chemical]
[General amount] levels of [chemical] in [plant part]

General amounts: Elevated, slightly elevated, low
Chemicals: Photorespiratory intermediates, methionine-derived glucosinolates, bound cyclopentenone jasmonates, twelve different amino acids, intermediates of

leucine biosynthesis, intermediates of methionine chain elongation, phenylpropanoid derivatives

Examples: Elevated levels of methionine-derived glucosinolates; Low levels of intermediates of leucine biosynthesis in leaves

Cellular and Physiological Processes

Photosynthesis-related chemical phenotype descriptions

Decreased post-illumination chlorophyll fluorescence
Complete loss of post-illumination chlorophyll fluorescence
Slightly decreased chlorophyll fluorescence
Reduced non-photochemical quenching
Slightly increased non-photochemical quenching
Abnormal photosynthesis acclimation response
Reduced electron transport
Decreased effective quantum yield of PSII
Excess absorbed light energy cannot be dissipated
Slightly decreased oxygen evolution in thylakoids
Reduced thylakoid membrane unsaturation
Reduced chlorophyll a/b ratio

DNA methylation phenotype descriptions

Decreased DNA methylation
Increased DNA methylation
Increased cytosine methylation
Decreased CpXpG DNA methylation
Reduced RNA-directed DNA methylation
Abnormal DNA methylation
Complete loss of telomeric DNA methylation
Complete loss of cytosine methylation

Chemical uptake and transport phenotype descriptions

Reduced nitrate uptake
Reduced nitrate influx in roots
Reduced potassium uptake
Reduced iron uptake
Reduced nitrogen transport
Reduced nitrate transport from root to shoot
Reduced sulfate transport in roots
Reduced basipetal auxin transport
Reduced phosphate transport in roots
Reduced aspartate transport in the phloem

<u>Other cellular process phenotype descriptions</u>

Increased homologous recombination frequency
Reduced somatic intrachromosomal homologous recombination
Increased intrachromosomal recombination frequency
Abnormal xylan modification
Abnormal insoluble lipid polyester biosynthesis
Abnormal aromatic suberin biosynthesis
Reduced 14C fatty acid elongation
Constitutively activated unfolded protein response
Decreased dienoic fatty acid desaturation
Decreased inward electrical currents in vacuoles
Reduced hydraulic conductivity in roots
Abnormal vacuolar trafficking
Abnormal stretch-activated channel activity
Reduced slow-activating vacuolar channel currents
Delayed lipid growth and breakdown

<u>Water Levels and Availability</u>

Reduced hydrotropism

Descriptors outlined after the underlined phrase below can replace [water condition]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Sensitive to [water condition]
Very sensitive to [water condition]
Resistant to [water condition]
[Plant part] growth sensitive to [water condition]
[Plant part] growth resistant to [water condition]
Sensitive to a combination of [water condition] and [other condition]
Phenotype enhanced under [water condition]
[Phenotype] under [water condition]
<u>Water conditions</u>: Drought, flood conditions, low humidity, high humidity

Examples: Sensitive to drought; Resistant to flood conditions; Root growth sensitive to high humidity; Phenotype enhanced under low humidity

<u>Temperature</u>

Altered response to high / low temperature
Reduced acclimation to high / low temperature
Lethal under high temperature
Sensitive to freezing when un-acclimated
Low germination rate without stratification
Delayed germination without stratification
Severely delayed germination without stratification

Descriptors outlined after the underlined phrase below can replace [temperature condition]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Sensitive to [temperature condition]
Very sensitive to [temperature condition]
Resistant to [temperature condition]
[Plant part] growth sensitive to [temperature condition]
[Plant part] growth resistant to [temperature condition]
Sensitive to a combination of [temperature condition] and [other condition]
[Phenotype] under a combination of [temperature condition] and [other condition]
[Phenotype] at high / low temperature
Phenotype enhanced under [temperature condition]
    Temperature conditions: High temperature, low temperature, altered temperature, freezing, heat shock

Examples: Sensitive to altered temperature; Resistant to high temperature; Leaf growth sensitive to heat shock; Cotyledon growth resistant to low temperature; Sensitive to a combination of high temperature and drought; Phenotype enhanced under low temperature

Light

General light response phenotype descriptions

Altered response to light
Abnormal phototropism
Reduced phototropism
Complete loss of phototropism
Dark-grown seedlings are de-etiolated

Red and far-red light phenotype phenotypes

Altered response to red: far-red light
Sensitive to red light
Sensitive to continuous red light

Descriptions of general mutant phenotypes can replace [phenotype]

[Phenotype] under far-red light
[Phenotype] under low fluences of far red light
[Phenotype] under hourly far red pulses
[Phenotype] under red light
[Phenotype] under low red/far red light

Examples: Short roots under far-red light; Long hypocotyl under low fluences of far red light; Upward-bending cotyledons under hourly far red pulses; Small leaves under low red/far red light

UV light condition phenotype descriptions

Sensitive to UV light
Resistant to UV light
Sensitive to UV-B light
Resistant to UV-B light
Sensitive to UV-C light
Resistant to UV-C light

Other light condition phenotype descriptions

Descriptions of general mutant phenotypes can replace [phenotype]

[Phenotype] under short days
[Phenotype] in the dark
[Phenotype] under continuous light
[Phenotype] under low light
[Phenotype] under high light
[Phenotype] under green shadelight
[Phenotype] under blue light
[Phenotype] under a variety of light fluence rates
[Phenotype] under a variety of light conditions
[Phenotype] under shadelight

Examples: Late flowering under short days; Small seedlings in the dark; Poor growth under a variety of light conditions

Mechanical Stimulus

Abnormal thigmotropism
Altered response to wounding

Names of any plant organs or structures can replace [plant part]

Abnormal [plant part] thigmotropism
Fragile [plant part]

Examples: Abnormal root thigmotropism; Fragile inflorescence stems

Miscellaneous Physical Conditions

Sensitive to ionizing radiation
Sensitive to x-rays
Sensitive to gamma rays
Sensitive to hypoxia
Freshly harvested seeds germinate well
Freshly harvested seeds exhibit delayed germination
Unable to regenerate shoots from callus

Descriptions of general mutant phenotypes can replace [phenotype]

[Phenotype] under vertical growth
[Phenotype] on tilted agar surface

Examples: Short roots under vertical growth; Small seedlings on tilted agar surface

Nutrient Levels and Availability

General nutrient availability phenotype descriptions
Descriptors outlined after the underlined phrase below can replace [nutrient]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Sensitive to [nutrient]
Sensitive to elevated [nutrient]
Sensitive to limited [nutrient]
Sensitive to [nutrient] starvation
[Plant part] growth sensitive to [nutrient]
[Plant part] growth sensitive to elevated [nutrient]
[Plant part] growth sensitive to limited [nutrient]
[Plant part] growth sensitive to [nutrient] starvation
Insensitive to [nutrient]
Insensitive to elevated [nutrient]
Insensitive to limited [nutrient]
Insensitive to [nutrient] starvation
Sensitive to a combination of [nutrient] and [other condition]

[Plant part] growth insensitive to [nutrient]
[Plant part] growth insensitive to elevated [nutrient]
[Plant part] growth resistant to limited [nutrient]
[Plant part] growth resistant to [nutrient] starvation
[Phenotype] in response to [nutrient]
[Phenotype] in response to elevated [nutrient]
[Phenotype] under limited [nutrient]
[Phenotype] under [nutrient] starvation
[Phenotype] when grown on nutrient plates
Under limited [nutrient]: [Phenotype description]
[Phenotype] when grown on both [nutrient] and [other chemical]

> Nutrients: Nitrogen, glucose, calcium, manganese, zinc, sodium, potassium, copper, nickel, alanine, urea, phosphate, carbon, sulfur, sucrose, nitrate, sulfate, iron, boron, molybdenum, carbon dioxide, sugar, calcium, ammonium, arabinose, L-glutamine, glutamate, magnesium

Examples: Sensitive to elevated glucose; Insensitive to manganese; Sensitive to a combination of ammonium and high temperature; Leaf growth sensitive to glucose; Root growth insensitive to elevated carbon; Short roots in response to glucose; Long hypocotyl under carbon starvation; Small leaves when grown on both sucrose and auxin

Nitrogen source phenotype descriptions
Names of nitrogen-containing nutrients can replace [nitrogen-containing nutrient]

Unable to use [nitrogen-containing nutrient] as primary nitrogen source
Reduced growth with [nitrogen-containing nutrient] as nitrogen source
Reduced growth with [nitrogen-containing nutrient] as sole nitrogen source
No growth with [nitrogen-containing nutrient] as sole nitrogen source
[Phenotype] with [nitrogen-containing nutrient] as sole nitrogen source

Examples: Unable to use urea as primary nitrogen source; Reduced growth with ammonium as nitrogen source; Short roots with nitrate as sole source of nitrogen

Exogenous Hormones

Descriptors outlined after the underlined phrase below can replace [hormone]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Altered response to [hormone]

Sensitive to [hormone]
Insensitive to [hormone]
[Phenotype] in response to [hormone]
[Plant part] growth sensitive to [hormone]
[Plant part] growth insensitive to [hormone]
Sensitive to a combination of [hormone] and [other condition]
[Phenotype] when grown on both [hormone] and [other chemical]

> <u>Hormones / hormone precursors and analogs</u>: SA, cytokinin, brassinosteroids, jasmonate, jasmonic acid, ethylene, saturating ethylene concentrations, IAA, IAA-Ala, IAA-Leu, MeIAA, IBA, auxin, IAA-amino acid conjugates**,** 2,4-D, 2,4-DB, pro-auxins, IAN (auxin precursor), INA (functional analog of SA), ACC (ethylene precursor), pyrabactin (synthetic ABA analog)

Examples: Altered response to ethylene; Sensitive to cytokinin; Short roots in response to jasmonic acid; Leaf growth insensitive to IAA; Sensitive to a combination of auxin and drought

Chemical Stress

Descriptors outlined after the underlined phrase below can replace [toxic chemical / chemical stress]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Altered response to [toxic chemical / chemical stress]
Sensitive to [toxic chemical / chemical stress]
Sensitive to elevated [toxic chemical]
Resistant to [toxic chemical / chemical stress]
[Plant part] growth sensitive to [toxic chemical / chemical stress]
[Plant part] growth resistant to [toxic chemical / chemical stress]
[Phenotype] in response to [toxic chemical / chemical stress]
Sensitive to a combination of [toxic chemical / chemical stress] and [other condition]
[Phenotype] when grown on both [toxic chemical / chemical stress] and [other chemical]

> <u>Toxic chemicals and chemical stress</u>:
> *Osmotic stress*
> Osmotic stress, salt stress, salt, mannitol, hyperosmotic stress
> *Oxidative stress*
> Oxidative stress, hydrogen peroxide, chlorate (inducer of oxidative stress), ozone, methyl viologen (inducer of oxidative stress), t-BOOH (organic peroxide), diamide (oxidizing agent)
> *DNA damaging agents*

DNA damaging agents, cisplatin, chemical mutagens, genotoxic stress, replication-inhibiting drugs, MMS (inducer of genotoxic stress), mitomycin C (DNA cross-linking agent), BLM (DNA damaging agent), hydroxyurea (inhibitor of DNA replication)

Transport inhibitors

NPA (inhibitor of polar auxin transport), TIBA (inhibitor of auxin transport), auxin transport inhibitors, concanamycin A (vacuole proton pump inhibitor)

Biosynthesis inhibitors

Paclobutrazol (inhibitor of GA synthesis), uniconazole (inhibitor of GA biosynthesis), DCB (inhibitor of cellulose synthesis), brassinazole (inhibitor of brassinosteroid biosynthesis), fosmidomycin (inhibitor of isoprenoid biosynthesis), lovastatin (inhibitor of isoprenoid biosynthesis), Latrunculin B (inhibitor of actin polymerization), buthionine sulfoximine (inhibitor of glutathione biosynthesis)

Toxic analogs

2,6-diaminopurine (toxic analog of adenine), fluoroacetate (toxic acetate analogue), fluorouridine (toxic uridine analog), PCIB (toxic anti-auxin), toxic purine analogues, herbicidal anthranilate analogs, toxic pyrimidine analogs

Cellular process / ultrastructure inhibitors

Oryzalin (microtubule-disrupting herbicide), DTT (ER homeostasis-perturbing compound), 5-fluorouracil (cytostatic drug), antimycin A (inhibitor of the cytochrome pathway of respiration), microtubule-disrupting drugs, tunicamycin (inducer of the unfolded protein response)

General herbicides

2,4-D, 2,4-DB, Ancymidol (herbicide), DAS734 (herbicide, novel phenyltriazole acetic acid compound), 6-methylanthranilate (herbicide), kanamycin, streptomycin, gentamicin, amikacin, tobramycin, apramycin, isoxaben (herbicide)

pH

Low pH, high pH

Miscellaneous toxic chemicals

Methotrexate, fungicides, methylglyoxal (cytotoxic byproduct of glycolysis), toxic D-alanine, TCO (inhibitor of ethylene signaling), BMAA (glutamate receptor competitor)

Examples: Altered response to osmotic stress; Sensitive to toxic pyrimidine analogs; Leaf growth resistant to paclobutrazol (inhibitor of GA synthesis); Short roots in response to cisplatin; Sensitive to a combination of hydrogen peroxide and low humidity

Miscellaneous Chemical Conditions

Descriptors outlined after the underlined phrase below can replace [miscellaneous chemical]***; Descriptions of general mutant phenotypes can replace*** [phenotype]***; Names of any plant organs or structures can replace*** [plant part]

Sensitive to [miscellaneous chemical]
Sensitive to elevated [miscellaneous chemical]
Sensitive to limited [miscellaneous chemical]
Sensitive to [miscellaneous chemical] starvation
[Plant part] growth sensitive to [miscellaneous chemical]
[Plant part] growth sensitive to elevated [miscellaneous chemical]
[Plant part] growth sensitive to limited [miscellaneous chemical]
[Plant part] growth sensitive to [miscellaneous chemical]starvation
Insensitive to [miscellaneous chemical]
Insensitive to elevated [miscellaneous chemical]
Insensitive to limited [miscellaneous chemical]
Insensitive to [miscellaneous chemical] starvation
[Plant part] growth insensitive to [miscellaneous chemical]
[Plant part] growth insensitive to elevated [miscellaneous chemical]
[Plant part] growth resistant to limited [miscellaneous chemical]
Plant part] growth resistant to [miscellaneous chemical] starvation
[Biological process] insensitive to [miscellaneous chemical]
[Phenotype] in response to [miscellaneous chemical]
[Phenotype] in response to elevated [miscellaneous chemical]
[Phenotype] under limited [miscellaneous chemical]
[Phenotype] under [miscellaneous chemical] starvation
Under limited [miscellaneous chemical]: [Phenotype description]
Sensitive to a combination of [miscellaneous chemical] and [other condition]
[Phenotype] when grown on both [miscellaneous chemical] and [other chemical]

> <u>Miscellaneous chemicals</u>: Aluminum, sirtinol, selenate, ethanol, potassium thiocyanate, sorbitol, cadmium, potassium chloride, cobalt, lithium, cadmium, arsenic, toxic compounds (including one in Bacto agar), TDIF (protein signaling molecule)

Examples: Sensitive to aluminum; Leaf growth resistant to cobalt; Short roots in response to elevated cadmium; Sensitive to a combination of lithium and cytokinin

Pathogens and Herbivores

Altered defense response
Complete loss of systemic acquired resistance development
Altered systemic acquired resistance response

Descriptions of general mutant phenotypes can replace [phenotype]

[Phenotype] under defense response conditions

Example: Dwarf under defense response conditions

Descriptors outlined after the underlined phrase below can replace [pathogen / herbivore]***; Names of any plant organs or structures can replace*** [plant part]

Susceptible to [pathogen / herbivore]
Resistant to [pathogen / herbivore]
Resistant to [pathogen / herbivore] in [plant part]
Altered response to [pathogen / herbivore]
Complete loss of hypersensitive response in response to [pathogen / herbivore]

> <u>Pathogens and herbivores</u>:
> *General categories*
> Disease, pathogens
> Viral infection, potyviruses
> Fungal infection, necrotrophic fungi, hemibiotrophic fungi, powdery mildew, oomycete infection, downy mildew
> Bacterial infection, avirulent bacteria, certain bacterial pathogens
> Parasitic wasps, green peach aphid
> *Specific species / strains*
> Tobacco etch virus, tobacco mosaic virus, barley powdery mildew, pea powdery mildew, potato late blight, lettuce mosaic virus, bacterial speck disease
> *Botrytis cinerea, Pseudomonas syringae, Albugo candida, Erysiphe cichoracearum, Leptosphaeria maculans, Alternaria brassicicola, Hyaloperonospora parasitica, Phytophthora brassicae, Piriformospora indica, Blumeria graminis hordei, Ralstonia solanacearum, Hyaloperonospora parasitica,* specific strains of *Pseudomonas syringae*

Examples: Susceptible to viral infection; Resistant to barley powdery mildew; Resistant to fungal infection in roots; Altered response to avirulent bacteria; Complete loss of hypersensitive response in response to *Blumeria graminis hordei*

Descriptors outlined after the underlined phrase below can replace [pathogen protein / signal]

Sensitive to [pathogen protein / signal]
Insensitive to [pathogen protein / signal]
Resistant to [pathogen protein / signal]

    Pathogen proteins and signals: elf18 (bacterial defense inducer), bacterial virulence gene B (AvrB), bacterial flagella protein

Example: Insensitive to bacterial virulence gene B (AvrB)

Descriptors outlined after the underlined phrase below can replace [pathogen-born toxin]

Resistant to [pathogen-born toxin]
Susceptible to [pathogen-born toxin]

    Pathogen-born toxins: Fumonisin B1 (fungal toxin), victorin (fungal toxin), fungal mycotoxin

Example: Susceptible to victorin (fungal toxin)

Other Biological Interactors

Resistant to Agrobacterium
Resistant to Agrobacterium transformation
Insensitive to growth stimulation of beneficial fungal interactor
Few tumors in roots in response to Agrobacterium infection

APPENDIX B: Arabidopsis Phenotype Classification System

This appendix describes the phenotype classification system developed for the Arabidopsis phenotype dataset. Phenotype group, class, and subset names and symbols are indicated by a series of indentions, type formatting, and text operators and punctuation (e.g. parentheses, commas, and colons) demonstrated at the beginning of the next page. Subset numbers and descriptions are also included.

Group Name (Symbol)

Class Name (Symbol)

Subset Number, Subset Symbol: Subset name and description

Essential (ESN)

Gametophyte (G)

1, GAM: Gametophyte defective (<2% mutant seeds)
2, GEM: Gametophyte, embryo defective (2-10% mutant seeds)
3, EMG: Embryo, gametophyte defective (>10% mutant seeds)
4, MGD: Miscellaneous gametophyte defective

Embryo-Seed (S)

5, EMB: True embryo defective; No known gametophyte defects
6, MSD: Miscellaneous seed defective

Lethal (L)

7, NHM: No homozygous mutant plants; Cause not determined
8, SRL: Seedling, rosette lethal; Severe seedling defective

Morphological (MRP)

Vegetative (V)

9, GER: Germination: Rate, frequency; seed dormancy
10, NLS: Non-lethal seedling: Cotyledon, hypocotyl
11, PIG: Pigmentation: Plant coloration
12, GRS: Plant growth rate, size
13, ROT: Root: Size, morphology, growth rate
14, LEF: Leaf: Size, morphology, number
15, IST: Inflorescence stem: Length, morphology
16, ARC: Shoot architecture: Branching; phyllotaxy; growth pattern
17, MSL: Miscellaneous shoot, leaf morphology

Reproductive (R)

18, FSM: Floral, silique morphology
19, OVP: Ovule, pollen; sporophytic
20, SRF: Sterility, reduced fertility; sporophytic
21, SSC: Seed, seed coat; maternal sporophytic

Morphological (continued)

Timing (T)

22, FLT: Flowering time
23, SEN: Senescence
24, CDR: Circadian rhythms
25, MTM: Miscellaneous timing; Phase change; vernalization

Cellular and Biochemical (CLB)

Cellular (C)

26, STT: Stomata, trichomes: Distribution, morphology
27, RTH: Root hairs: Distribution, morphology
28, TCM: Tissue, cell morphology: Structure, shape, patterning
29, CUL: Cell ultrastructure: Organelles, chromosomes, cytoskeleton

Biochemical (B)

30, PRA: Product accumulation: Hormones, metabolites, storage products
31, CPR: Cellular, physiological processes

Conditional (CND)

Physical (P)

32, WAT: Water levels, availability
33, TMP: Temperature
34, LIT: Light: Amount, type, duration, direction
35, MEC: Mechanical stimulus: Touch, pressure
36, MPH: Miscellaneous physical conditions

Chemical (H)

37, NUT: Nutrient levels, availability
38, HRM: Exogenous hormones
39, CHS: Chemical stress, toxins, mutagens
40, MCH: Miscellaneous chemicals

Biological (I)

41, PTH: Pathogens, herbivores
42, OBI: Other biological interactors

APPENDIX C: Single Gene Mutant Phenotype Dataset, Phenotype Information

This appendix includes a truncated version of the single gene mutant phenotype dataset. Emphasis was placed on phenotype and mutant information. Included data are locus numbers, gene names, confirmation statuses of gene-to-phenotype associations, phenotype group, class, and subset assignments, mutant phenotype descriptions, and the methods used to identify a disrupted gene responsible for a phenotype. The complete Arabidopsis phenotype dataset is available as a spreadsheet appended to the Plant Physiology publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S2).

Footnotes for the title row of the following table are described below:

[a] Gene responsible for mutant phenotype confirmed (C) or not confirmed (NC) through allelism tests, molecular complementation, or some other approach such as excision of a transposable element or cellular / biochemical analysis consistent with the mutant phenotype.

[b] Refer to Appendix B for explanation of abbreviations.

[c] RV, Reverse genetics; MB, Map-based cloning; TD, T-DNA insertion mutant identified through forward genetics; TN, Transposon insertion mutant identified through forward genetics; OTH, Other approach (e.g. analysis of altered biochemical pathway).

Locus	Gene Symbol	Identity Status[a]	Phenotype Group[b]	Phenotype Class[b]	Phenotype Subsets[b]	Description of Mutant Phenotype	Mutant Identification Method[c]
At1g01030	*NGA3*	C	MRP	R	FSM	Abnormal pistil morphology	RV
At1g01040	*SUS1*	C	ESN	S	EMB, W:FSM, W:OVP, W:SRF	Null: Embryo defective; Globular; Abnormal suspensor; Knockdown 1: Female sterile due to short integuments; Knockdown 2: Increased carpel number	MB; TD
At1g01060	*LHY*	C	MRP	T	CDR, LIT	Short circadian rhythms; Early flowering under short days	OTH
At1g01120	*KCS1*	C	MRP	V	IST, WAT	Thin inflorescence stems; Sensitive to low humidity	TD
At1g01280	*CYP703A2*	C	MRP	R	OVP, SRF	Reduced male fertility: Complete loss of pollen exine layer	RV
At1g01370	*CENH3*	C	ESN	S	EMB	Embryo defective	RV
At1g01460	*PIPK11*	C	CND	H	CHS	Pollen tube growth sensitive to latrunculin B (inhibitor of actin polymerization)	RV
At1g01480	*ACS2*	C	MRP	V	NLS, GRS, IST	Large cotyledons; Long hypocotyl; Slow growth; Tall inflorescence stems	RV
At1g01510	*AN*	C	MRP	V	LEF, FSM	Narrow leaves; Narrow, slightly elongated floral organs; Twisted siliques	MB
At1g01550	*BPS1*	C	ESN	L	SRL, ROT, LEF, MSL, STT, RTH, TCM, TMP	Few radially symmetric organs with very little vascular tissue and no trichomes; Short primary and lateral roots; Root hairs form close to root apex; Phenotype enhanced at low temperature	OTH
At1g01690	*PRD3*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	TD
At1g01860	*PFC1*	C	CND	P	TMP	Chlorosis at low temperature	TD
At1g01950	*ARK2*	C	MRP	V	ROT	Twisted root growth	MB
At1g02050	*LAP6*	C	MRP	R	OVP	Abnormal pollen exine layer	RV
At1g02065	*SPL8*	C	MRP	R	SRF	Reduced fertility	TN; RV
At1g02090	*FUS5*	C	MRP	V	PIG, LIT	Red cotyledons due to anthocyanin accumulation; Abnormal growth in the dark	OTH
At1g02120	*VAD1*	C	MRP	V	MSL, PTH	Chlorotic leaves; Resistant to bacterial infection	TD

At1g02140	*HAP1*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	TD
At1g02205	*CER1*	C	MRP	V	IST, FSM, WAT	Glossy inflorescence stems and siliques; Male sterile in low humidity	TN
At1g02280	*PPI1*	C	MRP	V	PIG	Pale green	TD
At1g02340	*HFR1*	C	CND	P	LIT	Long hypocotyl under far-red light	TD
At1g02560	*CLPP5*	C	ESN	S	EMB	Embryo defective; Globular	RV
At1g02580	*MEA*	C	ESN	S	MSD	Embryo and female gametophyte defective; Incomplete penetrance of endosperm formation without fertilization; 50% defective seeds	TN
At1g02730	*ATCSLD5*	C	MRP	V	GRS, ROT, LEF	Dwarf; Small rosette; Short roots	RV
At1g02780	*EMB2386*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g02860	*NLA*	C	CND	H	NUT	Early senescence under limited nitrogen	MB
At1g02910	*LPA1*	C	MRP	V	PIG, GRS	Pale green leaves; Dwarf	TD
At1g02970	*WEE1*	C	CND	H	CHS	Sensitive to replication-inhibiting drugs	RV
At1g03000	*PEX6*	C	MRP	V	PIG, GRS, HRM	Dwarf; Pale green; Insensitive to IBA	MB
At1g03060	*SPI*	C	MRP	V	NLS, STT, RTH, TCM	Short hypocotyl; Short root hairs; Abnormal trichome and pavement cell morphology	MB
At1g03160	*FZL*	C	MRP	V	PIG, FLT	Pale green leaves; Late flowering	RV
At1g03190	*UVH6*	C	ESN	L	NHM, W:PIG, W:GRS, W:LIT	Null: No homozygous mutant plants recovered; Knockdown: Pale green leaves; Dwarf; Sensitive to UV light	MB
At1g03310	*AtISA2*	C	CLB	B	PRA	Decreased starch levels	MB
At1g03360	*RRP4*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At1g03790	*SOM*	C	CND	P	LIT	Germination insensitive to darkness and far-red light	TD
At1g04010	*PSAT1*	C	MRP	T	SEN	Early leaf senescence; Low sterol ester content in leaves and seeds	RV
At1g04020	*BARD1*	C	MRP	V	GRS, MSL, TCM	Disorganized seedling and rosette growth; Dwarf; Tubular, finger-like structures form instead of leaves; Abnormal SAM organization	RV

At1g04110	*SDD1*	C	CLB	C	STT	Increased stomatal density	MB
At1g04120	*MRP5*	NC	MRP	V	ROT	Short roots; Increased lateral root formation	RV
At1g04220	*KCS2*	C	MRP	V	ROT	Short roots	RV
At1g04240	*SHY2*	C	MRP	V	ROT	Complete loss of root gravitropism	TD
At1g04250	*AXR3*	C	MRP	V	ROT	Complete loss of root gravitropism	MB
At1g04400	*FHA*	C	MRP	T	FLT	Late flowering	OTH
At1g04635	*EMB1687*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g04820	*TOR2*	C	MRP	V	NLS, LEF, ARC, CHS	Short, thick hypocotyl; Helical growth; Right-handed petiole torsions; Sensitive to microtubule-disrupting drugs	MB; RV
At1g04870	*AtPRMT10*	C	MRP	T	FLT	Late flowering	RV
At1g04940	*TIC20*	C	ESN	L	SRL, W:PIG	Null: Seedling lethal; Knockdown: Pale cotyledons; Pale leaves	RNAi
At1g04950	*EMB2781*	C	ESN	G	GEM	Male gametophyte defective; Embryo defective	RV
At1g05180	*AXR1*	C	MRP	V	GRS, ROT, ARC, SRF, RTH, HRM	Dwarf; Increased branching; Abnormal root gravitropism, lateral root formation, and root hair growth; Reduced fertility; Insensitive to auxin	MB
At1g05190	*EMB2394*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g05385	*LPA19*	C	MRP	V	PIG, GRS	Dwarf; Pale green leaves	MB; RV
At1g05470	*CVP2*	C	CLB	C	TCM	Altered vein patterning in cotyledons	MB
At1g05600	*EMB3101*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g05630	*At5PT13*	C	CLB	C	TCM	Altered vein patterning in cotyledons	RV
At1g05750	*PDE247*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At1g05760	*RTM1*	C	CND	I	PTH	Susceptible to tobacco etch virus	MB
At1g05850	*ELP*	C	MRP	V	GRS, ROT, RTH, TCM, LIT	Dwarf; Short roots; Long root hairs with increased density; Abnormal pith cell morphology; Short, thick hypocotyl and roots and exaggerated apical hook in the dark	MB
At1g05990	*RHS1*	C	CLB	C	RTH	Long root hairs	RV
At1g06040	*STO*	C	MRP	V	NLS	Short hypocotyl	RV
At1g06150	*EMB1444*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g06160	*ORA59*	C	CND	I	PTH	Susceptible to *Botrytis cinerea*	RV

At1g06220	*GFA1*	C	ESN	G	EMG	Embryo defective; Male and female gametophyte defective	TN
At1g06230	*GTE4*	C	MRP	V	GER, GRS, ROT, LEF, IST, FSM	Delayed germination and rosette development; Dwarf; Short roots; Abnormal lateral root formation; Small, slightly serrated leaves; Short, thin inflorescence stems; Decreased stamen number	RV
At1g06290	*ACX3*	C	CND	H	HRM	Insensitive to IBA	MB; RV
At1g06400	*ARA2*	C	CND	H	HRM, CHS	Sensitive to auxin and NPA (inhibitor of polar auxin transport)	RV
At1g06490	*CALS7*	C	MRP	V	ROT, IST, SRF	Short roots and inflorescence stems; Reduced fertility	RV
At1g06520	*GPAT1*	C	MRP	R	SRF	Reduced fertility; Pollen abortion (does not segregate in heterozygotes)	RV
At1g06570	*PDS1*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	OTH
At1g06780	*GAUT6*	C	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At1g06950	*TIC110*	C	ESN	S	EMB, S:PIG, S:MSL	Embryo defective; Globular; Heterozygotes: Pale green; Chlorotic	RV
At1g07130	*STN1*	C	MRP	V	LEF, IST, ARC, SRF	Fasciated stems and inflorescences; Increased branching; Small leaves; Abnormal floral phyllotaxy; Reduced fertility; Second generation: Very low germination rate and early developmental arrest due to short and eroding telomeres	RV
At1g07320	*EMB2784*	NC	ESN	S	EMB	Embryo defective; Globular	RV
At1g07360	*MAC5A*	C	MRP	V	ROT, LEF, SRF, FLT	Twisted, slightly serrated leaves; Long petioles; Short roots; Reduced fertility; Early flowering	RV
At1g07530	*SCL14*	C	CND	H	HRM, CHS	Sensitive to INA (functional analog of SA) and TIBA (inhibitor of auxin transport)	RV
At1g07630	*PLL5*	C	MRP	V	LEF	Abnormal leaf morphology	RV
At1g07890	*APX1*	NC	MRP	V	GRS, FLT, WAT, TMP	Slow growth; Late flowering; Sensitive to a combination of drought and high temperature	RV
At1g07930	*eEF1A2*	NC	CND	P	MPH	Short roots under vertical growth	RV

At1g08030	*TPST*	C	MRP	V	NLS, PIG, ROT, LEF, IST, SEN, TCM	Small cotyledons; Small, pale green leaves; Short roots and inflorescence stems; Early senescence; Abnormal vein morphology; Disorganized RAM	RV
At1g08060	*MOM*	C	CLB	B	CPR	Decreased DNA methylation	TD
At1g08090	*NRT2*	C	CLB	B	CPR	Reduced nitrate uptake	TD
At1g08130	*LIG1*	NC	ESN	S	EMB, W:GRS, W:ROT, W:LEF	Null: Embryo defective; Knockdown: Dwarf; Short roots; Small leaves	RV
At1g08190	*AtVPS41*	C	ESN	L	NHM	No homozygous mutant plants recovered	MB; RV
At1g08260	*EMB2284*	C	ESN	S	EMB, W:GRS, W:LEF, W:FSM, W:FLT	Null: Embryo defective; Globular; Knockdown: Dwarf; Small, narrow leaves; Small flowers; Early flowering independent of photoperiod	TD
At1g08370	*DCP1*	C	ESN	L	SRL	Seedling lethal	RV
At1g08430	*ALMT1*	C	CND	H	MCH	Sensitive to aluminum	RV
At1g08450	*CRT3*	NC	CND	I	PTH	Resistant to elf18 (bacterial defense inducer)	RV
At1g08510	*FATB*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g08520	*PDE166*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At1g08540	*ABC1*	C	MRP	V	PIG	Pale green	TD
At1g08550	*NPQ1*	C	CLB	B	CPR	Abnormal quenching of chlorophyll fluorescence	MB
At1g08560	*KN*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At1g08630	*THA1*	C	CLB	B	PRA	Elevated threonine levels in seeds	RV
At1g08660	*MGP2*	C	ESN	G	GAM	Complete male gametophyte defective	TN
At1g08720	*EDR1*	C	CND	I	PTH	Resistant to powdery mildew	MB
At1g08810	*MYB60*	C	CLB	C	STT, WAT	Reduced stomatal width; Resistant to drought	RV
At1g08840	*EMB2411*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g09090	*AtrbohB*	C	MRP	V	GER	Complete loss of seed after-ripening	TD; RV
At1g09100	*RPT5B*	C	CND	H	NUT	Sensitive to limited glucose	RV
At1g09210	*CRT1b*	C	MRP	V	NLS, CHS	Small seedlings; Resistant to tunicamycin	RV
At1g09270	*IMPA-4*	C	CND	I	OBI	Resistant to *Agrobacterium* transformation	RV

At1g09530	*PIF3*	C	MRP	V	NLS, LIT	Short hypocotyl; Sensitive to red light; Dwarf, open cotyledons and no apical hook in the dark	RV
At1g09540	*MYB61*	C	MRP	R	SSC	Reduced mucilage extrusion from seeds	TN
At1g09570	*FHY2*	C	CND	P	LIT	Long hypocotyl under far-red light	TD
At1g09700	*HYL1*	C	MRP	V	NLS, GRS, ROT, LEF, ARC, FSM, SRF, FLT, HRM	Short hypocotyl; Dwarf; Narrow, upward-bending leaves; Increased branching; Reduced root gravitropism; Small flowers; Twisted siliques; Late flowering; Reduced fertility due to short filaments; Sensitive to ABA; Insensitive to cytokinin	TN
At1g09770	*AtCDC5*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At1g09940	*HEMA2*	C	CLB	B	PRA	Decreased heme levels in roots; No other phenotypes detected	RV
At1g09970	*RLK7*	C	MRP	V	GER, CHS	Delayed germination; Sensitive to hydrogen peroxide	RV
At1g10130	*ECA3*	C	CND	H	NUT	Abnormal root growth in response to calcium and manganese	RV
At1g10170	*AtNFXL1*	C	CND	I	PTH	Susceptible to fungal mycotoxin; Altered defense response	RV
At1g10270	*GRP23*	C	ESN	S	EMB	Embryo defective; Preglobular	TN
At1g10310		C	CLB	B	PRA	Abnormal fatty acid levels	RV
At1g10370	*AtGSTU17*	C	CND	P	LIT, HRM	Reduced seedling biomass and fewer lateral roots on exogenous auxin; Long hypocotyl under low fluences of far-red light; Insensitive to ABA	RV
At1g10470	*ARR4*	NC	CND	P	LIT	Slightly longer petioles under short days; Short hypocotyl under red light	RV
At1g10510	*EMB2004*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g10760	*SEX1*	C	CLB	B	PRA	Elevated starch in leaves after prolonged darkness	MB
At1g10840	*eIF3h*	C	ESN	L	SRL, NLS, ROT, LEF, IST, ARC, FSM, RTH	High penetrance of rosette lethality; Abnormal cotyledon number and morphology; Warped leaves; Short primary root; Low penetrance of pin-formed inflorescences; Increased branching; Abnormal silique morphology; Few root hairs	RV
At1g10910	*EMB3103*	C	ESN	S	EMB	Embryo defective; Globular	RV

At1g10920	*LOV1*	C	CND	I	CHS, PTH	Resistant to victorin (fungal toxin); Susceptible to disease	MB
At1g10930	*RECQ4A*	C	CND	H	CPR, CHS	Sensitive to DNA damaging agents; Increased homologous recombination frequency	RV
At1g11000	*MLO4*	C	CND	P	MEC	Tight spiral-like root growth in response to touch	RV
At1g11130	*SUB*	C	MRP	V	IST, OVP	Short, twisted inflorescence stems; Abnormal ovules	MB
At1g11310	*MLO2*	C	CND	I	PTH	Resistant to powdery mildew	RV
At1g11350	*CBRLK1*	C	CND	I	PTH	Resistant to bacterial infection	RV
At1g11680	*EMB1738*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g11720	*AtSS3*	C	CLB	B	PRA	Elevated starch levels; Abnormal starch composition; No other phenotypes detected	RV
At1g11755	*LEW1*	C	ESN	L	NHM, W:GRS, W:MSL	Null: No homozygous mutant plants recovered; Knockdown: Dwarf; Wilted leaves	MB
At1g11870	*OVA7*	NC	ESN	G	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	RV
At1g11890	*SEC22*	C	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	RV
At1g12040	*LRX1*	C	CLB	C	RTH	Root hair defective	RV
At1g12110	*CHL1*	C	CLB	B	CPR, CHS	Reduced nitrate uptake; Resistant to chlorate	TD
At1g12220	*RPS5*	C	CND	I	PTH	Resistant to *Pseudomonas syringae*	MB
At1g12240	*VAC-INV*	C	MRP	V	ROT	Short roots	RV
At1g12260	*EMB2749*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g12360	*KEU*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At1g12370	*UVR2*	C	CND	P	LIT	Sensitive to UV-B light	OTH
At1g12410	*CLPR2*	C	ESN	S	EMB, W:PIG, W:GRS, W:FLT	Null: Embryo Defective; Cotyledon; Knockdown: Pale green; Dwarf; Late flowering	RV
At1g12480	*OZS1*	C	CND	H	CHS	Sensitive to ozone	TD
At1g12550	*HPR3*	C	CLB	B	PRA	Slightly elevated levels of photorespiratory intermediates; No other phenotypes detected	RV
At1g12770	*EMB1586*	C	ESN	S	EMB	Embryo defective; Globular	TD

At1g12840	*DET3*	C	CND	P	LIT, HRM	Abnormal seedling growth in the dark; Insensitive to brassinosteroids	MB
At1g12920	*eRF1-2*	C	CND	H	CHS	Resistant to paclobutrazol (inhibitor of GA synthesis)	RV
At1g12950	*RHS2*	C	CLB	C	RTH	Short root hairs	RV
At1g12980	*DRN*	C	MRP	V	NLS, TCM	Incomplete penetrance of cotyledon defects: Fused and cup-shaped cotyledons, increased cotyledon number; Abnormal embryonic cell patterning	RV
At1g13220	*LINC2*	C	CLB	C	CUL	Small nuclei; No other phenotypes detected	RV
At1g13230	*PII2*	C	CND	I	OBI	Insensitive to growth stimulation of beneficial fungal interactor	MB; RV
At1g13290	*DOT5*	NC	MRP	V	NLS, GRS, TCM	Delayed leaf growth; Abnormal divergence angle between cotyledons; Abnormal vein patterning in leaves	OTH
At1g13330	*AHP2*	C	MRP	R	SRF	Complete sterility due to defects in meiosis	TD
At1g13870	*DRL1*	C	MRP	V	ROT, LEF	Abnormal root and leaf growth	TN
At1g13930		C	CND	H	CHS	Sensitive to salt	RV
At1g13980	*EMB30*	C	ESN	S	EMB, SRL	Embryo and seedling defective	TD
At1g14000	*VIK*	C	CLB	C	TCM	Abnormal vein patterning	RV
At1g14150	*PQL1*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At1g14280	*PKS2*	NC	CND	P	LIT	Short hypocotyl and expanded cotyledon under hourly far red pulses	RV
At1g14320	*SAC52*	NC	ESN	G	GAM	Complete female gametophyte defective	RV
At1g14350	*FLP*	C	CLB	C	STT	Abnormal stomatal patterning	MB
At1g14400	*UBC1*	C	MRP	V	LEF	Few rosette leaves	RV
At1g14610	*TWN2*	C	ESN	G	EMG	Embryo defective; Suspensor-derived twin embryos; Female gametophyte defective	TD
At1g14660	*AtNHX8*	C	CND	H	MCH	Sensitive to lithium	RV
At1g14720	*XTH28*	C	MRP	R	FSM, SRF	Abnormal stamen morphology; Reduced fertility	RV
At1g14750	*SDS*	C	MRP	R	SRF	Severely reduced fertility due to defects in meiosis	TN
At1g14830	*ADL1C*	C	ESN	G	GAM	Complete male gametophyte defective	RV

At1g14870	*PCR2*	C	CND	H	NUT	Sensitive to limited and elevated zinc	RV
At1g14920	*GAI*	C	CND	H	CHS	Resistant to paclobutrazol (inhibitor of GA synthesis)	TD
At1g15020	*QSO2*	C	CND	H	CHS, MCH	Sensitive to salt, lithium, and, polyamines	RV
At1g15100	*RHA2a*	C	CND	H	HRM	Insensitive to ABA	RV
At1g15220	*AtCCMH*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g15510	*ECB2*	C	ESN	L	SRL, PIG, CUL	Seedling lethal; Albino; Abnormal chloroplast morphology	RV
At1g15520	*ABCG40*	C	CND	P	WAT, HRM	Sensitive to drought; Slow stomatal closure in response to ABA	RV
At1g15550	*GA4*	C	MRP	V	GRS, ROT, LEF, FLT	Semi-dwarf; Slightly smaller rosette; Slightly shorter roots; Late flowering	TD
At1g15570	*CYCA2;3*	C	CLB	C	STT, CUL	Abnormal trichome branching; Increased ploidy levels; No other phenotypes detected	RV
At1g15690	*AVP1*	C	MRP	V	NLS, ROT, LEF, FSM, SRF, FLT, TCM	Abnormal cotyledon morphology; Small rosette; Thick leaves with uneven margins; Thick roots; Collapsed root tip; High penetrance of complete loss of flowering; Complete loss of flower formation; Sterile; Disorganized vascular patterning	RV
At1g15820	*LHCB6*	C	MRP	V	GRS	Slightly slower growth; Reduced fresh weight	RV
At1g15950	*IRX4*	C	MRP	V	PIG, GRS, LEF, IST, TCM, TMP	Slow growth; Inflorescence stems cannot maintain an upright stance; Altered leaf morphology; Dark green; Collapsed xylem; Reduced fertility at high temperature	MB
At1g15960	*NRAMP6*	C	CND	H	MCH	Resistant to cadium	RV
At1g15980	*NDH48*	NC	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence; No other phenotypes mentioned	RV
At1g16060	*ADAP*	NC	MRP	V	GER, GRS, WAT, HRM, CHS	Early germination: Increased growth rate; Sensitive to drought; Insensitive to ABA; Resistant to salt stress	RV
At1g16150	*WAKL4*	C	MRP	V	ROT, NUT	Short roots; Sensitive to sodium, potassium, copper, and zinc; Resistant to nickel	RV

At1g16280	*SWA3*	C	ESN	G	GAM	Female gametophyte defective; Rare embryo defective (inferred)	TN
At1g16410	*SPS*	C	MRP	V	LEF, ARC, TCM	Increased branching; Crinkled leaves; Abnormal vascularization	TN
At1g16540	*ABA3*	C	MRP	V	GER, MSL, TMP, CHS	Reduced seed dormancy; Wilty; Low ABA levels; Altered response to low temperature and osmotic stress	MB
At1g16590	*REV7*	C	CND	P	LIT, CHS	Sensitive to UV-B light and cisplatin	RV
At1g16610	*SR45*	C	MRP	V	GRS, ROT, LEF, ARC, FSM, FLT, NUT	Semi-dwarf; Increased branching; Abnormal leaf and flower morphology; Slow root growth; Late flowering; Abnormal seedling growth in response to glucose	RV
At1g16720	*HCF173*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose; With exogenous sucrose: Absence of flowers	MB
At1g16970	*KU70*	C	CND	P	MPH, CHS	Sensitive to ionizing radiation and chemical mutagens	RV
At1g17110	*UBP15*	C	MRP	V	GRS, ROT, LEF, IST, FSM, SRF, FLT	Dwarf; Few, narrow, serrated rosette leaves; Short roots; Short, thin inflorescence stems; Small flowers; Reduced fertility; Early flowering	RV
At1g17140	*ICR1*	C	MRP	V	ROT	Short roots	RV; RNAi
At1g17220	*FUG1*	NC	ESN	S	EMB, W:NLS, W:PIG	Null: Embryo defective; Knockdown: Variegated seedlings	MB; RV
At1g17290	*AlaAT1*	C	CND	H	NUT	Elevated alanine levels in roots under hypoxia; Reduced growth with alanine as nitrogen source	RV
At1g17560	*HLL*	C	MRP	R	OVP, SRF	Abnormal integuments; Female sterile	MB
At1g17690	*NOF1*	C	ESN	G	GAM, W:EMB	Null: Complete female gametophyte defective; Knockdown: Embryo defective	TD; RV
At1g17840	*DSO4*	C	MRP	V	LEF, IST, ARC, TCM	Misshapen, torn rosette leaves; Short, thin inflorescence stems; Increased branching; Abnormal leaf venation; Abnormal cuticle	RNAi; RV
At1g17980	*PAPS1*	C	ESN	L	NHM	No homozygous mutant plants recovered	RV

At1g18080	*RACK1A*	C	MRP	V	NLS, LEF, FLT	Downward-bending cotyledons; Small, narrow, downward-bending rosette leaves; Late flowering	RV
At1g18100	*MFT*	C	CND	H	HRM	Sensitive to ABA	RV
At1g18370	*HIK*	C	ESN	L	SRL	Seedling lethal	MB
At1g18450	*ARP4*	C	MRP	V	W:NLS, W:GRS, W:SRF	Knockdown: Small seedlings; Dwarf; Completely sterile	RNAi
At1g18500	*IPMS1*	NC	MRP	V	GRS, LEF, MSL	Slow growth; Undulated, chlorotic leaves	RV
At1g18570	*MYB51*	C	CLB	B	PRA	Low glucosinolate levels	RV
At1g18580	*GAUT11*	C	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At1g18730	*NDF6*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At1g18890	*CPK10*	C	CND	P	WAT	Sensitive to drought	RV
At1g19080	*TTN10*	NC	ESN	S	EMB	Embryo defective; Preglobular	TD
At1g19220	*ARF19*	C	CND	H	S:HRM, MCH	Insensitive to ethylene and IAA; Resistant to 2,4-D and sirtinol (activator of auxin signaling); Heterozygotes: Intermediate 2,4-D resistance phenotype	MB
At1g19250	*FMO1*	NC	CND	I	PTH	Complete loss of systemic acquired resistance	RV
At1g19270	*DA1*	C	MRP	V	GRS, LEF, IST, FSM, SSC, SEN	Thick inflorescence stems; Increased biomass; Large, rounded leaves; Large flowers and seeds; Increased petal and carpel number; Large, slightly flattened siliques; Delayed senescence	MB
At1g19300	*PARVUS*	C	MRP	V	LEF, IST, MEC	Small rosette; Short, fragile inflorescence stems	RV
At1g19520	*NFD5*	NC	ESN	G	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	TD
At1g19750	*CSAat1B*	C	CND	H	CHS	Sensitive to genotoxic stress	RV
At1g19800	*TGD1*	C	ESN	S	EMB	Embryo defective; Cotyledon	OTH
At1g19850	*MP*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At1g20020	*FNR2*	NC	CND	P	LIT	Low fresh weight and pale green under short days	RV

At1g20050	*HYD1*	C	ESN	S	EMB, SRL	Embryo and seedling defective	TD
At1g20090	*ROP2*	C	CLB	C	STT	Increased stomatal width and opening rate	RV
At1g20110	*PDE330*	NC	MRP	V	PIG	Pigment defective embryo	RV
At1g20200	*EMB2719*	NC	ESN	G	GEM	Male gametophyte defective; Embryo defective	TD
At1g20330	*SMT2*	C	MRP	V	GRS, LEF, ARC, FSM, SRF, FLT, SEN, TCM	Dwarf; Increased branching; Small leaves; Scalloped petals; Severely serrated sepal and petal margins; Reduced fertility; Late flowering; Delayed senescence; Abnormal cotyledon venation	MB
At1g20450	*ERD10*	NC	MRP	V	GER, SSC, WAT, TMP	Low germination rate; Abnormal seed shape; Sensitive to low temperature and drought	RV
At1g20780	*SAUL1*	C	MRP	T	SEN	Early senescence	RV
At1g20840	*TMT1*	C	CLB	B	PRA, TMP	Slightly low fructose and glucose levels; Complete loss of glucose and fructose accumulation at low temperature; No other phenotypes detected	RV
At1g20960	*EMB1507*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g20980	*SPL14*	C	MRP	V	LEF, FLT	Elongated petioles; Serrated leaf margins; Late flowering	TD
At1g21270	*WAK2*	C	ESN	L	SRL, NLS, GRS, ROT, LEF	Incomplete penetrance of seedling lethality; Slow growth; Small seedlings; Short roots	RV
At1g21310	*RSH*	C	ESN	S	EMB, SRL	Embryo and seedling defective	TN
At1g21390	*EMB2170*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g21600	*PTAC6*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino	RV
At1g21650	*SECA2*	C	ESN	S	EMB	Embryo defective	RV
At1g21690	*EMB1968*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At1g21700	*AtSWI3C*	C	MRP	V	GRS, ROT, LEF, ARC, FSM, SRF, FLT	Semi-dwarf; Slow growth; Abnormal rosette growth; Downward-bending leaves; Very short roots; Decreased branching; Few cauline leaves; Abnormal floral morphology; Severely reduced fertility; Slightly early flowering	TD
At1g21760	*FBP7*	C	CND	P	TMP	Impaired translation at high or low temperature	RV
At1g21840	*UREF*	C	CND	H	NUT	Unable to use urea as primary nitrogen source	RV

At1g21970	*LEC1*	C	ESN	S	EMB	Embryo defective; Leafy cotyledons	TD
At1g22090	*EMB2204*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g22260	*ZYP1a*	C	MRP	R	SRF	Reduced fertility	RV
At1g22270	*SMO2*	C	MRP	V	GRS, ROT	Dwarf; Short roots	TD
At1g22275	*ZYP1b*	C	MRP	R	SRF	Reduced fertility	RV
At1g22310	*MBD8*	C	MRP	T	FLT	Early flowering independent of photoperiod	TD
At1g22400	*UGT85A1*	NC	CND	I	PTH	Susceptible to bacterial infection	RV
At1g22620	*AtSAC1*	C	MRP	V	NLS, GRS, ROT, IST, STT, TCM	Short roots; Short hypocotyl; Semi-dwarf; Crooked inflorescence stems; Abnormal trichome morphology; Abnormal pavement cell morphology	MB
At1g22700	*PYG7*	C	ESN	L	SRL, PIG, GRS, LEF	Seedling lethal on soil; Pale green seedlings; Thin leaves; Slow growth	MB; RV
At1g22710	*SUC2*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose	RV
At1g22770	*GI*	C	MRP	T	FLT	Late flowering	TD
At1g22780	*PFL*	C	MRP	V	GRS, ROT, LEF	Reduced fresh weight; Short roots; Pointed first true leaves	TD
At1g22920	*CSN5A*	C	MRP	V	PIG, GRS, LEF, ARC, FSM, STT, LIT, HRM	Purple cotyledons; Small, curled, pale green rosette leaves; Dwarf; Increased branching; Small flowers; Very few trichomes; Short hypocotyl in the dark; Altered response to jasmonic acid, light, and auxin	RV
At1g22940	*TH1*	NC	ESN	L	SRL	Seedling lethal without exogenous thiamine	OTH
At1g23010	*LPR1*	C	CND	H	NUT	Root growth resistant to limited phosphate	RV
At1g23090	*SULTR3;3*	C	MRP	V	LEF, FLT	Small rosette leaves; Early flowering; Slightly elevated sulfate content in seeds	RV
At1g23310	*GGT1*	C	MRP	V	PIG, GRS, TMP	Pale green; Slow growth; Severe leaf chlorosis at low temperature	MB; RV
At1g23400	*AtCAF2*	C	ESN	S	EMB; (W:SRL, W:PIG)	Null: Embryo defective; Transition; Knockdown: Seedling lethal; Pigment defective embryo	RV
At1g23420	*INO*	C	MRP	R	OVP	Abnormal integuments	MB
At1g24180	*IAR4*	C	MRP	V	ROT, RTH, HRM	Short primary root; Few, short root hairs; Insensitive to IAA-amino acid conjugates	MB

At1g24340	*EMB2421*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g24450	*NFD2*	NC	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	TD
At1g24490	*ALB4*	C	MRP	V	GRS, FLT, CUL	Slow growth; Early flowering; Arrested chloroplast division	RV
At1g24590	*DRNL*	C	MRP	V	NLS, ARC, FSM	Incomplete penetrance of fused cotyledons; Abnormal leaf phyllotaxy; Stamens frequently converted to a filamentous structure; Short, crinkled petals	MB; TN
At1g24706	*EMB2793*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g25350	*OVA9*	NC	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At1g25490	*RCN1*	C	MRP	V	NLS, ROT, LIT	Short hypocotyl and roots; Slightly reduced root curling; Abnormal apical hook in the dark	TD
At1g25540	*PFT1*	C	CND	I	PTH	Susceptible to necrotrophic fungi; Resistant to hemibiotrophic fungi in roots	RV
At1g26110	*DCP5*	C	ESN	L	SRL, W:PIG, W:LEF, W:FLT, W:TCM, W:MEC	Null: Seedling lethal; Knockdown: Pale green cotyledons; Serrated, pointed leaves; Slightly late flowering; Disorganized cotyledon venation; Fragile cotyledons	RV
At1g26630	*FBR12*	C	MRP	V	GRS, ROT, LEF, FSM, SRF	Dwarf; Short roots; Few, small rosette and cauline leaves; Few flowers; Abnormal flower morphology; Completely sterile	TD
At1g26670	*VTI1b*	NC	CND	H	NUT	Sensitive to nitrogen and carbon starvation	RV
At1g26780	*LOF1*	C	MRP	V	ARC, MSL	Downward-pointing auxiliary inflorescence stems; Cauline leaves fused to inflorescences; Complete loss of accessory shoot formation	RV
At1g26910	*RPL10B*	C	MRP	V	GRS, ROT, LEF	Dwarf; Abnormal leaf morphology; Short roots	RV
At1g27080	*NRT1.6*	C	MRP	R	SRF	Reduced fertility	RV
At1g27320	*AHK3*	C	CND	H	NUT, HRM	Insensitive to cytokinin; Sensitive to sucrose	MB
At1g27360	*SPL11*	C	MRP	V	LEF	Wide cauline leaves	RV

At1g27370	*SPL10*	C	MRP	V	LEF, STT	Wide cauline leaves; Increased trichome number on sepals	RV
At1g27390	*TOM20-2*	C	MRP	T	FLT	Late flowering	RV
At1g27440	*IRX10*	C	CLB	C	TCM	Slightly abnormal xylem	RV
At1g27450	*APT1*	C	MRP	R	SRF, CHS	Male sterile; Resistant to 2,6-diaminopurine (toxic analog of adenine)	OTH
At1g27760	*SAT32*	C	MRP	V	ROT, SRF	Long roots; Reduced fertility	RV
At1g27840	*CSAat1A*	C	CND	P	LIT	Sensitive to UV-B light	TD; RV
At1g27950	*LTPG*	C	CLB	B	PRA	Low cuticular wax levels; Abnormal cuticular wax composition	RV
At1g28300	*LEC2*	C	ESN	S	EMB	Embryo defective; Leafy cotyledons	MB
At1g28320	*DEG15*	C	CND	H	CHS	Resistant to 2,4-DB	RV
At1g28380	*NSL1*	C	MRP	V	GRS, MSL	Dwarf; Necrotic lesions on rosette and cauline leaves	TN
At1g28490	*OSM1*	C	MRP	V	MSL, CHS	Wilty; Sensitive to osmotic stress	TD
At1g28560	*SRD2*	C	MRP	V	ROT, TMP	Few lateral roots; Sensitive to high temperature	MB
At1g29260	*PEX7*	C	MRP	V	ROT, HRM, CHS	Few lateral roots; Insensitive to IBA; Resistant to 2,4-DB	RV
At1g29690	*CAD1*	C	MRP	V	GRS, MSL, SRF, SEN	Dwarf; Necrotic lesions on leaves; Sterile; Early leaf senescence	RV
At1g29900	*VEN3*	C	MRP	V	PIG, LEF	Pale green leaves; Small, reticulated rosette leaves; Heterozygotes: Intermediate phenotype	MB
At1g29940	*NRPA2*	C	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At1g29990	*PFD6*	C	CND	P	LIT, CHS	Short hypocotyl in the dark; Sensitive to oryzalin (microtubule-disrupting herbicide)	MB; RV
At1g30010	*CSS1*	C	MRP	V	GRS, CHS	Slow growth; Resistant to DCB (inhibitor of cellulose synthesis)	MB; RV
At1g30270	*CIPK23*	C	CND	P	WAT	Resistant to drought	RV
At1g30330	*ARF6*	C	MRP	R	IST, FSM, SRF, LIT	Short petals and stamens; Reduced fertility; Slightly shorter primary inflorescence stem; Short hypocotyl in the dark	RV
At1g30400	*MRP1*	C	CND	H	CHS	Sensitive to methotrexate	RV

At1g30450	*CCC1*	C	MRP	V	ROT, LEF, IST, ARC, SRF	Short roots and inflorescence stems; Increased branching; Slightly smaller rosette; Small cauline leaves; Reduced fertility	RV
At1g30520	*AAE14*	C	ESN	L	SRL	Seedling lethal	RV
At1g30610	*EMB2279*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g30620	*MUR4*	C	CLB	B	PRA, NUT	Abnormal starch, anthocyanin, and chlorophyll levels; Sensitive to sugar	MB; RV
At1g30825	*DIS2*	C	MRP	V	GRS, STT, LIT	Slightly reduced fresh weight; Abnormal trichomes; Short hypocotyl in the dark	MB; RV
At1g30950	*UFO*	C	MRP	R	FSM	Homeotic floral transformations	MB
At1g30970	*SUF4*	C	MRP	T	FLT	Early flowering	MB; RV
At1g31140	*GOA*	NC	MRP	R	FSM	Bent siliques	RNAi
At1g31170	*SRX*	NC	CND	H	CHS	Sensitive to oxidative stress	RV
At1g31180	*IPMDH1*	C	CLB	B	PRA	Elevated free leucine levels; Abnormal glucosinolate composition	RV
At1g31470	*NFD4*	NC	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	TD
At1g31480	*SGR2*	C	MRP	V	NLS, ARC	Abnormal hypocotyl and inflorescence stem gravitropism	MB
At1g31800	*CYP97A3*	C	CLB	B	PRA	Abnormal carotenoid levels	RV
At1g31810	*AFH14*	C	MRP	R	OVP	Decreased pollen number due to defects in meiosis	RV
At1g31817	*NFD3*	NC	ESN	G	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	TD
At1g31860	*HISN2*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At1g31880	*BRX*	C	MRP	V	ROT, HRM	Short roots; Sensitive to ABA	TD
At1g32130	*IWS1*	C	MRP	V	GRS	Semi-dwarf	RV
At1g32200	*ATS1*	C	ESN	L	W:SRL, W:GRS, W:SRF	Strong knockdown: Rosette lethal; Weak knockdown: Dwarf; Reduced fertility	RV

At1g32230	*RCD1*	C	MRP	V	GRS, ROT, LEF, FSM, FLT, LIT, CHS	Abnormal root architecture; Semi-dwarf; Malformed leaves; Small petals; Early flowering; Resistant to UV-B light; Sensitive to ozone	RV
At1g32450	*NRT1.5*	C	CLB	B	CPR	Reduced nitrate transport from root to shoot	RV
At1g32490	*EMB2733*	NC	ESN	S	EMB, W: GRS, W:LEF, W:FLT	Null: Embryo defective; Globular; Knockdown: Dwarf; Early flowering, Abnormal leaf morphology	TD
At1g32990	*PRPL11*	C	MRP	V	PIG, GRS	Pale green; Slow growth	TD
At1g33240	*GTL1*	C	CLB	C	STT	Large trichomes	RV
At1g33520	*MOS2*	C	CND	I	PTH	Susceptible to avirulent bacteria	MB; RV
At1g34120	*IP5PI*	C	CND	P	LIT, HRM	Long hypocotyl in the dark; Sensitive to ABA	RV
At1g34245	*EPF2*	C	CLB	C	STT, TCM	Increased stomatal and pavement cell density	RV
At1g34370	*STOP1*	C	CND	H	CHS, MCH	Root growth sensitive to low pH and aluminum	MB; RV
At1g34430	*EMB3003*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At1g34550	*EMB2756*	NC	ESN	S	EMB	Embryo defective; Transition	TD
At1g34790	*TT1*	C	MRP	R	PIG, SSC	Yellow seed coat	RV
At1g35580	*CINV1*	C	MRP	V	PIG, ROT	Short roots; Pale green leaves	RV
At1g35670	*AtCDPK2*	C	CND	P	WAT, HRM, CHS	Sensitive to drought and salt; Insensitive to ABA	RV
At1g35720	*AnnAt1*	C	CND	P	WAT	Sensitive to drought	RV
At1g36160	*ACC1*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	MB
At1g37130	*NIA2*	C	CND	H	CHS	Resistant to chlorate	MB
At1g42540	*GLR3.3*	C	MRP	V	ROT	Slightly reduced root gravitropism	RV
At1g42550	*PMI1*	C	CLB	C	CUL	Abnormal chloroplast movement under a variety of light fluence rates	MB; RV
At1g43170	*EMB2207*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g43620	*UGT80B1*	C	MRP	R	PIG, SSC	Pale seed coat; Small seeds	RV
At1g43700	*SUE3*	C	CND	H	NUT, CHS, MCH	Resistant to limited sulfur, cadmium, and oxidative stress	TD; RV
At1g43710	*EMB1075*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD

At1g43850	*SEU*	C	MRP	V	GRS, LEF, ARC, FSM, OVP	Dwarf; Narrow leaves; Increased branching; Homeotic floral transformations; Incomplete penetrance of abnormal integuments	MB
At1g44446	*CH1*	C	MRP	V	PIG	Pale yellow-green plants	OTH
At1g44575	*NPQ4*	C	CLB	B	CPR	Excess absorbed light energy cannot be dissipated; No other phenotypes mentioned	MB
At1g44900	*MCM2*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At1g45145	*ATTRX5*	C	CND	I	CHS, PTH	Resistant to victorin (fungal toxin)	MB
At1g46480	*WOX4*	NC	CND	H	MCH	Xylem development sensitive to TDIF (protein signaling molecule)	RV
At1g46768	*RAP2.1*	C	CND	P	WAT, TMP	Resistant to drought and low temperature	RV
At1g47720	*OSB1*	C	MRP	V	PIG, GRS, ROT, LEF, FSM, SRF	Dwarf; Short roots; Variegated leaves; Abnormal leaf and flower morphology; Reduced fertility	RV
At1g48050	*KU80*	C	CND	I	OBI	Resistant to *Agrobacterium* transformation	UNK
At1g48175	*EMB2191*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At1g48350	*EMB3105*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At1g48380	*RHL1*	C	CLB	C	RTH	Complete loss of root hairs on primary root	TD
At1g48410	*AGO1*	C	MRP	V	LEF, ARC	Altered leaf morphology; Decreased branching	TD
At1g48600	*PMEAMT*	NC	CLB	B	PRA	Abnormal phosphatidylmethylethanolamine levels; No other phenotypes detected	RV
At1g48850	*EMB1144*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At1g48920	*PARL1*	C	MRP	V	NLS, GRS, ROT, LEF, ARC, SRF, TCM	Narrow, slightly smaller cotyledons and leaves; Short roots; Semi-dwarf; Increased branching; Reduced fertility; Abnormal cotyledon, leaf, sepal, and petal venation	MB; RV
At1g49040	*SCD1*	C	MRP	V	GRS, ROT, LEF, FSM, SRF, STT, RTH, TCM	Dwarf; Small rosette; Short roots; Flower bud development arrests; Sterile; Abnormal stomata, root hair, and trichome development; Altered leaf pavement cell shape	UNK
At1g49400	*EMB1129*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At1g49430	*LACS2*	C	MRP	V	GRS, LEF	Dwarf; Few, small, wrinkled leaves	RV
At1g49510	*EMB1273*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD

At1g49540	*ELP2*	C	CND	H	HRM	Root growth sensitive to ABA	MB
At1g49720	*ABF1*	NC	CND	P	TMP	Sensitive to freezing when not acclimated	UNK
At1g49770	*RGE1*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g49820	*AtMTK*	C	CND	H	NUT	Sensitive to sulfur starvation	RV
At1g49880	*EMB3106*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At1g49970	*ClpR1*	C	MRP	V	GRS, MSL, CUL	Dwarf; Slow growth; Necrotic leaves; Abnormal chloroplast morphology	MB; RV
At1g50030	*TOR*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At1g50240	*FU*	C	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	MB; RV
At1g50320	*Trxx*	NC	MRP	V	LEF	Large rosette leaves	RV
At1g50430	*DWF5*	C	MRP	V	GRS	Dwarf; Low brassinosteroid levels	OTH
At1g50460	*HKL1*	C	CND	P	LIT	Dwarf under short days	RV
At1g50500	*HIT1*	C	ESN	G	EMG, W:TMP, W:CHS	Null: Male gametophyte defective; Embryo defective (inferred); Knockdown: Sensitive to high temperature and osmotic stress	MB; RV
At1g50900	*GDC1*	C	ESN	L	SRL	Seedling lethal	TD
At1g51190	*PLT2*	C	MRP	V	ROT, TCM	Slightly slower root growth; Increased columella cell density; Slightly reduced root meristem cell number	RV
At1g51450	*TRAUCO*	C	ESN	S	EMB	Embryo defective; Globular	RV
At1g51500	*CER5*	C	MRP	V	PIG, IST, CUL	Glossy, bright green inflorescence stems; Cytoplasm protrudes into vacuoles	MB; RV
At1g51760	*IAR3*	C	CND	H	HRM	Insensitive to IAA-Ala	MB
At1g51965	*ABO5*	C	CND	H	HRM	Seedling and root growth sensitive to ABA	TD
At1g52150	*ICU4*	C	CLB	C	TCM	Early shoot meristem is large; Slightly abnormal vascular development; No other phenotypes detected	MB; RV
At1g52230	*PSAH2*	NC	MRP	T	FLT	Early flowering	RV
At1g52240	*PIRF1*	NC	CND	P	LIT	Long roots in the dark	RV
At1g52340	*ABA2*	C	MRP	V	GER, MSL, CHS	Reduced seed dormancy; Severe wilting; Low ABA levels; Resistant to salt	MB

At1g52400	*BGLU18*	C	CND	P	MEC	Complete loss of wound-induced ER body formation	RV
At1g52760	*lysoPL2*	C	CND	H	NUT, CHS	Sensitive to zinc and hydrogen peroxide	RV
At1g52920	*GCR2*	C	CLB	C	STT, MPH	Large stomatal width; Freshly harvested seeds germinate well	RV
At1g53500	*MUM4*	C	MRP	R	SSC	Abnormal seed mucilage	MB
At1g53580	*ETHE1*	C	ESN	S	EMB	Embryo defective; Transition	TD
At1g53670	*MSRB1*	C	CND	P	TMP	Sensitive to low temperature	RV
At1g53850	*PAE1*	NC	CND	I	PTH	Susceptible to lettuce mosaic virus	RV
At1g53940	*GLIP2*	C	MRP	V	ROT, PTH	Increased lateral root number; Decreased root gravitropism; Susceptible to bacterial infection	RV
At1g54030	*MVP1*	C	CLB	C	CUL, CHS, PTH	Abnormal vacuole morphology; Sensitive to salt; Susceptible to fungal infection	MB
At1g54040	*TASTY*	C	CLB	B	PRA	Abnormal glucosinolate composition	OTH
At1g54060	*ASIL1*	C	MRP	V	PIG, GRS, LEF, FSM, SSC, FLT	Dwarf; Dark green leaves with abnormal morphology; Short petioles; Short siliques; Small seeds; Late flowering	RV
At1g54160	*NF-YA5*	C	CND	P	WAT	Sensitive to drought	RV
At1g54340	*ICDH*	C	MRP	V	GRS, PTH	Semi-dwarf; Resistant to bacterial infection	RV
At1g54490	*AIN1*	C	CND	H	HRM	Insensitive to ethylene	TD
At1g54960	*ANP2*	C	MRP	V	NLS	Short hypocotyl	RV
At1g54990	*AXR4*	C	MRP	V	ROT, HRM	Defective root gravitropism; Insensitive to auxin	MB
At1g55020	*LOX1*	C	MRP	V	ROT	Increased lateral root number	RV
At1g55180	*PLDE*	C	MRP	V	ROT, CHS	Small root system; Sensitive to hyperosmotic stress	RV
At1g55250	*HUB2*	NC	MRP	V	PIG, GRS, ROT, LEF, IST	Dwarf; Pale green leaves; Irregular leaf blade surface; Thin inflorescence stems; Reduced rosette biomass; Slightly shorter roots; Increased ploidy levels in leaves	RV
At1g55320	*AAE18*	C	CND	H	HRM	Insensitive to pro-auxins	RV
At1g55325	*GCT*	C	ESN	S	EMB, SRF	Embryo defective; Cotyledon; Abnormal cell specification; Reduced fertility	MB

At1g55350	*EMB1275*	C	ESN	S	EMB, W: SRL, W:NLS, W:TCM	Null: Embryo defective; Preglobular; Knockdown: Seedling lethal; Fused cotyledons; Epidermal cell defects	TD
At1g55370	*NDF5*	C	CLB	B	CPR	Complete loss of post-illumination chlorophyll fluorescence; No other phenotypes mentioned	RV
At1g55490	*Cpn60{beta}*	C	MRP	V	GRS, LEF, TMP, LIT	Dwarf; Wrinkled leaves; Variegated leaves under short days; Sensitive to high temperature	TD
At1g55580	*LAS*	C	MRP	V	ARC	Decreased branching	RV
At1g55600	*MINI3*	C	ESN	S	EMB	Embryo defective; Cotyledon	MB
At1g55670	*PSAG*	NC	MRP	V	PIG, GRS, FLT	Dwarf; Pale green; Late flowering	RV
At1g55870	*AtPARN*	C	ESN	S	EMB	Embryo defective	RV
At1g55900	*EMB1860*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At1g56070	*LOS1*	C	CND	P	TMP	Sensitive to freezing	MB
At1g56200	*EMB1303*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g56340	*CRT1a*	C	CND	H	CHS	Sensitive to tunicamycin (inducer of the unfolded protein response)	RV
At1g56510	*WRR4*	C	CND	I	PTH	Susceptible to *Albugo candida*	MB; RV
At1g56650	*PAP1*	C	CND	H	NUT	Cotyledons do not turn purple in response to sucrose	RV
At1g57750	*MAH1*	C	CLB	B	PRA	Low secondary alcohol and ketone levels in stem wax	RV
At1g57820	*VIM1*	C	CLB	C	CUL	Centromeres decondense during interphase; Increased cytosine methylation	MB; RV
At1g58210	*EMB1674*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g58250	*SAB*	C	MRP	V	ROT	Short, thick roots	TD
At1g58360	*AAP1*	C	CND	H	NUT	Insensitive to exogenous amino acids	TD
At1g58440	*SQE1*	C	MRP	V	PIG, GRS, WAT	Dwarf; Pale green leaves; Very sensitive to drought	MB; RV
At1g59560	*DAL2*	C	CND	I	PTH	Susceptible to avirulent bacteria	RV
At1g59640	*BPE*	C	MRP	R	FSM	Large petals	RV
At1g59820	*ALA3*	NC	ESN	G	MGD, ROT, STT, RTH	Male gametophyte defective; Homozygotes are viable: Short primary root; Long root hairs; Altered trichome branching	MB; RV

At1g59870	*PEN3*	C	CND	I	PTH	Susceptible to barley and pea powdery mildew, potato late blight; Resistant to *Erysiphe cichoracearum*	MB; RV
At1g59990	*EMB3108*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At1g60170	*EMB1220*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g60490	*AtVPS34*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At1g60600	*ABC4*	C	ESN	L	SRL, CUL	Seedling lethal without exogenous sucrose; Abnormal chloroplast development	TD
At1g60950	*AtFD2*	NC	MRP	V	PIG, GRS, LEF	Slow growth; Lower fresh and dry weights; Thin, rounded, pale yellow-green leaves	RV
At1g61120	*TPS04*	C	CLB	B	PRA	Low terpene levels; No other phenotypes mentioned	RV
At1g61210	*DWA3*	C	CND	H	HRM, CHS	Sensitive to ABA and salt	RV
At1g61720	*BAN*	C	MRP	R	PIG, SSC	Purple seed coats due to anthocyanin accumulation	TD
At1g62180	*APR2*	C	CLB	B	PRA	Elevated sulfate levels	MB; RV
At1g62300	*WRKY6*	C	CND	H	NUT	Resistant to limited phosphate	RV
At1g62340	*ALE1*	C	ESN	L	SRL, NLS, LEF, TCM	High penetrance of seedling lethality unless grown under high humidity; Small, crinkled cotyledons; Fused leaves; Abnormal cuticle	TN
At1g62360	*STM*	C	ESN	S	EMB, SRL, NLS, TCM	Embryo defective; Seedling lethal; Fused cotyledons; Complete loss of SAM	MB
At1g62640	*KAS3*	C	MRP	V	PIG	Pale green leaves	MB
At1g62750	*SCO1*	C	ESN	S	EMB, W:GER, W:PIG	Null: Embryo defective; Globular; Knockdown: Delayed germination; Pale cotyledons	MB
At1g62830	*LDL1*	C	MRP	T	FLT	Late flowering	RV
At1g62940	*ACOS5*	C	MRP	R	SRF	Completely sterile	RV
At1g62990	*KNAT7*	NC	CLB	C	TCM	Abnormal xylem	RV
At1g63000	*UER1*	C	CLB	C	RTH	Short root hairs	RV
At1g63160	*EMB2811*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At1g63440	*HMA5*	C	CND	H	NUT	Sensitive to copper	RV
At1g63650	*EGL3*	NC	CLB	C	RTH	Slightly increased root hair density in upper region of root	MB

At1g63680	*PDE316*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At1g63700	*YDA*	C	ESN	S	EMB, SRL	Embryo and seedling defective; Cotyledon	MB
At1g63880		C	CND	I	PTH	Susceptible to *Leptosphaeria maculans*	RV
At1g63900	*DAL1*	C	CND	I	PTH	Susceptible to avirulent bacteria	RV
At1g63970	*IspF*	C	ESN	L	SRL, PIG, CUL	Seedling lethal; Albino; Chloroplasts are filled with vesicles instead of thylakoids	RV
At1g63990	*SPO11-2*	C	MRP	R	SRF	Severely reduced fertility due to defects in meiosis	RV
At1g64030	*SRP3*	NC	CND	H	CHS	Resistant to genotoxic stress	RV
At1g64060	*AtrbohF*	C	MRP	V	GRS, PTH	Semi-dwarf; Resistant to fungal infection	RV
At1g64070	*RLM1*	C	CND	I	PTH	Susceptible to *Leptosphaeria maculans*	MB; RV
At1g64280	*NIM1*	C	CND	I	PTH	Complete loss of systemic acquired resistance; Susceptible to disease	MB
At1g64440	*RHD1*	C	CLB	C	RTH, TCM	Abnormal root hairs; Bulging root epidermis	MB
At1g64520	*RPN12a*	C	MRP	V	NLS, PIG, GRS, ROT, FLT, HRM	Low penetrance of decreased cotyledon number; Red hypocotyls and petioles due to anthocyanin accumulation; Short roots; Delayed rosette growth; Late flowering; Altered response to cytokinin; Resistant to auxin	RV
At1g64570	*DUO3*	C	ESN	G	GAM	Complete male gametophyte defective	MB
At1g64670	*BDG1*	C	MRP	V	GRS, LEF, ARC, CHS	Semi-dwarf; Increased branching; Curved, elongated, slightly serrated leaves; Incomplete penetrance of fused leaves; Sensitive to fungicides	TN; RV
At1g64770	*NDH45*	NC	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence; No other phenotypes mentioned	RV
At1g64790	*ILA*	NC	ESN	S	EMB	Embryo defective; Transition	RV
At1g64970	*TMT1*	C	MRP	V	GRS	Slightly reduced fresh weight; Low alpha and beta tocopherol levels	OTH
At1g65310	*XTH17*	NC	CND	P	LIT	Short petioles under green shadelight and low red:far-red light	RV
At1g65360	*AGL23*	C	ESN	G	MGD, GER, PIG	Female gametophyte defective; Albino embryos; Seeds do not germinate without exogenous sucrose	RV

At1g65380	*CLV2*	C	MRP	R	FSM, TCM, LIT	Abnormal pistil, pedicel, and stamen development; Large shoot and floral meristems; Fasciated stems and inflorescences, early flowering, and rescued floral phenotypes under short days	TD
At1g65410	*NAP11*	NC	MRP	V	GRS, ROT, LEF, SRF, FLT	Slow growth; Few rosette leaves; Short roots; Sterile; Late flowering	RV
At1g65420	*NPQ7*	C	CLB	B	CPR	Reduced non-photochemical quenching	RV
At1g65470	*FAS1*	C	MRP	V	GRS, ROT, LEF, IST, ARC, FSM, SRF, TCM	Slow growth; Short roots; Fasciated stems and inflorescences; Abnormal leaf morphology; Abnormal phyllotaxy; Decreased petal and stamen number; Narrow sepals and petals; Reduced fertility; Abnormal SAM and RAM morphology	TD
At1g65480	*FT*	C	MRP	T	FLT	Late flowering	OTH
At1g65620	*AS2*	C	MRP	V	LEF	Altered leaf morphology	MB
At1g65770	*AMR1*	C	CND	H	CHS	Resistant to ozone	RV
At1g66170	*MMD1*	C	MRP	R	FSM, SRF	Male sterile; Short filaments; Incomplete penetrance of decreased stamen number	TN
At1g66200	*GLN1;2*	C	CND	H	NUT	Small rosette leaves in response to nitrate	RV
At1g66340	*EIN1*	C	CND	H	HRM	Sensitive to ethylene	OTH
At1g66350	*RGL1*	C	CND	H	CHS	Resistant to paclobutrazol (inhibitor of GA synthesis)	OTH
At1g66520	*PDE194*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At1g66600	*ABO3*	C	CND	P	WAT, HRM	Sensitive to drought and ABA	RV
At1g66730	*LIG6*	C	MRP	V	GER, TMP, MPH, CHS	Delayed germination; Sensitive to low temperature, x-rays, and oxidative stress	RV
At1g66840	*WEB2*	C	CLB	C	CUL	Abnormal light-responsive chloroplast movement	MB
At1g67080	*ABA4*	C	CLB	B	PRA, CHS	Low ABA levels; Germination resistant to paclobutrazol (inhibitor of GA synthesis)	MB; RV
At1g67140	*SWEETIE*	C	MRP	V	GRS, LEF, SRF, SEN	Dwarf; Lancet-shaped leaves; Completely sterile; Early senescence	TD; RV

At1g67230	*LINC1*	C	CLB	C	CUL	Small nuclei with abnormal morphology	RV
At1g67320	*EMB2813*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At1g67370	*ASY1*	C	MRP	R	SRF	Severely reduced fertility due to defects in meiosis	TD
At1g67440	*EMB1688*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g67490	*KNF*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective	TD
At1g67500	*AtREV3*	C	CND	P	LIT	Sensitive to UV-B light	MB; RV
At1g67550	*URE*	C	CND	H	NUT	Unable to use urea as primary nitrogen source	RV
At1g67630	*EMB2814*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At1g67730	*KCR1*	C	ESN	S	EMB	Embryo defective; Globular	RV
At1g67940	*STAR1*	C	CND	H	MCH	Sensitive to aluminum	RV
At1g68050	*FKF1*	C	MRP	T	FLT	Late flowering	MB
At1g68100	*IAR1*	C	CND	H	HRM	Insensitive to IAA-Ala	MB
At1g68310	*AE7*	C	MRP	V	PIG, ROT, LEF, STT	Short primary root; Narrow, pale green, downward-bending leaves; Protruding trichome support cells	MB
At1g68370	*ARG1*	C	MRP	V	NLS, ROT	Abnormal hypocotyl and root gravitropism	MB
At1g68450	*PDE337*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino to pale yellow embryos	RV
At1g68480	*JAG*	C	MRP	V	LEF, FSM	Abnormal leaf, sepal, petal, and stamen morphology	RV
At1g68530	*CER6*	C	MRP	V	PIG, IST, SRF	Glossy, bright green inflorescence stems; Male sterile unless grown under high humidity	MB
At1g68540	*TKPR2*	C	MRP	R	OVP	Abnormal pollen exine layer	RV
At1g68560	*XYL1*	NC	MRP	V	LEF, FSM, STT	Slightly altered silique, trichome, and leaf morphology	RV
At1g68640	*PAN*	C	MRP	R	FSM	Homeotic floral transformations	TD
At1g68720	*TADA*	C	MRP	V	PIG, GRS, SRF	Delayed growth; Pale green leaves; Reduced fertility	RV
At1g68725	*AGP19*	C	MRP	V	NLS, PIG, GRS, LEF, IST, SRF	Short hypocotyl and inflorescence stems; Small, rounded, flat rosette leaves; Pale green leaves; Delayed growth; Reduced fertility	RV
At1g68730	*AtZR1*	NC	ESN	S	EMB	Embryo defective	RV

At1g68765	*IDA*	C	MRP	R	FSM, HRM	Indehiscent floral organs; Sensitive to ethylene	TD
At1g68800	*BRC2*	C	MRP	V	ARC	Increased branching	RV
At1g68890	*PHA*	C	MRP	V	PIG	Pale green seedlings; High chlorophyll fluorescence	MB; RV
At1g68990	*RPOTm*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	RV
At1g69120	*AP1*	C	MRP	R	FSM	Homeotic floral transformations	OTH
At1g69180	*CRC*	C	MRP	R	FSM	Abnormal carpel development	MB
At1g69190	*cytHPPK/DHPS*	NC	CND	H	CHS	Germination sensitive to hydrogen peroxide, mannitol, and salt	RV
At1g69270	*RPK1*	C	CND	H	HRM	Insensitive to ABA	RV
At1g69390	*AtMinE1*	C	CLB	C	CUL	Few, large chloroplasts; No other phenotypes detected	RV
At1g69440	*AGO7*	C	MRP	T	MTM	Early vegetative phase change	MB; RV
At1g69490	*NAP*	C	MRP	T	SEN	Severely delayed leaf senescence	RV
At1g69500	*CYP704B1*	C	MRP	R	OVP	Abnormal pollen exine layer (no reduction in fertility)	OTH; RV
At1g69770	*CMT3*	C	CLB	B	CPR	Decreased CpXpG DNA methylation	MB; RV
At1g69870	*NRT1.7*	C	CND	H	PRA, CPR, NUT	Sensitive to nitrogen starvation; Elevated nitrogen levels in leaves; Reduced nitrogen transport	RV
At1g69935	*SHW1*	C	MRP	T	FLT, LIT	Late flowering; Short hypocotyl under continuous light and in the dark	RV
At1g69940	*PPME1*	C	ESN	G	MGD	Abnormal pollen tube growth (no effect on fertility)	RV
At1g70070	*ISE2*	C	ESN	S	EMB, W:SRL, W:PIG	Null: Embryo defective; Cotyledon; Knockdown: Seedling lethal; Albino	TD
At1g70170	*MMP*	NC	MRP	T	FLT, SEN	Late flowering; Early senescence	TD
At1g70210	*CYCD1;1*	NC	MRP	V	GER	Delayed germination	RV
At1g70460	*RHS10*	C	CLB	C	RTH	Long root hairs	RV
At1g70560	*TIR2*	C	MRP	V	ROT, RTH, CHS	Few lateral roots; Reduced root gravitropism; Short root hairs; Resistant to NPA (inhibitor of polar auxin transport)	MB; RV

At1g70910	*DEP*	C	MRP	V	GER	Complete loss of seed dormancy	RV
At1g70940	*PIN3*	C	MRP	V	ROT, LIT	Abnormal root gravitropism; Abnormal phototropism	RV
At1g71100	*RSW10*	C	MRP	V	NLS, ROT	Thick hypocotyl and seedling roots	MB
At1g71230	*CSN5B*	C	CLB	C	RTH, LIT, HRM	Abnormal root hair development; Altered response to light and auxin	RV
At1g71270	*VPS52*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	RV
At1g71440	*PFI*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	TD
At1g71720	*PDE338*	NC	MRP	V	PIG	Pigment defective embryo	RV
At1g71880	*SUC1*	C	ESN	G	MGD, NUT	Male gametophyte defective; Homozygotes are viable: Low anthocyanin levels in response to sugar	RV
At1g72320	*APUM23*	C	MRP	V	GRS, ROT, LEF, TCM, MPH	Slow growth; Small, serrated, pointed rosette leaves; Short roots without exogenous sucrose; Abnormal leaf venation; Freshly harvested seeds exhibit delayed germination	RV
At1g72440	*SWA2*	C	ESN	G	GEM	Female and male gametophyte defective; Embryo defective	TD; RV
At1g72560	*PSD*	C	MRP	V	GRS, ROT, ARC, SRF	Delayed leaf growth; Few lateral roots; Abnormal phyllotaxy; Reduced fertility	MB; RV
At1g72770	*HAB1*	C	CND	H	HRM	Sensitive to ABA	RV
At1g72970	*HTH*	C	MRP	R	FSM, OVP, SRF	Abnormal sepal development; Fused floral organs; Reduced fertility; Low penetrance of abnormal ovules	MB
At1g73060	*LPA3*	C	MRP	V	PIG, GRS	Slow growth; Pale green	MB
At1g73177	*BNS*	C	MRP	V	IST	Short inflorescence stems	MB
At1g73360	*HDG11*	C	CLB	C	STT	Severely branched trichomes	RV
At1g73590	*PIN1*	C	MRP	V	NLS, LEF, IST, ARC, FSM	High penetrance of increased cotyledon number and abnormal cotyledon positioning; Naked, pin-shaped inflorescences; Abnormal leaf and flower number, morphology, and position	TN
At1g73660		C	CND	H	CHS	Resistant to salt	RV

At1g73720	*SMU1*	C	MRP	V	GRS, LEF, FSM	Severe dwarf; Small leaves; Absence of flowers	RV
At1g73730	*EIL3*	C	CND	H	NUT	Sensitive to sulfate starvation	MB
At1g73840	*ESP1*	C	MRP	T	FLT	Early flowering	MB
At1g73990	*SPPA1*	C	CLB	B	PRA, CPR	Increased non-photochemical quenching; Low anthocyanin levels; No other phenotypes detected	RV
At1g74030	*ENO1*	C	CLB	C	STT, RTH	Distorted trichomes; Decreased root hair density	RV
At1g74260	*PUR4*	C	ESN	G	GAM, S:GER, S:NLS, S:MSL	Complete male gametophyte defective; Female gametophyte defective; Heterozygotes: Delayed germination and early development; Low penetrance of chlorosis	RV
At1g74310	*HOT1*	C	CND	P	TMP	Reduced acclimation to high temperature	TD
At1g74710	*SID2*	C	CND	I	PTH	Susceptible to pathogens	MB; OTH
At1g74720	*QKY*	C	MRP	V	GRS, LEF, IST, ARC, FSM	Dwarf; Twisted leaves, inflorescence stems, and petals; Abnormal floral phyllotaxy	MB; RV
At1g74850	*PDE343*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	RV
At1g74900	*OTP43*	C	ESN	S	EMB, GER, GRS, LEF, SSC, FLT	Embryo defective; Cotyledon; Very low germination rate; Slow growth; Dwarf; Curled leaves; Late flowering; Abnormal, non-germinating seeds	RV
At1g74920	*ALDH10A8*	NC	CND	P	WAT, CHS	Sensitive to drought, salt, and mannitol	RV
At1g74960	*FAB1*	C	ESN	S	EMB, W:PRA, W:TMP	Null: Embryo lethal; Preglobular / Globular; Knockdown: Elevated 16:0 fatty acid levels; Sensitive to low temperature	OTH
At1g74970	*TWN3*	NC	ESN	S	EMB	Embryo defective; Cotyledon; Twin embryos	TD
At1g75010	*ARC3*	C	CLB	C	CUL	Few, large chloroplasts	MB
At1g75100	*JAC1*	C	CND	P	LIT	Abnormal chloroplast movement under weak blue light and in the dark	MB
At1g75350	*EMB2184*	NC	ESN	S	EMB	Embryo defective; Transition	TD
At1g75380	*BBD1*	C	CND	I	PRA, PTH	Susceptible to fungal infection; Low callose levels	RV

At1g75500	*WAT1*	NC	CND	P	LIT	Short inflorescences and decreased secondary cell wall thickness under short days	UNK
At1g75540	*LHUS*	C	CND	P	LIT	Long hypocotyl under shadelight	TD; RV
At1g75660	*XRN3*	NC	ESN	S	EMB, W:LEF, W:FLT	Null: Embryo lethal; Knockdown: Crinkled, rounded leaves; Late flowering	RV
At1g75820	*CLV1*	C	MRP	V	LEF, IST, ARC, FSM	Fasciated stems and inflorescences; Abnormal leaf phyllotaxy; Slightly rounded leaves; Incomplete penetrance of double leaf formation and increased floral organ number	MB
At1g75950	*ASK1*	C	MRP	R	SRF	Male sterile; Defective in homolog separation	TN
At1g76030	*VHA-B1*	C	CND	H	NUT	Insensitive to glucose	RV
At1g76060	*EMB1793*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At1g76260	*DWA2*	C	CND	H	HRM, CHS	Sensitive to ABA and salt	RV
At1g76420	*CUC3*	C	MRP	V	NLS	Partially fused cotyledons	MB; RV
At1g76490	*HMG1*	C	MRP	V	GRS, SRF, SEN	Dwarf; Completely sterile; Early senescence	RV
At1g76620	*PDE339*	NC	MRP	V	PIG	Pigment defective embryo	RV
At1g77080	*MAF1*	C	MRP	V	GRS, FLT, S:FLT	Dwarf; Early flowering; Heterozygotes: Early flowering	RV
At1g77140	*VPS45*	C	ESN	G	GAM, W:GRS	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Severe dwarf	RV
At1g77180	*SKIP*	C	MRP	V	GRS, SRF	Dwarf; Reduced fertility	RNAi
At1g77300	*EFS*	C	MRP	V	ARC	Increased branching	MB
At1g77390	*TAM1*	C	MRP	R	OVP	Abnormal pollen tetrad formation (no reduction in fertility); Delayed meiotic cell divisions	MB
At1g77470	*EMB2810*	C	ESN	S	EMB, W:GRS, W:LEF, W:FSM, W:SRF, W:HRM, W:PTH	Null: Embryo defective; Preglobular; Knockdown: Dwarf; Narrow leaves and petals; Reduced fertility; Sensitive to SA; Resistant to disease	RV

At1g77490	*tAPX*	C	CND	H	CHS	Elevated hydrogen peroxide levels under photooxidative stress	RV
At1g77860	*KOM*	NC	MRP	R	OVP	Abnormal pollen exine layer	MB
At1g78000	*SEL1*	C	CLB	B	CPR, MCH	Reduced sulfate transport in roots; Resistant to selenate	MB
At1g78240	*TSD2*	C	ESN	L	SRL, LEF, MSL	Incomplete penetrance of rosette lethality; Tumor-like tissue develops instead of leaves and inflorescences	MB
At1g78290	*SRK2C*	C	CND	P	WAT	Root growth sensitive to drought	RV
At1g78390	*NCED9*	C	CLB	B	PRA, CHS	Low ABA levels; Germination resistant to paclobutrazol (inhibitor of GA synthesis)	RV
At1g78570	*RHM1*	C	MRP	V	NLS, ROT, STT, RTH	Abnormal cotyledon growth; Slightly shorter roots and root hairs; Deformed trichomes	MB
At1g78580	*TPS1*	C	ESN	S	EMB	Embryo defective; Cotyledon	TN
At1g78590	*NADK3*	C	CND	H	HRM, CHS	Germination sensitive to ABA, salt, and mannitol; Seedling growth sensitive to oxidative stress	RV
At1g78630	*EMB1473*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g78770	*APC6*	C	ESN	G	GEM	Female gametophyte defective; Embryo defective (inferred)	TD
At1g78870	*UBC13A*	NC	CND	H	NUT	Abnormal root hair growth in response to iron starvation	RV
At1g78900	*VHA-A*	C	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	RV
At1g79000	*HAC1*	C	MRP	V	ROT, SRF, FLT	Short primary root; Reduced fertility; Late flowering	RV
At1g79040	*PsbR*	NC	CLB	B	CPR	Slightly decreased oxygen evolution in thylakoids; No other phenotypes detected under standard or low light conditions	RV
At1g79230	*STR1*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At1g79280	*NUA*	C	MRP	V	LEF, IST, ARC, FSM, SRF, FLT	Short inflorescence stems; Small rosette leaves; Abnormal phyllotaxy; Abnormal stamen, petal, and silique development; Reduced fertility; Very early flowering	RV
At1g79350	*EMB1135*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD

At1g79440	*SSADH1*	C	MRP	V	NLS, GRS, LEF, MSL, SRF, TMP, LIT	Dwarf; Short hypocotyl; Necrotic lesions; Small, bleached leaves; Few flowers; Sensitive to high temperature and UV light	RV
At1g79460	*GA2*	C	MRP	V	GER, PIG, GRS, SRF	Very low germination rate; Severe dwarf; Dark green; Sterile	OTH
At1g79490	*EMB2217*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At1g79560	*EMB1047*	C	ESN	S	EMB	Embryo defective; Globular	TD
At1g79580	*SMB*	C	CLB	C	TCM	Abnormal root cap cell morphology	MB; RV
At1g79650	*RAD23B*	C	MRP	V	GRS, ROT, IST, ARC, SRF	Slow growth; Abnormal phyllotaxy; Short roots and inflorescence stems; Few lateral roots; Reduced fertility	RV
At1g79810	*PEX2*	C	ESN	S	EMB	Embryo defective; Transition	OTH
At1g79840	*GL2*	C	CLB	C	STT, RTH	Abnormal trichome and root hair development	TD
At1g79850	*ORE4*	C	MRP	V	PIG, SEN	Pigment defective embryo; Delayed leaf senescence	TD
At1g79940	*AtERDJ2A*	C	ESN	G	GEM	Male gametophyte defective; Embryo defective (inferred)	RV
At1g80070	*SUS2*	C	ESN	S	EMB	Embryo defective; Globular; Abnormal suspensor	TD
At1g80080	*TMM*	C	CLB	C	STT	Abnormal stomatal patterning	MB
At1g80100	*AHP6*	C	CLB	C	TCM, HRM	Sporadic protoxylem differentiation along the root; No other seedling phenotypes detected; Root growth insensitive to cytokinin	MB; RV
At1g80260	*EMB1427*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At1g80350	*FRA2*	C	MRP	V	NLS, GRS, ROT, LEF, FSM, SRF, MEC	Dwarf; Short hypocotyl; Small rosette; Short roots; Small flowers; Reduced fertility; Fragile inflorescence stems	MB
At1g80380	*GLYK*	C	ESN	L	SRL	Seedling lethal under ambient air; Dwarf under elevated CO2	RV
At1g80410	*EMB2753*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At1g80420	*XRCC1*	NC	CND	P	MPH	Sensitive to gamma rays	RV

At1g80680	*SAR3*	C	MRP	V	ROT, IST, FSM, FLT	Short roots; Few lateral roots; Thick inflorescence stems; Small floral buds and siliques; Early flowering	MB; RV
At1g80760	*NIP6;1*	C	CND	H	NUT	Young leaf growth sensitive to limited and elevated boron	RV
At1g80770	*PDE318*	C	MRP	V	PIG	Pale green seeds and seedlings	TD
At1g80830	*NRAMP1*	C	CND	H	NUT	Sensitive to manganese starvation	RV
At2g01110	*APG2*	C	ESN	L	SRL, PIG	Seedling lethal; Albino and pale green seedlings	TN
At2g01140	*PDE345*	NC	MRP	V	PIG	Pigment defective embryo	RV
At2g01190	*PDE331*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	RV
At2g01290	*RPI2*	C	MRP	V	GRS, MSL, CUL, LIT	Semi-dwarf; Chlorotic; Abnormal chloroplast morphology; Low starch levels under short days	RV
At2g01350	*QPT*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At2g01390	*EMB3111*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At2g01420	*PIN4*	C	ESN	S	EMB, TCM	Embryo defective; Cotyledon; Abnormal seedling root cell patterning	TN
At2g01570	*RGA1*	C	MRP	V	PIG	Slightly pale green	MB
At2g01735	*RIE1*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At2g01830	*CRE1*	C	MRP	V	ROT, HRM	Short roots; Insensitive to cytokinin	TD
At2g01860	*EMB975*	C	ESN	S	EMB	Embryo defective; Globular	TD
At2g01918	*POL3*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At2g01940	*SGR5*	C	MRP	V	ARC	Reduced inflorescence stem gravitropism	MB
At2g01950	*BRL2*	C	MRP	T	SEN	Early leaf senescence	RV
At2g01980	*SOS1*	C	CND	H	NUT, CHS	Sensitive to salt stress and limited potassium	MB
At2g02150	*EMB2794*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At2g02220	*PSKR1*	C	MRP	V	ROT, SEN, HRM	Slightly shorter roots; Early leaf senescence; Complete loss of hormone-induced callus formation	RV
At2g02480	*STI*	C	CLB	C	STT	Unbranched trichomes	UNK
At2g02500	*ISPD*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino	RV

At2g02560	*CAND1*	C	MRP	V	GRS, LEF, ARC, MSL, SEN, HRM	Dwarf; Increased rosette leaf number; Aerial rosettes; Increased branching; Delayed senescence; Altered response to auxin	MB; RV
At2g02810	*AtUTr1*	NC	CLB	B	CPR	Constitutively activated unfolded protein response	RV
At2g02950	*PKS1*	C	CND	P	LIT	Pale under hourly far red pulses	RV
At2g02955	*MEE12*	C	ESN	G	GEM	Female gametophyte defective; Embryo defective (inferred)	TD; RV
At2g03050	*SOLDAT10*	C	ESN	S	EMB, W:PIG	Null: Embryo defective; Transition; Knockdown: Pale green cotyledons	RV
At2g03120	*AtSPP*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	RV
At2g03150	*EMB1579*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At2g03220	*MUR2*	C	CLB	B	PRA	Low fucosylated xyloglucan levels; No other phenotypes detected	MB
At2g03680	*SPR1*	C	MRP	V	ROT, LIT	Helical root growth; Helical shoot growth defects in the dark	UNK
At2g03720	*MRH6*	C	CLB	C	RTH	Abnormal root hair development	RV
At2g03760	*SOT12*	C	CND	H	HRM, CHS, PTH	Germination sensitive to ABA and salt; Seedling growth sensitive to SA; Susceptible to bacterial infection	RV
At2g03800	*GEK1*	C	CND	H	MCH	Sensitive to ethanol	MB
At2g03870	*EMB2816*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At2g04030	*EMB1956*	C	ESN	S	EMB	Embryo defective; Transition	TD
At2g04270	*RNEE/G*	C	ESN	L	SRL, PIG	Seedling lethal without exogenous sucrose; Pale green	RV
At2g04530	*TRZ2*	NC	ESN	S	EMB	Embryo defective; Globular	RV
At2g04550	*IBR5*	C	MRP	V	NLS, ROT, LEF, TCM	Long primary root; Few, short lateral roots; Short hypocotyl; Serrated leaves; Abnormal vascular patterning	MB
At2g04660	*APC2*	C	ESN	G	GAM	Female gametophyte defective; Rare embryo defective (inferred)	RV
At2g04842	*EMB2761*	NC	ESN	S	EMB	Embryo defective; Globular	RV

At2g05210	*AtPOT1a*	C	CLB	C	CUL	Short telomeres	RV
At2g05990	*MOD1*	C	MRP	V	GRS, LEF, MSL, FSM, SRF, SEN	Semi-dwarf; Chlorotic, curled leaves; Distorted siliques; Reduced fertility; Early primary inflorescence senescence	MB
At2g06050	*OPR3*	C	MRP	R	SRF	Male sterile	TD
At2g06510	*RPA70a*	C	MRP	R	SRF, CHS	Reduced fertility due to defects in meiosis; Sensitive to genotoxic stress	RV
At2g06925	*AtSPLA*	C	CND	I	PTH	Resistant to bacterial infection	RV
At2g07050	*CAS1*	C	ESN	G	MGD, W:NLS, W:PIG, W:FSM	Null: Male gametophyte defective; Knockdown: Variegated seedlings; Fused cotyledons; Albino inflorescence nodes; Variegated or albino late flowers	TD; RV
At2g13540	*ABH1*	C	CND	P	WAT, HRM	Resistant to drought; Abnormal stomatal regulation in response to ABA	TD
At2g13680	*CalS5*	C	MRP	R	FSM, SRF	Severely reduced fertility; Small, sterile anthers	RV
At2g14120	*DRP3B*	C	CLB	C	CUL	Elongated mitochondria; Abnormal peroxisome division; No other phenotypes detected	RV
At2g14540	*SRP2*	NC	CND	H	CHS	Resistant to MMS (inducer of genotoxic stress)	RV
At2g14560	*LURP1*	C	CND	I	PTH	Susceptible to oomycete infection	RV
At2g15290	*TIC21*	C	ESN	L	SRL, PIG	Seedling lethal without exogenous sucrose; Red cotyledons; White or transparent rosette leaves	RV
At2g15570	*ATM3*	C	MRP	V	PIG, GRS	Dwarf; Pale green	RV
At2g15790	*SQN*	C	MRP	V	LEF	Few leaves	MB
At2g15820	*OTP51*	C	ESN	L	SRL, PIG	Lethal on soil or in normal light; Pale yellow; With exogenous sucrose under low light: Pale green; Dwarf; Slow growth	RV
At2g16390	*DRD1*	C	CLB	B	CPR	Reduced RNA-directed DNA methylation	MB
At2g16910	*AMS*	C	MRP	R	FSM, SRF	Completely male sterile; Very short filaments	TD
At2g17090	*SSP*	C	ESN	S	MSD	Embryo defective; 50% defective seeds	MB
At2g17250	*EMB2762*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g17265	*DMR1*	C	CND	I	PTH	Resistant to downy mildew; Susceptible to other pathogens	MB
At2g17290	*CPK6*	C	CND	H	NUT, HRM	Reduced stomatal closing in response to ABA and calcium	RV

At2g17430	*NTA*	C	ESN	G	MGD, SRF	Female gametophyte defective; Homozygotes are viable: Reduced fertility	MB; RV
At2g17510	*EMB2763*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At2g17870	*CSP3*	C	CND	P	TMP	Sensitive to freezing	RV
At2g17950	*WUS*	C	MRP	V	ARC, MSL, FSM	Complete loss of primary inflorescence growth; Disorganized bunches of rosette leaves; Complete loss of carpels; Single, central stamen	MB
At2g18020	*EMB2296*	C	ESN	S	EMB	Embryo defective; Globular	TD
At2g18290	*EMB2783*	C	ESN	S	EMB	Embryo defective	RV
At2g18390	*TTN5*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	TD
At2g18470	*PERK4*	C	CND	H	HRM	Insensitive to ABA	RV
At2g18510	*EMB2444*	NC	ESN	S	EMB	Embryo defective; Transition	TD
At2g18710	*SCY1*	C	ESN	L	SRL, PIG	Seedling lethal; Albino embryos	RV
At2g18790	*PHYB*	C	MRP	V	NLS, PIG, ROT, LEF, IST, ARC, FSM, FLT, RTH, LIT	Pale green; Long hypocotyl and petioles; Short roots; Small leaves; Few rosette leaves; Tall inflorescence stems; Decreased branching; Few siliques; Early flowering independent of photoperiod; Long root hairs; Altered response to red:far-red light	OTH
At2g18950	*HPT1*	NC	MRP	V	GRS, TMP, LIT	Semi-dwarf; Sensitive to a combination of high light and low temperature	MB
At2g19080	*METAXIN*	C	MRP	V	GRS, LEF, FSM, SRF	Dwarf; Abnormal leaf morphology; Abnormal floral development; Sterile; Elevated starch levels	RV
At2g19430	*DWA1*	C	CND	H	HRM, CHS	Sensitive to ABA and salt	RV
At2g19450	*TAG1*	C	ESN	S	EMB, GER	Embryo defective; Cotyledon; Wrinkled seeds; Delayed germination; Abnormal triacylglycerol levels and fatty acid composition in seeds	OTH
At2g19520	*FVE*	C	MRP	T	FLT	Late flowering	MB
At2g19560	*EER5*	C	MRP	V	ROT, HRM	Short roots; Very short hypocotyl in response to saturating ethylene concentrations	MB
At2g19570	*CDA1*	NC	CND	I	PTH	Susceptible to bacterial infection	RV

At2g19690	*PLA2-BETA*	C	MRP	V	LEF, IST	Short inflorescence stems and petioles	RV
At2g19760	*PRF1*	C	MRP	V	NLS	Abnormal seedling morphology	TD
At2g19810	*AtOZF1*	NC	CND	H	CHS	Sensitive to oxidative stress	RV
At2g20000	*HBT*	C	ESN	L	SRL, ROT	Seedling lethal; Severe reduction to complete loss of root growth	UNK
At2g20120	*COV1*	C	MRP	V	GRS, LEF, FSM, TCM	Slow growth; Semi-dwarf; Slightly twisted leaves; Short, wrinkled siliques; Severely increased vascular tissue in inflorescence stems	MB
At2g20180	*PIL5*	C	CND	P	LIT	Short hypocotyl under far-red light; Abnormal hypocotyl gravicurvature under red and far-red light	RV
At2g20190	*CLASP*	C	MRP	V	GRS, ROT, SRF	Dwarf; Short roots; Reduced fertility	RV
At2g20300	*ALE2*	C	MRP	V	LEF, SRF	Malformed leaves; Leaf fusion; Female sterile	RV
At2g20310	*RIN13*	C	CND	I	PTH	Susceptible to *Pseudomonas syringae*	RV
At2g20370	*MUR3*	C	CLB	C	CUL	Disorganized endomembranes and actin filaments	MB; RV
At2g20580	*RPN1A*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g20585	*NFD6*	NC	ESN	G	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	TD
At2g20610	*SUR1*	C	MRP	V	ROT	Abnormal lateral root formation	TD
At2g20630	*PIA1*	C	CND	I	PTH	Resistant to bacterial infection	RV
At2g20750	*AtEXPB1*	NC	CND	P	LIT	Short hypocotyl and small cotyledons under red light	RV
At2g20810	*GAUT10*	C	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At2g20890	*THF1*	C	MRP	V	PIG, GRS	Slow growth; Variegated leaves	RV
At2g20990	*SYTA*	NC	CND	I	W:PTH	Knockdown: Resistant to viral infection	RV
At2g21070	*FIO1*	C	MRP	T	FLT, CDR	Early flowering; Abnormal circadian rhythms	MB
At2g21150	*XCT*	C	MRP	T	CDR	Short circadian rhythms independent of light conditions	MB; RV
At2g21170	*cpTPI*	C	ESN	L	SRL	Seedling lethal	RV
At2g21470	*EMB2764*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At2g21660	*CCR2*	NC	CND	H	HRM, CHS	Germination and root growth sensitive to ABA; Sensitive to a combination of salt and mannitol	RV

At2g21710	*EMB2219*	C	ESN	S	EMB	Embryo defective; Transition	TD; RV
At2g21790	*RNR1*	C	MRP	V	PIG, ROT, LEF, MSL, FSM, CUL	Short roots; Bleached to yellow leaf sections; Abnormal leaf and flower morphology; Few, large chloroplasts	MB
At2g21870	*MGP1*	C	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	TN
At2g22010	*RKP*	C	CND	I	PRA, PTH	Resistant to viral infection; Low callose levels	RV
At2g22125	*CSI1*	C	ESN	G	MGD, NLS, GRS, ROT	Male gametophyte defective; Homozygotes are viable; Short, thick hypocotyl and roots; Dwarf	RV
At2g22300	*SR1*	C	MRP	V	MSL, PTH	Necrotic lesions on leaves; Susceptible to fungal and bacterial infection	RV
At2g22410	*SLO1*	C	MRP	V	GRS	Dwarf; Slow growth	TD; RV
At2g22540	*SVP*	C	MRP	T	FLT	Early flowering	TN
At2g22630	*AGL17*	C	MRP	T	FLT	Late flowering	RV
At2g22640	*BRK1*	C	CLB	C	STT, TCM	Abnormal trichome and pavement cell morphology	RV
At2g22770	*NAI1*	NC	CLB	C	CUL	Complete loss of ER body formation	MB
At2g22780	*PMDH1*	C	CND	P	LIT	Short hypocotyl in the dark	RV
At2g22810	*ACS4*	C	MRP	V	NLS, IST	Large cotyledons; Long hypocotyl; Tall inflorescence stems; Elevated ethylene levels	RV
At2g22870	*EMB2001*	C	ESN	S	EMB	Embryo defective; Transition	TD
At2g22990	*SNG1*	C	CLB	B	PRA	Low sinapoylmalate and elevated sinapoylglucose levels	MB
At2g23380	*CLF*	C	MRP	V	LEF	Altered leaf morphology	TN
At2g24120	*PDE319*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At2g24270	*ALDH11A3*	NC	MRP	V	GRS	Slow growth	RV
At2g24490	*RPA2*	C	MRP	V	GRS, FLT, STT	Dwarf; Decreased trichome density; Early flowering	MB; RV
At2g24790	*COL3*	C	CND	P	LIT	Long hypocotyl under red light and short days; Early flowering and reduced lateral branching under short days; Short roots and few lateral roots under continuous light	RV
At2g24840	*AGL61*	C	ESN	G	GAM	Female gametophyte defective; Rare embryo defective (inferred)	RV

At2g25110	*SDF2*	C	CND	H	CHS	Sensitive to tunicamycin (inducer of the unfolded protein response) and DTT (ER homeostasis-perturbing compound)	RV
At2g25170	*PKL*	C	MRP	V	PIG, ROT	Incomplete penetrance of thick, green distal end of primary root	MB
At2g25180	*ARR12*	C	MRP	V	ROT, TCM	Short roots; Large RAM arrests development over time	RV
At2g25490	*EBF1*	C	CND	H	HRM	Altered response to ACC (ethylene precursor)	RV
At2g25600	*SPIK*	C	ESN	G	MGD	Impaired pollen tube growth (no effect on fertility)	TD
At2g25660	*EMB2410*	C	ESN	S	EMB	Embryo defective; Globular	TD
At2g25680	*MOT1*	C	CLB	B	PRA, NUT	Low molybdenum levels; Shoot growth sensitive to limited molybdenum	RV
At2g25710	*HCS1*	C	ESN	G	GEM	Female gametophyte defective; Embryo defective	RV
At2g25840	*OVA4*	NC	ESN	G	EMG	Ovule abortion; Female gametophyte defective; Early embryo defective (inferred)	RV
At2g25850	*PAPS2*	NC	ESN	L	NHM	No homozygous mutant plants recovered	RV
At2g25930	*ELF3*	C	MRP	V	NLS, FLT	Long hypocotyl; Early flowering	MB
At2g26000	*BRIZ2*	C	ESN	L	SRL, GER, PIG	Seedling lethal; Pale green embryos; Delayed germination	RV
At2g26060	*EMB1345*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At2g26070	*RTE1*	C	CND	H	HRM	Leaf senescence insensitive to ethylene	MB; RV
At2g26140	*FtsH4*	C	CND	P	LIT	Asymmetric rosette leaves with irregular serration under short days	RV
At2g26150	*HsfA2*	C	CND	P	TMP	Sensitive to high temperature	RV
At2g26170	*CYP711A1*	C	MRP	V	GRS, LEF, ARC	Semi-dwarf; Increased branching; Rounded rosette leaves	TD
At2g26250	*FDH*	C	MRP	V	LEF, FSM, STT	Fused leaves and floral organs; Abnormal trichomes	TN
At2g26300	*GPA1*	C	ESN	G	MGD, NLS, TCM, HRM	Low pollen germination rate; Short pollen tubes; Homozygotes are viable: Short hypocotyl; Large leaf cells; Short roots in response to auxin	TD

At2g26330	*ER*	C	MRP	V	LEF, IST, FSM	Short inflorescence stems; Short petioles; Blunt siliques	TD
At2g26350	*PEX10*	C	ESN	S	EMB	Embryo defective; Transition	RV
At2g26460	*SMU2*	C	MRP	V	NLS, GRS, SSC	Slow growth; Incomplete penetrance of abnormal cotyledon number and heavy seeds	RV
At2g26510	*PDE135*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At2g26550	*HO2*	C	MRP	V	PIG, FLT, LIT	Pale green; Early flowering; Long hypocotyl growth under red and far-red light	MB
At2g26570	*WEB1*	C	CLB	C	CUL	Abnormal light-responsive chloroplast movement	MB
At2g26650	*AKT1*	NC	CLB	B	CPR	Reduced potassium uptake	RV
At2g26670	*HY6*	C	MRP	V	NLS, PIG, GRS, LIT	Dwarf; Pale green; Long hypocotyl; Slow growth and small, chlorotic leaves under continuous light	MB
At2g26710	*BAS1*	C	MRP	V	IST, LIT	Tall inflorescence stems; Short hypocotyl under a variety of light conditions	RV
At2g26830	*EMB1187*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At2g26890	*GRV2*	C	ESN	S	EMB, W:GRS, W:IST	Null: Embryo defective; Knockdown: Dwarf; Abnormal shoot gravitropism	MB
At2g26930	*PDE277*	C	ESN	L	SRL, PIG	Seedling lethal; Albino embryos and seedlings	TD
At2g26990	*FUS12*	C	ESN	L	SRL, PIG, GRS	Rosette lethal; Red due to anthocyanin accumulation; Dwarf	OTH
At2g27040	*AGO4*	NC	CLB	B	CPR	Decreased DNA methylation	RV
At2g27050	*EIL1*	C	CND	H	HRM	Insensitive to ethylene	RV
At2g27100	*SE*	C	MRP	V	LEF, MTM, TCM	Serrated leaves; Abnormal vegetative phase change; Increased leaf venation complexity	MB
At2g27150	*AAO3*	C	MRP	V	MSL, CHS	Wilty leaves; Low ABA levels; Germination resistant to uniconazole (inhibitor of GA biosynthesis)	MB
At2g27170	*TTN7*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged endosperm nuclei	TD
At2g27230	*LHW*	C	MRP	V	ROT	Complete loss of root bilateral symmetry	MB

At2g27250	*CLV3*	C	MRP	V	IST, ARC, FSM, TCM	Fasciated stems and inflorescences; Increased floral organ number; Large shoot and floral meristems	TN; TD
At2g27300	*NTL8*	C	MRP	V	ROT	Short lateral roots	RV
At2g28000	*SLP*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At2g28110	*FRA8*	C	MRP	V	GRS, LEF, FSM, SRF	Dwarf; Small leaves, flowers, and siliques; Sterile due to anther and pollen defects	RV
At2g28160	*FRU*	C	ESN	L	SRL	Seedling lethal without exogenous iron	RV
At2g28290	*SYD*	C	MRP	V	GRS, LEF, IST, ARC, FSM, SRF, TCM	Short inflorescence stems; Decreased branching; Slow growth; Small, upward-bending leaves; Abnormal floral organ morphology, position, and number; Sterile; Premature SAM termination	MB
At2g28550	*TOE1*	NC	MRP	T	FLT	Early flowering	RV
At2g28560	*RAD51B*	C	CND	H	CHS	Sensitive to mitomycin C (DNA cross-linking agent)	RV
At2g28610	*PRS*	C	MRP	R	FSM	Abnormal flower morphology	MB
At2g28670	*ESB2*	C	CND	P	PRA, WAT	Resistant to drought; Elevated suberin levels in roots	RV
At2g28800	*ALB3*	C	MRP	V	PIG	Pale green seeds and seedlings	TN
At2g28880	*EMB1997*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At2g28890	*PLL4*	NC	MRP	V	LEF	Abnormal leaf morphology	RV
At2g28900	*AtOEP16-1*	C	ESN	L	SRL	Seedling lethal unless grown under continuous light	RV
At2g29090	*CYP707A2*	C	CND	P	TMP	Severely delayed germination without stratification	RV
At2g29630	*THIC*	C	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At2g29980	*FAD3*	C	CLB	B	PRA	Abnormal fatty acid composition	MB
At2g30020	*AP2C1*	C	CLB	C	STT, HRM	Increased stomatal width; Germination sensitive to ABA	RV
At2g30110	*AtUBA1*	C	CND	I	PTH	Susceptible to bacterial infection	MB
At2g30200	*EMB3147*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At2g30240	*AtCHX13*	C	CND	H	NUT	Slow growth and chlorotic, bleached leaves under low potassium	RV

At2g30280	*RDM4*	C	MRP	V	GER, PIG, GRS, LEF, ARC, SRF, FLT	Increased seed dormancy; Pale green seedlings; Slow growth; Dwarf; Abnormal phyllotaxy; Abnormal rosette leaf morphology; Reduced fertility; Late flowering; Altered DNA methylation	TD
At2g30410	*KIS*	C	ESN	S	EMB, CUL	Embryo defective; Enlarged embryo cells and endosperm nuclei	TD
At2g30432	*TCL1*	C	CLB	C	STT	Increased trichome density on inflorescences; Abnormal trichome patterning	RV
At2g30490	*C4H*	C	MRP	V	GRS, IST, ARC, SRF	Dwarf; Increased branching; Thick lateral branch bases; Male sterile due to indehiscent anthers	MB
At2g30520	*RPT2*	C	CND	P	LIT	Complete loss of root phototropism	MB
At2g30570	*PsbW*	C	CLB	B	CPR	Slightly decreased chlorophyll fluorescence; No other phenotypes detected	RV; RNAi
At2g30770	*CYP71A13*	C	CND	I	PTH	Susceptible to *Alternaria brassicicola*	RV
At2g30920	*EMB3002*	NC	ESN	S	EMB	Embryo defective; Preglobular	TD
At2g30950	*VAR2*	C	MRP	V	PIG, LEF	Pigment defective embryo; Variegated leaves	MB
At2g31060	*EMB2785*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g31170	*SYCO*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective; Abnormal female gametophyte morphology	MB
At2g31190	*RUS2*	C	MRP	V	ROT, LIT	Short roots; Seedling lethal when roots are exposed to UV-B light	MB
At2g31260	*APG9*	C	CND	H	NUT	Early chlorosis and reduced fertility under nitrogen starvation	RV
At2g31305	*INH3*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g31340	*EMB1381*	C	ESN	S	EMB	Embryo defective; Transition	TD
At2g31380	*STH*	NC	CND	P	LIT	Short hypocotyl in red and far-red light	RV
At2g31400	*GUN1*	NC	CND	H	NLS, NUT, HRM	Seedling growth sensitive to ABA; Low anthocyanin levels in response to sucrose; Slightly slower seedling growth	RV
At2g31530	*EMB2289*	C	ESN	S	EMB	Embryo defective; Globular	TD
At2g31650	*ATX1*	C	MRP	V	GRS, FLT	Dwarf; Late flowering	RV

At2g31660	*SAD2*	C	CND	H	HRM	Germination and seedling growth sensitive to ABA	TD
At2g31865	*PARG2*	NC	CND	I	PTH	Susceptible to *Botrytis cinerea*	RV
At2g31870	*TEJ*	C	MRP	T	CDR	Long circadian rhythms	MB
At2g31970	*RAD50*	C	MRP	R	SRF, CUL, NUT, CHS	Completely sterile due to defects in meiosis; Short telomeres; Dwarf when grown on nutrient plates; Sensitive to genotoxic stress	TD
At2g32590	*EMB2795*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At2g32700	*LUH*	C	MRP	V	GER, GRS, ROT	Delayed germination; Low germination rate; Slow growth; Short roots	RV
At2g32940	*AGO6*	C	CLB	B	CPR	Decreased DNA methylation	TD
At2g32950	*COP1*	C	ESN	L	SRL, GER, PIG, LIT	Seedling lethal; Red embryos, cotyledons, and roots due to anthocyanin accumulation; Severely delayed germination; Abnormal growth in the dark	TD
At2g33100	*CSLD1*	NC	ESN	G	MGD	Male gametophyte defective	RV
At2g33150	*PED1*	C	ESN	L	SRL, HRM	Seedling lethal without exogenous sucrose; Insensitive to 2,4-DB	OTH
At2g33430	*DAL1*	C	ESN	L	SRL, PIG	Seedling lethal without exogenous sucrose; Pale green embryos and seedlings	TN
At2g33460	*RIC1*	C	CLB	C	CUL	Disorganized microtubules in pavement cells	RV
At2g33540	*CPL3*	C	MRP	V	GRS, FLT	Slow growth; Early flowering	TD
At2g33770	*PHO2*	C	CLB	B	PRA	Elevated phosphate levels	OTH
At2g33800	*EMB3113*	C	ESN	S	EMB, W:PIG	Null: Embryo defective; Preglobular; Knockdown: Pigment defect	RV
At2g33860	*ETT*	C	MRP	R	FSM	Abnormal flower morphology	TD
At2g33880	*STIP*	C	ESN	L	SRL, NLS, ROT	Seedling lethal; Small, upward-bending cotyledons; Incomplete penetrance of complete loss of primary root	RV
At2g34220	*PDD12*	NC	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	TD
At2g34470	*UREG*	C	CND	H	NUT	Unable to use urea as primary nitrogen source	RV
At2g34490	*CYP710A2*	C	CLB	B	PRA	Low sterol levels	RV

At2g34640	*PTAC12*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino	RV
At2g34650	*PID*	C	ESN	S	EMB, NLS, MSL, FSM	Embryo defective; Abnormal cotyledon number; Fused cotyledons; Inflorescence terminates prematurely in a pin-like structure; Abnormal floral morphology	RV
At2g34660	ABCC2	NC	CND	H	MCH	Sensitive to arsenic	RV
At2g34680	*SETH1*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	TD; RV
At2g34690	*ACD11*	C	ESN	L	SRL	High penetrance of rosette lethality	TN
At2g34780	*EMB1611*	C	ESN	S	EMB, W:IST, W:TCM	Null: Embryo defective; Preglobular; Knockdown: Short inflorescence stems; Abnormal SAM	TD
At2g34790	*EDA28*	NC	ESN	G	GEM, EMG	Female gametophyte defective; Embryo defective (inferred)	TD
At2g35000	*ATL9*	C	CND	I	PTH	Susceptible to powdery mildew	RV
At2g35035	*URED*	C	CND	H	NUT	Unable to use urea as primary nitrogen source	RV
At2g35070	*PGD4*	NC	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	TD
At2g35100	*ARAD1*	C	CLB	B	PRA	Abnormal cell wall composition; Low arabinose levels	RV
At2g35210	*RPA*	C	ESN	G	MGD, RTH	Slow pollen tube growth (no effect on fertility); Homozygotes are viable: Abnormal root hair development	RV
At2g35230	*IKU1*	C	ESN	S	MSD	Small seeds due to reduced endosperm growth (segregates in heterozygotes)	MB
At2g35350	*PLL1*	C	MRP	R	FSM	Short pedicel	RV
At2g35510	*SRO1*	C	MRP	V	ROT, FLT, CHS	Long roots; Increased lateral root number; Late flowering; Resistant to oxidative and osmotic stress	RV
At2g35630	*GEM1*	C	ESN	G	MGD	Male and female gametophyte defective; Homozygotes are viable: Increased percentage of abnormal pollen	MB
At2g35650	*CSLA7*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective	RV

At2g35670	*FIS2*	C	ESN	S	MSD	Initiation of seed development in absence of fertilization; 50% defective seeds	MB; TN
At2g35720	*OWL1*	C	CND	P	LIT	Long hypocotyl and partially unfolded cotyledons under far-red light	TD; RV
At2g35930	*PUB23*	C	CND	P	WAT	Resistant to drought	RV
At2g35940	*BLH1*	C	CND	P	LIT	Altered response to continuous far-red light and deep canopy shadelight	RV
At2g36000	*EMB3114*	NC	ESN	S	EMB	Embryo defective; Globular	RV
At2g36120	*DOT1*	C	MRP	V	LEF, TCM	Rough leaves; Fused leaves; Abnormal venation	MB
At2g36190	*AtCWINV4*	C	CLB	B	PRA	Complete loss of nectar production	RV
At2g36230	*HISN3*	C	ESN	G	EMG, W:PIG	Null: Embryo defective; Gametophyte defective (inferred); Knockdown: Pigment defective embryo	RV
At2g36270	*ABI5*	C	CND	H	HRM	Altered response to ABA	MB
At2g36390	*SBE2.1*	C	CLB	B	PRA	Abnormal amylopectin structure	RV
At2g36490	*DML1*	C	CLB	B	CPR	Increased DNA methylation	MB
At2g36530	*LOS2*	C	CND	P	TMP	Sensitive to freezing	MB
At2g36830	*TIP1;1*	C	ESN	L	SRL, W:GRS, W:SEN	Null: Seedling lethal; Knockdown: Dwarf; Early senescence	RV
At2g36850	*GSL8*	C	ESN	G	GEM, W:GRS	Null: Male gametophyte defective; Embryo defective; Knockdown: Dwarf	RV
At2g36910	*AtPGP1*	C	MRP	V	NLS	Short hypocotyl	RV
At2g36990	*SIGF*	C	MRP	V	PIG	Pale green cotyledons	RV
At2g37090	*IRX9*	NC	MRP	V	GRS, TCM	Dwarf; Collapsed xylem; Low cellulose levels	RV
At2g37250	*ADK*	NC	MRP	V	ROT, LIT	Long roots; Increased biomass under continuous light; Late flowering in the dark	RV
At2g37260	*TTG2*	C	MRP	R	PIG, SSC, STT	Yellow seed coat; Abnormal trichomes	TN
At2g37330	*ALS3*	NC	CND	H	MCH	Sensitive to aluminum	MB
At2g37560	*ORC2*	C	ESN	S	EMB	Embryo defective; Globular	TN
At2g37630	*AS1*	C	MRP	V	LEF	Altered leaf morphology	MB
At2g37680	*PAT3*	C	CND	P	LIT	Long hypocotyl under far-red light	TD
At2g37860	*LCD1*	C	CND	H	CHS	Pale plants in response to ozone	MB

At2g37920	*EMB1513*	NC	ESN	S	EMB	Embryo defective; Transition	TD
At2g37970	*SOUL-1*	NC	CND	P	LIT	Short hypocotyl and large cotyledons under red light	RV
At2g38020	*VCL1*	C	ESN	S	EMB	Embryo defective	TD
At2g38050	*DET2*	C	MRP	V	PIG, GRS, ARC, FSM, SRF, FLT, SEN, LIT	Dwarf; Increased branching; Dark green; Small flowers; Reduced fertility; Late flowering; Abnormal senescence; Dark-grown seedlings are de-etiolated	MB
At2g38110	*GPAT6*	C	CLB	C	TCM, CUL	Complete loss of cuticle and nanoridges on petals	RV
At2g38120	*AUX1*	C	MRP	V	ROT, HRM	Abnormal root gravitropism; Root growth insensitive to auxin	TD
At2g38170	*CAX1*	C	MRP	V	ROT, IST, ARC	Short roots; Few, short lateral roots; Short inflorescence stems; Decreased branching	RV
At2g38230	*PDX1.1*	C	MRP	V	ROT	Short roots	RV
At2g38280	*FAC1*	C	ESN	S	EMB	Embryo defective; Preglobular	MB
At2g38440	*ITB1*	C	CLB	C	STT, LIT	Abnormal trichome morphology; Short hypocotyl in the dark	MB
At2g38460	*IREG1*	C	CLB	B	PRA	Complete loss of cobalt accumulation	RV
At2g38470	*WRKY33*	C	CND	H	CHS	Sensitive to salt stress	RV
At2g38560	*TFIIS*	C	MRP	V	GER, FLT	Reduced seed dormancy; Slightly early flowering	RV
At2g38670	*PECT1*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At2g38750	*AnnAt4*	C	CND	H	HRM, CHS	Germination and early seedling growth sensitive to osmotic stress and ABA	RV
At2g38770	*EMB2765*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g39080	*EMB2799*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At2g39140	*PDE328*	C	MRP	V	PIG	Pale green seeds and seedlings	RV
At2g39290	*PGP1*	C	MRP	V	PIG	Pale green	MB
At2g39450	*MTP11*	C	CND	H	NUT	Sensitive to elevated manganese	RV
At2g39470	*PPL2*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence; No other phenotypes detected	RV
At2g39550	*AtGGT1B*	C	CND	H	HRM	Decreased stomatal width in response to ABA	RV

At2g39660	*BIK1*	C	CND	I	PTH	Susceptible to necrotrophic fungi; Resistant to bacterial infection	RV
At2g39770	*CYT1*	C	ESN	S	EMB, W:LIT, W:CHS	Null: Embryo defective; Cotyledon; Knockdown: Low vitamin C levels; Sensitive to ozone and UV light	MB
At2g39800	*P5CS1*	C	CND	H	CHS	Lethality in response to salt stress	RV
At2g39810	*HOS1*	C	MRP	T	FLT	Early flowering	MB
At2g39930	*ISA1*	C	CLB	B	PRA	Low starch levels	RV
At2g39940	*COI1*	C	MRP	R	SRF, MEC, HRM	Male sterile; Altered response to wounding; Insensitive to jasmonate	MB
At2g39990	*AteIF3f*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective	TN
At2g40080	*ELF4*	C	MRP	V	NLS, LEF, CDR, LIT	Long hypocotyl and petioles; Abnormal circadian rhythms; Early flowering in non-inductive photoperiods	TD
At2g40140	*SZF2*	C	CND	H	HRM, PTH	Germination sensitive to ABA; Susceptible to *Botrytis cinerea*	RV
At2g40170	*GEA6*	C	MRP	R	FSM, SSC	Premature dehydration of seeds and dehiscence of siliques at distal end	RV
At2g40180	*PP2C5*	C	CLB	C	STT, HRM	Increased stomatal width; Seed germination sensitive to ABA	RV
At2g40190	*LEW3*	C	MRP	V	GRS, MSL, SRF, TCM	Dwarf; Wilted leaves; Reduced fertility; Collapsed xylem; Low cellulose levels	MB; RV
At2g40220	*ABI4*	C	CND	H	HRM	Germination insensitive to ABA	MB
At2g40550	*ETG1*	C	MRP	V	LEF	Serrated leaves	RV
At2g40840	*DPE2*	C	MRP	V	GRS	Dwarf; Elevated maltose and chloroplast starch levels; Elevated sucrose levels at night	RV
At2g40850	*AtPI4KG1*	NC	MRP	R	SRF	Reduced fertility due to pollen defects	RV
At2g40890	*REF8*	C	MRP	V	GRS, TCM	Dwarf; Collapsed vessel elements; Reduced lignin	MB
At2g40930	*PDE323*	NC	MRP	V	PIG	Pale green seeds and seedlings	TD
At2g40950	*BZIP17*	C	CND	H	CHS	Sensitive to salt	RV
At2g40970	*MYBC1*	C	CND	P	TMP	Resistant to freezing	RV

At2g41110	*CAM2*	C	ESN	G	MGD	Male gametophyte defective; Homozygotes appear wild type	TN
At2g41310	*ARR8*	NC	MRP	V	ROT	Slightly fewer lateral roots	RV
At2g41350	*EMB2819*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At2g41370	*BOP2*	NC	MRP	V	IST, ARC, FSM	Fused, fasciated stems and inflorescences; Incomplete penetrance of multiple flowers developing at one node	RV
At2g41500	*EMB2776*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective	MB
At2g41540	*GPDHc1*	C	CND	H	FLT, HRM, CHS	Germination and seedling growth sensitive to ABA; Sensitive to salt; Slightly early flowering	RV
At2g41560	*ACA4*	C	MRP	V	MSL	Low penetrance of faint chlorotic spots	RV
At2g41660	*MIZ1*	C	CND	P	WAT	Reduced hydrotropism	MB; RV
At2g41670	*SIN2*	C	MRP	V	GER, GRS, ARC, FSM, SRF, FLT, TCM	Low germination rate; Slow growth; Increased branching; Abnormal pistil and sepals; Female sterile due to short integuments; Late flowering; Vascular discontinuity in petals	MB; RV
At2g41680	*NTRC*	NC	MRP	V	PIG, GRS, WAT, CHS	Small, pale green rosette; Dwarf; Sensitive to drought, oxidative stress, and salt stress	RV
At2g41720	*EMB2654*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At2g41850	*ADPG2*	C	CND	P	WAT	Reduced silique shattering under drought	RV
At2g41940	*ZFP8*	C	CLB	C	STT	Severely reduced trichome density on upper cauline leaves and inflorescences	RV
At2g42160	*BRIZ1*	C	ESN	L	SRL, GER, PIG	Seedling lethal; Pale embryos; Delayed germination	RV
At2g42200	*SPL9*	C	MRP	V	LEF	Slightly fewer rosette leaves; Slightly increased cauline leaf number	RV
At2g42260	*UVI4*	C	CLB	C	STT, LIT	Increased trichome branching; Resistant to UV-B light	MB
At2g42380	*bZIP34*	C	MRP	R	OVP	Abnormal pollen shape and exine layer	RV
At2g42430	*LBD16*	C	MRP	V	ROT	Slightly fewer lateral roots	RV
At2g42580	*TTL3*	C	CLB	C	TCM, HRM	Abnormal vein patterning; Altered response to auxin and brassinosteroid	RV

At2g42620	*ORE9*	C	MRP	V	NLS, ARC, SEN, CHS	Increased branching; Long hypocotyl and cotyledonary petioles; Delayed senescence; Resistant to oxidative stress	MB
At2g42870	*PAR1*	NC	MRP	V	ARC, SRF	Increased branching; Reduced fertility	RV
At2g43010	*SRL2*	C	CND	P	LIT	Sensitive to continuous red light	TD
At2g43040	*NPG1*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At2g43090	*AtLeuD3*	C	ESN	G	EMG	Female gametophyte defective; Embryo defective (inferred)	RV
At2g43350	*ATGPX3*	C	CND	P	WAT, CHS	Increased water loss under drought; Germination and seedling growth sensitive to hydrogen peroxide	RV
At2g43360	*BIO2*	C	ESN	S	EMB	Embryo defective; Globular	OTH
At2g43400	*ETFQO*	C	MRP	R	SRF, LIT	Reduced female fertility; Early senescence in the dark	RV
At2g43410	*FPA*	C	MRP	T	FLT	Late flowering	MB
At2g43650	*EMB2777*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At2g43710	*SSI2*	C	MRP	V	MSL, PTH	Necrotic lesions; Resistant to *Phytophthora parasitica*	MB
At2g43790	*AtMPK6*	C	CND	H	TMP, NUT, HRM	Stratification and after-ripening not required for germination; Germination resistant to ABA and glucose	RV
At2g43910	*HOL1*	C	CND	I	MCH, PTH	Susceptible to bacterial infection; Sensitive to potassium thiocyanate	RV
At2g44170	*NMT2*	NC	MRP	T	FLT	Early flowering	RV
At2g44190	*EMB3116*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At2g44490	*PEN2*	C	CND	I	PTH	Susceptible to fungal infection	MB
At2g44745	*WRKY12*	C	MRP	V	GRS	Increased above-ground biomass	RV
At2g44810	*DAD1*	C	MRP	R	FSM, SRF	Delayed flower bud opening; Male sterile due to indehiscent anthers; Slightly smaller pollen	TD
At2g44950	*HUB1*	C	MRP	V	PIG, ROT, LEF	Pale green leaves; Abnormal leaf shape; Reduced rosette biomass; Short primary root	MB; RV
At2g44990	*CCD7*	C	MRP	V	GRS, LEF, ARC	Increased branching; Semi-dwarf; Short leaves and petioles	MB
At2g45000	*EMB2766*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV

At2g45190	*FIL*	C	MRP	V	MSL, FSM	Clusters of filamentous structures and flowers; Altered floral organ number and shape	MB
At2g45270	*GCP1*	C	ESN	S	EMB	Embryo defective; Globular	RV
At2g45280	*AtRAD51C*	C	MRP	R	SRF, MPH, CHS	Male and female sterile due to defects in meiosis; Sensitive to cisplatin and gamma radiation	RV
At2g45330	*EMB1067*	C	ESN	S	EMB	Embryo defective; Globular	TD
At2g45350	*CRR4*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence; No other phenotypes detected	MB
At2g45400	*BEN1*	C	MRP	V	LEF, IST	Tall inflorescence stems; Elongated leaves	RV
At2g45420	*LBD18*	C	MRP	V	ROT	Few lateral roots	RV
At2g45430	*AHL22*	C	MRP	V	NLS	Slightly longer hypocotyl	RV
At2g45440	*DHDPS2*	C	MRP	V	ROT, LEF	Small rosette; Short roots; Elevated threonine levels	RV
At2g45660	*AGL20*	C	MRP	T	FLT	Late flowering independent of photoperiod	RV
At2g45690	*SSE*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At2g45770	*cpFtsY*	C	MRP	V	MSL	Severe chlorosis	RV
At2g45790	*PMM*	C	CND	P	TMP	Lethal at high temperature	MB
At2g45890	*RHS11*	C	CLB	C	RTH	Short root hairs	RV
At2g45970	*LCR*	C	MRP	V	LEF	Fused leaves	TN
At2g46020	*BRM*	C	ESN	G	MGD, GRS, ROT, LEF, FSM, SRF	Male and female gametophyte defective; Homozygotes are viable: Dwarf; Slow growth; Abnormal leaf, root and flower morphology; Completely sterile	RV
At2g46240	*AtBAG6*	C	MRP	V	S:PIG, S:ROT, S:LEF, S:ARC, S:FLT, S:SEN	Heterozygotes: Increased branching and lateral root number; Early flowering and senescence; Incomplete penetrance of purple leaves; Homozygotes not mentioned	RV
At2g46340	*SPA1*	C	CND	P	LIT	Sensitive to continuous far-red light	MB
At2g46370	*FIN219*	C	CND	P	LIT, HRM	Long hypocotyl under far-red light; Insensitive to jasmonate	MB
At2g46410	*CPC*	C	CLB	C	RTH	Abnormal root hairs	TD

At2g46510	*AtAIB*	C	CND	H	HRM	Insensitive to ABA	RV
At2g46590	*DAG2*	C	MRP	V	IST, TMP, LIT	Tall inflorescence stems; Low germination rate in the dark and at low temperature	RV
At2g46720	*HIC*	C	CND	H	NUT	Increased stomatal density in response to elevated CO2	TD
At2g46770	*ANAC043*	C	MRP	R	FSM, TCM	Indehiscent siliques; Loss of secondary walls at valve margins	RV
At2g46790	*APRR9*	NC	CND	P	LIT	Long hypocotyl and small cotyledons under red light	RV
At2g46800	*MTP1*	C	CND	H	NUT	Sensitive to zinc	RV
At2g46830	*CCA1*	C	MRP	T	CDR	Short circadian rhythms in leaf movements	TD
At2g46920	*POL*	C	MRP	R	FSM, TCM	Slow flower development; Slightly smaller meristems	MB
At2g46970	*PIL1*	C	CND	P	LIT	Abnormal hypocotyl length and cotyledon size under red and far-red light	RV
At2g47000	*AtPGP4*	C	CLB	B	CPR, MPH	Reduced basipetal auxin transport; Increased root gravitropism under vertical growth	RV
At2g47040	*VGD1*	C	ESN	G	MGD, SRF	Male gametophyte defective; Homozygotes are viable: Reduced fertility	TD
At2g47160	*BOR1*	C	CND	H	NUT	Sensitive to boron starvation	MB
At2g47240	*LACS1*	C	MRP	V	IST	Glossy inflorescence stems	RV
At2g47430	*CKI1*	C	ESN	G	GAM	Complete female gametophyte defective	RV
At2g47450	*CAO*	C	MRP	V	PIG, MSL	Pale green; Chlorotic	TN
At2g47460	*MYB12*	C	CLB	B	PRA	Low flavonoid levels	RV
At2g47470	*UNE5*	NC	ESN	G	GEM, EMG	Female gametophyte defective; Embryo defective (inferred)	TD
At2g47510	*TGD16*	NC	ESN	G	EMG	Male and female gametophyte defective; Embryo defective (inferred)	TD
At2g47620	*AtSWI3A*	C	ESN	G	EMG	Embryo defective; Gametophyte defective	RV
At2g47750	*KEN*	NC	ESN	G	MGD	Female gametophyte defective	RV
At2g47760	*ALG3*	C	CLB	B	PRA	Abnormal N-glycan composition; No other phenotypes detected	RV
At2g47940	*EMB3117*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV

At2g47980	*SCC3*	NC	ESN	L	NHM, S:CUL	No homozygous mutant plants recovered; Heterozygotes: Reduced sister chromatid alignment	RV
At2g47990	*SWA1*	C	ESN	G	GAM, W:ROT	Null: Complete female gametophyte defective; Male gametophyte defective; Knockdown: Short roots	TN; RNAi
At2g48070	*RPH1*	C	MRP	V	GRS, PTH	Dwarf; Low chlorophyll levels (not visibly pale); Susceptible to *Phytophthora brassicae*	TD
At2g48120	*PAC*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g01020	*ISU2*	NC	MRP	V	GRS, IST, ARC	Dwarf; Thin inflorescence stems; Increased branching	RNAi
At3g01040	*GAUT13*	NC	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At3g01080	*WRKY58*	NC	CND	I	PTH	Curled, pointed, small, leaves with rough texture under defense response conditions	RV
At3g01090	*AKIN10*	NC	CND	H	NUT	Reduced starch transport under phosphate starvation	RV
At3g01120	*MTO1*	C	CLB	B	PRA	Elevated methionine levels	MB
At3g01140	*NOK*	C	CLB	C	STT	Increased trichome branching	MB
At3g01220	*AtHB20*	C	MRP	V	GER, HRM	Increased seed dormancy; Sensitive to ABA	RV
At3g01370	*AtCFM2*	C	ESN	S	EMB, W:PIG	Null: Embryo defective; Knockdown: Pale green leaves	RV
At3g01440	*PQL2*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At3g01460	*MBD9*	C	MRP	V	ARC, FLT	Increased branching; Early flowering	RV
At3g01480	*CYP38*	C	MRP	V	PIG, GRS, LIT	Pale green leaves; Dwarf; Sensitive to high light	RV
At3g01510	*LSF1*	C	CLB	B	PRA	Elevated starch levels	RV
At3g01610	*EMB1354*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At3g01780	*TPLATE*	C	ESN	G	GAM	Complete male gametophyte defective	RV; RNAi
At3g02000	*ROXY1*	C	MRP	R	FSM	Decreased petal number	RV
At3g02130	*RPK2*	C	MRP	V	IST, ARC, OVP, SRF	Spindly inflorescence stems; Increased branching; Male sterile due to abnormal anther dehiscence and pollen maturation	RV

At3g02140	*TMAC2*	NC	CND	H	NUT, HRM, CHS	Insensitive to ABA; Resistant to salt; Sensitive to glucose and sorbitol	RV
At3g02150	*PTF1*	C	CND	P	LIT	Pale cotyledons and slow growth under short days	RV
At3g02260	*TIR3*	C	MRP	V	ROT, LEF, IST, ARC, SRF	Short inflorescence stems; Increased branching; Short roots and petioles; Short siliques; Reduced auxin transport	MB; TD
At3g02280	*ATR3*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At3g02350	*GAUT9*	C	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At3g02410	*ICME-LIKE2*	C	CND	H	HRM, CHS	Sensitive to ABA; Resistant to salt and osmotic stress	RV
At3g02470	*SAMDC*	C	MRP	V	NLS, GRS, LEF, TCM	Dwarf; Short hypocotyl and petioles; Abnormal vascular bundle patterning	RV
At3g02580	*DWF7*	C	MRP	V	GRS	Dwarf; Low brassinosteroid levels	OTH
At3g02660	*EMB2768*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At3g02680	*NBS1*	C	CND	H	CHS	Sensitive to MMS (inducer of genotoxic stress) and mitomycin C (DNA cross-linking agent)	RV
At3g02850	*SKOR*	C	CLB	B	PRA	Low potassium levels in shoot and xylem sap	RV
At3g02870	*VTC4*	C	CLB	B	PRA	Low ascorbate levels	RV
At3g02875	*ILR1*	C	CND	H	HRM	Insensitive to IAA-Leu	MB
At3g02885	*GASA5*	C	MRP	V	GRS, FLT	Increased stem growth rate; Early flowering independent of photoperiod	RV
At3g03050	*KJK*	C	CLB	C	RTH	Defective root hairs	MB
At3g03090	*AtVGT1*	C	MRP	V	GER, FLT	Low germination rate; Late flowering	RV
At3g03450	*RGL2*	NC	CND	H	CHS	Germination resistant to paclobutrazol (inhibitor of GA biosynthesis)	RV
At3g03530	*NPC4*	C	CND	P	WAT, HRM, CHS	Sensitive to drought and salt; Insensitive to ABA	RV
At3g03630	*CS26*	C	MRP	V	PIG, GRS	Dwarf; Pale green leaves	RV
At3g03710	*PDE326*	C	MRP	V	PIG	Pale green seeds and seedlings	RV
At3g04240	*SEC*	NC	CND	H	CHS	Sensitive to paclobutrazol (GA biosynthesis inhibitor)	RV
At3g04260	*PDE324*	C	MRP	V	PIG	Pale green seeds and seedlings	RV

At3g04340	*EMB2458*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g04400	*EMB2171*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At3g04460	*PEX12*	C	ESN	S	EMB, W:SRL, W:GER, W:ROT, W:IST, W:HRM	Null: Embryo defective; Transition; Knockdown: Low penetrance of seedling lethality; Low germination rate; Short roots and inflorescence stems; Root growth resistant to 2,4-DB	RV
At3g04520	*THA2*	C	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At3g04580	*EIN4*	NC	MRP	V	LEF, HRM	Abnormal leaf morphology; Insensitive to ethylene	RV
At3g04680	*CLPS3*	C	ESN	G	EMG	Embryo defective; Female gametophyte defective	RV
At3g04740	*SWP*	C	MRP	V	NLS, PIG, GRS, ROT, LEF, IST, ARC, FSM, SRF, TCM	Lanceolate, slightly darker green cotyledons; Dwarf; Fasciated stems and inflorescences; Few, small leaves; Slightly reduced root growth; Abnormal floral morphology; Sterile; SAM becomes increasingly disrupted over time	TD
At3g04790	*EMB3119*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At3g04870	*PDE181*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g05000	*TGD8*	NC	ESN	G	EMG	Male gametophyte defective; Embryo defective (inferred)	TD
At3g05040	*HST*	C	MRP	V	NLS, ROT, LEF, ARC, FSM, SRF, MTM, TCM, LIT, NUT	Short hypocotyl and primary root; Small leaves, sepals, and petals; Few, upward-bending leaves; Abnormal phyllotaxy; Reduced fertility; Early vegetative phase change; Late flowering under short days; Large, rounded SAM; Dark-grown seedlings on sucrose: Open apical hook; Abnormal cotyledon positioning	MB
At3g05200	*ATL6*	C	CND	H	NUT	Sensitive to nitrogen starvation and glucose	RV
At3g05530	*RPT5a*	C	ESN	G	GAM, W:MGD, W:GRS, W:ROT, W:SRF	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes are viable: Dwarf; Short roots; Reduced fertility	RV
At3g05630	*PLDP2*	C	MRP	V	ROT, HRM	Short roots with reduced gravitropism;	RV

						Insensitive to auxin	
At3g05680	*EMB2016*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g05770	*PGD8*	NC	ESN	G	GEM	Male gametophyte defective; Embryo defective (inferred)	TD
At3g06120	*MUTE*	C	MRP	V	PIG, GRS, SRF, STT	Dwarf; Pale green; Sterile; Complete loss of stomata formation	MB
At3g06350	*EMB3004*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g06370	*NAX4*	C	CND	H	CHS	Resistant to salt stress	RV
At3g06400	*CHR11*	NC	ESN	G	GAM	Female gametophyte defective	RNAi
At3g06430	*EMB2750*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g06490	*MYB108*	C	MRP	R	SRF, SEN	Reduced fertility due to delayed anther dehiscence; Delayed floral organ senescence	RV
At3g06510	*SFR2*	C	CND	P	TMP	Sensitive to freezing	MB
At3g06560	*PAPS3*	C	ESN	G	MGD	Gametophyte defective	RV
At3g06730	*TRXP*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino to pale yellow	RV
At3g06810	*IBR3*	C	CND	H	HRM	Insensitive to IBA; Resistant to 2, 4-DB	MB; RV
At3g06860	*MFP2*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose	MB; RV
At3g06910	*ELS1*	C	MRP	V	GRS, IST	Dwarf; Thin inflorescence stems	RV
At3g06960	*PDE320*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g07020	*UGT80A2*	NC	MRP	R	SSC	Small seeds	RV
At3g07040	*RPM1*	C	CND	I	PTH	Resistant to certain bacterial pathogens	MB
At3g07060	*EMB1974*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g07100	*Sec24A*	NC	ESN	L	NHM, W:CUL	Null: No homozygous mutant plants recovered; Knockdown: Abnormal ER morphology	RV
At3g07130	*PAP15*	C	MRP	R	OVP	Low pollen germination rate	RV
At3g07160	*AtGSL10*	C	ESN	G	MGD, W:GRS	Null: Male gametophyte defective; Knockdown: Dwarf	RV
At3g07430	*EMB1990*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g07525	*ATG10*	C	MRP	V	GRS, SRF, FLT, SEN, NUT	Slightly slower rosette growth; Reduced fertility; Late flowering; Early senescence; Sensitive to carbon starvation and limited nitrogen	RV

At3g07560	*PEX13*	C	MRP	V	ROT, IST, HRM	Short inflorescence stems; Short roots; Root growth resistant to 2,4-DB	MB
At3g07610	*IBM1*	C	MRP	V	LEF, FSM, SRF	Small, narrow leaves; Arrested flower development; Reduced fertility	MB; RV
At3g07650	*COL9*	C	MRP	V	LEF, FLT	Few leaves; Early flowering	RV
At3g07970	*QRT2*	C	MRP	R	OVP	Tetrad pollen	RV
At3g08010	*AtAB2*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino	RV
At3g08040	*FRD3*	C	CLB	B	PRA	Elevated iron, manganese, and zinc levels	UNK
At3g08550	*KOB1*	C	MRP	V	GRS	Dwarf; Cellulose deficient	TD
At3g08710	*TRXH9*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose	RV
At3g08720	*S6K2*	C	MRP	R	SRF	Reduced fertility	RV
At3g08850	*RAPTOR1*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At3g08950	*HCC1*	C	ESN	S	EMB	Embryo defective; Transition	RV
At3g08970	*AtERdj3A*	C	ESN	G	MGD, TMP	Male gametophyte defective; Homozygotes are viable: Severely reduced male fertility at high temperature; Fertility phenotype rescued at low temperature	TD; RV
At3g09090	*DEX1*	C	MRP	R	OVP	Abnormal pollen exine layer	TD
At3g09150	*HY2*	C	MRP	V	NLS	Long hypocotyl	MB
At3g09260	*PYK10*	C	CND	I	PTH	Resistant to *Piriformospora indica*	RV
At3g09840	*CDC48*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective	RV
At3g10220	*EMB2804*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At3g10370	*SDP6*	C	ESN	L	SRL, GER	Seedling lethal without exogenous sucrose; Delayed germination	MB; RV
At3g10380	*SEC8*	C	ESN	G	GAM, W:MGD	Null: Complete male gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes appear wild type	RV
At3g10400	*U11/U12-31K*	NC	ESN	S	EMB, W:LEF, W:IST, W:MSL	Null: Embryo defective; Knockdown: Short inflorescence stems; Serrated leaves; Rosette leaf formation continues after bolting	RV; RNAi

At3g10420	*SPD1*	C	ESN	L	SRL, PIG	High penetrance of seedling lethality; Cotyledons and upper hypocotyl are mostly albino with small clusters of green cells	MB
At3g10570	*CYP77A6*	C	CLB	C	TCM, CUL	Complete loss of cuticle and nanoridges on petals	RV
At3g10670	*AtNAP7*	C	ESN	S	EMB	Embryo defective; Globular	RV
At3g10690	*AtGYRA*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At3g10800	*BZIP28*	C	CND	P	TMP	Severe chlorosis at high temperature	RV
At3g10870	*MES17*	C	MRP	V	NLS, HRM	Long hypocotyl; Long roots in response to MeIAA	RV
At3g10960	*AZG1*	C	CND	H	CHS	Resistant to toxic purine analogues	RV
At3g11050	*AtFER2*	C	CND	H	CHS	Germination sensitive to methyl viologen (inducer of oxidative stress)	RV
At3g11170	*FAD7*	C	CLB	B	CPR	Decreased dienoic fatty acid desaturation in chloroplast lipids	MB
At3g11220	*ELO1*	C	MRP	V	GER, NLS, ROT, LEF, IST, ARC	Very low germination rate; Slow seedling growth; Narrow leaves; Short primary root; Short inflorescence stems with abnormal architecture	RV
At3g11410	*PP2CA*	C	CND	H	HRM	Sensitive to ABA	RV
At3g11430	*GPAT5*	C	CLB	B	CPR	Abnormal insoluble lipid polyester biosynthesis	RV
At3g11480	*BSMT1*	NC	CLB	B	PRA, PTH	Low MeSA levels; Susceptible to parasitic wasps	RV
At3g11540	*SPY*	C	MRP	V	NLS, PIG, IST, FSM, SRF, FLT, CHS	Long hypocotyl; Pale green; Tall inflorescence stems; Reduced fertility; Siliques form without fertilization; Early flowering; Resistant to paclobutrazol (inhibitor of GA synthesis)	TD
At3g11670	*DGD1*	C	MRP	V	PIG	Pale green seeds and seedlings	OTH
At3g11820	*SYP121*	C	CND	I	PTH	Susceptible to *Blumeria graminis hordei*	MB
At3g11940	*AML1*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective	TD
At3g11980	*MS2*	C	MRP	R	SRF	Male sterile	TN
At3g12080	*EMB2738*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g12120	*FAD2*	C	CND	P	TMP	Sensitive to low temperature	MB

At3g12160	*RABA4D*	C	ESN	G	MGD	Altered pollen tube growth and morphology; Homozygotes are viable: 100% abnormal pollen	RV
At3g12280	*Rb*	C	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At3g12360	*ITN1*	C	CND	H	CHS	Seedling growth resistant to salt stress	MB; RV
At3g12380	*ARP5*	C	MRP	V	GRS, CHS	Dwarf; Sensitive to genotoxic stress	RV
At3g12400	*ELC*	C	CLB	C	STT, CUL	Clustered trichomes with multiple nuclei	RV
At3g12490	*CYS6*	C	MRP	V	GER, NLS	Early germination; Fast seedling growth	RV
At3g12670	*EMB2742*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g12810	*PIE1*	C	MRP	T	FLT	Early flowering independent of photoperiod	TD; RV
At3g13065	*SRF4*	C	MRP	V	LEF	Small leaves	RV
At3g13170	*AtSPO11-1*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	MB; RV
At3g13200	*EMB2769*	NC	ESN	S	EMB	Embryo defective; Globular	RV
At3g13220	*ABCG26*	C	MRP	R	SRF, SSC	Reduced fertility; Large seeds	RV
At3g13300	*VCS*	C	MRP	V	GRS, LEF, TMP	Dwarf; Narrow, asymmetric leaves; Sensitive to altered temperature	RV
At3g13490	*OVA5*	NC	ESN	G	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	RV
At3g13540	*MYB5*	C	MRP	R	SSC	Abnormal seed coat; Reduced mucilage extrusion from seeds	RV
At3g13550	*COP10*	C	ESN	L	SRL, PIG, ROT, LEF, MSL, SRF, STT, LIT	Red hypocotyl and cotyledons; Small rosette; Complete loss of petiole elongation; Red lower leaf surfaces due to anthocyanin accumulation; Green roots that become thick and purple over time; Low penetrance of sterile flowers without bolting; Abnormal trichome branching; Altered growth in dark	MB
At3g13870	*RHD3*	C	CLB	C	RTH	Abnormal root hair morphology	TD
At3g13890	*AtMYB26*	C	MRP	R	SRF	Male sterile due to failure of anther dehiscence	TN
At3g14110	*FLU*	C	ESN	L	SRL, LIT	Seedling lethal unless grown under continuous light; Elevated protochlorophyllide levels in the dark	MB
At3g14210	*ESM1*	C	CLB	B	PRA	Low nitrile levels; Heterozygotes: Intermediate phenotype	RV

At3g14230	*AtRAP2.2*	NC	ESN	L	NHM	No homozygous mutant plants recovered	RV
At3g14270	*FAB1B*	C	MRP	V	LEF	Curled leaves	RV
At3g14370	*WAG2*	C	CND	P	MPH	Wavy roots under vertical growth	RV
At3g14440	*NCED3*	C	CND	H	NUT, MCH	Insensitive to potassium and calcium; Sensitive to lithium	TD
At3g14900	*EMB3120*	C	ESN	S	EMB	Embryo defective; Transition	RV
At3g15150	*AtMMS21*	C	MRP	V	GRS, MPH	Dwarf; Short primary root under vertical growth	RV
At3g15170	*CUC1*	NC	MRP	V	NLS	Low penetrance of heart-shaped cotyledons	TD
At3g15390	*SDE5*	C	MRP	V	NLS, LEF, STT	Small seedlings; Elongated, curled leaves; Long petioles; Slightly early trichome development	MB; RV
At3g15500	*ANAC055*	NC	CND	I	PTH	Susceptible to bacterial infection	RV
At3g15620	*UVR3*	C	CND	P	LIT	Sensitive to UV light	OTH
At3g15730	*PLDA1*	C	CND	H	HRM	Abnormal stomatal regulation in response to ABA	RV
At3g15820	*ROD1*	C	CLB	B	PRA	Abnormal unsaturated fatty acid levels in seeds	MB
At3g15850	*FAD5*	C	CLB	B	CPR	Reduced thylakoid membrane unsaturation	OTH
At3g15950	*NAI2*	C	CLB	C	CUL	Complete loss of ER body formation	OTH; RV
At3g15990	*SULTR3;4*	C	MRP	V	LEF, FLT	Small rosette leaves; Early flowering; Slightly elevated sulfate levels in seeds	RV
At3g16290	*EMB2083*	C	ESN	S	EMB	Embryo defective; Transition	TD
At3g16630	*KINESIN-13A*	C	CLB	C	STT	Abnormal trichome branching	RV
At3g16640	*TCTP*	NC	ESN	G	GEM	Male gametophyte defective; Embryo defective (inferred)	RV
At3g16720	*ATL2*	C	CND	H	NUT	Sensitive to nitrogen starvation and glucose	RV
At3g16857	*ARR1*	NC	MRP	V	ROT	Long roots	RV
At3g16890	*PPR40*	C	MRP	V	GER, LEF, HRM	Slightly delayed germination; Small rosette; Sensitive to ABA	TD; RV
At3g16910	*ACN1*	C	CND	H	CHS	Resistant to fluoroacetate (toxic acetate analogue)	RV
At3g16950	*ptLPD1*	C	CND	H	MCH	Sensitive to arsenate	TD; RV
At3g17170	*RFC3*	C	CND	H	NUT	Abnormal lateral root formation in response to sucrose	MB
At3g17300	*EMB2786*	C	ESN	S	EMB	Embryo defective; Preglobular	RV

At3g17390	*MTO3*	C	CLB	B	PRA	Elevated methionine levels	MB
At3g17609	*HYH*	C	MRP	V	PIG, FLT, LIT	Slightly pale green; Early flowering; Long hypocotyl under blue light	RV
At3g17650	*PDE321*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g17910	*EMB3121*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At3g18110	*EMB1270*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g18165	*MOS4*	C	MRP	R	SRF, FLT	Reduced fertility; Late flowering	MB; RV
At3g18290	*EMB2454*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At3g18390	*EMB1865*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g18440	*AtALMT9*	C	CLB	B	PRA, CPR	Low malate levels; Decreased inward electrical currents in vacuoles; No other phenotypes detected	RV
At3g18630	*UNG*	C	CND	H	CHS	Resistant to 5-fluorouracil	RV
At3g18660	*GUX1*	C	CLB	B	CPR	Abnormal xylan modification	RV
At3g18680	*DPT1*	C	ESN	L	SRL, PIG, GRS	Seedling lethal without exogenous sucrose; Slow growth; Pale green leaves	MB
At3g18690	*MKS1*	NC	CND	I	PTH	Susceptible to *Pseudomonas syringae*	RV
At3g18730	*TSK*	C	MRP	V	ROT, IST, ARC	Short roots; Fasciated stems and inflorescences	TD
At3g18780	*ACT2*	C	CLB	C	RTH	Short root hairs	MB
At3g18990	*VRN1*	C	MRP	T	MTM	Reduced vernalization response	MB
At3g19040	*HAF2*	C	MRP	V	PIG	Pale green cotyledons; Yellow early leaves	RV
At3g19170	*PreP1*	C	MRP	V	MSL	Slightly chlorotic leaves	RV
At3g19180	*CDP1*	C	CLB	C	CUL	Few chloroplasts with abnormal morphology	RV
At3g19210	*AtRAD54*	C	CND	P	MPH, CHS	Sensitive to gamma radiation and cisplatin	RV
At3g19220	*CYO1*	C	ESN	L	SRL, PIG	Seedling lethal; Albino cotyledons	TD
At3g19570	*SCO3*	C	ESN	L	NHM, W:NLS, W:GRS	Null: No homozygous mutant plants recovered; Knockdown: Chlorotic cotyledons; Slight delay in growth	MB; RV
At3g19580	*AZF2*	C	CND	H	HRM	Germination sensitive to ABA	RV
At3g19590	*Bub3.1*	NC	ESN	G	MGD	Male and female gametophyte defective	UNK
At3g19700	*IKU2*	C	ESN	S	EMB	Embryo defective; Cotyledon	MB

At3g19710	*BCAT4*	C	CLB	B	PRA	Elevated free methionine levels in leaves; Low levels of methionine-derived glucosinolates	RV
At3g19720	*ARC5*	C	CLB	C	CUL	Few, large chloroplasts	MB
At3g19770	*AtVPS9A*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At3g19820	*DWF1*	C	MRP	V	GRS, SRF	Dwarf; Severely reduced fertility; Low brassinosteroid levels	TD
At3g19980	*EMB2736*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At3g20070	*TTN9*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged endosperm nuclei	TD
At3g20320	*TGD2*	C	MRP	V	PIG, GRS	Dwarf; Slightly pale green	MB
At3g20400	*EMB2743*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g20440	*EMB2729*	C	ESN	S	EMB, W:PIG, W:GRS	Null: Embryo defective; Transition; Knockdown: Dwarf; Pale	TD
At3g20470	*GRP5*	C	MRP	V	ROT, LEF, IST	Small leaves; Short roots and inflorescence stems	RNAi
At3g20475	*MSH5*	C	MRP	R	SRF	Reduced fertility	RV
At3g20550	*DDL*	C	MRP	V	ROT, FSM, SRF, FLT	Short roots; Abnormal floral organ number and morphology; Reduced fertility; Late flowering	RV
At3g20600	*NDR1*	C	CND	I	PTH	Susceptible to disease	MB
At3g20630	*TTN6*	C	ESN	S	EMB, CUL	Embryo defective; Globular; Enlarged endosperm nuclei	TD
At3g20740	*FIE*	C	ESN	S	MSD	Initiation of seed development in absence of fertilization; 50% defective seeds	MB
At3g20770	*EIN3*	C	CND	H	HRM	Insensitive to ethylene	TD
At3g20780	*BIN3*	C	ESN	L	SRL	Seedling lethal	RV
At3g20810	*JMJ30*	C	MRP	T	CDR	Abnormal circadian rhythms in leaf movements	RV
At3g20840	*PLT1*	C	MRP	V	ROT, TCM	Slightly slower root growth; Increased cell number in columella root cap and quiescent center	TD
At3g20870	*ZTP29*	C	CND	H	CHS	Germination and seedling growth sensitive to salt	RV
At3g21070	*NADK1*	NC	MRP	V	GRS, MPH, CHS	Dwarf; Sensitive to radiation and oxidative stress	RV

At3g21150		NC	CND	P	LIT	Short hypocotyl and small cotyledons under red light	RV
At3g21200	*PGR7*	C	MRP	V	PIG, GRS	Semi-dwarf; Slightly pale green	MB
At3g21560	*UGT84A2*	C	CLB	B	PRA	Sinapoylmalate levels low in leaves and elevated in trichomes	MB
At3g21630	*CERK1*	C	CND	I	PTH	Susceptible to fungal infection	RV
At3g21640	*UCU2*	C	MRP	V	LEF	Rolled leaves	MB
At3g22170	*FHY3*	C	CND	P	**LIT**	Short hypocotyl and complete loss of circadian rhythms under red light	RV
At3g22200	*POP2*	C	ESN	G	MGD, SRF	Male and female gametophyte defective; Homozygotes are viable: Sterile	MB
At3g22370	*AOX1A*	C	CND	H	CHS	Sensitive to antimycin A (inhibitor of the cytochrome pathway of respiration)	RV
At3g22380	*TIC*	C	MRP	V	PIG, LEF, MSL, FLT, CDR, NUT	Pale green; Slow leaf growth; Chlorosis; Early flowering; Abnormal circadian rhythms; Sensitive to iron	MB
At3g22400	*LOX5*	C	MRP	V	ROT	Slightly longer primary root; Increased lateral root number	RV
At3g22590	*CDC73*	C	MRP	T	FLT	Early flowering independent of photoperiod	TD; RV
At3g22680	*RDM1*	C	CLB	B	CPR	Decreased DNA methylation	MB; RV
At3g22780	*TSO1*	C	MRP	R	FSM, OVP, SRF	Serrated sepals; Unfused carpels; Long stigma papillae; Sterile; Abnormal integuments; Collapsed pollen	RV
At3g22880	*DMC1*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	RV
At3g22942	*AGG2*	C	MRP	V	ROT	Abnormal root architecture; Decreased basipetal auxin transport	RV
At3g22990	*LFR*	C	MRP	V	NLS, GRS, LEF, FSM, SRF, TCM	Upward-bending cotyledons and young leaves; Slow growth; Small rosette; Short, narrow leaves with long petioles; Downward-curling petals; Abnormal floral organ number; Short filaments; Reduced fertility; Abnormal cotyledon vasculature	MB; RV
At3g23050	*AXR2*	C	MRP	V	NLS	Slightly longer hypocotyl	MB
At3g23110	*EMB2800*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV

At3g23130	*SUP*	C	MRP	R	FSM	Homeotic floral transformations	MB
At3g23150	*ETR2*	C	CLB	C	STT	Abnormal trichome branching	RV
At3g23400	*FIB4*	C	CND	H	CHS, PTH	Sensitive to ozone; Susceptible to bacterial speck disease	RV
At3g23430	*PHO1*	C	CLB	B	CPR	Reduced phosphate transport in roots	MB
At3g23440	*EDA6*	NC	ESN	G	GAM, GEM	Female gametophyte defective; Embryo defective (inferred)	TD
At3g23560	*ALF5*	C	CND	H	MCH	Root growth sensitive to toxic compounds (including one in Bacto agar)	MB
At3g23820	*GAE6*	C	CLB	C	RTH	Short root hairs	RV
At3g23980	*BLI*	C	ESN	G	MGD, GER, NLS, GRS, LEF, FSM	Male gametophyte defective; Homozygotes are viable: Delayed germination; Dwarf; Slow growth; Small leaves and cotyledons with blister-like outgrowths; Abnormal flower morphology	RV
At3g24140	*FAMA*	C	MRP	V	PIG, GRS, LEF, ARC, SRF, STT	Pale green; Dwarf; Small rosette leaves; Increased branching; Sterile; Absence of stomata	RV
At3g24220	*NCED6*	C	CLB	B	PRA, CHS	Low ABA levels in seeds; Germination resistant to paclobutrazol (inhibitor of GA synthesis)	RV
At3g24260	*SEP3*	C	MRP	R	FSM	Sepal-like petals; Low penetrance of extra flowers forming at base of sepals	TN
At3g24320	*MSH1*	C	MRP	V	PIG	Variegated leaves	MB; RV
At3g24560	*RSY3*	C	ESN	S	EMB	Embryo defective; Globular	MB
At3g24590	*PLSP1*	C	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At3g24650	*ABI3*	C	MRP	V	GER, HRM	Reduced seed dormancy; Insensitive to ABA	MB
At3g25100	*CDC45*	C	MRP	R	SRF	Partial to complete sterility due to defects in meiosis	RNAi
At3g25140	*QUA1*	C	MRP	V	GRS, TCM	Dwarf; Reduced cell adhesion; Low pectin levels	TD
At3g25230	*ROF1*	C	CND	P	TMP	Sensitive to high temperature	RV
At3g25250	*OXI1*	C	CLB	C	RTH, PTH	Abnormal root hair development; Susceptible to virulent and avirulent bacteria	RV
At3g25520	*ATL5*	C	MRP	V	LEF	Slightly pointed, serrated leaves	MB

At3g25690	*CHUP1*	NC	CLB	C	CUL	Abnormal chloroplast positioning	OTH
At3g25860	*PLE2*	C	ESN	S	EMB	Embryo defective; Transition	RV
At3g26090	*RGS1*	C	MRP	V	ROT, LIT	Long primary roots; Short hypocotyl in the dark	RV
At3g26410	*TRM11*	NC	MRP	V	ROT, FLT	Short roots; Early flowering	RV
At3g26420	*AtRZ-1a*	C	CND	P	TMP	Germination and seedling growth sensitive to low temperature	RV
At3g26570	*PHT2;1*	C	MRP	V	LEF, NUT	Small rosettes; Low phosphate levels in response to elevated phosphate	RV
At3g26680	*SNM1*	C	CND	H	CHS	Sensitive to BLM (DNA damaging agent) and hydrogen peroxide	RV
At3g26744	*ICE1*	C	CLB	C	STT	Abnormal stomata morphology	RV
At3g26790	*FUS3*	C	ESN	S	EMB	Embryo defective; Leafy cotyledons	MB
At3g26830	*PAD3*	C	CND	I	PRA, PTH	Susceptible to fungal infection; Low camalexin levels	MB
At3g26900	*SKL1*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	RV
At3g27000	*ARP2*	C	CLB	C	STT, RTH, TCM	Distorted trichomes; Abnormal pavement and hypocotyl cell morphology; Abnormal root hairs; Complete loss of stomata on hypocotyl	MB; RV
At3g27060	*TSO2*	C	MRP	V	PIG, LEF, IST, ARC, FSM, SRF	Variegated leaves; Abnormal leaf and floral organ margins; Low penetrance of fasciated stems and inflorescences and stamens exhibiting carpel characteristics; Reduced fertility	MB
At3g27160	*GHS1*	C	MRP	V	PIG, LEF, NUT	Pale green; Small leaves; Sensitive to glucose	RV
At3g27460	*SGF29A*	NC	CND	P	LIT	Fewer, smaller rosette leaves and late flowering under short days	RV
At3g27530	*MAG4*	C	MRP	V	GRS	Dwarf	MB; RV
At3g27660	*OLEO4*	NC	CND	P	TMP	Germination sensitive to freezing	RV
At3g27670	*RST1*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g27730	*RCK*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	RV
At3g27740	*VEN6*	C	MRP	V	PIG, LEF	Small, pale green, curled leaves; Heterozygotes: Intermediate phenotype	MB; RV

At3g27750	*EMB3123*	C	ESN	S	EMB, W:PIG	Null: Embryo defective; Cotyledon; Knockdown: Pigment defective embryo	RV
At3g27810	*AtMYB21*	C	MRP	R	SRF	Severely reduced fertility	RV
At3g27820	*MDAR4*	C	ESN	L	SRL	Seedling lethal	MB; RV
At3g27920	*GL1*	C	CLB	C	STT	Reduced, abnormal trichomes	TD
At3g28030	*UVH3*	C	MRP	T	SEN, LIT, MPH	Early senescence; Sensitive to UV light and ionizing radiation	MB
At3g28470	*TDF1*	C	MRP	R	FSM, SRF	Male sterile; Abnormal anther development; Complete loss of pollen development	MB
At3g28730	*SSRP1*	C	MRP	V	LEF, ARC, FSM, SRF, FLT	Increased branching and leaf number; Abnormal flower and leaf morphology; Reduced fertility; Early flowering	RV
At3g28860	*PGP19*	C	MRP	V	NLS, LEF, IST, FLT	Downward-bending cotyledons and first true leaves; Curled, wrinkled rosette leaf margins; Slow inflorescence growth; Late flowering	RV
At3g28910	*MYB30*	C	CND	H	CHS	Sensitive to brassinazole (inhibitor of brassinosteroid biosynthesis)	RV
At3g29030	*EXPA5*	NC	MRP	V	NLS, ROT, LEF	Short hypocotyl and roots; Small rosette	RV
At3g29290	*EMB2076*	NC	ESN	S	EMB	Embryo defective; Transition	TD
At3g29320	*PHS1*	C	MRP	V	MSL	Chlorotic leaves	RV
At3g30180	*BR6OX2*	C	MRP	V	NLS, PIG, LEF, IST, FSM, SRF	Slightly smaller seedlings; Slightly shorter inflorescence stems; Rounded, curled, dark green leaves; Short petioles; Abnormal cauline leaf and stamen formation; Reduced fertility	RV
At3g33520	*AtARP6*	C	MRP	V	NLS, LEF, IST, FSM, SRF, FLT	Slightly longer hypocotyl; Short inflorescence stems; Small, curled leaves with serrated margins; Small flowers; Increased sepal and petal numbers; Reduced fertility; Early flowering independent of photoperiod	MB; RV
At3g42170	*DAYSLEEPER*	C	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At3g43210	*TES*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis; Large pollen	MB
At3g43300	*AtMIN7*	C	CND	I	PTH	Sensitive to avirulent bacteria	RV

At3g44110	*J3*	C	CND	H	CHS	Sensitive to a combination of salt and high pH	RV
At3g44200	*NEK6*	C	MRP	V	NLS, LEF, STT, TCM	Abnormal hypocotyl and petiole protrusions; Abnormal trichome branching; Disordered cell files in root epidermis	RV
At3g44260	*AtCAF1a*	C	CND	H	CHS	Sensitive to methyl viologen (inducer of oxidative stress); Germination resistant to salt stress	RV
At3g44310	*NIT1*	C	CND	H	HRM	Insensitive to IAN (auxin precursor)	MB
At3g44480	*RPP1*	C	CND	I	PTH	Altered response to fungal infection	OTH
At3g44530	*HIRA*	C	ESN	S	EMB	Embryo defective	RV
At3g44540	*FAR4*	NC	CLB	B	PRA	Abnormal suberin composition in roots and seed coat; No other phenotypes detected	RV
At3g44550	*FAR5*	C	CLB	B	W:PRA	Knockdown: Abnormal suberin composition in roots and seed coat; No other phenotypes detected	RV
At3g44880	*ACD1*	C	MRP	V	MSL	Necrotic lesions	OTH
At3g45100	*SETH2*	NC	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	RV
At3g45130	*LAS1*	C	CLB	B	PRA	Low sterol levels	RV
At3g45140	*LOX2*	C	CLB	B	PRA	Low levels of bound cyclopentenone jasmonates	RV
At3g45150	*TCP16*	NC	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	RNAi
At3g45300	*AtIVD*	C	CLB	B	PRA	Elevated levels of twelve different amino acids in seeds	OTH; RV
At3g45640	*AtMPK3*	NC	CND	H	CHS	Damaged, brittle leaves in response to ozone	RV
At3g45780	*NPH1*	C	CND	P	LIT	Reduced phototropism	TD
At3g45890	*RUS1*	C	MRP	V	ROT, LIT	Short roots; Seedling lethal when roots are exposed to UV-B light	MB
At3g46530	*RPP13*	C	CND	I	PTH	Altered response to fungal infection	MB
At3g46550	*SOS5*	C	MRP	V	ROT, CHS	Thick roots and root tips; Root growth sensitive to salts	MB
At3g46560	*EMB2474*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At3g46640	*PCL1*	C	MRP	T	CDR	Abnormal circadian rhythms	MB
At3g46740	*TOC75*	C	ESN	S	EMB	Embryo defective; Preglobular	RV

At3g46790	*CRR2*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence; No other phenotypes detected	MB
At3g46970	*PHS2*	C	MRP	V	LEF	Slightly larger rosette; Elevated maltose levels at night	RV
At3g47390	*PHS1*	C	MRP	V	GRS, MSL, LIT	Dwarf; Bleached leaves; Phenotype enhanced under high light	MB
At3g47440	*TIP5;1*	NC	CND	H	NUT	Short pollen tubes under nitrogen starvation	RV
At3g47450	*NOA1*	C	MRP	V	PIG, GRS, CHS	Pale green cotyledons; Delayed growth; Young leaves are pale; Resistant to fosmidomycin (inhibitor of isoprenoid biosynthesis)	RV
At3g47500	*CDF3*	NC	CND	P	LIT	Short hypocotyl under red light	RV
At3g47620	*AtTCP14*	C	CND	P	MPH, HRM, CHS	Freshly harvested seeds exhibit delayed germination; Germination sensitive to ABA and paclobutrazol (inhibitor of GA synthesis)	RV
At3g47690	*AtEB1a*	NC	MRP	V	ROT, MEC	Abnormal root gravitropism and thigmotropism	RV
At3g47710	*BNQ3*	C	MRP	R	PIG, FSM	Smaller floral organs; Albino or pale green sepals and carpels; Purple inflorescences and carpels	RV
At3g47860	*CHL*	C	CND	P	WAT, CHS	Sensitive to drought and photooxidative stress	RV
At3g47870	*SCP*	C	ESN	G	MGD	Male gametophyte defective; Homozygotes are viable: Abnormal pollen	MB; RV
At3g47930	*AtGLDH*	NC	ESN	L	SRL, GER	Seedling lethal without exogenous ascorbate; Delayed germination	RV
At3g47950	*AHA4*	C	MRP	V	ROT, IST, S:CHS	Slightly shorter roots and inflorescence stems; Sensitive to salt stress; Heterozygotes: Intermediate salt sensitive phenotype	TD
At3g47990	*SIS3*	C	CND	H	NUT	Insensitive to elevated sugar	MB; RV
At3g48090	*EDS1*	C	CND	I	PTH	Susceptible to fungal infection	TN
At3g48100	*ARR5*	NC	CND	P	LIT	Small rosette leaves under short days; Short hypocotyl under red light	RV
At3g48110	*EDD*	C	ESN	S	EMB	Embryo defective; Globular	TN
At3g48160	*DEL1*	C	CLB	C	CUL	Abnormal ploidy levels	RV
At3g48190	*ATM*	C	MRP	R	SRF	Reduced female fertility	RV

At3g48250	*BIR6*	C	MRP	V	GRS, CHS	Dwarf; Resistant to buthionine sulfoximine (inhibitor of glutathione biosynthesis), mannitol, and salt stress	MB; RV
At3g48360	*BT2*	C	CND	H	NUT, HRM	Sensitive to sugar and ABA	RV
At3g48430	*REF6*	NC	MRP	V	LEF, FLT	Short petioles and leaf blades; Late flowering	RV
At3g48470	*EMB2423*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At3g48500	*PDE312*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g48670	*IDN2*	C	MRP	T	FLT	Late flowering; Decreased DNA methylation	MB
At3g48690	*AtCXE12*	C	CND	H	HRM	Resistant to 2,4-D-methyl	RV
At3g48750	*CDC2*	C	ESN	G	MGD, MSD	Male gametophyte defective; Bicellular pollen; 50% defective seeds	RV
At3g48930	*EMB1080*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At3g49170	*EMB2261*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At3g49180	*RID3*	C	CND	P	TMP	Shoots fail to regenerate from callus at high temperature	MB
At3g49240	*EMB1796*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g49250	*DMS3*	C	CLB	B	CPR	Abnormal DNA methylation	MB
At3g49500	*SGS2*	C	CND	I	PTH	Susceptible to viral infection	MB
At3g49600	*UBP26*	C	ESN	S	MSD, SRF, SSC	50% defective seeds; Low penetrance of endosperm development without fertilization; Reduced fertility; Shriveled seeds	MB; RV
At3g49660	*AtMUT11*	NC	ESN	S	EMB	Embryo defective	RV
At3g49700	*ACS9*	C	MRP	V	NLS, IST, FLT	Tall inflorescence stems; Large cotyledons; Long hypocotyl; Early flowering; Enhanced ethylene production	RV
At3g49940	*LBD38*	NC	CND	H	NUT	Elevated anthocyanin levels in response to nitrogen	RV
At3g50060	*MYB77*	C	CND	H	HRM	Abnormal lateral root number in response to IAA	RV
At3g50500	*SnRK2.2*	NC	MRP	V	GER, STT, HRM	Slightly reduced seed dormancy; Abnormal stomata; Insensitive to ABA	RV
At3g50660	*DWF4*	C	MRP	V	GRS	Dwarf	TD

At3g50820	*PsbO2*	NC	MRP	V	PIG, GRS, LEF	Slow growth; Long, dark green leaves with bent margins	RV
At3g50870	*MNP*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At3g51060	*STY1*	NC	MRP	R	FSM, SRF	Abnormal style morphology; Slightly reduced fertility	RV
At3g51160	*MUR1*	C	MRP	V	GRS	Dwarf; Low L-fucose levels in cell wall	MB
At3g51240	*TT6*	C	MRP	R	PIG, SSC	Yellow seed coat	TN
At3g51460	*RHD4*	C	CLB	C	RTH	Short root hairs with randomly formed bulges	MB
At3g51550	*FER*	C	ESN	G	GEM	Female gametophyte defective; Embryo defective (inferred)	MB
At3g51770	*ETO1*	NC	CND	H	CHS	Necrotic lesions in response to ozone	RV
At3g51780	*AtBAG4*	C	MRP	V	S:PIG, S:ROT, S:LEF, S:ARC, S:FLT, S:SEN	Heterozygotes: Increased branching and lateral root number; Early flowering and senescence; Incomplete penetrance of purple leaves; Homozygotes not mentioned	RV
At3g51820	*PDE325*	C	MRP	V	PIG	Pale green seeds and seedlings	RV
At3g51840	*ACX4*	C	CND	H	HRM	Resistant to 2,4-DB	RV
At3g51860	*CAX3*	C	CND	H	NUT	Sensitive to calcium	RV
At3g51970	*ASAT1*	C	CLB	B	PRA	Low sterol ester levels in leaves	RV
At3g52115	*AtGR1*	C	MRP	R	SRF	Sterile due to defects in meiosis	RV
At3g52180	*SEX4*	C	MRP	V	GRS, FLT	Dwarf; Late flowering; Elevated starch levels	RV
At3g52190	*PHF1*	C	CND	H	NUT	Under limited phosphate: Dwarf; Many, large root hairs; Elevated anthocyanin levels	MB
At3g52280	*GTE6*	C	MRP	V	LEF	Abnormal leaf shape	RV
At3g52380	*PDE322*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At3g52430	*PAD4*	C	CND	I	PRA, PTH	Susceptible to fungal infection; Low camalexin levels	MB
At3g52450	*PUB22*	C	CND	P	WAT	Resistant to drought	RV
At3g52560	*UEV1D-4*	C	CND	H	CHS	Germination and seedling growth sensitive to MMS (inducer of genotoxic stress)	RV
At3g52590	*EMB2167*	NC	ESN	G	GEM, EMG	Male and female gametophyte defective; Embryo defective	TD

At3g52770	*ZPR3*	C	MRP	V	GRS	Dwarf	RV
At3g52940	*FK*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At3g53020	*STV1*	C	MRP	V	NLS, GRS, ROT, LEF, FSM, OVP, SRF, TCM	Low penetrance of fused cotyledons and decreased cotyledon number; Dwarf; Small, pointed leaves; Slow root growth; Abnormal pistil morphology; Short integuments; Reduced fertility; Abnormal cotyledon vasculature	TD; RV
At3g53110	*LOS4*	C	MRP	T	FLT, TMP, HRM	Early flowering; Resistant to freezing; Sensitive to elevated temperatures; Germination sensitive to ABA	MB
At3g53130	*LUT1*	C	CLB	B	PRA	Low lutein levels; No other phenotypes detected	MB
At3g53420	*PIP2;2*	C	CLB	B	CPR	Reduced hydraulic conductivity in roots	RV
At3g53480	*ABCG37*	C	CND	H	HRM	Sensitive to auxin	MB
At3g53720	*AtCHX20*	C	CLB	C	STT	Reduced stomatal width	RV
At3g53760	*GCP4*	C	MRP	V	GRS, SRF	Dwarf; Sterile	RNAi
At3g53900	*UPP*	C	ESN	L	SRL, PIG, GRS, ROT, MEC	Seedling lethal without exogenous sucrose; Dwarf; Pale green to albino; Few lateral roots; Fragile roots	RV
At3g54010	*PAS1*	C	ESN	S	EMB, SRL	Embryo and seedling defective	TD
At3g54050	*HCEF1*	C	MRP	V	GRS	Slow growth	MB
At3g54110	*PUMP1*	C	MRP	V	GRS	Decreased inflorescence biomass; Decrease in photosynthesis	RV
At3g54170	*FIP37*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g54220	*SCR*	C	MRP	V	ROT	Slow root growth	MB
At3g54280	*RGD3*	C	CND	P	TMP, HRM	Unable to regenerate shoots from callus; Phenotype enhanced at high temperature	MB; RV
At3g54320	*WRI1*	C	ESN	S	EMB	Embryo defective; Cotyledon	MB
At3g54340	*AP3*	C	MRP	R	FSM	Homeotic floral transformations	OTH
At3g54350	*EMB1967*	C	ESN	S	EMB	Embryo defective; Transition	TD
At3g54610	*GCN5*	C	MRP	V	GRS, ROT, LEF, ARC, MSL, FSM, SRF	Dwarf; Increased branching; Short roots; Small rosette; Serrated, chlorotic leaves; Short stamens and petals; Reduced fertility	RV

At3g54640	*TRP3*	C	ESN	L	SRL, CHS	Seedling lethal without exogenous tryptophan; Resistant to anthranilate analogs (herbicide)	OTH
At3g54650	*FBL17*	C	ESN	G	MGD, MSD	Male gametophyte defective; Bicellular pollen; 50% defective seeds	RV
At3g54660	*EMB2360*	C	ESN	S	EMB	Embryo defective; Globular	TD
At3g54670	*TTN8*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged endosperm nuclei	TD
At3g54690	*SETH3*	C	ESN	G	GAM	Complete male gametophyte defective	TD
At3g54720	*AMP1*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB
At3g54810	*BME3*	C	MRP	V	GER, TMP	Low germination rate; Reduced response to cold stratification	RV
At3g54870	*MRH2*	C	CLB	C	RTH	Wavy, branched root hairs	MB; RV
At3g54920	*PMR6*	C	CND	I	PTH	Resistant to powdery mildew	TD
At3g55010	*EMB2818*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At3g55120	*TT5*	C	MRP	R	PIG, SSC	Yellow seed coat	OTH
At3g55130	*AtWBC19*	C	CND	H	CHS	Sensitive to kanamycin	RV
At3g55250	*PDE329*	NC	MRP	V	PIG	Pigment defective embryo	RV
At3g55270	*MKP1*	C	CND	H	CHS	Sensitive to genotoxic stress	TD
At3g55360	*CER10*	C	MRP	V	NLS, GRS, LEF, IST, ARC, FSM, SRF	Downward-bending cotyledons; Dwarf; Glossy, thin, zig-zag inflorescences; Small, crinkled leaves; Fused floral buds; Short, crooked stamen filaments; Reduced male fertility	MB; RV
At3g55400	*OVA1*	NC	ESN	G	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	RV
At3g55480	*PAT2*	C	ESN	L	SRL, GER, ROT, ARC	Low penetrance of seedling lethality; Low germination rate over time; Short roots; Few lateral roots; Abnormal inflorescence stem gravitropism	MB; RV
At3g55510	*RBL*	NC	ESN	S	EMB	Embryo defective; Transition	MB; RV
At3g55530	*SDIR1*	C	MRP	V	ROT	Long primary root	RV
At3g55610	*P5CS2*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At3g55620	*EMB1624*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At3g55630	*FPGS3*	NC	CLB	B	PRA	Low methionine levels	RV

At3g55830	*EPC1*	C	ESN	L	SRL, NLS, PIG, ROT, LEF, ARC, MSL, SRF, MEC	High penetrance of seedling lethality on soil; Curled, thick cotyledons; Short hypocotyls; Short roots; Increased lateral root number; Pale, bleached, small rosette leaves; Complete loss of branching; Severely reduced fertility; Fragile cotyledons	RV
At3g55990	*ESK1*	C	CND	P	TMP	Resistant to freezing	MB; RV
At3g56040	*UGP3*	C	CLB	B	PRA	Complete loss of sulfolipid accumulation; No other phenotypes detected	RV
At3g56400	*WRKY70*	C	CND	H	HRM, PTH	Elevated anthocyanin levels in response to jasmonic acid; Susceptible to fungal infection	RV
At3g56800	*CaM3*	C	CND	P	TMP	Sensitive to high temperature	RV
At3g56940	*CHL27*	C	MRP	V	PIG, GRS, MSL	Dwarf; Pale green; Chlorotic	RV
At3g56960	*PIP5K4*	C	CLB	C	STT	Delayed, decreased stomatal opening	RV
At3g57040	*ARR9*	NC	MRP	V	ROT	Slightly fewer lateral roots	RV
At3g57090	*FIS1A*	NC	MRP	V	GRS, CUL	Semi-dwarf; Abnormal mitochondria and peroxisome morphology	RV
At3g57130	*BOP1*	C	MRP	V	NLS, LEF, FSM, SEN	Ectopic organ outgrowths on the basal portion of cauline leaves and the petioles of cotyledons and rosette leaves; Fused rosette leaf petioles; Reduced leaf number; Abnormal floral organ number and morphology; Delayed senescence	MB
At3g57150	*AtCBF5*	C	ESN	L	NHM	No homozygous mutant plants recovered	RV
At3g57180	*BPG2*	C	MRP	V	PIG, CHS	Pale green cotyledons; Resistant to brassinazole (inhibitor of brassinosteroid synthesis)	TD; RV
At3g57510	*ADPG1*	C	MRP	R	FSM	Reduced silique shattering	RV
At3g57650	*LPAT2*	C	ESN	G	GAM, GEM, S:LEF	Female gametophyte defective; Embryo defective (inferred); Heterozygotes: Slightly shorter rosette leaves	RV
At3g57670	*NTT*	C	MRP	R	SRF	Reduced fertility	RV
At3g57860	*OSD1*	C	MRP	R	OVP, CUL	Dyad pollen; Increased ploidy levels	RV
At3g57870	*EMB1637*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD

At3g57920	*SPL15*	C	MRP	V	GRS, LEF	Dwarf; Increased rosette leaf number	RV
At3g58070	*GIS*	C	CLB	C	STT	Abnormal trichomes on inflorescence organs; Heterozygotes: Intermediate phenotype	RV
At3g59030	*TT12*	C	MRP	R	PIG, SSC	Yellow seed coat	TD
At3g59050	*PAO3*	C	ESN	G	MGD, SRF	Male gametophyte defective; Homozygotes are viable: Reduced fertility	RV
At3g59060	*PIL6*	C	CND	P	LIT	Short hypocotyl and large cotyledons under red light	RV
At3g59220	*PRN*	C	CND	H	TMP, HRM	Delayed germination without stratification; Germination and early seedling growth sensitive to ABA	RV
At3g59380	*FTA*	C	MRP	V	GRS, IST, ARC, FSM, SRF, FLT, TCM	Dwarf; Slow growth; Low penetrance of fasciated stems and inflorescences; Increased floral organ number; Reduced fertility; Late flowering; Large shoot meristem	MB; RV
At3g59400	*GUN4*	C	MRP	V	PIG, GRS	Dwarf; Albino or yellow	MB; RV
At3g59420	*ACR4*	C	MRP	V	ROT, OVP, TCM	Few lateral roots; Abnormal integuments; Increased lateral root meristem number	RV
At3g59550	*SYN3*	C	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At3g59770	*SAC9*	C	MRP	V	PIG, GRS, LEF	Slow growth; Upward-bending, purple leaves	MB; RV
At3g60190	*ADL1E*	C	CND	I	PTH	Resistant to *Erysiphe cichoracearum* and *Botrytis cinerea*	MB
At3g60330	*AHA7*	NC	CLB	C	RTH	Decreased root hair density	RV
At3g60370	*AtFKBP20-2*	C	MRP	V	PIG, GRS, LEF	Dwarf; Small, pale green leaves	RV
At3g60460	*DUO1*	C	ESN	G	GAM	Complete male gametophyte defective	MB
At3g60500	*CER7*	C	MRP	V	GER, PIG, IST, FSM	Very low germination rate; Bright green, glossy stems, inflorescences, and siliques	MB; RV
At3g60740	*TTN1*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	MB; TD
At3g60830	*ARP7*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At3g61110	*ARS27*	C	CND	H	CHS	Sensitive to DNA damaging agents	TD

At3g61140	*FUS6*	C	ESN	L	SRL, PIG, LIT, NUT	Seedling lethal; Red seeds and cotyledons due to anthocyanin accumulation; Abnormal growth in the dark; Short roots in response to sugar	TD
At3g61190	*BAP1*	C	MRP	V	LEF, PTH	Small, curled leaves; Resistant to disease	RV
At3g61430	*PIP1;2*	C	CLB	B	CPR	Reduced root hydrostatic hydraulic conductivity	RV
At3g61440	*CYS-C1*	C	CLB	C	RTH	Abnormal root hairs	RV
At3g61510	*ACS1*	C	MRP	V	NLS, IST, FLT	Large cotyledons; Long hypocotyl; Thin inflorescence stems; Early flowering; Low ethylene levels	RV
At3g61710	*ATG6*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At3g61730	*RMF*	NC	MRP	V	GRS, LEF, FSM	Increased growth rate; Large leaves and flowers	RNAi
At3g61780	*EMB1703*	C	ESN	S	EMB	Embryo defective; Transition	TD
At3g61850	*DAG1*	C	MRP	V	GER, LIT	Reduced seed dormancy; Seeds germinate in darkness; Altered response to red and far-red light	RV
At3g61890	*AtHB-12*	C	CND	H	HRM	Long roots in response to ABA	RV
At3g62030	*ROC4*	C	CND	H	CHS	Sensitive to osmotic stress and elevated salt	RV
At3g62090	*PIF6*	C	MRP	V	GER	Low germination rate	RV
At3g62800	*DRB4*	NC	MRP	V	LEF	Downward-bending leaf margins	RV
At3g62910	*APG3*	C	ESN	L	SRL, PIG	Albino seeds and seedlings	TN
At3g62980	*TIR1*	C	MRP	V	NLS, ROT, HRM	Abnormal hypocotyl and lateral root formation; Insensitive to auxin	TD
At3g63190	*HFP108*	NC; C	ESN	S	EMB, W:SRL	Null: Embryo defective; Knockdown: Seedling lethal without exogenous sucrose	MB; RV
At3g63250	*HMT2*	C	CLB	B	PRA	Elevated methionine levels in seeds	MB; RV
At3g63300	*FKD1*	C	CLB	C	TCM	Abnormal cotyledon vascular patterning; No other phenotypes detected	MB; RV
At3g63410	*APG1*	C	ESN	L	SRL, PIG	Seedling lethal; Pale green	MB; RV
At3g63420	*AGG1*	C	MRP	V	ROT	Abnormal root architecture; Increased basipetal auxin transport	RV
At3g63490	*EMB3126*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV

At3g63520	*CCD1*	C	CLB	B	PRA	Elevated carotenoid levels in seeds; No other phenotypes detected	RV
At3g63530	*BB*	C	MRP	R	FSM	Large floral organs	MB; RV
At4g00020	*AtBRCA2a*	NC	ESN	G	MGD, CHS	Female gametophyte defective; Homozygotes are viable: Sensitive to genotoxic stress	RV
At4g00100	*PFL2*	C	MRP	V	ROT, LEF, STT, LIT	Narrow, pointed first true leaves; Short roots; Decreased density and abnormal branching of trichomes; Late flowering under continuous light	TN
At4g00220	*JLO*	C	ESN	S	EMB	Embryo defective; Globular	RV
At4g00310	*EDA8*	NC	ESN	G	GAM, GEM	Female gametophyte defective; Embryo defective (inferred)	TD
At4g00330	*PDD25*	NC	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	TD
At4g00450	*CRP*	NC	MRP	R	SRF, TCM	Reduced fertility; Large SAM	RV
At4g00620	*EMB3127*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At4g00650	*FRI*	C	MRP	T	MTM	Altered vernalization requirement for flowering	MB
At4g00710	*BSK3*	C	CND	P	LIT, HRM	Short hypocotyl in the dark; Insensitive to brassinosteroids	RV
At4g00730	*ANL2*	C	MRP	V	ROT	Abnormal root architecture; Low anthocyanin levels in subepidermal cells	TN
At4g00800	*SETH5*	NC	ESN	G	GAM	Male gametophyte defective; Female gametophyte defective; Rare embryo defective (inferred)	TD; RV
At4g01050	*TROL*	C	MRP	V	PIG, GRS, LEF, CUL	Slow growth; Small rosette; Thick leaves; Incomplete penetrance of yellow inflorescences and siliques; Small chloroplasts with altered morphology	RV
At4g01060	*CPL3*	NC	CLB	C	STT, RTH	Increased trichome density; Abnormal root hairs	RV
At4g01100	*ADNT1*	C	MRP	V	ROT	Slightly shorter roots; Decreased cellular respiration	RV
At4g01190	*PIPK10*	C	CND	H	CHS	Pollen tube growth sensitive to latrunculin B (inhibitor of actin polymerization)	RV

At4g01220	*MGD4*	C	ESN	G	GAM, W:MGD, W:SRF	Null: Complete male gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes are viable: Reduced fertility	TN; RV
At4g01370	*MPK4*	C	MRP	V	GRS, LEF, SRF, PTH	Dwarf; Curled leaves; Reduced fertility; Resistant to bacterial and oomycete infection	TN
At4g01470	*TIP1;3*	NC	CND	H	NUT	Short pollen tubes under nitrogen starvation	RV
At4g01500	*NGA4*	C	MRP	R	FSM	Altered pistil morphology	RV
At4g01540	*NTM1*	NC	MRP	V	NLS	Long hypocotyl	RV
At4g01800	*AGY1*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	TD
At4g02060	*PRL*	C	ESN	G	EMG	Embryo defective; Female gametophyte defective	TN
At4g02150	*MOS6*	C	CND	I	PTH	Susceptible to oomycete infection	MB
At4g02195	*SYP42*	NC	ESN	G	GAM	Complete male gametophyte defective	RV
At4g02280	*SUS3*	C	CLB	B	PRA	Elevated sucrose levels; Low fructose and starch levels; No other phenotypes detected	RV
At4g02460	*PMS1*	C	ESN	G	MGD, SRF	Male and female gametophyte defective; Homozygotes are viable: Reduced fertility	RV
At4g02510	*PPI2*	C	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At4g02560	*LD*	C	MRP	T	FLT	Late flowering	TD
At4g02570	*AXR6*	C	ESN	G	EMG, S:HRM	Embryo defective; Male and female gametophyte defective; Heterozygotes: Resistant to 2,4-D	MB
At4g02700	*SULTR3;2*	C	MRP	V	LEF, FLT	Small rosette leaves; Early flowering; Slightly elevated sulfate levels in seeds	RV
At4g02780	*GA1*	C	MRP	V	GER	Complete loss of germination without exogenous GA	OTH
At4g02790	*EMB3129*	C	ESN	S	EMB	Embryo defective; Globular	RV
At4g02980	*ABP1*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g03110	*RBP-DR1*	C	CND	I	PTH	Susceptible to bacterial infection	RV
At4g03240	*AtFH*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At4g03280	*PGR1*	C	CLB	B	W:CPR	Knockdown: Reduced electron transport at saturating light intensities; No other phenotypes detected	MB

At4g03430	*EMB2770*	C	ESN	S	EMB, W:LEF, W:IST, W:FLT	Null: Embryo defective; Transition; Knockdown: Small leaves with abnormal morphology; Short inflorescence stems; Early flowering	RV
At4g03550	*AtGSL5*	C	CND	P	MEC, PTH	Altered response to wounding; Resistant to powdery mildew	RV
At4g03560	*AtTPC1*	C	CND	H	NUT, HRM	Insensitive to ABA; Abnormal stomatal regulation in response to calcium	RV
At4g04350	*EMB2369*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g04720	*CPK21*	C	CND	H	CHS	Resistant to hyperosmotic stress	RV
At4g04770	*LAF6*	C	MRP	V	PIG, LIT	Slightly pale green seedlings; Long hypocotyl in far-red light	TN
At4g04780	*MED21*	C	ESN	L	NHM, W:PTH	Null: No homozygous mutant plants recovered; Knockdown: Susceptible to necrotrophic fungi	RV
At4g04885	*PCFS4*	C	MRP	T	FLT	Late flowering independent of photoperiod	RV
At4g05120	*FUR1*	C	CND	H	CHS	Insensitive to fluorouridine (toxic uridine analog)	MB; RV
At4g05190	*AtK5*	C	CLB	C	CUL	Abnormal mitotic spindle morphogenesis	RV
At4g05410	*YAO*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective	TN
At4g05450	*PGD6*	NC	ESN	G	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	TD
At4g05530	*IBR1*	C	CND	H	HRM	Insensitive to IBA	RV
At4g08150	*BP*	C	MRP	V	IST, FSM	Short inflorescence stems; Downward-pointing flowers and siliques	MB
At4g08390	*sAPX*	C	CND	H	CHS	Elevated hydrogen peroxide levels under photooxidative stress	RV
At4g08810	*SUB1*	C	CND	P	LIT	Sensitive to blue and far-red light	TD
At4g08870	*ARGAH2*	NC	MRP	V	ROT	Increased lateral and adventitious root number; Elevated nitric oxide levels	RV
At4g08900	*ARGAH1*	NC	MRP	V	ROT	Increased lateral and adventitious root number; Elevated nitric oxide levels	RV
At4g08920	*HY4*	C	MRP	V	NLS	Long hypocotyl	TD
At4g08950	*EXO*	C	MRP	V	GRS, HRM	Reduced biomass; Root growth sensitive to brassinosteroids	RV

At4g09020	*ISA3*	NC	CLB	B	PRA	Severely elevated starch levels; No other phenotypes detected	RV
At4g09080	*TOC75-IV*	C	CLB	C	CUL	Slightly altered etioplast morphology; No other phenotypes detected	RV
At4g09570	*CPK4*	C	CND	H	HRM, CHS	Insensitive to ABA; Resistant to salt	RV
At4g09650	*PDE332*	NC	ESN	L	SRL, PIG	Seedling lethal; Pale yellow seedlings; Pigment defective embryo	RV
At4g09820	*TT8*	C	MRP	R	PIG, SSC	Yellow seed coat	TD
At4g09980	*EMB1691*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g10090	*ELP6*	C	CND	H	HRM	Root growth sensitive to ABA	MB
At4g10180	*DET1*	C	MRP	V	PIG, GRS, LIT	Dwarf; Red cotyledons and lower leaf surfaces; Green roots; Dark-grown seedlings are de-etiolated	MB
At4g10380	*NIP5;1*	C	CND	H	NUT	Sensitive to limited boron	RV
At4g10710	*SPT16*	C	MRP	V	LEF, ARC, FSM, SRF, FLT	Increased branching and leaf number; Early flowering; Abnormal flower and leaf morphology; Reduced fertility	RV
At4g10760	*EMB1706*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g11130	*RDR2*	NC	CLB	B	CPR	Complete loss of telomeric DNA methylation	UNK
At4g11150	*EMB2448*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g11260	*EDM1*	C	CND	I	PTH	Susceptible to downy mildew	MB
At4g11280	*ACS6*	C	MRP	V	NLS, IST, FLT	Large cotyledons; Long hypocotyl; Tall inflorescence stems; Early flowering	RV
At4g11660	*HsfB2b*	C	CND	I	PTH	Resistant to disease	RV
At4g11720	*HAP2*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective (inferred)	RV
At4g11820	*FKP1*	C	MRP	R	SRF	Male sterile	TD
At4g12030	*BASS5*	C	CLB	B	PRA	Elevated methionine levels; Low levels of methionine-derived glucosinolates; No other phenotypes detected	RV
At4g12420	*SKU5*	C	CND	P	MPH	Skewed root growth on tilted agar surface	TD
At4g12470	*AZI1*	C	CND	I	PTH	Complete loss of systemic acquired resistance	RV
At4g12560	*CPR30*	C	MRP	V	GRS, MSL, PTH	Dwarf; Severe chlorosis; Resistant to bacterial infection	RV

At4g12570	*UPL5*	C	MRP	T	SEN	Early senescence	RV
At4g12720	*NUDT7*	C	MRP	V	GRS, LEF	Dwarf; Curled leaves	RV
At4g13420	*HAK5*	NC	CND	H	NUT, CHS	Reduced fresh weight under limited potassium and elevated salt	RV
At4g13430	*LeuC1*	C	CLB	B	PRA	Abnormal aliphatic glucosinolate composition; Elevated levels of intermediates of leucine biosynthesis and methionine chain elongation	RV
At4g13510	*AMT1;1*	C	CND	H	LEF, NUT	Seedling lethal when grown on both sucrose and ammonium; Slightly thicker leaves	RV
At4g13520	*SMAP1*	C	CND	H	HRM, CHS	Resistant to 2,4-D and PCIB (toxic anti-auxin)	MB; RV
At4g13750	*EMB2597*	C	ESN	S	EMB, W:ROT, W:LEF, W:TCM	Null: Embryo defective; Cotyledon; Knockdown: Narrow rosette leaves; Short roots; Reduced rosette leaf venation	TD
At4g13770	*CYP83A1*	C	CLB	B	PRA	Low levels of phenylpropanoid derivatives; No other phenotypes detected	MB
At4g13890	*EDA36;EDA37*	NC	ESN	G	GAM, GEM	Female gametophyte defective; Embryo defective (inferred)	TD
At4g13940	*EMB1395*	C	ESN	S	EMB, W:GRS	Null: Embryo defective; Globular; Knockdown: Delayed growth	TD
At4g14070	*AAE15*	C	CLB	B	CPR	Reduced 14C fatty acid elongation; No other phenotypes detected	RV
At4g14110	*COP9*	C	ESN	L	SRL, PIG, LIT	Seedling lethal; Red embryos and cotyledons due to anthocyanin accumulation; Dark-grown seedlings are de-etiolated	TD
At4g14130	*XTH15*	NC	CND	P	LIT	Short petioles under green shadelight and low red:far-red light	RV
At4g14180	*AtPRD1*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	RV
At4g14210	*PDE226*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At4g14590	*EMB2739*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At4g14713	*PPD1*	C	MRP	V	LEF, FSM	Curved leaves; Abnormal silique width; Heterozygotes: Intermediate phenotype	MB; RV
At4g14750	*FRC3*	C	CLB	C	STT	Reduced trichome branching	MB

At4g14790	*PDD17;PDD26*	NC	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	TD
At4g14850	*LOI1*	C	MRP	V	GRS, CHS	Slow growth; Resistant to lovastatin (inhibitor of isoprenoid biosynthesis)	MB
At4g14870	*SECE1*	C	ESN	L	SRL, PIG	Seedling lethal; Albino embryos	RV
At4g14880	*OLD3*	NC	ESN	L	SRL	Seedling lethal	MB
At4g14960	*TUA6*	NC	MRP	V	NLS	Short, thick hypocotyl	RV
At4g15090	*FAR1*	C	CND	P	LIT	Altered response to far-red light	MB
At4g15180	*SDG2*	C	MRP	V	GRS, SRF	Dwarf; Completely sterile	RV
At4g15230	*AtPDR2*	NC	CLB	B	CPR	Abnormal root exudate profiles	RV
At4g15560	*CLA*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At4g15570	*MAA3*	NC	ESN	G	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	MB
At4g15802	*HSBP*	C	MRP	R	SRF, FLT	Reduced fertility; Early flowering	RV
At4g15880	*ESD4*	C	MRP	V	GRS, FLT	Dwarf; Early flowering independent of photoperiod	MB; RV
At4g15900	*PRL1*	C	CND	H	NUT	Sensitive to glucose and sucrose	RV
At4g15950	*RDM2*	C	CLB	B	CPR	Decreased DNA methylation	RV
At4g16110	*ARR2*	C	MRP	V	LEF, FLT, HRM	Small rosette; Early flowering; Insensitive to cytokinin and ethylene	RV
At4g16130	*ARA1*	C	CND	H	NUT	Sensitive to arabinose	MB
At4g16144	*AMSH3*	C	ESN	L	SRL	Seedling lethal	RV
At4g16155	*ptLPD2*	C	CND	H	MCH	Sensitive to arsenate	RV
At4g16280	*FCA*	C	MRP	T	FLT	Late flowering	MB
At4g16340	*SPK1*	C	ESN	L	SRL	Seedling lethal	TD
At4g16370	*OPT3*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At4g16390	*SVR7*	C	MRP	V	PIG, LEF	Small, pale green rosette	MB
At4g16420	*PRZ1*	C	CND	H	HRM	Altered response to auxin and cytokinin	TD
At4g16845	*VRN2*	C	MRP	T	MTM	Altered vernalization response	MB
At4g16860	*RPP4*	C	CND	I	PTH	Altered response to fungal infection	MB
At4g16950	*RPP5*	C	CND	I	PTH	Resistant to downy mildew	MB
At4g16990	*RLM3*	C	CND	I	PTH	Susceptible to necrotrophic fungi	RV

At4g17040	*CLPR4*	C	ESN	L	SRL, PIG	Seedling lethal without exogenous sucrose; Pigment defective embryo	RV
At4g17090	*CT-BMY*	C	MRP	V	GRS, LEF	Slow growth; Small rosette; Elevated starch levels in leaves	RV
At4g17300	*OVA8*	NC	ESN	G	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	RV
At4g17380	*MSH4*	C	MRP	R	SRF	Severely reduced fertility due to defects in meiosis	RV
At4g17615	*CBL1*	C	CND	P	WAT, CHS	Sensitive to drought and salt stress	RV
At4g17870	*PYR1*	C	CND	H	HRM	Insensitive to pyrabactin (synthetic ABA analog)	MB
At4g17970	*ALMT12*	C	CND	P	LIT, NUT, HRM	Abnormal stomatal regulation in response to darkness, CO2, and ABA	RV
At4g18240	*AtSS4*	C	MRP	V	GRS, LEF, FLT	Slow growth; Small rosette; Late flowering	RV
At4g18370	*DEG5*	C	MRP	V	GRS, LIT	Slightly slower growth; Small rosettes under high light	RV
At4g18470	*SNI1*	C	MRP	V	GRS, LEF	Dwarf; Narrow leaves	MB
At4g18480	*CH42*	C	ESN	L	SRL, GER, S:PIG, CHS	Seedling lethal; Albino seedlings; Yellow-green embryos; Delayed germination; Resistant to acifluorfen (herbicide); Heterozygotes: Yellow-green leaves and stems	TD
At4g18640	*MRH1*	NC	CLB	C	RTH	Short, straight root hairs	RV
At4g18710	*BIN2*	C	CND	H	HRM	Sensitive to brassinosteroids	MB; RV
At4g18750	*DOT4*	C	MRP	V	ROT, LEF	Short roots; Small rosette; Abnormal leaf morphology	MB
At4g18770	*MYB98*	C	ESN	G	MGD, SRF	Female gametophyte defective, Homozygotes are viable: Severely reduced fertility	RV
At4g18780	*IRX1*	C	CLB	C	TCM	Collapsed xylem; Cellulose-deficient secondary walls	MB
At4g18830	*OFP5*	NC	ESN	G	MGD	Female gametophyte defective	RV
At4g18960	*AG*	C	MRP	R	FSM	Homeotic floral transformations	TD
At4g18980	*S40-3*	NC	MRP	T	SEN	Delayed senescence	RV
At4g19030	*NIP1;1*	C	CND	H	MCH	Resistant to arsenite	RV
At4g19040	*EDR2*	C	CND	I	PTH	Resistant to powdery mildew	MB; RV

At4g19100	*PAM68*	C	MRP	V	PIG, GRS	Pale green cotyledons and leaves; Slow growth	TD; RV
At4g19230	*CYP707A1*	C	CLB	B	PRA, TMP	Low ABA levels; Low germination rate without stratification	RV
At4g19350	*EMB3006*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At4g19490	*AtVPS54*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	RV
At4g19690	*IRT1*	C	MRP	V	MSL, SRF, S:LIT	Chlorotic; Few flowers; Sterile; Reduced iron uptake; Phenotype enhanced under short days; Heterozygotes: Early flowering under short days	RV
At4g20050	*QRT3*	C	MRP	R	OVP	Tetrad pollen	TD; RV
At4g20060	*EMB1895*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g20090	*EMB1025*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g20370	*TSF*	C	CND	P	LIT	Late flowering under short days	RV
At4g20380	*LSD1*	C	CND	H	HRM, CHS, PTH	Sensitive to avirulent *Pseudomonas syringae*, BTH (SA mimic), and oxidative stress	MB
At4g20400	*AtJmj4*	C	MRP	T	FLT	Early flowering independent of photoperiod	RV
At4g20740	*EMB3131*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At4g20780	*CML42*	C	CLB	C	STT	Abnormal trichome morphology; Increased trichome branching	RV
At4g20900	*MS5*	C	MRP	R	SRF	Male sterile	TD
At4g20910	*CRM2*	C	MRP	V	LEF, ARC, FSM, SRF, FLT	Corymb-like inflorescences; Increased cauline leaf number; Increased flower growth rate; Short stamens; Reduced fertility; Late flowering	MB
At4g21100	*DDB1b*	NC	ESN	L	NHM	Null: No homozygous mutant plants recovered	RV
At4g21130	*EMB2271*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g21150	*HAP6*	NC	ESN	G	GAM	Complete male gametophyte defective	TD
At4g21190	*EMB1417*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g21200	*AtGA2ox8*	C	MRP	V	NLS, LIT, CHS	Long hypocotyl; Few rosette leaves, many cauline leaves under short days; Germination resistant to ancymidol (herbicide)	RV
At4g21270	*ATK1*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	TN
At4g21320	*Hsa32*	C	CND	P	TMP	Sensitive to high temperature	RV
At4g21330	*DYT1*	C	MRP	R	SRF	Male sterile due to anther defects	MB

At4g21540	*SphK1*	C	CND	H	HRM	Increased germination rate and abnormal stomatal regulation in response to ABA	RV
At4g21670	*FRY2*	C	CND	P	TMP, HRM, CHS	Seedling growth sensitive to freezing; Germination insensitive to ABA and resistant to salt stress	MB
At4g21680	*NRT1.8*	C	CND	H	NUT, MCH	Sensitive to a combination of nitrate and cadmium	UNK
At4g21710	*EMB1989*	C	ESN	G	GAM, W:EMB	Null: Complete female gametophyte defective; Male gametophyte defective; Knockdown: Embryo defective	TD
At4g21790	*TOM1*	C	CND	I	PTH	Resistant to tobacco mosaic virus	MB
At4g21800	*QQT2*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At4g21860	*MSRB2*	C	CND	P	TMP	Sensitive to low temperature	RV
At4g22140	*EBS*	C	MRP	V	GER, FLT	Reduced seed dormancy; Early flowering	MB
At4g22200	*AKT2/3*	C	CLB	B	CPR	Decreased potassium permeability of the plasma membrane in leaf mesophyll cell layers	RV
At4g22220	*ISU1*	C	MRP	V	GRS, IST, ARC	Dwarf; Thin inflorescence stems; Increased branching	RV; RNAi
At4g22260	*IM*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	MB
At4g22300	*SOBER1*	NC	CND	I	PTH	Resistant to bacterial infection	OTH
At4g22950	*AGL19*	C	CND	P	LIT	Slightly late flowering under short days	RV
At4g22970	*AESP*	C	ESN	S	EMB	Embryo defective; Globular	RV
At4g23100	*RML1*	C	ESN	S	EMB, SRL, W:ROT, W:TCM, W:MCH	Null: Embryo and seedling defective; Knockdown: Short roots; Abnormal shoot meristem; Sensitive to cadmium	OTH
At4g23250	*EMB1290*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g23430	*TIC32*	C	ESN	S	EMB	Embryo defective; Transition	RV
At4g23450	*AtAIRP1*	C	CND	H	HRM	Germination insensitive to ABA	RV
At4g23640	*TRH1*	C	CLB	C	RTH	Altered root hair development	TD
At4g23650	*CPK3*	C	CND	H	CHS	Sensitive to salt	RV
At4g23660	*AtPPT1*	NC	ESN	S	EMB	Embryo defective; Transition	RV
At4g23700	*AtCHX17*	C	CND	H	NUT, CHS	Low potassium levels in roots under salt stress and potassium starvation	RV

At4g23810	*WRKY53*	NC	CND	I	PTH	Susceptible to bacterial infection	RV
At4g23920	*UGE2*	NC	CND	P	LIT	Short hypocotyl in the dark	RV
At4g24020	*NLP7*	C	MRP	V	GRS, LEF, FLT, WAT	Small rosette; Delayed growth; Late flowering; Resistant to drought	RV
At4g24120	*YSL1*	C	CLB	B	PRA	Low iron and nicotianamine levels in seeds; Elevated nicotianamine levels in shoots	RV
At4g24160	*CGI-58*	C	CLB	B	PRA	Elevated triacylglycerol levels in leaves	RV
At4g24190	*SHD*	C	ESN	G	MGD, ROT, FSM, TCM	Male gametophyte defective; Homozygotes are viable: Short roots; Increased lateral root and carpel number; Thick pistils; Large SAM	TD
At4g24210	*SLY1*	C	MRP	V	GER, PIG, GRS, SRF, FLT	Increased seed dormancy; Dwarf; Dark green; Late flowering; Reduced fertility	MB
At4g24230	*ACBP3*	NC	CND	P	LIT	Delayed leaf senescence in the dark	UNK
At4g24270	*EMB140*	NC	ESN	S	EMB	Embryo defective; Globular	RV
At4g24280	*cpHsc70-1*	C	MRP	V	PIG, GRS, LEF, MPH	Variegated cotyledons; Malformed leaves; Dwarf; Short roots under vertical growth	RV
At4g24510	*CER2*	C	MRP	V	PIG, IST	Bright green stems, inflorescences, and siliques	MB
At4g24540	*AGL24*	C	MRP	T	FLT	Late flowering	OTH
At4g24580	*REN1*	C	ESN	G	GAM	Complete male gametophyte defective	TD; RV
At4g24620	*PGI1*	C	CLB	B	PRA, LIT	Low starch levels in leaves; Late flowering under short days	OTH
At4g24960	*HVA22D*	NC	MRP	R	SRF	Reduced fertility	RV
At4g24972	*TPD1*	C	MRP	R	SRF	Completely male sterile due to anther defects	TD
At4g25000	*AMY1*	NC	MRP	T	FLT	Early flowering	RV
At4g25050	*ACP4*	C	MRP	V	PIG, GRS, LEF, MSL, PTH	Pale green; Dwarf; Slow growth; Small, chlorotic rosette; Altered fatty acid composition; Altered systemic acquired resistance response	MB; RV
At4g25080	*CHLM*	C	ESN	L	SRL, PIG	Seedling lethal; Albino embryos and seedlings	RV
At4g25140	*OLEO1*	C	CND	P	CUL, TMP	Germination sensitive to freezing; Large oil bodies	RV
At4g25230	*RIN2*	C	CND	I	PTH	Decreased ion leakage in response to *Pseudomonas syringae*	RV

At4g25350	*SHB1*	C	MRP	R	SSC, LIT	Slightly reduced seed mass; Short hypocotyl under blue light	RV
At4g25420	*GA5*	C	MRP	V	GRS, ARC, FSM, SRF	Semi-dwarf; Increased branching; Short, indehiscent anthers and sterility in early flowers	MB
At4g25470	*CBF2*	C	CND	P	WAT, TMP, CHS	Resistant to drought, freezing, and salt stress	RV
At4g25480	*DREB1A*	NC	CND	P	LIT	Short hypocotyl under red light	RV
At4g25560	*LAF1*	C	CND	P	LIT	Long hypocotyl under far-red light	TN
At4g25640	*FFT*	C	MRP	V	GER, ROT, SRF, SSC	Altered germination rate; Increased root growth rate; Abnormal seed coat; Reduced fertility; Abnormal flavonoid levels	RV
At4g26070	*MEK1*	NC	CND	I	PTH	Susceptible to virulent and avirulent *Pseudomonas syringae*	RV
At4g26080	*ABI1*	C	CND	H	HRM	Sensitive to ABA	MB
At4g26090	*RPS2*	C	CND	I	PTH	Resistant to *Pseudomonas syringae*	MB
At4g26200	*ACS7*	C	MRP	T	FLT	Early flowering; Low ethylene levels	RV
At4g26300	*EMB1027*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At4g26420	*GAMT1*	C	CND	H	CHS	Germination resistant to ancymidol (GA biosynthesis inhibitor)	RV
At4g26430	*CSN6B*	NC	CND	P	LIT	Short hypocotyl in the dark and under blue light	RV
At4g26440	*WRKY34*	C	CND	P	TMP	Male gametophyte defective under cold stress	RV
At4g26466	*LRE*	C	ESN	G	EMG	Embryo defective; Female gametophyte defective	MB; TD
At4g26500	*EMB1374*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At4g26690	*SHV3*	C	CLB	C	RTH	Root hair growth blocked due to tip rupture	RV
At4g26850	*VTC2*	NC	MRP	V	GRS, MSL, PTH	Slow growth; Necrotic lesions; Low ascorbic acid levels; Resistant to *Pseudomonas syringae*	RV
At4g26900	*HISN4*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At4g27010	*EMB2788*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At4g27030	*FAD4*	C	CLB	B	PRA	Abnormal fatty acid composition; Elevated palmitic acid levels	MB; RV

At4g27060	*TOR1*	C	MRP	V	ROT, LEF, FSM	Abnormal root gravitropism; Anti-clockwise twisting rosette leaves, cauline leaves, and petals	MB
At4g27330	*SPL*	C	MRP	R	PIG, FSM, SRF, SEN	Complete male and female sterile; Albino stamens; Delayed senescence	TN
At4g27600	*NARA5*	C	ESN	L	SRL, PIG	Seedling lethal without exogenous sucrose; Pale green seedlings	MB; RV
At4g27750	*ISI1*	C	MRP	V	GRS, SRF	Dwarf; Reduced fertility	MB; RV
At4g27760	*FEY*	C	ESN	L	SRL, LEF, TCM	High penetrance of rosette lethality; Stunted leaves; Abnormal leaf position; Flattened, disorganized SAM	TD
At4g27800	*TAP38*	C	CND	P	LIT	Increased growth rate under low light	RV
At4g28210	*EMB1923*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g28320	*MAN5*	NC	MRP	V	GER	Delayed germination	RV
At4g28580	*MGT5*	C	ESN	G	MGD	Male gametophyte defective	RV
At4g28590	*PDE333*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	RV
At4g28750	*PSAE1*	C	MRP	V	PIG, GRS	Pale green; Slow growth; Dwarf	TN
At4g28980	*CDKF;1*	C	ESN	L	SRL, GRS, LEF	Rosette lethal; Slow growth; Small, wavy leaves with abnormal serration	RV
At4g29010	*AIM1*	C	MRP	V	PIG, LEF, ARC, FSM, SRF, SSC, TCM, LIT	Slightly smaller, darker green leaves; Increased branching; Few, abnormal flowers; Severely reduced fertility; Dark seeds with abnormal morphology; Disorganized floral meristems; Very small, twisted rosette leaves under short days	TD
At4g29040	*RPT2a*	C	MRP	V	ROT	Short roots	MB; RV
At4g29060	*EMB2726*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g29130	*HXK1*	C	MRP	V	ROT, LEF, IST, SRF, SEN, NUT	Short petioles and inflorescence stems; Small root system; Very small leaves; Few flowers; Delayed senescence; Insensitive to glucose	MB
At4g29170	*AtMND1*	C	MRP	R	SRF	Completely sterile due to defects in meiosis	RV
At4g29660	*EMB2752*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g29810	*AtMKK2*	C	CND	P	TMP, CHS	Sensitive to low temperature and salt stress	RV

At4g29840	*MTO2*	C	MRP	V	GRS, ROT	Short roots; Slow growth; Low threonine levels; Severely elevated methionine levels in rosettes	TD
At4g29860	*EMB2757*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g29910	*EMB2798*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At4g30120	*HMA3*	C	CND	H	NUT, MCH	Sensitive to zinc and cadmium	RV
At4g30580	*EMB1995*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g30720	*PDE327*	C	MRP	V	PIG	Pigment defective embryo	RV
At4g30870	*AtMUS81*	C	CND	H	CHS	Sensitive to genotoxic stress	RV
At4g30930	*NFD1*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	RV
At4g30950	*FAD6*	C	CND	P	PRA, TMP, CHS	Chlorotic leaves and slow growth at low temperature; Sensitive to salt stress; Low trienoic fatty acid levels; Elevated monounsaturated fatty acid levels	TD
At4g30960	*CIPK6*	C	MRP	V	NLS, ROT, CHS	Fused cotyledons; Thick hypocotyl; Slightly shorter primary root; Few, short lateral roots; Sensitive to salt stress	RV
At4g31120	*SKB1*	C	MRP	V	PIG, GRS, LEF, FLT	Increased rosette leaf number; Curled, slightly darker green leaves; Slow growth; Late flowering	RV
At4g31160	*DCAF1*	C	ESN	S	EMB	Embryo defective; Globular	RV
At4g31400	*CTF7*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective; Female gametophytes develop slowly	RV
At4g31500	*SUR2*	C	ESN	L	SRL, IST, ARC	High penetrance of seedling lethality; Short primary inflorescence stem; Complete loss of branching	RV
At4g31560	*HCF153*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose	RV
At4g31700	*RPS6A*	C	MRP	V	GRS, LEF	Slightly delayed growth; Small leaves	RV
At4g31770	*DBR1*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g31780	*EMB2797*	C	ESN	S	EMB, W:PIG	Null: Embryo defective; Globular; Knockdown: Yellow-green	RV
At4g31800	*WRKY18*	NC	CND	I	PTH	Resistant to bacterial infection; Susceptible to fungal infection	RV
At4g31820	*ENP*	NC	MRP	R	FSM	Fused floral organs; Abnormal flower number	MB

At4g31870	*GPX7*	C	CND	H	CHS	Sensitive to photooxidative stress	RV
At4g31970	*JAH1*	C	CND	H	HRM, PTH	Sensitive to jasmonic acid; Susceptible to necrotrophic fungi	TD
At4g32150	*AtVAMP711*	C	CND	H	CHS	Resistant to salt	RV
At4g32260	*PDE334*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect); Albino embryos	RV
At4g32400	*SHS1*	C	ESN	S	EMB, W:TMP, W:NUT, W:HRM, W:CHS	Null: Embryo defective; Globular; Knockdown: Sensitive to low temperature, salt, sugar; Insensitive to ABA	TD
At4g32410	*RSW1*	C	ESN	G	GAM, W:EMB, W:NLS, W:ROT	Null: Complete male gametophyte defective; Strong knockdown: Embryo defective; Weak knockdown: Thick roots and seedlings	MB; RV
At4g32551	*LUG*	C	MRP	R	LEF, FSM	Narrow leaves; Homeotic floral transformations	MB
At4g32650	*KC1*	C	CND	H	NUT	Sensitive to potassium starvation	UNK
At4g32700	*TEB*	C	MRP	V	ROT, LEF, IST, ARC	Short roots; Serrated leaves; Fasciated stems and inflorescences	TD; RV
At4g32720	*AtLA1*	C	ESN	S	EMB	Embryo defective; Globular	RV
At4g32770	*VTE1*	C	CLB	B	PRA, LIT	Complete loss of tocopherol production; Low anthocyanin levels under high light; No other phenotypes detected	MB
At4g32810	*CCD8*	C	MRP	V	LEF, ARC	Short petioles; Increased branching	RV
At4g32850	*PAPS4*	C	ESN	L	NHM	No homozygous mutant plants recovered	RV
At4g32980	*ATH1*	NC	CND	P	LIT	Slightly early flowering under short days	RV
At4g33000	*CBL10*	C	CND	H	CHS	Sensitive to salt stress	RV
At4g33030	*SQD1*	C	CLB	B	PRA	Low sulfolipid levels; No other phenotypes detected	OTH
At4g33090	*APM1*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At4g33210	*SLOMO*	C	MRP	V	GRS	Slow growth	MB; RV
At4g33240	*FAB1A*	C	MRP	V	LEF	Curled leaves	RV
At4g33330	*GUX2*	C	CLB	B	PRA	Abnormal xylan modification	RV

At4g33360	*FLDH*	C	CND	H	HRM	Germination and stomatal closure insensitive to ABA	RV
At4g33430	*BAK1*	C	MRP	V	GRS, HRM	Semi-dwarf; Insensitive to brassinosteroids	RV
At4g33460	*EMB2751*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g33470	*HDA14*	NC	CLB	C	RTH	Increased root hair density	RV
At4g33495	*RPD1*	C	ESN	S	EMB	Embryo defective; Transition	MB; RV
At4g33520	*PAA1*	C	MRP	V	GRS	Slow growth; High chlorophyll fluorescence	MB
At4g33650	*DRP3A*	C	CLB	C	CUL	Severely elongated mitochondria; No other phenotypes detected	MB
At4g33680	*AGD2*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At4g33790	*CER4*	C	MRP	V	PIG, IST	Glossy stems and inflorescences	MB; RV
At4g33950	*OST1*	C	CND	P	WAT	Reduced stomatal closing under drought	MB
At4g33990	*EMB2758*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At4g34350	*HDR*	NC	ESN	L	SRL, PIG	Albino seeds and seedlings	MB
At4g34390	*XLG2*	C	CND	I	PTH	Susceptible to bacterial infection	RV
At4g34460	*AGB1*	C	MRP	V	LEF, IST, FSM	Rounded leaves; Short petioles; Slightly shorter inflorescence stems; Short, blunt siliques	MB
At4g34520	*FAE1*	C	MRP	V	IST, WAT	Thin inflorescence stems; Sensitive to low humidity	RV
At4g34620	*SSR16*	C	ESN	S	EMB	Embryo defective; Transition	TN
At4g34700	*AtCIB22*	C	MRP	V	W:GRS, W:ROT, W:LEF, W:FLT	Knockdown: Short roots; Dwarf; Few, small leaves; Late flowering	RV; RNAi
At4g34710	*ADC2*	C	MRP	V	ROT, CHS	Increased lateral root number; Sensitive to salt	MB
At4g34740	*AtGPRAT2*	C	CND	H	CHS	Resistant to DAS734 (herbicide)	MB
At4g34830	*PDE346*	NC	MRP	V	PIG	Pigment defective embryo	RV
At4g34850	*LAP5*	C	MRP	R	OVP	Abnormal pollen exine layer	RV
At4g34890	*AtXDH1*	C	CLB	B	CPR	Complete loss of XDH and ROS-generation	RV
At4g34940	*ARO1*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At4g34990	*AtMYB32*	C	ESN	G	MGD, SRF	Collapsed pollen; Homozygotes are viable: Reduced fertility	RV
At4g35040	*bZIP19*	C	CND	H	NUT	Sensitive to limited zinc	RV

At4g35090	*CAT2*	C	CND	P	LIT	Dwarf, pale green, and few lateral roots under low light	RV
At4g35420	*TKPR1*	C	MRP	R	SRF	Reduced fertility	RV
At4g35440	*CLCE*	C	CLB	B	PRA, CPR	Low nitrate content; Elevated nitrite content; Reduced nitrate influx in roots	RV
At4g35450	*ARK2A*	C	MRP	V	GRS, LEF, FLT	Dwarf; Small, curled rosette leaves; Late flowering	RV
At4g35490	*MRPL11*	C	MRP	V	PIG, GRS	Semi-dwarf; Dark green leaves	RV
At4g35520	*MLH3*	C	MRP	R	SRF	Reduced fertility	RV
At4g35900	*FD*	C	MRP	T	FLT	Late flowering	MB
At4g35920	*MCA1*	C	CND	P	MEC	Abnormal root thigmotropism	RV
At4g36220	*FAH1*	C	CLB	B	PRA	Low sinapoylmalate levels in leaves	RV
At4g36380	*ROT3*	C	MRP	V	LEF, FSM	Short, rounded leaves; Short petioles and floral organs	TD
At4g36480	*EMB2779*	C	ESN	G	GAM, W:EMB	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Embryo defective	RV
At4g36630	*EMB2754*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At4g36830	*HOS3*	C	CND	H	HRM, CHS	Sensitive to ABA and salt	TD; RV
At4g36890	*IRX14*	NC	CLB	C	TCM, WAT	Abnormal xylem; Low xylose levels in cell walls; Drought tolerant	RV
At4g36920	*AP2*	C	MRP	R	FSM	Homeotic floral transformations	TD
At4g36930	*SPT*	C	MRP	R	FSM	Abnormal carpel development	OTH
At4g37000	*ACD2*	C	MRP	V	MSL	Necrotic lesions	MB
At4g37050	*PLAIVC*	NC	MRP	V	NLS, NUT	Long hypocotyl; Root growth insensitive to phosphate starvation	RV
At4g37070	*PLAIVA*	C	MRP	V	ROT	Few lateral roots	RV
At4g37200	*HCF164*	C	ESN	L	SRL	Seedling lethal	TD
At4g37270	*HMA1*	C	CND	P	LIT	Variegated leaves under high light	RV
At4g37450	*AGP18*	NC	ESN	G	GEM	Female gametophyte defective; Embryo defective (inferred)	RNAi
At4g37470	*HTL*	C	CND	P	LIT	Long hypocotyls and petioles and small cotyledons and leaves under red, far-red, and blue light	MB; RV

At4g37540	*LBD39*	NC	CND	H	NUT	Elevated anthocyanin levels in response to nitrogen	RV
At4g37580	*HLS1*	C	MRP	V	NLS	Complete loss of apical hook	TD
At4g37650	*SHR*	C	MRP	V	ROT	Abnormal root growth	RV
At4g37750	*ANT*	C	MRP	R	FSM, OVP	Abnormal flower and ovule development	TD
At4g37925	*NDH-M*	C	CLB	B	CPR	Complete loss of post-illumination chlorophyll fluorescence; Slightly increased non-photochemical quenching	RV
At4g37930	*SHM1*	C	ESN	L	SRL	Rosette lethal at ambient CO2 levels	MB; RV
At4g38130	*HD1*	C	CND	P	TMP	At high temperature: Disorganized embryonic root and shoot; Incomplete penetrance of pin-formed and tubular cotyledons and decreased cotyledon number; Slightly narrow cotyledons	TD; RV
At4g38160	*PDE191*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At4g38190	*CSLD4*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At4g38240	*CGL1*	C	CND	H	CHS	Sensitive to mannitol and potassium chloride	RV
At4g38600	*KAK*	C	CLB	C	STT	Increased trichome branching	TD
At4g38620	*MYB4*	C	CND	P	PRA, LIT	Resistant to UV-B light; Elevated sinapate ester levels in leaves	RV
At4g38630	*RPN10*	C	MRP	V	GER, GRS, MSL, FSM, SRF, SEN	Very low germination rate; Slow growth; Chlorotic leaves; Decreased stamen number; Reduced fertility; Early rosette leaf senescence	RV
At4g38800	*MTN1*	C	CND	H	NUT	Reduced growth with MTA as source of nitrogen	RV
At4g39030	*EDS5*	C	CLB	B	PRA, PTH	Low SA levels; Susceptible to disease	MB
At4g39090	*RD19*	C	CND	I	PTH	Sensitive to *Ralstonia solanacearum*	RV
At4g39120	*HISN7*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At4g39350	*CESA2*	C	MRP	V	NLS, SRF	Short hypocotyl; Reduced fertility	TN
At4g39400	*BRI1*	C	MRP	V	PIG, GRS, ARC, SRF, FLT, SEN, HRM	Dwarf; Dark green; Increased branching; Completely male sterile; Late flowering; Delayed leaf senescence; Insensitive to brassinosteroids	MB
At4g39460	*SAMC1*	C	MRP	V	GER, PIG, GRS, FLT	Low germination rate; Dwarf; Pale green leaves; Late flowering	RV

At4g39620	*EMB2453*	C	ESN	S	EMB	Embryo defective; Globular	TD
At4g39640	*GGT1*	C	MRP	V	GRS, MSL	Dwarf; Chlorotic	RV
At4g39710	*FKBP16-2*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At4g39800	*AtIPS1*	C	MRP	V	NLS, MSL, TCM	Short hypocotyl; Abnormal cotyledon shape; Necrotic lesions on leaves; Root cap disorganized; Abnormal veins in cotyledons	RV
At4g39850	*PXA1*	C	ESN	L	SRL, HRM	Seedling lethal; Insensitive to IBA	MB
At4g39920	*POR*	C	ESN	S	EMB, CUL	Embryo defective; Preglobular; Enlarged embryo cells and endosperm nuclei	TD
At5g01220	*SQD2*	C	CND	H	PRA, NUT	Sensitive to limited phosphate; Low sulfolipid levels	OTH
At5g01360	*TBL3*	C	MRP	V	IST	Short, thin inflorescence stems	RV; RNAi
At5g01400	*ESP4*	C	MRP	V	NLS, FLT	Bleached cotyledons; Early flowering	MB
At5g01410	*RSR4*	C	MRP	V	PIG, ROT, MSL, SRF	Pale green, slightly chlorotic rosette leaves; Short roots; Reduced fertility	MB
At5g01490	*CAX4*	C	CND	H	NUT, HRM, MCH	Abnormal root growth in response to cadmium, manganese and auxin	RV
At5g01500	*TAAC*	NC	MRP	V	PIG	Pale green leaves	RV
At5g01540	*LecRKA4.1*	C	CND	H	HRM	Germination sensitive to ABA	RV
At5g01550	*LecRKA4.2*	C	CND	H	HRM	Germination sensitive to ABA	RV
At5g01560	*LecRKA4.3*	C	CND	H	HRM	Germination sensitive to ABA	RV
At5g01600	*AtFER1*	C	MRP	T	SEN	Early senescence	RV
At5g01630	*AtBRCA2b*	C	CND	H	CHS	Sensitive to genotoxic stress	RV
At5g01820	*CIPK14*	NC	CND	P	LIT	Etiolated cotyledons following a far red to white light shift	UNK
At5g01840	*OFP1*	C	CND	H	CHS	Sensitive to genotoxic stress	RV
At5g01920	*STN8*	NC	CLB	C	CUL	Increased thylakoid stacking	RV
At5g01930	*MAN6*	NC	MRP	V	GER	Delayed germination	RV
At5g02030	*LSN*	C	MRP	V	GRS, ARC, FSM	Dwarf; Increased branching; Short siliques; Complete loss of septum formation	TD
At5g02120	*PDE335*	NC	MRP	V	PIG	Pigment defective embryo	RV

At5g02190	*AtASP38*	C	ESN	G	EMG	Embryo defective; Male and female gametophyte defective	RV
At5g02200	*FHL*	C	MRP	V	NLS	Long hypocotyl; Open cotyledons	RV
At5g02250	*EMB2730*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g02310	*PRT6*	C	MRP	V	GER, ROT	Delayed after-ripening; Short roots without exogenous sucrose	MB
At5g02600	*NaKR1*	C	MRP	V	ROT, FLT	Short roots; Late flowering	OTH
At5g02810	*PRR7*	C	MRP	V	NLS	Long hypocotyl; Narrow cotyledons	MB
At5g02820	*BIN5*	C	MRP	V	GRS, LEF, ARC, LIT, HRM	Dwarf; Increased branching; Downward-bending leaves; Short petioles; Dark-grown seedlings are de-etiolated; Insensitive to brassinosteroids	MB
At5g02870	*RPL4A*	C	MRP	V	GRS, ROT, LEF, FLT	Narrow, pointed first true leaves; Dwarf; Short roots; Late flowering	TD; RV
At5g03150	*JKD*	C	MRP	V	ROT	Slightly shorter roots; Early lateral root formation	RV
At5g03280	*EIN2*	C	MRP	V	NLS, SEN, HRM, CHS	Long hypocotyl; Delayed senescence; Insensitive to ethylene, cytokinin and ABA; Resistant to auxin transport inhibitors	MB
At5g03455	*CDC25*	C	CND	H	CHS	Sensitive to hydroxyurea (inhibitor of DNA replication)	RV
At5g03540	*AtEXO70A1*	C	MRP	V	ARC, SRF	Increased branching; Reduced fertility	RV
At5g03570	*IREG2*	C	CND	H	PRA, NUT, MCH	Sensitive to cobalt and nickel; Elevated cobalt levels in shoots	RV
At5g03730	*CTR1*	C	MRP	V	NLS, PIG, GRS, ROT, LEF, SRF, FLT	Short hypocotyl and roots; Exaggerated apical hook; Slow growth; Dark green cotyledons; Dwarf; Small rosette; Sterile early flowers; Late flowering	MB; TD
At5g03790	*LMI1*	C	MRP	V	LEF	Abnormal leaf morphology; Base of rosette divided into leaflets	RV
At5g03800	*EMB1899*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g03840	*TFL1*	C	MRP	V	IST, ARC, FLT	Inflorescences terminate early with a single flower; Early flowering independent of photoperiod	TD
At5g03860	*MLS*	C	MRP	V	NLS	Slightly slower seedling growth	RV

At5g03940	*FFC*	C	MRP	V	PIG	Yellow first true leaves	OTH
At5g04040	*SDP1*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose	MB
At5g04140	*GLS1*	C	MRP	V	MSL	Chlorotic unless grown under non-photorespiratory conditions	OTH
At5g04240	*ELF6*	C	MRP	T	FLT	Early flowering	TD; RV
At5g04290	*KTF1*	C	CLB	B	CPR	Decreased DNA methylation	TD; RV
At5g04430	*BTR1*	C	CND	I	PTH	Susceptible to tobacco mosaic virus	RV
At5g04470	*SIM*	C	CLB	C	STT	Multicellular trichomes	MB
At5g04490	*VTE5*	C	CLB	B	PRA	Low tocopherol levels in seeds	MB
At5g04560	*DME*	C	ESN	S	MSD	Embryo defective; 50% defective seeds	TD
At5g04770	*AtCAT6*	C	MRP	V	PIG, NUT	Purple leaves; No growth with L-glutamine as sole nitrogen source	RV
At5g04810	*AtPPR4*	C	ESN	S	EMB	Embryo defective	RV
At5g04890	*RTM2*	C	CND	I	PTH	Altered response to tobacco etch virus	MB
At5g05000	*TOC34*	C	MRP	V	ROT	Short roots	RV
At5g05170	*CEV1*	C	ESN	G	GAM, W:ROT	Null: Complete male gametophyte defective; Knockdown: Short roots; Elevated jasmonate and ethylene levels	MB; RV
At5g05410	*DREB2A*	C	CND	P	WAT, TMP	Sensitive to drought and high temperature	RV
At5g05490	*SYN1*	NC	MRP	R	SRF	Completely male and female sterile due to defects in meiosis	TD
At5g05560	*EMB2771*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At5g05580	*FAD8*	C	CLB	B	PRA	Low trienoic acid levels	MB
At5g05680	*EMB2789*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g05690	*CBB3*	C	MRP	V	GRS, SRF	Dwarf; Male sterile	TD
At5g05700	*ATE1*	C	MRP	T	SEN	Delayed leaf senescence	TD
At5g05730	*TRP5*	C	CND	H	CHS	Resistant to 6-methylanthranilate (herbicide)	MB
At5g05780	*RPN8A*	C	MRP	V	GRS, LEF, ARC, FSM, FLT, STT	Semi-dwarf; Long, narrow rosette leaves; Increased rosette leaf number; Incomplete penetrance of cauline leaves forming additional ectopic leaves; Abnormal cauline leaf phyllotaxy; Long pedicels; Abnormal floral organ number; Late flowering; Abnormal trichome morphology	MB

At5g05970	*NEDD1*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	RV
At5g06070	*RBE*	C	MRP	R	FSM	Abnormal petal morphology	MB; RV
At5g06240	*EMB2735*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g06410	*AtHscB*	C	MRP	V	PIG, IST, SRF, STT	Glossy, bright green stems; Reduced fertility; Abnormal trichome development	RV
At5g06580	*AtD-LDH1*	C	CND	H	NUT, CHS	Sensitive to D-lactate and methylglyoxal (cytotoxic byproduct of glycolysis)	RV
At5g06650	*GIS2*	C	CLB	C	STT	Complete loss of trichomes on floral organs	RV
At5g06700	*TBR*	C	MRP	V	IST, LIT	Short inflorescence stems; Short hypocotyl in the dark	MB; RNAi
At5g06760	*LEA4-5*	C	CND	P	WAT, CHS	Sensitive to drought; Germination sensitive to osmotic stress	RV
At5g07280	*EXS*	C	ESN	S	EMB	Embryo defective; Cotyledon	MB
At5g07440	*GDH2*	C	CND	H	NUT	Reduced growth with glutamate as sole source of nitrogen	RV
At5g07500	*PEI*	C	ESN	S	EMB	Embryo defective; Cotyledon	RNAi
At5g07990	*TT7*	C	MRP	R	PIG, SSC	Yellow seed coat	OTH
At5g08130	*BIM1*	NC	ESN	S	EMB, SRL	Embryo defective; Cotyledon; Low penetrance of patterning defects and seedling lethality	RV
At5g08170	*EMB1873*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g08370	*AtAGAL2*	C	MRP	V	LEF, FLT	Curly rosette leaves: Late flowering	RV
At5g08470	*EMB2817*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	RV
At5g08550	*ILP1*	C	MRP	V	NLS	Short hypocotyl	RV
At5g08610	*PDE340*	NC	MRP	V	PIG	Pigment defective embryo	RV
At5g08640	*FLS1*	C	MRP	V	PIG	Purple due to anthocyanin accumulation; Low flavonol levels	RV
At5g09640	*SNG2*	C	CLB	B	PRA	Elevated sinapoylglucose levels; Low sinapoylcholine levels	MB
At5g09660	*PMDH2*	C	MRP	V	NLS	Short hypocotyl without exogenous sucrose	RV
At5g09680	*RLF1*	C	MRP	V	GRS, ROT	Semi-dwarf; Fewer lateral roots; Short primary roots	MB; RV
At5g09690	*MRS2-7*	C	CND	H	NUT	Sensitive to limited magnesium	RV

At5g09750	*HEC3*	C	MRP	R	SRF	Slightly reduced fertility	RV
At5g09790	*PDE336*	NC	MRP	V	PIG	Pigment defective embryo	RV
At5g09810	*ACT7*	C	MRP	V	ROT, HRM	Short roots; Slow hormone-induced callus formation	TD
At5g09900	*EMB2107*	C	ESN	S	EMB, GRS, LEF, FSM, SRF	Embryo defective; Cotyledon; Dwarf; Abnormal leaf and flower morphology; Severely reduced fertility	TD
At5g10140	*FLC*	C	MRP	T	FLT	Early flowering	MB
At5g10170	*AtIPS3*	NC	ESN	L	NHM	No homozygous mutant plants recovered	RV
At5g10250	*DOT3*	C	MRP	V	GRS, ROT, TCM	Dwarf; Very short primary root; Abnormal leaf venation	MB
At5g10330	*HISN6A*	C	ESN	S	EMB, W:ROT	Null: Embryo defective; Preglobular; Knockdown: Short roots	TD
At5g10440	*CYCD4;2*	C	CLB	C	STT	Decreased stomatal density	RV
At5g10470	*KAC1*	C	CLB	C	CUL	Severely reduced chloroplast movement	MB; RV
At5g10480	*PAS2*	C	ESN	S	EMB	Embryo defective; Cotyledon	MB
At5g11040	*TRS120*	C	ESN	L	SRL	Seedling lethal	RV
At5g11110	*AtSPS2F*	C	MRP	R	OVP	Abnormal pollen exine layer	MB
At5g11260	*HY5*	C	MRP	V	NLS, ROT	Long hypocotyl; Altered root waving and gravitropism	TD
At5g11270	*OCP3*	C	MRP	V	PIG, GRS, PTH	Slow growth; Pale young leaves; Resistant to necrotrophic fungi	MB
At5g11530	*EMF1*	C	MRP	V	NLS, GRS, LEF, IST, MSL, FSM, FLT, TCM	Short hypocotyl; Oval cotyledons with no petiole; Very small, sessile rosette leaves; Very short inflorescence stems; Single flower develops; Only carpel-like floral organs form; Severe early flowering; Large SAM	MB
At5g11710	*EPSIN1*	C	CLB	B	CPR	Abnormal vacuolar trafficking	RV
At5g11890	*EMB3135*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At5g12080	*MSL10*	C	CLB	B	CPR	Abnormal stretch-activated channel activity	RV
At5g12130	*PDE149*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At5g12200	*PYD2*	C	CND	H	NUT	Unable to use urea as primary nitrogen source	RV

At5g12210	*RGBT1*	C	MRP	V	GRS, LEF, ARC, FSM, SRF	Dwarf; Small rosette leaves; Increased branching; Abnormal flower morphology; Reduced fertility	RV
At5g12390	*FIS1B*	NC	MRP	V	GRS, CUL	Semi-dwarf; Abnormal mitochondria and peroxisome morphology	RNAi
At5g12840	*EMB2220*	NC	ESN	S	MSD	Embryo defective; 50% defective seeds	TD
At5g12860	*pOMT1*	NC	MRP	V	GRS	Slow growth	RV
At5g13010	*EMB3011*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At5g13080	*WRKY75*	C	CND	I	PTH	Susceptible to bacterial infection	RV
At5g13150	*EXO70C1*	NC	ESN	G	MGD, GRS, ROT, SRF	Male gametophyte defective; Homozygotes are viable: Short roots; Slow growth; Reduced fertility	RV
At5g13160	*PBS1*	C	CND	I	PTH	Susceptible to specific strains of *Pseudomonas syringae*	MB
At5g13170	*SAG29*	C	CND	H	CHS	Resistant to salt	RV
At5g13290	*CRN*	C	MRP	R	FSM	Club-shaped siliques; Floral defects	MB
At5g13300	*SFC*	C	CLB	C	TCM	Abnormal vein patterning	MB
At5g13320	*PBS3*	NC	CND	I	PTH	Susceptible to avirulent bacteria	MB
At5g13480	*FY*	C	ESN	S	EMB, W:FLT	Null: Embryo defective; Preglobular; Knockdown: Late flowering	UNK
At5g13510	*EMB3136*	NC	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g13530	*KEG*	C	ESN	L	SRL	Seedling lethal	RV
At5g13550	*SULTR4;1*	NC	MRP	R	SSC	Slightly reduced seed mass	RV
At5g13570	*DCP2*	C	ESN	L	SRL, TCM	Seedling lethal; Abnormal vasculature	RV
At5g13630	*GUN5*	C	MRP	V	PIG	Pale green	OTH
At5g13650	*SVR3*	C	CND	P	TMP	Leaf chlorosis at low temperature	MB; RV
At5g13680	*ELO2*	C	MRP	V	GER, NLS, ROT, LEF, IST, ARC, WAT	Very low germination rate; Slow seedling growth; Narrow leaves; Short inflorescence stems and primary root; Altered inflorescence architecture; Resistant to drought	MB
At5g13690	*CYL1*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At5g13710	*SMT1*	C	ESN	S	EMB	Embryo defective; Cotyledon	TN
At5g13800	*PPH*	C	MRP	V	MSL	Leaves stay green during senescence	RV
At5g13910	*LEP*	C	MRP	V	NLS	Short hypocotyl; Small cotyledons	TD

At5g13930	*TT4*	C	MRP	R	PIG, SSC	Yellow seed coat	OTH
At5g13960	*KYP*	C	CLB	B	CPR	Complete loss of cytosine methylation resulting in the reactivation of endogenous transposons	MB
At5g14100	*NAP14*	C	MRP	V	GER	Complete loss of germination without exogenous sucrose	RV
At5g14170	*EMB262*	NC	ESN	S	EMB, W:GRS, W:OBI	Null: Embryo defective; Cotyledon; Knockdown: Dwarf; Resistant to *Agrobacterium* transformation in roots	RV
At5g14180	*MPL1*	C	CND	I	PTH	Susceptible to green peach aphid	RV
At5g14200	*IMD1*	C	CLB	B	PRA	Abnormal glucosinolate composition	RV
At5g14250	*FUS11*	C	ESN	L	SRL, PIG	Seedling lethal; Red seedlings due anthocyanin accumulation	OTH
At5g14320	*EMB3137*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g14570	*AtNRT2.7*	C	CLB	B	PRA	Low nitrate levels in seeds	RV
At5g14660	*PDF1B*	NC	ESN	L	SRL, PIG	Seedling lethal; Albino	RV
At5g14750	*WER1*	C	CLB	C	STT, RTH, TCM	Increased root hair production; Increased stomatal density on hypocotyls; Abnormal root epidermal cell patterning	MB
At5g14760	*AO*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g14800	*EMB2772*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g14870	*CNGC18*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At5g14960	*E2FD*	C	MRP	V	ROT	Long roots	RV
At5g15130	*WRKY72*	C	CND	I	PTH	Susceptible to fungal infection	RV
At5g15170	*TDP*	C	MRP	V	GRS, ARC, FLT	Dwarf; Increased branching; Early flowering	TD
At5g15410	*DND1*	C	MRP	V	GRS, PTH	Dwarf; Complete loss of hypersensitive response in response to avirulent *Pseudomonas syringae*	MB
At5g15450	*CLPB3*	C	ESN	L	SRL	Seedling lethal without exogenous sucrose; With exogenous sucrose: Pale green	RV
At5g15470	*GAUT14*	C	CLB	B	PRA	Abnormal xylan and pectin levels in cell walls	RV
At5g15540	*EMB2773*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g15700	*RPOTmp*	C	MRP	V	GRS, LEF	Slow growth; Wrinkly rosette leaves	RV
At5g15840	*CO*	C	MRP	T	FLT	Late flowering	MB
At5g15920	*EMB2782*	C	ESN	S	EMB	Embryo defective; Preglobular	RV

At5g16000	*NIK1*	C	CND	I	PTH	Susceptible to viral infection	RV
At5g16020	*GEX3*	NC	ESN	G	MGD	Female gametophyte defective	RNAi
At5g16260	*ELF9*	C	CND	P	LIT	Early flowering under short days	TD
At5g16270	*SYN4*	C	CLB	C	CUL	Reduced sister chromatid alignment; No other phenotypes detected	RV
At5g16390	*CAC1A*	C	ESN	G	EMG	Embryo defective; Male gametophyte defective	RV
At5g16530	*PIN5*	C	MRP	V	NLS, ROT, HRM	Abnormal hypocotyl and root growth; Insensitive to IAA	RV
At5g16560	*KAN*	C	MRP	V	LEF, FSM, OVP, STT	Cupped first true leaves; Rolled leaves that become flat over time; Abnormal pistil development; Ectopic ovules on outside of carpels; Abnormal trichome patterning	TD
At5g16620	*PDE120*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At5g16715	*EMB2247*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g16750	*TOZ*	C	ESN	G	EMG	Embryo defective; Female gametophyte defective	TN
At5g16780	*MDF*	C	ESN	L	SRL, NLS	Seedling lethal; Increased cotyledon number	RV
At5g16830	*SYP21*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At5g16910	*CSLD2*	C	CLB	C	RTH	Short, abnormal root hairs	RV
At5g17220	*TT19*	C	MRP	R	PIG, SSC	Pale seed coat	TN; RV
At5g17290	*APG5*	C	MRP	V	GRS, FLT	Dwarf; Late flowering	RV
At5g17330	*GAD*	C	CLB	B	PRA	Low GABA levels in roots	RV
At5g17400	*ER-ANT1*	C	MRP	V	PIG, GRS, ROT, ARC, SSC	Very slow growth; Dwarf; Short roots; Increased branching; Pale green; Small, translucent seeds	RV
At5g17420	*IRX3*	C	CLB	C	TCM	Collapsed xylem; Cellulose-deficient secondary walls	MB
At5g17520	*RCP1*	C	MRP	V	PIG, GRS	Dwarf; Pale green; Elevated maltose levels	MB
At5g17690	*TFL2*	C	MRP	V	GRS, FSM, FLT	Dwarf; Abnormal flower morphology; Early flowering	MB
At5g17710	*EMB1241*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At5g17770	*AtCBR*	C	CLB	B	PRA	Low hydroxyl fatty acid levels in seeds	MB
At5g17880	*CSA1*	C	CND	P	LIT	Long petioles and erect, pale leaves under high red:far-red light	TD

At5g17890	*CHS3*	C	CND	P	TMP	Sensitive to low temperature	MB
At5g17990	*TRP1*	C	ESN	L	SRL	Seedling lethal without exogenous tryptophan	OTH
At5g18000	*VDD*	C	ESN	G	GEM	Female gametophyte defective; Embryo defective	RV
At5g18170	*GDH1*	C	CND	H	NUT	Seedling growth sensitive to inorganic nitrogen	OTH
At5g18560	*PUCHI*	C	MRP	V	ROT	Abnormal lateral root formation	MB
At5g18570	*EMB3138*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g18580	*FS1*	C	ESN	S	EMB, SRL	Embryo and seedling defective	MB; TD
At5g18660	*PCB2*	C	MRP	V	PIG	Pale green	MB
At5g18700	*EMB3013*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g18820	*EMB3007*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At5g18930	*BUD2*	C	MRP	V	NLS, GRS, LEF, TCM	Dwarf; Short hypocotyl and petioles; Altered vascular bundle patterning	TD; RV
At5g19220	*ADG2*	C	CLB	B	PRA	Low starch levels in leaves	OTH
At5g19400	*SMG7*	NC; C	ESN	L	NHM, W:SRL, W:GRS, W:LEF, W:TCM	Null: No homozygous mutant plants recovered; Knockdown 1: Seedling lethal; Dwarf; Decreased leaf number; Knockdown 2: Slow growth; Abnormal rosette leaf morphology; High penetrance of rosette lethality; Large SAM	RV
At5g19520	*MSL9*	C	CLB	B	CPR	Abnormal stretch-activated channel activity	RV
At5g19530	*ACL5*	C	MRP	V	IST, SRF	Short inflorescence stems; Few flowers	MB
At5g19550	*AAT2*	C	CLB	B	CPR	Reduced aspartate transport in the phloem	OTH
At5g19600	*SULTR3;5*	C	MRP	V	LEF, FLT	Small rosette leaves; Early flowering; Slightly elevated sulfate levels in seeds	RV
At5g19610	*GNL2*	C	ESN	G	GAM	Complete male gametophyte defective	TD; RV
At5g19620	*OEP80*	C	ESN	S	EMB	Embryo defective; Globular	RV
At5g19660	*S1P*	C	CND	H	CHS, MCH	Sensitive to salt, potassium chloride, lithium chloride and mannitol	RV
At5g19690	*STT3A*	C	MRP	V	ROT	Thick lateral roots	RV
At5g19770	*TUA3*	NC	MRP	V	NLS	Short, thick hypocotyl	RV
At5g19820	*EMB2734*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g20040	*AtIPT9*	NC	MRP	V	MSL	Chlorotic; Low cytokinin levels	RV

At5g20240	*PI*	C	MRP	R	FSM	Homeotic floral transformations	OTH
At5g20270	*HHP1*	C	CND	H	HRM, CHS	Sensitive to ABA and osmotic stress	RV
At5g20320	*DCL4*	C	MRP	V	LEF	Elongated, narrow, curled leaves	MB
At5g20350	*TIP1*	C	ESN	G	MGD, GRS, LEF, SRF, FLT, SEN, RTH	Male gametophyte defective; Homozygotes are viable: Semi-dwarf; Small rosette; Reduced male fertility; Late flowering; Early senescence; Short, branched root hairs	MB
At5g20480	*EFR*	C	CND	I	PTH	Sensitive to elf18 (bacterial defense inducer)	RV
At5g20730	*NPH4*	C	MRP	V	ARC, LIT	Altered inflorescence gravitropism; Reduced phototropism	MB
At5g20850	*AtRAD51*	C	MRP	R	SRF	Completely male and female sterile due to defects in meiosis	RV
At5g20910	*AIP2*	C	CND	H	HRM	Sensitive to ABA	RV
At5g20920	*EMB1401*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g20930	*TSL*	C	MRP	R	FSM	Abnormal flower morphology	TD
At5g21140	*EMB1379*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At5g21150	*AGO9*	C	ESN	G	MGD	Abnormal ovule morphology (no effect on fertility); Homozygotes are viable: Increased percentage of abnormal ovules	RV
At5g22010	*AtRFC1*	C	ESN	S	EMB	Embryo defective	RV
At5g22110	*CYL2*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g22130	*PNT1*	C	ESN	G	GEM	Male gametophyte defective; Embryo defective	MB
At5g22250	*AtCAF1b*	C	CND	H	CHS	Sensitive to methyl viologen (inducer of oxidative stress); Germination resistant to salt stress	RV
At5g22260	*MS1*	C	MRP	R	SRF	Male sterile	MB
At5g22330	*AtTIP49a*	NC	ESN	G	EMG, W:SRL, W:TCM	Null: Female gametophyte defective; Embryo defective (inferred); Knockdown: Seedling lethal; Abnormal meristem development	RV
At5g22350	*ELM1*	C	MRP	V	GRS, CUL	Dwarf; Slow growth; Elongated mitochondria	MB
At5g22360	*ATVAMP714*	NC	CND	H	CHS	Resistant to salt stress	RV
At5g22370	*EMB1705*	C	ESN	S	EMB	Embryo defective; Preglobular	TD

At5g22500	*FAR1*	C	CLB	B	W:PRA	Knockdown: Abnormal suberin composition in roots and seed coat; No other phenotypes detected	RV
At5g22640	*EMB1211*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g22800	*EMB1030*	C	ESN	S	EMB	Embryo defective; Transition	TD
At5g23010	*MAM1*	C	CLB	B	PRA	Abnormal glucosinolate composition	MB
At5g23020	*IMS2*	C	CLB	B	PRA	Low C8 glucosinolate levels	RV
At5g23060	*CaS*	C	MRP	V	GRS	Dwarf	RV
At5g23080	*TGH*	C	MRP	V	NLS, GRS, LEF, FSM, SRF, TCM	Low penetrance of increased cotyledon number; Abnormal cotyledon shape; Dwarf; Small, lanceolate leaves; Short, sterile anthers; Severely reduced fertility; Reduced vascularization	RV
At5g23120	*HCF136*	C	ESN	L	SRL, PIG	Seedling lethal; Pale green cotyledons	TD
At5g23190	*CYP86B1*	C	CLB	B	PRA	Abnormal fatty acid composition	RV
At5g23230	*NIC2*	C	MRP	V	GER, SSC	Low germination rate; Pale seed coat	RV
At5g23260	*TT16*	C	MRP	R	PIG, SSC	Abnormal seed coat coloration; Large seeds	TD
At5g23290	*PFD5*	C	MRP	V	NLS, PIG, GRS, FLT, TCM, CUL, CHS	Dwarf; Slow growth; Dark green; Short hypocotyl; Late flowering; Abnormal pavement cell morphology and microtubule development; Sensitive to salt	RV
At5g23570	*SGS3*	C	CND	I	PTH	Susceptible to viral infection	MB
At5g23630	*MIA*	C	MRP	V	LEF, OVP, SRF, FLT, SEN	Small rosette leaves; Severely reduced fertility and silique size; Low pollen germination rate; Late flowering; Delayed senescence	RV
At5g23730	*RUP2*	NC	CND	P	LIT	Sensitive to UV-B light	RV
At5g23880	*EMB1265*	NC	ESN	S	EMB, W:FLT	Null: Embryo defective; Preglobular / Globular; Knockdown: Early flowering	TD
At5g23940	*EMB3009*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At5g24270	*SOS3*	C	CND	H	NUT, CHS, MCH	Sensitive to lithium, salt stress, and limited potassium	MB
At5g24300	*SSI1*	C	CLB	B	PRA, CPR	Low amylopectin levels; Abnormal amylopectin modification	RV
At5g24310	*ABIL3*	NC	CLB	C	STT	Distorted trichomes	RNAi
At5g24314	*PDE225*	NC	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD

At5g24400	*EMB2024*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g24470	*APRR5*	C	MRP	T	FLT, CDR, LIT	Short circadian rhythms; Late flowering; Sensitive to red light	RV
At5g24520	*TTG1*	C	MRP	R	PIG, SSC, STT, RTH	Yellow seed coat; Abnormal trichome and root hair development	MB
At5g24530	*DMR6*	C	CND	I	PTH	Resistant to *Hyaloperonospora parasitica*	MB
At5g24630	*BIN4*	C	MRP	V	NLS, GRS, ROT, LEF, STT, RTH, CUL, HRM	Severe dwarf; Small cotyledons; Short hypocotyl, roots, and petioles; Abnormal trichomes and root hairs; Increased ploidy levels due to endoreduplication; Insensitive to brassinosteroids	MB; RV
At5g24670	*EMB2820*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g25350	*EBF2*	NC	CND	P	LIT, HRM	Altered response to ACC (ethylene precursor) in the dark	RV
At5g25370	*PLDALPHA3*	C	MRP	T	FLT, WAT, CHS	Late flowering; Sensitive to drought and salt	RV
At5g25380	*CYCA2;1*	C	CLB	C	CUL	Increased ploidy levels	RV
At5g25900	*GA3*	C	MRP	V	GER, PIG, GRS, LEF, FSM, SRF	Very low germination rate; Dwarf; Short, dark green leaves; Abnormal flower morphology; Reduced fertility	MB
At5g26030	*FC1*	NC	CLB	B	PRA	Low heme levels in roots	RV
At5g26240	*CLC-D*	C	MRP	V	ROT, CHS	Short roots; Sensitive to concanamycin A (vacuole proton pump inhibitor)	RV
At5g26570	*AtGWD3*	C	CLB	B	PRA	Elevated starch levels	RV
At5g26742	*EMB1138*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At5g26820	*MAR1*	C	CND	H	CHS	Resistant to kanamycin, streptomycin, gentamicin, amikacin, tobramycin, and apramycin	MB; RV
At5g26860	*LON1*	C	MRP	V	NLS, GRS, ROT, CUL, TMP	Dwarf; Delayed root growth and seedling establishment; Abnormal mitochondria morphology; Low germination rate at high temperature	MB; RV
At5g26920	*CBP60g*	C	CND	I	PTH	Susceptible to bacterial infection	RV
At5g26980	*SYP41*	NC	ESN	G	GAM	Complete male gametophyte defective	RV
At5g27150	*NHX1*	C	MRP	V	LEF	Abnormal leaf growth	RV

At5g27270	*EMB976*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g27380	*GSH2*	C	ESN	L	SRL, PIG	Seedling lethal; Albino seeds and seedlings	RV
At5g27420	*CNI1*	C	CND	H	NUT	Sensitive to nitrogen starvation and glucose	RV
At5g27540	*EMB2473*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g27720	*EMB1644*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g27740	*EMB2775*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g28030	*DES1*	C	MRP	T	SEN, CHS	Early leaf senescence; Elevated cysteine levels in leaves; Tolerant to oxidative stress	RV
At5g28640	*AN3*	C	MRP	V	NLS, LEF, FSM	Narrow cotyledons, leaves, and petals; Increased rosette leaf number	RV
At5g33290	*XGD1*	C	CLB	B	PRA	Low xylose levels in cell walls	RV
At5g33320	*PPT*	C	MRP	V	LEF, CUL	Reticulated leaves; Abnormal chloroplasts in leaf mesophyll layer	TD
At5g34850	*PAP26*	NC	CLB	B	PRA, NUT	Low phosphate levels; Sensitive to phosphate starvation	RV
At5g35220	*EGY1*	C	MRP	V	NLS, PIG	Yellow-green cotyledons; Abnormal hypocotyl gravicurvature	MB
At5g35410	*SOS2*	C	CND	H	NUT	Sensitive to salt stress and limited potassium	MB
At5g35520	*MIS12*	NC	ESN	L	NHM, W:TMP	Null: No homozygous mutant plants recovered; Knockdown: Slow growth at high temperature	RV
At5g35550	*TT2*	C	MRP	R	PIG, SSC	Yellow seed coat	TD
At5g35620	*LSP1*	C	CND	I	PTH	Resistant to potyviruses	MB
At5g35770	*SAP*	C	MRP	R	FSM	Abnormal flower morphology	TN
At5g35840	*PHYC*	C	CND	P	LIT	Long hypocotyl under red light	RV
At5g37020	*ARF8*	C	MRP	V	NLS, IST, SRF, LIT	Long hypocotyl; Slightly shorter inflorescence stems; Reduced fertility; Short hypocotyl in the dark	RV
At5g37055	*SEF*	C	MRP	V	LEF, FSM, FLT	Serrated leaves; Increased petal number; Small siliques; Early flowering	RV
At5g37260	*CIR1*	NC	MRP	T	FLT	Slightly early flowering	RV
At5g37500	*GORK*	NC	CLB	C	STT	Decreased stomatal closure; No other phenotypes detected	TD

At5g37510	*EMB1467*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g37630	*EMB2656*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At5g37850	*SOS4*	C	CND	H	NUT	Sensitive to salt stress and limited potassium	MB
At5g38660	*APE1*	NC	CLB	B	CPR	Abnormal photosynthesis acclimation response	RV
At5g39050	*PMaT1*	C	CLB	B	PRA	Elevated naphthol levels	RV
At5g39400	*AtPTEN1*	NC	ESN	G	MGD	Collapsed pollen	RNAi
At5g39500	*ERMO1*	C	CLB	C	CUL	Disorganized ER morphology	MB
At5g39510	*ZIG*	C	MRP	V	NLS, ARC	Abnormal hypocotyl and inflorescence gravitropism	MB
At5g39610	*ANAC092*	NC	CND	I	PTH	Susceptible to bacterial infection	RV
At5g39680	*EMB2744*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At5g39710	*EMB2745*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g39740	*ANG3*	C	MRP	V	NLS, ROT, LEF, FLT	Short hypocotyl; Narrow, elongated rosette leaves; Short roots; Late flowering	MB; RV
At5g39750	*EMB3008*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g39830	*DEG8*	C	MRP	V	GRS, LIT	Slightly slower growth; Small rosette under high light	RV
At5g39980	*EMB3140*	C	ESN	S	EMB	Embryo defective	RV
At5g40160	*EMB506*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g40280	*ERA1*	C	CND	H	HRM	Abnormal stomatal regulation in response to ABA	TD
At5g40330	*MYB23*	C	CLB	C	STT	Decreased trichome branching	RV
At5g40420	*OLEO2*	C	MRP	V	GER, CUL	Abnormal germination; Large oil bodies	RV
At5g40480	*EMB3012*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g40770	*PHB3*	C	MRP	V	GER, GRS, ROT, LEF	Delayed germination; Semi-dwarf; Small, curled rosette leaves; Slow root growth	RV
At5g40780	*LHT1*	C	MRP	V	MSL, CHS, PTH	Leaf chlorosis; Resistant to toxic D-alanine; Resistant to bacterial and fungal infection	RV
At5g40870	*AtUK/UPRT1*	C	CND	H	CHS	Resistant to toxic pyrimidine analogs	RV
At5g40890	*CLCA*	NC	CND	H	NUT	Low nitrate levels under elevated nitrate	TD
At5g40990	*GLIP1*	C	CND	I	PTH	Susceptible to *Alternaria brassicicola*	RV

At5g41040	*RWP1*	C	CLB	B	CPR	Abnormal aromatic suberin biosynthesis	RV
At5g41150	*UVH1*	C	MRP	T	SEN, LIT, MPH	Early senescence; Sensitive to UV light and ionizing radiation	MB
At5g41315	*GL3*	C	CLB	C	STT	Reduced, abnormal trichomes	OTH
At5g41370	*XPB1*	C	MRP	V	GRS, CHS	Slow growth; Sensitive to alkylating agents	RV
At5g41410	*BEL1*	C	MRP	R	OVP	Abnormal integuments	TD
At5g41480	*GLA1*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD
At5g42080	*ADL1A*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g42270	*VAR1*	C	MRP	V	PIG	Variegated	TD
At5g42400	*ATXR7*	C	MRP	V	LEF, FLT	Decreased young leaf number; Early flowering independent of photoperiod	RV
At5g42630	*KAN4*	C	MRP	R	OVP	Complete loss of integuments	MB; RV
At5g42650	*AOS*	C	MRP	R	SRF	Male sterile	RV
At5g42790	*ARS5*	C	CND	H	MCH	Resistant to arsenic	MB
At5g42800	*TT3*	C	MRP	R	PIG, SSC	Yellow seed coat	OTH
At5g42970	*COP8*	C	ESN	L	SRL, PIG, LIT, NUT	Seedling lethal; Red embryos and cotyledons due to anthocyanin accumulation; Abnormal growth in the dark; Short roots in response to sugar	TD
At5g43270	*SPL2*	C	MRP	V	LEF, STT	Wide cauline leaves; Increased trichome density on sepals	RV
At5g43430	*ETFBETA*	C	MRP	R	SRF	Reduced fertility	RV
At5g43470	*RPP8*	C	CND	I	PTH	Altered response to fungal infection	OTH
At5g43650	*bHLH92*	C	CND	H	CHS	Root growth sensitive to mannitol	RV
At5g43750	*NDH18*	C	CLB	B	CPR	Decreased post-illumination chlorophyll fluorescence	RV
At5g43810	*ZLL*	C	ESN	L	IST, ARC, TCM	Complete loss of primary inflorescence; Fasciated adventitious stems and inflorescences; Arrested SAM development	MB
At5g43940	*HOT5*	C	MRP	V	PIG, GRS, LEF, ARC, SRF, TMP, NUT	Semi-dwarf; Increased branching; Few rosette leaves; Distorted, pale green leaves; Reduced fertility; Sensitive to high temperature; Lethal when grown on nutrient plates	MB
At5g44030	*CESA4*	C	MRP	V	IST, TCM	Short inflorescence stems; Increased xylem	MB

At5g44070	*CAD1*	C	CLB	B	PRA, MCH	Low phytochelatin levels; Sensitive to cadmium	MB
At5g44160	*AtIDD8*	C	MRP	T	FLT	Late flowering	RV
At5g44190	*GLK2*	C	MRP	R	PIG, FSM	Pale green siliques	RV
At5g44370	*PHT4;6*	C	CND	H	CHS	Sensitive to salt	TD; RV
At5g44510	*TAO1*	C	CND	I	PTH	Resistant to bacterial virulence gene B (AvrB)	RV
At5g44740	*POLH*	C	CND	P	LIT	Sensitive to UV-B light	RV
At5g44750	*REV1*	C	CND	P	LIT	Sensitive to UV-B light	RV
At5g44790	*RAN1*	C	CND	H	CHS	Sensitive to TCO (inhibitor of ethylene signaling)	MB
At5g45140	*NRPC2*	C	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At5g45250	*RPS4*	C	CND	I	PTH	*Resistant to Pseudomonas syringae*	MB
At5g45260	*RRS1*	C	CND	I	PTH	Susceptible to fungal infection	RV
At5g45340	*CYP707A3*	C	CND	P	WAT	Resistant to drought	RV
At5g45380	*AtDUR3*	C	CND	H	NUT	Chlorosis and elevated anthocyanin levels with urea as sole source of nitrogen	RV
At5g45610	*HUS2*	C	CND	H	CHS	Sensitive to genotoxic stress	MB; RV
At5g45710	*RHA1*	C	MRP	V	ROT, HRM	Reduced root gravitropism; Insensitive to auxin	TD
At5g45830	*DOG1*	C	MRP	V	GER	Increased seed dormancy	MB
At5g46110	*APE2*	NC	CLB	B	CPR	Abnormal photosynthesis acclimation response	RV
At5g46180	*dOAT*	C	CND	H	NUT	Seedling lethal with ornithine or arginine as sole nitrogen source	RV
At5g46210	*CUL4*	C	MRP	V	ROT, STT, TCM	Few lateral roots; Abnormal leaf stomata and vascular tissue	RV
At5g46290	*KAS1*	C	ESN	S	EMB, PIG, GRS, LEF, SRF	Embryo defective; Cotyledon; Homozygotes are viable: Semi-dwarf; Small, curled, variegated rosette leaves; Reduced fertility; Shriveled seeds; 2nd generation: Seedling lethal	RV
At5g46330	*FLS2*	C	CND	I	PTH	Resistant to bacterial flagella protein	MB
At5g46350	*WRKY8*	C	CND	I	PTH	Resistant to *Pseudomonas syringae*; Susceptible to *Botrytis cinerea*	RV
At5g46470	*RPS6*	C	CND	I	PTH	Susceptible to *Pseudomonas syringae*	MB

At5g46700	*TRN2*	C	MRP	V	LEF, IST, ARC, FSM, SRF	Twisted, irregular leaves lacking large parts of the lamina; Twisted inflorescence stems and floral whorls; Reduced sepal, petal, and stamen number; Incomplete penetrance of unfused carpels with exposed ovules; Sterile	MB
At5g46800	*BOU*	C	ESN	L	SRL	Seedling lethal	TN
At5g46860	*SGR3*	NC	ESN	G	MGD, W:GRS, W:LEF, W:ARC, W:FLT	Null: Male gametophyte defective; Knockdown 1: Serrated, wavy leaves; Semi-dwarf; Late flowering; Knockdown 2: Reduced inflorescence gravitropism	MB
At5g47010	*LBA1*	C	ESN	L	SRL, W:SSC	Null: Seedling lethal; Knockdown: Large seeds	RV
At5g47040	*LON2*	C	MRP	V	ROT, HRM	Short roots; Insensitive to IBA	RV
At5g47100	*CBL9*	C	CND	H	NUT, HRM, CHS	Sensitive to ABA, osmotic stress, and glucose	RV
At5g47120	*AtBI1*	C	CND	P	TMP, CHS, PTH	Sensitive to heat shock, fumonisin B1 (fungal toxin), and tunicamycin (inducer of the unfolded protein response)	RV
At5g47560	*TDT*	C	CLB	B	PRA	Low malate levels in leaves	RV
At5g47910	*RbohD*	NC	MRP	V	GRS	Semi-dwarf	RV
At5g47990	*CYP705A5*	NC	CLB	B	PRA	Elevated thalian-diol levels; No other phenotypes mentioned	RV
At5g48000	*CYP708A2*	C	CLB	B	PRA	Elevated thalianol levels; No other phenotypes mentioned	RV
At5g48010	*OSC*	NC	CLB	B	PRA	Complete loss of thalianol accumulation in roots	RV
At5g48030	*GFA2*	C	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	RV
At5g48100	*TT10*	C	MRP	R	PIG, SSC	Pale brown seed coat with dark-brown chalazal zone	RV
At5g48230	*EMB1276*	C	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g48300	*ADG1*	C	CLB	B	PRA	Low starch levels in leaves	OTH
At5g48485	*DIR1*	C	CND	I	PTH	Altered systemic acquired resistance response	TD
At5g48600	*SMC4*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective	RV

At5g48670	*FEM111*	C	ESN	G	GAM	Complete female gametophyte defective	TD
At5g48720	*XRI1*	C	ESN	G	MGD, MSD	Male gametophyte defective; Bicellular pollen; 50% defective seeds	RV
At5g48840	*PTS*	C	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g48850	*AtSDI1*	NC	CND	H	NUT	Elevated sulfate levels in roots under sulfate starvation	RV
At5g48870	*SAD1*	C	CND	H	HRM, CHS	Germination sensitive to ABA and salt	MB
At5g48910	*LPA66*	C	MRP	V	PIG, GRS	Dwarf; Pale green leaves	MB; RV
At5g49010	*EMB2812*	NC	ESN	S	EMB	Embryo defective	RV
At5g49030	*OVA2*	NC	ESN	G	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	RV
At5g49160	*MET1*	C	ESN	S	EMB	Embryo defective	MB
At5g49190	*SUS2*	C	CLB	B	PRA	Elevated sucrose levels; Low fructose and starch levels; No other phenotypes detected	RV
At5g49270	*SHV2*	C	CLB	C	RTH	Short root hairs	MB
At5g49360	*BXL1*	C	MRP	R	SSC	Abnormal seed mucilage	TD
At5g49510	*PFD3*	C	MRP	V	NLS, PIG, GRS, FLT, TCM, CUL, CHS	Dwarf; Slow growth; Slightly darker green; Short hypocotyl; Late flowering; Abnormal pavement cell morphology and microtubule development; Sensitive to salt	RV
At5g49630	*AAP6*	NC	MRP	V	LEF, SSC	Increased cauline leaf number; Large rosette leaves and seeds	RV
At5g49680	*KIP*	C	ESN	G	MGD, SRF, RTH	Twisted, branched pollen tubes; Homozygotes are viable: Reduced fertility; Short, thick root hairs	TD
At5g49720	*KOR1*	C	MRP	V	NLS, CUL	Abnormal seedling morphology, cell plates, and cell walls	TD
At5g49830	*EXO84B*	C	MRP	V	GRS, LEF, SRF, STT, TCM	Dwarf; Abnormal leaf morphology; Sterile; Abnormal trichomes and epidermal cell morphology	RV
At5g49890	*AtCLCc*	C	CLB	C	STT, CHS	Abnormal stomatal response to light; Sensitive to salt	RV
At5g49930	*EMB1441*	C	ESN	S	EMB	Embryo defective; Globular	TD

At5g49970	*AtPPOX*	C	MRP	V	GRS, ROT, SRF, LIT, NUT, CHS	Small root system; Reduced fertility; Sensitive to high light; Increased growth in response to sucrose; Resistant to salt	RV
At5g50200	*WR3*	C	CND	H	NUT	Sensitive to limited nitrate	RV
At5g50210	*QS*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g50280	*EMB1006*	NC	ESN	S	EMB	Embryo defective; Globular	TD
At5g50300	*AZG2*	C	CND	H	CHS	Resistant to toxic purine analogues	RV
At5g50320	*ELO3*	C	MRP	V	GER, NLS, GRS, ROT, LEF, ARC	Very low germination rate; Delayed seedling growth; Narrow leaves; Short primary root; Short inflorescence stems with abnormal architecture --	MB
At5g50375	*CPI1*	C	MRP	V	GRS, ROT, SRF	Dwarf; Reduced root gravitropism; Sterile	TN
At5g50390	*EMB3141*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g50850	*MAB1*	NC	ESN	S	EMB	Embryo defective	MB
At5g50920	*DCA1*	C	MRP	V	PIG, MSL, CUL	Chlorosis; Pale green; Aberrant chloroplast biogenesis	RV
At5g50950	*FUM2*	C	CLB	B	PRA	Low fumarate levels; Low amino acid levels in the daytime; Elevated amino acid levels at night	RV
At5g50960	*AtNBP35*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	RV
At5g51020	*CRL*	C	ESN	S	EMB, PIG, GRS, ROT, LEF, IST, SRF, CUL	Embryo defective; Cotyledon; Dwarf; Crumpled, pale green leaves; Short roots; Thin inflorescence stems; Severely reduced fertility; Few, large chloroplasts	TD
At5g51060	*RHD2*	C	CLB	C	RTH	Short root hairs	RV
At5g51100	*APG8*	C	MRP	V	PIG	Pale green seedlings	RV
At5g51200	*EMB3142*	NC	ESN	S	EMB	Embryo defective; Preglobular	RV
At5g51230	*EMF2*	C	MRP	V	NLS, LEF, IST, MSL, FSM, FLT, TCM	Short hypocotyl; Oval cotyledons with no petiole; Very small, sessile rosette leaves; Very short inflorescence stem; Single flower develops; Only carpel-like floral organs; Severe early flowering; Large SAM	MB
At5g51330	*SWI1*	C	MRP	R	SRF, CUL	Sterile due to defects in meiosis; Reduced sister chromatid cohesion	TD
At5g51430	*EYE*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD

At5g51545	*LPA2*	C	MRP	V	PIG, GRS	Pale green; Slow growth	RV
At5g51600	*PLE*	C	MRP	V	ROT	Short, wavy roots with abnormal architecture; Increased lateral root number	MB
At5g51700	*PBS2*	C	CND	I	PTH	Susceptible to specific strains of *Pseudomonas syringae*	MB
At5g51760	*AHG1*	C	CND	H	HRM	Sensitive to ABA	MB
At5g51810	*GA20ox2*	NC	MRP	V	NLS, GRS, FSM, FLT	Semi-dwarf; Short hypocotyl; Short siliques (no reduction in fertility); Late flowering	RV
At5g51820	*PGM*	C	CLB	B	PRA	Low starch levels	RV
At5g52290	*SHOC1*	C	MRP	R	SRF	Reduced fertility due to defects in meiosis	RV
At5g52520	*OVA6*	NC	ESN	G	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	RV
At5g52560	*AtUSP*	C	ESN	G	GAM	Complete male gametophyte defective	TD
At5g52920	*PKP1*	C	ESN	S	EMB	Embryo defective; Cotyledon	RV
At5g53170	*FTSH11*	C	CND	P	TMP	Lethal, pale plants at high temperature	MB
At5g53200	*TRY*	C	CLB	C	STT	Low penetrance of clustered trichomes	RV
At5g53210	*SPCH*	C	MRP	V	PIG, STT	Pale green seedlings; Complete loss of stomata	RV
At5g53280	*PDV1*	C	CLB	C	CUL	Large, constricted chloroplasts	MB
At5g53400	*BOB1*	C	ESN	S	EMB	Embryo defective; Globular	MB
At5g53460	*GLT1*	NC	CLB	B	PRA, NUT	Low chlorophyll levels (no other phenotypes detected); Reduced fresh weight and low glutamate levels when grown under 1% CO2	RV
At5g53470	*ACBP1*	NC	CND	P	TMP	Resistant to freezing	UNK
At5g53760	*MLO11*	C	CND	P	MEC	Tight spiral-like root growth in response to touch	RV
At5g53860	*EMB2737*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g53950	*CUC2*	NC	MRP	V	NLS	Low penetrance of heart-shaped cotyledons	TD
At5g54160	*COMT1*	C	CND	I	PTH	Susceptible to fungal infection	RV
At5g54250	*AtCNGC4*	C	MRP	V	LEF, MSL, PTH	Small leaves; Short petioles; Necrotic lesions; Resistant to *Pseudomonas syringae*	TD; RV
At5g54260	*MRE11*	C	MRP	V	GRS, SRF, CUL, CHS	Dwarf; Sterile; Long telomeres; Sensitive to genotoxic stress	RV
At5g54310	*NEV*	C	MRP	R	FSM	Indehiscent floral organs; Abnormal silique morphology	RV

At5g54380	*THE1*	C	MRP	V	NLS	Short hypocotyl	MB
At5g54440	*TRS130*	C	ESN	L	SRL	Seedling lethal; Seedlings are amorphous and club-like	MB; RV
At5g54590	*CRLK1*	C	CND	P	TMP	Sensitive to freezing	RV
At5g54640	*RAT5*	C	CND	I	OBI	Resistant to *Agrobacterium* root transformation	TD
At5g54650	*FH5*	C	ESN	S	MSD	Delayed endosperm cellularization; No other phenotypes detected	TD
At5g54690	*GAUT12*	C	MRP	V	LEF, FSM, CUL	Small leaves, siliques, flowers; Decreased secondary cell wall thickness	RV
At5g54770	*TZ*	C	ESN	L	SRL	Seedling lethal without exogenous thiamine	OTH
At5g54800	*GPT1*	C	ESN	G	GEM	Male and female gametophyte defective; Embryo defective (inferred)	RV
At5g54810	*TRP2*	C	ESN	L	SRL	Seedling lethal without exogenous tryptophan	OTH
At5g55170	*SUM3*	NC	MRP	T	FLT	Late flowering independent of photoperiod	RV
At5g55280	*FtsZ1*	C	CLB	C	CUL	Few, large chloroplasts	RV
At5g55310	*TOP1*	C	MRP	V	LEF, IST, ARC, FSM	Twisted inflorescence stems and leaf margins; Multiple flowers form at single node	TD
At5g55390	*EDM2*	C	CND	I	PTH	Susceptible to fungal infection	MB
At5g55470	*NHX3*	C	CND	H	NUT	Sensitive to potassium starvation	RV
At5g55540	*TRN1*	C	CLB	C	TCM	Abnormal division and positioning of lateral root cap	MB
At5g55590	*QRT1*	C	MRP	R	OVP	Tetrad pollen	MB; RV
At5g55630	*AtKCO1*	NC	CLB	B	CPR	Reduced slow-activating vacuolar channel currents; Visible phenotypes not discussed	RV
At5g55700	*BAM4*	C	MRP	V	GRS	Semi-dwarf; Elevated starch levels	RV
At5g55740	*CRR21*	C	CLB	B	CPR	Complete loss of post-illumination chlorophyll fluorescence	RV
At5g55760	*SRT2*	NC	CND	I	PTH	Resistant to disease	RV
At5g55810	*AtNMNAT*	C	ESN	G	GAM	Male gametophyte defective; Rare embryo defective	RV
At5g55940	*EMB2731*	NC	ESN	G	EMG	Embryo defective; Gametophyte defective (inferred)	TD
At5g56110	*AtMYB103*	C	MRP	R	OVP, SRF	Male sterile; Abnormal pollen exine layer	MB

At5g56270	*WRKY2*	C	CND	H	HRM	Germination and seedling growth sensitive to ABA	RV
At5g56280	*CSN6A*	NC	MRP	V	NLS	Short hypocotyl	RV
At5g56290	*EMB2790*	C	ESN	S	EMB	Embryo defective; Globular	RV
At5g56360	*PSL4*	C	CND	I	PTH	Insensitive to elf18 (bacterial defense inducer)	MB
At5g56550	*OXS3*	NC	CND	H	CHS	Sensitive to t-BOOH (organic peroxide) and diamide (oxidizing agent)	RV
At5g56580	*MKK6*	C	MRP	V	NLS, GRS, ROT, LEF, TCM	Dwarf; Small leaves; Short roots; Rough cotyledons; Cell outgrowths on root epidermis	RV
At5g56680	*EMB2755*	NC	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g56860	*GNC*	C	MRP	V	PIG	Pale green leaves	RV
At5g56930	*EMB1789*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g57020	*NMT1*	C	ESN	L	SRL	Seedling lethal	RV
At5g57030	*LUT2*	C	CLB	B	PRA	Complete loss of lutein accumulation; Elevated carotenoid levels; Heterozygotes: Low lutein levels	MB
At5g57090	*AGR1*	C	MRP	V	NLS, ROT	Abnormal root and hypocotyl gravicurvature	MB
At5g57160	*AtLIG4*	C	CND	H	CHS	Seedling growth sensitive to genotoxic stress	RV
At5g57180	*CIA2*	C	MRP	V	PIG	Pale green	MB
At5g57320	*VLN5*	C	ESN	G	MGD	Male gametophyte defective	RV
At5g57350	*AHA3*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At5g57360	*ZTL*	C	MRP	T	CDR	Abnormal circadian rhythms	MB
At5g57380	*VIN3*	C	CND	H	NUT	Sensitive to hypoxia	RV
At5g57390	*AIL5*	C	CND	H	NUT	Seedlings insensitive to elevated nitrate	MB
At5g57590	*BIO1*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g57740	*XBAT32*	C	MRP	V	GRS, ROT	Few lateral roots; Slow growth	RV
At5g57800	*CER3*	C	MRP	V	IST, SRF	Dull stems and inflorescences; Reduced male fertility	OTH
At5g57880	*MPS1*	C	MRP	R	SRF	Reduced male and female fertility	TD; RV
At5g57930	*EMB1629*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g58070	*TIL1*	C	CND	P	TMP	Sensitive to high temperature	RV

At5g58140	*PHOT2*	C	CLB	C	CUL	Complete loss of chloroplast movement in response to light; Heterozygotes: Slow chloroplast movement in response to light	RV
At5g58230	*MSI1*	C	ESN	S	MSD	Embryo defective; 50% defective seeds	RV
At5g58250	*EMB3143*	NC	ESN	S	EMB	Embryo defective; Cotyledon	RV
At5g58270	*Sta1*	C	MRP	V	GRS, LEF, MSL	Dwarf; Chlorotic; Abnormal leaf morphology	TD
At5g58290	*BIM409*	C	CND	H	CHS	Resistant to BMAA (glutamate receptor competitor)	MB
At5g58600	*PMR5*	C	MRP	V	LEF, PTH	Short, rounded leaves; Elevated pectin and uronic acid levels in cell wall; Resistant to fungal infection	MB
At5g58960	*GIL1*	C	CND	P	LIT	Upward hypocotyl growth under red light	RV
At5g59220	*PP2CA2*	NC	CND	H	HRM, CHS	Germination insensitive to ABA and salt	RV
At5g59340	*WOX2*	C	ESN	S	EMB	Embryo defective; Cotyledon; Abnormal cell patterning; Homozygotes appear wild type	RV
At5g59440	*ZEUS1*	C	ESN	S	EMB	Embryo defective; Preglobular	TD
At5g59560	*SRR1*	C	CND	P	LIT	Altered response to red light	RV
At5g59710	*VIP2*	NC	CND	I	OBI	Few root tumors in response to *Agrobacterium* infection	RV
At5g59780	*MYB59*	C	MRP	V	ROT	Long roots	RV
At5g59890	*ADF4*	C	CND	I	PTH	Susceptible to avirulent bacteria	RV
At5g59920	*ULI3*	C	CND	P	LIT	Long hypocotyl under UV-B light	MB
At5g60410	*AtSIZ1*	C	CND	H	NUT	Sensitive to phosphate starvation	RV
At5g60540	*EMB2407*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g60600	*HDS*	C	MRP	V	GRS, LEF, PTH	Dwarf; Curled leaves; Resistant to *Hyaloperonospora parasitica*	MB
At5g60690	*REV*	C	MRP	V	LEF, ARC	Altered leaf morphology; Complete loss of auxiliary inflorescences	MB; TD
At5g60760		C	CLB	B	PRA	Low phytic acid levels in seeds	RV
At5g60910	*AGL8*	C	MRP	R	FSM, SRF, SSC	Short siliques that are crowded with small seeds; Reduced fertility	TN

At5g60920	*COB*	C	CLB	C	TCM	Abnormal cell expansion orientation; Reduced crystalline cellulose in root	MB
At5g61070	*HDA18*	NC	CLB	C	RTH, TCM	Increased root hair density; Abnormal root epidermal cell patterning	RV
At5g61150	*VIP4*	C	MRP	T	FSM, FLT	Early flowering; Slightly altered flower morphology	MB
At5g61160	*AtACT*	C	CLB	B	PRA	Complete loss of hydroxycinnamic acid amide accumulation	RV
At5g61230	*ANK6*	C	ESN	G	EMG	Ovule abortion; Female gametophyte defective; Early embryo defective (inferred)	RV
At5g61380	*TOC1*	C	MRP	T	CDR	Short circadian rhythms in light	MB
At5g61410	*EMB2728*	C	ESN	S	EMB	Embryo defective; Cotyledon	TD
At5g61420	*MYB28*	C	CLB	B	PRA	Low glucosinolate levels in seeds	RV
At5g61460	*MIM*	C	CND	H	CPR, CHS	Sensitive to DNA damaging agents; Reduced somatic intrachromosomal homologous recombination	TD
At5g61640	*PMSR2*	C	CND	P	LIT	Dwarf under short days	RV
At5g61850	*LFY*	C	MRP	V	ARC, MSL, FSM	Increased branching; Flowers show some characteristics of secondary inflorescences; Flowers often subtended by leafy bracts	MB
At5g61900	*BON1*	C	MRP	V	LEF, TMP, PTH	Small, curled leaves; Dwarf at low temperature; Resistant to disease	TD
At5g62000	*ARF2*	C	MRP	V	NLS, PIG, LEF, SRF, SSC, FLT, SEN	Large cotyledons; Short hypocotyl; Large, dark green rosette leaves; Reduced fertility; Large seeds; Late flowering; Delayed senescence	RV
At5g62310	*IRE*	C	CLB	C	RTH	Short root hairs	TD
At5g62320	*AtMYB99*	NC	MRP	R	OVP, SRF	Reduced fertility; Thin tapetal cells	RV
At5g62390	*BAG7*	C	CND	P	TMP, CHS	Sensitive to high and low temperature and tunicamycin (inducer of the unfolded protein response)	RV
At5g62410	*TTN3*	C	ESN	G	EMG, CUL	Embryo defective; Large nuclei in endosperm; Gametophyte defective	TD
At5g62440	*DOM1*	C	ESN	S	EMB	Embryo defective; Globular	TD

At5g62470	*MYB96*	C	MRP	V	ROT, WAT	Increased lateral root number; Sensitive to drought	RV
At5g62500	*AtEB1B*	C	MRP	V	ROT, MEC	Abnormal root gravitropism and thigmotropism	RV
At5g62790	*PDE129*	C	ESN	L	SRL, PIG	Seedling lethal (inferred from pigment defect)	TD
At5g62810	*PED2*	C	ESN	L	SRL, HRM	Seedling lethal without exogenous sucrose; Insensitive to 2,4-DB	MB
At5g62920	*ARR6*	NC	CND	P	LIT	Short hypocotyl under red light	RV
At5g62990	*EMB1692*	C	ESN	S	EMB	Embryo defective; Transition	TD
At5g63050	*EMB2759*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g63110	*HDA6*	C	MRP	T	FLT, SEN	Late flowering; Delayed leaf senescence	MB; RV
At5g63310	*NDPK2*	C	CND	P	LIT	Short hypocotyl and reduced cotyledon opening and apical hook strengthening under far-red light	RV
At5g63420	*EMB2746*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g63780	*SHA1*	C	ESN	L	SRL	Rosette lethal	TD
At5g63840	*RSW3*	C	MRP	V	ROT	Thick roots	MB
At5g63860	*UVR8*	C	CND	P	LIT	Sensitive to UV-B light	MB
At5g63890	*HISN8*	C	ESN	G	GAM, W:MGD	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Male and female gametophyte defective	RV
At5g63920	*TOP3A*	NC	ESN	L	SRL, W:SRF	Null: Seedling lethal; Knockdown: Sterile	RV
At5g63950	*CHR24*	NC	CND	P	LIT	Sensitive to UV light	RV
At5g63980	*FRY1*	C	MRP	T	FLT, RTH, TCM, WAT, TMP, MPH, HRM, CHS	Late flowering; Abnormal leaf venation; Long root hairs; Few lateral roots under vertical growth; Sensitive to drought, freezing, ABA, and salt stress	MB; RV
At5g64050	*OVA3*	C	ESN	G	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	RV
At5g64330	*NPH3*	C	CND	P	LIT	Reduced phototropism	MB
At5g64370	*PYD3*	C	CND	H	NUT	Lethal with urea as sole source of nitrogen	RV
At5g64440	*AtFAAH*	C	MRP	V	NLS, ROT	Short primary root; Narrow cotyledons; Short hypocotyl	RV
At5g64560	*MGT9*	C	ESN	G	GAM	Complete male gametophyte defective	RV
At5g64580	*EMB3144*	C	ESN	S	EMB	Embryo defective; Globular	RV

At5g64630	*FAS2*	C	MRP	V	GRS, ROT, LEF, IST, ARC, FSM, SRF, TCM	Slow growth; Short roots; Fasciated stems and inflorescences; Abnormal leaf morphology; Abnormal phyllotaxy; Reduced petal and stamen number; Narrow sepals and petals; Reduced fertility; Abnormal SAM and RAM morphology	OTH
At5g64740	*IXR2*	C	MRP	V	GRS, ROT, CUL, CHS	Dwarf; Short roots; Cell wall defective; Resistant to isoxaben (herbicide)	TD
At5g64750	*ABR1*	C	CND	H	NUT, HRM, CHS	Sensitive to ABA, glucose, and osmotic stress	RV
At5g64813	*LIP1*	C	MRP	T	CDR, LIT	Short circadian rhythms; Altered response to light	MB; RV
At5g64860	*DPE1*	C	MRP	V	GRS	Slightly reduced fresh weight; Elevated starch levels	TD
At5g64930	*CPR5*	C	MRP	V	MSL, STT	Spontaneous chlorotic lesions; Abnormal trichome development	TD
At5g65050	*AGL31*	C	MRP	T	MTM	Abnormal vernalization response	TD
At5g65090	*BST1*	C	CLB	C	RTH	Short root hairs	MB
At5g65110	*ACX2*	NC	CLB	B	CPR	Delayed lipid elongation and breakdown	RV
At5g65165	*SDH2-3*	C	MRP	V	GER	Low germination rate	RV
At5g65420	*CYCD4;1*	C	MRP	V	ROT	Few lateral roots	RV
At5g65720	*NFS1*	NC	ESN	L	NHM, W:GRS, W:LEF, W:ARC, W:MSL	Null: No homozygous mutant plants recovered; Knockdown: Dwarf; Increased branching; Scalloped, chlorotic leaves	RV; RNAi
At5g65800	*ACS5*	C	MRP	V	NLS, IST, HRM	Tall inflorescence stems; Long hypocotyl; Large cotyledons; Low ethylene levels in response to cytokinin	MB
At5g65930	*ZWI*	C	CLB	C	STT	Abnormal trichome morphology	TD
At5g65940	*CHY1*	C	CND	H	HRM	Insensitive to IBA	MB
At5g66055	*EMB2036*	C	ESN	S	EMB	Embryo defective; Globular	TD
At5g66130	*RAD17*	C	CND	H	CPR, CHS	Sensitive to DNA damaging agents; Increased intrachromosomal recombination frequency	RV
At5g66190	*AtLFNR1*	C	MRP	V	PIG, LEF	Reduced rosette size; Pale green leaves	RV

At5g66460	*MAN7*	NC	MRP	V	GER	Delayed germination	RV
At5g66570	*PsbO*	C	MRP	V	GRS	Dwarf	OTH
At5g66680	*DGL1*	C	ESN	S	EMB	Embryo defective; Preglobular / Globular	TD; RV
At5g66750	*DDM1*	C	CLB	B	CPR	Decreased DNA methylation; Variety of morphological defects upon repeated self-pollination due to release of endogenous transposons	UNK
At5g66760	*SDH1-1*	C	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	RV; RNAi
At5g66880	*SnRK2.3*	NC	MRP	V	GER, STT, HRM	Slightly reduced seed dormancy; Abnormal stomata; Insensitive to ABA	RV
At5g67030	*ABA1*	C	MRP	V	MSL	Wilty; Low ABA levels	MB
At5g67100	*ICU2*	C	ESN	G	GAM, W:LEF, W:FSM, W:FLT	Null: Male and female gametophyte defective; Rare embryo defective; Knockdown: Curled leaves; Abnormal floral morphology; Early flowering	MB; RV
At5g67160	*EPS1*	C	CLB	B	PRA, PTH	Low SA levels; Susceptible to virulent and avirulent bacteria	MB; RV
At5g67270	*AtEB1C*	NC	MRP	V	ROT	Thin roots that grow in a clockwise spiral fashion	RV
At5g67320	*HOS15*	C	CND	P	TMP	Sensitive to low temperature and freezing	TD
At5g67360	*AtSBT1.7*	C	MRP	R	SSC	Abnormal seed mucilage	RV
At5g67420	*LBD37*	C	CND	H	NUT	Elevated anthocyanin levels in response to nitrogen	RV
At5g67570	*EMB1408*	C	ESN	S	EMB	Embryo defective; Transition	TD
At5g67590	*FRO1*	C	MRP	V	LEF, TMP	Abnormal leaf morphology; Reduced acclimation to low temperature	MB

.

APPENDIX D: Single Gene Mutant Phenotype Dataset, Gene Information

This appendix includes a truncated version of the single gene mutant phenotype dataset. Emphasis was placed on gene identifier information and features of an encoded protein. Included data are locus numbers, gene names and aliases, full gene names, genetic redundancy class, protein product function descriptions, and mitochondria or chloroplast localization ranks. The complete Arabidopsis phenotype dataset is available as a spreadsheet appended to the Plant Physiology publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S2).

Footnotes for the title row of the following table are described below:

[a] Unique, No additional genes with a similar sequence (BLASTP e-30 cutoff) found in the Arabidopsis genome; Moderate, One or more genes identified with moderate similarity (BLASTP e-30 to e-80, or BLASTP >e-80 if <80% of protein lengths aligned) in the Arabidopsis genome; High, One or more genes identified with high similarity (BLASTP >e-80 with >80% aligned) in the Arabidopsis genome.

[b] Based on manual curation of information presented in publications. To streamline efforts and facilitate comparisons of greatest interest, assignments were limited to unique genes, essential seed and gametophyte genes, and proteins localized to chloroplasts and mitochondria.

[c] Likelihood of protein localization to chloroplasts or mitochondria based on experimental data and prediction programs; from high (5 CPT; 6 MIT) to low (1).

Locus	**Gene Symbol**	**Alias Symbols**	**Full Gene Name**	**Genetic Redundancy Class**[a]	**Predicted Function of Gene Product**[b]	**MIT Localization (Rank)**[c]	**CPT Localization (Rank)**[c]
At1g01030	*NGA3*	*TOP1*	Ngatha	Moderate			
At1g01040	*SUS1*	*DCL1; SIN1; CAF*	Abnormal Suspensor	Moderate	RNA Helicase		
At1g01060	*LHY*		Late Elongated Hypocotyl	Moderate			
At1g01120	*KCS1*		3-Ketoacyl-CoA Synthase Defective	High			
At1g01280	*CYP703A2*		Cytochrome P450	High			
At1g01370	*CENH3*		Centromere-Specific Histone	Unique	Centromere-Specific Histone		
At1g01460	*PIPK11*		Phosphatidylinositol Phosphate Kinase	High			Not Evaluated
At1g01480	*ACS2*		Aminocyclopropane Carboxylate Synthase	High			
At1g01510	*AN*		Angustifolia	Unique	CtBP Protein; Putative Transcriptional Repressor		
At1g01550	*BPS1*		Bypass	High			
At1g01690	*PRD3*		Putative Recombination Initiation Defect	Unique	Role in Meiotic DSB Formation		
At1g01860	*PFC1*		Paleface	Unique	16S rRNA Methylase; Pre-rRNA Modification		
At1g01950	*ARK2*		Armadillo Repeat Kinesin	High			
At1g02050	*LAP6*	*PKSA*	Less Adhesive Pollen	High			Not Evaluated
At1g02065	*SPL8*		Squamosa Promoter Binding Protein-Like	Moderate			Not Evaluated

At1g02090	*FUS5*	*COP15*	Fusca	Unique	Component of COP9 Signalosome; Light-Regulated Signal Transduction and Protein Degradation		
At1g02120	*VAD1*		Vascular-Associated Death	Unique	Uncertain; Putative Lipid or Protein Binding Signaling Protein		
At1g02140	*HAP1*	*MAGO; MEE63*	Hapless	Unique	Component of Exon Junction Complex		
At1g02205	*CER1*		Eceriferum	High			
At1g02280	*PPI1*	*TOC33*	Plastid Protein Import	High	Chloroplast Protein Import		CPT Localized (3)
At1g02340	*HFR1*	*REP1; RSF1*	Long Hypocotyl in Far-Red Light	Unique	bHLH Transcription Factor		
At1g02560	*CLPP5*	*NCLPP1; NCLPP5*	Clp Protease	Moderate	Chloroplast Clp Protease Subunit		CPT Localized (4)
At1g02580	*MEA*	*EMB173; FIS1*	Medea	Moderate	SET Domain Polycomb Protein; Chromatin Structure Modulation		
At1g02730	*ATCSLD5*	*SOS6*	Cellulose Synthase Like	High			
At1g02780	*EMB2386*		Embryo Defective	High	Cytosolic Ribosomal Protein L19		
At1g02860	*NLA*	*BAH1*	Nitrogen Limitation Adaptation	Moderate			
At1g02910	*LPA1*		Low PSII Accumulation	Unique	Chloroplast Integral Membrane Chaperone		CPT Localized (4)
At1g02970	*WEE1*		Arabidopsis wee1 Kinase Homolog	Unique	WEE1 Kinase; Cell Cycle Inhibition Signaling		
At1g03000	*PEX6*		Peroxin	Moderate			
At1g03060	*SPI*		Spirrig	High			

At1g03160	*FZL*		FZO-Like	Unique	Dynamin-Like GTPase; Regulation of Thylakoid Organization		CPT Localized (4)
At1g03190	*UVH6*	*AtXPD*	Ultraviolet Hypersensitive	Moderate	Nucleotide Excision Repair		
At1g03310	*AtISA2*	*DBE1*	Isoamylase	High	Multimeric Isoamylase Complex; Polysaccharide Biosynthesis		CPT Localized (4)
At1g03360	*RRP4*		Ribosomal RNA Processing	Unique	rRNA Processing; Exonuclease	MIT Localized (4)	
At1g03790	*SOM*		Somnus	Moderate			
At1g04010	*PSAT1*		Phospholipid Sterol Acyl Transferase	Unique	Sterol Ester Biosynthesis; Free Sterol Homeostasis		
At1g04020	*BARD1*		BRCA1-Associated Ring Domain	Moderate			
At1g04110	*SDD1*		Stomatal Density, Distribution	High			
At1g04120	*MRP5*	*ABCC5*	Multidrug Resistance-Associated Protein	High			
At1g04220	*KCS2*	*DAISY*	3-Ketoacyl-CoA Synthase	High			
At1g04240	*SHY2*	*IAA3*	Short Hypocotyl	Moderate			
At1g04250	*AXR3*	*IAA17*	Auxin Resistant	Moderate			
At1g04400	*FHA*	*CRY2*	Late Flowering	High			
At1g04635	*EMB1687*		Embryo Defective	Unique	Ribonuclease P Family (POP5); tRNA Processing		
At1g04820	*TOR2*	*TUA4*	Tortifolia	High			
At1g04870	*AtPRMT10*		Protein Arginine Methyltransferase	Moderate			

At1g04940	*TIC20*		Translocon Inner Envelope Membrane of Chloroplasts	High	Chloroplast Protein Import		CPT Localized (1)
At1g04950	*EMB2781*	*TAF6; TAFII59*	Embryo Defective	High	TATA Box Binding Protein; Transcriptional Regulation		
At1g05180	*AXR1*		Auxin Resistant	High			
At1g05190	*EMB2394*		Embryo Defective	Unique	Chloroplast 50S Ribosomal Protein L6		CPT Localized (4)
At1g05385	*LPA19*		Low Photosystem II Accumulation	Unique	PSII Biogenesis and Assembly		Not Evaluated
At1g05470	*CVP2*	*At5PT11*	Cotyledon Vascular Pattern	Moderate			
At1g05600	*EMB3101*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing	MIT Localized (4)	
At1g05630	*At5PT13*		Inositol Polyphosphate 5' Phosphatase	High			
At1g05750	*PDE247*	*CLB19*	Pigment Defective Embryo	High	PPR Protein; Organellular mRNA Processing		CPT Localized (2)
At1g05760	*RTM1*		Restricted TEV Movement	Moderate			
At1g05850	*ELP*	*CTL1; HOT2; ERH2*	Ectopic Lignin in Pith	High			
At1g05990	*RHS1*		Root Hair Specific	Moderate			
At1g06040	*STO*		Salt Tolerance	High			
At1g06150	*EMB1444*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		

At1g06160	*ORA59*		Octadecanoid-Responsive AP2/ERF	Moderate			
At1g06220	*GFA1*	*CLO; MEE5*	Gametophyte Factor	High	Putative RNA Splicing Protein		
At1g06230	*GTE4*		Global Transcription Factor	Moderate			
At1g06290	*ACX3*	*IBR4*	Acyl-CoA Oxidase	High			
At1g06400	*ARA2*	*AtRAB11E; AtRABA1A*		High			
At1g06490	*CALS7*	*GSL7*	Callose Synthase	High			Not Evaluated
At1g06520	*GPAT1*		Glycerol-3-Phosphate Acyltransferase	High			
At1g06570	*PDS1*	*HPD*	Phytoene Desaturase	Unique	p-Hydroxyphenylpyruvate Dioxygenase; Plastoquinone and Tocopherol Biosynthesis		
At1g06780	*GAUT6*		Galacturonosyltransferase	High			
At1g06950	*TIC110*		Translocon at Inner Envelope Membrane of Chloroplasts	Unique	Chloroplast Import Protein		CPT Localized (4)
At1g07130	*STN1*		Arabidopsis Ortholog of Yeast STN1	Unique	Role in Telomere Capping		
At1g07320	*EMB2784*		Embryo Defective	Unique	Plastid Ribosomal Protein L4		CPT Localized (4)
At1g07360	*MAC5A*		MOS4-Associated Complex Subunit	Moderate			Not Evaluated

At1g07530	*SCL14*	*GRAS2*	Scarecrow-Like	High			
At1g07630	*PLL5*		POL-Like	High			
At1g07890	*APX1*		Ascorbate Peroxidase	High	Cytosolic Ascorbate Peroxidase; Peroxide Detoxification		
At1g07930	*eEF1A2*		Eukaryotic Elongation Factor	High	Multifunctional Protein: Translation Elongation Factor; Actin Filament Formation and Bundling; Role in Several Signaling Pathways	MIT Localized (1)	
At1g08030	*TPST*		Tyrosylprotein Sulfotransferase	Unique	Tyrosylprotein Sulfotransferase; Tyrosine Sulfation		
At1g08060	*MOM*		Maintenance of Methylation	Unique	SWI/SNF2-Related Protein; Putative Role in Chromatin Remodeling		
At1g08090	*NRT2*	*LIN1*	Nitrate Transport Defective	High			
At1g08130	*LIG1*		DNA Ligase	High	DNA Replication and Repair; Adjacent Polynucleotide Joining	MIT Localized (2)	
At1g08190	*AtVPS41*	*ZIP2*		Unique	Vacuole and Golgi Vesicle Trafficking		
At1g08260	*EMB2284*	*TIL1; EMB529; AtPOL2a; ABO4; ESD7*	Embryo Defective	High	Subunit of DNA Polymerase Epsilon; DNA Replication		
At1g08370	*DCP1*		Decapping	Unique	Decapping Protein; Role in mRNA Turnover and Decay		

At1g08430	*ALMT1*		Aluminum-Activated Malate Transporter	High			
At1g08450	*CRT3*	*EBS2; PSL1*	Calreticulin	Moderate			Not Evaluated
At1g08510	*FATB*		Fatty Acyl-ACP Thioesterase B	Moderate	Acyl-Acyl Carrier Protein Thioesterase; Saturated Fatty Acid Biosynthesis		CPT Localized (1)
At1g08520	*PDE166*	*CHLD*	Pigment Defective Embryo	Moderate	Magnesium Chelatase; Chlorophyll Biosynthesis		CPT Localized (4)
At1g08540	*ABC1*	*SIG2*	Aberrant Chloroplasts	Moderate	RNA Polymerase Sigma Factor		CPT Localized (4)
At1g08550	*NPQ1*	*AVDE1*	Nonphotochemical Quenching Defective	Unique	Violaxanthin De-epoxidase; Zeaxanthin Biosynthesis		CPT Localized (3)
At1g08560	*KN*	*SYP111*	Knolle	Moderate	Cytokinesis-Specific Syntaxin; Promotes Vesicle Fusion in Cell Division Plane		
At1g08630	*THA1*		Threonine Aldolase	High			
At1g08660	*MGP2*		Male Gametophyte Defective	High	Golgi-localized Sialyltransferase		
At1g08720	*EDR1*		Enhanced Disease Resistance	Moderate			
At1g08810	*MYB60*		MYB Domain Protein	Moderate			
At1g08840	*EMB2411*	*DNA2*	Embryo Defective	Moderate	Helicase/Nuclease; DNA Replication; Okazaki Fragment Metabolism		
At1g09090	*AtrbohB*		Respiratory Burst Oxidase Homolog	High			

At1g09100	*RPT5B*			High			
At1g09210	*CRT1b*		Calreticulin	High			Not Evaluated
At1g09270	*IMPA-4*		Importin Alpha Isoform	High			
At1g09530	*PIF3*	*PAP3; POC1*	Phytochrome Interacting Factor	Unique	Phytochrome Signaling		
At1g09540	*MYB61*		MYB Gene Knockout	High			
At1g09570	*FHY2*	*PHYA; HY8*	Long Hypocotyl in Far-Red Light	High			
At1g09700	*HYL1*	*DRB1*	Hyponastic Leaves	Unique	Putative dsRNA Binding Protein		
At1g09770	*AtCDC5*		Cell Division Cycle	Unique	MYB Domain Transcription Factor		
At1g09940	*HEMA2*			High			
At1g09970	*RLK7*		Receptor-Like Kinase	High			Not Evaluated
At1g10130	*ECA3*		ER-Type Calcium Transporting ATPase	High			
At1g10170	*AtNFXL1*		NF-X-Like	Moderate			
At1g10270	*GRP23*		Glutamine Rich Protein	Moderate	Novel PPR Protein; Putative Transcriptional Regulator		
At1g10310				Unique	Fatty Acid Short Chain Dehydrogenase		
At1g10370	*AtGSTU17*	*ERD9*	Glutathione S-Transferase	High			Not Evaluated
At1g10470	*ARR4*	*MEE7*	Response Regulator	Moderate			
At1g10510	*EMB2004*		Embryo Defective	Unique	Uncertain; Chloroplast-localized LRR Protein		CPT Localized (2)

At1g10760	*SEX1*	*GWD1; SOP1*	Starch Excess	High	Regulator of Starch Phosphorylation and Degradation		CPT Localized (3)
At1g10840	*eIF3h*	*TIF3H1*	Eukaryotic Initiation Factor	Unique	Translation Initiation Factor		Not Evaluated
At1g10910	*EMB3103*		Embryo Defective	Moderate	Unknown; Putative PPR Protein		CPT Localized (1)
At1g10920	*LOV1*		Locus Orchestrating Victorin Effects	High			
At1g10930	*RECQ4A*			High			
At1g11000	*MLO4*		Mildew Resistance Locus O	High			
At1g11130	*SUB*		Strubbelig	Moderate			
At1g11310	*MLO2*	*PMR2*	Mildew Resistance Locus	High			
At1g11350	*CBRLK1*		Calmodulin-Binding Receptor-Like Kinase	High			
At1g11680	*EMB1738*	*CYP51*	Embryo Defective	Unique	Obtusifoliol 14-Alpha Demethylase; Cytochrome P450 monooxygenase; Sterol Biosynthesis		
At1g11720	*AtSS3*		Starch Synthase	Moderate	Starch Synthase; Negative Regulator of Starch Synthesis		CPT Localized (3)
At1g11755	*LEW1*		Leaf Wilting	Unique	Cis-Prenyltransferase; Dolichol Biosynthesis		
At1g11870	*OVA7*		Ovule Abortion	Moderate	Serine Amino Acyl tRNA Synthetase	MIT Localized (1)	
At1g11890	*SEC22*		Secretion	Unique	v-SNARE Protein; ER and Golgi Secretory Trafficking		

At1g12040	*LRX1*		Leucine-Rich Repeat, Extensin Protein	Moderate			
At1g12110	*CHL1*	*NRT1*	Chlorate Resistant	High			
At1g12220	*RPS5*		Resistant to P. syringae	High			
At1g12240	*VAC-INV*		Vacuolar Invertase	High			
At1g12260	*EMB2749*		Embryo Defective	High	NAM-Like Protein; NAC Domain Putative Transcription Factor		
At1g12360	*KEU*		Keule	High	Cytokinesis-Related Sec1 Protein; Regulator of Vesicle Trafficking		
At1g12370	*UVR2*	*PHR1*	UV Repair Defective	Unique	Type II CPD Photolyase; UV-Damaged DNA Repair		
At1g12410	*CLPR2*		Clp Protease	Moderate	Chloroplast Clp Protease Proteolytic Subunit		CPT Localized (4)
At1g12480	*OZS1*		Ozone Sensitive	Moderate			
At1g12550	*HPR3*		Hydroxypyruvate Reductase	High			Not Evaluated
At1g12770	*EMB1586*	*ISE1*	Embryo Defective	Moderate	DEAD/DEAH Box RNA Helicase; RNA Binding Protein	MIT Localized (4)	
At1g12840	*DET3*	*VHA-C*	De-etiolated	Unique	Vacuolar H(+)-ATPase Subunit		
At1g12920	*eRF1-2*		Eukaryotic Release Factor	High			
At1g12950	*RHS2*		Root Hair Specific	High			
At1g12980	*DRN*	*ESR1*	Dornroschen	Unique	AP2 Domain Transcription Factor		
At1g13220	*LINC2*		Little Nuclei	High			

At1g13230	*PII2*		Piriformospora indica Insensitive	High			
At1g13290	*DOT5*		Defectively Organized Tributaries	Moderate			
At1g13330	*AHP2*		Arabidopsis Homolog Pairing	Unique	Putative Role in Homologous Chromosome Pairing		
At1g13870	*DRL1*	*KTI12*	Deformed Roots and Leaves	Unique	Putative ATP/GTP Binding Protein; Regulator of Transcription Elongation		
At1g13930		*ST6-66*		Unique	Unknown		
At1g13980	*EMB30*	*GN; VAN7*	Embryo Defective	High	ARF Guanine Exchange Factor; Large Membrane-Associated ARF GEF; Role in Vesicle Trafficking and Cell Polarity		
At1g14000	*VIK*		VH1-Interacting Kinase	High			
At1g14150	*PQL1*		PsbQ-Like	Unique	PsbQ-like Protein; NDH Complex Subunit		Not Evaluated
At1g14280	*PKS2*		Phytochrome Kinase Substrate	Moderate			
At1g14320	*SAC52*		Suppressor of Acaulis	High	Ribosomal Protein L10		
At1g14350	*FLP*	*MYB124*	Four Lips	High			
At1g14400	*UBC1*		Ubiquitin Carrier Protein	High			
At1g14610	*TWN2*	*ValRS*	Twin	High	Mitochondrial or Cytoplasmic Valyl tRNA Synthetase	MIT Localized (5)	

At1g14660	*AtNHX8*		Sodium Hydrogen Exchanger	High			
At1g14720	*XTH28*		Xyloglucan Endotransglucosylase/Hydrolases	High			
At1g14750	*SDS*		Solo Dancers	Unique	Cyclin-Like Protein		
At1g14830	*ADL1C*	*ADL5; DRP1C*	Arabidopsis Dynamin-Like Protein	High	Dynamin-Like GTPase; Plasma Membrane Dynamics	MIT Localized (2)	
At1g14870	*PCR2*		Plant Cadmium Resistance	Moderate			Not Evaluated
At1g14920	*GAI*	*RGA2*	GA-Insensitive	High			
At1g15020	*QSO2*		Quiescin-Sulhydryl Oxidase	High			
At1g15100	*RHA2a*		RING-H2 Finger	Moderate			
At1g15220	*AtCCMH*		Cytochrome C Maturation	Unique	Mitochondrial Cytochrome C Maturation	MIT Localized (1)	
At1g15510	*ECB2*		Early Chloroplast Biogenesis	High	PPR Protein; Organellular mRNA Processing		CPT Localized (4)
At1g15520	*ABCG40*	*PDR12*	ATP-Binding Cassette	High			Not Evaluated
At1g15550	*GA4*	*GA3ox1*	GA Deficient	High			
At1g15570	*CYCA2;3*		Cyclin	High			
At1g15690	*AVP1*		Arabidopsis V-PPase	High			
At1g15820	*LHCB6*		Light Harvesting Complex	Moderate	PSII Antenna Protein		CPT Localized (4)
At1g15950	*IRX4*	*CCR1*	Irregular Xylem	High			
At1g15960	*NRAMP6*		Natural Resistance Associated Macrophage Protein	High			

At1g15980	*NDH48*	*NDF1*	NAD(P)H Dehydrogenase Subunit	Unique	NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (4)
At1g16060	*ADAP*		ARIA-Interacting Double AP2 Domain Protein	High			
At1g16150	*WAKL4*		Wall-Associated Kinase-Like	High			
At1g16280	*SWA3*	*AtRH36*	Slow Walker	High	DEAD-Box RNA Helicase; Role in rRNA Biogenesis		
At1g16410	*SPS*	*BUS1*	Supershoot	High			
At1g16540	*ABA3*	*LOS5; SIR3*	ABA Deficient	Unique	Molybdenum Cofactor Sulfurase		
At1g16590	*REV7*			Unique	Translesion Synthesis; Crosslinking DNA Repair		
At1g16610	*SR45*		Arginine/Serine-Rich	Unique	Plant-Specific RNA Splicing Factor		Not Evaluated
At1g16720	*HCF173*		High Chlorophyll Fluorescence	Unique	Unknown; Putative Short-Chain Dehydrogenase/Reductase		CPT Localized (4)
At1g16970	*KU70*		Homolog of Yeast KU70	Unique	Putative Role in DNA DSB Repair		
At1g17110	*UBP15*		Ubiquitin-Specific Protease	Moderate			
At1g17140	*ICR1*	*RIP1*	Interactor of Constitutive Active ROPS	High			Not Evaluated
At1g17220	*FUG1*	*cpIF2*	Fu-Gaeri	Moderate	Chloroplast Translation Initiation Factor		CPT Localized (3)

At1g17290	*AlaAT1*		Alanine Aminotransferase	High			
At1g17560	*HLL*		Huellenlos	Moderate	Mitochondrial Ribosomal Protein L14	MIT Localized (2)	
At1g17690	*NOF1*		Nucleolar Factor	Unique	Putative Nucleolar Protein; Putative Role in rRNA Biogenesis		Not Evaluated
At1g17840	*DSO4*	*ABCG11;* *WBC11;* *COF1*	Desperado	High			
At1g17980	*PAPS1*		Poly(A) Polymerase	Moderate			
At1g18080	*RACK1A*		Receptor for Activated C Kinase	High			
At1g18100	*MFT*		Mother of FT and TFL1	Moderate			Not Evaluated
At1g18370	*HIK*	*NACK1*	Hinkel	High			
At1g18450	*ARP4*		Actin-Related Protein	Moderate	Actin-Related Protein; Proposed Role in Chromatin Remodeling		
At1g18500	*IPMS1*		Isopropylmalate Synthase	High	Leucine Biosynthesis		CPT Localized (4)
At1g18570	*MYB51*	*BW51A;* *BW5B;* *HIG1*	MYB Domain Protein	High			
At1g18580	*GAUT11*		Galacturonosyltransferase	High			
At1g18730	*NDF6*		NDH Dependent Flow	Unique	Putative Subunit of Plastid NAD(P)H Dehydrogenase		CPT Localized (4)
At1g18890	*CPK10*	*CDPK1*	Calcium-Dependent Kinase	High			Not Evaluated

At1g19080	*TTN10*	*PSF3*	Titan	High	GINS Complex Subunit; DNA Replication Initiation		
At1g19220	*ARF19*	*IAA22; ARF11*	Auxin Response Factor	Moderate			
At1g19250	*FMO1*		Flavin-Dependent Monooxygenase	High			
At1g19270	*DA1*		Da	High			
At1g19300	*PARVUS*	*GATL1; GLZ1*	Parvus	High			
At1g19520	*NFD5*		Nuclear Fusion Defective	Moderate	Mitochondrial Ribosomal Protein L21	MIT Localized (4)	
At1g19750	*CSAat1B*		Cockayne Syndrome A-like Protein	High			Not Evaluated
At1g19800	*TGD1*		Trigalactosyldiacylglycerol	Unique	Chloroplast Envelope Protein; Putative Lipid Transporter Component		CPT Localized (3)
At1g19850	*MP*	*ARF5*	Monopteros	Moderate	B3 Domain Transcription Factor		
At1g20020	*FNR2*	*LFNR2*	Ferredoxin-NADP(+)-Oxidoreductase	High	Ferredoxin-NADP(+) Oxidoreductase		CPT Localized (4)
At1g20050	*HYD1*		Hydra	Unique	Sterol Isomerase; Sterol Biosynthesis		
At1g20090	*ROP2*	*AtRAC4*	Rho-Related Protein	High			
At1g20110	*PDE330*		Pigment Defective Embryo	Unique	Zinc Finger Protein; Putative Transcriptional Regulator		CPT Localized (1)
At1g20200	*EMB2719*	*HAP15; RPN3*	Embryo Defective	High	26S Proteasome Regulatory Subunit		
At1g20330	*SMT2*	*CVP1; FRL1*	Sterol Methyltransferase	High			
At1g20450	*ERD10*	*LTI29; LTI45*	Early Responsive to Dehydration	Moderate			Not Evaluated

At1g20780	*SAUL1*	*PUB44*	Senescence-Associated E3 Ubiquitin Ligase	High			
At1g20840	*TMT1*		Tonoplast Monosaccharide Transporter	High			
At1g20960	*EMB1507*		Embryo Defective	High	Spliceosome-Associated RNA Helicase		
At1g20980	*SPL14*	*FBR6; SPL1R2*	Squamosa Promoter Binding Protein-Like	High			
At1g21270	*WAK2*		Wall-Associated Kinase	High			
At1g21310	*RSH*	*EXT3*	Root-Shoot-Hypocotyl Defective	Unique	Cell Wall Hydroxyproline-Rich Glycoprotein; Role in Cell Shape and Cell Plate Positioning during Cytokinesis		
At1g21390	*EMB2170*		Embryo Defective	Moderate	Unknown		
At1g21600	*PTAC6*		Plastid Transcriptionally Active	Unique	Unknown		CPT Localized (4)
At1g21650	*SECA2*			Moderate	Chloroplast Sec Translocase		Not Evaluated
At1g21690	*EMB1968*		Embryo Defective	Moderate	Replication Factor C; DNA Polymerase Loading ATPase		
At1g21700	*AtSWI3C*	*CHB4*	Switch/Sucrose Nonfermenting 3C	Moderate	Chromatin-Remodeling Complex Subunit		
At1g21760	*FBP7*		F-Box Protein 7	Unique	Putative Role in Translation During Temperature Stress		

At1g21840	*UREF*		Urease Accessory Protein	Unique	Urea Hydrolase Accessory Protein; Urea Catabolism		
At1g21970	*LEC1*	*EMB212*	Leafy Cotyledon	Moderate	Transcriptional Regulator		
At1g22090	*EMB2204*		Embryo Defective	Moderate	Unknown		
At1g22260	*ZYP1a*			High			
At1g22270	*SMO2*		Small Organ	Moderate			
At1g22275	*ZYP1b*			High			
At1g22310	*MBD8*		Methyl-CpG Binding Domain	Unique	Putative Methyl-CpG-Binding Domain Protein		
At1g22400	*UGT85A1*		UDP-Glucosyl Transferase	High			
At1g22620	*AtSAC1*	*FRA7*	Suppressor of Actin	Moderate			
At1g22700	*PYG7*		Pale Yellow Green	Unique	TPR protein; Photosystem I Subunit		CPT Localized (4)
At1g22710	*SUC2*	*SUT1*	Sucrose Transporter	High			
At1g22770	*GI*	*FB*	Gigantea	Unique	Regulator of Degradation of CONSTANS Repressor		
At1g22780	*PFL*	*RPS18A*	Pointed First Leaves	Moderate			
At1g22920	*CSN5A*	*AJH1*	COP9 Signalosome 5A	High			
At1g22940	*TH1*	*THIE*	Thiamine Requiring	Unique	Bifunctional Hydroxymethylpyrimidine Kinase; Thiamin Biosynthesis		
At1g23010	*LPR1*		Low Phosphate Root	High			
At1g23090	*SULTR3;3*	*AST91*	Sulfate Transporter	High			Not Evaluated
At1g23310	*GGT1*	*ADAT1*	Glutamate:Glyoxylate Aminotransferase	High			

At1g23400	*AtCAF2*		Ortholog of Maize CAF2	Moderate	Chloroplast Intron Splicing Factor		CPT Localized (3)
At1g23420	*INO*		Inner No Outer	Moderate			
At1g24180	*IAR4*	*ETA5*	IAA-Alanine Resistant	High	Putative Mitochondrial Pyruvate Dehydrogenase Subunit	MIT Localized (5)	
At1g24340	*EMB2421*		Embryo Defective	Unique	Polyketide Hydroxylase Related Monooxygenase		
At1g24450	*NFD2*		Nuclear Fusion Defective	Unique	Ribonuclease III		
At1g24490	*ALB4*	*ARTEMIS*	Albina	Moderate	Thylakoid Protein Integration and Complex Stabilization		CPT Localized (2)
At1g24590	*DRNL*	*SOB2; ESR2*	Dornroschen-Like	Unique	AP2-Like Transcription Factor		
At1g24706	*EMB2793*	*THO2*	Embryo Defective	Unique	THO/TREX Complex Component; Transcription Elongation; mRNP Biogenesis		
At1g25350	*OVA9*		Ovule Abortion	Moderate	AARS (Glutamine)		
At1g25490	*RCN1*	*EER1; REGA*	Altered Responses to NPA	High			
At1g25540	*PFT1*		Phytochrome and Flowering Time	Unique	Mediator Complex Subunit; Transcriptional Coregulator		
At1g26110	*DCP5*		Decapping	Moderate			
At1g26630	*FBR12*	*ELF5A-2*	Fumonisin B1-Resistant	Moderate			
At1g26670	*VTI1b*	*VTI12*	Vesicle Transport V-Snare	Moderate			
At1g26780	*LOF1*	*MYB117*	Lateral Organ Fusion	Moderate			

At1g26910	*RPL10B*		Ribosomal Protein L10	High			Not Evaluated
At1g27080	*NRT1.6*		Nitrate Transporter	High			
At1g27320	*AHK3*		Arabidopsis Histidine Kinase	High			
At1g27360	*SPL11*		Squamosa Promoter Binding Protein-Like	High			
At1g27370	*SPL10*		Squamosa Promoter Binding Protein-Like	High			
At1g27390	*TOM20-2*		Translocase of the Outer Mitochondrial Membrane	Moderate	Mitochondrial Protein Import	MIT Localized (1)	
At1g27440	*IRX10*	*GUT2*	Irregular Xylem	High			
At1g27450	*APT1*		Adenine Phosphoribosyl Transferase	Moderate	Adenine Phosphoribosyltransferase		CPT Localized (2)
At1g27760	*SAT32*		Salt Tolerance	Unique	ABA Signaling		
At1g27840	*CSAat1A*		Cockayne Syndrome A-like Protein	High			Not Evaluated
At1g27950	*LTPG*		Glycosylphosphatidylinositol-Anchored Lipid Protein Transfer	Unique	Glycosylphosphatidylinositol-Anchored Lipid Transfer Protein; Cuticular Lipid Export Machinery Component		
At1g28300	*LEC2*		Leafy Cotyledon	Moderate	B3 Domain Transcription Factor		
At1g28320	*DEG15*			Unique	DEG15 Serine Protease; Cleaves Peroxisomal Targeting Signals		
At1g28380	*NSL1*		Necrotic Spotted Lesions	High			

At1g28490	*OSM1*	*SPY61*	Osmotic Sensitive Mutant	Unique	SNARE Family Syntaxin 6/10-Like Protein; Vesicular Transport		
At1g28560	*SRD2*		Shoot Redifferentiation Defective	Unique	snRNA Transcriptional Activator		
At1g29260	*PEX7*		Peroxin	Unique	Peroxisomal Protein Import		
At1g29690	*CAD1*		Constitutively Activated Cell Death	High			
At1g29900	*VEN3*	*CarB*	Venosa	Unique	Carbamoyl Phosphate Synthetase Subunit; Arginine Biosynthesis		Not Evaluated
At1g29940	*NRPA2*		Nuclear RNA Polymerase	High	Nuclear RNA Polymerase		
At1g29990	*PFD6*		Prefoldin	Unique	Microtubule Chain-Building Chaperone		
At1g30010	*CSS1*	*nMat1a*	Changed Sensitivity to Cellulose Synthesis Inhibitors	High	Mitochondrial Splicing Factor	MIT Localized (1)	
At1g30270	*CIPK23*	*SnRK3.23;* *LSK1*	CBL-Interacting Protein Kinase	High			
At1g30330	*ARF6*		Auxin Response Factor	Moderate			
At1g30400	*MRP1*	*ABCC1;* *EST1*	Multidrug Resistance-Associated Protein	High			
At1g30450	*CCC1*	*HAP5*	Cation-Chloride Co-Transporter	Unique	Chloride-Cation Cotransporter		
At1g30520	*AAE14*		Acyl-Activating Enzyme	Moderate			

At1g30610	*EMB2279*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At1g30620	*MUR4*	*HSR8; UXE1*	Murus	High			
At1g30825	*DIS2*	*ARPC2A*	Distorted	Moderate			
At1g30950	*UFO*		Unusual Floral Organs	Unique	F-Box Protein; Putative Role in Ubiquination		
At1g30970	*SUF4*		Suppressor of Frigidia4	Unique	C2H2 Zinc Finger Transcription Factor		
At1g31140	*GOA*	*AGL64*	Gordita	Unique	MIKC-Type MADS Domain Transcription Factor		Not Evaluated
At1g31170	*SRX*		Sulfiredoxin	Unique	Sulfiredoxin; Reduces Sulfinic Form of PRX Protein	MIT Localized (1)	Not Evaluated
At1g31180	*IPMDH1*	*IMD3*	Isopropylmalate Dehydrogenase	High	Glucosinolate and Leucine Biosynthesis		CPT Localized (3)
At1g31470	*NFD4*		Nuclear Fusion Defective	High	Uncertain; Mitochondrial Nodulin-Like Protein	MIT Localized (1)	
At1g31480	*SGR2*		Shoot Gravitropism	Unique	Putative Phospholipase A1; Putative Role in Gravity Sensing		
At1g31800	*CYP97A3*	*LUT5*	Cytochrome P450-Type Monooxygenase	Moderate	Cytochrome P450 Monooxygenase; Lutein Biosynthesis		CPT Localized (4)
At1g31810	*AFH14*		Formin Homology	Moderate			Not Evaluated
At1g31817	*NFD3*		Nuclear Fusion Defective	Unique	Mitochondrial Ribosomal Protein S11	MIT Localized (4)	
At1g31860	*HISN2*		Histidine Auxotroph	Unique	Histidine Biosynthesis		CPT Localized (3)

At1g31880	*BRX*	*NIP3;1; NLM9*	Brevis Radix	High			
At1g32130	*IWS1*		Interact-With-Spt6	Moderate			Not Evaluated
At1g32200	*ATS1*	*ACT1*	Acyltransferase	Unique	Phosphatidylglycerol Biosynthesis		CPT Localized (4)
At1g32230	*RCD1*	*ATP8; CEO1*	Radical-Induced Cell Death	High			
At1g32450	*NRT1.5*		Nitrate Transporter	High			
At1g32490	*EMB2733*	*ESP3; PRP2*	Embryo Defective	High	RNA Helicase; Putative Role in Pre-mRNA Splicing		
At1g32990	*PRPL11*		Plastid Ribosomal Protein L11	Moderate	Chloroplast Ribosomal Protein L11		CPT Localized (4)
At1g33240	*GTL1*		GT-2-Like	Moderate			
At1g33520	*MOS2*		Modifier of SNC1,2	High			
At1g34120	*IP5PI*	*At5PTase1*	Inositol Polyphosphate 5-Phosphatase I	High			
At1g34245	*EPF2*		Epidermal Patterning Factor	Unique	Secretory Protein; Regulator of Epidermal Cell Density		
At1g34370	*STOP1*		Sensitive to Proton Rhizotoxicity	Moderate	Zinc Finger Transcription Factor		
At1g34430	*EMB3003*		Embryo Defective	Moderate	Dihydrolipoamide S-Acetyltransferase; Chloroplast Pyruvate Decarboxylase Complex; Putative E3 Binding Protein; Acetyl-CoA Formation		CPT Localized (4)
At1g34550	*EMB2756*		Embryo Defective	High	Unknown		
At1g34790	*TT1*	*WIP1*	Transparent Testa	Moderate			

At1g35580	*CINV1*		Cytosolic Invertase	High			
At1g35670	*AtCDPK2*	*CPK11*	Calcium-Dependent Protein Kinase	High			
At1g35720	*AnnAt1*	*OXY5*	Annexin	High			
At1g36160	*ACC1*	*PAS3; GK; EMB22*	Acetyl CoA Carboxylase	High	Acetyl-CoA Carboxylase; Formation of Malonyl-CoA in Fatty Acid Biosynthesis		
At1g37130	*NIA2*	*CHL3; NR2*	Nitrate Reductase	High			
At1g42540	*GLR3.3*		Glutamate Receptor	High			Not Evaluated
At1g42550	*PMI1*		Plastid Movement Impaired	Unique	Calcium-Mediated Signal Transduction		
At1g43170	*EMB2207*	*RP1; RPL3A*	Embryo Defective	High	Cytosolic Ribosomal Protein L3		
At1g43620	*UGT80B1*	*TT15*	UDP-Glucose:Sterol Glucosyltransferase	Moderate			
At1g43700	*SUE3*	*VIP1*	Sulphate Utilization Efficiency	Moderate			Not Evaluated
At1g43710	*EMB1075*		Embryo Defective	Unique	Serine Decarboxylase; Ethanolamine Biosynthesis		
At1g43850	*SEU*		Seuss	Moderate			
At1g44446	*CH1*	*CAO*	Chlorina	Unique	Chlorophyll A Oxygenase		CPT Localized (4)
At1g44575	*NPQ4*	*PsbS*	Nonphotochemical Quenching	Unique	Chlorophyll-Binding Protein of PSII		CPT Localized (4)
At1g44900	*MCM2*		Minichromosome Maintenance	Moderate	Putative DNA Helicase Subunit; DNA Replication		
At1g45145	*ATTRX5*	*ATH5; LIV1*	Thioredoxin h5	Moderate			
At1g46480	*WOX4*		Wuschel Related Homeobox	Unique	Homeobox Transcription Factor		Not Evaluated

At1g46768	*RAP2.1*		Related to AP2	Moderate			Not Evaluated
At1g47720	*OSB1*		Organellar Single-Stranded DNA Binding Protein	Unique	Mitochondrial DNA Binding Protein; Regulator of Stoichiometry of Alternative Forms of mtDNA	MIT Localized (1)	
At1g48050	*KU80*			Unique	Nonhomologous End-Joining Complex Subunit; ds T-DNA Binding and Integration		
At1g48175	*EMB2191*	*TAD2*	Embryo Defective	Unique	Adenosine Deaminase; Modification of tRNA Wobble Position		
At1g48350	*EMB3105*		Embryo Defective	Unique	Chloroplast 50S Ribosomal Protein L18		CPT Localized (4)
At1g48380	*RHL1*	*HPY7*	Root Hairless	Unique	DNA Topoisomerase VI Complex Subunit; Role in Mitotic Cell Cycle and Endoreduplication		
At1g48410	*AGO1*	*ICU9*	Argonaute	High			
At1g48600	*PMEAMT*		Phosphoethanolamine N-Methyltrasnferase	High			Not Evaluated
At1g48850	*EMB1144*		Embryo Defective	Unique	Chorismate Synthase; Aromatic Amino Acid Biosynthesis		CPT Localized (3)
At1g48920	*PARL1*	*AtNUC-L1*	Parallel	Moderate			
At1g49040	*SCD1*		Stomatal Cytokinesis Defective	Unique	DENN Domain Protein; Role in Pathogen Defense Signaling		

At1g49400	*EMB1129*		Embryo Defective	Moderate	Cytosolic Ribosomal Protein S17		
At1g49430	*LACS2*	*SMA4; LRD2*	Long-Chain Acyl-CoA Synthetase	High			
At1g49510	*EMB1273*		Embryo Defective	Unique	Unknown		CPT Localized (2)
At1g49540	*ELP2*			Unique	Histone Acetyl-Transferase Complex Subunit		
At1g49720	*ABF1*		ABRE Binding Factor	High			
At1g49770	*RGE1*		Retarded Growth of Embryo	Unique	bHLH Transcription Factor		
At1g49820	*AtMTK*		Arabidopsis thaliana S-Methyl-5-Thioribose Kinase	Unique	Methylthioribose Kinase; Methionine Recycling		
At1g49880	*EMB3106*		Embryo Defective	Unique	Mitochondrial Sulfhydryl Oxidase; Disulfide Bond Formation	MIT Localized (1)	
At1g49970	*ClpR1*	*SVR1; NCLPP5*		Moderate	Plastid Clp Protease		CPT Localized (4)
At1g50030	*TOR*		Target of Rapamycin	Moderate	Protein Kinase (Target of Rapamycin)		
At1g50240	*FU*	*TIO*	Fused	Moderate	Serine/Threonine Protein Kinase		
At1g50320	*Trxx*		Thioredoxin	Unique	Plastidial Thioredoxin		Not Evaluated
At1g50430	*DWF5*	*LE; PA*	Dwarf	Moderate	Sterol Delta 7 Reductase; Sterol Biosynthesis		
At1g50460	*HKL1*		Hexokinase Like	High			

At1g50500	*HIT1*	*AtVPS53*	Heat-Intolerant	Moderate	Vacuole Protein Sorting; Endosome-Golgi Vesicle Trafficking		
At1g50900	*GDC1*	*LTD*	Grana Deficient Chloroplast	Unique	Ankyrin Domain Protein; Grana Formation in Chloroplasts		Not Evaluated
At1g51190	*PLT2*		Plethora	High			
At1g51450	*TRAUCO*		Trauco	Unique	Trithorax Class Transcriptional Regulator		
At1g51500	*CER5*	*D3;* *ABCG12;* *WBC12*	Eceriferum	High			
At1g51760	*IAR3*	*JR3*	IAA-Alanine Resistant	High			
At1g51965	*ABO5*		ABA Overly-Sensitive	Moderate	PPR Protein; Mitochondrial RNA Splicing	MIT Localized (1)	Not Evaluated
At1g52150	*ICU4*	*CNA;* *ATHB-15*	Incurvata	High			
At1g52230	*PSAH2*	*PSI-H*	Photosystem I Subunit H2	Moderate	Photosystem I Subunit H		CPT Localized (4)
At1g52240	*PIRF1*		Phytochrome-Interacting RopGEF	High			Not Evaluated
At1g52340	*ABA2*	*SRE1;* *GIN1; ISI4;* *SIS4*	ABA Deficient	Moderate			
At1g52400	*BGLU18*	*BGL1;* *ATBG1*	Beta Glucosidase	High			
At1g52760	*lysoPL2*		Lysophospholipase	Moderate			Not Evaluated
At1g52920	*GCR2*		G-Protein Coupled Receptor	High			
At1g53500	*MUM4*	*RHM2*	Mucilage Modified	High			

At1g53580	*ETHE1*	*GLX2*	Similar to Human ETHE1	Unique	Glyoxylate-Like Protein		
At1g53670	*MSRB1*		Methionine Sulfoxide Reductase B	Unique	Methionine Sulfoxide Reductase		CPT Localized (3)
At1g53850	*PAE1*		20S Proteasome Alpha Subunit	High			Not Evaluated
At1g53940	*GLIP2*		GDSL-Motif Lipase	High			
At1g54030	*MVP1*		Modified Vacuole Phenotype	Moderate			
At1g54040	*TASTY*	*ESP; ESR*	Tasty	High			
At1g54060	*ASIL1*		Arabidopsis 6b-Interacting Protein 1-Like	Moderate			
At1g54160	*NF-YA5*	*NFYA5*	Nuclear Factor Y, Subunit A5	Moderate			
At1g54340	*ICDH*		Isocitrate Dehydrogenase	High			Not Evaluated
At1g54490	*AIN1*	*EIN5; EIN7; XRN4*	ACC Insensitive	Moderate			
At1g54960	*ANP2*	*MAPKKK2*	Arabidopsis NPK1-Related Protein Kinase	High			Not Evaluated
At1g54990	*AXR4*	*RGR1*	Auxin Resistant	Unique	ER Accessory Protein; Trafficking of Plasma Membrane Proteins		
At1g55020	*LOX1*		Lipoxygenase	High			
At1g55180	*PLDE*	*PLDA4*	Phospholipase D	High			
At1g55250	*HUB2*		Histone Mono-Ubiquitination	High			
At1g55320	*AAE18*		Acyl-Activation Enzyme	High			

At1g55325	*GCT*	*MAB2*	Grand Central	Unique	Mediator Complex Subunit; Transcriptional Regulator		Not Evaluated
At1g55350	*EMB1275*	*AtDEK1*	Embryo Defective	Unique	Calpain-Type Cysteine Protease		
At1g55370	*NDF5*		NAD(P)H Dehydrogenase-Dependent Cyclic Electron Flow	Unique	Putative NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (2)
At1g55490	*Cpn60{beta}*	*LEN1*	Chaperonin 60{beta}	High	Plastid Molecular Chaperone		CPT Localized (4)
At1g55580	*LAS*	*SCL18*	Lateral Suppressor	Moderate			
At1g55600	*MINI3*	*WRKY10*	Mini Seed	Unique	WRKY Transcription Factor		
At1g55670	*PSAG*	*PSI-G*	Photosystem I Subunit G	Unique	Stabilization of PSI Core		CPT Localized (4)
At1g55870	*AtPARN*	*AHG2*	Poly(A) Ribonuclease	Moderate	Poly (A) Ribonuclease; CAF1 Family Ribonuclease		
At1g55900	*EMB1860*	*TIM50*	Embryo Defective	Unique	Inner Mitochondrial Membrane Protein; Import of Mitochondrial Matrix Proteins	MIT Localized (5)	
At1g56070	*LOS1*		Low Response to Osmotic Stress	High			
At1g56200	*EMB1303*		Embryo Defective	Unique	Unknown		CPT Localized (5)
At1g56340	*CRT1a*		Calreticulin	High			Not Evaluated
At1g56510	*WRR4*		White Rust Resistance	High			

At1g56650	*PAP1*	*MYB75; SIAA1*	Production of Anthocyanin Pigment	High			
At1g57750	*MAH1*	*CYP96A15*	Mid-Chain Alkane Hydroxylase	High			
At1g57820	*VIM1*	*ORTH*	Variant in Methylation	High			
At1g58210	*EMB1674*		Embryo Defective	Moderate	Uncertain		
At1g58250	*SAB*		Sabre	High			
At1g58360	*AAP1*	*NAT2*	Amino Acid Permease	High			
At1g58440	*SQE1*	*DRY2*	Squalene Epoxidase	High			
At1g59560	*DAL2*		DIAP1-Like Protein	High			Not Evaluated
At1g59640	*BPE*	*ZCW32*	Big Petal	Moderate			
At1g59820	*ALA3*	*ITB2*	Aminophospholipid ATPase	High	Lipid Translocation; Secretory Vesicle Formation		
At1g59870	*PEN3*	*PDR8*	Penetration	High			
At1g59990	*EMB3108*		Embryo Defective	Unique	Putative RNA Helicase		CPT Localized (2)
At1g60170	*EMB1220*		Embryo Defective	Moderate	PRP31 Splicing Factor; Spliceosome Subunit		
At1g60490	*AtVPS34*	*PI3K*	Vacuolar Sorting Protein	Moderate	Phosphatidylinositol 3-Kinase		
At1g60600	*ABC4*		Aberrant Chloroplast Development	Unique	Phylloquinone Biosynthesis		CPT Localized (2)
At1g60950	*AtFD2*	*FED A*	Ferredoxin	Moderate	Chloroplast Ferredoxin		CPT Localized (4)
At1g61120	*TPS04*	*GES*	Terpene Synthase	High			
At1g61210	*DWA3*		DWD Hypersensitive to ABA	High			Not Evaluated

At1g61720	*BAN*		Banyuls	Moderate			
At1g62180	*APR2*	*APSR; PRH43*	5'Adenylylphosphosulfate Reductase	High	5'Adenylylphosphosulfate Reductase		CPT Localized (4)
At1g62300	*WRKY6*		WRKY Transcription Factor	High			
At1g62340	*ALE1*		Abnormal Leaf Shape	High			
At1g62360	*STM*	*BUM; WAM1; SHL*	Shoot Meristemless	Moderate	Knotted Class Homeodomain Transcription Factor; Regulation of Shoot Meristem Formation		
At1g62640	*KAS3*		3-Ketoacyl-Acyl Carrier Protein Synthase	Unique	3-Ketoacyl-ACP Synthase; Plastidial De Novo Fatty Acid Biosynthesis		Not Evaluated
At1g62750	*SCO1*		Snowy Cotyledon	High	Plastid Elongation Factor G		CPT Localized (4)
At1g62830	*LDL1*	*LSD1; SWP1*	LSD1-Like	High			
At1g62940	*ACOS5*		Acyl-CoA Synthetase	High			
At1g62990	*KNAT7*	*IRX11*	Knotted-Like Homeobox of Arabidopsis thaliana	High			
At1g63000	*UER1*	*NRS/ER*	UDP-4-Keto-6-Deoxy-D-Glucose-3,5-Epimerase-4-Reductase	High			Not Evaluated
At1g63160	*EMB2811*	*RFC5*	Embryo Defective	Moderate	DNA Replication Factor; DNA Replication		

At1g63440	*HMA5*		Heavy Metal ATPase 5	High	P-Type ATPase; Copper Homeostasis	MIT Localized (4)	
At1g63650	*EGL3*	*EGL1;* *AtMYC-2*	Enhancer of Glabra	High			
At1g63680	*PDE316*	*APG 13*	Pigment Defective Embryo	Unique	Similar to Bacterial mur E Protein; Putative Role in Transcription		CPT Localized (2)
At1g63700	*YDA*	*EMB71;* *MAPKKK4*	Yoda	Moderate	MAP3K Protein Kinase; Role in Signal Transduction		
At1g63880				High			
At1g63900	*DAL1*		DIAP1-Like Protein	High			Not Evaluated
At1g63970	*IspF*	*MECPS*	Isoprenoid	Unique	Isoprenoid Biosynthesis; Plastid MEP Pathway		CPT Localized (4)
At1g63990	*SPO11-2*		Sporulation 11-2	Moderate	DNA Topoisomerase IV Homolog; Meiotic DSB Induction		
At1g64030	*SRP3*		Serpin	High			
At1g64060	*AtrbohF*		Respiratory Burst Oxidase Protein	High			
At1g64070	*RLM1*		Resistance to Leptosphaeria maculans	High			
At1g64280	*NIM1*	*NPR1; SAI1*	Non-Induced Immunity	High			
At1g64440	*RHD1*	*REB1;* *UGE4*	Root Hair Defective	High			
At1g64520	*RPN12a*		Regulatory Particle Non-ATPase	High			
At1g64570	*DUO3*		Duo Pollen	Unique	Uncertain		
At1g64670	*BDG1*		Bodyguard	High			

At1g64770	*NDH45*	*NDF2*	NAD(P)H Dehydrogenase Subunit	Unique	NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (3)
At1g64790	*ILA*	*GCN1*	Ilithyia	Unique	Translational Activator		CPT Localized (1)
At1g64970	*TMT1*	*VTE4*	Tocopherol Methyltransferase	Unique	Gamma-Tocopherol Methyltransferase; Vitamin E Biosynthesis		CPT Localized (2)
At1g65310	*XTH17*		Xyloglucan Endotransglucosylase/Hydrolase	High			Not Evaluated
At1g65360	*AGL23*		Agamous-Like	Moderate	MADS Box Transcription Factor		
At1g65380	*CLV2*	*RLP10*	Clavata	Moderate			
At1g65410	*NAP11*	*ABCI13;* *TGD3*	Non-Intrinsic ABC Protein	Unique	Putative Role in Iron Transport or Homeostasis		Not Evaluated
At1g65420	*NPQ7*		Nonphotochemical Quenching	Unique	Unknown; YCF20 Protein		Not Evaluated
At1g65470	*FAS1*	*NFB2*	Fasciata	Unique	Chromatin Assembly Factor Subunit		
At1g65480	*FT*		Flowering Locus T	High			
At1g65620	*AS2*	*LBD6*	Asymmetric Leaves	Moderate			
At1g65770	*AMR1*		Ascorbic Acid and Mannose Pathway Regulator	High			
At1g66170	*MMD1*		Male Meiocyte Death	High			
At1g66200	*GLN1;2*	*GSR2*	Glutamine Synthase	High			Not Evaluated
At1g66340	*EIN1*	*ETR1*	Ethylene Insensitive	High			
At1g66350	*RGL1*		RGA-Like	High			

At1g66520	*PDE194*		Pigment Defective Embryo	Unique	Methionyl-tRNA Formyltransferase; Putative Role in Translation Initiation		CPT Localized (1)
At1g66600	*ABO3*	*WRKY63*	ABA Overly Sensitive	High			Not Evaluated
At1g66730	*LIG6*		DNA Ligase	Moderate			Not Evaluated
At1g66840	*WEB2*	*PMI2*	Weak Chloroplast Movement Under Blue Light	High			Not Evaluated
At1g67080	*ABA4*		Abscisic Acid (ABA)-Deficient 4	Unique	Chloroplast Membrane Protein; Carotenoid Biosynthesis		CPT Localized (4)
At1g67140	*SWEETIE*		Sweetie	Unique	Putative ABC Transporter		
At1g67230	*LINC1*		Little Nuclei	Moderate			
At1g67320	*EMB2813*	*POLA3*	Embryo Defective	Unique	DNA Polymerase Alpha; DNA Replication		
At1g67370	*ASY1*		Asynaptic	Moderate	Uncertain		
At1g67440	*EMB1688*		Embryo Defective	Moderate	Uncertain; Putative Ribosome Biogenesis GTPase	MIT Localized (4)	
At1g67490	*KNF*	*GCS*	Knopf	High	Alpha Glucosidase I; N-Glycan Trimming of Glycoproteins		
At1g67500	*AtREV3*			Moderate	DNA Polymerase Gamma Catalytic Subunit; Translesion Synthesis		
At1g67550	*URE*		Urease	Unique	Urea Hydrolase; Urea Catabolism		
At1g67630	*EMB2814*	*POLA2*	Embryo Defective	Unique	DNA Polymerase Alpha; DNA Replication		

At1g67730	*KCR1*		Beta-Ketoacyl Reductase	Moderate	B-Ketoacyl-Coenzyme A Reductase; Long-Chain Fatty Acid Biosynthesis		
At1g67940	*STAR1*	*ABCI17; NAP3*		Moderate	Bacterial-Type ABC Transporter		Not Evaluated
At1g68050	*FKF1*	*ADO3*	Flavin Binding, Kelch Repeat, F-Box	High			
At1g68100	*IAR1*		IAA-Alanine Resistant	Unique	Unknown Transmembrane Protein; Role in Auxin Sensitivity		
At1g68310	*AE7*		AS1/2 Enhancer	Moderate			Not Evaluated
At1g68370	*ARG1*		Altered Response to Gravity	High			
At1g68450	*PDE337*		Pigment Defective Embryo	Unique	Uncertain		CPT Localized (1)
At1g68480	*JAG*		Jagged	Unique	C2H2 Zinc Finger Transcription Factor		
At1g68530	*CER6*	*POP1; CUT1*	Eceriferum	High			
At1g68540	*TKPR2*	*CCRL2*	Tetraketide Alpha-Pyrone Reductase	High			Not Evaluated
At1g68560	*XYL1*	*TRG1*	Xylosidase	High			
At1g68640	*PAN*		Perianthia	Moderate			
At1g68720	*TADA*		tRNA Adenosine Deaminase	Unique	Chloroplast tRNA Adenosine Deaminase		CPT Localized (2)
At1g68725	*AGP19*		Arabinogalactan-Protein	Unique	Arabinogalactan Protein		
At1g68730	*AtZR1*			Unique	Zinc Finger Protein; Transcriptional Regulation		

At1g68765	*IDA*		Inflorescence Deficient in Abscission	Unique	Putative Cell to Cell Signaling Peptide; Floral Abscission Signaling		
At1g68800	*BRC2*	*TCP12*	Branched	Unique	TCP Transcription Factor		
At1g68890	*PHA*		Phylloquinone Absence	Unique	Menaquinone Biosynthesis; Organellular mRNA Processing		CPT Localized (1)
At1g68990	*RPOTm*	*RPOMT*	DNA-Directed RNA Polymerase	High	Mitochondrial Phage-Type RNA Polymerase	MIT Localized (2)	
At1g69120	*AP1*	*AGL7*	Apetala	High			
At1g69180	*CRC*		Crabs Claw	Moderate	Putative YABBY Transcription Factor		
At1g69190	*cytHPPK/DHPS*		Cytosolic HPPK/DHPS	High			
At1g69270	*RPK1*		Receptor-Like Protein Kinase	High			
At1g69390	*AtMinE1*		Arabidopsis Homologue of Bacterial MinE1	Unique	Unknown; Role in Plastid Division Site Placement		CPT Localized (5)
At1g69440	*AGO7*	*ZIP*	Argonaute	High			
At1g69490	*NAP*		NAC-Like, Activated by AP3/PI	Moderate			
At1g69500	*CYP704B1*		Cytochrome P450	High			
At1g69770	*CMT3*		Chromomethylase	High			
At1g69870	*NRT1.7*		Nitrate Transporter	High			
At1g69935	*SHW1*		Short Hypocotyl in White Light	Unique	Regulator of Light and ABA Signaling		
At1g69940	*PPME1*		Pollen Pectin Methylesterase	High	Pectin Methylesterase		

At1g70070	*ISE2*	*PDE317; EMB25;*	Increased Size Exclusion Limit	Moderate	DEAD Box Helicase; Putative RNA Binding Protein		
At1g70170	*MMP*		Matrix Metalloproteinase	High			
At1g70210	*CYCD1;1*		Cyclin D1;1	Moderate			
At1g70460	*RHS10*		Root Hair Specific	Moderate			
At1g70560	*TIR2*		Transport Inhibitor Response	High			
At1g70910	*DEP*		Despierto	Unique	C3HC4 RING-Finger Protein; Putative Role in ABA Signaling		
At1g70940	*PIN3*		Pin-Formed	High			
At1g71100	*RSW10*		Radial Swelling	High			
At1g71230	*CSN5B*	*AJH2*	COP9-Signalosome	High			
At1g71270	*VPS52*	*POK; TTD8*	Vacuolar Sorting Protein	High	Membrane Trafficking		
At1g71440	*PFI*	*TFCE*	Pfifferling	Unique	Tubulin Folding Cofactor E; Regulation of Tubulin Folding and Microtubule Dynamics		
At1g71720	*PDE338*		Pigment Defective Embryo	Unique	RNA Binding Protein		CPT Localized (4)
At1g71880	*SUC1*		Sucrose-Proton Symporter	High	Plasma Membrane Sugar Transporter; Sucrose Signaling		
At1g72320	*APUM23*		Pumilio	Unique	Nucleolar Protein; Pre-rRNA Processing		Not Evaluated
At1g72440	*SWA2*	*EDA25*	Slow Walker	Unique	18S Ribosomal RNA Biogenesis		
At1g72560	*PSD*		Paused	Unique	Putative Exportin-t; Nuclear tRNA Export		
At1g72770	*HAB1*		Homology to ABI1	High			

At1g72970	*HTH*	*ACE; EDA17*	Hothead	High			
At1g73060	*LPA3*		Low Photosystem II Accumulation	Unique	Photosystem II Assembly		Not Evaluated
At1g73177	*BNS*		Bonsai	Unique	Putative Anaphase Promoting Complex Component		
At1g73360	*HDG11*		Homeodomain Glabrous	High			
At1g73590	*PIN1*		Pin-Formed	High			
At1g73660		*AT6*		Moderate			
At1g73720	*SMU1*		Suppressors of MEC-8 and UNC-52	Unique	Putative Auxiliary Spliceosome Protein; Role in Pre-mRNA Splicing		
At1g73730	*EIL3*	*SLIM1*	Ethylene-Insensitive3-Like3	Moderate			
At1g73840	*ESP1*		Enhanced Silencing Phenotype	Unique	RNA Processing Factor		
At1g73990	*SPPA1*		Signal Peptide Peptidase	Unique	Plastid Signal Peptide Peptidase; Light-Dependent Protein Degradation		CPT Localized (3)
At1g74030	*ENO1*		Enolase	High	Putative Plastid Phosphoenolpyruvate Enolase		CPT Localized (5)
At1g74260	*PUR4*		Purine Biosynthesis	Unique	De Novo Purine Biosynthesis Pathway	MIT Localized (3)	
At1g74310	*HOT1*	*HSP101*	Sensitive to Hot Temperatures	Moderate			
At1g74710	*SID2*	*EDS16; ICS1*	SA Induction Deficient	High	Plastidic Isochorismate Synthase; Salicylic Acid Biosynthesis		CPT Localized (3)

At1g74720	*QKY*		Quirky	Moderate			
At1g74850	*PDE343*	*PTAC2*	Pigment Defective Embryo	Moderate	PPR; TPR Domain Protein; Organellular mRNA Processing		CPT Localized (4)
At1g74900	*OTP43*		Organelle Transcript Processing	Moderate	PPR Protein; Mitochondrial Splicing; Organellular mRNA Processing	MIT Localized (1)	
At1g74920	*ALDH10A8*		Aldehyde Dehydrogenase	High			Not Evaluated
At1g74960	*FAB1*	*KAS2*	Fatty Acid Biosynthesis	Moderate	Ketoacyl-Acyl Carrier Protein Synthase; Fatty Acid Metabolism		CPT Localized (4)
At1g74970	*TWN3*		Twin	Unique	Chloroplast Ribosomal Protein S9		CPT Localized (3)
At1g75010	*ARC3*		Accumulation and Replication of Chloroplasts	Unique	Z-Ring Accessory Protein; Stromal Plastid Division Machinery Component		
At1g75100	*JAC1*		J-Domain Protein Required for Chloroplast Accumulation Response	Moderate			
At1g75350	*EMB2184*		Embryo Defective	Unique	Chloroplast Ribosomal Protein L31		CPT Localized (4)
At1g75380	*BBD1*		Bifunctional Nuclease in Basal Defense Response	High			
At1g75500	*WAT1*		Walls Are Thin	High			Not Evaluated
At1g75540	*LHUS*	*BBX21; STH2*	Long Hypocotyl Under Shade	Moderate			Not Evaluated

At1g75660	*XRN3*		Exoribonuclease	High	PTGS Suppressor; Nuclear Degradation of Aberrant RNAs		
At1g75820	*CLV1*	*FLO5; FAS3*	Clavata	High			
At1g75950	*ASK1*	*SKP1A; UIP1*	Arabidopsis SKP1-Like	Moderate			
At1g76030	*VHA-B1*		Vacuolar H(+)-ATPase	High			
At1g76060	*EMB1793*		Embryo Defective	Unique	Uncertain; Complex 1 LYR Motif		
At1g76260	*DWA2*		DWD Hypersensitive to ABA	High			Not Evaluated
At1g76420	*CUC3*		Cup Shaped Cotyledon	Moderate			
At1g76490	*HMG1*	*HMGR1*	Hydroxy Methylglutaryl CoA Reductase	High			
At1g76620	*PDE339*		Pigment Defective Embryo	High	Unknown		CPT Localized (1)
At1g77080	*MAF1*	*FLM; AGL27*	MADS Affecting Flowering	Moderate			
At1g77140	*VPS45*		Vacuolar Sorting Protein	Unique	Vacuolar Sorting Receptor Recycling		
At1g77180	*SKIP*			Unique	SNW⁄SKIP Protein; Transcriptional Co-Regulator		Not Evaluated
At1g77300	*EFS*	*CCR1; SDG8*	Early Flowering in Short Days	Moderate			
At1g77390	*TAM1*	*DYP; CYCA1; CYCA1;2*	Tardy Asynchronous Meiosis	High			

At1g77470	*EMB2810*	*RFC5*	Embryo Defective	Moderate	DNA Replication Factor; DNA Replication		
At1g77490	*tAPX*		Thylakoidal Ascorbate Peroxidase	Moderate	Thylakoid Ascorbate Peroxidase; Detoxifies H2O2		CPT Localized (4)
At1g77860	*KOM*		Kompeito	Moderate			
At1g78000	*SEL1*	*SULTR1;2*	Selenate Resistant	High			
At1g78240	*TSD2*	*QUA2*	Tumorous Shoot Development	High			
At1g78290	*SRK2C*		SNF1-Related Protein Kinase	High			
At1g78390	*NCED9*		Nine-Cis-Epoxycarotenoid Dioxygenase	Moderate	ABA Biosynthesis; Cleavage of 9-Cis-Epoxycarotenoids		CPT Localized (2)
At1g78570	*RHM1*	*ROL1*	Rhamnose Biosynthesis	High			
At1g78580	*TPS1*		Trehalose-6-Phosphate Synthase	Moderate	Trehalose-6-Phosphate Synthase 1		
At1g78590	*NADK3*		NAD(H) Kinase	Unique	Cytoplasmic NADH Kinase; NADPH Biosynthesis		
At1g78630	*EMB1473*		Embryo Defective	Unique	Chloroplast Ribosomal Protein L13		CPT Localized (4)
At1g78770	*APC6*	*NOMEGA; CDC16*	Anaphase-Promoting Complex	Unique	Anaphase Promoting Complex Subunit		
At1g78870	*UBC13A*		Ubiquitin Conjugating Enzyme	High			Not Evaluated
At1g78900	*VHA-A*		Vacuolar ATP Synthase Subunit	Unique	Vacuolar Proton Pump		
At1g79000	*HAC1*		Histone Acetyltransferase CBP Family	High			

At1g79040	*PsbR*		Photosystem II Subunit R	Unique	Photosystem II Subunit		CPT Localized (4)
At1g79230	*STR1*	*MST1; RDH1; ST1*	Sulfurtransferase	High	Mitochondrial Sulfurtransferase 1	MIT Localized (2)	
At1g79280	*NUA*	*AtTPR*	Nuclear Pore Anchor	Unique	Nuclear Pore Complex Subunit; Nuclear mRNA Export		
At1g79350	*EMB1135*		Embryo Defective	Unique	DNA-Binding Protein; Putative Transcription Factor		
At1g79440	*SSADH1*	*ALDH5F1*	Succinic Semialdehyde Dehydrogenase	High	Succinic Semialdehyde Dehydrogenase; Constituent of GABA Shunt; Biosynthesis of Succinate from GABA	MIT Localized (5)	
At1g79460	*GA2*	*KS1*	GA Deficient	High	Ent-Kaurene Synthase; GA Biosynthesis		CPT Localized (2)
At1g79490	*EMB2217*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		
At1g79560	*EMB1047*	*FTSH12*	Embryo Defective	Moderate	AAA ATPase Protein; Chloroplast FtsH-Like Protease		CPT Localized (1)
At1g79580	*SMB*	*ANAC033*	Sombrero	Moderate			Not Evaluated
At1g79650	*RAD23B*		Radiation Sensitive	High			Not Evaluated
At1g79810	*PEX2*	*TED3*	Peroxisomal Protein	Unique	Peroxisomal Protein; Putative Role in Photomorphogenic Pathway		
At1g79840	*GL2*		Glabra	High			

At1g79850	*ORE4*	*PRPS17*	Oresara	Unique	Chloroplast Ribosomal Protein S17		CPT Localized (4)
At1g79940	*AtERDJ2A*			High	ER J Domain Protein; Protein Translocation		
At1g80070	*SUS2*	*EMB177;* *EMB14;* *EMB33*	Abnormal Suspensor	High	PRP8 Splicing Factor; Spliceosome Subunit		
At1g80080	*TMM*	*RLP17*	Too Many Mouths	Moderate			
At1g80100	*AHP6*		Arabidopsis Histidine Phosphotransfer Protein	Unique	Cytokinin Signaling		
At1g80260	*EMB1427*	*GCP5*	Embryo Defective	High	Gamma Tubulin; Microtubule Nucleation		
At1g80350	*FRA2*	*BOT1;* *ERH3;* *KTN1*	Fragile Fiber	Moderate			
At1g80380	*GLYK*		D-Glycerate 3-Kinase	Unique	D-Glycerate 3-Kinase; Photorespiratory C2 Cycle		CPT Localized (4)
At1g80410	*EMB2753*	*FEY*	Embryo Defective	Unique	N-Terminal Acetyltransferase; Proposed Role in Protein Modification		
At1g80420	*XRCC1*			Unique	DNA Repair Protein		Not Evaluated
At1g80680	*SAR3*	*MOS3; PRE*	Suppressor of Auxin Resistance	Moderate	Nuclear Pore Complex Subunit		
At1g80760	*NIP6;1*		NOD26-Like Intrinsic Protein	High			
At1g80770	*PDE318*		Pigment Defective Embryo	Unique	Uncertain; GTP Binding Protein		

At1g80830	*NRAMP1*	*PMIT1*	Natural Resistance-Associated Macrophage Protein	High			Not Evaluated
At2g01110	*APG2*	*UNE2*	Albino and Pale Green	Unique	Chloroplast Protein Translocation		CPT Localized (4)
At2g01140	*PDE345*		Pigment Defective Embryo	High	Fructose-Biphosphate Aldolase; Carbohydrate Metabolism		CPT Localized (5)
At2g01190	*PDE331*		Pigment Defective Embryo	Moderate	Uncertain		CPT Localized (1)
At2g01290	*RPI2*		Ribose-5-Phosphate Isomerase	High			
At2g01350	*QPT*		Quinolinic Acid Phosphoribosyl Transferase	Unique	NAD Biosynthesis		CPT Localized (2)
At2g01390	*EMB3111*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing	MIT Localized (2)	
At2g01420	*PIN4*		Pin-Formed	High	Transmembrane Auxin Efflux Carrier		
At2g01570	*RGA1*	*RGA*	Repressor of GA1	High			
At2g01735	*RIE1*		Ring Finger Protein for Embryogenesis	High	Uncertain; RING-H2 Zinc Finger Protein		
At2g01830	*CRE1*	*WOL; AHK4*	Cytokinin Response	High			
At2g01860	*EMB975*		Embryo Defective	Unique	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At2g01918	*POL3*		PsbQ-Like	Unique	NDH Complex Assembly		Not Evaluated
At2g01940	*SGR5*	*AtIDD15*	Shoot Gravitropism	Moderate			
At2g01950	*BRL2*	*VH1*	BRI1-Like	High			
At2g01980	*SOS1*	*NHX7*	Salt Overly Sensitive	Moderate			

At2g02150	*EMB2794*		Embryo Defective	High	Putative PPR Protein; Organellular mRNA Processing		
At2g02220	*PSKR1*		Phytosulfokin Receptor	High			
At2g02480	*STI*		Stichel	High			
At2g02500	*ISPD*	*AtMEPCT*	Isoprenoid	Unique	Isoprenoid Biosynthesis		CPT Localized (3)
At2g02560	*CAND1*	*ETA2; HVE; TID120*	Cullin-Associated and Neddylation Dissociated	Unique	HEAT-Repeat Unit Protein; Roles in SCF-Mediated Protein Degradation and Auxin Signaling		
At2g02810	*AtUTr1*		UDP-Galactose Transporter	High			
At2g02950	*PKS1*		Phytochrome Kinase Substrate	High			
At2g02955	*MEE12*	*CCG*	Maternal Effect Embryo Arrest	Unique	Nuclear Zinc Finger Protein		
At2g03050	*SOLDAT10*		Soldat	Moderate	Plastid mTERF-Related Protein; Plastid Signaling		
At2g03120	*AtSPP*		Signal Peptide Peptidase	Unique	Signal Peptide Peptidase		
At2g03150	*EMB1579*		Embryo Defective	Unique	Uncertain; Putative Calcium Binding Protein		
At2g03220	*MUR2*	*FUT1*	Cell Wall Mutant	High			
At2g03680	*SPR1*	*SKU6*	Spiral	Unique	Unknown		
At2g03720	*MRH6*		Morphogenesis of Root Hair	Moderate			
At2g03760	*SOT12*	*RAR047; ST1*	Sulphotransferase	High			Not Evaluated

At2g03800	*GEK1*		Geko	Unique	D-Aminoacyl-tRNA Deacylase; Recycling of Misacylated tRNA		
At2g03870	*EMB2816*	*LSM7*	Embryo Defective	Unique	snRNP; RNA Splicing and Processing		
At2g04030	*EMB1956*	*HSP90*	Embryo Defective	High	Heat Shock Protein; Molecular chaperone		CPT Localized (5)
At2g04270	*RNEE/G*		RNase E/G-Like	Unique	Endoribonuclease E		CPT Localized (3)
At2g04530	*TRZ2*		tRNase Z	Moderate	Plastid tRNA Biosynthesis		CPT Localized (3)
At2g04550	*IBR5*	*DSPTP1E*	Indole-3-Butyric Acid Response	Unique	Putative Dual-Specificity Phosphatase; Phytohormone Signaling		
At2g04660	*APC2*		Anaphase-Promoting Complex	Unique	Ubiquitin Protein Ligase Subunit		
At2g04842	*EMB2761*		Embryo Defective	High	Plastid and Mitochondrial Threonine tRNA Synthetase	MIT Localized (1)	
At2g05210	*AtPOT1a*		Protection of Telomeres	Moderate			
At2g05990	*MOD1*	*ENR*	Mosaic Death	Unique	Enoyl-Acyl Carrier Protein Reductase; Fatty Acid Synthase Complex		CPT Localized (4)
At2g06050	*OPR3*	*DDE1*	Oxophytodienoate Reductase	High	12-Oxophytodienoic Acid Reductase; Jasmonic Acid Biosynthesis		CPT Localized (0)
At2g06510	*RPA70a*	*RPA1a*	Replication Protein A	High			

At2g06925	*AtSPLA*		Phospholipase	Unique	Secreted Phospholipase; Negative Regulator of AtMYB30-Mediated Defense		Not Evaluated
At2g07050	*CAS1*		Cycloartenol Synthase	High	Sterol Biosynthesis; 2,3-Oxidosqualene Cyclase		
At2g13540	*ABH1*	*ENS*	ABA Hypersensitive	Unique	Nuclear mRNA Cap Binding Protein		
At2g13680	*CalS5*	*Gsl2*	Callose Synthase	High			
At2g14120	*DRP3B*		Dynamin Related Protein	High			
At2g14540	*SRP2*		Serpin	High			
At2g14560	*LURP1*		Late Upregulated in Response to Hyaloperonospora Parasitica	Moderate			
At2g15290	*TIC21*	*PIC1*	Translocon at Inner Membrane of Chloroplasts	Unique	Chloroplast Import Protein		CPT Localized (5)
At2g15570	*ATM3*	*GAT1; TRX-M3; AtHM3*	ATP-Binding Cassette Transporter of Mitochondria	Unique	ABC Transporter		
At2g15790	*SQN*	*CYP40*	Squint	Moderate			
At2g15820	*OTP51*		Organelle Transcript Processing	Unique	Plastid mRNA Processing		CPT Localized (2)
At2g16390	*DRD1*	*DMS1; CHR35*	Defective in RNA-Directed DNA Methylation	Moderate			
At2g16910	*AMS*		Aborted Microspores	Unique	bHLH Transcription Factor		

At2g17090	*SSP*		Short Suspensor	High	Cytoplasmic Receptor Kinase; Role in Signal Transduction		
At2g17250	*EMB2762*		Embryo Defective	Unique	U3 SnoRNP; Proposed Role in Ribosome Biogenesis		
At2g17265	*DMR1*	*HSK*	Downy Mildew Resistant	Unique	Homoserine Kinase; Pathogen Response Signaling		CPT Localized (4)
At2g17290	*CPK6*	*AtCDPK3*	Calcium-Dependent Protein Kinase	High			
At2g17430	*NTA*	*MLO7*	Nortia	High	MLO Protein; Plant Signaling Pathways		Not Evaluated
At2g17510	*EMB2763*	*RRP44A*	Embryo Defective	Moderate	Ribonuclease II; Exosome Component; Proposed Role in Ribosomal RNA Processing		
At2g17870	*CSP3*		Cold Shock Domain Protein	Moderate			
At2g17950	*WUS*	*PGA6*	Wuschel	Unique	Homeodomain Transcription Factor		
At2g18020	*EMB2296*		Embryo Defective	High	Mitochondrial or Cytoplasmic Ribosomal Protein L8/L2		
At2g18290	*EMB2783*	*APC10*	Embryo Defective	Unique	Anaphase-Promoting Complex; Ubiquitin Protein Ligase		
At2g18390	*TTN5*	*HAL*	Titan	Moderate	ARL2 GTPase; Regulator of Tubulin Folding and Microtubule Dynamics		

At2g18470	*PERK4*		Proline-Rich Extensin-Like Receptor Kinase	Moderate			
At2g18510	*EMB2444*	*SAP49*	Embryo Defective	Moderate	Spliceosome Associated Protein; RNA Recognition Motif Protein; Post-Transcriptional Regulation		
At2g18710	*SCY1*		SecY Homolog	Unique	Chloroplast Sec Translocase		Not Evaluated
At2g18790	*PHYB*	*HY3; OOP1*	Phytochrome B	High			
At2g18950	*HPT1*	*VTE2; TPT1*	Homogentisate Phytyltransferase	Moderate	Vitamin E Synthesis; Homogentisate Phytyltransferase		CPT Localized (3)
At2g19080	*METAXIN*		Metaxin	Unique	Mitochondrial Protein Import; Putative Role in Assembly of Membrane Beta-Barrel Proteins	MIT Localized (1)	
At2g19430	*DWA1*	*THO6*	DWD Hypersensitive to ABA	Unique	CUL4 E3 Ligase Receptor; ABA Signaling		Not Evaluated
At2g19450	*TAG1*	*RDS1; ABX45; AS11; DGAT*	Triacylglycerol Biosynthesis	Unique	Diacylglycerol Transferase; Storage Lipid Biosynthesis		
At2g19520	*FVE*	*MIS4*	Late Flowering	High			
At2g19560	*EER5*		Enhanced Ethylene Response	Unique	PAM Domain Protein; Ethylene Signaling		
At2g19570	*CDA1*	*DESZ*	Cytidine Deaminase	High			
At2g19690	*PLA2-BETA*		Phospholipase	Moderate			
At2g19760	*PRF1*	*PFN1*	Profilin	Moderate			

At2g19810	*AtOZF1*		Oxidation-Related Zinc Finger	High			Not Evaluated
At2g20000	*HBT*	*CDC72b*	Hobbit	High			
At2g20120	*COV1*		Continuous Vascular Ring	High			
At2g20180	*PIL5*	*PIF1*	Phytochrome Interacting Factor 3-Like	Moderate			
At2g20190	*CLASP*		CLIP-Associated Protein	Unique	Microtubule-Associated Protein; Role in Microtubule Organization		
At2g20300	*ALE2*		Abnormal Leaf Shape	High			
At2g20310	*RIN13*		RPM1 Interacting Protein	Moderate	RPM1 Disease Resistance Signaling Complex Component		
At2g20370	*MUR3*	*KAM1*	Murus	Moderate			
At2g20580	*RPN1A*		Proteasome Regulatory Subunit	High	26S Proteasome Subunit; Protein Degradation and Cell Cycle Progression		
At2g20585	*NFD6*		Nuclear Fusion Defective	Unique	Unknown; Mitochondrial Protein	MIT Localized (0)	
At2g20610	*SUR1*	*RTY; ALF1; HLS3*	Super Root	High			
At2g20630	*PIA1*		PP2C Induced by AvrRpm	High			
At2g20750	*AtEXPB1*		Expansin	High			
At2g20810	*GAUT10*	*LGT4*	Galacturonosyltransferase	High			
At2g20890	*THF1*	*PSB29*	Thylakoid Formation	Unique	G-Protein-Coupled, Sugar-Signaling Pathway		CPT Localized (5)

At2g20990	*SYTA*	*SYTA*	Synaptotagmin	High			Not Evaluated
At2g21070	*FIO1*		Fiona	Unique	Unknown; Role in Circadian Clock Regulation		
At2g21150	*XCT*		XAP5 Circadian Timekeeper	Unique	Unknown; Circadian Clock Light Regulator		
At2g21170	*cpTPI*	*TIM*	Plastid Isoform Triose Phosphate Isomerase	High			Not Evaluated
At2g21470	*EMB2764*	*SAE2*	Embryo Defective	Moderate	SUMO Activating Enzyme ; Nuclear Protein Modification		
At2g21660	*CCR2*	*GRP7*	Cold, Circadian Rhythm, and RNA Binding	Moderate			
At2g21710	*EMB2219*		Embryo Defective	Moderate	Uncertain; mTERF Domain Protein		
At2g21790	*RNR1*	*CLS8*	Ribonucleotide Reductase	Unique	3'-5'-Exoribonuclease		CPT Localized (0)
At2g21870	*MGP1*		Male Gametophyte Defective	Unique	Mitochondrial ATP Synthase Subunit	MIT Localized (5)	
At2g22010	*RKP*		Related to KPC1	Unique	Ubiquitin E3 Ligase		
At2g22125	*CSI1*		Cellulose Synthase-Interactive Protein	High	Armadillo Repeat-Containing Protein; Cellulose Biosynthesis		Not Evaluated
At2g22300	*SR1*	*CAMTA3*	Signal Responsive	High			
At2g22410	*SLO1*		Slow Growth	High	Mitochondrial RNA Editing	MIT Localized (4)	Not Evaluated
At2g22540	*SVP*	*AGL22*	Short Vegetative Phase	Moderate			
At2g22630	*AGL17*		Agamous-Like	High			

At2g22640	*BRK1*		Brick	Unique	ARP2/3 Complex Regulator; Regulator of F-Actin Polymerization		
At2g22770	*NAI1*			Moderate			
At2g22780	*PMDH1*		Peroxisomal NAD-Malate Dehydrogenase	High			
At2g22810	*ACS4*		Aminocyclopropane Carboxylate Synthase	High			
At2g22870	*EMB2001*		Embryo Defective	Moderate	Uncertain; Putative Ribosome Biogenesis GTPase	MIT Localized (4)	
At2g22990	*SNG1*	*SCPL8*	Sinapoylglucose Accumulator	High			
At2g23380	*CLF*	*ICU1*	Curly Leaf	High			
At2g24120	*PDE319*	*SCA3*	Pigment Defective Embryo	High	Chloroplast DNA-Dependent RNA Polymerase; Plastid Transcription		CPT Localized (4)
At2g24270	*ALDH11A3*	*NP-GAPDH*		Moderate			
At2g24490	*RPA2*	*ROR1*	Replicon Protein	Moderate			
At2g24790	*COL3*		Constans-Like	High			
At2g24840	*AGL61*	*DIA*	Agamous-Like	Moderate	Type I MADS Domain Transcription Factor		
At2g25110	*SDF2*	*SDL*	Stromal Cell-Derived Factor	Unique	Unknown; Unfolded Protein Response Component		Not Evaluated
At2g25170	*PKL*	*GYM; SSL2*	Pickle	High			
At2g25180	*ARR12*		Arabidopsis Response Regulator	High			
At2g25490	*EBF1*	*FBL6*	EIN3-Binding F Box Protein	High			

At2g25600	*SPIK*	*AKT6*	Shaker Family K+ Channel	High	Shaker Family K+ Channel		
At2g25660	*EMB2410*		Embryo Defective	Unique	Unknown		CPT Localized (2)
At2g25680	*MOT1*		Molybdate Transporter	High	Mitochondrial Molybdenum Transporter	MIT Localized (2)	
At2g25710	*HCS1*		Holocarboxylase Synthetase	High	Holocarboxylase Synthetase		
At2g25840	*OVA4*		Ovule Abortion	Unique	Tryptophan Amino Acyl tRNA Synthetase	MIT Localized (1)	
At2g25850	*PAPS2*		Poly(A) Polymerase	High			
At2g25930	*ELF3*		Early Flowering	Unique	Putative Transcriptional Regulator		
At2g26000	*BRIZ2*		BRAP2 RING ZnUBP Domain-Containing Protein	High			Not Evaluated
At2g26060	*EMB1345*	*CIAO1*	Embryo Defective	High	WD Repeat Protein; Putative Transcription Factor Binding Protein		
At2g26070	*RTE1*		Reversion-To-Ethylene Sensitivity	Moderate			
At2g26140	*FtsH4*		FtsH Protease	High	Mitochondrial Inner Membrane-Bound ATP-Dependent Metalloprotease	MIT Localized (1)	
At2g26150	*HsfA2*		Heat Shock Transcription Factor	Moderate			Not Evaluated
At2g26170	*CYP711A1*	*MAX1*	Phytochrome P450	Unique	Positive Regulator of the Flavonoid Pathway		
At2g26250	*FDH*	*KCS10*	Fiddlehead	High			
At2g26300	*GPA1*		G-Protein Alpha Subunit	Moderate	G-Protein Alpha Subunit		

At2g26330	*ER*	*QRP1*	Erecta	High			
At2g26350	*PEX10*		Peroxisomal Protein	Unique	Membrane-Associated Peroxisomal Protein		
At2g26460	*SMU2*		Suppressors of MEC-8 and UNC-52	Unique	Putative Auxiliary Spliceosome Protein; Role in Pre-mRNA Splicing		
At2g26510	*PDE135*		Pigment Defective Embryo	High	Permease; Membrane Transport		
At2g26550	*HO2*		Heme Oxygenase	Moderate	Heme Oxygenase; Phytochrome Chromophore Biosynthesis		CPT Localized (2)
At2g26570	*WEB1*		Weak Chloroplast Movement Under Blue Light	High			Not Evaluated
At2g26650	*AKT1*		Arabidopsis Potassium Transport	High			
At2g26670	*HY6*	*GUN2; HY6; TED4; HY1; HO1*	Elongated Hypocotyl	High	Heme Oxygenase; Phytochrome Chromophore Biosynthesis		CPT Localized (5)
At2g26710	*BAS1*	*CYP72B1; CYP734A1*	PHYB Activation Tagged Suppressor	High			
At2g26830	*EMB1187*		Embryo Defective	Moderate	Choline Kinase; Phospholipid (Phosphatidylcholine) Biosynthesis		
At2g26890	*GRV2*	*KAM2; RME-8*	Gravitropism Defective	Unique	DnaJ Domain Protein; Endocytosis; Vacuolar Sorting; Protein Trafficking		

At2g26930	*PDE277*	*CDPMEK;* *ISPE*	Pigment Defective Embryo	Unique	Isoprenoid Biosynthesis in Plastids		CPT Localized (2)
At2g26990	*FUS12*	*CSN2;* *COP12*	Fusca	Unique	COP9 Signalosome Component		
At2g27040	*AGO4*	*OCP11*	Argonaute	High			
At2g27050	*EIL1*		Ethylene-Insensitive3-Like	High			
At2g27100	*SE*		Serrate	Unique	C2H2-Type Zinc Finger Protein; Role in Primary miRNA Processing		
At2g27150	*AAO3*		Aldehyde Oxidase	High			
At2g27170	*TTN7*	*SMC3*	Titan	Unique	Cohesin; Structural Maintenance of Chromosome Protein		
At2g27230	*LHW*		Lonesome Highway	Moderate			
At2g27250	*CLV3*		Clavata	Unique	Secreted Signaling Glycopeptide		
At2g27300	*NTL8*	*ANAC040*	NTM1-Like	Moderate			
At2g28000	*SLP*	*CPN60A*	Schlepperless	High	Chaperonin-60 alpha; Plastid Protein Folding		CPT Localized (5)
At2g28110	*FRA8*	*IRX7*	Fragile Fiber	High			
At2g28160	*FRU*	*FIT1;* *BHLH029*	FER-Like Regulator of Iron Uptake	Unique	Putative Transcription Factor		
At2g28290	*SYD*	*CHR3*	Splayed	Moderate			
At2g28550	*TOE1*	*RAP2.7*	Target of Early Activation Tagged	Moderate			Not Evaluated
At2g28560	*RAD51B*		Rad51 Paralog	Unique	Putative DNA Recombinase; Somatic DNA Recombination		
At2g28610	*PRS*	*WOX3*	Pressed Flower	Unique	Homeodomain Transcription Factor		
At2g28670	*ESB2*		Enhanced Suberin	Moderate			

At2g28800	*ALB3*	*Oxa1p*	Albino	Moderate	Chloroplast Protein Translocase; Integration of Proteins into Thylakoid Membranes		CPT Localized (4)
At2g28880	*EMB1997*	*ADCS*	Embryo Defective	Moderate	Bifunctional PABA Synthase; Para-Aminobenzoic Acid Biosynthesis; Glutamine Amidotransferase		CPT Localized (2)
At2g28890	*PLL4*		Poltergeist Like	High			
At2g28900	*AtOEP16-1*		Outer Plastid Envelope Protein	Unique	Plastid Protein Translocator		CPT Localized (4)
At2g29090	*CYP707A2*		Cytochrome P450	High			
At2g29630	*THIC*		ThiaminC	Unique	Thiamine Biosynthesis		CPT Localized (4)
At2g29980	*FAD3*		Fatty Acid Desaturase	High			
At2g30020	*AP2C1*			High			Not Evaluated
At2g30110	*AtUBA1*	*MOS5*	Ubiquitin-Activating Enzyme	High			
At2g30200	*EMB3147*		Embryo Defective	Unique	ACP-S-Malonyltransferase; Fatty Acid Biosynthesis		
At2g30240	*AtCHX13*		Cation/H+ Exchanger	High			
At2g30280	*RDM4*	*DMS4*	RNA-Directed DNA Methylation	Unique	RNA-Directed DNA Methylation		
At2g30410	*KIS*	*TFCA*	Kiesel	Unique	Tubulin Folding Cofactor A; Regulation of Tubulin Folding and Microtubule Dynamics		
At2g30432	*TCL1*		Trichomeless	Moderate			

At2g30490	*C4H*	*REF3; CYP73A5*	Cinnamate 4-Hydroxylase	Moderate			
At2g30520	*RPT2*		Root Phototropism	High			
At2g30570	*PsbW*		Photosystem II Reaction Center	Unique	PSII Protein Complex Subunit; PSII-LHCII Supercomplex Accumulation and Stability		Not Evaluated
At2g30770	*CYP71A13*		Cytochrome P450	High			
At2g30920	*EMB3002*	*COQ3*	Embryo Defective	Unique	Hexaprenyldihydroxybenzoate Methyltransferase; Ubiquinone Biosynthesis	MIT Localized (4)	
At2g30950	*VAR2*	*FtsH2*	Variegated	High	Chloroplast Homolog of FtsH; ATP-Dependent Zinc Metalloprotease; Photosystem II Repair		CPT Localized (4)
At2g31060	*EMB2785*		Embryo Defective	High	E2Fa Transcriptional Activator		
At2g31170	*SYCO*	*FIONA*	Syco Arath	High	Mitochondrial Cysteinyl-tRNA Synthetase	MIT Localized (1)	Not Evaluated
At2g31190	*RUS2*		Root UV-B Sensitive	Moderate	Unknown Function; Role in Polar Auxin Transport		CPT Localized (2)
At2g31260	*APG9*		Autophagy Defective	Unique	Unknown; Autophagy-Related Protein		
At2g31305	*INH3*		Inhibitor	Unique	Protein Phosphatase 1 Regulatory Subunit		
At2g31340	*EMB1381*		Embryo Defective	Unique	Unknown		
At2g31380	*STH*		Salt Tolerance Homologue	High			

At2g31400	*GUN1*		Genomes Uncoupled	Moderate			Not Evaluated
At2g31530	*EMB2289*	*SECY2*	Embryo Defective	Moderate	Chloroplast Protein Translocase; Plastid Translocation of Nuclear-Encoded Genes		
At2g31650	*ATX1*		Arabidopsis Homologue of Trithorax	High			
At2g31660	*SAD2*	*URM9*	Super Sensitive to ABA and Drought	High			
At2g31865	*PARG2*		Poly(ADP-Ribose) Glycohydrolase	High			Not Evaluated
At2g31870	*TEJ*		Sanskrit for 'Bright'	High			
At2g31970	*RAD50*		Radiation Sensitive	Unique	MRN Complex Subunit; Role in Repair and Metabolism of DNA Breaks		
At2g32590	*EMB2795*		Embryo Defective	Unique	Non-SMC Condensin Complex Subunit H; Sister Chromatid Segregation in Mitosis		
At2g32700	*LUH*		Leunig Homolog	Moderate			
At2g32940	*AGO6*		Argonaute	High			
At2g32950	*COP1*	*FUS1; EMB168*	Constitutive Photomorphogenesis	Moderate	Nuclear Protein that Represses Photomorphogenesis in the Dark; HY5 Protein Degradation		
At2g33100	*CSLD1*		Cellulose Synthase Like	High	Putative Glycosyltransferase; Cell Wall Biosynthesis		

At2g33150	*PED1*	*KAT2;* *PKT3*	Peroxisome Defective	High			
At2g33430	*DAL1*		Differentiation and Greening-Like	Moderate	Plastid rRNA Processing		CPT Localized (3)
At2g33460	*RIC1*		ROP-Interacting CRIB Motif-Containing Protein	Moderate			
At2g33540	*CPL3*		C-Terminal Domain Phosphatase-Like	Moderate			
At2g33770	*PHO2*		Phosphate	Moderate			
At2g33800	*EMB3113*		Embryo Defective	Unique	Chloroplast 30S Ribosomal Protein S5		CPT Localized (4)
At2g33860	*ETT*	*ARF3*	Ettin	Moderate			
At2g33880	*STIP*	*HB-3;* *WOX9*	Stimpy	Moderate			
At2g34220	*PDD12*	*MEE20*	Pollen Development Defective	High	Unknown		
At2g34470	*UREG*	*PSKF109*	Urease Accessory Protein	Unique	Urea Hydrolase Accessory Protein; Urea Catabolism		
At2g34490	*CYP710A2*		Cytochrome P450, Family 710, Subfamily A, Polypeptide 2	High			
At2g34640	*PTAC12*	*HMR*	Plastid Transcriptionally Active	Unique	Unknown		CPT Localized (3)
At2g34650	*PID*	*ABR*	Pinoid	High	Serine-Threonine Protein Kinase; Positive Regulator of Polar Auxin Transport		
At2g34660	ABCC2	*MRP2;* *EST4*	ATP-Binding Cassette	High			Not Evaluated

At2g34680	*SETH1*	*AIR9*		Unique	Microtubule-Associated Protein		
At2g34690	*ACD11*		Accelerated Cell Death	Moderate			
At2g34780	*EMB1611*	*UMB; MEE22*	Embryo Defective	Unique	Uncertain; Putative Role in Promoting Cell Division		
At2g34790	*EDA28*	*MEE23*	Embryo Sac Development Arrest	High	FAD Binding Domain Protein		
At2g35000	*ATL9*	*ATL2g*	Arabidopsis Toxicos en Levadura	Moderate			Not Evaluated
At2g35035	*URED*		Urease Accessory Protein	Unique	Urea Hydrolase Accessory Protein; Urea Catabolism		
At2g35070	*PGD4*		Pollen Germination Defective	Moderate	Unknown	MIT Localized (4)	
At2g35100	*ARAD1*		Arabinan Deficient	High			
At2g35210	*RPA*	*AGD10; MEE28*	Root and Pollen ARFGAP	High	ADP-Ribosylation Factor; GTPase Activating Factor; Intracellular Membrane Trafficking		
At2g35230	*IKU1*		Haiku	Moderate	LRR Kinase; Role in IKU Pathway		Not Evaluated
At2g35350	*PLL1*		Poltergeist Like	Moderate			
At2g35510	*SRO1*		Similar to RCD One	High			
At2g35630	*GEM1*	*MOR1*	Gemini Pollen	Unique	Microtubule Organization; Phragmoplast Orientation		

At2g35650	*CSLA7*		Cellulose Synthase Like	High	Cellulose Synthase-Like Glycosyltransferase; Cell Wall Polysaccharide Biosynthesis		
At2g35670	*FIS2*	*FIE2*	Fertilization Independent Seed	Moderate	Zinc Finger Transcriptional Regulator; Chromatin Structure Modulation		
At2g35720	*OWL1*		Orientation Under Very Low Fluences of Light	Unique	J-Domain Protein; Very Low Fluence Response Signaling		
At2g35930	*PUB23*		Plant U-Box	High			
At2g35940	*BLH1*	*EDA29*	BEL1-Like Homeodomain	Moderate			
At2g36000	*EMB3114*		Embryo Defective	Moderate	Uncertain; mTERF Domain Protein		CPT Localized (1)
At2g36120	*DOT1*		Defectively Organized Tributaries	Unique	Unknown; Glycine-Rich Protein		
At2g36190	*AtCWINV4*		Cell Wall Invertase	High			
At2g36230	*HISN3*	*APG10*	Histidine Auxotroph	Unique	Histidine Biosynthesis		CPT Localized (1)
At2g36270	*ABI5*	*GIA1*	ABA Insensitive	Unique	Putative Leucine Zipper Transcription Factor		
At2g36390	*SBE2.1*	*BE3*	Starch Branching Enzyme	High	Starch Branching Enzyme		CPT Localized (3)
At2g36490	*DML1*	*ROS1*	Demeter-Like	Moderate			
At2g36530	*LOS2*	*ENO2*	Low Response to Osmotic Stress	High			
At2g36830	*TIP1;1*	*GAMMA-TIP*	Tonoplast Intrinsic Protein	High			
At2g36850	*GSL8*		Glucan Synthase-Like	High	Callose Biosynthesis		

At2g36910	*AtPGP1*	*ABCB1*	P Glycoprotein	High			
At2g36990	*SIGF*	*SIG6; SOLDAT8*	RNA Polymerase Sigma-Subunit	Moderate	RNA Polymerase Sigma Factor		CPT Localized (3)
At2g37090	*IRX9*		Irregular Xylem	Moderate			
At2g37250	*ADK*	*AtPADK1*	Adenosine Kinase	High			
At2g37260	*TTG2*	*DSL1*	Transparent Testa Glabra	Moderate			
At2g37330	*ALS3*		Aluminum Sensitive	Unique	ABC Transporter-Like Protein; Aluminum Transport		Not Evaluated
At2g37560	*ORC2*		Origin Recognition Complex	Unique	Origin Recognition Complex Subunit 2; Role in DNA Replication, Chromatin Structure, and Gene Silencing		
At2g37630	*AS1*	*MYB91*	Asymmetric Leaves	Unique	MYB Transcription Factor		
At2g37680	*PAT3*	*FHY1*	Phytochrome A Transduction	Unique	Unknown		
At2g37860	*LCD1*	*SOZ2*	Lower Cell Density	Moderate	Unknown		CPT Localized (2)
At2g37920	*EMB1513*		Embryo Defective	Unique	Unknown		
At2g37970	*SOUL-1*			Unique	Unknown		
At2g38020	*VCL1*	*MAN; EMB258; VPS16*	Vacuoleless	Unique	Vacuolar Protein Sorting; Vacuole Biogenesis and Protein Trafficking to the Vacuole		
At2g38050	*DET2*	*DWF6*	De-etiolated	Unique	Sterol Reductase; Brassinosteroid Biosynthesis		

At2g38110	*GPAT6*		Glycerol-3-Phosphate Acyltransferase	High			
At2g38120	*AUX1*	*WAV5; MAP1*	Auxin Resistant	High			
At2g38170	*CAX1*		Cation Exchanger	High			
At2g38230	*PDX1.1*		Pyridoxine Biosynthesis	High			
At2g38280	*FAC1*		Embryonic Factor	Unique	AMP Deaminase; Purine Biosynthesis		
At2g38440	*ITB1*	*SCAR2; DIS3; WAVE1*	Irregular Trichome Branch	Moderate			
At2g38460	*IREG1*	*FPN1*	Iron Regulated	High			
At2g38470	*WRKY33*		WRKY DNA-Binding Protein	Moderate			
At2g38560	*TFIIS*		Transcript Elongation Factor IIS	Unique	Transcript Elongation Factor		
At2g38670	*PECT1*		CTP:Phosphorylethanolamine Cytidylyltransferase	Unique	Phosphatidylethanolamine Biosynthesis		
At2g38750	*AnnAt4*		Annexin	Moderate			Not Evaluated
At2g38770	*EMB2765*	*AQUARIUS*	Embryo Defective	Unique	U5 Associated Protein; Putative Role in Pre-mRNA Splicing		
At2g39080	*EMB2799*		Embryo Defective	Unique	Unknown; Potential Role in Chloroplast Nutrient Transport		CPT Localized (4)
At2g39140	*PDE328*	*SVR1*	Pigment Defective Embryo	Moderate	Pseudouridine Synthase; RNA Binding and Modification		CPT Localized (4)

At2g39290	*PGP1*	*PGPS1*	Phosphatidylglycerolphosphate Synthase	Moderate	Phosphatidylglycerol Biosynthesis	MIT Localized (2)	CPT Localized (4)
At2g39450	*MTP11*			High			
At2g39470	*PPL2*		PsbP-Like Protein	Moderate	NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (3)
At2g39550	*AtGGT1B*	*PGGT-I;* *GGB*	Geranylgeranyltransferase	Unique	Geranylgeranyltransferase; Role in Regulation of ABA Signaling in Guard Cells		
At2g39660	*BIK1*		Botrytis-Induced Kinase	High			
At2g39770	*CYT1*	*EMB101;* *VTC1*	Cytokinesis Defective	High	Mannose-1-Phosphate Guanyltransferase; GDP-Mannose Pyrophosphorylase; Role in N-Glycosylation and Vitamin C Biosynthesis		
At2g39800	*P5CS1*		Delta1-Pyrroline-5-Carboxylate Synthase	High			
At2g39810	*HOS1*		High Response to Osmotic Stress	Unique	RING E3 Ligase; Negative Regulator of Cold Response		
At2g39930	*ISA1*		Isoamylase	High	Isoamylase-Type Debranching Enzyme		CPT Localized (3)
At2g39940	*COI1*		Coronatine Insensitive	High			
At2g39990	*AteIF3f*	*EIF2*	Eukaryotic Translation Initiation Factor	Unique	Translation Initiation Factor		

At2g40080	*ELF4*		Early Flowering	Unique	Unknown		
At2g40140	*SZF2*	*CZF1; ZFAR1*	Salt-Inducible Zinc Finger	High			
At2g40170	*GEA6*	*EM6*	Late Embryogenesis Abundant	Unique	Regulator of ABA Response		
At2g40180	*PP2C5*		Phosphatase	Moderate			Not Evaluated
At2g40190	*LEW3*		Leaf Wilting	Unique	Alpha-1,2-Mannosyltransferase; Protein N-Glycosylation		
At2g40220	*ABI4*	*GIN6; ISI3; SAN5; SUN6; SIS5*	ABA Insensitive	Unique	AP2 Domain Transcription Factor		
At2g40550	*ETG1*		E2F Target Gene	Unique	DNA Replication; Replisome Complex Component		
At2g40840	*DPE2*		Disproportionating Enzyme	Unique	Cytosolic Amylomatase; Maltose Metabolism		
At2g40850	*AtPI4KG1*		Arabidopsis Phosphoinositide 4-Kinase	High			
At2g40890	*REF8*	*CYP98A3*	Reduced Epidermal Fluorescence	High			
At2g40930	*PDE323*	*UBP5*	Pigment Defective Embryo	High	Ubiquitin-Specific Protease; Protein Degradation		
At2g40950	*BZIP17*			High			
At2g40970	*MYBC1*		MYB transcription factor	Moderate			Not Evaluated
At2g41110	*CAM2*	*AtCAL5*	Calmodulin	High	Calmodulin; Role in Calcium Signaling		
At2g41310	*ARR8*		Arabidopsis Response Regulator	Moderate			

At2g41350	*EMB2819*		Embryo Defective	Unique	HAUS1 Subunit of Augmin Complex; Mitotic Spindle Formation		
At2g41370	*BOP2*		Blade on Petiole	High			
At2g41500	*EMB2776*	*PRP4; LIS*	Embryo Defective	Moderate	U4/U6 snRNP; ; Putative Role in Pre-mRNA Splicing		
At2g41540	*GPDHc1*			High			
At2g41560	*ACA4*		Autoinhibited Ca(2+)-ATPase	High			Not Evaluated
At2g41660	*MIZ1*		Mizu-Kussei	Moderate			
At2g41670	*SIN2*		Short Integuments	Moderate	DAR GTPase; Mitochondrial Ribosome Assembly	MIT Localized (0)	
At2g41680	*NTRC*		NADPH-Dependent Thioredoxin Reductase	Moderate	Plastid NADPH Thioredoxin Reductase		CPT Localized (4)
At2g41720	*EMB2654*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		
At2g41850	*ADPG2*	*PGAZAT*	Arabidopsis Dehiscence Zone Polygalacturonase	High			
At2g41940	*ZFP8*		Zinc Finger Protein	Moderate			
At2g42160	*BRIZ1*		BRAP2 RING ZnUBP Domain-Containing Protein	High			Not Evaluated
At2g42200	*SPL9*		Squamosa Promoter Binding Protein-Like	Moderate			
At2g42260	*UVI4*		UV-B-Insensitive	Moderate			
At2g42380	*bZIP34*			High			
At2g42430	*LBD16*	*ASL18*	Lateral Organ Boundaries-Domain	Moderate			

At2g42580	*TTL3*	*VIT*	Tetratricopetide-Repeat Thioredoxin-Like	High			
At2g42620	*ORE9*	*MAX2; PPS*	Oresara	Unique	F-Box Protein; SCF Complex Subunit; Role in Light Signaling Pathways		
At2g42870	*PAR1*	*HLH1*	PHY Rapidly Regulated	Unique	Putative bHLH Transcription Factor		
At2g43010	*SRL2*	*PIF4*	Short Hypocotyl in Red Light	High			
At2g43040	*NPG1*		No Pollen Germination	High	Calmodulin Binding Protein		
At2g43090	*AtLeuD3*		Leucine	High	Isopropylmalate Isomerase; Leucine Biosynthesis		Not Evaluated
At2g43350	*ATGPX3*		Glutathione Peroxidase	Moderate			
At2g43360	*BIO2*	*EMB49*	Biotin Auxotroph	Unique	Biotin Synthase; Mitochondrial Biotin Biosynthesis	MIT Localized (4)	
At2g43400	*ETFQO*		Electron-Transfer Flavoprotein:Ubiquinone Oxidoreductase	Unique	Leucine Catabolism	MIT Localized (3)	
At2g43410	*FPA*		Late Flowering	Moderate	Spen Family Protein; RNA Binding Protein		
At2g43650	*EMB2777*	*EMB2796; UTP3*	Embryo Defective	Moderate	U3 snoRNP; Processome Small Subunit; Putative Regulator of Chromatin Silencing		

At2g43710	*SSI2*	*FAB2*	Suppressor of Salicylic Acid Insensitive	High	Stearoyl-ACP Desaturase; Fatty Acid Desaturation		CPT Localized (4)
At2g43790	*AtMPK6*	*MAPK6*	Map Kinase	High			
At2g43910	*HOL1*		Harmless to Ozone Layer	High			
At2g44170	*NMT2*		N-Myristoyltransferase	High			
At2g44190	*EMB3116*	*EDE1*	Embryo Defective	High	Novel Microtubule Associated Protein		
At2g44490	*PEN2*	*BGLU26*		High			
At2g44745	*WRKY12*		WRKY DNA-Binding Protein	Moderate			Not Evaluated
At2g44810	*DAD1*		Defective in Anther Dehiscence	High	Chloroplast Phospholipase A1; Jasmonic Acid Biosynthesis		CPT Localized (3)
At2g44950	*HUB1*	*RDO4; ANG4*	Histone Mono-Ubiquitination	High			
At2g44990	*CCD7*	*MAX3*	Carotenoid Cleavage Dioxygenase	Unique	Carotenoid Cleavage Dioxygenase; Regulates Starch Phosphorylation, Degradation		CPT Localized (3)
At2g45000	*EMB2766*	*SEC31*	Embryo Defective	Unique	COPII Coat Protein; Putative Chloroplast-Localized Vesicular Trafficking Protein		
At2g45190	*FIL*	*AFO*	Filamentous Flower	Moderate			
At2g45270	*GCP1*		Glycoprotease	Unique	Mitochondrial Glycoprotease; HSP70 Superfamily Protein	MIT Localized (0)	

At2g45280	*AtRAD51C*		RAS Associated with Diabetes	Moderate	DSB Repair		
At2g45330	*EMB1067*		Embryo Defective	Moderate	2' tRNA Phosphotransferase; Catalytic Role in tRNA Splicing		
At2g45350	*CRR4*		Chlororespiratory Reduction	Moderate	PPR Protein; Plant Combinatorial and Modular Protein		CPT Localized (2)
At2g45400	*BEN1*		bri1-5 Enhanced	Moderate			
At2g45420	*LBD18*	*ASL20*	Lateral Organ Boundaries-Domain	Moderate			
At2g45430	*AHL22*		AT-Hook Motif Nuclear Localized Protein	Moderate			
At2g45440	*DHDPS2*		Dihydrodipicolinate Synthase	High	Dihydrodipicolinate Synthase; Lysine Biosynthesis		CPT Localized (2)
At2g45660	*AGL20*	*SOC1*	Agamous-Like	Moderate			
At2g45690	*SSE*	*PEX16*	Shrunken Seed	Unique	Peroxisomal Biogenesis Factor; Protein and Oil Body Biogenesis		
At2g45770	*cpFtsY*			Moderate	Thylakoidal Protein Integration		CPT Localized (4)
At2g45790	*PMM*	*DGR1*	Phosphomannomutase	Unique	Phosphomannomutase; Guanosine Diphosphate Mannose Biosynthesis		
At2g45890	*RHS11*		Root Hair Specific	High			
At2g45970	*LCR*	*CYP86A8*	Lacerata	High			
At2g46020	*BRM*	*CHA2; CHR2*	Brahma	Moderate	SNF2 Protein; Chromatin Remodeling		
At2g46240	*AtBAG6*		BCL-2-Associated Athanogene	Unique	Chaperone Regulator		

At2g46340	*SPA1*		Suppressor of phyA-105	High			
At2g46370	*FIN219*	*JAR1*	Far-Red Insensitive	High			
At2g46410	*CPC*		Caprice	Unique	MYB Transcription Factor		
At2g46510	*AtAIB*		ABA-Inducible bHLH-Type Transcription Factor	High			
At2g46590	*DAG2*		Dof Affecting Germination	High			
At2g46720	*HIC*	*KCS13*	High Carbon Dioxide	High			
At2g46770	*ANAC043*	*NST1*	Arabidopsis NAC Domain Containing Protein	High			
At2g46790	*APRR9*	*TL1*	Arabidopsis Pseudo-Response Regulator	Moderate			
At2g46800	*MTP1*	*ZAT1; CDF1*		Moderate			
At2g46830	*CCA1*		Circadian Clock Associated	Moderate			
At2g46920	*POL*		Poltergeist	Moderate			
At2g46970	*PIL1*		Phytochrome Interacting Factor 3-Like	Moderate			
At2g47000	*AtPGP4*	*ABCB4; MDR4*	P-Glycoprotein	High			
At2g47040	*VGD1*		Vanguard	High	Pectin Methylesterase; Putative Cell Wall Modification		
At2g47160	*BOR1*		Requires High Boron	High			

At2g47240	*LACS1*	*CER8*	Long-Chain Acyl-CoA Synthase	High			
At2g47430	*CKI1*		Cytokinin Independent	Moderate	Histidine Kinase; Cytokinin Perception		
At2g47450	*CAO*	*CPSRP43*	Chaos	Unique	Chloroplast Signal Recognition Particle		CPT Localized (3)
At2g47460	*MYB12*	*PFG1*	MYB Domain Protein	High			
At2g47470	*UNE5*	*TED18;* *PDI11;* *MEE30*	Unfertilized Embryo Sac	Moderate	Protein Disulfide Isomerase		
At2g47510	*TGD16*	*FUM1*	Pollen Tube Growth Defective	High	Fumarase; Catalyzes the Interconversion of Fumarate and S-Malate	MIT Localized (6)	
At2g47620	*AtSWI3A*		Arabidopsis Ortholog of Switch	Moderate	DNA Binding Protein; Chromatin Remodeling Complex Subunit		
At2g47750	*KEN*	*GH3.9*	Kerridwin	High	GH3 Family Protein; Indole-3-Acetic Acid-Amido Synthetase		
At2g47760	*ALG3*		Asparagine-Linked Glycosylation	Unique	Alpha 1,3-Mannosyltransferase; Protein N-Glycosylation		Not Evaluated
At2g47940	*EMB3117*		Embryo Defective	Moderate	Chloroplast DegP2 Protease		CPT Localized (4)
At2g47980	*SCC3*		Sister-Chromatid Cohesion Protein	Unique	Cohesin; Role in DSB Repair		
At2g47990	*SWA1*	*EDA13;* *EDA19*	Slow Walker	Unique	18S Ribosomal RNA Biogenesis		
At2g48070	*RPH1*		Resistance to Phytophthora	Unique	Unknown; Integral Membrane Plastid Protein		CPT Localized (4)

At2g48120	*PAC*		Pale Cress	Unique	Uncertain; Putative Role in Plastid mRNA Maturation		CPT Localized (2)
At3g01020	*ISU2*			Moderate	Iron-Sulfur Cluster Assembly	MIT Localized (5)	
At3g01040	*GAUT13*		Galacturonosyltransferase	High			
At3g01080	*WRKY58*		WRKY DNA-Binding Protein	Moderate			
At3g01090	*AKIN10*		Arabidopsis SNF1 Kinase Homolog\	High			
At3g01120	*MTO1*	*CGS1; CYS1*	Methionine Overaccumulation	Moderate			Not Evaluated
At3g01140	*NOK*	*MYB106*	NOECK	High			
At3g01220	*AtHB20*		Homeobox Protein	High			
At3g01370	*AtCFM2*		CRM Family Member	Moderate	Chloroplast Intron Splicing Factor		CPT Localized (1)
At3g01440	*PQL2*		PsbQ-Like	Unique	NDH Complex Assembly		Not Evaluated
At3g01460	*MBD9*		Methyl-CpG Binding Domain	Unique	Unknown; Methyl-CpG-Binding Domain Protein		
At3g01480	*CYP38*		Cyclophilin	Moderate	Chloroplast Cyclophilin; Photosystem II Assembly		CPT Localized (4)
At3g01510	*LSF1*		Like SEX4	Unique	Starch Degradation; Putative Phosphatase		CPT Localized (3)
At3g01610	*EMB1354*	*CD48C*	Embryo Defective	Moderate	AAA ATPase; Putative Cell Division Control Protein		
At3g01780	*TPLATE*			Unique	Vesicle Trafficking; Cell Wall Modification		
At3g02000	*ROXY1*			Moderate			

At3g02130	*RPK2*	*TOAD2*	Receptor-Like Protein Kinase	Moderate			
At3g02140	*TMAC2*	*AFP4*	Two or More ABRES-Containing Gene	Unique	ABI Five Binding Protein; Regulator of ABA Signaling		
At3g02150	*PTF1*	*TCP13; TFPD*	psbD Transcription Factor	Moderate			
At3g02260	*TIR3*	*DOC1; BIG; CRM1; UMB1*	Transport Inhibitor Response	Unique	Calossin-Like Protein; Role in Hormone Transport / Signaling		
At3g02280	*ATR3*		Arabidopsis thaliana P450 Reductase	Moderate	Cytochrome P450 Reductase Like; NR1 Subfamily of Diflavin Reductases		
At3g02350	*GAUT9*		Galacturonosyltransferase	High			
At3g02410	*ICME-LIKE2*		Isoprenylcysteine Methylesterase-Like	High			Not Evaluated
At3g02470	*SAMDC*		S-Adenosylmethionine Decarboxylase	High			
At3g02580	*DWF7*	*BUL; STE1*	Dwarf	High			
At3g02660	*EMB2768*		Embryo Defective	Unique	Plastid and Mitochondrial Tyrosine tRNA Synthetase	MIT Localized (1)	CPT Localized (4)
At3g02680	*NBS1*		Nijmegen Breakage Syndrome	Unique	MRN Complex Subunit; Role in Repair and Metabolism of DNA Breaks		
At3g02850	*SKOR*		Defect in SKOR K+ Channel	High			

At3g02870	*VTC4*		Vitamin C	Moderate	L-Gal-1-P Phosphatase; Ascorbate and Myoinositol Biosynthesis		
At3g02875	*ILR1*		IAA-Leucine Resistant	High			
At3g02885	*GASA5*		GAST1 Protein Homolog	Unique	Regulator of GA Response		
At3g03050	*KJK*	*CSLD3*	Kojak	High			
At3g03090	*AtVGT1*		Vacuolar Glucose Transporter	High			
At3g03450	*RGL2*		RGA-Like	High			
At3g03530	*NPC4*		Non-Specific Phospholipase	High			Not Evaluated
At3g03630	*CS26*		Cysteine Synthase	Moderate			Not Evaluated
At3g03710	*PDE326*	*RIF10*	Pigment Defective Embryo	Moderate	Plastid Polynucleotide Phosphorylase; Proposed Role in 23S rRNA 3' End Processing		CPT Localized (3)
At3g04240	*SEC*		Secret Agent	Moderate	O-Linked N-Acetylglucosamine Transferase; Post-Translational Modification		
At3g04260	*PDE324*	*PTAC3*	Pigment Defective Embryo	Unique	SAP Domain Protein; Plastid Gene Expression		CPT Localized (4)
At3g04340	*EMB2458*		Embryo Defective	Moderate	FtsH Protease; AAA ATPase; Chloroplast ATP-Dependent Zinc Metalloprotease		CPT Localized (4)

At3g04400	*EMB2171*		Embryo Defective	Moderate	Mitochondrial or Cytoplasmic Ribosomal Protein L17/L23		
At3g04460	*PEX12*	*APM4*	Peroxisomal Protein	Unique	RING Finger Protein; Peroxisome Biogenesis		
At3g04520	*THA2*		Threonine Aldolase	High	Threonine Aldolase; Amino Acid Metabolism		
At3g04580	*EIN4*		Ethylene Insensitive	High			
At3g04680	*CLPS3*		CLP1-Similar Protein	High	Polyadenylation Factor; mRNA Processing		
At3g04740	*SWP*	*MED14*	Struwwelpeter	Unique	Transcriptional Activator; Role in RNA Polymerase Recruitment		
At3g04790	*EMB3119*		Embryo Defective	Moderate	Ribulose-5-Phosphate Isomerase; Carbohydrate Metabolism		CPT Localized (4)
At3g04870	*PDE181*	*SPC1; ZDS*	Pigment Defective Embryo	Moderate	Zeta Carotene Desaturase; Carotenoid Biosynthesis		CPT Localized (4)
At3g05000	*TGD8*		Pollen Tube Growth Defective	Unique	Transport Protein Particle Component; Vesicle Transport		
At3g05040	*HST*	*HST1*	Hasty	Unique	Nucleocytoplasmic Transport Receptor		
At3g05200	*ATL6*		Arabidopsis Toxicos En Levadura	High			
At3g05530	*RPT5a*		Regulatory Particle	High	Proteasome AAA-ATPase		
At3g05630	*PLDP2*	*PDLZ2*	Phospholipase D {zeta}	High			
At3g05680	*EMB2016*		Embryo Defective	Unique	Unknown		

At3g05770	*PGD8*		Pollen Germination Defective	High	Unknown		
At3g06120	*MUTE*		Mute	Moderate			
At3g06350	*EMB3004*	*MEE32*	Embryo Defective	Unique	Dehydroquinate Dehydratase; Shikimate Dehydrogenase; Chorismate Biosynthesis		CPT Localized (3)
At3g06370	*NAX4*		Na+/H+ Exchanger	High			
At3g06400	*CHR11*		Chromatin Remodeling Factor	High	Chromatin-Remodeling Protein		
At3g06430	*EMB2750*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At3g06490	*MYB108*	*BOS1*	MYB Domain Protein	High			
At3g06510	*SFR2*		Sensitive to freezing	Moderate			Not Evaluated
At3g06560	*PAPS3*		Poly(A) Polymerase	High	Cytoplasm localized; mRNA 3' End Formation		
At3g06730	*TRXP*	*TRXZ*	Thioredoxin Putative Plastidic	Unique	Chloroplast Thioredoxin		CPT Localized (3)
At3g06810	*IBR3*		IBA-Response	Unique	Peroxisomal Acyl-CoA Dehydrogenase		
At3g06860	*MFP2*		Multifunctional Protein	High			
At3g06910	*ELS1*	*ULP1A*	ESD4-Like SUMO Protease	High			Not Evaluated
At3g06960	*PDE320*		Pigment Defective Embryo	Moderate	Uncertain; Lipid Transport Between ER and Plastid		
At3g07020	*UGT80A2*		UDP-Glucose:Sterol Glucosyltransferase	Moderate			

At3g07040	*RPM1*	*RPS3*	Resistance to P. syringae pv. maculicola	Moderate			
At3g07060	*EMB1974*		Embryo Defective	Unique	Unknown		
At3g07100	*Sec24A*	*G92; ERMO2*		Moderate			
At3g07130	*PAP15*		Purple Acid Phosphatase	High			
At3g07160	*AtGSL10*		Glucan Synthase-Like	High	Callose Synthesis		
At3g07430	*EMB1990*		Embryo Defective	Moderate	Uncertain; Integral Membrane, Chloroplast Division Protein		CPT Localized (2)
At3g07525	*ATG10*		Autophagy	Unique	E2-Conjugating Enzyme; Role in Vesicle Trafficking to Vacuole		
At3g07560	*PEX13*	*APM2*	Peroxin	Unique	Peroxisomal Protein Transport		
At3g07610	*IBM1*		Increase in Bonsai Methylation	Moderate			
At3g07650	*COL9*		Constans-Like	High			
At3g07970	*QRT2*		Quartet	High			
At3g08010	*AtAB2*		Arabidopsis TAB2	Unique	RNA Binding Protein; Putative PPR Protein		CPT Localized (4)
At3g08040	*FRD3*	*MAN1*	Ferric Reductase Defective	High			
At3g08550	*KOB1*	*ABI8; ELD1*	Kobito	High			
At3g08710	*TRXH9*	*TH9*	Thioredoxin	Moderate	Plasma Membrane Thioredoxin; Putative Role in Cell-to-Cell Signaling		Not Evaluated
At3g08720	*S6K2*	*PK2; PK19*	P70 Ribosomal S6 Kinase	High			Not Evaluated

At3g08850	*RAPTOR1*	*RAPTOR1b*	Raptor	High	Binding Partner of Target of Rapamycin (TOR) Kinase; Signal Transduction		
At3g08950	*HCC1*		Homolog of the Copper Chaperone SCO1	Moderate	Mitochondrial Chaperone; Cytochrome C Oxidase Assembly	MIT Localized (4)	Not Evaluated
At3g08970	*AtERdj3A*	*TMS1*		Unique	ER DnaJ Domain Protein; Disulfide Isomerase; Molecular Chaperone		
At3g09090	*DEX1*		Defective in Exine Patterning	Unique	Unknown; Plant-Specific Membrane Protein with Calcium Binding Domains		
At3g09150	*HY2*	*GUN3*	Elongated Hypocotyl	Unique	Phytochromobilin Synthase; Ferredoxin-Dependent Biliverdin Reductase		CPT Localized (2)
At3g09260	*PYK10*	*PSR3.1; BGLU23*		High			
At3g09840	*CDC48*	*CDC48A*	Cell Division Cycle	High	AAA-ATPase Chaperone		
At3g10220	*EMB2804*		Embryo Defective	Unique	Tubulin Folding Cofactor B; Microtubule Polymerization		
At3g10370	*SDP6*		Sugar Dependent	Unique	Mitochondrial FAD-G3P Dehydrogenase; Role in Gluconeogenesis / Glycerol Catabolism	MIT Localized (1)	
At3g10380	*SEC8*		Subunit of Exocyst Complex	Unique	Plasma Membrane Vesicle Docking		

At3g10400	*U11/U12-31K*			Unique	U12-Type Spliceosomal Protein		Not Evaluated
At3g10420	*SPD1*		Seedling Plastid Development	High			Not Evaluated
At3g10570	*CYP77A6*		Cytochrome P450	High			
At3g10670	*AtNAP7*		Non-Intrinsic ABC Protein	Unique	Plastidic SufC-Like ABC/ATPase; Fe-S Cluster Maintenance and Repair		CPT Localized (4)
At3g10690	*AtGYRA*		DNA Gyrase	Unique	DNA Gyrase Subunit A; Replication and Transcription in Chloroplasts and Mitochondria	MIT Localized (1)	CPT Localized (4)
At3g10800	*BZIP28*			High			
At3g10870	*MES17*		Methyl Esterases	Moderate			
At3g10960	*AZG1*		AZA-Guanine Resistant	High			
At3g11050	*AtFER2*		Ferritin	Moderate			
At3g11170	*FAD7*	*FADD*	Fatty Acid Desaturase	High	Chloroplast Omega 3 Fatty Acid Desaturase		CPT Localized (4)
At3g11220	*ELO1*	*ELP4*	Elongata	Unique	Histone Acetyl Transferase Complex Subunit		
At3g11410	*PP2CA*	*AHG3*	Protein Phosphatase	Moderate			
At3g11430	*GPAT5*		Glycerol-3-Phosphate Acyltransferase	High			
At3g11480	*BSMT1*			High			Not Evaluated

At3g11540	*SPY*		Spindly	Moderate	O-Linked N-Acetylglucosamine Transferase; Role in Gibberellin Signaling		
At3g11670	*DGD1*		Digalactosyl Diacylglycerol Deficient	Moderate	Digalactosyl Diacylglycerol Synthase; Thylakoidal Galactolipid Biosynthesis		CPT Localized (0)
At3g11820	*SYP121*	*SYR1; PEN1*	Syntaxin of Plants	Moderate			
At3g11940	*AML1*	*RPS5A*	Arabidopsis Minute-Like	High	Cytosolic Ribosomal Protein S5		
At3g11980	*MS2*	*FAR2*	Male Sterile	High			
At3g12080	*EMB2738*	*ENGA*	Embryo Defective	Moderate	Uncertain; Putative Ribosome Biogenesis GTPase		CPT Localized (4)
At3g12120	*FAD2*		Fatty Acid Desaturase	Moderate			
At3g12160	*RABA4D*		Rab GTPase Homolog	High	Rab GTPase; Membrane Trafficking		
At3g12280	*Rb*	*RBR*	Retinoblastoma	Unique	Repressor of cell proliferation		
At3g12360	*ITN1*		Increased Tolerance to NaCl	High			
At3g12380	*ARP5*		Actin Related Protein	Unique	Chromatin Remodeling Complex Subunit		
At3g12400	*ELC*		ELCH	High			
At3g12490	*CYS6*	*CYSB*	Phytocystatin	Moderate			
At3g12670	*EMB2742*		Embryo Defective	High	CTP Synthase; UTP-Ammonia Ligase; Ribonucleotide Metabolism		

At3g12810	*PIE1*		Photoperiod-Independent Early Flowering	Moderate			
At3g13065	*SRF4*		Strubbelig-Receptor Family	High			
At3g13170	*AtSPO11-1*			Moderate			
At3g13200	*EMB2769*	*CWC15*	Embryo Defective	Unique	U5 Associated Protein; Putative Role in Pre-mRNA Splicing		
At3g13220	*ABCG26*	*WBC27*	ATP-Binding Cassette	High			Not Evaluated
At3g13300	*VCS*		Varicose	High			
At3g13490	*OVA5*		Ovule Abortion	High	Amino Acyl tRNA Synthetase (Lysine)	MIT Localized (2)	
At3g13540	*MYB5*		MYB Domain Protein	Moderate			
At3g13550	*COP10*	*FUS9;* *CIN4;* *EMB144*	Constitutive Photomorphogenesis	Moderate			
At3g13870	*RHD3*		Root Hair Defective	High			
At3g13890	*AtMYB26*	*MS35*	MYB Domain Protein	Moderate			
At3g14110	*FLU*		Fluorescent in Blue Light	Unique	TPR Protein; Negative Regulator of Tetrapyrrole Biosynthesis		CPT Localized (4)
At3g14210	*ESM1*		Epithiospecifier Modifier	High			
At3g14230	*AtRAP2.2*			High			
At3g14270	*FAB1B*			High			
At3g14370	*WAG2*			High			

At3g14440	*NCED3*	*STO1, SIS7*	Nine-Cis-Epoxycarotenoid Dioxygenase	High	ABA Biosynthesis; Cleavage of 9-Cis-Epoxycarotenoids		CPT Localized (4)
At3g14900	*EMB3120*		Embryo Defective	Unique	Unknown		CPT Localized (2)
At3g15150	*AtMMS21*	*HPY2*	Methyl Methane Sulfonate Sensitivity	Unique	SUMO E3 Ligase; DNA Damage Repair		
At3g15170	*CUC1*	*ANAC054; AtNAC1*	Cup-Shaped Cotyledon	Moderate			
At3g15390	*SDE5*		Silencing Defective	Unique	Putative mRNA Export Factor		
At3g15500	*ANAC055*	*NAC3*	Arabidopsis NAC Domain Containing Protein	High			
At3g15620	*UVR3*		UV Repair Defective	Moderate	6-4 Photolyase; Pyrimidine Dimer Repair		
At3g15730	*PLDA1*		Phospholipase	High			
At3g15820	*ROD1*	*PDCT*	Reduced Oleate Desaturation	High			
At3g15850	*FAD5*	*FADB*	Fatty Acid Desaturase	High	Palmitate-Specific Monogalactosyldiacylglycerol Desaturase		CPT Localized (2)
At3g15950	*NAI2*			High			
At3g15990	*SULTR3;4*		Sulfate Transporter	High			Not Evaluated
At3g16290	*EMB2083*		Embryo Defective	Moderate	FtsH Protease; AAA ATPase; Chloroplast ATP-Dependent Zinc Metalloprotease		CPT Localized (4)
At3g16630	*KINESIN-13A*			Moderate			

At3g16640	*TCTP*		Translationally Controller Tumor Protein	Moderate	GTPase; TOR Signaling Pathway		
At3g16720	*ATL2*		Arabidopsis Toxicos En Levadura	Moderate			
At3g16857	*ARR1*		Arabidopsis Response Regulator	High			
At3g16890	*PPR40*		Pentatricopeptide (PPR) Domain Protein	Moderate	Uncertain; Role in Mitochondrial Complex III Function	MIT Localized (1)	
At3g16910	*ACN1*	*AAE7*	Ac Non-Utilizing	High			
At3g16950	*ptLPD1*	*LPD1*	Lipoamide Dehydrogenase	High			Not Evaluated
At3g17170	*RFC3*		Regulator of Fatty-Acid Composition	Unique	Plastid Ribosomal Protein S6-Like Protein		CPT Localized (2)
At3g17300	*EMB2786*		Embryo Defective	Unique	Unknown; Complex 1 (LYR Domain) Protein		
At3g17390	*MTO3*	*SAMS3*	Methionine Over-Accumulation	High			
At3g17609	*HYH*		HY5-Homolog	Unique	bZIP Transcription Factor		
At3g17650	*PDE321*	*YSL5*	Pigment Defective Embryo	High	OPT Transporter; Putative Role in Heavy Metal Transport		
At3g17910	*EMB3121*		Embryo Defective	Moderate	Cytochrome C Oxidase Assembly in Mitochondria	MIT Localized (1)	
At3g18110	*EMB1270*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		
At3g18165	*MOS4*		Modifier of snc1, 4	Unique	Unknown		

At3g18290	*EMB2454*	*BTS*	Embryo Defective	Moderate	Zinc Finger Protein; Putative Transcription Factor		CPT Localized (1)
At3g18390	*EMB1865*	*CRS1*	Embryo Defective	Moderate	Chloroplast Intron Splicing Factor		CPT Localized (2)
At3g18440	*AtALMT9*		Aluminum-Activated Malate Transporter	High			
At3g18630	*UNG*		Uracil DNA Glycosylase	Moderate			Not Evaluated
At3g18660	*GUX1*	*PGSIP1*	Glucuronic Acid Substitution of Xylan	Moderate			Not Evaluated
At3g18680	*DPT1*		Defect in PsaA/B Transcript Accumulation	Moderate	Uncertain		CPT Localized (4)
At3g18690	*MKS1*		MAP Kinase Substrate	Unique	Nuclear Factor in MAP Kinase Signaling Cascade		Not Evaluated
At3g18730	*TSK*	*BRU1; MGO3*	Tonsoku	Unique	LGN Repeat Protein; Putative role in DNA repair and epigenetic gene silencing		
At3g18780	*ACT2*	*DER1; ENL2; LSR2*	Actin	High			
At3g18990	*VRN1*	*REM39*	Reduced Vernalization Response	Moderate			
At3g19040	*HAF2*	*TAF1, TAF1b*	Histone Acetyltransferase of the TAFII250 Family	High			
At3g19170	*PreP1*		Presequence Protease	High	Zinc Metallooligopeptidase	MIT Localized (2)	CPT Localized (5)

At3g19180	*CDP1*	*PARC6*	Chloroplast Division Site Positioning	Unique	Unknown; Role in Chloroplast Division		CPT Localized (2)
At3g19210	*AtRAD54*	*CHR25*	Homolog of RAD54	Moderate			
At3g19220	*CYO1*	*SCO2*	Shi-Yo-U Means Cotyledon in Japanese	Unique	DnaJ Protein; Chaperone Activity		CPT Localized (2)
At3g19570	*SCO3*	*QWRF1*	Snowy Cotyledon	High			Not Evaluated
At3g19580	*AZF2*		Arabidopsis Zinc Finger Protein	Moderate			Not Evaluated
At3g19590	*Bub3.1*			High	Spindle Checkpoint Protein		
At3g19700	*IKU2*		Haiku	High	LRR Kinase		
At3g19710	*BCAT4*		Branched-Chain Aminotransferase	High			
At3g19720	*ARC5*		Accumulation and Replication of Chloroplast	Moderate	Cytosolic Dynamin-Like GTPase; Chloroplast Division Machinery Component		
At3g19770	*AtVPS9A*		Vacuolar Protein Sorting	High	Rab5 Guanine Exchange Factor; Proposed Role in Endocytosis		
At3g19820	*DWF1*	*DIM; CBB1; EVE1*	Dwarf	Unique	FAD-Binding Domain Protein; Brassinosteroid Biosynthesis		
At3g19980	*EMB2736*		Embryo Defective	High	Serine/Threonine Protein Phosphatase 6; Putative Role in Cell Cycle Control		
At3g20070	*TTN9*		Titan	Unique	Unknown		
At3g20320	*TGD2*		Trigalactosyldiacylglycerol	Unique	Phosphatidic Acid Binding Protein; Lipid Trafficking		CPT Localized (4)

At3g20400	*EMB2743*		Embryo Defective	Unique	Uncertain; Potential F Box Protein		
At3g20440	*EMB2729*	*BE1*	Embryo Defective	Moderate	1,4-Alpha-Glucan Branching Enzyme; Starch Debranching Enzyme		CPT Localized (2)
At3g20470	*GRP5*		Glycine Rich Protein	Unique	Vacuolar Glycine-Rich Protein		
At3g20475	*MSH5*		MUTS-Homologue	Moderate	Uncertain Role in Meiotic Recombination		
At3g20550	*DDL*		Dawdle	Unique	RNA Binding Protein; miRNA and siRNA Biogenesis		
At3g20600	*NDR1*		Non Race-Specific Disease Resistance	High			
At3g20630	*TTN6*	*PER1; UBP14*	Titan	Unique	UBP14 Deubiquitinating Enzyme; Ubiquitin Processing and Recycling		
At3g20740	*FIE*	*FIS3*	Fertilization Independent Endosperm	Unique	WD Polycomb Protein; Chromatin Structure Modulation		
At3g20770	*EIN3*		Ethylene Insensitive	High			
At3g20780	*BIN3*	*TOP6B; HYP6; RHL3*	Brassinosteroid Insensitive	Unique	Topoisomerase; Role in Transcription		
At3g20810	*JMJ30*	*JMJD5*	Jumonji Domain Containing	Unique	Histone Demethylase; Chromatin Remodeling		Not Evaluated
At3g20840	*PLT1*		Plethora	High			
At3g20870	*ZTP29*		Zinc Transporter	Unique	Putative Zinc Transporter		Not Evaluated
At3g21070	*NADK1*		NAD Kinase	Moderate	NADH Kinase; NADPH Synthesis		

At3g21150				Unique	B-Box Type Zinc Finger Transcription Factor		
At3g21200	*PGR7*		Proton Gradient Regulation	Unique	Chloroplast Protein; Unknown Function		Not Evaluated
At3g21560	*UGT84A2*	*BRT1*	UDP-Glucosyl Transferase	High			
At3g21630	*CERK1*	*LysM RLK1*	Chitin Elicitor Receptor Kinase	Moderate			
At3g21640	*UCU2*	*TWD1*	Ultracurvata	Moderate	SHAGGY/GSK3-Like Kinase; Auxin and Brassinosteroid Signaling		
At3g22170	*FHY3*		Far-Red Elongated Hypocotyls	High			
At3g22200	*POP2*	*GABA-T; HER1*	Pollen-Pistil Incompatibility	Moderate	GABA Transaminase; GABA Degradation	MIT Localized (5)	
At3g22370	*AOX1A*		Alternative Oxidase	High	Alternative Oxidase	MIT Localized (5)	
At3g22380	*TIC*		Time for Coffee	Unique	Clock Gene Circuit Regulator		
At3g22400	*LOX5*		Lipoxygenase	High			
At3g22590	*CDC73*	*PHP*	Cell Division Cycle	Unique	RNA Polymerase II-Associated Complex Subunit		Not Evaluated
At3g22680	*RDM1*		RNA-Directed DNA Methylation	Unique	RdDM Effector Complex Subunit; Putative Role in Linking siRNA and DNA Methylation		Not Evaluated
At3g22780	*TSO1*		Tso	High			
At3g22880	*DMC1*	*ARLIM15;*	Homolog of Yeast DMC 1	High			

At3g22942	*AGG2*		G-Protein Gamma Subunit	Unique	G-Protein Complex Subunit; Regulator of Auxin Transport		
At3g22990	*LFR*		Leaf and Flower Related	Unique	Unknown; Nuclear Armadillo-Repeat Protein		
At3g23050	*AXR2*	*IAA7*	Auxin Resistant	High			
At3g23110	*EMB2800*	*AtRLP37*	Embryo Defective	High	LRR Protein; Putative Signaling Function		
At3g23130	*SUP*	*FLO10; FON1*	Superman	Unique	Zinc Finger, Leucine Zipper Transcription Factor		
At3g23150	*ETR2*		Ethylene Receptor	High			
At3g23400	*FIB4*		Fibrillin	Unique	Fibrillin; Role in the Regulation of Plastoglobule Content		Not Evaluated
At3g23430	*PHO1*		Low Inorganic Phosphate	High			
At3g23440	*EDA6*	*MEE46*	Embryo Sac Development Arrest	Unique	Unknown		
At3g23560	*ALF5*		Aberrant Lateral Root Formation	High			
At3g23820	*GAE6*		UDP-D-Glucuronate 4-Epimerase	Moderate			Not Evaluated
At3g23980	*BLI*	*KOS1*	Blister	Unique	Uncertain; Nuclear Coiled-Coil SMC-Domain Protein		Not Evaluated
At3g24140	*FAMA*		FAMA	Moderate			
At3g24220	*NCED6*		Nine-Cis-Epoxycarotenoid Dioxygenase	High	ABA Biosynthesis; Cleavage of 9-Cis-Epoxycarotenoids		CPT Localized (2)
At3g24260	*SEP3*	*AGL9*	Sepallata	Moderate	MADS-Box Transcription Factor		

At3g24320	*MSH1*	*CHM1*	MUTL Protein Homolog	Unique	Putative Role in Mitochondrial Genome Replication	MIT Localized (4)	
At3g24560	*RSY3*		Raspberry	Unique	Uncertain; ATP Binding Motif Protein		
At3g24590	*PLSP1*		Plastidic Type I Signal Peptidase	Moderate	Plastidic Type1 Signal Peptidase		CPT Localized (3)
At3g24650	*ABI3*	*SIS10*	ABA Insensitive	Moderate			
At3g25100	*CDC45*		Cell Division Cycle	Unique	Uncertain Role During Meiosis		
At3g25140	*QUA1*	*GAUT8*	Quasimodo	High			
At3g25230	*ROF1*	*FKBP62*	Rotamase FKBP	High			
At3g25250	*OXI1*		Oxidative Signal-Inducible	High			
At3g25520	*ATL5*	*PGY3;* *OLI5;* *RPL5A*	Arabidopsis thaliana Ribosomal Protein L5	High			
At3g25690	*CHUP1*		Chloroplast Unusual Positioning	Moderate	Actin-Binding Chloroplast Outer Membrane Protein		CPT Localized (4)
At3g25860	*PLE2*		Plastid E2 Subunit of Pyruvate Decarboxylase	Moderate	Chloroplast Pyruvate Decarboxylase E2 Subunit; Acetyl-CoA Formation		CPT Localized (4)
At3g26090	*RGS1*		Regulator of G-Protein Signaling	Unique	Regulator of G-Protein Signaling; Plasma Membrane Glucose Sensor		
At3g26410	*TRM11*		tRNA Modification	Unique	tRNA Modification Protein		Not Evaluated
At3g26420	*AtRZ-1a*			Unique	Zinc Finger-Containing Glycine-Rich RNA-Binding Protein		

At3g26570	*PHT2;1*	*ORF02*	Phosphate Transporter	Unique	Plastid Phosphate Transporter; Phosphorus Metabolism		CPT Localized (4)
At3g26680	*SNM1*		Sensitive to Nitrogen Mustard	Moderate			
At3g26744	*ICE1*	*SCRM*	Inducer of CBF Expression	High			
At3g26790	*FUS3*		Fusca	Moderate	B3 Domain Transcription Factor		
At3g26830	*PAD3*		Phytoalexin Deficient	High			
At3g26900	*SKL1*		Shikimate Kinase Like	Unique	Uncertain; Shikimate Kinase-Like		CPT Localized (4)
At3g27000	*ARP2*	*WRM*	Actin Related Protein	High			
At3g27060	*TSO2*		TSO Meaning 'Ugly' in Chinese	High			
At3g27160	*GHS1*		Glucose Hypersensitive	Unique	Chloroplast Ribosomal Protein S21		CPT Localized (4)
At3g27460	*SGF29A*		SAGA Associated Factor	High			Not Evaluated
At3g27530	*MAG4*	*GC6*	Maigo	Unique	Golgi-Localized Tethering Factor; Transport of Storage Protein Precursors from ER to Golgi		Not Evaluated
At3g27660	*OLEO4*	*OLE3*	Oleosin	Moderate			
At3g27670	*RST1*		Resurrection	Unique	Unknown; Cuticular Wax Formation		
At3g27730	*RCK*	*MER3*	Rock-N-Rollers	Moderate			
At3g27740	*VEN6*	*CarA*	Venosa	Unique	Carbamoyl Phosphate Synthetase Subunit; Arginine Biosynthesis		Not Evaluated

At3g27750	*EMB3123*		Embryo Defective	Unique	Uncertain; VPS9 Domain Protein		CPT Localized (2)
At3g27810	*AtMYB21*	*MYB3*	MYB Domain Protein	Moderate			
At3g27820	*MDAR4*		Monodehydroascorbate Reductase	High			
At3g27920	*GL1*	*MYB0*	Glabra	Moderate			
At3g28030	*UVH3*	*UVR1*	Ultraviolet Hypersensitive	Unique	Putative Endonuclease; Role in Nucleotide Excision Repair		
At3g28470	*TDF1*	*AtMYB35*	Defective in Tapetal Development and Function	Moderate			
At3g28730	*SSRP1*	*HMG; NFD*		Unique	FACT Complex Subunit; Facilitator of Transcription through Destabilization of Nucleosomes		
At3g28860	*PGP19*	*ABCB19; MDR1; MDR11; MDL15.2*	P-Glycoprotein	High			
At3g28910	*MYB30*		MYB Domain Protein	High			
At3g29030	*EXPA5*		Expansin	High			
At3g29290	*EMB2076*		Embryo Defective	Unique	PPR Protein; Organellular mRNA Processing		
At3g29320	*PHS1*		Alpha-Glucan Phosphorylase	High	Plastidial Alpha-Glucan Phosphorylase; Drought Tolerance		CPT Localized (4)
At3g30180	*BR6OX2*	*CYP85A2*	Brassinosteroid-6-Oxidase	High			

At3g33520	*AtARP6*	*SUF3; ESD1*	Actin-Related Protein	Moderate			
At3g42170	*DAYSLEEPER*		Daysleeper	Moderate	hAT Transposase		
At3g43210	*TES*	*STD*	Tetraspore	High			
At3g43300	*AtMIN7*		HopM Interactor	High			
At3g44110	*J3*		DNAJ Homolog	High			Not Evaluated
At3g44200	*NEK6*		NIMA (Never In Mitosis, Gene A)-Related	Moderate			
At3g44260	*AtCAF1a*		CCR4 Associated Factor	High			
At3g44310	*NIT1*		Resistant to Indole-3-Acetonitrile	High			
At3g44480	*RPP1*	*COG1; RPP10*	Recognition of Peronospora parasitica	High			
At3g44530	*HIRA*		Arabidopsis Ortholog of Hira	Moderate	Chromatin Remodeling Factor; Putative Histone Chaperone		
At3g44540	*FAR4*		Fatty Acid Reductase	High			Not Evaluated
At3g44550	*FAR5*		Fatty Acid Reductase	High			Not Evaluated
At3g44880	*ACD1*	*LLS1; PaO*	Accelerated Cell Death	Moderate	Pheophorbide A Oxygenase; Chlorophyll Breakdown		CPT Localized (4)
At3g45100	*SETH2*			Unique	GPI Anchor Biosynthesis		
At3g45130	*LAS1*		Lanosterol Synthase	High			
At3g45140	*LOX2*		Lipoxygenase	High	Lipoxygenase; Jasmonic Acid Biosynthesis		CPT Localized (4)

At3g45150	*TCP16*		TCP Domain Protein	Unique	Putative Transcription Factor		
At3g45300	*AtIVD*		Isovaleryl-CoA Dehydrogenase	Moderate	Putative Isovaleryl-CoA Dehydrogenase; Leucine and Valine Catabolism	MIT Localized (6)	
At3g45640	*AtMPK3*		Mitogen-Activated Protein Kinase	High			
At3g45780	*NPH1*	*RPT1*	Non-Phototropic Hypocotyl	Moderate			
At3g45890	*RUS1*		Root UV-B Sensitive	Moderate	Unknown; Role in UV light perception		CPT Localized (2)
At3g46530	*RPP13*	*RPP11*	Recognition of Peronospora parasitica	High			
At3g46550	*SOS5*		Salt Overly Sensitive	Unique	Putative Cell Surface Adhesion Protein		
At3g46560	*EMB2474*	*TIM9*	Embryo Defective	Unique	Small Zinc Finger-Like Protein; Component of Mitochondrial Protein Import Apparatus	MIT Localized (1)	
At3g46640	*PCL1*	*LUX*	Phytoclock	Moderate			
At3g46740	*TOC75*	*AtTOC75-III*	Translocon at outer envelope membrane of chloroplasts	Moderate	Chloroplast Import Protein; Protein Translocation at the Inner Envelope of Chloroplasts		CPT Localized (4)
At3g46790	*CRR2*		Chlororespiratory Reduction	High	PPR Protein; Intergenic Processing of Chloroplast RNA		CPT Localized (3)
At3g46970	*PHS2*		Alpha-Glucan Phosphorylase	High			

At3g47390	*PHS1*		Photosensitive	Unique	Deaminase–Reductase Domain Protein; Role in Riboflavin Pathway		Not Evaluated
At3g47440	*TIP5;1*		Tonoplast Intrinsic Protein	Moderate	Pollen Aquaporin; Water and Urea Transport	MIT Localized (4)	Not Evaluated
At3g47450	*NOA1*	*NOS1; RIF1*	Nitric Oxide Associated	Unique	Chloroplast GTPase; Ribosome Function		CPT Localized (3)
At3g47500	*CDF3*	*HPPBF-2a*	Cycling Dof Factor	High			
At3g47620	*AtTCP14*		Teosinte Branched1, Cycloidea and PCF	Moderate			
At3g47690	*AtEB1a*		End Binding	High			
At3g47710	*BNQ3*	*bHLH161*	Banquo	Unique	bHLH Transcription Factor		Not Evaluated
At3g47860	*CHL*		Chloroplastic Lipocalin	Unique	Chloroplastic Lipocalin; Role in Protection from Oxidative Stress		CPT Localized (4)
At3g47870	*SCP*	*ASL29*	Sidecar Pollen	Unique	Nuclear LOB/AS2 Domain Protein		Not Evaluated
At3g47930	*AtGLDH*		L-Galactono-1,4-Lactone Dehydrogenase	Unique	Ascorbate Biosynthesis	MIT Localized (5)	
At3g47950	*AHA4*		Arabidopsis Plasma Membrane H+ ATPase	High			
At3g47990	*SIS3*		Sugar Insensitive	Unique	RING Finger Protein; Positive Regulator of Sugar Signaling		Not Evaluated
At3g48090	*EDS1*		Enhanced Disease Susceptibility	High			
At3g48100	*ARR5*	*IBC6*	Arabidopsis Response Regulator	Moderate			

At3g48110	*EDD*		Embryo Defective Development	Unique	Chloroplast Glycyl tRNA Synthetase		CPT Localized (5)
At3g48160	*DEL1*	*E2L3; E2Fe*	DP-E2F-Like 1	Moderate			
At3g48190	*ATM*		Ataxia-Telangiectasia Mutated	Moderate	Protein Kinase; DNA Damage Signaling		
At3g48250	*BIR6*		Buthionine Sulfoximine-Insensitive Roots	Moderate	PPR Protein; Splicing of Mitochondrial NAD7 Transcript	MIT Localized (0)	Not Evaluated
At3g48360	*BT2*		BTB and TAZ Domain Protein	High			
At3g48430	*REF6*		Relative of Early Flowering	Moderate			
At3g48470	*EMB2423*		Embryo Defective	Unique	Uncertain		
At3g48500	*PDE312*	*PTAC10*	Pigment Defective Embryo	Unique	Uncertain; Putative Role in Plastid Gene Expression		CPT Localized (1)
At3g48670	*IDN2*		Involved in De Novo	High			
At3g48690	*AtCXE12*		Carboxyesterase	High			
At3g48750	*CDC2*	*CDC2A; CDC2AAT; CDK2; CDKA;1*	Cell Division Control	High	Cyclin-Dependent Kinase; Division of Generative Cell in Pollen		
At3g48930	*EMB1080*		Embryo Defective	Moderate	Cytosolic Ribosomal Protein S11		
At3g49170	*EMB2261*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At3g49180	*RID3*		Root Initiation Defective	Unique	Unknown; WD40 Domain Protein		

At3g49240	*EMB1796*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing	MIT Localized (2)	CPT Localized (1)
At3g49250	*DMS3*	*IDN1*	Defective in Meristem Silencing	Moderate	RNA-Directed DNA Methylation		
At3g49500	*SGS2*	*SDE1*	Suppressor of Gene Silencing	High			
At3g49600	*UBP26*		Ubiquitin-Specific Protease	Unique	Ubiquitin-Specific Protease		
At3g49660	*AtMUT11*		Arabidopsis MUT11 Homolog	High	Subunit of Histone Methyltransferase Complex; Heterochromatin Maintenance		
At3g49700	*ACS9*	*ETO3*	Aminocyclopropane Carboxylate Synthase	High			
At3g49940	*LBD38*		LOB Domain-Containing Protein	High			
At3g50060	*MYB77*		MYB Domain Protein	Moderate			
At3g50500	*SnRK2.2*	*SPK-2-2; SRK2D*	SNF1-Related Protein Kinase	High			
At3g50660	*DWF4*	*CLM; SAV1; SNP2*	Dwarf	High			
At3g50820	*PsbO2*	*OEC; PsbO-2*	Photosystem II Subunit	High			
At3g50870	*MNP*	*GATA18; HAN*	Monopole	Moderate	GATA Factor Transcriptional Regulator		
At3g51060	*STY1*	*SRS1*	Stylish	Moderate			
At3g51160	*MUR1*	*GMD2*	Cell Wall Mutant	High			
At3g51240	*TT6*	*F3H*	Transparent Testa	Moderate			

At3g51460	*RHD4*		Root Hair Defective	High			
At3g51550	*FER*	*SIR*	Feronia	High	Plasma-Membrane Localized Receptor-Like Kinase		
At3g51770	*ETO1*		Ethylene Overproducer	High			
At3g51780	*AtBAG4*		BCL-2-Associated Athanogene	Moderate			
At3g51820	*PDE325*	*CHLG; ATG4*	Pigment Defective Embryo	Unique	Chlorophyll Synthase; Chlorophyll Biosynthesis		CPT Localized (4)
At3g51840	*ACX4*		Acyl-CoA Oxidase	Moderate	Acyl-CoA Oxidase		
At3g51860	*CAX3*	*CAX1-LIKE; AtHCX1*	Cation Exchanger	High			
At3g51970	*ASAT1*		Acyl-CoA Sterol Acyl Transferase	Moderate			
At3g52115	*AtGR1*	*AtCOM1*	Gamma Response Gene	Unique	DNA DSB Repair		
At3g52180	*SEX4*	*AtPTPKIS1; DSP4*	Starch-Excess	Moderate	Phosphoglucan Phosphatase; Starch Breakdown		CPT Localized (4)
At3g52190	*PHF1*		Phosphate Transporter Traffic Facilitator	Unique	SEC12-Related Plant-Specific Protein; Phosphate Transport		
At3g52280	*GTE6*		General Transcription Factor Group E6	Moderate			
At3g52380	*PDE322*	*CP33*	Pigment Defective Embryo	Moderate	Chloroplast RNA Binding Protein; Putative Role in Plastid mRNA Stabilization		CPT Localized (3)

At3g52430	*PAD4*		Phytoalexin Deficient	Moderate	Putative Triacyl Glycerol Lipase; Role in Defense Signaling		
At3g52450	*PUB22*		Plant U-Box	High			
At3g52560	*UEV1D-4*	*UEV1D*	Ubiquitin E2 Variant	Moderate			
At3g52590	*EMB2167*	*HAP4; UbA52*	Embryo Defective	Moderate	Ubiquitin Fused to Ribosomal Protein L40		
At3g52770	*ZPR3*		Little Zipper	Unique	Leucine Zipper-Containing Protein; Negative Regulator of HD-ZIP III Activity		
At3g52940	*FK*	*HYD2; ELL*	Fackel	Moderate	Sterol C-14 Reductase; Sterol Biosynthesis		
At3g53020	*STV1*	*RPL24; RPL24B*	Short Valve	Moderate			
At3g53110	*LOS4*	*CRYOPHYTE*	Low Expression of Osmotically Responsive Genes	Moderate			
At3g53130	*LUT1*	*CYP97C1*	Lutein Deficient	High	Cytochrome P450 Monooxygenase; Carotenoid Hydroxylase; Lutein Biosynthesis		CPT Localized (4)
At3g53420	*PIP2;2*		Plasma Membrane Intrinsic Protein	High			Not Evaluated
At3g53480	*ABCG37*	*PIS1; PDR9*	ATP-Binding Cassette	High			Not Evaluated
At3g53720	*AtCHX20*		Cation/H+ Exchanger	High			
At3g53760	*GCP4*		Gamma-Tubulin Complex Protein	Unique	Gamma-Tubulin Complex Protein; Microtubule Array Organization		Not Evaluated

At3g53900	*UPP*		Uracil Phosphoribosyltransferase	Unique	Uracil Phosphoribosyltransferase		CPT Localized (4)
At3g54010	*PAS1*	*DEI1*	Pasticcino	Moderate	Immunophilin-like FK506 Binding Protein; Putative Role in Hormone Signaling		
At3g54050	*HCEF1*		High Cyclic Electron Flow	High			Not Evaluated
At3g54110	*PUMP1*	*UCP1*	Plant Uncoupling Mitochondrial Protein	High	Mitochondrial Inner Membrane Uncoupling Protein; Dissipation of Proton Gradient	MIT Localized (1)	
At3g54170	*FIP37*		FKBP Interacting Protein	Unique	FKBP12 Interacting Protein; Putative Role in Alternative Pre-mRNA Splicing		
At3g54220	*SCR*	*SGR1*	Scarecrow	Moderate			
At3g54280	*RGD3*	*CHA16;* *CHR16;* *BTAF1*	Root Growth Defective	Moderate	TATA-Binding Protein-Associated Factor		
At3g54320	*WRI1*		Wrinkled Seed	Moderate	Transcription Factor; AP2/EREB Domain Protein		
At3g54340	*AP3*		Apetala	Unique	MADS Box Transcription Factor		
At3g54350	*EMB1967*		Embryo Defective	Moderate	Forkhead-Associated Domain Protein; Putative Role in Signal Transduction		
At3g54610	*GCN5*	*BGT;* *HAC3;* *HAG1;* *HAT1*	General Control Non-Repressible	Unique	Histone Acyltransferase		

At3g54640	*TRP3*	*TSA1*	Tryptophan Biosynthesis	High	Tryptophan Synthase Alpha Subunit		CPT Localized (4)
At3g54650	*FBL17*			Unique	F-Box Protein; Division of Generative Cell in Pollen		
At3g54660	*EMB2360*	*AtGR2; GR*	Embryo Defective	High	Glutathione Reductase; Protection Against Oxidative Stress	MIT Localized (2)	CPT Localized (4)
At3g54670	*TTN8*	*SMC1*	Titan	Moderate	Cohesin; Structural Maintenance of Chromosome Protein		
At3g54690	*SETH3*			Unique	Arabinose-5-Phosphate Isomerase		
At3g54720	*AMP1*	*COP2; HPT; PT*	Altered Meristem Program	High	Putative Glutamate Carboxypeptidase; Putative Role in Signaling		
At3g54810	*BME3*	*BME3-ZF*	Blue Micropylar End	Unique	GATA Zinc Finger Transcription Factor		
At3g54870	*MRH2*	*ARK1*	Morphogenesis of Root Hair	Moderate			
At3g54920	*PMR6*		Powdery Mildew Resistant	High			
At3g55010	*EMB2818*	*PUR5; AtPURM*	Embryo Defective	Unique	Phosphoribosylformylglycinamidine Cyclo-ligase; AIR synthetase; Purine Biosynthesis		CPT Localized (4)
At3g55120	*TT5*	*CFI*	Transparent Testa	Moderate			
At3g55130	*AtWBC19*		White-Brown Complex Homolog	High			
At3g55250	*PDE329*		Pigment Defective Embryo	Unique	Uncertain; Similar to Calcium Homeostasis Regulator		CPT Localized (4)

At3g55270	*MKP1*		MAP Kinase Phosphatase	Unique	MAP Kinase Phosphatase; Stress Signaling		
At3g55360	*CER10*	*ECR; TSC13*	Eceriferum	Unique	Enoyl-CoA Reductase; Very Long Chain Fatty Acid Biosynthesis		
At3g55400	*OVA1*		Ovule Abortion	Moderate	Amino Acyl tRNA Synthetase (Methionine)	MIT Localized (2)	
At3g55480	*PAT2*	*AP-3 BETA*	Protein Affected Trafficking	Unique	Putative Beta-Subunit of the AP-3 Complex; Lytic Vacuole Biogenesis		Not Evaluated
At3g55510	*RBL*		Rebelote	High	Uncertain; Noc2 Domain Protein		
At3g55530	*SDIR1*		Salt- and Drought-Induced RING Finger	Unique	E3 Ubiquitin Ligase		
At3g55610	*P5CS2*		Pyrroline-5-Carboxylate Synthetase	High	Delta 1-Pyrroline-5-Carboxylate Synthetase; Proline Biosynthesis		CPT Localized (2)
At3g55620	*EMB1624*	*EIF-6*	Embryo Defective	High	Translation Initiation Factor		
At3g55630	*FPGS3*	*DFD*	Folylpolyglutamate Synthetase	High			Not Evaluated
At3g55830	*EPC1*		Ectopically Parting Cells	Unique	Uncertain; GT64 Glycosyltransferase		
At3g55990	*ESK1*		Eskimo	Moderate			
At3g56040	*UGP3*		UDP-Glucose Pyrophosphorylase	Unique	UDP-Glucose Pyrophosphorylase; Sulfolipid Biosynthesis		CPT Localized (3)
At3g56400	*WRKY70*		WRKY DNA-Binding Protein	Moderate			
At3g56800	*CaM3*		Calmodulin	High			

At3g56940	*CHL27*	*CRD1;* *ACSF*		Unique	Chlorophyll Biosynthesis		CPT Localized (4)
At3g56960	*PIP5K4*		Phosphatidyl Inositol Monophosphate 5 Kinase	High			
At3g57040	*ARR9*	*AtRR4*	Arabidopsis Response Regulator	High			
At3g57090	*FIS1A*	*BIGYIN1*	Fission	Moderate	DRP Organelle Anchor Protein; Mitochondria and Peroxisome Division	MIT Localized (1)	
At3g57130	*BOP1*		Blade on Petiole	High			
At3g57150	*AtCBF5*	*AtNAP57*	Centromere Binding Factor	Unique	snoRNP Generation; RNA Processing		
At3g57180	*BPG2*		Brassinazole-Insensitive-Pale Green	Moderate	Chloroplast Zinc Finger GTPase		CPT Localized (4)
At3g57510	*ADPG1*	*PGA9;* *SAC70*	Arabidopsis Dehiscence Zone Polygalacturonase	High			
At3g57650	*LPAT2*		Lysophosphatidyl Acyltransferase	High	Lysophosphatidic Acid Metabolism		
At3g57670	*NTT*		No Transmitting Tract	Moderate			
At3g57860	*OSD1*	*UVI4-L*	Omission of Second Division	Moderate			
At3g57870	*EMB1637*	*SCE1*	Embryo Defective	Unique	SUMO Conjugating Enzyme; Protein Modification		
At3g57920	*SPL15*		Squamosa Promoter Binding Protein-Like	Moderate			
At3g58070	*GIS*		Glabrous Inflorescence Stems	Moderate			

At3g59030	*TT12*		Transparent Testa	High			
At3g59050	*PAO3*		Polyamine Oxidase	High	Peroxisomal Protein; Spermidine Metabolism		Not Evaluated
At3g59060	*PIL6*	*PIF5*	Phytochrome Interacting Factor 3-Like	High			
At3g59220	*PRN*	*PRN1; AtPirin1*	Pirin	High			
At3g59380	*FTA*	*PFT/PGGT-Iα; PLP*	Farnesyltransferase	Unique	Alpha-Subunit of Farnesyltransferase and Geranylgeranyltransferase-I; Meristem Signaling		
At3g59400	*GUN4*		Genomes Uncoupled	Unique	Chlorophyll Synthesis and Intracellular Signaling		CPT Localized (4)
At3g59420	*ACR4*		Arabidopsis Crinkly	High			
At3g59550	*SYN3*	*AtRAD21.2*		Moderate	α-Kleisin Cohesin Protein		
At3g59770	*SAC9*		Supressor of Actin	Moderate	SAC Domain Phosphatase; Phosphoinositide Signaling		
At3g60190	*ADL1E*	*ADL4; ADLP2; DRP1E; EDR3*	Arabidopsis Dynamin-Like	High	Dynamin-Related GTPase; Role in Salicylic Acid Signaling and Programmed Cell Death	MIT Localized (1)	
At3g60330	*AHA7*		Arabidopsis H+ ATPase	High			
At3g60370	*AtFKBP20-2*		FK-506 Binding Protein	Unique	Immunophilin; Peptidyl-Prolyl Isomerase; Protein Folding		CPT Localized (3)
At3g60460	*DUO1*		Duo Pollen	Moderate	R2R3 MYB Transcription Factor		

At3g60500	*CER7*	*G3*	Eceriferum	Moderate				
At3g60740	*TTN1*	*CHO; EMB133*	Titan	Unique	Tubulin Folding Cofactor D; Regulator of Tubulin Folding and Microtubule Dynamics			
At3g60830	*ARP7*		Actin-Related Protein	Moderate	Actin-Related Protein; Proposed Role in Chromatin Remodeling			
At3g61110	*ARS27*		Arabidopsis Ribosomal Protein	Moderate				
At3g61140	*FUS6*	*COP11; EMB78*	Fusca	Unique	Component of COP9 Signalosome; Role in Light-Regulated Signal Transduction and Protein Degradation			
At3g61190	*BAP1*		BON Association Protein	Moderate				
At3g61430	*PIP1;2*		Plasma Membrane Intrinsic Protein	High				Not Evaluated
At3g61440	*CYS-C1*		Cysteine Synthase	High	Mitochondrial β-Cyanoalanine Synthase; Cyanide Detoxification		MIT Localized (5)	Not Evaluated
At3g61510	*ACS1*		Aminocyclopropane Carboxylate Synthase	High				
At3g61710	*ATG6*	*AtVPS30*	Autophagy	Unique	Vacuolar Protein Sorting			
At3g61730	*RMF*		Reduced Male Fertility	High				Not Evaluated
At3g61780	*EMB1703*		Embryo Defective	Moderate	Unknown			CPT Localized (1)
At3g61850	*DAG1*		Dof Affecting Germination	High				
At3g61890	*AtHB-12*	*AtHB12*	Homeobox 12	Moderate				

At3g62030	*ROC4*	*AtCYP20-3*	Rotamase CyP	Moderate	Cyclophilin; Peptidyl Prolyl Isomerase; Protein Folding		CPT Localized (4)
At3g62090	*PIF6*	*PIL2*	Phytochrome Interacting Factor	Moderate			Not Evaluated
At3g62800	*DRB4*		Double-Stranded-RNA-Binding Protein	Moderate			
At3g62910	*APG3*		Albino and Pale Green	Moderate	Cytosolic Translation Releasing Factor RF-1		CPT Localized (3)
At3g62980	*TIR1*		Transport Inhibitor Response	High			
At3g63190	*HFP108*	*RRF*	High Chlorophyll Fluorescence and Pale Green Mutant	Unique	Plastid Ribosome Recycling Factor		Not Evaluated
At3g63250	*HMT2*	*AtHMT-2*	Homocysteine Methyltransferase	High			
At3g63300	*FKD1*		Forked	High			Not Evaluated
At3g63410	*APG1*	*VTE3*	Albino or Pale Green Mutant	Unique	Methylation of Plastoquinone		CPT Localized (4)
At3g63420	*AGG1*		G-Protein Gamma Subunit	Unique	G-Protein Complex Subunit; Regulator of Auxin Transport		
At3g63490	*EMB3126*		Embryo Defective	Moderate	Chloroplast 50S Ribosomal Protein L1		CPT Localized (4)
At3g63520	*CCD1*	*NCED1*	Carotenoid Cleavage Dioxygenase	High			
At3g63530	*BB*	*BB2*	Big Brother	Moderate	E3 Ubiquitin Ligase		
At4g00020	*AtBRCA2a*	*EDA20; MEE43*	Breast Cancer Associated	High	DSB Repair; Homologous Recombination		
At4g00100	*PFL2*	*RPS13A*	Pointed First Leaves	High			

At4g00220	*JLO*		Jagged Lateral Organs	Moderate	LOB Domain Transcription Factor		
At4g00310	*EDA8*	*MEE23*	Embryo Sac Development Arrest	Unique	Unknown		
At4g00330	*PDD25*	*CRCK2*	Pollen Development Defective	Moderate	Calmodulin-Binding Receptor-Like Kinase		
At4g00450	*CRP*	*CCT*	Cryptic Precocious	Unique	Putative Transcriptional Repressor		
At4g00620	*EMB3127*		Embryo Defective	High	Folic Acid Biosynthesis; Vitamin Biosynthesis		CPT Localized (4)
At4g00650	*FRI*	*FLA*	Frigida	Unique	Putative Transcriptional Activator		
At4g00710	*BSK3*		BR-Signaling Kinase	High			
At4g00730	*ANL2*	*AHDP*	Anthocyaninless	High			
At4g00800	*SETH5*			Unique	Putative Vps8 Homolog		
At4g01050	*TROL*		Thylakoid Rhodanese-Like	Unique	Thylakoid Rhodanese-Like Protein; Tethers Ferredoxin:NADP(+) Oxidoreductase to Thylakoid Membrane		
At4g01060	*CPL3*	*ETC3*	Caprice-Like MYB	Unique	R3 MYB-Domain Transcriptional Regulator		
At4g01100	*ADNT1*		Adenine Nucleotide Transporter	Moderate	Mitochondrial Adenine Nucleotide Transporter	MIT Localized (1)	
At4g01190	*PIPK10*		Phosphatidylinositol Phosphate Kinase	High			Not Evaluated
At4g01220	*MGD4*		Male Gametophyte Defective	High	Xylosyltransferase		
At4g01370	*MPK4*		MAP Kinase	High			
At4g01470	*TIP1;3*		Tonoplast Intrinsic Protein	High			Not Evaluated
At4g01500	*NGA4*		Ngatha	Moderate			

At4g01540	*NTM1*		NAC with Transmembrane Motif	Moderate			
At4g01800	*AGY1*	*AtCPSECA*	Albino or Glassy Yellow	Moderate	Thylakoid Protein Translocase; Protein Transport		CPT Localized (4)
At4g02060	*PRL*		Prolifera	Moderate	DNA Replication Licensing Factor; Regulation of Initiation of DNA Replication		
At4g02150	*MOS6*	*IMPA-3*	Modifier of SNC1,6	High			
At4g02195	*SYP42*	*AtTLG2B*	Syntaxin of Plants	High	Transport Vesicle-Membrane Fusion		
At4g02280	*SUS3*		Sucrose Synthase	High			Not Evaluated
At4g02460	*PMS1*		Post Meiotic Segregation	Moderate	DNA Mismatch Repair Protein		
At4g02510	*PPI2*	*TOC159*	Plastid Protein Import	Moderate	Chloroplast Import Protein		CPT Localized (4)
At4g02560	*LD*		Luminidependens	Unique	Putative Transcriptional Regulator		
At4g02570	*AXR6*	*CUL1*	Auxin Resistant	High	Cullin; SCF Ubiquitin Ligase Complex Component		
At4g02700	*SULTR3;2*		Sulfate Transporter	High			Not Evaluated
At4g02780	*GA1*	*ABC33; CPS1*	GA Deficient	Moderate	Ent-Kaurene Synthase; GA Biosynthesis		CPT Localized (2)
At4g02790	*EMB3129*		Embryo Defective	Unique	Uncertain; Putative Ribosome Biogenesis GTPase		CPT Localized (1)
At4g02980	*ABP1*		Auxin Binding Protein	Unique	Auxin Binding Protein; Role in Auxin Signaling		

At4g03110	*RBP-DR1*		RNA-Binding Protein-Defense Related	High			Not Evaluated
At4g03240	*AtFH*		Frataxin	Unique	Frataxin; Biogenesis of Mitochondrial Fe-S Proteins	MIT Localized (4)	
At4g03280	*PGR1*	*PETC*	Proton Gradient Regulation	Unique	Rieske Subunit of Cytochrome b6f Complex; Photosynthetic Electron Transfer		CPT Localized (4)
At4g03430	*EMB2770*	*STA1; PRP6*	Embryo Defective	Moderate	U5 snRNP; Putative Role in Pre-mRNA Splicing		
At4g03550	*AtGSL5*	*PMR4*	Glucan Synthase-Like	High			
At4g03560	*AtTPC1*	*FOU2; AtCCH1*	Two-Pore Channel	Unique	Vacuolar Calcium Channel		
At4g04350	*EMB2369*		Embryo Defective	Unique	Plastid or Cytoplasmic Leucyl tRNA Synthetase		CPT Localized (5)
At4g04720	*CPK21*		Calcium-Dependent Protein Kinase	High			Not Evaluated
At4g04770	*LAF6*	*ABC1; NAP1*	Long After Far-Red Light	High	ABC Transporter; Fe-S Cluster Assembly (SufB)		CPT Localized (5)
At4g04780	*MED21*		Mediator	Unique	Mediator Subunit; Regulator of RNA Polymerase		
At4g04885	*PCFS4*		PCF11P-Similar Protein	Moderate			
At4g05120	*FUR1*	*ENT3*	Fluorouridine Insensitive	High			
At4g05190	*AtK5*		Kinesin	High			
At4g05410	*YAO*		Yaozhe	Moderate	snoRNP Protein; rRNA Biogenesis		

At4g05450	*PGD6*	*MFDX1*	Pollen Germination Defective	High	Mitochondrial Adrenodoxin-Like Ferredoxin	MIT Localized (2)	
At4g05530	*IBR1*	*SDRa*	Indole-3-Butyric Acid Response	Unique	Putative Peroxisomal Oxidoreductase; IAA Biosynthesis		
At4g08150	*BP*	*KNAT1*	Brevipedicellus	Moderate			
At4g08390	*sAPX*		Stromal Ascorbate Peroxidase	Moderate	Stromal Ascorbate Peroxidase; Detoxifies H2O2		CPT Localized (4)
At4g08810	*SUB1*		Short Under Blue Light	High			
At4g08870	*ARGAH2*		Arginine Amidohydrolase	High	Arginine Amidohydrolase; Urea Biosynthesis	MIT Localized (5)	
At4g08900	*ARGAH1*		Arginine Amidohydrolase	High	Arginine Amidohydrolase; Urea Biosynthesis	MIT Localized (1)	
At4g08920	*HY4*	*CRY1; BLU1; OOP2*	Elongated Hypocotyl	High			
At4g08950	*EXO*		Exordium	High			
At4g09020	*ISA3*		Isoamylase	High	Starch Debranching Enzyme		CPT Localized (4)
At4g09080	*TOC75-IV*		Translocon Outer Membrane Complex	High	Protein Translocation Channel in Etioplasts		CPT Localized (2)
At4g09570	*CPK4*		Calcium Dependent Protein Kinase	High			
At4g09650	*PDE332*	*ATPD*	Pigment Defective Embryo	Unique	Chloroplast ATP Synthase Delta Chain		CPT Localized (4)
At4g09820	*TT8*	*BHLH42*	Transparent Testa	Moderate			

At4g09980	*EMB1691*		Embryo Defective	Unique	DNA Methyltransferase; DNA Methylation; Chromatin Structure		
At4g10090	*ELP6*			Unique	Histone Acetyl-Transferase Complex Subunit		
At4g10180	*DET1*	*FUS2*	De-etiolated	Unique	Nuclear-Localized Protein; Role in Light-Regulated Signal Transduction		
At4g10380	*NIP5;1*	*NLM6; NLM8*	Nodulin26-Like Intrinsic Protein	High			
At4g10710	*SPT16*			Moderate			
At4g10760	*EMB1706*	*MTA*	Embryo Defective	Unique	Methyltransferase MT-A70; Pre-mRNA Adenine Methylation		
At4g11130	*RDR2*	*SMD1*	RNA-Dependent RNA Polymerase	High			Not Evaluated
At4g11150	*EMB2448*	*VHAE1; TUF*	Embryo Defective	High	Vacuolar H+ ATPase		
At4g11260	*EDM1*	*SGT1B; ETA3*	Enhanced Downy Mildew Susceptibility	High			
At4g11280	*ACS6*		Aminocyclopropane Carboxylate Synthase	High			
At4g11660	*HsfB2b*		Heat Shock Factor	Moderate			
At4g11720	*HAP2*	*GCS1*	Hapless	Unique	Uncertain; Putative Membrane Protein		
At4g11820	*FKP1*	*HMGS; MVA1*	Flaky Pollen	Unique	3-Hydroxy-3-Methylglutaryl-Coenzyme A Synthase; Isoprenoid Biosynthesis		Not Evaluated

At4g12030	*BASS5*	*BAT5*	Bile Acid:Sodium Symporter Family Protein	High	Bile Acid:Sodium Symporter; Transport of Glucosinolate Intermediates		CPT Localized (2)
At4g12420	*SKU5*		Skewed Root Growth	High			
At4g12470	*AZI1*		Azelaic Acid Induced	Moderate			
At4g12560	*CPR30*		Constitutive Expresser of PR Genes	High			
At4g12570	*UPL5*		Ubiquitin Protein Ligase	Moderate			Not Evaluated
At4g12720	*NUDT7*	*GFG1*	Nudix Hydrolase Homolog	High			
At4g13420	*HAK5*		High Affinity K+ Transporter	High			
At4g13430	*LeuC1*	*MAM-IL1; IPMI; LSU1*		Unique	Leucine Biosynthesis; Methionine Chain Elongation		CPT Localized (4)
At4g13510	*AMT1;1*		Ammonium Transporter	High			
At4g13520	*SMAP1*		Small Acidic Protein	Unique	Unknown; Small Acidic Protein		
At4g13750	*EMB2597*	*NOV*	Embryo Defective	Moderate	Uncertain; Plant-Specific Nuclear Protein		
At4g13770	*CYP83A1*	*REF2*	Cytochrome P450	High			
At4g13890	*EDA36;EDA37*	*PDD4; PDD33*	Embryo Sac Development Arrest	High	Serine Hydroxymethyltransferase		

At4g13940	*EMB1395*	*HOG1; MEE58*	Embryo Defective	High	S-Adenosyl Homocysteine Hydrolase; Amino Acid and Nucleotide Metabolism		
At4g14070	*AAE15*		Acyl-Activating Enzyme	High	Plastid Acyl-Acyl Carrier Protein Synthetase; Fatty Acid Elongation		CPT Localized (4)
At4g14110	*COP9*	*FUS7; EMB143*	Constitutive Photomorphogenesis	Unique	Component of COP9 Signalosome; Role in Light-Regulated Signal Transduction and Protein Degradation		
At4g14130	*XTH15*	*XTR7*	Xyloglucan Endotransglucosylase/Hydrolase	High			Not Evaluated
At4g14180	*AtPRD1*		Putative Recombination Initiation Defect	Unique	Putative Role in Meiotic DSB Formation		
At4g14210	*PDE226*	*PDS1*	Pigment Defective Embryo	Moderate	Phytoene Desaturase; Carotenoid Biosynthesis		CPT Localized (2)
At4g14590	*EMB2739*		Embryo Defective	Unique	Uncertain; Potential Role in snRNA 3' End Formation (Integrator Complex)		
At4g14713	*PPD1*	*TIFY4A*	Peapod	High			
At4g14750	*FRC3*	*IQD19*	Furca	Unique	Plant-Specific Calmodulin-Binding Protein		
At4g14790	*PDD17;PDD26*	*AtSUV3*	Pollen Development Defective	High	RNA Helicase	MIT Localized (4)	

At4g14850	*LOI1*	*MEF11*	Lovastatin Insensitive	High	Mitochondrial PPR Protein; RNA Binding Protein	MIT Localized (0)	
At4g14870	*SECE1*			Unique	Chloroplast Sec Translocase		Not Evaluated
At4g14880	*OLD3*	*OASA1;*	Onset of Leaf Death	High			Not Evaluated
At4g14960	*TUA6*		Tubulin Alpha	High			
At4g15090	*FAR1*		Far-Red Impaired Response	High			
At4g15180	*SDG2*	*ATXR3*	Set Domain Group	Unique	SET Domain Protein; Histone Methylation		Not Evaluated
At4g15230	*AtPDR2*	*ABCG30*	Pleiotropic Drug Resistance	High			
At4g15560	*CLA*	*DEF; DXS*	Chloroplastos Alterados	High	1-Deoxyxylulose 5-Phosphate Synthase; Isoprenoid Biosynthesis		CPT Localized (5)
At4g15570	*MAA3*		Magatama	Moderate	RNA Helicase		
At4g15802	*HSBP*		Heat Shock Factor Binding Protein	Unique	Heat Shock Factor Binding Protein; Regulator of Heat Shock Response		Not Evaluated
At4g15880	*ESD4*		Early in Short Days	High			
At4g15900	*PRL1*		Pleiotropic Regulatory Locus	High			
At4g15950	*RDM2*	*NRPD4; NRPE4*	RNA-Directed DNA Methylation	Unique	RNA-Directed DNA Methylation		
At4g16110	*ARR2*		Arabidopsis Response Regulator	High			
At4g16130	*ARA1*	*ISA1; ATISA1*	Arabinose Sensitive	High			

At4g16144	*AMSH3*		Associated Molecule with the SH3 Domain of STAM	High			Not Evaluated
At4g16155	*ptLPD2*	*LPD2*	Lipoamide Dehydrogenase	High			Not Evaluated
At4g16280	*FCA*		Late Flowering	Moderate			
At4g16340	*SPK1*		Spike	Unique	Guanine Nucleotide Exchange Factor; Regulator of Actin Polymerization		
At4g16370	*OPT3*		Oligopeptide Transporter	High	Oligopeptide Transporter		
At4g16390	*SVR7*		Suppressor of Variegation	High			Not Evaluated
At4g16420	*PRZ1*	*ADA2B*	Proporz	High			
At4g16845	*VRN2*		Reduced Vernalization Response	Moderate			
At4g16860	*RPP4*		Recognition of Peronospora parasitica	High			
At4g16950	*RPP5*		Recognition of Peronospora Parasitica	High			
At4g16990	*RLM3*		Resistance to Leptosphaeria Maculans	Moderate			
At4g17040	*CLPR4*		Clp Protease	Moderate	Clp Protease Subunit		CPT Localized (4)
At4g17090	*CT-BMY*	*BAM3;* *BMY8*	Chloroplast Beta-Amylase	High			

At4g17300	*OVA8*		Ovule Abortion	High	Asparagine Amino Acyl tRNA Synthetase	MIT Localized (1)	
At4g17380	*MSH4*		MutS Homolog	Moderate	Putative Role in Meiotic Recombination		
At4g17615	*CBL1*	*SCABP5*	Calcineurin B-Like Protein	High			
At4g17870	*PYR1*	*RCAR11*	Pyrabactin Resistance	Moderate			Not Evaluated
At4g17970	*ALMT12*		Aluminum-Activated Malate Transporter	High			Not Evaluated
At4g18240	*AtSS4*	*SSIV*	Starch Synthase	Moderate	Soluble Starch Synthase		CPT Localized (3)
At4g18370	*DEG5*	*HHOA*	DEGP Protease	Moderate	DEGP Protease; Misfolded Protein Degradation		CPT Localized (3)
At4g18470	*SNI1*		Suppressor of npr1 Inducible	Unique	Leucine Rich Nuclear Protein; Transcriptional Repressor		
At4g18480	*CH42*	*PDE314;* *CHLI1;* *ACI5*	Chlorina	High	Magnesium Chelatase; Chlorophyll Biosynthesis		CPT Localized (4)
At4g18640	*MRH1*		Morphogenesis of Root Hair	High			
At4g18710	*BIN2*	*DWF12;* *SK21;* *UCU1*	Brassinosteroid Insensitive	High			
At4g18750	*DOT4*		Defectively Organized Tributaries	High			
At4g18770	*MYB98*		MYB Domain Protein	Moderate	R2R3 Transcription Factor; Synergid Cell Development		

At4g18780	*IRX1*	*LEW2*	Irregular Xylem	High			
At4g18830	*OFP5*		Ovate Family Protein	Unique	Unknown		
At4g18960	*AG*		Agamous	Moderate			
At4g18980	*S40-3*			Unique	Unknown		Not Evaluated
At4g19030	*NIP1;1*	*NLM1*	Nodulin26-Like Intrinsic Protein	High			
At4g19040	*EDR2*		Enhanced Disease Resistance	High			
At4g19100	*PAM68*		Photosynthesis Affected Mutant	Unique	Photosystem II Biogenesis		Not Evaluated
At4g19230	*CYP707A1*		Cytochrome P450	High			
At4g19350	*EMB3006*		Embryo Defective	Unique	Unknown		
At4g19490	*AtVPS54*		VPS54 Homolog	Unique	Vesicle Trafficking		
At4g19690	*IRT1*		Iron Transport	High			
At4g20050	*QRT3*		Quartet	High			
At4g20060	*EMB1895*		Embryo Defective	Unique	Unknown		
At4g20090	*EMB1025*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing	MIT Localized (1)	CPT Localized (1)
At4g20370	*TSF*		Twin Sister of FT	Moderate			
At4g20380	*LSD1*		Lesions Simulating Disease Resistance	Unique	Zinc Finger Transcription Factor		
At4g20400	*AtJmj4*		Jumonji	Moderate			
At4g20740	*EMB3131*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At4g20780	*CML42*		Calmodulin Like	Moderate			
At4g20900	*MS5*	*TDM1*	Male Sterile	High			
At4g20910	*CRM2*	*HEN1*	Corymbosa	High			
At4g21100	*DDB1b*		DNA Damaged Binding Protein	High			Not Evaluated

At4g21130	*EMB2271*		Embryo Defective	High	WD-40 Repeat; U3 snoRNP Associated Protein; Ribosome Biogenesis; Pre-rRNA Processing		
At4g21150	*HAP6*		Hapless	Unique	Membrane Trafficking		
At4g21190	*EMB1417*	*APR3*	Embryo Defective	Moderate	5' Adenylsulfate Reductase; Sulfate Reduction	MIT Localized (4)	
At4g21200	*AtGA2ox8*		Gibberellin 2-Oxidase	Moderate			
At4g21270	*ATK1*		Arabidopsis thaliana Kinesin	High			
At4g21320	*Hsa32*		Heat-Stress-Associated	Unique	Heat Shock Chaperone		
At4g21330	*DYT1*		Dysfunctional Tapetum	Unique	bHLH Transcription Factor		
At4g21540	*SphK1*		Shingosine Kinase	High	Shingosine Kinase; ABA Signaling		
At4g21670	*FRY2*	*CPL1*	Fiery	High			
At4g21680	*NRT1.8*		Nitrate Transporter	High			Not Evaluated
At4g21710	*EMB1989*	*NRPB2*	Embryo Defective	High	RNA Polymerase II Subunit		
At4g21790	*TOM1*		Tobamovirus Multiplication	High			
At4g21800	*QQT2*		Quatre-Quart	Unique	ATP/GTP Binding Protein; Proposed Role in Microtubule Localization		
At4g21860	*MSRB2*		Methionine Sulfoxide Reductase B	Moderate	Methionine Sulfoxide Reductase		CPT Localized (3)

At4g22140	*EBS*		Early Bolting in Short Days	Moderate			
At4g22200	*AKT2/3*		Arabidopsis Potassium Transport	High			
At4g22220	*ISU1*			Moderate	Iron-Sulfur Cluster Assembly	MIT Localized (5)	
At4g22260	*IM*		Immutans	Unique	Chloroplast Homolog of Mitochondrial Alternative Oxidase; Cofactor for Carotenoid Desaturation		CPT Localized (3)
At4g22300	*SOBER1*		Suppressor of AvrBsT Elicited Resistance	High	Carboxylesterase; Putative Role in Defense Response		
At4g22950	*AGL19*		Agamous-Like	High			
At4g22970	*AESP*		Arabidopsis Separase	Moderate	Separase; Sister Chromatid Separation		
At4g23100	*RML1*	*CAD2; PAD2*	Root Meristemless	Unique	Gamma-Glutamylcysteine Synthetase; Glutathione Biosynthesis		CPT Localized (4)
At4g23250	*EMB1290*	*CRK17; RKC1*	Embryo Defective	Moderate	Serine-Threonine Protein Kinase		
At4g23430	*TIC32*		Translocon at inner envelope membrane of chloroplasts	High	Short chain dehydrogenase; Chloroplast Protein Import		CPT Localized (1)
At4g23450	*AtAIRP1*		ABA Insensitive RING Protein	Unique	Cytosolic RING E3 Ubiquitin Ligase; Regulator of ABA-Dependent Drought Response		Not Evaluated

At4g23640	*TRH1*	*ATKT3; KUP4*	Tiny Root Hair	High			
At4g23650	*CPK3*	*CDPK6*	Calcium-Dependent Protein Kinase	High			Not Evaluated
At4g23660	*AtPPT1*		Polyprenyl Diphosphate Transferase	Unique	4-Hydroxybenzoate Polyprenyl Diphosphate Transferase; Ubiquinone Biosynthesis	MIT Localized (5)	
At4g23700	*AtCHX17*		Cation/H(+) Exchanger	High			
At4g23810	*WRKY53*		WRKY DNA-Binding Protein	Moderate			
At4g23920	*UGE2*		UDP-D-Glucose/UDP-D-Galactose 4-Epimerase	High			
At4g24020	*NLP7*		NIN-Like Protein	Moderate			
At4g24120	*YSL1*		Yellow Stripe Like	High			
At4g24160	*CGI-58*			Unique	Enzymatic Hydrolysis of Stored Lipids		Not Evaluated
At4g24190	*SHD*	*HSP90-7*	Shepherd	Moderate	GRP94 Ortholog; HSP90-Like Protein		
At4g24210	*SLY1*		Sleepy	Unique	F-Box Protein; SCF E3 Ubiquitin Ligase Subunit		
At4g24230	*ACBP3*		Acyl-CoA Binding Domain	Unique	Acyl-CoA Binding Protein; Regulator of Phospholipid Metabolism and ATG8-PE Complex Formation		Not Evaluated
At4g24270	*EMB140*		Embryo Defective	Unique	Uncertain; RNA Recognition Motif Protein		

At4g24280	*cpHsc70-1*		Heat Shock Cognate Factor	High	Chaperone; Heat Shock Protein		CPT Localized (4)
At4g24510	*CER2*	*VC2*	Eceriferum	Moderate			
At4g24540	*AGL24*		Agamous-Like	Moderate			
At4g24580	*REN1*		ROP1 Enhancer	Moderate	Rho GTPase-Activating Protein		
At4g24620	*PGI1*		Phosphoglucose Isomerase	Moderate	Phosphoglucose Isomerase		CPT Localized (4)
At4g24960	*HVA22D*		HVA Homolog	Moderate			
At4g24972	*TPD1*		Tapetum Determinant	Moderate			
At4g25000	*AMY1*		Alpha-Amylase-Like	High			
At4g25050	*ACP4*		Acyl Carrier Protein	Unique	Acyl Carrier Protein; Fatty Acid Biosynthesis		CPT Localized (4)
At4g25080	*CHLM*		Magnesium-Protoporphyrin IX Methyltransferase	Unique	Magnesium Protoporphyrin IX Methyltransferase; Chlorophyll Biosynthesis		CPT Localized (4)
At4g25140	*OLEO1*	*OLE1*	Oleosin	Moderate			
At4g25230	*RIN2*		RPM1 Interacting Protein	High			
At4g25350	*SHB1*		Short Hypocotyl Under Blue	High			
At4g25420	*GA5*	*GA20ox1*	GA Deficient	High			
At4g25470	*CBF2*	*DREB1C; FTQ4*	C-Repeat/DRE Binding Factor	High			
At4g25480	*DREB1A*	*CBF3*	Dehydration Response Element	High			
At4g25560	*LAF1*	*AtMYB18*	Long After Far-Red Light	Moderate			
At4g25640	*FFT*	*AtDTX35*	Flower Flavonoid Transporter	High			

At4g26070	*MEK1*	*MKK1; NMAPKK*	Map Kinase/ERK Kinase	High			
At4g26080	*ABI1*		ABA Insensitive	High			
At4g26090	*RPS2*		Resistant to P. syringae	High			
At4g26200	*ACS7*		Aminocyclopropane Carboxylate Synthase	High			
At4g26300	*EMB1027*		Embryo Defective	High	Cytosolic Arginyl tRNA Synthetase		CPT Localized (4)
At4g26420	*GAMT1*			High			
At4g26430	*CSN6B*		COP9 Signalosome Subunit	High			
At4g26440	*WRKY34*	*MSP3*	WRKY DNA-Binding Protein	Moderate			Not Evaluated
At4g26466	*LRE*		Lorelei	Moderate	GPI Anchor Protein		
At4g26500	*EMB1374*	*AtSufE*	Embryo Defective	Unique	Activator of Plastidic and Mitochondrial Desulfurases; Fe-S Cluster Protein	MIT Localized (0)	CPT Localized (5)
At4g26690	*SHV3*	*MRH5; GPDL2*	Shaven	High			
At4g26850	*VTC2*		Vitamin C Defective	High			
At4g26900	*HISN4*		Histidine Auxotroph	Unique	Histidine Biosynthesis		CPT Localized (4)
At4g27010	*EMB2788*		Embryo Defective	Moderate	Uncertain		
At4g27030	*FAD4*		Fatty Acid Desaturase	High	Fatty Acid Desaturation		CPT Localized (3)
At4g27060	*TOR1*	*CN; SPR2*	Tortifolia	High			
At4g27330	*SPL*	*NZZ*	Sporocyteless	Unique	MADS Box Transcription Factor		

At4g27600	*NARA5*		Necessary for the Achievement of Rubisco Accumulation	Unique	Unknown; Carbohydrate Kinase Motifs		CPT Localized (2)
At4g27750	*ISI1*		Impaired Sucrose Induction	Unique	Uncertain; Putative Armadillo Repeat Protein		
At4g27760	*FEY*	*FEY3*	FoRVer Young	High			
At4g27800	*TAP38*	*PPH1*	Thylakoid-Associate Phosphatase	Unique	Plastid Protein Phosphatase; Role in LHCII Dephosphorylation		Not Evaluated
At4g28210	*EMB1923*		Embryo Defective	Unique	Unknown		CPT Localized (2)
At4g28320	*MAN5*		Endo-Β-Mannanase	High			Not Evaluated
At4g28580	*MGT5*		Magnesium Transporter	High	Mitochondrial Magnesium Transporter	MIT Localized (1)	
At4g28590	*PDE333*		Pigment Defective Embryo	Unique	Unknown		CPT Localized (1)
At4g28750	*PSAE1*		psa E1 Knockout	Moderate	Photosystem I, Subunit E		CPT Localized (4)
At4g28980	*CDKF;1*	*CAK1AT*	Cyclin-Dependent Kinase	Unique	CDK-Activating Kinase		
At4g29010	*AIM1*		Abnormal Inflorescence Meristem	High			
At4g29040	*RPT2a*	*HLR*	Regulatory Particle AAA-ATPase	High			
At4g29060	*EMB2726*		Embryo Defective	Unique	Cytosolic Translation Elongation Factor Ts		CPT Localized (4)
At4g29130	*HXK1*	*GIN2*	Hexokinase	High			
At4g29170	*AtMND1*			Unique	Putative Role in Meiotic DSB Repair		

At4g29660	*EMB2752*		Embryo Defective	Unique	Unknown		
At4g29810	*AtMKK2*	*MK1*	Map Kinase Kinase	High			
At4g29840	*MTO2*	*TS*	Methionine Over-Accumulation	High	Threonine Synthase		CPT Localized (4)
At4g29860	*EMB2757*	*TAN*	Embryo Defective	Unique	Uncertain; WD-40 Repeat Protein		
At4g29910	*EMB2798*	*ORC5*	Embryo Defective	Unique	Origin of Replication Complex; DNA Replication Initiation		
At4g30120	*HMA3*		Heavy Metal Associated	High			
At4g30580	*EMB1995*	*ATS2; LPAAT*	Embryo Defective	Unique	Lysophosphatidic Acid Acyltransferase; Fatty Acid and Phospholipid Metabolism		CPT Localized (4)
At4g30720	*PDE327*		Pigment Defective Embryo	Unique	Unknown		CPT Localized (4)
At4g30870	*AtMUS81*		MMS and UV Sensitive	Moderate			
At4g30930	*NFD1*	*At4g30925*	Nuclear Fusion Defective	Unique	Mitochondrial Ribosomal Subunit L21	MIT Localized (5)	
At4g30950	*FAD6*	*FADC*	Fatty Acid Desaturase	Unique	Chloroplast Omega 6 Fatty Acid Desaturase		CPT Localized (4)
At4g30960	*CIPK6*	*SnRK3.14; SIP3*	CBL-Interacting Protein Kinase	High			
At4g31120	*SKB1*	*PRMT5*	SHK1 Binding Protein	Unique	Histone Methylation		
At4g31160	*DCAF1*		DDB1-CUL4 Associated Factor	Unique	Nuclear Ubiquitin E3 Ligase; Protein Degradation		
At4g31400	*CTF7*		Arabidopsis Homolog of Yeast CTF	Unique	Sister Chromatid Cohesion Factor		Not Evaluated

At4g31500	*SUR2*	*CYP83B1; RED1; RNT1*	Superroot	High			Not Evaluated
At4g31560	*HCF153*			Unique	Unknown; Putative Role in Cytochrome b(6)f Complex Biogenesis		CPT Localized (3)
At4g31700	*RPS6A*		Ribosomal Protein S6	High			Not Evaluated
At4g31770	*DBR1*		Lariat Debranching Enzyme	Unique	Lariat Debranching Enzyme; Removal of Spliced Introns; Generation of snoRNAs		
At4g31780	*EMB2797*	*MGD1; MGDA*	Embryo Defective	High	Monogalactosyldiacylglycerol (Galactolipid) Biosynthesis		CPT Localized (5)
At4g31800	*WRKY18*		WRKY DNA-Binding Protein	High			
At4g31820	*ENP*	*MAB4; NPY1*	Enhancer of Pinoid	High			
At4g31870	*GPX7*		Glutathione Peroxidase	High	Glutathione Peroxidase; Plastid Antioxidant		CPT Localized (3)
At4g31970	*JAH1*	*CYP82C2*	Jasmonic Acid Hypersensitive	High			Not Evaluated
At4g32150	*AtVAMP711*		Vesicle-Associated Membrane Protein	High			
At4g32260	*PDE334*		Pigment Defective Embryo	Unique	ATP Synthase Family		CPT Localized (4)
At4g32400	*SHS1*	*EMB104; AtBT1*	Sodium Hypersensitive	Moderate	Transport Protein; Plastid Nucleotide Export		CPT Localized (3)
At4g32410	*RSW1*	*CESA1*	Radially Swollen Root	High	Cellulose Synthase; Primary Cell Wall Formation		

At4g32551	*LUG*	*RON2*	Leunig	Moderate			
At4g32650	*KC1*		K+ Rectifying Channel	Moderate			
At4g32700	*TEB*		Tebichi	Moderate	Regulator of DNA DSB Repair		
At4g32720	*AtLA1*		Arabidopsis LA1 Protein	Moderate	RNA Binding Protein; RNA Maturation and Stability in Nucleus		
At4g32770	*VTE1*	*AtSDX1*	Vitamin E Deficient	Unique	Tocopherol Cyclase; Vitamin E Biosynthesis		CPT Localized (5)
At4g32810	*CCD8*	*MAX4*	Carotenoid Cleavage Dioxygenase	Moderate	Carotenoid Cleavage Dioxygenase; Apocarotenoid Hormone Biosynthesis		CPT Localized (2)
At4g32850	*PAPS4*	*NPAP; PAP(IV)*	Poly(A) Polymerase	High			
At4g32980	*ATH1*		Homeobox Gene	Moderate			
At4g33000	*CBL10*		Calcineurin B-Like	Moderate			
At4g33030	*SQD1*		Sulfoquinovosyl Diacylglycerol Deficient	Unique	Sulfolipid Biosynthesis		CPT Localized (2)
At4g33090	*APM1*		Aminopeptidase PM	Unique	Bifunctional M1 Aminopeptidase; Proposed Role in Cellular Trafficking		
At4g33210	*SLOMO*		Slow Motion	Unique	F-Box Protein; Putative Role in Auxin Transport or Biosynthesis		Not Evaluated
At4g33240	*FAB1A*			High			
At4g33330	*GUX2*	*PGSIP3*	Glucuronic Acid Substitution of Xylan	Moderate			Not Evaluated

At4g33360	*FLDH*		Farnesol Dehydrogenase	Unique	Farnesol Dehydrogenase; Regulator of ABA Signaling		Not Evaluated
At4g33430	*BAK1*	*ELG*	BRI 1-Associated Receptor Kinase	High			
At4g33460	*EMB2751*		Embryo Defective	Unique	ABC Transporter		CPT Localized (2)
At4g33470	*HDA14*		Histone Deacetylase	Moderate	Histone Acetylation		
At4g33495	*RPD1*		Root Primordium Defective	Moderate	PORR Domain Protein; Putative Role in Organellular RNA Splicing or Metabolism	MIT Localized (4)	
At4g33520	*PAA1*	*HMA6*	P-Type ATP-ase	High	P-type ATPase; Plastid Copper Transport		CPT Localized (4)
At4g33650	*DRP3A*	*ADL2*	Dynamin-Related Protein	High			
At4g33680	*AGD2*		Aberrant Growth and Death	High	Class 2 Aminotransferase; Amino Acid Metabolism		CPT Localized (4)
At4g33790	*CER4*	*FAR3; G7*	Eceriferum	High			
At4g33950	*OST1*	*SNRK2.6; SRK2E; P44*	Open Stomata	High			
At4g33990	*EMB2758*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing	MIT Localized (4)	
At4g34350	*HDR*	*CLB6; IspH*	4-Hydroxy-3-Methylbut-2-Enyl Diphosphate Reductase	Unique	Isoprenoid Biosynthesis		CPT Localized (4)
At4g34390	*XLG2*		Extra-Large GTP-Binding Protein	Moderate			

At4g34460	*AGB1*	*ELK4*	Arabidopsis G Protein Beta Subunit	Unique	Heterotrimeric G-Protein Beta Subunit; Role in Defense Signaling		
At4g34520	*FAE1*	*KCS18*	Fatty Acid Elongation	High			
At4g34620	*SSR16*		Small Subunit Ribosomal Protein	Moderate	Mitochondrial Ribosomal Protein S16	MIT Localized (1)	CPT Localized (4)
At4g34700	*AtCIB22*		Mitochondrial Complex I Subunit	Unique	Mitochondrial Complex I Subunit	MIT Localized (4)	
At4g34710	*ADC2*	*SPE2*	Arginine Decarboxylase	High			
At4g34740	*AtGPRAT2*	*AtPURF2; CIA1; AtASE2*	Glutamine Phosphoribosylamidotransferase	High	Purine Biosynthesis		CPT Localized (4)
At4g34830	*PDE346*	*MRL1*	Pigment Defective Embryo	Moderate	Uncertain; Putative PPR Protein		CPT Localized (4)
At4g34850	*LAP5*	*PKSB*	Less Adhesive Pollen	High			Not Evaluated
At4g34890	*AtXDH1*		Xanthine Dehydrogenase	High			
At4g34940	*ARO1*	*SETH4*	Armadillo Repeat Only	High	Armadillo Repeat Protein		
At4g34990	*AtMYB32*		MYB Domain Protein	High	R2R3 MYB Transcription Factor		
At4g35040	*bZIP19*		bZIP Transcription Factor	High			Not Evaluated
At4g35090	*CAT2*		Catalase	High			
At4g35420	*TKPR1*	*DRL1*	Tetraketide Alpha-Pyrone Reductase	Moderate			Not Evaluated
At4g35440	*CLCE*		Chloride Channel	High	Nitrate Transporter; Nitrate Homeostasis		CPT Localized (2)
At4g35450	*ARK2A*	*AFT*	Ankyrin Repeat-Containing Protein	High			Not Evaluated

At4g35490	*MRPL11*		Mitochondrial Ribosomal Protein	Unique	Mitochondrial Ribosomal Protein L11	MIT Localized (4)	
At4g35520	*MLH3*		MutL Protein Homolog	Unique	DNA Mismatch Repair Protein		
At4g35900	*FD*	*AtBZIP14*	Late Flowering	Moderate			
At4g35920	*MCA1*		MID1-Complementing Activity	High			
At4g36220	*FAH1*	*CYP84A1*	Ferulic Acid 5-Hydroxylase	High			
At4g36380	*ROT3*	*CYP90C1*	Rotundifolia	High			
At4g36480	*EMB2779*	*LCB1; FBR11*	Embryo Defective	Moderate	Serine Palmitoyltransferase; Sphingolipid Biosynthesis		
At4g36630	*EMB2754*	*VPS39*	Embryo Defective	Unique	Putative Vacuolar Protein; Proposed Role in Vacuolar Protein Sorting		
At4g36830	*HOS3*		High Expression of Osmotically Responsive Genes	High			
At4g36890	*IRX14*		Irregular Xylem	High			Not Evaluated
At4g36920	*AP2*	*FLO2; FL1*	Apetala	Moderate			
At4g36930	*SPT*		Spatula	Unique	bHLH Transcription Factor		
At4g37000	*ACD2*	*AtRCCR*	Accelerated Cell Death	Unique	Red Chlorophyll Catabolite Reductase; Breakdown of Porphyrin		CPT Localized (5)
At4g37050	*PLAIVC*	*PLP4*	Phospholipase A	High			Not Evaluated

At4g37070	*PLAIVA*	*PLP1*	Phospholipase A	High			Not Evaluated
At4g37200	*HCF164*		High Chlorophyll Fluorescence	Unique	Thioredoxin-Like; Disulfide Reductase; Cytochrome b(6)f Complex Biogenesis		CPT Localized (4)
At4g37270	*HMA1*		Heavy Metal ATPase	Moderate	ATPase; Chloroplast Copper Import		CPT Localized (3)
At4g37450	*AGP18*		Arabinogalactan Protein	Unique	Cell Surface Proteoglycan		
At4g37470	*HTL*		Hyposensitive to Light	High			Not Evaluated
At4g37540	*LBD39*		LOB Domain-Containing Protein	Moderate			
At4g37580	*HLS1*	*COP3; UNS2*	Hookless	High			
At4g37650	*SHR*	*SGR7*	Short Root	Moderate			
At4g37750	*ANT*	*DRG*	Aintegumenta	Moderate			
At4g37925	*NDH-M*		Subunit NDH-M of NAD(P)H:Plastoquinone Dehydrogenase Complex	Unique	Subunit of NAD(P)H:Plastoquinone Dehydrogenase Complex		CPT Localized (3)
At4g37930	*SHM1*		Serine Hydroxymethyltransferase	High	Photorespiratory C2 Cycle Protein; Catalyzes the conversion of two molecules of glycine into one molecule each of CO2, NH4+, and serine	MIT Localized (5)	
At4g38130	*HD1*	*HDA1; HDA19; RPD3a*	Histone Deacetylase	High			
At4g38160	*PDE191*		Pigment Defective Embryo	Unique	Uncertain; mTERF Domain Protein		

At4g38190	*CSLD4*		Cellulose Synthase Like	High	Putative Glycosyltransferase; Cell Wall Biosynthesis		
At4g38240	*CGL1*	*GNTI*	Complex Glycan	Unique	N-Acetyl-Glucosaminyltransferase; Role in N-Glycosylation		
At4g38600	*KAK*	*UPL3*	Kaktus	Moderate			
At4g38620	*MYB4*		MYB Gene Knockout	High			
At4g38630	*RPN10*	*MBP1;* *MCB1*	Regulatory Particle Non-ATPase	Unique	26S Proteasome Subunit		
At4g38800	*MTN1*	*MTAN1*	Methylthioadenosine Nucleosidase	High			Not Evaluated
At4g39030	*EDS5*	*SID1*	Enhanced Disease Susceptibility	High			
At4g39090	*RD19*	*RD19A*	Responsive to Dehydration	High			
At4g39120	*HISN7*	*IMPL2;* *HPP*	Histidine Biosynthesis	Unique	Histidinol-Phosphate Phosphatase; Histidine Biosynthesis		CPT Localized (4)
At4g39350	*CESA2*	*ATH-A*	Cellulose Synthase	High			
At4g39400	*BRI1*	*CBB2; BIN1*	Brassinosteroid Insensitive	High			
At4g39460	*SAMC1*	*SAMT1*	S-Adenosylmethionine Carrier	High	Plastid SAM Importer		CPT Localized (4)
At4g39620	*EMB2453*	*PPR5*	Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		
At4g39640	*GGT1*		Gamma-Glutamyl Transpeptidase	High			

At4g39710	*FKBP16-2*		FK506 Binding Protein	Moderate	NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (4)
At4g39800	*AtIPS1*	*MIPS1*	Inositol-3-Phosphate Synthase	High			
At4g39850	*PXA1*	*PED3; CTS*	Peroxisomal ABC Transporter	Moderate	Peroxisomal ABC Transporter		
At4g39920	*POR*	*TFCC*	Porcino	Unique	Tubulin Folding Cofactor C; Regulation of Tubulin Folding and Microtubule Dynamics		
At5g01220	*SQD2*		Sulfoquinovosyl Diacylglycerol Deficient	Unique	Sulfoquinovosyltransferase ; Sulfolipid Biosynthesis		CPT Localized (2)
At5g01360	*TBL3*		Trichome Birefringence-Like	High			Not Evaluated
At5g01400	*ESP4*		Enhanced Silencing Phenotype	Moderate			
At5g01410	*RSR4*	*PDX1.3*	Reduced Sugar Response	High			
At5g01490	*CAX4*		Cation Exchanger	High			
At5g01500	*TAAC*		Thylakoid ATP/ADP Carrier	Moderate	Thylakoid Membrane ATP/ADP Carrier		CPT Localized (2)
At5g01540	*LecRKA4.1*		Lectin Receptor Kinase	High			
At5g01550	*LecRKA4.2*		Lectin Receptor Kinase	High			
At5g01560	*LecRKA4.3*		Lectin Receptor Kinase	High			
At5g01600	*AtFER1*		Ferritin	High	Ferritin; Iron Homeostasis		CPT Localized (4)
At5g01630	*AtBRCA2b*		Breast Cancer Associated	High			

At5g01820	*CIPK14*	*SR1; SNRK3.15*	CBL-Interacting Protein Kinase	High			Not Evaluated
At5g01840	*OFP1*		Ovate Family Protein	Unique	KU-70 Interacting Protein; DNA Repair		Not Evaluated
At5g01920	*STN8*		State Transition	Moderate			Not Evaluated
At5g01930	*MAN6*		Endo-B-Mannanase	High			Not Evaluated
At5g02030	*LSN*	*BLR; PNY; RPL; VAN*	Larson	Moderate			
At5g02120	*PDE335*	*OHP*	Pigment Defective Embryo	Unique	Uncertain; Thylakoid One Helix Protein		CPT Localized (4)
At5g02190	*AtASP38*	*PCS1*	Aspartic Protease	High	Aspartic Protease		
At5g02200	*FHL*		Far-Red-Elongated Hypocotyl1-Like	Unique	phyA Signaling		
At5g02250	*EMB2730*	*RNR1*	Embryo Defective	Unique	Ribonuclease II Family Protein; Plastid rRNA Maturation		CPT Localized (3)
At5g02310	*PRT6*		Proteolysis	Unique	E3 Ubiquitin Ligase		
At5g02600	*NaKR1*	*NPCC6*	Sodium Potassium Root Defective	Unique	Uncertain; Metal Binding Protein		Not Evaluated
At5g02810	*PRR7*		Pseudo-Response Regulator	Moderate			
At5g02820	*BIN5*	*RHL2*	Brassinosteroid Insensitive	Moderate			
At5g02870	*RPL4A*		Ribosomal Protein L4A	High			Not Evaluated
At5g03150	*JKD*		Jackdaw	Moderate			
At5g03280	*EIN2*	*CKR1; ORE2; ORE3*	Ethylene Insensitive	Unique	Integral Membrane Protein; Ethylene Signaling		

At5g03455	*CDC25*	*ACR2*	Cell Division Cycle	Unique	Protein Phosphatase; Positive Regulator of Cell Cycle Progression		Not Evaluated
At5g03540	*AtEXO70A1*		Exocyst Subunit EXO70 Family Protein A	High			
At5g03570	*IREG2*	*FPN2*	Iron Regulated	High			
At5g03730	*CTR1*	*SIS1*	Constitutive Triple Response	Moderate			
At5g03790	*LMI1*		Late Meristem Identity	Moderate			
At5g03800	*EMB1899*	*EMB175;* *EMB166*	Embryo Defective	High	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At5g03840	*TFL1*		Terminal Flower	Moderate			
At5g03860	*MLS*		Malate Synthase	Unique	Malate Synthase		
At5g03940	*FFC*	*54CP;* *CPSRP54*	Yellow First Leaves	Moderate	Sorting of Thylakoid Proteins		CPT Localized (4)
At5g04040	*SDP1*		Sugar-Dependent	High			
At5g04140	*GLS1*	*GLU1*	Glutamate Synthase	High	Glutamate Synthase		CPT Localized (4)
At5g04240	*ELF6*		Early Flowering	Moderate			
At5g04290	*KTF1*	*SPT5L*	KOW Domain-Containing Transcription Factor	Moderate	RNA-Directed DNA Methylation		
At5g04430	*BTR1*		Binding to ToMV RNA	Unique	Viral RNA Binding Protein; Negative Regulator of Viral Spread		
At5g04470	*SIM*		Siamese	Unique	Plant-Specific CDK Inhibitor; Regulator of Endoreplication		
At5g04490	*VTE5*		Vitamin E Pathway Gene	Moderate	Phytol Kinase; Vitamin E Biosynthesis		CPT Localized (4)

At5g04560	*DME*	*EMB1649*	Demeter	Moderate	DNA Glycosylase		
At5g04770	*AtCAT6*		Cationic Amino Acid Transporter	High			
At5g04810	*AtPPR4*		Pentatricopeptide Repeat Protein	Moderate	PPR Protein; Plastid RNA Editing		CPT Localized (2)
At5g04890	*RTM2*		Restricted TEV Movement	Unique	Unknown; Putative Small Heat Shock Protein		
At5g05000	*TOC34*	*OEP34; PPI3*	Translocon at the Outer Membrane of Chloroplasts	High	Chloroplast Protein Import		CPT Localized (3)
At5g05170	*CEV1*	*IXR1; CESA3*	Constitutive Expression of VSP 1	High	Cellulose Synthase CeSA3		
At5g05410	*DREB2A*		DRE-binding Protein 2A	Moderate			
At5g05490	*SYN1*	*DIF1; REC8; BP8*	Meiotic Synaptic Defective	Unique	Rad21-Like Cohesin Protein		
At5g05560	*EMB2771*	*APC1*	Embryo Defective	Unique	E3 Ubiquitin Ligase; Anaphase Promoting Complex Subunit; Cell Cycle Regulation		
At5g05580	*FAD8*		Fatty Acid Desaturase	High	Chloroplast Omega 3 Fatty Acid Desaturase		CPT Localized (4)
At5g05680	*EMB2789*	*Nup88*	Embryo Defective	Unique	Nuclear Envelope Protein; Nuclear Protein Export		
At5g05690	*CBB3*	*CPD; DWF3*	Cabbage	High			
At5g05700	*ATE1*	*DLS1*	Arginine-tRNA Protein Transferase	High			
At5g05730	*TRP5*	*AMT1; ASA1*	Tryptophan Biosynthesis	High	Anthranilate Synthase Alpha Subunit; Tryptophan Biosynthesis		CPT Localized (2)
At5g05780	*RPN8A*	*AE3*	RP Non-ATPase Subunit	High			

At5g05970	*NEDD1*		Neural Precursor Cell Expressed, Developmentally Down-Regulated Gene	Unique	WD40 Protein; Microtubule Organization		
At5g06070	*RBE*	*RAB*	Rabbit Ears	Unique	Transcription Factor		
At5g06240	*EMB2735*		Embryo Defective	Unique	Unknown		
At5g06410	*AtHscB*			Unique	Iron Sulfur Protein Biogenesis		
At5g06580	*AtD-LDH1*		D-Lactate Dehydrogenase	Moderate	Lactate Metabolism	MIT Localized (2)	
At5g06650	*GIS2*		Glabrous Inflorescence Stems	Unique	C2H2 Transcription Factor		
At5g06700	*TBR*		Trichome Birefringence	High			Not Evaluated
At5g06760	*LEA4-5*		Late Embryogenesis Abundant	Unique	Unknown; Role in Desiccation Tolerance During Late Embryogenesis		Not Evaluated
At5g07280	*EXS*	*GNE2; EMS1*	Extra Sporogenous Cells	High	LRR Receptor Kinase; Signal Transduction		
At5g07440	*GDH2*		Glutamate Dehydrogenase	High	Glutamate Dehydrogenase		CPT Localized (0)
At5g07500	*PEI*			Moderate	Zinc Finger Transcriptional Regulator		
At5g07990	*TT7*	*CYP75B1*	Transparent Testa	High			
At5g08130	*BIM1*			Moderate	bHLH Protein Interactor of Transcription Factors; Brassinosteroid Signaling		

At5g08170	*EMB1873*	*AIH*	Embryo Defective	Unique	Agmatine Iminohydrolase; Polyamine Biosynthesis		
At5g08370	*AtAGAL2*		Alpha-Galactosidase	High			
At5g08470	*EMB2817*	*PEX1*	Embryo Defective	Moderate	AAA ATPase; Peroxisome Biogenesis		
At5g08550	*ILP1*	*ILP1-1D*	Increased Level of Polyploidy1-1D	Moderate			
At5g08610	*PDE340*		Pigment Defective Embryo	Moderate	DEAD Box RNA Helicase		CPT Localized (4)
At5g08640	*FLS1*		Flavonol Synthase	High			
At5g09640	*SNG2*	*SCPL19*	Sinapoylglucose Accumulator	High			
At5g09660	*PMDH2*		Peroxisomal NAD-Malate Dehydrogenase	High			
At5g09680	*RLF1*		Reduced Lateral Root Formation	Unique	Cytosolic Cytochrome b5-Like Protein; Positive Regulator of Early Cell Division in Lateral Root Initiation		Not Evaluated
At5g09690	*MRS2-7*			High			
At5g09750	*HEC3*		Hecate	Unique	BHLH Transcription Factor		
At5g09790	*PDE336*	*ATXR5*	Pigment Defective Embryo	High	SET-Domain Protein; Putative Histone Methyltransferase		CPT Localized (4)
At5g09810	*ACT7*		Actin	High			
At5g09900	*EMB2107*	*RPN5A; MSA*	Embryo Defective	Moderate	26S Proteasome Regulatory Subunit		
At5g10140	*FLC*	*FLF*	Flowering Locus C	Moderate			

At5g10170	*AtIPS3*	*MIPS3*	Inositol-3-Phosphate Synthase	High			
At5g10250	*DOT3*		Defectively Organized Tributaries	High			
At5g10330	*HISN6A*	*HPA1; EMB2196*	Histidine Auxotroph	High	Histidinol Phosphate Aminotransferase; Histidine Biosynthesis		CPT Localized (1)
At5g10440	*CYCD4;2*		Cyclin	High			
At5g10470	*KAC1*	*KCA1*	Kinesin Like Protein for Actin Based Chloroplast Movement	High			Not Evaluated
At5g10480	*PAS2*	*PEPINO*	Pasticcino	Unique	3-Hydroxy-Acyl-CoA Dehydratase; Very-Long-Chain Fatty Acid Biosynthesis		
At5g11040	*TRS120*			Unique	Tethering Factor; Cell Plate Biogenesis		Not Evaluated
At5g11110	*AtSPS2F*	*SPS1; KNS2*	Sucrose Phosphate Synthase	High			
At5g11260	*HY5*	*TED5*	Elongated Hypocotyl	Unique	bZIP Transcription Factor		
At5g11270	*OCP3*		Overexpressor of Cationic Peroxidase	Unique	Homeodomain Transcription Factor		
At5g11530	*EMF1*		Embryonic Flower	Unique	Polycomb-Group Mediated Transcriptional Repression		
At5g11710	*EPSIN1*		Epsin N-Terminal Homology Domain Protein	Moderate			

At5g11890	*EMB3135*		Embryo Defective	Unique	Unknown		CPT Localized (1)
At5g12080	*MSL10*		Mechanosensitive Channel of Small Conductance-Like	High			
At5g12130	*PDE149*	*ATTERC*	Pigment Defective Embryo	Unique	Transmembrane Transport Protein		CPT Localized (4)
At5g12200	*PYD2*		Pyrimidine	Unique	Dihydropyrimidinase; Uracil Catabolism		
At5g12210	*RGBT1*		RAB Geranylgeranyl Transferase	High			Not Evaluated
At5g12390	*FIS1B*		Fission	Moderate	DRP Organelle Anchor Protein; Mitochondria and Peroxisome Division	MIT Localized (0)	
At5g12840	*EMB2220*	*HAP2A*	Embryo Defective	Moderate	CCAAT Box Transcription Factor		
At5g12860	*pOMT1*	*DIT1*	Plastidic 2-Oxoglutarate/Malate Transporter	High			Not Evaluated
At5g13010	*EMB3011*	*OMA*	Embryo Defective	Moderate	RNA Helicase		
At5g13080	*WRKY75*		WRKY Transcription Factor	Moderate			
At5g13150	*EXO70C1*		Exocyst Subunit	High	Component of Exocyst Complex		Not Evaluated
At5g13160	*PBS1*	*AVRPPHB*	avrPphB Susceptible	High			
At5g13170	*SAG29*	*SWEET15*	Senescence Associated Gene	Moderate			Not Evaluated
At5g13290	*CRN*	*SOL2*	Coryne	Moderate			
At5g13300	*SFC*	*AGD3; VAN3*	Scarface	High			
At5g13320	*PBS3*	*GDG1; WIN3*	AvrPphB Susceptible	High			

At5g13480	*FY*		Late Flowering	Unique	Nuclear RNA Binding Protein; Polyadenylation Factor		
At5g13510	*EMB3136*		Embryo Defective	Moderate	Chloroplast 50S Ribosomal Protein L10		CPT Localized (4)
At5g13530	*KEG*		Keep On Going	Moderate			Not Evaluated
At5g13550	*SULTR4;1*		Sulfate Transporter	High			Not Evaluated
At5g13570	*DCP2*	*TDT*	Decapping	Unique	mRNA Decapping Complex Subunit		
At5g13630	*GUN5*	*CHLH; CCH*	Genomes Uncoupled	Unique	Magnesium Chelatase, Subunit H		CPT Localized (5)
At5g13650	*SVR3*		Suppressor of Variegation	High			Not Evaluated
At5g13680	*ELO2*	*ABO1*	Elongata	Unique	Elongator Complex Subunit; Roles in transcription elongation, secretion, and tRNA modification		
At5g13690	*CYL1*	*NAGLU*	Cyclops	Unique	Alpha-N-Acetyl-Glucosaminidase; Arabinogalactan Protein Metabolism		
At5g13710	*SMT1*	*CPH*	Sterol Methyltransferase	Moderate	Sterol Methyltransferase; Sterol Biosynthesis		
At5g13800	*PPH*		Pheophytinase	Unique	Pheophytin Hydrolase; Chlorophyll Breakdown		CPT Localized (3)
At5g13910	*LEP*		Leafy Petiole	Unique	AP2 Transcription Factor		
At5g13930	*TT4*	*CHS*	Transparent Testa	Moderate			

At5g13960	*KYP*	*SDG33; SUVH4*	Kryptonite	High			
At5g14100	*NAP14*	*ABCI11*	Non-Intrinsic ABC Protein	Unique	Putative Role in Iron Transport or Homeostasis		Not Evaluated
At5g14170	*EMB262*	*CHC1*	Embryo Defective	Moderate	Chromodomain Remodeling Complex; Chromatin Modification		
At5g14180	*MPL1*		Myzus persicae-Induced Lipase	Moderate			Not Evaluated
At5g14200	*IMD1*	*MAM-D1*		High	Methionine Chain Elongation; Glucosinolate Biosynthesis		CPT Localized (3)
At5g14250	*FUS11*	*COP13; CSN3*	Fusca	Unique	COP9 Signalosome Component		
At5g14320	*EMB3137*		Embryo Defective	Unique	Chloroplast 30S Ribosomal Protein S13		CPT Localized (5)
At5g14570	*AtNRT2.7*		High Affinity Nitrate Transporter	High			
At5g14660	*PDF1B*	*DEF2*	Peptide Deformylase	Unique	Peptide Deformylase		CPT Localized (5)
At5g14750	*WER1*	*MYB66*	Werewolf	Moderate			
At5g14760	*AO*		Aspartic Oxidase	Moderate	NAD Biosynthesis		CPT Localized (4)
At5g14800	*EMB2772*		Embryo Defective	Unique	Proline Biosynthesis		
At5g14870	*CNGC18*		Cyclic Nucleotide-Gated Channel	High	Cyclic Nucleotide Gated Channel		
At5g14960	*E2FD*	*DEL2; E2L1*		High			
At5g15130	*WRKY72*		WRKY DNA-Binding Protein	Moderate			Not Evaluated

At5g15170	*TDP*		Tyrosyl-DNA Phosphodiesterase	Unique	Tyrosyl-DNA Phosphodiesterase; DNA Repair		Not Evaluated
At5g15410	*DND1*	*AtCNGC2*	Defense No Death	High			
At5g15450	*CLPB3*	*CLPB-P; APG6*	Casein Lytic Proteinase	High	Chloroplast Hsp101 Homolog; Molecular Chaperone		CPT Localized (4)
At5g15470	*GAUT14*		Galacturonosyltransferase	High			
At5g15540	*EMB2773*	*AtSCC2*	Embryo Defective	Unique	Adherin; Sister Chromatid Cohesion		
At5g15700	*RPOTmp*	*RPOT2*	DNA-Directed RNA Polymerase	High	Phage-Type RNA Polymerase	MIT Localized (1)	CPT Localized (4)
At5g15840	*CO*	*FG*	Constans	High			
At5g15920	*EMB2782*	*MSS2; SMC5*	Embryo Defective	Unique	SMC Family Protein; Chromosome Dynamics		
At5g16000	*NIK1*		NSP-Interacting Kinase	High			
At5g16020	*GEX3*		Gamete Expressed	Unique	Unknown; Plasma-Membrane Localized		
At5g16260	*ELF9*		Early flowering	Unique	RNA Binding Protein; Role in Nonsense-Mediated mRNA Decay		
At5g16270	*SYN4*		Sister Chromatid Cohesion 1 Protein	Moderate			
At5g16390	*CAC1A*		Biotin Carboxyl Carrier Protein	Moderate	Biotin Carboxyl Carrier Protein; Acetyl-CoA carboxylase subunit; Fatty Acid Biosynthesis		CPT Localized (4)
At5g16530	*PIN5*		Pin Formed	Moderate			
At5g16560	*KAN*		Kanadi	Moderate			
At5g16620	*PDE120*	*TIC40*	Pigment Defective Embryo	Unique	Chloroplast Protein Import;		CPT Localized (4)

At5g16715	*EMB2247*		Embryo Defective	High	Amino Acyl tRNA Synthetase (Valine)	MIT Localized (2)	CPT Localized (4)
At5g16750	*TOZ*		Tormoz	Unique	Uncertain; Nucleolar WD-40 Repeat Protein		
At5g16780	*MDF*	*DOT2*	Meristem Defective	Unique	RS Domain Protein; Putative Role in Transcription or RNA Processing		
At5g16830	*SYP21*	*PEP12*	Syntaxin of Plants	Moderate	Transport Vesicle-Membrane Fusion		
At5g16910	*CSLD2*		Cellulose Synthase Like	High			
At5g17220	*TT19*	*GSTF12; GST26*	Transparent Testa	Moderate			Not Evaluated
At5g17290	*APG5*	*ATG5*	Autophagy	Unique	Putative Role During Autophagy		
At5g17330	*GAD*	*GAD1*	Glutamate Decarboxylate	High			
At5g17400	*ER-ANT1*		Endoplasmic Reticulum-Denine Nucleotide Transporter	High			
At5g17420	*IRX3*	*MUR10*	Irregular Xylem	High			
At5g17520	*RCP1*	*MEX1*	Root Cap	Moderate	Maltose Transporter		
At5g17690	*TFL2*	*LHP1*	Terminal Flower	Unique	Polycomb Chromatin Remodeling Protein		
At5g17710	*EMB1241*		Embryo Defective	Moderate	Chloroplast GrpE Protein; Chloroplast Protein Maintenance; Interacts with Hsp70		CPT Localized (3)
At5g17770	*AtCBR*	*CBR1*	NADH:Cytochrome B5 Reductase	Moderate			

At5g17880	*CSA1*		Constitutive Shade-Avoidance	High			
At5g17890	*CHS3*	*DAR4*	Chilling Sensitive	Moderate			Not Evaluated
At5g17990	*TRP1*	*PAT1*	Tryptophan Biosynthesis	Unique	TPR Protein; Tryptophan Biosynthesis		CPT Localized (4)
At5g18000	*VDD*		Verdandi	High	Putative Transcription Factor		Not Evaluated
At5g18170	*GDH1*		Glutamate Dehydrogenase	High	Glutamate Dehydrogenase; Glutamate Biosynthesis	MIT Localized (2)	CPT Localized (0)
At5g18560	*PUCHI*			Unique	ERF/AP2 Transcription Factor Family		
At5g18570	*EMB3138*		Embryo Defective	Moderate	Chloroplast Obg-Like GTPase; Thylakoid Biogenesis		CPT Localized (4)
At5g18580	*FS1*	*TON2;* *EMB40;* *PP2A*	Fass	Unique	Protein Phosphatase; Role in Signal Transduction		
At5g18660	*PCB2*		Pale-Green and Chlorophyll B Reduced	Unique	Divinyl Protochlorophyllide 8-Vinyl Reductase		CPT Localized (4)
At5g18700	*EMB3013*		Embryo Defective	Moderate	Microtubule-Associated Kinase; Cell Plate Expansion in Cytokinesis		
At5g18820	*EMB3007*		Embryo Defective	High	Chaperonin		CPT Localized (1)
At5g18930	*BUD2*	*SAMDC4*	Bushy and Dwarf	Moderate			
At5g19220	*ADG2*	*APL1*	ADP Glucose Pyrophosphorylase Deficient	High	ADP Glucose Pyrophosphorylase Large Subunit		CPT Localized (4)

At5g19400	*SMG7*		Suppressor with Morphogenic Effects on Genetalia	Moderate			Not Evaluated
At5g19520	*MSL9*		Mechanosensitive Channel of Small Conductance-Like	High			
At5g19530	*ACL5*		Acaulis	Moderate	Thermospermine Synthase		
At5g19550	*AAT2*	*ASP2*	Aspartate Aminotransferase	High			
At5g19600	*SULTR3;5*		Sulfate Transporter	High			Not Evaluated
At5g19610	*GNL2*		GNOM-Like	High	ADP-Ribosylation Factor-Guanine Nucleotide Exchange Factor		
At5g19620	*OEP80*		Outer Envelope Protein	Moderate	Chloroplast Outer Envelope Protein; Chloroplast Protein Import		CPT Localized (3)
At5g19660	*S1P*		Site-1 Protease	Unique	Subtilase Serine Protease		
At5g19690	*STT3A*		Staurosporin and Temperature Sensitive 3-Like A	High			
At5g19770	*TUA3*		Tubulin Alpha	High			
At5g19820	*EMB2734*		Embryo Defective	Moderate	Karyopherin Beta 3 Transportin; Nuclear Import of Ribosomal Proteins		

At5g20040	*AtIPT9*		Isopentenyltransferase	Unique	tRNA Isopentenyltransferase; cZ-Type Cytokinin Biosynthesis		
At5g20240	*PI*		Pistillata	Unique	MADS Box Transcription Factor		
At5g20270	*HHP1*		Heptahelical Transmembrane Protein	Moderate			
At5g20320	*DCL4*		Dicer-Like	High			
At5g20350	*TIP1*		Tip Growth Defective	High	Uncertain; Ankyrin Repeat Protein		
At5g20480	*EFR*		EF-TU Receptor	High			
At5g20730	*NPH4*	*BIP; MSG1; TIR5*	Non-Phototropic Hypocotyl	Moderate			
At5g20850	*AtRAD51*		RAS Associated with Diabetes Protein	High			
At5g20910	*AIP2*		ABI3 Interacting Protein	Unique	E3 Ligase; ABA Signaling Regulator		
At5g20920	*EMB1401*	*EIF2-BETA*	Embryo Defective	Moderate	Translation Initiation Factor; Role in Ribosome Small Subunit Attachment		
At5g20930	*TSL*		Tousled	Unique	Serine-Threonine Protein Kinase; Transcriptional Repressor		
At5g21140	*EMB1379*		Embryo Defective	Unique	Uncertain		
At5g21150	*AGO9*		Argonaute	High	RNA Binding Protein; Small RNA Metabolism		Not Evaluated
At5g22010	*AtRFC1*		Replication Factor C	Unique	Replication Factor C Large Subunit; DNA Replication and Repair		

At5g22110	*CYL2*		Cyclops	Unique	DNA Polymerase Epsilon, Subunit; DNA Replication		
At5g22130	*PNT1*		Peanut	Unique	ER-Localized Mannosyl Transferase; Production of GPI Anchor; Proposed Role in Cell Wall Biogenesis		
At5g22250	*AtCAF1b*		CCR4 Associated Factor	High			
At5g22260	*MS1*		Male Sterile	High			
At5g22330	*AtTIP49a*	*RIN1*		High	RPM1-Interacting Protein; Associated with TATA Binding Protein		
At5g22350	*ELM1*		Elongated Mitochondria	High			
At5g22360	*ATVAMP714*		Vesicle-Associated Membrane Protein	Moderate			
At5g22370	*EMB1705*	*QQT1*	Embryo Defective	Moderate	GPN-Loop GTPase; Microtubule Organization		
At5g22500	*FAR1*		Fatty Acid Reductase	High			Not Evaluated
At5g22640	*EMB1211*		Embryo Defective	Unique	Uncertain; MORN Repeat Protein		CPT Localized (1)
At5g22800	*EMB1030*		Embryo Defective	High	Plastid and Mitochondrial Alanine tRNA Synthetase	MIT Localized (1)	CPT Localized (4)
At5g23010	*MAM1*	*IMS3*	Methylthioalkylmalate Synthase	High	Methylthioalkylmalate Synthase; Glucosinolate Biosynthesis		CPT Localized (2)

At5g23020	*IMS2*	*MAM3; MAM-L*	2-Isopropylmalate Synthase	High	2-Isopropylmalate Synthase; Methionine-Derived Glucosinolate Chain Elongation		CPT Localized (3)
At5g23060	*CaS*		Calcium Sensing Receptor	Unique	Thylakoid Membrane Phosphoprotein; Calcium Sensing Receptor		CPT Localized (5)
At5g23080	*TGH*		Tough	Unique	Putative Role in RNA Binding and Processing		
At5g23120	*HCF136*		High Chlorophyll Fluorescence	Unique	PS II Chaperone-Like Assembly Factor		CPT Localized (4)
At5g23190	*CYP86B1*		Cytochrome P450	High			
At5g23230	*NIC2*		Nicotinamidase	High			
At5g23260	*TT16*	*ABS*	Transparent Testa	Moderate	MADS Box Transcription Factor		
At5g23290	*PFD5*	*GIM1*	Prefoldin	Unique	Prefoldin Complex Subunit; Role in Tubulin and Actin Folding		
At5g23570	*SGS3*		Suppressor of Gene Silencing	Unique	Unknown		
At5g23630	*MIA*		Male Gametogenesis Impaired Anthers	Unique	Type V Subfamily P-Type ATPase Cation Pump		
At5g23730	*RUP2*	*EFO2*	Repressor of UV-B Photomorphogenesis	High			Not Evaluated
At5g23880	*EMB1265*	*ESP5*	Embryo Defective	Moderate	mRNA Cleavage and Polyadenylation Specificity Factor		
At5g23940	*EMB3009*		Embryo Defective	Moderate	BAHD Transferase Family; Secondary Metabolite Modification		

At5g24270	*SOS3*	*CBL4*	Salt Overly Sensitive	Moderate			
At5g24300	*SSI1*		Starch Synthase 1	High	Starch Synthase; Amylopectin Synthesis		CPT Localized (4)
At5g24310	*ABIL3*		ABL Interactor-Like Protein	High			Not Evaluated
At5g24314	*PDE225*	*PTAC7*	Pigment Defective Embryo	Unique	Unknown		
At5g24400	*EMB2024*	*PGL3*	Embryo Defective	Moderate	6-Phosphogluconolactonase; Role in Pentose Phosphate Pathway		CPT Localized (4)
At5g24470	*APRR5*		Arabidopsis Pseudo-Response Regulator	Moderate			
At5g24520	*TTG1*	*URM23*	Transparent Testa Glabra	High			
At5g24530	*DMR6*		Downy Mildew Resistant	High			
At5g24630	*BIN4*		Brassinosteroid-Insensitive	Unique	DNA Topoisomerase VI Complex Component		
At5g24670	*EMB2820*	*TAD3*	Embryo Defective	Unique	Adenosine Deaminase; tRNA Wobble Position Modification		
At5g25350	*EBF2*		EIN3-Binding F Box Protein	High			
At5g25370	*PLDALPHA3*		Phospholipase D Alpha	High			
At5g25380	*CYCA2;1*	*CYCLINA2*	Cyclin	High			
At5g25900	*GA3*	*KO1;* *CYP701A3*	GA Deficient	Moderate			
At5g26030	*FC1*		Ferrochelatase	Moderate			
At5g26240	*CLC-D*		Chloride Channel D	High			

At5g26570	*AtGWD3*	*PWD; OK1*	Glucan Water Dikinase/ Phosphoglucan Water Dikinase	Unique	Glucan, Water Dikinase; Starch Degradation		CPT Localized (4)
At5g26742	*EMB1138*		Embryo Defective	Moderate	DEAD/DEAH Box RNA Helicase; RNA Binding Protein		CPT Localized (4)
At5g26820	*MAR1*	*IREG3; RTS3*	Multiple Antibiotic Resistance	Unique	Plastid Transporter; Iron Homeostasis		CPT Localized (4)
At5g26860	*LON1*		LON Protease	High	Mitochondrial Protease	MIT Localized (3)	
At5g26920	*CBP60g*		CAM-Binding Protein 60-Like	Moderate			
At5g26980	*SYP41*	*AtTLG2A*	Syntaxin of Plants	High	Transport Vesicle-Membrane Fusion		
At5g27150	*NHX1*		Na+/H+ Exchanger	High			
At5g27270	*EMB976*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At5g27380	*GSH2*	*GSHB*	Glutathione Synthetase	Unique	Glutathione Biosynthesis		CPT Localized (3)
At5g27420	*CNI1*	*ATL31*	Carbon/Nitrogen Insensitive	High			
At5g27540	*EMB2473*	*MIRO1*	Embryo Defective	High	Mitochondrial GTPase; Regulation of Mitochondrial Morphology	MIT Localized (1)	
At5g27720	*EMB1644*	*LSm4*	Embryo Defective	Unique	U6 snRNA Associated Protein; Spliceosome Component		
At5g27740	*EMB2775*	*RFC3*	Embryo Defective	Unique	DNA Replication Factor		
At5g28030	*DES1*		L-Cysteine Desulfhydrase	High			

At5g28640	*AN3*	*GIF1*	Angustifolia	Unique	Putative Transcriptional Coactivator		
At5g33290	*XGD1*		Xylogalacturonan Deficient	High			
At5g33320	*PPT*	*CUE1*	Phosphate/Phosphoenolpyruvate Translocator	High	Plastid Phosphoenolpyruvate/Phosphate Translocator		CPT Localized (4)
At5g34850	*PAP26*		Purple Acid Phosphatase	High			Not Evaluated
At5g35220	*EGY1*		Ethylene-Dependent Gravitropism-Deficient and Yellow-Green	Moderate	ATP-Independent Metalloprotease		CPT Localized (5)
At5g35410	*SOS2*	*CIPK24; SNRK3.11*	Salt Overly Sensitive	High			
At5g35520	*MIS12*		Minichromosome Instability 12 (MIS12)-Like	Unique	Unknown; Kinetochore Component		
At5g35550	*TT2*	*MYB123*	Transparent Testa	Moderate			
At5g35620	*LSP1*	*EIF4E2; EIFISO4E*	Loss of Susceptibility to Potyviruses	Moderate			
At5g35770	*SAP*		Sterile Apetala	Unique	Putative Transcription Factor		
At5g35840	*PHYC*		Phytochrome C	High			
At5g37020	*ARF8*		Auxin Response Factor	Moderate			
At5g37055	*SEF*		Serrated Leaves and Early Flowering	Unique	Zinc Finger Transcription Factor		
At5g37260	*CIR1*	*RVE2*	Circadian 1	Unique	MYB Transcription Factor		
At5g37500	*GORK*		Gated Outwardly-Rectifying K+ Channel	High			

At5g37510	*EMB1467*		Embryo Defective	Unique	Mitochondrial NADH Dehydrogenase; Subunit of Mitochondrial Complex I	MIT Localized (2)	
At5g37630	*EMB2656*		Embryo Defective	Unique	Chromosome Condensation		
At5g37850	*SOS4*		Salt Overly Sensitive	Unique	Pyridoxal Kinase; Vitamin B6 Biosynthesis		
At5g38660	*APE1*		Acclimation of Photosynthesis to Environment	Unique	Unknown		CPT Localized (4)
At5g39050	*PMaT1*			High			Not Evaluated
At5g39400	*AtPTEN1*			Moderate	Tyrosine Phosphatase		
At5g39500	*ERMO1*	*GNL1*	ER Morphology	High			
At5g39510	*ZIG*	*SGR4;* *VTI11*	Zigzag Stem	Moderate			
At5g39610	*ANAC092*	*NAC2;* *NAC6;* *ORE1*	Arabidopsis NAC Domain Containing Protein	High			
At5g39680	*EMB2744*		Embryo Defective	High	PPR Protein		
At5g39710	*EMB2745*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing	MIT Localized (4)	
At5g39740	*ANG3*	*RPL5B;* *OLI7*	Angusta	High			Not Evaluated
At5g39750	*EMB3008*		Embryo Defective	High	MADS-Box Family Protein; Putative Transcription Factor		
At5g39830	*DEG8*		DEG Protease	Moderate	D1 Protein Turnover		CPT Localized (4)

At5g39980	*EMB3140*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At5g40160	*EMB506*	*EMB139*	Embryo Defective	Moderate	Uncertain; Ankyrin Repeat Protein		CPT Localized (4)
At5g40280	*ERA1*	*WIG; AtFTB*	Enhanced Response to ABA	Unique	Farnesyltransferase Beta Subunit; Protein Farnesylation		
At5g40330	*MYB23*	*AtMYBRTF*	MYB Domain Protein	Moderate			
At5g40420	*OLEO2*	*OLE2*	Oleosin-deficient mutant	Moderate			
At5g40480	*EMB3012*	*Nup210*	Embryo Defective	Unique	Nuclear Pore Complex Protein; Nuclear Protein Export		
At5g40770	*PHB3*		Prohibitin	High	Mitochondrial Type-I Prohibitin; Uncertain role in cell division or mitochondrial biogenesis	MIT Localized (2)	
At5g40780	*LHT1*		Lysine Histidine Transporter	High			Not Evaluated
At5g40870	*AtUK/UPRT1*		Uridine Kinase/Uracil Phosphoribosyltransferase	High			
At5g40890	*CLCA*		Chloride Channel	High			
At5g40990	*GLIP1*		GDSL Lipase	High			
At5g41040	*RWP1*			High			
At5g41150	*UVH1*	*RAD1*	Ultraviolet Hypersensitive	Unique	DNA Repair Endonuclease Subunit		
At5g41315	*GL3*		Glabra	High			

At5g41370	*XPB1*		XPB/RAD25 Knockout	High			
At5g41410	*BEL1*		Bell-Shaped Ovules	Moderate			
At5g41480	*GLA1*		Globular Arrest	Unique	Dihydrofolate Synthetase; Folate Biosynthesis	MIT Localized (4)	
At5g42080	*ADL1A*	*ACW2; RSW9*	Arabidopsis Dynamin Like	High	Dynamin-Like Protein; Putative Function in Vesicle Trafficking and Cytokinesis		
At5g42270	*VAR1*	*FTSH5*	Variegated	High	FtsH Metalloprotease; PS II Subunit Degradation		CPT Localized (4)
At5g42400	*ATXR7*	*SDG25*	Arabidopsis Trithorax-Related	Moderate	Histone H3 Methylase		
At5g42630	*KAN4*	*ATS*	KANADI 4/ Aberrant Testa Shape	Moderate			
At5g42650	*AOS*	*DDE2*	Allene Oxide Synthase	Moderate	Allene Oxide Synthase; Jasmonic Acid Biosynthesis		CPT Localized (5)
At5g42790	*ARS5*	*PAF1*	Arsenic Tolerance	High			
At5g42800	*TT3*	*DFR*	Transparent Testa	Moderate			
At5g42970	*COP8*	*FUS4; EMB134; FUS8*	Constitutive Photomorphogenesis	Unique	Component of COP9 Signalosome; Role in Light-Regulated Signal Transduction and Protein Degradation		
At5g43270	*SPL2*		Squamosa Promoter Binding Protein-Like	Moderate			
At5g43430	*ETFBETA*		Electron Transfer Flavoprotein	Unique	Mitochondrial Electron Transfer Flavoprotein	MIT Localized (1)	

At5g43470	*RPP8*	*HRT; RCY1*	Recognition of Peronospora parasitica	High			
At5g43650	*bHLH92*		Basic Helix-Loop-Helix Transcription Factor	Unique	bHLH Transcription Factor		
At5g43750	*NDH18*		NAD(P)H Dehydrogenase	Unique	NAD(P)H Dehydrogenase Complex Subunit		CPT Localized (4)
At5g43810	*ZLL*	*PNH*	Zwille	High			
At5g43940	*HOT5*	*ADH2; GSNOR*	Sensitive to Hot Temperatures	High			
At5g44030	*CESA4*	*IRX5/NWS2*	Cellulose Synthase	High			
At5g44070	*CAD1*	*ARA8; PCS1*	Cadmium Sensitive	High			
At5g44160	*AtIDD8*	*NUC*	Indeterminate Domain	High			Not Evaluated
At5g44190	*GLK2*	*GPR12*	Golden2-Like	Moderate			
At5g44370	*PHT4;6*		Phosphate Transporter	Moderate			
At5g44510	*TAO1*		Target of AvrB Operation	High			
At5g44740	*POLH*		Y-Family DNA Polymerase	Unique	Y-Family DNA Polymerase; Role in DNA Repair		
At5g44750	*REV1*		Reversionless	Unique	Y-Family DNA Polymerase; Role in Translesion Synthesis DNA Repair		
At5g44790	*RAN1*	*HMA7*	Responsive to Antagonist	High			
At5g45140	*NRPC2*		Nuclear RNA Polymerase	High	Nuclear RNA Polymerase		

At5g45250	*RPS4*		Resistant to P. syringae	High			
At5g45260	*RRS1*		Resistance to Ralstonia solanacearum	High			
At5g45340	*CYP707A3*		Cytochrome P450 CYP707A	High			
At5g45380	*AtDUR3*		Degradation of Urea	Unique	Plasma Membrane Urea Transporter		
At5g45610	*HUS2*	*SUV2*	Hydroxyurea Sensitive	Unique	ATRIP Ortholog; Putative Role in DNA Damage Response		
At5g45710	*RHA1*	*AT-HSFA4C*	Root-Handedness Altered	High			
At5g45830	*DOG1*		Delay of Germination	Moderate			
At5g46110	*APE2*	*TPT*	Acclimation of Photosynthesis to Environment	Moderate	Triose Phosphate Transmembrane Transporter		CPT Localized (3)
At5g46180	*dOAT*		Ornithine-Delta-Aminotransferase	Moderate	Ornithine Aminotransferase; Arginine Catabolism	MIT Localized (4)	
At5g46210	*CUL4*		Cullin	High			
At5g46290	*KAS1*		Ketoacyl-ACP Synthase	High	3-Ketoacyl-Acyl Carrier Protein Synthase 1; Fatty Acid Biosynthesis		Not Evaluated
At5g46330	*FLS2*		Flagellin Signaling	High			
At5g46350	*WRKY8*		WRKY DNA-Binding Protein	Moderate			Not Evaluated
At5g46470	*RPS6*		Resistant to Pseudomonas syringae	High			
At5g46700	*TRN2*		Tornado	Moderate			

At5g46800	*BOU*		A Bout de Souffle	Moderate	Mitochondrial Carnitine Acyl Carrier; Putative Acylcarnitine Translocator	MIT Localized (1)	
At5g46860	*SGR3*	*SYP22; VAM3*	Shoot Gravitropism	High	Transport Vesicle-Vacuole Fusion		
At5g47010	*LBA1*	*UPF1*	Low-Level Beta-Amylase	Moderate	RNA Helicase; Role in Nonsense-Mediated mRNA Decay		
At5g47040	*LON2*		LON Protease	High			
At5g47100	*CBL9*		Calcineurin B-like Calcium Sensor Protein	High			
At5g47120	*AtBI1*		BAX Inhibitor 1	Moderate			
At5g47560	*TDT*		Tonoplast Dicarboxylate Transporter	Unique	Vacuolar Malate Transporter		
At5g47910	*RbohD*		Respiratory Burst Oxidase Homologue	High			
At5g47990	*CYP705A5*		Cytochrome P450	High			
At5g48000	*CYP708A2*	*THAH*	Cytochrome P450	High			
At5g48010	*OSC*		Oxidosqualene Cyclase	High			
At5g48030	*GFA2*		Gametophytic Factor	Moderate	Mitochondrial Chaperone; DNA J Protein	MIT Localized (5)	
At5g48100	*TT10*		Transparent Testa	High			
At5g48230	*EMB1276*	*ACAT2*	Embryo Defective	High	Acetyl CoA Acetyl Transferase (Thiolase); Fatty Acid Oxidation; Breakdown of Fatty Acids for Energy		

At5g48300	*ADG1*	*APS1*	ADP Glucose Pyrophosphorylase Deficient	High	ADP Glucose Pyrophosphorylase Small Subunit		CPT Localized (4)
At5g48485	*DIR1*		Defective in Induced Resistance	Moderate			
At5g48600	*SMC4*	*AtCAP-C; SMC3*	Structural Maintenance of Chromosomes	Moderate	Condensin; Chromatin Condensation		
At5g48670	*FEM111*	*AGL80*		Moderate	MADS-Box Transcription Factor		
At5g48720	*XRI1*		X-Ray Induced Transcript	Unique	MND1/AHP2 Complex; DNA Repair		
At5g48840	*PTS*		Pantothenate Synthetase	Unique	Pantothenate Synthetase; Biosynthesis of Vitamin B5; Coenzyme A (CoA) Function		
At5g48850	*AtSDI1*		Sulphate Deficiency Induced	High			
At5g48870	*SAD1*		Supersensitive to ABA and Drought	Unique	Sm-Like snRNP Protein; mRNA Splicing, Export, and Degradation		
At5g48910	*LPA66*		Low PSII Accumulation	High	PPR Protein; Plastid RNA Editing		CPT Localized (3)
At5g49010	*EMB2812*	*SLD5*	Embryo Defective	Unique	DNA Replication, GINS Complex; DNA Replication		
At5g49030	*OVA2*		Ovule Abortion	High	Isoleucine Amino Acyl tRNA Synthetase	MIT Localized (1)	
At5g49160	*MET1*		Methyltransferase	High	Methyltransferase; CpG DNA Methylation		
At5g49190	*SUS2*		Sucrose Synthase	High			Not Evaluated

At5g49270	*SHV2*	*DER9;* *MRH4;* *COBL9*	Shaven	High			
At5g49360	*BXL1*	*PTY*	Beta-Xylosidase	High			
At5g49510	*PFD3*	*GIM2*	Prefoldin	Unique	Prefoldin Complex Subunit; Role in Tubulin and Actin Folding		
At5g49630	*AAP6*		Amino Acid Permease	High			Not Evaluated
At5g49680	*KIP*	*TTD*	Kinky Pollen	High	Unknown; SABRE-Like Protein		
At5g49720	*KOR1*	*RSW2;* *TSD1;* *KOR1*	Korrigan	High			
At5g49830	*EXO84B*		Exocyst Complex Component	High			Not Evaluated
At5g49890	*AtCLCc*		Chloride Channel	High			Not Evaluated
At5g49930	*EMB1441*	*SDCCAG1*	Embryo Defective	Unique	Uncertain; Putative RNA Binding Protein		
At5g49970	*AtPPOX*	*PDX3*	Pyridoxin (Pyrodoxamine) 5'-phosphate Oxidase	Unique	Pyridoxin (Pyrodoxamine) 5'-phosphate Oxidase; Role in Vitamin B6 Salvage Pathway		
At5g50200	*WR3*	*NRT3.1*	Wound-Responsive	Moderate			
At5g50210	*QS*	*OLD5*	Quinolinate Synthase	Moderate	NAD Biosynthesis		CPT Localized (4)
At5g50280	*EMB1006*		Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At5g50300	*AZG2*		AZA-Guanine Resistant	High			

At5g50320	*ELO3*		Elongata	Unique	Histone Acetyl Transferase Complex		
At5g50375	*CPI1*		Cyclopropyl Isomerase	Unique	Cyclopropyl Isomerase; Sterol Biosynthesis		
At5g50390	*EMB3141*		Embryo Defective	High	PPR Protein; Organellular mRNA Processing		CPT Localized (1)
At5g50850	*MAB1*		Macchi-Bou	Moderate	Mitochondrial Pyruvate Dehydrogenase E1 Beta Subunit	MIT Localized (2)	
At5g50920	*DCA1*	*CLPC1;* *HSP93-V*	Deregulated CAO Accumulation	High			
At5g50950	*FUM2*		Fumarase	High			Not Evaluated
At5g50960	*AtNBP35*		Nucleotide Binding Protein	Moderate	Cytosolic Iron–Sulfur Cluster Assembly and Delivery		
At5g51020	*CRL*		Crumpled Leaf	Unique	Plastid Outer Envelope Membrane Protein; Required for Plastid Division		CPT Localized (4)
At5g51060	*RHD2*	*AtRbohC*	Root Hair Defective	High			
At5g51100	*APG8*	*FSD2*	Albino Pale Green	Moderate	Iron Superoxide Dismutase		CPT Localized (4)
At5g51200	*EMB3142*	*Nup205*	Embryo Defective	Unique	Nuclear Pore Complex Protein; Nuclear Protein Export		
At5g51230	*EMF2*	*CYR1;* *VEF2*	Embryonic Flower	Moderate			
At5g51330	*SWI1*	*DYAD*	Switch	Moderate	Unknown; Role in Sister Chromatid Alignment During Meiosis		

At5g51430	*EYE*		Embryo Yellow	Unique	Subunit of Golgi (COG) Complex; Proposed Role in Formation of Extracellular Matrix		
At5g51545	*LPA2*		Low PSII Accumulation	Unique	Thylakoid Membrane Protein		CPT Localized (3)
At5g51600	*PLE*	*MAP65-3*	Pleiade	Moderate			
At5g51700	*PBS2*	*AtRAR1*	avrPphB Susceptible	Unique	Protein Cochaperone		
At5g51760	*AHG1*		ABA-Hypersensitive Germination	Moderate			
At5g51810	*GA20ox2*	*AT2353*	Gibberellin 20 Oxidase	High			
At5g51820	*PGM*	*STF1*	Phosphoglucomutase	High	Plastidic Phosphoglucomutase		CPT Localized (3)
At5g52290	*SHOC1*		Shortage in Chiasmata	Unique	XPF Endonuclease; Putative Role in the Formation of Meiotic Crossovers		
At5g52520	*OVA6*	*ProRS1*	Ovule Abortion	High	Amino Acyl tRNA Synthetase (Proline)	MIT Localized (2)	
At5g52560	*AtUSP*		UDP-Sugar Pyrophosphorylase	Unique	UDP-Sugar Phosphorylase; Salvage Pathway Enzyme		
At5g52920	*PKP1*		Plastidic Pyruvate Kinase	High	Plastidic Pyruvate Kinase B1 Subunit; Seed Oil Biosynthesis		CPT Localized (4)
At5g53170	*FTSH11*		FtsH Protease	Moderate	FtsH Protease	MIT Localized (1)	CPT Localized (4)
At5g53200	*TRY*		Triptychon	Moderate			
At5g53210	*SPCH*		Speechless	Unique	Transcription Factor		

At5g53280	*PDV1*		Plastid Division	Unique	Plastidic Integral Outer Membrane Protein; Plastid Division		CPT Localized (2)
At5g53400	*BOB1*	*NUDC*	Bobber	Moderate	Noncanonical Small Heat Shock Protein; Putative Molecular Chaperone		
At5g53460	*GLT1*			Moderate	Glutamate Biosynthesis		CPT Localized (4)
At5g53470	*ACBP1*		Acyl-CoA Binding Domain	High			Not Evaluated
At5g53760	*MLO11*		Mildew Resistance Locus O	High			
At5g53860	*EMB2737*		Embryo Defective	Unique	Unknown; Putative Auxin-Regulated Protein		CPT Localized (1)
At5g53950	*CUC2*	*ANAC098*	Cup-Shaped Cotyledon	Moderate			
At5g54160	*COMT1*		Caffeate O-Methyltransferase	High			
At5g54250	*AtCNGC4*	*HML1; DND2*	Cyclic Nucleotide-Gated Cation Channel	High			
At5g54260	*MRE11*		Meiotic Recombination	Unique	MRN Complex Subunit; Role in Repair and Metabolism of DNA Breaks		
At5g54310	*NEV*	*AGD5*	Nevershed	Moderate			
At5g54380	*THE1*		Theseus	High			
At5g54440	*TRS130*	*CLUB*		Unique	Putative TRAPPII Tethering Factor; Cell Plate Assembly		Not Evaluated
At5g54590	*CRLK1*		Calcium/Calmodulin Regulated Receptor-Like Kinase	Moderate			Not Evaluated

At5g54640	*RAT5*	*HTA1*	Resistant to Agrobacterium Transformation	Moderate			
At5g54650	*FH5*		Formin Homology	Moderate	Actin-Organizing Protein; Role in Cytokinesis		
At5g54690	*GAUT12*		Galacturonosyltransferase	High			
At5g54770	*TZ*	*THI1; THI4*	Thiazole Requiring	Unique	Thiamine (Vitamin B1) Biosynthesis	MIT Localized (1)	CPT Localized (5)
At5g54800	*GPT1*		Glucose 6-Phosphate/Phosphate Translocator	High	Plastid Glucose Import		
At5g54810	*TRP2*	*TSB1*	Tryptophan Biosynthesis	High	Tryptophan Synthase Beta Subunit; Tryptophan Biosynthesis		CPT Localized (4)
At5g55170	*SUM3*	*SUMO3*	Small Ubiquitin-Like Modifier	Unique	Small Ubiquitin-Like Protein; Defense Signaling		Not Evaluated
At5g55280	*FtsZ1*			Moderate	Stromal Tubulin-Like Chloroplast Division Protein		CPT Localized (5)
At5g55310	*TOP1*		Topoisomerase 1 Alpha	Moderate			
At5g55390	*EDM2*		Enhanced Downy Mildew	Moderate			
At5g55470	*NHX3*		Sodium Hydrogen Exchanger	High			Not Evaluated
At5g55540	*TRN1*	*LOP1*	Tornado	Unique	Putative Plant-Specific Signaling Protein		
At5g55590	*QRT1*		Quartet	High			

At5g55630	*AtKCO1*		Two Pore K-Channel	Moderate			
At5g55700	*BAM4*		Beta Amylase	High			
At5g55740	*CRR21*		Chlororespiratory Reduction	High	Chloroplast RNA Editing		CPT Localized (3)
At5g55760	*SRT2*		Sirtuin	Unique	NAD+-Dependent Deacetylase; Putative Regulator of SA Synthesis		Not Evaluated
At5g55810	*AtNMNAT*		Nicotinate/Nicotinamide Mononucleotide Adenyltransferase	Unique	NAD Biosynthesis/ Pollen development		
At5g55940	*EMB2731*	*NOC4*	Embryo Defective	Unique	Processome Protein; 18S rRNA Biogenesis		
At5g56110	*AtMYB103*	*MS188*	MYB Domain Protein	Moderate			
At5g56270	*WRKY2*		WRKY Transcription Factor	Moderate			
At5g56280	*CSN6A*		COP9 Signalosome	High			
At5g56290	*EMB2790*		Embryo Defective	Unique	Peroxisome Targeting; Peroxisomal Protein Translocation		
At5g56360	*PSL4*		Priority in Sweet Life	Moderate			
At5g56550	*OXS3*		Oxidative Stress	Unique	Putative Chromatin Remodeling Factor		
At5g56580	*MKK6*	*ANQ1*	Map Kinase Kinase	High			Not Evaluated
At5g56680	*EMB2755*		Embryo Defective	High	Cytosolic Asparaginyl-tRNA Synthetase		

At5g56860	*GNC*		GATA, Nitrate-Inducible, Carbon Metabolism-Involved	Moderate	GATA Transcription Factor		
At5g56930	*EMB1789*		Embryo Defective	Unique	Uncertain; Putative Zinc Finger Domain		
At5g57020	*NMT1*		Myristoyl-CoA:Protein N-Myristoyltransferase	Unique	N-Myristoyltransferase Protein; Posttranslational Modification		
At5g57030	*LUT2*		Lutein Deficient	Moderate			
At5g57090	*AGR1*	*PIN2; WAV6; EIR1*	Agravitropic	High			
At5g57160	*AtLIG4*		DNA Ligase IV	Unique	DNA Ligase; Non-Homologous End-Joining of DNA Double Strand Breaks		
At5g57180	*CIA2*		Chloroplast Import Apparatus	High			
At5g57320	*VLN5*		Villin	High	Actin Binding Protein; Role in Actin Filament Dynamics		
At5g57350	*AHA3*		Arabidopsis H+-ATPase	High	Plasma Membrane Proton Pump		
At5g57360	*ZTL*	*ADO1; LKP1*	Zeitlupe	High			
At5g57380	*VIN3*		Vernalization Insensitive	High			
At5g57390	*AIL5*	*CHO1*	Aintegumenta-Like	Moderate			

At5g57590	*BIO1*		Biotin Auxotroph	Unique	7-KAP, DAP Aminotransferase; Dethiobiotin Synthetase; Mitochondrial Biotin Synthesis	MIT Localized (0)	
At5g57740	*XBAT32*		XBA3 Ortholog 2 in Arabidopsis thaliana	High			Not Evaluated
At5g57800	*CER3*	*FLP1; YRE; WAX2*	Eceriferum	High			
At5g57880	*MPS1*	*PRD2*	Multipolar Spindle	Unique	Putative Coiled-Coil Protein; Meiotic Spindle Formation		
At5g57930	*EMB1629*	*APO2*	Embryo Defective	Moderate	Accumulation of Iron-Sulfur Complexes in Chloroplasts		CPT Localized (1)
At5g58070	*TIL1*		Temperature-Induced Lipocalin	Unique	Lipocalin; Putative Role in Thermotolerance		
At5g58140	*PHOT2*		Phototropin	High			
At5g58230	*MSI1*	*MEE70*	Multicopy Suppressor of IRA	High	WD-40 Repeat Protein; Chromatin-Modifying Complex Component		
At5g58250	*EMB3143*		Embryo Defective	Unique	Unknown		CPT Localized (4)
At5g58270	*Sta1*	*ATM3*	Starik	High	Mitochondrial ABC Transporter; Role in Iron-Sulfur Cluster Biosynthesis	MIT Localized (6)	
At5g58290	*BIM409*		BMAA Insensitive Morphology	High			
At5g58600	*PMR5*		Powdery Mildew Resistant	High			
At5g58960	*GIL1*		Gravitropic in Light	Moderate			

At5g59220	*PP2CA2*		Protein Phosphatase 2C	Moderate			
At5g59340	*WOX2*		Wuschel Related Homeobox	Unique	Homeodomain Protein; Transcriptional Regulation		
At5g59440	*ZEUS1*		Zeus	Unique	Thymidylate Kinase; Biosynthesis of dTDP; Regulation of Replication	MIT Localized (1)	
At5g59560	*SRR1*		Sensitivity to Red Light Reduced	Unique	phyB Signaling		
At5g59710	*VIP2*		VIRE2 Interacting Protein	High			
At5g59780	*MYB59*		MYB Transcription Factor	High			
At5g59890	*ADF4*		Actin-Depolymerizing Factor	Moderate			
At5g59920	*ULI3*		UV-B Light Insensitive	High			
At5g60410	*AtSIZ1*			Unique	SUMO E3 Ligase		
At5g60540	*EMB2407*	*PDX2*	Embryo Defective	Unique	Imidazoleglycerol-Phosphate Synthase Subunit H; Pyridoxine (Vitamin B6) Biosynthesis		
At5g60600	*HDS*	*CSB3/ CLB4; ISPG*	4-Hydroxy-3-Methylbut-2-Enyl Diphosphate Synthase	Unique	Isoprenoid Biosynthesis; Plastid MEP Pathway		CPT Localized (4)
At5g60690	*REV*	*IFL1*	Revoluta	High			
At5g60760				High			Not Evaluated

At5g60910	*AGL8*	*FUL*	Agamous-Like	Moderate			
At5g60920	*COB*		Cobra	High			
At5g61070	*HDA18*		Histone Deacetylase of HDA1 Superfamily	Moderate			
At5g61150	*VIP4*		Vernalization Independence	Unique	Putative Transcriptional Regulator		
At5g61160	*AtACT*		Agmatine Coumaroyltransferase	High			
At5g61230	*ANK6*		Ankyrin Repeat Protein	Moderate	Mitochondrial Ankyrin Repeat Protein; Putative role in male-female gamete recognition	MIT Localized (0)	
At5g61380	*TOC1*	*APRR1*	Timing of CAB Expression	Unique	Putative Transcriptional Regulator		
At5g61410	*EMB2728*	*RPE*	Embryo Defective	Moderate	Ribulose-5-Phosphate-3-Epimerase; Role in Calvin Cycle and Oxidative Pentose Phosphate Pathway		CPT Localized (4)
At5g61420	*MYB28*	*PMG1; HAG1*	MYB Domain Protein	High			
At5g61460	*MIM*	*RAD18; SMC6B*	MMS, Irradiation, Mitomycin C Sensitive	High			
At5g61640	*PMSR2*	*MSRA1*	Peptide Methionine Sulfoxide Reductase	High			
At5g61850	*LFY*	*LFY3*	Leafy	Unique	Transcription Factor		
At5g61900	*BON1*	*CPN1*	Bonzai	High			
At5g62000	*ARF2*	*HSS; ORE14*	Auxin Response Factor	Moderate			

At5g62310	*IRE*		Incomplete Root Hair Elongation	High			
At5g62320	*AtMYB99*	*MYBCU15*	MYB Domain Protein	Moderate			
At5g62390	*BAG7*		BCL-2-Associate Athanogene	Unique	Bcl-2-Associated Athanogene Protein; Uncertain Role in the Unfolded Protein Response		Not Evaluated
At5g62410	*TTN3*	*AtCAP-E1; SMC2*	Titan	High	Condensin; Large Chromosomal ATPase; Chromosome Condensation		
At5g62440	*DOM1*	*EMB514*	Domino	Unique	Uncertain; Nucleolar Function		
At5g62470	*MYB96*		MYB Transcription Factor	High			
At5g62500	*AtEB1B*		END Binding Protein	High			
At5g62790	*PDE129*	*DXR*	Pigment Defective Embryo	Unique	1-Deoxyxylulose 5-Phosphate Reductoisomerase; Isoprenoid Biosynthesis		CPT Localized (4)
At5g62810	*PED2*	*PEX14*	Peroxisome Defective	Unique	Pex14p Peroxisomal Import Protein		
At5g62920	*ARR6*		Arabidopsis Response Regulator	Moderate			
At5g62990	*EMB1692*		Embryo Defective	Moderate	PORR Domain Protein; Putative Role in Organellular RNA Splicing or Metabolism		CPT Localized (1)
At5g63050	*EMB2759*		Embryo Defective	Unique	Unknown	MIT Localized (4)	

At5g63110	*HDA6*	*SIL1; AXL1*	Histone Deacetylase	High			
At5g63310	*NDPK2*		Nucleoside Diphosphate Kinase	Moderate	Nucleoside Diphosphate Kinase; Phytochrome Signaling		CPT Localized (5)
At5g63420	*EMB2746*		Embryo Defective	Unique	Metallo-Beta-Lactamase Family Protein; Putative Chloroplast RNA Endonuclease (RNase J)		CPT Localized (4)
At5g63780	*SHA1*		Shoot Apical Meristem Arrest	High			
At5g63840	*RSW3*	*PSL5*	Radial Swelling	Moderate			
At5g63860	*UVR8*		UV Repair Defective	Moderate			
At5g63890	*HISN8*	*HDH; PDD3*	Histidine Biosynthesis	Unique	Histidine Biosynthesis		
At5g63920	*TOP3A*		Topoisomerase Alpha	Moderate			
At5g63950	*CHR24*		Chromatin Remodeling	Moderate			
At5g63980	*FRY1*	*HOS2; ALX8; SAL1; RON1*	Fiery	High	Inositol Polyphosphate 1-Phosphatase ABA and Stress Signaling		CPT Localized (3)
At5g64050	*OVA3*	*ERS*	Ovule Abortion	Unique	Glutamate Amino Acyl tRNA Synthetase	MIT Localized (5)	
At5g64330	*NPH3*	*RPT3*	Non-Phototropic Hypocotyl	High			
At5g64370	*PYD3*	*BETA-UP*	Pyrimidine	Unique	Cytosolic Beta-Ureidopropionase; Uracil Catabolism		
At5g64440	*AtFAAH*		Fatty Acid Amide Hydrolase	Unique	Fatty Acid Amide Hydrolase; N-acylethanolamine Metabolism		

At5g64560	*MGT9*		Magnesium Transporter	High	Low-Affinity Magnesium Transporter		
At5g64580	*EMB3144*		Embryo Defective	Moderate	Uncertain; AAA ATPase		CPT Localized (2)
At5g64630	*FAS2*	*NFB1*	Fasciata	Moderate	Chromatin Assembly Factor 1 Subunit		
At5g64740	*IXR2*	*PRC1;* *CESA6*	Isoxaben Resistant	High			
At5g64750	*ABR1*		ABA Repressor	Unique	Transcription Factor		
At5g64813	*LIP1*		Light Insensitive Period	High			
At5g64860	*DPE1*		Disproportionating Enzyme	Unique	Alpha-1,4-Glucanotransferase; Starch Degradation		CPT Localized (4)
At5g64930	*CPR5*	*HYS1*	Constitutive Expression of PR Genes	Unique	Regulator of Hormone, Defense, and Senescence Signaling		
At5g65050	*AGL31*	*MAF2*	Agamous Like	High			
At5g65090	*BST1*	*DER4*	Bristled	High			
At5g65110	*ACX2*		Acyl-CoA Oxidase	High			
At5g65165	*SDH2-3*		Succinate Dehydrogenase	Moderate	Iron-Sulfur Subunit of Mitochondrial Complex II	MIT Localized (4)	
At5g65420	*CYCD4;1*		Cyclin	High			
At5g65720	*NFS1*	*NIFS1*	Nitrogen Fixation S-Like	Unique	Iron-Sulfur Cluster Assembly	MIT Localized (6)	
At5g65800	*ACS5*	*ETO2/ CIN5*	ACC Synthase	High			
At5g65930	*ZWI*	*KCBP*	Zwichel	Moderate			
At5g65940	*CHY1*		CoA Ester Hydrolase	High			
At5g66055	*EMB2036*	*EMB16;* *AKRP*	Embryo Defective	Moderate	Uncertain; Ankyrin Repeat Protein		CPT Localized (4)

At5g66130	*RAD17*		Radiation Sensitive	Unique	Regulator of DNA Repair		
At5g66190	*AtLFNR1*	*FNR1*	Leaf FNR	High	Ferredoxin NADP Oxidoreductase		CPT Localized (4)
At5g66460	*MAN7*		Endo-B-Mannanase	High			Not Evaluated
At5g66570	*PsbO*	*MSP-1;* *OE33;* *OEE1;* *OEE33;*	PS II Oxygen-Evolving Complex	High	Photosystem II Oxygen-Evolving Complex Subunit		CPT Localized (4)
At5g66680	*DGL1*		Defective Glycosylation	Unique	OST Complex Subunit; Proposed Role in N-Linked Glycosylation of Proteins		
At5g66750	*DDM1*	*SOM1;* *SOM4;* *CHA1;* *CHR1*	Decreased DNA Methylation	Moderate			
At5g66760	*SDH1-1*		Succinate Dehydrogenase	High	Component of Mitochondrial Succinate Dehydrogenase Complex	MIT Localized (5)	
At5g66880	*SnRK2.3*		SNF1-Related Protein Kinase	High			
At5g67030	*ABA1*	*NPQ2;* *IBS3; LOS6;* *ZEP*	ABA Deficient	Unique	Zeaxanthin Epoxidase; ABA Biosynthesis		CPT Localized (4)
At5g67100	*ICU2*		Incurvata	Moderate	DNA Polymerase Alpha		
At5g67160	*EPS1*		Enhanced Pseudomonas Susceptibility	High			
At5g67270	*AtEB1C*		Microtubule End Binding Protein	Moderate			

At5g67320	*HOS15*		High Expression of Osmotically Responsive Genes	Unique	Histone Deacetylation		
At5g67360	*AtSBT1.7*	*ARA12*	Subtilisin-Like Serine Protease	High			
At5g67420	*LBD37*		LOB Domain-Containing Protein	High			
At5g67570	*EMB1408*	*DG1*	Embryo Defective	Moderate	PPR Protein; Organellular mRNA Processing		CPT Localized (2)
At5g67590	*FRO1*		Frostbite	Unique	NADH Dehydrogenase; Mitochondrial Complex 1 Fe-S Subunit	MIT Localized (6)	

APPENDIX E: Arabidopsis Genes with Gametophyte Phenotypes

This appendix includes a truncated version of the dataset of Arabidopsis genes with gametophyte phenotypes. Genes in this dataset show defects in male or female gametophyte development. These defects are associated in this appendix with nine categories: strong male and female defects; severe male and weak female defects; severe female and weak male defects; strong female defects; GEM loci exhibiting aborted embryos (2-10% expected); GEM or EMG classification uncertain; EMG class of embryo and gametophyte defects; gametophyte defects, homozygous plants obtained; and gametophyte defects, classification uncertain. The complete dataset is available as a supplementary table (Table S2) to Muralla et al. (2011).

Footnotes for the title row of the following table are described below:

[a] Gene responsible for mutant phenotype confirmed (C) or not confirmed (NC) through allelism tests, molecular complementation, or some other approach such as excision of a transposable element or cellular / biochemical analysis consistent with the mutant phenotype.

[b] Unique, No additional genes with a similar sequence (BLASTP e-30 cutoff) found in the Arabidopsis genome; Moderate, One or more genes identified with moderate similarity (BLASTP e-30 to e-80, or BLASTP >e-80 if <80% of protein lengths aligned) in the Arabidopsis genome; High, One or more genes identified with high similarity (BLASTP >e-80 with >80% aligned) in the Arabidopsis genome.

[c] GAM, < 2% mutant seeds predicted or observed; GEM, 2-10% mutant seeds predicted or observed; EMG, > 10% mutant seeds predicted or observed; Viable, Viable homozygotes produced; No embryo defects documented; Uncertain, Insufficient details on transmission efficiency to assign subclass

[d] See Table 4 for a description of these abbreviations. LRMS, Low ratio of mutant seeds; NRSD, non-random distribution of mutant seeds within a silique.

[e] NA, No homozygotes expected; absence of male or female transmission; EMBi, defect in embryo development inferred from reduced transmission efficiency and absence of homozygous mutant plants; [EMBi], rare defect in embryo development inferred (< 2% mutant seeds); EMB, defect in embryo development observed; ND, not determined; cannot be inferred from limited data presented; OVA, ovule abortion phenotype observed; VEG, homozygotes viable; vegetative defects observed; GAM, homozygotes viable; gametophyte defects observed; COND, homozygotes viable; conditional defects observed; CELL, homozygotes viable; cellular defects observed; WT, homozygotes viable; appear wild type

[f] D, Defective in pollen development; G, defective in pollen germination; T, defective in pollen-tube growth; F, defective in fertilization

Chromosome Locus	Identity Status[a]	Gene Symbol	Genetic Redundancy Class[b]	Gametophyte Subclass[c]	Description of Mutant Phenotype	Transmission Defect[d]	HMZ[e]	Male Gametophyte Phenotype[f]
Strong Male and Female Defects (T.E. Both < 0.4) (14 Loci)								
At1g11890	C	*SEC22*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / FFF	NA	D
At1g19520	NC	*NFD5*	Moderate	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	MMM / FF	[EMBi]	
At1g24450	NC	*NFD2*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / FFF	NA	
At1g31817	NC	*NFD3*	Unique	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	MMM / FF	[EMBi]	
At1g50240	C	*FU*	Moderate	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / FFF	NA	D
At2g20585	NC	*NFD6*	Unique	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	MMM / FF	[EMBi]	
At2g34220	NC	*PDD12*	High	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / FF	NA	D
At2g35070	NC	*PGD4*	Moderate	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / FF	NA	G
At3g12280	C	*Rb*	Unique	GAM	Complete female gametophyte defective; Male gametophyte defective	MMM / 0 ♀	NA	D
At3g59550	C	*SYN3*	Moderate	GAM	Complete female gametophyte defective; Male gametophyte defective	MM / 0 ♀	NA	G

At4g05450	NC	*PGD6*	High	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	MM / FF	[EMBi]	G
At4g21710	C	*EMB1989*	High	GAM	Null: Complete female gametophyte defective; Male gametophyte defective; Knockdown: Embryo defective	MM / 0 ♀	NA	T
At5g45140	C	*NRPC2*	High	GAM	Complete female gametophyte defective; Male gametophyte defective	MM / 0 ♀	NA	T
At5g67100	C	*ICU2*	Moderate	GAM	Null: Male and female gametophyte defective; Rare embryo defective; Knockdown: Curled leaves; Abnormal floral morphology; Early flowering	MM / FF	EMB	
Severe Male Defect (T.E. <0.1); Weak Female Defect (44 Loci)								
At1g02140	C	*HAP1*	Unique	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	T
At1g08660	C	*MGP2*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	GT
At1g14830	C	*ADL1C*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	D
At1g60490	C	*AtVPS34*	Moderate	GAM	Complete male gametophyte defective	0 ♂ / +	NA	D
At1g64570	C	*DUO3*	Unique	GAM	Complete male gametophyte defective	0 ♂ / +	NA	Not G
At1g71270	C	*VPS52*	High	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	T
At1g74260	C	*PUR4*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective; Heterozygotes: Delayed germination and early development; Low penetrance of chlorosis	0 ♂ / F	NA	D

At1g77140	C	*VPS45*	Unique	GAM	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Severe dwarf	0 ♂ / F	NA	G
At1g78900	C	*VHA-A*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / F	NA	D
At2g03120	C	*AtSPP*	Unique	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	G
At2g21870	C	*MGP1*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / F	NA	D
At2g34680	C	*SETH1*	Unique	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	GT
At2g39990	C	*AteIF3f*	Unique	GAM	Male gametophyte defective; Rare embryo defective	MMM / +	EMB	G
At2g43040	C	*NPG1*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	G
At3g01780	C	*TPLATE*	Unique	GAM	Complete male gametophyte defective	0 ♂ / +	NA	DG
At3g05530	C	*RPT5a*	High	GAM	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes are viable: Dwarf; Short roots; Reduced fertility	0 ♂ / F	NA	D
At3g10380	C	*SEC8*	Unique	GAM	Null: Complete male gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes appear wild type	0 ♂ / +	NA	G
At3g45100	NC	*SETH2*	Unique	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	GT

At3g45150	NC	*TCP16*	Unique	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / F	NA	D
At3g54690	C	*SETH3*	Unique	GAM	Complete male gametophyte defective	0 ♂ / +	NA	Not D
At3g60460	C	*DUO1*	Moderate	GAM	Complete male gametophyte defective	0 ♂ / +	NA	F
At3g61710	C	*ATG6*	Unique	GAM	Complete male gametophyte defective	0 ♂ / F	NA	G
At4g00330	NC	*PDD25*	Moderate	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / F	NA	D
At4g00800	NC	*SETH5*	Unique	GAM	Male gametophyte defective; Female gametophyte defective; Rare embryo defective (inferred)	MMM / F	[EMBi]	G
At4g01220	C	*MGD4*	High	GAM	Null: Complete male gametophyte defective; Knockdown: Male gametophyte defective; Homozygotes are viable: Reduced fertility	0 ♂ / +	NA	T
At4g02195	NC	*SYP42*	High	GAM	Complete male gametophyte defective	0 ♂ / X	NA	G
At4g11720	C	*HAP2*	Unique	GAM	Male gametophyte defective; Rare embryo defective (inferred)	MMM / +	[EMBi]	TF
At4g21150	NC	*HAP6*	Unique	GAM	Complete male gametophyte defective	0 ♂ / F	NA	T
At4g24580	C	*REN1*	Moderate	GAM	Complete male gametophyte defective	0 ♂ / +	NA	T
At4g32410	C	*RSW1*	High	GAM	Null: Complete male gametophyte defective; Strong knockdown: Embryo defective; Weak knockdown: Thick roots and seedlings	0 ♂ / X	NA	D
At4g34940	C	*ARO1*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	Not D

At4g36480	C	*EMB2779*	Moderate	GAM	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Embryo defective	0 ♂ / F	NA	D
At4g38190	C	*CSLD4*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	G
At5g05170	C	*CEV1*	High	GAM	Null: Complete male gametophyte defective; Knockdown: Short roots; Elevated jasmonate and ethylene levels	0 ♂ / X	NA	D
At5g14870	C	*CNGC18*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	T
At5g16830	C	*SYP21*	Moderate	GAM	Complete male gametophyte defective	0 ♂ / X	NA	G
At5g19610	C	*GNL2*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	G
At5g26980	NC	*SYP41*	High	GAM	Complete male gametophyte defective	0 ♂ / X	NA	
At5g52560	C	*AtUSP*	Unique	GAM	Complete male gametophyte defective	0 ♂ / X	NA	
At5g55810	C	*AtNMNAT*	Unique	GAM	Male gametophyte defective; Rare embryo defective	MMM / +	EMB	T
At5g57350	C	*AHA3*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	D
At5g63890	C	*HISN8*	Unique	GAM	Null: Complete male gametophyte defective; Female gametophyte defective; Knockdown: Male and female gametophyte defective	0 ♂ / F	NA	D
At5g64560	C	*MGT9*	High	GAM	Complete male gametophyte defective	0 ♂ / +	NA	D
At5g66760	C	*SDH1-1*	High	GAM	Complete male gametophyte defective; Female gametophyte defective	0 ♂ / F	NA	D

Severe Female Defect (T.E. <0.1); Weak Male Defect (12 Loci)								
At1g14320	NC	*SAC52*	High	GAM	Complete female gametophyte defective	+ / 0 ♀	NA	
At1g16280	C	*SWA3*	High	GAM	Female gametophyte defective; Rare embryo defective (inferred)	+ / FFF	[EMBi]	
At1g25350	NC	*OVA9*	Moderate	GAM	Complete female gametophyte defective; Male gametophyte defective	M / 0 ♀	NA	
At1g29940	C	*NRPA2*	High	GAM	Complete female gametophyte defective; Male gametophyte defective	M / 0 ♀	NA	T
At2g04660	C	*APC2*	Unique	GAM	Female gametophyte defective; Rare embryo defective (inferred)	+ / FFF	[EMBi]	
At2g24840	C	*AGL61*	Moderate	GAM	Female gametophyte defective; Rare embryo defective (inferred)	+ / FFF	[EMBi]	
At2g47430	C	*CKI1*	Moderate	GAM	Complete female gametophyte defective	M / 0 ♀	NA	
At2g47990	C	*SWA1*	Unique	GAM	Null: Complete female gametophyte defective; Male gametophyte defective; Knockdown: Short roots	M / 0 ♀	NA	
At3g06400	NC	*CHR11*	High	GAM	Female gametophyte defective	+ / FFF	ND	
At4g15570	NC	*MAA3*	Moderate	GAM	Male and female gametophyte defective; Rare embryo defective (inferred)	M / FFF	[EMBi]	
At5g48030	C	*GFA2*	Moderate	GAM	Complete female gametophyte defective; Male gametophyte defective	M / 0 ♀	NA	
At5g48670	C	*FEM111*	Moderate	GAM	Complete female gametophyte defective	+ / 0 ♀	NA	
Strong Female Defect (T.E. <0.4) (4 Loci)								
At3g23440	NC	*EDA6*	Unique	GAM or GEM	Female gametophyte defective; Embryo defective (inferred)	X / FF	ND	

At3g57650	C	*LPAT2*	High	GAM or GEM	Female gametophyte defective; Embryo defective (inferred); Heterozygotes: Slightly shorter rosette leaves	+ / (FF)	ND	
At4g00310	NC	*EDA8*	Unique	GAM or GEM	Female gametophyte defective; Embryo defective (inferred)	X / FF	ND	
At4g13890	NC	*EDA36;EDA37*	High	GAM or GEM	Female gametophyte defective; Embryo defective (inferred)	X / FF	ND	
GEM Loci - Aborted Embryos (2-10%) Expected (25 Loci)								
At1g04950	C	*EMB2781*	High	GEM	Male gametophyte defective; Embryo defective	MM / +	EMB	T
At1g20200	NC	*EMB2719*	High	GEM	Male gametophyte defective; Embryo defective	MMM / +	EMB	T
At1g31470	NC	*NFD4*	High	GEM	Male and female gametophyte defective; Embryo defective (inferred)	M / FF	EMBi	
At1g68990	C	*RPOTm*	High	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MMM / FF	[EMBi]	
At1g72440	C	*SWA2*	Unique	GEM	Female and male gametophyte defective; Embryo defective	M / FF	EMB	D
At1g78770	C	*APC6*	Unique	GEM	Female gametophyte defective; Embryo defective (inferred)	M / FF	ND	
At1g79940	C	*AtERDJ2A*	High	GEM	Male gametophyte defective; Embryo defective (inferred)	MM / +	EMBi	G
At2g02955	C	*MEE12*	Unique	GEM	Female gametophyte defective; Embryo defective (inferred)	+ / FF	EMBi	
At2g25710	Y	*HCS1*	High	GEM	Female gametophyte defective; Embryo defective	+ / FF	EMB	
At2g36850	C	*GSL8*	High	GEM	Null: Male gametophyte defective; Embryo defective; Knockdown: Dwarf	MM / X	EMB	D
At2g41500	C	*EMB2776*	Moderate	GEM	Male and female gametophyte defective; Embryo defective	M / FFF	EMB	

At3g05770	NC	*PGD8*	High	GEM	Male gametophyte defective; Embryo defective (inferred)	MM / +	EMBi	G
At3g09840	C	*CDC48*	High	GEM	Male and female gametophyte defective; Embryo defective	MMM / F	EMB	GT
At3g11940	Y	*AML1*	High	GEM	Male and female gametophyte defective; Embryo defective	MM / FF	EMB	
At3g16640	NC	*TCTP*	Moderate	GEM	Male gametophyte defective; Embryo defective (inferred)	MMM / +	[EMBi]	T
At3g51550	C	*FER*	High	GEM	Female gametophyte defective; Embryo defective (inferred)	M / FF	EMBi	F
At4g14790	NC	*PDD17;PDD26*	High	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MMM / F	[EMBi]	D
At4g19490	C	*AtVPS54*	Unique	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MM / FF	[EMBi]	
At4g26466	C	*LRE*	Moderate	GEM	Embryo defective; Female gametophyte defective	+ / F	EMB	
At4g30930	C	*NFD1*	Unique	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MM / FF	[EMBi]	
At4g37450	NC	*AGP18*	Unique	GEM	Female gametophyte defective; Embryo defective (inferred)	+ / (F)	EMBi	
At5g05970	C	*NEDD1*	Unique	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MM / F	EMBi	D
At5g22130	N	*PNT1*	Unique	GEM	Male gametophyte defective; Embryo defective	MMM / +	EMB	
At5g48600	C	*SMC4*	Moderate	GEM	Male and female gametophyte defective; Embryo defective	(M) / FF	EMB	D
At5g54800	C	*GPT1*	High	GEM	Male and female gametophyte defective; Embryo defective (inferred)	MM / FF	EMBi	D

GEM / EMG Classification Uncertain / Conflicted (3 Loci)								
At2g34790	NC	*EDA28*	High	GEM or EMG	Female gametophyte defective; Embryo defective (inferred)	X / F	ND	
At2g47470	NC	*UNE5*	Moderate	GEM or EMG	Female gametophyte defective; Embryo defective (inferred)	X / F	ND	
At3g52590	NC	*EMB2167*	Moderate	GEM or EMG	Male and female gametophyte defective; Embryo defective	MM / F (LRMS)	EMB	T
EMG Class of Embryo / Gametophyte Defectives (44 Loci)								
At1g11870	NC	*OVA7*	Moderate	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	X / (F)	OVA	
At1g14610	C	*TWN2*	High	EMG	Embryo defective; Suspensor-derived twin embryos; Female gametophyte defective	+ / F	EMB	
At1g31860	C	*HISN2*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At1g36160	C	*ACC1*	High	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At1g43710	NC	*EMB1075*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At1g48850	NC	*EMB1144*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	NRSD	EMB	
At1g50500	C	*HIT1*	Moderate	EMG	Null: Male gametophyte defective; Embryo defective (inferred); Knockdown: Sensitive to high temperature and osmotic stress	MM / F	EMBi	
At1g67320	C	*EMB2813*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	(LRMS)	EMB	
At1g67490	C	*KNF*	High	EMG	Embryo defective; Male gametophyte defective	(M) / X	EMB	
At1g80410	NC	*EMB2753*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	

At2g03870	NC	*EMB2816*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	(LRMS)	EMB	
At2g25840	NC	*OVA4*	Unique	EMG	Ovule abortion; Female gametophyte defective; Early embryo defective (inferred)	+ / F	OVA	
At2g35650	C	*CSLA7*	High	EMG	Embryo defective; Male gametophyte defective	MM / +	EMB	
At2g36230	C	*HISN3*	Unique	EMG	Null: Embryo defective; Gametophyte defective (inferred); Knockdown: Pigment defective embryo	LRMS; NRSD	EMB	
At2g41350	NC	*EMB2819*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	(LRMS)	EMB	
At2g47620	C	*AtSWI3A*	Moderate	EMG	Embryo defective; Gametophyte defective	Complex	EMB	
At3g02660	C	*EMB2768*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	(LRMS; NRSD)	EMB	
At3g04680	C	*CLPS3*	High	EMG	Embryo defective; Female gametophyte defective	+ / F	EMB	
At3g05000	NC	*TGD8*	Unique	EMG	Male gametophyte defective; Embryo defective (inferred)	MM / +	EMBi	T
At3g13490	NC	*OVA5*	High	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	M / F	OVA	
At3g48930	NC	*EMB1080*	Moderate	EMG	Embryo defective; Gametophyte defective (inferred)	NRSD	EMB	
At3g55400	NC	*OVA1*	Moderate	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	M / F	OVA	
At3g57870	C	*EMB1637*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS	EMB	
At4g02060	C	*PRL*	Moderate	EMG	Embryo defective; Female gametophyte defective	LRMS	EMB	

At4g02570	C	*AXR6*	High	EMG	Embryo defective; Male and female gametophyte defective; Heterozygotes: Resistant to 2,4-D	M / F	EMB	
At4g05410	C	*YAO*	Moderate	EMG	Embryo defective; Male gametophyte defective	M / +	EMB	
At4g17300	NC	*OVA8*	High	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	X / (F)	OVA	
At4g26900	C	*HISN4*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At5g02190	C	*AtASP38*	High	EMG	Embryo defective; Male and female gametophyte defective	M / F	EMB	
At5g08470	C	*EMB2817*	Moderate	EMG	Embryo defective; Gametophyte defective (inferred)	(LRMS)	EMB	
At5g16390	C	*CAC1A*	Moderate	EMG	Embryo defective; Male gametophyte defective	MM / +	EMB	
At5g16750	C	*TOZ*	Unique	EMG	Embryo defective; Female gametophyte defective	+ / F	EMB	
At5g18700	NC	*EMB3013*	Moderate	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS	EMB	
At5g22330	NC	*AtTIP49a*	High	EMG	Null: Female gametophyte defective; Embryo defective (inferred); Knockdown: Seedling lethal; Abnormal meristem development	+ / FF	EMBi	
At5g27540	C	*EMB2473*	High	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At5g37510	NC	*EMB1467*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At5g39750	NC	*EMB3008*	High	EMG	Embryo defective; Gametophyte defective (inferred)	NRSD	EMB	
At5g40480	NC	*EMB3012*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS	EMB	

At5g48230	C	*EMB1276*	High	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS	EMB	
At5g49030	NC	*OVA2*	High	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	M / F	OVA	
At5g52520	NC	*OVA6*	High	EMG	Ovule abortion; Gametophyte defective; Early embryo defective (inferred)	X / (F)	OVA	
At5g55940	NC	*EMB2731*	Unique	EMG	Embryo defective; Gametophyte defective (inferred)	LRMS; NRSD	EMB	
At5g62410	C	*TTN3*	High	EMG	Embryo defective; Large nuclei in endosperm; Gametophyte defective	LRMS; NRSD	EMB	
At5g64050	C	*OVA3*	Unique	EMG	Ovule abortion; Male and female gametophyte defective; Early embryo defective (inferred)	M / F	OVA	
Gametophyte Defective; Homozygous Plants Obtained (14 Loci)								
At1g59820	NC	*ALA3*	High	Viable	Male gametophyte defective; Homozygotes are viable: Short primary root; Long root hairs; Altered trichome branching	MM / +	VEG	GT
At1g69940	C	*PPME1*	High	Viable	Abnormal pollen tube growth (no effect on fertility)	+ / +	GAM	T
At1g71880	C	*SUC1*	High	Viable	Male gametophyte defective; Homozygotes are viable: Low anthocyanin levels in response to sugar	MMM / +	COND	G
At2g25600	C	*SPIK*	High	Viable	Impaired pollen tube growth (no effect on fertility)	(M) / X	GAM	GT
At2g35630	C	*GEM1*	Unique	Viable	Male and female gametophyte defective; Homozygotes are viable: Increased percentage of abnormal pollen	MM / FF	GAM	D

At2g46020	C	*BRM*	Moderate	Viable	Male and female gametophyte defective; Homozygotes are viable: Dwarf; Slow growth; Abnormal leaf, root and flower morphology; Completely sterile	M / F	VEG	
At2g47040	C	*VGD1*	High	Viable	Male gametophyte defective; Homozygotes are viable: Reduced fertility	MMM / +	GAM	T
At3g08970	C	*AtERdj3A*	Unique	Viable	Male gametophyte defective; Homozygotes are viable: Severely reduced male fertility at high temperature; Fertility phenotype rescued at low temperature	MM / +	GAM	T
At3g12160	C	*RABA4D*	High	Viable	Altered pollen tube growth and morphology; Homozygotes are viable: 100% abnormal pollen	+ / +	GAM	T
At3g22200	C	*POP2*	Moderate	Viable	Male and female gametophyte defective; Homozygotes are viable: Sterile	M / +	GAM	T
At4g00020	NC	*AtBRCA2a*	High	Viable	Female gametophyte defective; Homozygotes are viable: Sensitive to genotoxic stress	X / FF	COND	
At4g18770	C	*MYB98*	Moderate	Viable	Female gametophyte defective, Homozygotes are viable: Severely reduced fertility	+ / FFF	GAM	
At4g24190	C	*SHD*	Moderate	Viable	Male gametophyte defective; Homozygotes are viable: Short roots; Increased lateral root and carpel number; Thick pistils; Large SAM	MMM / +	VEG	T

At5g49680	C	*KIP*	High	Viable	Twisted, branched pollen tubes; Homozygotes are viable: Reduced fertility; Short, thick root hairs	+ / +	CELL	T
Gametophyte Defective; Classification Uncertain (13 Loci)								
At2g07050	C	*CAS1*	High	Uncertain	Null: Male gametophyte defective; Knockdown: Variegated seedlings; Fused cotyledons; Albino inflorescence nodes; Variegated or albino late flowers	(M) / X	ND	
At2g33100	NC	*CSLD1*	High	Uncertain	Male gametophyte defective	(M) / X	ND	G
At2g41110	C	*CAM2*	High	Uncertain	Male gametophyte defective; Homozygotes appear wild type	M / +	WT	GT
At2g47750	NC	*KEN*	High	Uncertain	Female gametophyte defective	X / (F)	ND	
At3g06560	C	*PAPS3*	High	Uncertain	Gametophyte defective	Uncertain	ND	
At3g07160	C	*AtGSL10*	High	Uncertain	Null: Male gametophyte defective; Knockdown: Dwarf	(M) / X	ND	D
At3g19590	NC	*Bub3.1*	High	Uncertain	Male and female gametophyte defective	(M) / (F)	ND	D
At4g18830	NC	*OFP5*	Unique	Uncertain	Female gametophyte defective	X / (F)	ND	
At4g28580	C	*MGT5*	High	Uncertain	Male gametophyte defective	(M) / X	ND	D
At5g16020	NC	*GEX3*	Unique	Uncertain	Female gametophyte defective	+ / X	ND	
At5g39400	NC	*AtPTEN1*	Moderate	Uncertain	Collapsed pollen	(M) / X	ND	D
At5g46860	NC	*SGR3*	High	Uncertain	Null: Male gametophyte defective; Knockdown 1: Serrated, wavy leaves; Semi-dwarf; Late flowering; Knockdown 2: Reduced inflorescence gravitropism	(M) / X	ND	
At5g57320	C	*VLN5*	High	Uncertain	Male gametophyte defective	(M) / X	ND	T

APPENDIX F: Protein Function Classification System

This appendix outlines the protein function classification utilized throughout this thesis. The system includes eleven defined protein functions. Six of these classes are also associated with more detailed subclasses. Two additional classes are incorporated to classify proteins with unknown or unclassified functions. A total of 31 classes and subclasses are outlined.

Phenotype Function Classes

1. DNA Synthesis and Repair
2. RNA Synthesis and Modification
    - 2.1 Transcription Machinery
    - 2.2 PPR and RNA Binding Proteins
    - 2.3 RNA Splicing, Modification, and Degradation
3. Protein Synthesis
    - 3.1 Ribosomal Proteins
    - 3.2 Aminoacyl-tRNA Synthetases
    - 3.3 Translation Machinery
4. Protein Modification and Transport
    - 4.1 Modification; Chaperones
    - 4.2 Protein Transport and Import
5. Protein Degradation
6. Chromosome Dynamics
    - 6.1 Chromatin Structure and Modification
    - 6.2 Chromosome Mechanics; Cell Cycle
7. Transcriptional Regulation
8. Signaling and Regulatory Pathways
9. Energy; Electron Transport
10. Metabolism
    - 10.1 Biosynthesis of Amino Acids, Vitamins, Nucleotides, Fatty Acids
    - 10.2 Biosynthesis of Chlorophyll, Carotenoids, Terpenoids
    - 10.3 Biosynthesis of Lipids; Modification of Fatty Acids and Lipids
    - 10.4 Biosynthesis and Modification of Complex Carbohydrates
    - 10.5 Other Metabolic Pathways and Enzymes
11. Cell Structure; Membrane Function and Trafficking
    - 11.1 Cytoskeleton; Cell Wall; Organelle Biogenesis and Division; Other Structural Proteins
    - 11.2 Membrane Transporters
    - 11.3 Vesicle and Membrane Trafficking and Secretion
12. Remain to be Classified
13. Uncertain and Unknown

APPENDIX G: Multiple Mutant Phenotype Dataset, Gene Information

This appendix includes a truncated version of the dataset describing phenotypes resulting from the disruption of multiple genetically redundant genes. Each row of this appendix represents a gene that contributes to a multiple mutant phenotype. Included data are locus numbers, gene names and aliases, phenotypes observed in single, double, triple, or higher-order multiple mutant combinations, methods used to identify a disrupted gene, types of clusters a gene was associated with (complete / incomplete; simple / complex), and the highest order mutants where genes are found. The full multiple mutant phenotype dataset is available as a spreadsheet appended to the *Plant Physiology* publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S6).

Footnotes for the title row of the following table are described below:

[a] Phenotype class of designated single or multiple mutant. Refer to Appendix B for phenotype class abbreviations. Dash, absence of documented phenotype. When a single row includes an entry in more than one column, the phenotype becomes more severe with increasing order (single mutant, double mutant, triple mutant, etc).

[b] RV, Reverse genetics; MB, Map-based cloning; TD, T-DNA insertion mutant identified through forward genetics; TN, Transposon insertion mutant identified through forward genetics; OTH, Other approach (e.g. analysis of altered biochemical pathway).

[c] Complete clusters involve disruptions of all putative paralogs (BLASTP e-30 cutoff). “Yes” indicates that the phenotype class noted for the highest order multiple mutant includes all putative paralogs.

[d] Exclusive, Single mutants lack an established phenotype; Asymmetric, One (or more) members of the cluster are included in the single gene dataset but others are

not; Symmetric, All members exhibit single mutant phenotypes that differ from that of the multiple mutant; Complex, Three or more genes involved, phenotypes found with two or more groupings of mutants within a single cluster.

[e] Maximal number of genes included in a cluster of putative paralogs with a loss-of-function phenotype. For example, “Double” indicates the gene in question is part of at least one double mutant (but not triple or higher-order mutant) with a documented phenotype.

Locus	**Gene Symbol**	**Alias**	**Single Mutant Phenotype Class**[a]	**Double Mutant Phenotype Class**[a]	**Triple Mutant Phenotype Class**[a]	**>Triple Mutant Phenotype Class**[a]	**Mutant ID Method**[b]	**Complete Cluster Constituent?**[c]	**Cluster Type**[d]	**Highest Order**[e]
At1g01030	*NGA3*	*TOP1*	R	R			RV	No	Complex	Double
At1g01460	*PIPK11*		H	G			RV	No	Symmetric	Double
At1g01480	*ACS2*		V	V	-	S	RV	No	Complex	Octuple
At1g01610	*GPAT4*		-	C			RV	No	Exclusive	Double
At1g02280	*PPI1*	*TOC33*	V	S			TD	Yes	Symmetric	Double
At1g02300	*CathB1*		-	-	I		RV	Yes	Exclusive	Triple
At1g02305	*CathB2*		-	-	I		RV	Yes	Exclusive	Triple
At1g02880	*TPK1*		-	L			RV	Yes	Exclusive	Double
At1g03430	*AHP5*		-	-	V	V	RV	No	Complex	Quadruple
At1g03630	*PORC*		-	L			RV	No	Exclusive	Double
At1g03770	*AtRING1B*		-	L			RV	Yes	Exclusive	Double
At1g04510	*MAC3A*		-	V			RV	Yes	Exclusive	Double
At1g04580	*AAO4*		-	B			RV	No	Complex	Double
At1g05180	*AXR1*		V	S			MB	Yes	Asymmetric	Double
At1g06390	*BIL2*	*GSK1; SK2-3; SK22; GSK1*	-	H	V		RV	No	Complex	Triple
At1g06430	*FTSH8*		-	S			RV	No	Complex	Double
At1g06770	*DRIP1*		-	V			RV	Yes	Exclusive	Double
At1g07360	*MAC5A*		V	L			RV	No	Asymmetric	Double
At1g08320	*TGA9*	*bZIP21*	-	R			RV	No	Exclusive	Double
At1g08860	*BON3*		-	L	L		RV	Yes	Complex	Triple
At1g09000	*ANP1*	*MAPKKK1*	-	V	G		RV	No	Complex	Triple
At1g09240	*NAS3*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At1g09340	*CRB*	*CSP41a*	-	S			RV	Yes	Exclusive	Double
At1g10290	*DRP2A*		-	G			RV	No	Exclusive	Double
At1g10470	*ARR4*	*MEE7*	P	P	H	V	RV	No	Complex	Sextuple
At1g10570	*OTS2*		-	T			RV	Yes	Exclusive	Double
At1g11310	*MLO2*	*PMR2*	I	I			RV	No	Complex	Double

At1g12780	*UGE1*		-	V	V	V	RV	No	Complex	Quadruple
At1g12820	*AFB3*		-	H			UNK	No	Complex	Double
At1g13320	*PP2AA3*		-	V			RV	No	Complex	Double
At1g13860	*QUL1*		-	-	V		RV	No	Asymmetric	Triple
At1g14290	*SBH2*		-	L			RV	Yes	Exclusive	Double
At1g14350	*FLP*	*MYB124*	C	C			MB	Yes	Asymmetric	Double
At1g14360	*AtUTr3*		-	G			RV	Yes	Asymmetric	Double
At1g14400	*UBC1*		V	V	V		RV	No	Complex	Triple
At1g15500	*AtNTT2*		-	P			RV	Yes	Exclusive	Double
At1g15550	*GA4*	*GA3ox1*	V	V	V		TD	No	Complex	Triple
At1g15750	*TPL*	*WSIP1*	-	I	I	L	RV	No	Complex	Pentuple
At1g16190	*RAD23A*		-	-	L		RV	No	Complex	Triple
At1g16300	*GAPCp2*		-	V			RV	No	Exclusive	Double
At1g16460	*STR2*	*RHD2; MST2; ST2*	-	S			RV	Yes	Asymmetric	Double
At1g16890	*UBC13B*		-	C			RV	No	Asymmetric	Double
At1g17060	*CYP72C1*	*SOB7; CHI2*	-	V			RV	No	Asymmetric	Double
At1g17420	*LOX3*		-	V			RV	No	Exclusive	Double
At1g17730	*CHMP1B*		-	S			RV	Yes	Exclusive	Double
At1g17920	*HDG12*		-	C			RV	No	Asymmetric	Double
At1g18080	*RACK1A*		V	V			RV	No	Complex	Double
At1g18800	*NRP2*		-	V			RV	Yes	Exclusive	Double
At1g18870	*ICS2*		-	L			RV	Yes	Asymmetric	Double
At1g20840	*TMT1*		B	B	B		RV	No	Complex	Triple
At1g20900	*ESC*	*ORE7; AHL27*	-	P			RV	No	Exclusive	Double
At1g22920	*CSN5A*	*AJH1*	V	L			RV	No	Symmetric	Double
At1g22990	*HIPP22*		-	-	H		RV	No	Exclusive	Triple
At1g23190	*PGM3*		-	G			RV	No	Exclusive	Double
At1g23380	*KNAT6*	*KNAT6L; KNAT6S*	-	L			RV	No	Asymmetric	Double
At1g23820	*SPDS1*		-	S			RV	No	Exclusive	Double

At1g25410	*AtIPT6*		-	-	-	V	RV	No	Complex	Pentuple
At1g25490	*RCN1*	*EER1; REGA*	V	V			TD	No	Complex	Double
At1g26260	*CIB5*		-	P			RV	No	Exclusive	Double
At1g26310	*CAL*	*AGL10*	-	R			OTH	No	Asymmetric	Double
At1g26670	*VTI1b*	*VTI12*	H	S			RV	No	Symmetric	Double
At1g26780	*LOF1*	*MYB117*	V	V			RV	No	Asymmetric	Double
At1g26830	*AtCUL3*	*AtCUL3A*	-	G			RV	No	Exclusive	Double
At1g27320	*AHK3*		H	V	V		MB	No	Complex	Triple
At1g27390	*TOM20-2*		T	-	V		RV	No	Asymmetric	Triple
At1g27440	*IRX10*	*GUT2*	C	V			RV	No	Asymmetric	Double
At1g29170	*WAVE2*	*AtSCAR3*	-	-	C	C	RV	No	Complex	Quadruple
At1g29400	*AML5*		-	-	-	V	RV	No	Complex	Pentuple
At1g30000	*MNS3*		-	-	V		RV	No	Complex	Triple
At1g30330	*ARF6*		R	V			RV	No	Symmetric	Double
At1g30400	*MRP1*	*ABCC1; EST1*	H	H			RV	No	Symmetric	Double
At1g30490	*PHV*	*AtHB9*	-	V	S	V	RV	No	Complex	Quadruple
At1g31180	*IPMDH1*	*IMD3*	B	G			RV	No	Asymmetric	Double
At1g31340	*RUB1*	*NEDD8*	-	G			RV	No	Exclusive	Double
At1g32230	*RCD1*	*ATP8; CEO1*	V	S			RV	No	Symmetric	Double
At1g32240	*KAN2*		-	R			MB	No	Asymmetric	Double
At1g32770	*ANACO12*	*NST3; SND1*	-	R			RV	No	Asymmetric	Double
At1g33280	*BRN1*	*ANAC015*	-	C	C		RV	No	Complex	Triple
At1g34130	*STT3B*		-	G			RV	Yes	Asymmetric	Double
At1g34210	*SERK2*		-	R			RV	No	Exclusive	Double
At1g35580	*CINV1*		V	V			RV	No	Asymmetric	Double
At1g35720	*AnnAt1*	*OXY5*	P	P			RV	No	Symmetric	Double
At1g37130	*NIA2*	*CHL3; NR2*	H	H			MB	No	Asymmetric	Double
At1g43850	*SEU*		V	S			MB	No	Complex	Double
At1g47056	*VFB1*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At1g48410	*AGO1*	*ICU9*	V	S			TD	No	Symmetric	Double

At1g48605	*HAL3B*		-	S			RV	Yes	Exclusive	Double
At1g48630	*RACK1B*		-	V			RV	No	Complex	Double
At1g49430	*LACS2*	*SMA4; LRD2*	V	V			RV	No	Symmetric	Double
At1g49630	*PreP2*		-	V			RV	Yes	Asymmetric	Double
At1g49760	*PAB8*		-	V	L		RV	No	Complex	Triple
At1g50250	*FTSH1*		-	L			RV	No	Complex	Double
At1g50960	*AtGA2ox7*		-	V			RV	No	Asymmetric	Double
At1g51590	*AtMANIb*		-	H	V		RV	No	Complex	Triple
At1g52150	*ICU4*	*CNA; ATHB-15*	C	V	S	V	MB; RV	No	Complex	Quadruple
At1g53240	*mMDH1*		-	V			RV	No	Exclusive	Double
At1g53470	*MSL4*		-	-	-	B	RV	No	Complex	Pentuple
At1g53700	*WAG1*	*PK3AT*	-	P			RV	No	Asymmetric	Double
At1g54210	*ATG12A*		-	T			RV	Yes	Exclusive	Double
At1g54960	*ANP2*	*MAPKKK2*	V	V	G		RV	No	Complex	Triple
At1g56430	*NAS4*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At1g57820	*VIM1*	*ORTH*	C	B	V		MB; RV	No	Complex	Triple
At1g58200	*MSL3*		-	V			RV	Yes	Exclusive	Double
At1g58300	*HO4*		-	V	V		RV	No	Complex	Triple
At1g59610	*DRP2B*		-	G			RV	No	Exclusive	Double
At1g59750	*ARF1*		-	R			RV	No	Asymmetric	Double
At1g59940	*ARR3*		-	P	H	V	RV	No	Complex	Sextuple
At1g60220	*ULP1D*	*OTS1*	-	T			RV	Yes	Exclusive	Double
At1g60440	*AtPANK1*	*AtCoaA*	-	S			RV	No	Exclusive	Double
At1g61560	*MLO6*		-	I			RV	No	Complex	Double
At1g62360	*STM*	*BUM; WAM1; SHL*	S	L			MB	No	Asymmetric	Double
At1g62830	*LDL1*	*LSD1; SWP1*	T	T			RV	No	Asymmetric	Double
At1g63180	*UGE3*		-	R	V	V	RV	No	Complex	Quadruple
At1g64060	*AtrbohF*		V	L			RV	No	Symmetric	Double

At1g64440	*RHD1*	*REB1; UGE4*	C	V	V	V	MB	No	Complex	Quadruple
At1g64990	*GTG1*		-	H			RV	Yes	Exclusive	Double
At1g65650	*UCH2*		-	V			RV	Yes	Exclusive	Double
At1g65660	*SMP1*		-	L			MB; RV	No	Exclusive	Double
At1g66050	*VIM2*		-	-	V		RV	No	Complex	Triple
At1g66340	*EIN1*	*ETR1*	H	V			OTH	No	Asymmetric	Double
At1g68050	*FKF1*	*ADO3*	T	-	T		MB	Yes	Asymmetric	Triple
At1g68460	*AtIPT1*		-	-	-	V	RV	No	Complex	Pentuple
At1g68740	*PHO1;H1*		-	L			RV	No	Asymmetric	Double
At1g69120	*AP1*	*AGL7*	R	R			OTH	No	Asymmetric	Double
At1g69270	*RPK1*		H	S			RV	No	Symmetric	Double
At1g69560	*LOF2*	*MYB105*	-	V			RV	No	Asymmetric	Double
At1g69640	*SBH1*		-	L			RV	Yes	Exclusive	Double
At1g69670	*CUL3B*		-	G			RV	No	Exclusive	Double
At1g69720	*HO3*		-	V	V		RV	No	Complex	Triple
At1g70310	*SPDS2*		-	S			RV	No	Exclusive	Double
At1g70410	*BCA4*		-	C			TD; RV	No	Exclusive	Double
At1g70730	*PGM2*		-	G			RV	No	Exclusive	Double
At1g71050	HIPP20		-	-	H		RV	No	Exclusive	Triple
At1g71230	*CSN5B*	*AJH2*	C	L			RV	No	Symmetric	Double
At1g71830	*SERK1*		-	R			RV	No	Exclusive	Double
At1g72520	*LOX4*		-	V			RV	No	Exclusive	Double
At1g73030	*CHMP1A*		-	S			RV	Yes	Exclusive	Double
At1g73360	*HDG11*		C	C			RV	No	Asymmetric	Double
At1g74560	*NRP1*		-	V			RV	Yes	Exclusive	Double
At1g74710	*SID2*	*EDS16; ICS1*	I	L			MB; OTH	Yes	Asymmetric	Double
At1g75950	*ASK1*	*SKP1A; UIP1*	R	S			TN	No	Asymmetric	Double
At1g76490	*HMG1*	*HMGR1*	V	G			RV	Yes	Asymmetric	Double
At1g76500	*SOB3*	*AHL29*	-	P			RV	No	Exclusive	Double
At1g77760	*NIA1*	*NR1*	-	H			RV	No	Asymmetric	Double

At1g78240	*TSD2*	*QUA2*	L	-	V		MB	No	Asymmetric	Triple
At1g78610	*MSL6*		-	-	-	B	RV	No	Complex	Pentuple
At1g78870	*UBC13A*		H	C			RV	No	Asymmetric	Double
At1g79230	*STR1*	*MST1; RDH1; ST1*	S	S			RV	Yes	Asymmetric	Double
At1g79250	*AGC1.7*		-	G			RV	No	Exclusive	Double
At1g79530	*GAPCp1*		-	V			RV	No	Exclusive	Double
At1g79580	*SMB*	*ANAC033*	C	-	C		MB; RV	No	Complex	Triple
At1g79650	*RAD23B*		V	-	L		RV	No	Complex	Triple
At1g80300	*AtNTT1*		-	P			RV	Yes	Exclusive	Double
At1g80330	*GA3ox4*		-	V	V		RV	No	Complex	Triple
At1g80340	*GA3ox2*		-	V	R		RV	No	Complex	Triple
At1g80490	*TPR1*		-	I	I	L	RV	No	Complex	Pentuple
At1g80560	*IPMDH2*		-	G			RV	No	Asymmetric	Double
At1g80840	*WRKY40*		-	I	I		RV	Yes	Complex	Triple
At2g01830	*CRE1*	*WOL; AHK4*	V	-	V		TD	No	Complex	Triple
At2g02760	*AtUBC2*		-	V	V		RV	No	Complex	Triple
At2g02810	*AtUTr1*		B	G			RV	Yes	Asymmetric	Double
At2g02820	*MYB88*		-	C			RV	Yes	Asymmetric	Double
At2g03480	*QUL2*		-	-	V		RV	No	Asymmetric	Triple
At2g11810	*MGDC*	*MGD3*	-	H			RV	No	Exclusive	Double
At2g13560	*AtNAD-ME1*		-	B			RV	No	Exclusive	Double
At2g14120	*DRP3B*		C	V			RV	No	Symmetric	Double
At2g14750	*APK1*		-	V	G		RV	No	Complex	Triple
At2g14820	*NPY2*	*MEL3*	-	-	-	V	RV	No	Asymmetric	Pentuple
At2g16500	*ADC1*	*ARGDC; SPE1*	-	S			RV	Yes	Asymmetric	Double
At2g16640	*TOC132*		-	S			UNK	No	Asymmetric	Double
At2g17370	*HMG2*	*HMGR2*	-	G			RV	Yes	Asymmetric	Double
At2g17420	*NTRA*		-	V			RV	No	Exclusive	Double
At2g17780	*MCA2*		-	V			RV	Yes	Asymmetric	Double
At2g18915	*LKP2*	*ADO2*	-	-	T		RV	Yes	Asymmetric	Triple

At2g18960	*AHA1*	*OST2; PMA*	-	S			RV	No	Exclusive	Double
At2g19110	*HMA4*		-	L			RV	No	Exclusive	Double
At2g19480	*AtNAP1;2*	*NFA2*	-	-	P		RV	No	Exclusive	Triple
At2g20000	*HBT*	*CDC72b*	L	G			UNK	Yes	Asymmetric	Double
At2g20570	*GPRI1*	*GLK1*	-	V			RV	Yes	Asymmetric	Double
At2g21410	*VHA-A2*		-	V			RV	No	Exclusive	Double
At2g21770	*CESA9*		-	-	G		RV	No	Complex	Triple
At2g22300	*SR1*	*CAMTA3*	V	P			RV	No	Asymmetric	Double
At2g22310	*UBP4*		-	G			RV	Yes	Exclusive	Double
At2g22330	*CYP79B3*		-	V			RV	No	Exclusive	Double
At2g22780	*PMDH1*		P	L			RV	No	Symmetric	Double
At2g22810	*ACS4*		V	V	-	S	RV	No	Complex	Octuple
At2g23050	*NPY4*	*MEL4*	-	-	-	V	RV	No	Asymmetric	Pentuple
At2g23150	*NRAMP3*		-	H			RV	No	Exclusive	Double
At2g23350	*PAB4*		-	V	L		RV	No	Complex	Triple
At2g23760	*BLH4*	*SAW2*	-	V			RV	No	Exclusive	Double
At2g24050	*eIFiso4G2*		-	V			RV	No	Exclusive	Double
At2g25000	*WRKY60*		-	I	I		RV	Yes	Complex	Triple
At2g25490	*EBF1*	*FBL6*	H	V			RV	No	Symmetric	Double
At2g26040	*PYL2*	*RCAR14*	-	-	-	H	RV	No	Complex	Quadruple
At2g26080	*AtGLDP2*		-	L			RV	Yes	Exclusive	Double
At2g26330	*ER*	*QRP1*	V	V			TD	No	Complex	Double
At2g26670	*HY6*	*GUN2; HY6; TED4; HY1; HO1*	V	V	V		MB	No	Complex	Triple
At2g26710	*BAS1*	*CYP72B1; CYP734A1*	V	V			RV	No	Asymmetric	Double
At2g27150	*AAO3*		V	B			MB	No	Complex	Double
At2g27990	*BLH8*	*PNF*	-	V			RV	No	Asymmetric	Double
At2g28110	*FRA8*	*IRX7*	V	V			RV	No	Asymmetric	Double
At2g28550	*TOE1*	*RAP2.7*	T	T	-	T	RV	No	Complex	Quadruple
At2g29580	*MAC5B*		-	L			RV	No	Asymmetric	Double

At2g30110	*AtUBA1*	*MOS5*	I	L			MB	Yes	Asymmetric	Double
At2g30250	*WRKY25*		-	H			RV	No	Asymmetric	Double
At2g30580	*DRIP2*		-	V			RV	Yes	Exclusive	Double
At2g30950	*VAR2*	*FtsH2*	V	S			MB	No	Complex	Double
At2g30980	*ASKdZeta*	*BIL1;* *AtSK2-2;* *AtSK23*	-	H	V		RV	No	Complex	Triple
At2g32370	*HDG3*		-	V			RV	No	Complex	Double
At2g32410	*AXL*		-	S			RV	Yes	Asymmetric	Double
At2g32700	*LUH*		V	S			RV	Yes	Symmetric	Double
At2g33340	*MAC3B*		-	V			RV	Yes	Exclusive	Double
At2g33860	*ETT*	*ARF3*	R	V			TD	No	Asymmetric	Double
At2g34150	*WAVE1*	*AtRanGAP2;* *SCAR1*	-	-	C	C	RV	No	Complex	Quadruple
At2g34660	ABCC2	*MRP2;* *EST4*	H	H			RV	No	Symmetric	Double
At2g34710	*PHB*	*AtHB14*	-	L	S	V	RV	No	Complex	Quadruple
At2g35350	*PLL1*		R	S			RV	No	Symmetric	Double
At2g35490	*FIB2*		-	-	V		RV	Yes	Exclusive	Triple
At2g35510	*SRO1*		V	S			RV	No	Symmetric	Double
At2g35635	*RUB2*	*UBQ7*	-	G			RV	No	Exclusive	Double
At2g35930	*PUB23*		P	-	I		RV	No	Asymmetric	Triple
At2g35990	*LOG2*		-	H			RV	No	Complex	Double
At2g36250	*FTSZ2-1*		-	C			RV	No	Exclusive	Double
At2g36910	*AtPGP1*	*ABCB1*	V	V			RV	No	Symmetric	Double
At2g37040	*PAL1*		-	R			RV	No	Exclusive	Double
At2g37210	*LOG3*		-	-	V		RV	No	Complex	Triple
At2g38170	*CAX1*		V	V			RV	No	Symmetric	Double
At2g38230	*PDX1.1*		V	S			RV	No	Symmetric	Double
At2g38310	*PYL4*	*RCAR10*	-	-	H	H	RV	No	Complex	Quadruple
At2g38440	*ITB1*	*SCAR2;* *DIS3;* *WAVE1*	C	C	C	C	MB	No	Complex	Quadruple

At2g38470	*WRKY33*		H	H			RV	No	Asymmetric	Double
At2g38750	*AnnAt4*		H	P			RV	No	Symmetric	Double
At2g39200	*MLO12*		-	I			RV	No	Complex	Double
At2g39250	*SNZ*		-	-	-	T	RV	No	Complex	Quadruple
At2g40300	*AtFER4*		-	-	H		RV	No	Asymmetric	Triple
At2g40750	*WRKY54*		-	B			RV	Yes	Asymmetric	Double
At2g40940	*ERS1*		-	V			RV	No	Asymmetric	Double
At2g41210	*PIP5K5*		-	G			RV	No	Asymmetric	Double
At2g41310	*ARR8*		V	V	-	V	RV	No	Complex	Sextuple
At2g41560	*ACA4*		V	V			RV	No	Asymmetric	Double
At2g42680	*AtMBF1a*		-	-	H		RV	Yes	Exclusive	Triple
At2g42790	*CSY3*		-	V			RV	No	Exclusive	Double
At2g42830	*SHP2*	*AGL5*	-	R			RV	No	Exclusive	Double
At2g42890	*AML2*		-	-	L	V	RV	No	Complex	Pentuple
At2g43790	*AtMPK6*	*MAPK6*	H	S			RV	No	Symmetric	Double
At2g44750	*TPK2*		-	L			RV	Yes	Exclusive	Double
At2g44900	*ARABIDILLO-1*		-	P			RV	Yes	Exclusive	Double
At2g45150	*CDS4*		-	G			RV	Yes	Exclusive	Double
At2g45160	*HAM1*	*LOM1*	-	-	V		RV	No	Exclusive	Triple
At2g45190	*FIL*	*AFO*	V	V			MB	No	Asymmetric	Double
At2g46070	*MPK12*		-	C			RV	No	Exclusive	Double
At2g46770	*ANAC043*	*NST1*	R	R			RV	No	Asymmetric	Double
At2g46790	*APRR9*	*TL1*	P	T			RV	No	Symmetric	Double
At2g46870	*NGA1*		-	R			RV	No	Complex	Double
At2g46920	*POL*		R	S			MB	No	Symmetric	Double
At2g47240	*LACS1*	*CER8*	V	V			RV	No	Symmetric	Double
At3g01150	*PTB1*		-	G			RV	No	Exclusive	Double
At3g01500	*BCA1*	*SABP3; CA1*	-	C			TD; RV	No	Exclusive	Double
At3g01650	*RGLG1*		-	V			RV	No	Exclusive	Double
At3g02130	*RPK2*	*TOAD2*	V	S			RV	No	Symmetric	Double
At3g02230	*RGP1*		-	G			RV	No	Exclusive	Double

At3g02470	*SAMDC*		V	S			RV	No	Symmetric	Double
At3g02540	*RAD23C*	*RAD23-3*	-	-	L		RV	No	Complex	Triple
At3g03110	*XPO1B*	*CRM1B*	-	G			RV	Yes	Exclusive	Double
At3g03250	*UGP1*		-	V			RV	Yes	Exclusive	Double
At3g03900	*APK3*		-	-	G		RV	No	Complex	Triple
At3g04240	*SEC*		H	G			RV	Yes	Symmetric	Double
At3g04690	*ANX1*		-	G			RV	No	Exclusive	Double
At3g05120	*GID1a*		-	V	V		TD; RV	No	Complex	Triple
At3g05630	*PLDP2*	*PDLZ2*	V	H			RV	Yes	Asymmetric	Double
At3g06030	*ANP3*	*MAPKKK12*	-	V	G		RV	No	Complex	Triple
At3g06490	*MYB108*	*BOS1*	R	R			RV	No	Complex	Double
At3g06930	*PRMT4b*		-	T			RV	No	Exclusive	Double
At3g07740	*ADA2a*	*HAC10; HXA2*	-	V			RV	Yes	Asymmetric	Double
At3g07780	*OBE1*		-	L			RV	No	Exclusive	Double
At3g07980	*MAPKKK6*	*MAP3k{e}2*	-	G			RV	No	Exclusive	Double
At3g08500	*MYB83*		-	V			RV	No	Exclusive	Double
At3g08720	*S6K2*	*PK2; PK19*	R	G			RV	No	Asymmetric	Double
At3g08730	*S6K1*	*PK1; PK6*	-	G			RV	No	Asymmetric	Double
At3g09560	*AtPAH1*		-	H			RV	Yes	Exclusive	Double
At3g10160	*FPGS2*	*DFC*	-	S			RV	No	Complex	Double
At3g11330	*PIRL9*		-	G			RV	No	Exclusive	Double
At3g11540	*SPY*		V	G			TD	Yes	Symmetric	Double
At3g11840	*PUB24*		-	-	I		RV	No	Asymmetric	Triple
At3g12250	*TGA6*	*BZIP45*	-	-	I		RV	No	Exclusive	Triple
At3g12690	*AGC1.5*		-	G			RV	No	Exclusive	Double
At3g12990	*RRP45a*		-	G			RV	Yes	Asymmetric	Double
At3g13530	*MAPKKK7*	*MAP3k{e}1*	-	G			RV	No	Exclusive	Double
At3g13682	*LDL2*		-	T			RV	No	Asymmetric	Double
At3g13730	*CYP90D1*		-	V			RV	No	Asymmetric	Double
At3g13970	*ATG12B*		-	T			RV	Yes	Exclusive	Double
At3g14270	*FAB1B*		V	G			RV	No	Symmetric	Double

At3g14370	*WAG2*		P	P			RV	No	Asymmetric	Double
At3g14810	*MSL5*		-	-	-	B	RV	No	Complex	Pentuple
At3g15020	*mMDH2*		-	V			RV	No	Exclusive	Double
At3g15170	*CUC1*	*ANAC054; AtNAC1*	V	S			TD	No	Symmetric	Double
At3g15880	*TPR4*	*WSIP2*	-	-	I	L	RV	No	Complex	Pentuple
At3g16320	*CDC27a*		-	G			RV	Yes	Asymmetric	Double
At3g16785	*PLDP1*	*PLDZ1, PLD(Z)1*	-	H			RV	Yes	Asymmetric	Double
At3g16830	*TPR2*		-	-	-	L	RNAi	No	Complex	Pentuple
At3g17360	*POK1*		-	V			RV	No	Exclusive	Double
At3g18030	*HAL3A*		-	S			RV	Yes	Exclusive	Double
At3g18040	*MPK9*		-	C			RV	No	Exclusive	Double
At3g18130	*RACK1C*		-	V			RV	No	Complex	Double
At3g18660	*GUX1*	*PGSIP1*	B	B			RV	No	Symmetric	Double
At3g19050	*POK2*		-	V			RV	No	Exclusive	Double
At3g19170	*PreP1*		V	V			RV	Yes	Asymmetric	Double
At3g19290	*AREB2*	*ABF4*	-	V			RV	No	Exclusive	Double
At3g19450	*CAD-C*	*CAD4*	-	V			RV	No	Exclusive	Double
At3g21160	*AtMANIa*		-	H	V		RV	No	Complex	Triple
At3g21510	*AHP1*		-	-	H	V	RV	No	Complex	Quadruple
At3g23430	*PHO1*		B	L			MB	No	Asymmetric	Double
At3g23580	*RNR2A*		-	L			RV	Yes	Asymmetric	Double
At3g23630	*AtIPT7*		-	-	V	V	RV	No	Complex	Pentuple
At3g23670	*PAKRP1L*	*KINESIN-12B*	-	G			RV	No	Exclusive	Double
At3g23920	*BAM1*		-	B	B		RV	No	Complex	Triple
At3g24500	*AtMBF1c*		-	-	H		RV	Yes	Exclusive	Triple
At3g25800	*PP2AA2*	*PDF1; PR65*	-	V			RV	No	Complex	Double
At3g26810	*AFB2*		-	H			UNK	No	Complex	Double
At3g27060	*TSO2*		V	L			MB	Yes	Asymmetric	Double
At3g27080	*TOM20-3*		-	-	V		RV	No	Asymmetric	Triple

At3g27280	*PHB4*		-	L			RV	No	Asymmetric	Double
At3g28860	*PGP19*	*ABCB19; MDR1; MDR11; MDL15.2*	V	V			RV	No	Symmetric	Double
At3g29350	*AHP2*		-	H	V	V	RV	No	Complex	Quadruple
At3g30180	*BR6OX2*	*CYP85A2*	V	V			RV	No	Asymmetric	Double
At3g43190	*SUS4*		-	B			RV	No	Exclusive	Double
At3g45640	*AtMPK3*		H	S			RV	No	Symmetric	Double
At3g45780	*NPH1*	*RPT1*	P	C			TD	No	Symmetric	Double
At3g47460	*AtSMC2*	*AtCAP-E2*	-	G			TD	No	Asymmetric	Double
At3g48100	*ARR5*	*IBC6*	P	P	-	V	RV	No	Complex	Sextuple
At3g48190	*ATM*		R	R			RV	No	Asymmetric	Double
At3g48780	*LCB2a*	*AtSPT1*	-	G			RV	No	Exclusive	Double
At3g48870	*HSP93-III*		-	G			RV	No	Asymmetric	Double
At3g49670	*BAM2*		-	V	V		RV	No	Complex	Triple
At3g49700	*ACS9*	*ETO3*	V	V	-	S	RV	No	Complex	Octuple
At3g50080	*VFB2*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At3g50220	*IRX15*		-	B			RV	No	Exclusive	Double
At3g50500	*SnRK2.2*	*SPK-2-2; SRK2D*	V	V			RV	No	Symmetric	Double
At3g51490	*TMT3*		-	-	B		RV	No	Complex	Triple
At3g51860	*CAX3*	*CAX1-LIKE; AtHCX1*	H	V			RV	No	Symmetric	Double
At3g52450	*PUB22*		P	-	I		RV	No	Asymmetric	Triple
At3g52750	*FTSZ2-2*		-	C			RV	No	Exclusive	Double
At3g53260	*PAL2*		-	R			RV	No	Exclusive	Double
At3g53450	*LOG4*		-	-	V		RV	No	Complex	Triple
At3g54990	*SMZ*		-	-	-	T	RV	No	Complex	Quadruple
At3g55630	*FPGS3*	*DFD*	B	G			RV	No	Complex	Double
At3g56090	*AtFER3*		-	-	H		RV	No	Asymmetric	Triple
At3g56400	*WRKY70*		H	B			RV	Yes	Asymmetric	Double

At3g56960	*PIP5K4*		C	G			RV	No	Asymmetric	Double
At3g57040	*ARR9*	*AtRR4*	V	V	-	V	RV	No	Complex	Sextuple
At3g57330	*ACA11*		-	V			RV	No	Asymmetric	Double
At3g58680	*AtMBF1b*		-	-	H		RV	Yes	Exclusive	Triple
At3g58750	*CSY2*		-	V			RV	No	Exclusive	Double
At3g58780	*SHP1*	*AGL1*	-	R			RV	No	Exclusive	Double
At3g60350	*ARABIDILLO-2*		-	P			RV	Yes	Exclusive	Double
At3g60500	*CER7*	*G3*	V	G			MB; RV	Yes	Asymmetric	Double
At3g60620	*CDS5*		-	G			RV	Yes	Exclusive	Double
At3g60630	*HAM2*	*LOM2*	-	-	V		RV	No	Exclusive	Triple
At3g61650	*TubG1*		-	G			RV	No	Exclusive	Double
At3g61970	*NGA2*		-	R			RV	No	Complex	Double
At3g62980	*TIR1*		V	H			TD	No	Complex	Double
At3g63010	*GID1b*		-	V	V		TD; RV	No	Complex	Triple
At3g63110	*AtIPT3*		-	-	V	V	RV	No	Complex	Pentuple
At3g63130	*RG1*		-	G			RV	No	Exclusive	Double
At3g63140	*CSP41a*		-	S			RV	Yes	Exclusive	Double
At4g00150	*HAM3*	*LOM3*	-	-	V		RV	No	Exclusive	Triple
At4g00180	*YAB3*		-	V			RV	No	Asymmetric	Double
At4g00400	*GPAT8*		-	C			RV	No	Exclusive	Double
At4g00570	*AtNAD-ME2*		-	B			RV	No	Exclusive	Double
At4g01190	*PIPK10*		H	G			RV	No	Symmetric	Double
At4g01610	*CathB3*		-	-	I		RV	Yes	Exclusive	Triple
At4g02510	*PPI2*	*TOC159*	L	S			RV	No	Asymmetric	Double
At4g04020	*FIB1a*		-	-	V		RV	Yes	Exclusive	Triple
At4g04890	*PDF2*		-	L			RV	No	Complex	Double
At4g07400	*VFB3*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At4g08040	*ACS11*		-	-	-	S	RV	No	Complex	Octuple
At4g09510	*CINV2*		-	V			RV	No	Asymmetric	Double
At4g10350	*BRN2*		-	C	C		RV	No	Complex	Triple
At4g10960	*UGE5*		-	-	V	V	RV	No	Complex	Quadruple

At4g11260	*EDM1*	*SGT1B; ETA3*	I	S			MB	Yes	Asymmetric	Double
At4g11280	*ACS6*		V	V	-	S	RV	No	Complex	Octuple
At4g11660	*HsfB2b*		I	I			RV	No	Asymmetric	Double
At4g11960	*PGRL1B*		-	V			RV	Yes	Exclusive	Double
At4g13260	*YUC2*		-	V	V	V	RV	No	Complex	Quadruple
At4g14150	*PAKRL1*	*KINESIN-12A*	-	G			RV	No	Exclusive	Double
At4g16420	*PRZ1*	*ADA2B*	H	V			TD	Yes	Asymmetric	Double
At4g16760	*ACX1*		-	L			RV	No	Asymmetric	Double
At4g17090	*CT-BMY*	*BAM3; BMY8*	V	B	B		RV	No	Complex	Triple
At4g17190	*FPS2*		-	L			RV	Yes	Exclusive	Double
At4g17360			-	V			RV	Yes	Exclusive	Double
At4g17600	*LIL3:1*		-	V			RV	Yes	Exclusive	Double
At4g17870	*PYR1*	*RCAR11*	H	-	H	H	MB	No	Complex	Quadruple
At4g18120	*AML3*		-	-	-	V	RV	No	Complex	Pentuple
At4g18480	*CH42*	*PDE314; CHLI1*	L	L			TD	No	Asymmetric	Double
At4g18710	*BIN2*	*DWF12; SK21; UCU1*	H	-	V		MB; RV	No	Complex	Triple
At4g20140	*GSO1*		-	S			RV	No	Exclusive	Double
At4g20270	*BAM3*		-	-	V		RV	No	Complex	Triple
At4g21200	*AtGA2ox8*		V	V			RV	No	Asymmetric	Double
At4g21690	*GA3ox3*		-	R	V		RV	No	Complex	Triple
At4g21750	*AtML1*		-	L			RV	No	Complex	Double
At4g22240	*FIB1b*		-	-	V		RV	Yes	Exclusive	Triple
At4g22890	*PGRL1A*		-	V			RV	Yes	Exclusive	Double
At4g23570	*SGT1a*		-	S			RV	Yes	Asymmetric	Double
At4g23920	*UGE2*		P	V	V	V	RV	No	Complex	Quadruple
At4g24280	*cpHsc70-1*		V	G			RV	No	Asymmetric	Double
At4g25230	*RIN2*		I	B			RV	Yes	Asymmetric	Double

At4g25420	*GA5*	*GA20ox1*	V	V			MB	No	Symmetric	Double
At4g25520	*SLK1*		-	V			RV	No	Complex	Double
At4g25700	*BETA-OHASE1*	*B1; BCH1; CHY1*	-	V			RV	Yes	Exclusive	Double
At4g26110	*AtNAP1;1*		-	-	P		RV	No	Exclusive	Triple
At4g26200	*ACS7*		T	V	-	S	RV	No	Complex	Octuple
At4g26690	*SHV3*	*MRH5; GPDL2*	C	V			RV	No	Asymmetric	Double
At4g26840	*SUM1*	*SUMO1*	-	S			RV	Yes	Exclusive	Double
At4g26850	*VTC2*		V	L			RV	Yes	Asymmetric	Double
At4g27440	*PORB*		-	L			RV	No	Exclusive	Double
At4g27630	*GTG2*		-	H			RV	Yes	Exclusive	Double
At4g27780	*ACBP2*		-	S			RV	Yes	Asymmetric	Double
At4g28490	*HAE*	*RLK5*	-	R			RV	No	Exclusive	Double
At4g30110	*HMA2*		-	L			RV	No	Exclusive	Double
At4g30190	*AHA2*	*PMA2*	-	S			RV	No	Exclusive	Double
At4g31700	*RPS6A*		V	G			RV	Yes	Asymmetric	Double
At4g31800	*WRKY18*		I	I	I		RV	Yes	Complex	Triple
At4g31820	*ENP*	*MAB4; NPY1*	R	-	-	V	MB	No	Asymmetric	Pentuple
At4g32180	*AtPANK2*		-	S			RV	No	Exclusive	Double
At4g32540	*YUC1*		-	V	V	V	RV	No	Complex	Quadruple
At4g32551	*LUG*	*RON2*	R	S			MB	Yes	Symmetric	Double
At4g32730	*PC-MYB1*	*MYB3R1*	-	V			RV	No	Exclusive	Double
At4g32880	*AtHB8*		-	-	-	V	RV	No	Complex	Quadruple
At4g33010	*AtGLDP1*		-	L			RV	Yes	Exclusive	Double
At4g33240	*FAB1A*		V	G			RV	No	Symmetric	Double
At4g33330	*GUX2*	*PGSIP3*	B	B			RV	No	Symmetric	Double
At4g33650	*DRP3A*	*ADL2*	C	V			MB	No	Symmetric	Double
At4g34000	*ABF3*	*DPBF5*	-	V			RV	No	Exclusive	Double
At4g34110	*PAB2*	*PABP2*	-	V	L		RV	No	Complex	Triple
At4g34230	*CAD-D*	*CAD5*	-	V			RV	No	Exclusive	Double
At4g34530	*CIB1*		-	P			RV	No	Exclusive	Double

At4g34710	*ADC2*	*SPE2*	V	S			MB	Yes	Asymmetric	Double
At4g34840	*MTN2*	*MTAN2*	-	R			RV	Yes	Asymmetric	Double
At4g35300	*TMT2*		-	B	B		RV	No	Complex	Triple
At4g35460	*NTRB*		-	V			RV	No	Exclusive	Double
At4g35920	*MCA1*		P	V			RV	Yes	Asymmetric	Double
At4g36280	*CRH1*		-	I			RV	No	Exclusive	Double
At4g36290	*CRT1*		-	I			RV	No	Exclusive	Double
At4g36380	*ROT3*	*CYP90C1*	V	V			TD	No	Asymmetric	Double
At4g36870	*BLH2*	*SAW1*	-	V			RV	No	Exclusive	Double
At4g36890	*IRX14*		C	V			RV	Yes	Asymmetric	Double
At4g36990	*HsfB1*		-	I			RV	No	Asymmetric	Double
At4g37120	*SMP2*		-	L			OTH	No	Exclusive	Double
At4g37590	*NPY5*	*MEL1*	-	-	-	V	RV	No	Asymmetric	Pentuple
At4g37770	*ACS8*		-	-	-	S	RV	No	Complex	Octuple
At4g38800	*MTN1*	*MTAN1*	H	R			RV	Yes	Asymmetric	Double
At4g39080	*VHA-A3*		-	V			RV	No	Exclusive	Double
At4g39350	*CESA2*	*ATH-A*	V	V	G		TN	No	Complex	Triple
At4g39910	*UBP3*		-	G			RV	Yes	Exclusive	Double
At4g39940	*APK2*		-	V	P		RV	No	Complex	Triple
At4g39950	*CYP79B2*		-	V			RV	No	Exclusive	Double
At5g01410	*RSR4*	*PDX1.3*	V	S			MB	No	Symmetric	Double
At5g01600	*AtFER1*		T	-	H		RV	No	Asymmetric	Triple
At5g01730	*AtSCAR4*		-	C	-	C	RV	No	Complex	Quadruple
At5g02030	*LSN*	*BLR; PNY; RPL; VAN*	V	V			TD	No	Asymmetric	Double
At5g02810	*PRR7*		V	T			MB	No	Symmetric	Double
At5g04950	*NAS1*		-	-	-	V	RV	Yes	Exclusive	Quadruple
At5g05000	*TOC34*	*OEP34*	V	S			TD	Yes	Symmetric	Double
At5g05620	*TubG2*		-	G			RV	No	Exclusive	Double
At5g05850	*PIRL1*		-	G			RV	No	Exclusive	Double
At5g05980	*FPGS1*	*DFB*	-	G			RV	No	Complex	Double
At5g06300	*LOG7*		-	H	V		RV	No	Complex	Triple

At5g06460	*AtUBA2*		-	L			RV	Yes	Asymmetric	Double
At5g06839	*TGA10*	*bZIP65*	-	R			RV	No	Exclusive	Double
At5g06950	*TGA2*	*AHBP-1B*	-	-	I		RV	No	Exclusive	Triple
At5g06960	*TGA5*	*OBF5*	-	-	I		RV	No	Exclusive	Triple
At5g07180	*ERL2*		-	R			RV	No	Complex	Double
At5g07290	*AML4*		-	L	L	V	RV	No	Complex	Pentuple
At5g07300	*BON2*	*CPN1?*	-	L	L		RV	Yes	Complex	Triple
At5g07350	*TSN1*	*TUDOR1*	-	V			RV	Yes	Exclusive	Double
At5g07440	*GDH2*		H	P			RV	No	Symmetric	Double
At5g07690	*AtMYB29*		-	V			RV	No	Complex	Double
At5g09410	*CAMTA1*		-	P			RV	No	Asymmetric	Double
At5g09660	*PMDH2*		V	L			RV	No	Symmetric	Double
At5g09790	*PDE336*	*ATXR5*	V	V			RV	Yes	Asymmetric	Double
At5g09870	*CESA5*		-	L			RV	No	Complex	Double
At5g09900	*EMB2107*	*RPN5A;* *MSA*	S	G			TD	Yes	Asymmetric	Double
At5g10030	*TGA4*	*OBF4*	-	I			RV	No	Exclusive	Double
At5g10360	*EMB3010*	*RPS6B*	-	G			TD	Yes	Asymmetric	Double
At5g10470	*KAC1*	*KCA1*	C	C			MB; RV	No	Asymmetric	Double
At5g10490	*MSL2*		-	V			RV	Yes	Exclusive	Double
At5g11320	*YUC4*		-	V	V	V	RV	No	Complex	Quadruple
At5g11510	*MYB3R-4*		-	V			RV	No	Exclusive	Double
At5g12080	*MSL10*		B	B	-	B	RV	No	Complex	Pentuple
At5g12180	*CPK17*		-	G			RV	No	Exclusive	Double
At5g12870	*MYB46*		-	V			RV	No	Exclusive	Double
At5g14420	*RGLG2*		-	V			RV	No	Exclusive	Double
At5g15650	*RGP2*		-	G			RV	No	Exclusive	Double
At5g16310	*UCH1*		-	V			RV	Yes	Exclusive	Double
At5g16560	*KAN*		V	R			TD	No	Asymmetric	Double
At5g17020	*XPO1A*	*AtCRM1;* *AtXPO1*	-	G			RV	Yes	Exclusive	Double
At5g17310	*UGP2*		-	V			RV	Yes	Exclusive	Double

At5g17450	HIPP21		-	-	H		RV	No	Exclusive	Triple
At5g18170	*GDH1*		H	P			OTH	No	Symmetric	Double
At5g18930	*BUD2*	*SAMDC4*	V	S			TD; RV	No	Symmetric	Double
At5g19040	*AtIPT5*		-	-	V	V	RV	No	Complex	Pentuple
At5g19320	*RG2*		-	G			RV	No	Exclusive	Double
At5g19360	*CPK34*		-	G			RV	No	Exclusive	Double
At5g19520	*MSL9*		B	B	-	B	RV	No	Complex	Pentuple
At5g19690	*STT3A*		V	G			RV	Yes	Asymmetric	Double
At5g20410	*MGD2*		-	H			TD	No	Exclusive	Double
At5g20830	*SUS1*		-	B			RV	No	Exclusive	Double
At5g20960	*AAO1*	*ATAO*	-	B			RV	No	Complex	Double
At5g22940	*F8H*		-	V			RV	No	Asymmetric	Double
At5g23670	*LCB2c*		-	G			RV	No	Exclusive	Double
At5g23730	*RUP2*	*EFO2*	P	P			RV	No	Asymmetric	Double
At5g24330	*ATXR6*		-	V			RV	Yes	Asymmetric	Double
At5g25350	*EBF2*		P	V			RV	No	Symmetric	Double
At5g25620	*YUC6*		-	V	V	V	RV	No	Complex	Quadruple
At5g25980	*TGG2*		-	B			RV	No	Exclusive	Double
At5g26000	*TGG1*		-	B			RV	No	Exclusive	Double
At5g27030	*TPR3*		-	-	-	L	RV	No	Complex	Pentuple
At5g27320	*GID1c*		-	V	V		RV	No	Complex	Triple
At5g28680	*ANX2*		-	G			RV	No	Exclusive	Double
At5g35750	*AHK2*		-	V	V		RV	No	Complex	Triple
At5g37020	*ARF8*		V	V			RV	No	Symmetric	Double
At5g38470	*RAD23D*		-	-	L		RV	No	Complex	Triple
At5g38970	*BR6OX1*		-	V			RV	No	Asymmetric	Double
At5g39340	*AHP3*		-	H	V	V	RV	No	Complex	Quadruple
At5g39510	*ZIG*	*SGR4;* *VTI11*	V	S			MB	No	Symmetric	Double
At5g39550	*VIM3*		-	B	V		RV	No	Complex	Triple
At5g40770	*PHB3*		V	L			RV	No	Asymmetric	Double
At5g40820	*AtRAD3*	*AtATR*	-	R			RV	No	Asymmetric	Double

At5g40930	*TOM20-4*		-	-	V		RV	No	Asymmetric	Triple
At5g42190	*ASK2*	*SKP1B*	-	S			RV	No	Asymmetric	Double
At5g42270	*VAR1*	*FTSH5*	V	L			TD	No	Complex	Double
At5g42870	*AtPAH2*		-	H			RV	Yes	Exclusive	Double
At5g43810	*ZLL*	*PNH*	L	S			MB	No	Symmetric	Double
At5g44190	*GLK2*	*GPR12*	R	V			RV	Yes	Asymmetric	Double
At5g44280	*AtRING1A*		-	L			RV	Yes	Exclusive	Double
At5g44700	*GSO2*	*EDA23*	-	S			RV	No	Exclusive	Double
At5g45930	*CHLI2*		-	L			RV	No	Asymmetric	Double
At5g46790	*PYL1*	*RCAR12*	-	-	H	H	RV	No	Complex	Quadruple
At5g47110	*LIL3:2*		-	V			RV	Yes	Exclusive	Double
At5g47435	PurU		-	V			RV	Yes	Exclusive	Double
At5g47770	*FPS1*		-	L			RV	Yes	Exclusive	Double
At5g47910	*RbohD*		V	L			RV	No	Symmetric	Double
At5g48160	*OBE2*		-	L			RV	No	Exclusive	Double
At5g49020	*PRMT4a*		-	T			RV	No	Exclusive	Double
At5g49910	*cpHsc70-2*		-	G			RV	No	Asymmetric	Double
At5g50920	*DCA1*	*CLPC1;* *HSP93-V*	V	G			RV	No	Asymmetric	Double
At5g51450	*RIN3*		-	B			RV	Yes	Asymmetric	Double
At5g51810	*GA20ox2*	*AT2353*	V	V			RV	No	Symmetric	Double
At5g52250	*RUP1*	*EFO1*	-	P			RV	No	Asymmetric	Double
At5g52570	*B2*	*CHY2;* *BCH2*	-	V			RV	Yes	Exclusive	Double
At5g53180	*PTB2*		-	G			RV	No	Exclusive	Double
At5g53470	*ACBP1*		P	S			UNK	Yes	Asymmetric	Double
At5g53950	*CUC2*	*ANAC098*	V	S			TD	No	Symmetric	Double
At5g55120	*VTC5*		-	L			RV	Yes	Asymmetric	Double
At5g55160	*SUM2*	*SUMO2*	-	S			RV	Yes	Exclusive	Double
At5g55480	*SVL1*		-	V			RV	No	Asymmetric	Double
At5g55700	*BAM4*		V	B	B		RV	No	Complex	Triple
At5g56080	*NAS2*		-	-	-	V	RV	Yes	Exclusive	Quadruple

At5g56950	*AtNAP1;3*	*NFA3*	-	-	P		RV	No	Exclusive	Triple
At5g57360	*ZTL*	*ADO1; LKP1*	T	-	T		MB	Yes	Asymmetric	Triple
At5g57870	*eIFiso4G1*		-	V			RV	No	Exclusive	Double
At5g58140	*PHOT2*		C	C			RV	No	Symmetric	Double
At5g60120	*TOE2*		-	T	-	T	RV	No	Complex	Quadruple
At5g60450	*ARF4*		-	V			RV	No	Asymmetric	Double
At5g60690	*REV*	*IFL1*	V	L	S		MB; TD	No	Complex	Triple
At5g61420	*MYB28*	*PMG1; HAG1*	B	V			RV	No	Complex	Double
At5g61780	*TSN2*		-	V			RV	Yes	Exclusive	Double
At5g61840	*IRX10-L*		-	V			RV	No	Asymmetric	Double
At5g61900	*BON1*	*CPN1*	V	L	L		TD	Yes	Complex	Triple
At5g61960	*AML1*		-	L	L	V	RV	No	Complex	Pentuple
At5g62000	*ARF2*	*HSS; ORE14*	V	R			RV	No	Asymmetric	Double
At5g62090	*SLK2*		-	S			RV	No	Complex	Double
At5g62230	*ERL1*		-	V			RV	No	Complex	Double
At5g62410	*TTN3*	*AtCAP-E1; SMC2*	G	G			TD	No	Asymmetric	Double
At5g62540	*UBC3*		-	-	V		RV	No	Complex	Triple
At5g62920	*ARR6*		P	P	H	V	RV	No	Complex	Sextuple
At5g64740	*IXR2*	*PRC1; CESA6*	V	L	G		TD	No	Complex	Triple
At5g64760	*RPN5B*		-	G			RV	Yes	Asymmetric	Double
At5g65110	*ACX2*		B	L			RV	No	Asymmetric	Double
At5g65210	*TGA1*		-	I			RV	No	Exclusive	Double
At5g65460	*KAC2*		-	C			RV	No	Asymmetric	Double
At5g65700	*BAM1*		-	V	V		RV	No	Complex	Triple
At5g65710	*HSL2*		-	R			RV	No	Exclusive	Double
At5g65800	*ACS5*	*ETO2/ CIN5*	V	V	-	S	MB	No	Complex	Octuple
At5g66880	*SNRK2.3*		V	V			RV	No	Symmetric	Double
At5g67210	*IRX15-L*		-	B			RV	No	Exclusive	Double
At5g67230	*IRX14L*	*I14H*	-	V			RV	Yes	Asymmetric	Double

At5g67250	*VFB4*	*SKIP2*	-	-	-	V	RV	Yes	Exclusive	Quadruple
At5g67330	*AtNRAMP4*		-	H			RV	No	Exclusive	Double
At5g67440	*NPY3*	*MEL2*	-	-	-	V	RV	No	Asymmetric	Pentuple
At5g67520	*APK4*		-	B	G		RV	No	Complex	Triple

APPENDIX H: Multiple Mutant Phenotype Dataset, Grouping Information

This appendix includes a truncated version of the dataset describing phenotypes resulting from the disruption of multiple genetically redundant genes. Each row of this appendix represents a phenotype grouping resulting from the disruption of multiple genes. Included data are grouping identifiers, total numbers of loci involved, locus numbers and names of associated genes, phenotype group, class, and subset assignments, descriptions of mutant phenotypes, and complete grouping statuses. The full multiple mutant phenotype dataset is available as a spreadsheet appended to the *Plant Physiology* publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S6).

Footnotes for the title row of the following table are described below:

[a] Internal tracking system for different groupings within a single cluster. The letters and numbers correspond to the associated cluster. For complex clusters, this identifier precedes the decimal point.

[b] Refer to Appendix B for explanations of phenotype group, class, and subset abbreviations.

[c] Complete groupings involve disruptions of all putative paralogs (BLASTP e-30 cutoff). "Yes" indicates that the phenotype noted includes all putative paralogs.

Grouping ID[a]	**Number of Loci**	**Loci**	**Gene Symbols**	**Group**[b]	**Class**[b]	**Subsets**[b]	**Description of Mutant Phenotype**	**Complete Grouping**[c]
ED001	2	At1g01610, At4g00400	*GPAT4, GPAT8*	MRP	C	STT, CUL, WAT, PTH	Abnormal stomata morphology; Low cutin levels; Sensitive to drought; Susceptible to disease	No
ED002	2	At1g02880, At2g44750	*TPK1, TPK2*	ESN	L	SRL	Seedling lethal without exogenous thiamine pyrophosphate	Yes
ED003	2	At1g03630, At4g27440	*PORC, PORB*	ESN	L	SRL, PIG	Seedling lethal; Pigment defective embryo	No
ED004	2	At1g03770, At5g44280	*RING1B, RING1A*	ESN	L	SRL, NLS, LEF, IST, ARC, FSM, SRF, TCM	Low penetrance of seedling lethality; Incomplete penetrance of lobed cotyledons; Serrated, lobed, downward-curling leaves; Thick inflorescence stems; Abnormal floral phyllotaxy; Increased floral organ number; Fused floral organs; Homeotic floral transformations; Complete sterility; Cotyledons and rosette leaves form meristem structures	Yes
ED005	2	At1g04510, At2g33340	*MAC3A, MAC3B*	MRP	V	PIG, GRS, FLT, PTH	Semi-dwarf; Dark green leaves; Late flowering; Susceptible to disease	Yes
ED006	2	At1g06770, At2g30580	*DRIP1, DRIP2*	MRP	V	GRS	Slightly delayed growth	Yes
ED007	2	At1g08320, At5g06839	*TGA9, TGA10*	MRP	R	SRF	Male sterile due to anther defects	No
ED008	2	At1g09340, At3g63140	*CSP41b, CSP41a*	ESN	S	EMB	Embryo defective	Yes
ED009	2	At1g10290, At1g59610	*DRP2A, DRP2B*	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	No
ED010	2	At1g10570, At1g60220	*OTS2, OTS1*	MRP	T	FLT, CHS	Early flowering; Sensitive to salt	Yes
ED011	2	At1g14290, At1g69640	*SBH2, SBH1*	ESN	L	SRL	Seedling lethal	Yes

ED012	2	At1g15500, At1g80300	*AtNTT2*, *AtNTT1*	CND	P	LIT	Dwarf with necrotic lesions under short days	Yes
ED013	2	At1g16300, At1g79530	*GAPCp2*, *GAPCp1*	MRP	V	GRS, ROT, SRF	Dwarf; Abnormal root growth; Sterile	No
ED014	2	At1g17420, At1g72520	*LOX3*, *LOX4*	MRP	V	IST, ARC, SRF	Tall inflorescence stems; Increased branching; Male sterile due to short, indehiscent anthers and inviable pollen	No
ED015	2	At1g17730, At1g73030	*CHMP1B*, *CHMP1A*	ESN	S	EMB, SRL, NLS, STT, TCM	Embryo defective; Seedling lethal; Increased cotyledon number; Clustered stomata; Altered leaf venation; Disorganized SAM and RAM; Large root epidermal cells	Yes
ED016	2	At1g18800, At1g74560	*NRP2*, *NRP1*	MRP	V	ROT, CHS	Short roots; Sensitive to genotoxic stress	Yes
ED017	2	At1g20900, At1g76500	*AHL27*, *AHL29*	CND	P	LIT	Long hypocotyl under a variety of non-standard light conditions	No
ED018	2	At1g23190, At1g70730	*PGM3*, *PGM2*	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	No
ED019	2	At1g23820, At1g70310	*SPDS1*, *SPDS2*	ESN	S	EMB	Embryo defective	No
ED020	2	At1g26260, At4g34530	*CIB5*, *CIB1*	CND	P	LIT	Slightly delayed flowering under photoperiodic inductive conditions	No
ED021	2	At1g26830, At1g69670	*CUL3A*, *CUL3B*	ESN	G	EMG	Embryo defective; Male and female gametophyte defective	No
ED022	2	At1g31340, At2g35635	*RUB1*, *RUB2*	ESN	G	GEM, W:GRS, W:HRM	Null: Male and female gametophyte defective; Embryo defective; Knockdown: Severe dwarf; Insensitive to auxin	No
ED023	2	At1g34210, At1g71830	*SERK2*, *SERK1*	MRP	R	SRF	Male sterile due to anther defects	No
ED024	2	At1g48605, At3g18030	*HAL3B*, *HAL3A*	ESN	S	EMB	Embryo defective	Yes

ED025	2	At1g53240, At3g15020	*mMDH1, mMDH2*	MRP	V	GRS	Dwarf; Slow growth	No
ED026	2	At1g54210, At3g13970	*ATG12A, ATG12B*	MRP	T	SEN, NUT	Early senescence; Sensitive to nitrogen and fixed carbon starvation	Yes
ED027	2	At1g58200, At5g10490	*MSL3, MSL2*	MRP	V	PIG, LEF, TCM, CUL	Variegated leaves that become more severe over time; Abnormal leaf shape; Large intracellular air spaces in leaves; Large; misshapen leaf cells; Large chloroplasts	Yes
ED028	2	At1g60440, At4g32180	*AtPANK1, AtPANK2*	ESN	S	EMB	Embryo defective	No
ED029	2	At1g64990, At4g27630	*GTG1, GTG2*	CND	H	HRM	Germination and seedling growth insensitive to ABA	Yes
ED030	2	At1g65650, At5g16310	*UCH2, UCH1*	MRP	V	LEF, ARC, FSM, SRF, FLT, SEN	Short petioles; Small, upward-bending leaves; Lanceolate cauline leaves; Decreased branching; Abnormal flower morphology; Reduced fertility; Late flowering; Delayed senescence; Low chlorophyll levels	Yes
ED031	2	At1g65660, At4g37120	*SMP1, SMP2*	ESN	L	NHM, W:GRS, W:ROT, W:LEF, W:SRF	Null: No homozygous double mutant plants recovered; Knockdown: Dwarf; Abnormal leaf morphology; Slightly shorter roots; Reduced fertility	No
ED032	2	At1g70410, At3g01500	*BCA4, BCA1*	CLB	C	STT	Increased stomatal density; Stomatal regulation insensitive to CO2	No
ED033	2	At1g79250, At3g12690	*AGC1.7, AGC1.5*	ESN	G	GAM	Male gametophyte defective	No
ED034	2	At2g11810, At5g20410	*MGD3, MGD2*	CND	H	NUT	Decreased fresh weight, root growth, and photosynthetic performance under limited phosphate	No

ED035	2	At2g13560, At4g00570	*AtNAD-ME1, AtNAD-ME2*	CLB	B	PRA	Elevated mono- and disaccharide and 2-oxoglutarate/oxaloacetate-derived amino acid levels; Low citrate levels	No
ED036	2	At2g17420, At4g35460	*NTRA, NTRB*	MRP	V	GRS, SSC, LIT, CHS	Slow growth; Wrinkled seeds; Resistant to UV-C light; Sensitive to buthionine sulfoximine (inhibitor of glutathione biosynthesis)	No
ED037	2	At2g18960, At4g30190	*AHA1, AHA2*	ESN	S	EMB	Embryo defective	No
ED038	2	At2g19110, At4g30110	*HMA4, HMA2*	ESN	L	SRL	Seedling lethal	No
ED039	2	At2g21410, At4g39080	*VHA-A2, VHA-A3*	MRP	V	GRS, MSL, FSM, LIT, NUT	Dwarf; Necrotic leaf tips and flowers; Low nitrate levels; Degree of dwarfism is inversely proportional to day length; Sensitive to zinc	No
ED040	2	At2g22310, At4g39910	*UBP4, UBP3*	ESN	G	GAM	Complete male gametophyte defective	Yes
ED041	2	At2g22330, At4g39950	*CYP79B3, CYP79B2*	MRP	V	LEF	Slightly shorter petioles; Smaller leaves	No
ED042	2	At2g23150, At5g67330	*NRAMP3, NRAMP4*	CND	H	NUT	Seedling lethal under limited iron	No
ED043	2	At2g23760, At4g36870	*SAW2, SAW1*	MRP	V	LEF	Serrated leaf margins; Revolute leaves with abaxially-curled margins	No
ED044	2	At2g24050, At5g57870	*eIFiso4G2, eIFiso4G1*	MRP	V	GER, GRS, ROT, ARC, MSL, SRF, FLT, RTH	Low germination rate; Slow growth; Slightly chlorotic; Decreased branching; Short primary roots; Few lateral roots; Reduced fertility; Late flowering; Decreased root hair density	No
ED045	2	At2g26080, At4g33010	*AtGLDP2, AtGLDP1*	ESN	L	SRL	Seedling lethal; Non-photorespiratory conditions: Delayed lethality	Yes

ED046	2	At2g36250, At3g52750	*FTSZ2-1, FTSZ2-2*	CLB	C	CUL	Abnormal chloroplast division	No
ED047	2	At2g37040, At3g53260	*PAL1, PAL2*	MRP	R	SRF	Male sterile	No
ED048	2	At2g42790, At3g58750	*CSY3, CSY2*	MRP	V	GER	Complete loss of germination; Germination proceeds after removal of seed coat and application of sucrose	No
ED049	2	At2g42830, At3g58780	*SHP2, SHP1*	MRP	R	FSM	Indehiscent siliques	No
ED050	2	At2g44900, At3g60350	*ARABIDILLO-1, ARABIDILLO-2*	CND	P	MPH	Few lateral roots under vertical growth	Yes
ED051	2	At2g45150, At3g60620	*CDS4, CDS5*	ESN	G	EMG	Embryo defective; Male gametophyte defective (inferred)	Yes
ED052	2	At2g46070, At3g18040	*MPK12, MPK9*	CLB	C	STT, HRM, CHS	Abnormal stomata; Stomata movement insensitive to ABA and hydrogen peroxide	No
ED053	2	At3g01150, At5g53180	*PTB1, PTB2*	ESN	G	GAM	Male gametophyte defective	No
ED054	2	At3g01650, At5g14420	*RGLG1, RGLG2*	MRP	V	ARC	Increased branching; Abnormal phyllotaxy	No
ED055	2	At3g02230, At5g15650	*RGP1, RGP2*	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	No
ED056	2	At3g03110, At5g17020	*XPO1B, XPO1A*	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	Yes
ED057	2	At3g03250, At5g17310	*UGP1, UGP2*	MRP	V	GRS, SRF	Dwarf; Slow growth; Sterile	Yes
ED058	2	At3g04690, At5g28680	*ANX1, ANX2*	ESN	G	GAM	Male gametophyte defective; Pollen tubes rupture before reaching female gametophyte	No
ED059	2	At3g06930, At5g49020	*PRMT4b, PRMT4a*	MRP	T	FLT	Late flowering	No
ED060	2	At3g07780, At5g48160	*OBE1, OBE2*	ESN	L	SRL, ROT, TCM	Seedling lethal; Abnormal root growth; Complete loss of SAM and RAM	No
ED061	2	At3g07980, At3g13530	*MAPKKK6, MAPKKK7*	ESN	G	GAM	Complete male gametophyte defective	No

ED062	2	At3g08500, At5g12870	*MYB83*, *MYB46*	MRP	V	GRS, TCM	Dwarf; Severely deformed vessel elements; Reduced secondary wall thickening	No
ED063	2	At3g09560, At5g42870	*AtPAH1*, *AtPAH2*	CND	H	NUT	Sensitive to phosphate starvation	Yes
ED064	2	At3g11330, At5g05850	*PIRL9*, *PIRL1*	ESN	G	GAM	Complete male gametophyte defective	No
ED065	2	At3g17360, At3g19050	*POK1*, *POK2*	MRP	V	NLS, GRS, ROT, SRF	Small cotyledons; Short, wide roots; Dwarf; Reduced fertility	No
ED066	2	At3g19290, At4g34000	*AREB2*, *ABF3*	MRP	V	IST	Slightly shorter inflorescence stems	No
ED067	2	At3g19450, At4g34230	*CAD-C*, *CAD-D*	MRP	V	PIG, GRS, IST, FLT, SEN	Slightly slower growth; Short, less rigid inflorescence stems; Purple lower inflorescence stems; Late flowering; Early senescence	No
ED068	2	At3g23670, At4g14150	*PAKRP1L*, *PAKRL1*	ESN	G	MGD, SRF	Male and female gametophyte defective; Homozygotes are viable: Reduced fertility	No
ED069	2	At3g43190, At5g20830	*SUS4*, *SUS1*	CLB	B	PRA, WAT	Elevated sugar levels in leaves; Slow growth and reduced root weight under flood conditions	No
ED070	2	At3g48780, At5g23670	*LCB2b*, *LCB2a*	ESN	G	GAM	Male gametophyte defective	No
ED071	2	At3g50220, At5g67210	*IRX15*, *IRX15-L*	CLB	C	CUL, PRA	Low xylose levels in inflorescence stems; Abnormal secondary cell wall margins in fiber cells; Decreased xylan polymerization	No
ED072	2	At3g61650, At5g05620	*TubG1*, *TubG2*	ESN	G	GAM, W:SRL	Null: Male and female gametophyte defective; Knockdown: Seedling lethal	No
ED073	2	At3g63130, At5g19320	*RG1*, *RG2*	ESN	G	GAM	Complete female gametophyte defective	No
ED074	2	At4g11960, At4g22890	*PGRL1B*, *PGRL1A*	MRP	V	PIG, GRS	Slow growth; Pale green leaves	Yes

ED075	2	At4g17190, At5g47770	*FPS2*, *FPS1*	ESN	L	SRL	Seedling lethal without exogenous sucrose	Yes
ED076	2	At4g17360, At5g47435	, *PurU*	MRP	V	PIG, GRS, SRF, FLT	Dwarf; Pale green; Sterile; Late flowering	Yes
ED077	2	At4g17600, At5g47110	*LIL3:1*, *LIL3:2*	MRP	V	PIG, GRS	Yellow green leaves; Slow growth	Yes
ED078	2	At4g20140, At5g44700	*GSO1*, *GSO2*	ESN	S	EMB, NLS, WAT	Embryo defective; Abnormal embryo morphology; Short hypocotyl; Concave cotyledons; Cotyledons adhere to first true leaves; Seedling lethal under low humidity	No
ED079	2	At4g25700, At5g52570	*B1*, *B2*	MRP	V	PIG, GRS	Dwarf; Pale green; Altered carotenoid composition	Yes
ED080	2	At4g26840, At5g55160	*SUM1*, *SUM2*	ESN	S	EMB	Embryo defective	Yes
ED081	2	At4g28490, At5g65710	*HAE*, *HSL2*	MRP	R	FSM	Indehiscent floral organs	No
ED082	2	At4g32730, At5g11510	*MYB3R-1*, *MYB3R-4*	MRP	V	NLS, IST, CUL	Low penetrance of abnormal seedling morphology and short inflorescence stems; Multinucleate cells due to abnormal cytokinesis	No
ED083	2	At4g36280, At4g36290	*CRH1*, *CRT1*	CND	I	PTH	Susceptible to *Pseudomonas syringae*	No
ED084	2	At5g07350, At5g61780	*TSN1*, *TSN2*	MRP	V	GRS, ROT, CHS	Slightly shorter roots and slower growth; Sensitive to salt stress	Yes
ED085	2	At5g10030, At5g65210	*TGA4*, *TGA1*	CND	I	PTH	Susceptible to *Pseudomonas syringae*	No
ED086	2	At5g12180, At5g19360	*CPK17*, *CPK34*	ESN	G	GAM	Complete male gametophyte defective	No
ED087	2	At5g25980, At5g26000	*TGG2*, *TGG1*	CLB	B	PRA	Elevated indole glucosinolate levels	No
ET001	3	At1g02300, At1g02305, At4g01610	*CathB1*, *CathB2*, *CathB3*	CND	I	SEN, PTH	Susceptible to bacterial infection; Slightly delayed senescence	Yes

ET002	3	At1g22990, At1g71050, At5g17450	*HIPP22*, *HIPP20*, *HIPP21*	CND	H	MCH	Sensitive to cadmium	No
ET003	3	At2g19480, At4g26110, At5g56950	*AtNAP1;2*, *AtNAP1;1*, *AtNAP1;3*	CND	P	LIT, HRM	Sensitive to UV-C light and ABA	No
ET004	3	At2g35490, At4g04020, At4g22240	*FIB2*, *FIB1a*, *FIB1b*	MRP	V	IST, CHS	Short inflorescence stems; Sensitive to photooxidative stress	Yes
ET005	3	At2g42680, At3g24500, At3g58680	*AtMBF1a*, *AtMBF1c*, *AtMBF1b*	CND	H	CHS	Sensitive to oxidative and osmotic stress	Yes
ET006	3	At2g45160, At3g60630, At4g00150	*HAM1*, *HAM2*, *HAM3*	MRP	V	LEF, IST, ARC, FSM, TCM	Abnormal rosette leaf morphology and phyllotaxy; Decreased branching; Tall inflorescence stems; Abnormal flower and SAM morphology	No
ET007	3	At3g12250, At5g06950, At5g06960	*TGA6*, *TGA2*, *TGA5*	CND	I	PTH	Susceptible to *Botrytis cinerea*	No
EQ001	4	At1g09240, At1g56430, At5g04950, At5g56080	*NAS3*, *NAS4*, *NAS1*, *NAS2*	MRP	V	MSL, SRF	Chlorotic leaves; Sterile	Yes
EQ002	4	At1g47056, At3g50080, At4g07400, At5g67250	*VFB1*, *VFB2*, *VFB3*, *VFB4*	MRP	V	GRS, ROT, LEF	Abnormal lateral root formation; Small rosette; Delayed root and plant growth	Yes
AD001	2	At1g05180, At2g32410	*AXR1*, *AXL*	ESN	S	EMB, SRL	Embryo defective; Seedling lethal	Yes
AD002	2	At1g07360, At2g29580	*MAC5A*, *MAC5B*	ESN	L	NHM	No homozygous double mutant plants recovered	No
AD003	2	At1g14350, At2g02820	*MYB124*, *MYB88*	CLB	C	STT	Clustered stomata	Yes
AD004	2	At1g14360, At2g02810	*AtUTr3*, *AtUTr1*	ESN	G	GAM	Male and female gametophyte defective	Yes
AD005	2	At1g16460, At1g79230	*STR2*, *STR1*	ESN	S	EMB	Embryo defective	Yes
AD006	2	At1g16890, At1g78870	*UBC13B*, *UBC13A*	CLB	C	RTH	Few, short root hairs	No
AD007	2	At1g17060, At2g26710	*CYP72C1*, *CYP72B1*	MRP	V	LEF, IST, FSM	Large rosette; Tall primary inflorescence stem; Long siliques	No

AD008	2	At1g17920, At1g73360	*HDG12, HDG11*	CLB	C	STT	Severely branched trichomes	No
AD009	2	At1g18870, At1g74710	*ICS2, ICS1*	ESN	L	SRL	Seedling lethal without exogenous sucrose	Yes
AD010	2	At1g23380, At1g62360	*KNAT6, STM*	ESN	L	SRL, TCM	Seedling lethal; Cotyledons fuse; Complete loss of SAM formation	No
AD011	2	At1g26310, At1g69120	*CAL, AP1*	MRP	R	FSM	Homeotic floral transformations	No
AD012	2	At1g26780, At1g69560	*LOF1, LOF2*	MRP	V	LEF, IST, FSM	Fusion of cauline leaves and pedicels with primary inflorescence stem	No
AD013	2	At1g27440, At5g61840	*IRX10, IRX10-L*	MRP	V	PIG, GRS, SRF	Severe dwarf; Slow growth; Dark green; Complete sterility	No
AD014	2	At1g31180, At1g80560	*IPMDH3, IPMDH2*	ESN	G	GAM	Complete male gametophyte defective; Female gametophyte defective	No
AD015	2	At1g32240, At5g16560	*KAN2, KAN*	MRP	R	FSM, OVP	Abnormal external carpel structures and outer integuments	No
AD016	2	At1g32770, At2g46770	*ANAC012, ANAC043*	MRP	R	FSM	Indehiscent siliques	No
AD017	2	At1g34130, At5g19690	*STT3B, STT3A*	ESN	G	MGD	Male and female gametophyte defective	Yes
AD018	2	At1g35580, At4g09510	*CINV1, CINV2*	MRP	V	GRS, ROT	Dwarf; Short roots	No
AD019	2	At1g37130, At1g77760	*NIA2, NIA1*	CND	H	NUT	Reduced growth with nitrate as primary source of nitrogen	No
AD020	2	At1g49630, At3g19170	*PreP2, PreP1*	MRP	V	PIG, GRS	Pale green leaves; Reduced biomass	Yes
AD021	2	At1g50960, At4g21200	*AtGA2ox7, AtGA2ox8*	MRP	V	NLS	Long hypocotyl	No
AD022	2	At1g53700, At3g14370	*WAG1, WAG2*	CND	P	MPH	Wavy roots under vertical growth	No
AD023	2	At1g59750, At5g62000	*ARF1, ARF2*	MRP	R	FSM, FLT, SEN	Delayed floral organ dehiscence; Short stamens; Long carpels; Late flowering; Delayed leaf senescence; Low leaf chlorophyll levels	No

AD024	2	At1g62830, At3g13682	*LDL1*, *LDL2*	MRP	T	FLT	Late flowering	No
AD025	2	At1g66340, At2g40940	*EIN1*, *ERS1*	MRP	V	NLS, LEF, SRF, FLT	Small seedlings; Small rosette; Sterile; Late flowering	No
AD026	2	At1g68740, At3g23430	*PHO1;H1*, *PHO1*	ESN	L	SRL	Seedling lethal without exogenous phosphate	No
AD027	2	At1g75950, At5g42190	*ASK1*, *ASK2*	ESN	S	EMB, SRL	Low penetrance of embryo defects; Seedling lethal	No
AD028	2	At1g76490, At2g17370	*HMG1*, *HMG2*	ESN	G	GAM	Male gametophyte defective	Yes
AD029	2	At2g16500, At4g34710	*ADC1*, *ADC2*	ESN	S	EMB	Embryo defective	Yes
AD030	2	At2g16640, At4g02510	*TOC132*, *TOC159*	ESN	S	EMB	Embryo defective	No
AD031	2	At2g17780, At4g35920	*MCA2*, *MCA1*	MRP	V	GRS, ROT, NUT	Slow growth; Short roots; Sensitive to magnesium	Yes
AD032	2	At2g20000, At3g16320	*CDC72b*, *CDC27a*	ESN	G	GAM	Female gametophyte defective	Yes
AD033	2	At2g20570, At5g44190	*GLK1*, *GLK2*	MRP	V	PIG, GRS	Dwarf; Pale green	Yes
AD034	2	At2g22300, At5g09410	*CAMTA3*, *CAMTA1*	CND	P	TMP	At high or low temperature: Dwarf, chlorotic old leaves, and reduced acclimation to low temperature	No
AD035	2	At2g27990, At5g02030	*PNF*, *PNY*	MRP	V	LEF, FLT	Abnormal leaf morphology; Complete loss of flowering	No
AD036	2	At2g28110, At5g22940	*FRA8*, *F8H*	MRP	V	GRS, TCM	Dwarf; Deformed vessel elements	No
AD037	2	At2g30110, At5g06460	*AtUBA1*, *AtUBA2*	ESN	L	NHM	No homozygous double mutant plants recovered	Yes
AD038	2	At2g30250, At2g38470	*WRKY25*, *WRKY33*	CND	H	CHS	Sensitive to salt stress	No
AD039	2	At2g33860, At5g60450	*ARF3*, *ARF4*	MRP	V	PIG, GRS, LEF, ARC, MSL, FSM	Dwarf; Narrow; dark green leaves with ectopic blade outgrowths; Abnormal phyllotaxy; Abnormal flower morphology	No
AD040	2	At2g40750, At3g56400	*WRKY54*, *WRKY70*	CLB	B	PRA	Elevated free SA levels	Yes
AD041	2	At2g41210, At3g56960	*PIP5K5*, *PIP5K4*	ESN	G	MGD	Slow pollen germination and tube growth	No

AD042	2	At2g41560, At3g57330	*ACA4, ACA11*	MRP	V	MSL	Necrotic lesions on leaves; Necrosis covers entire rosette leaf over time	No
AD043	2	At2g45190, At4g00180	*FIL, YAB3*	MRP	V	NLS, LEF, FSM, SRF, TCM	Narrow cotyledons and leaves; Radialized floral organs; Complete loss of petals; Reduced fertility due to incomplete penetrance of complete loss of stamens; Abnormal leaf vasculature	No
AD044	2	At3g05630, At3g16785	*PLDP2, PLDP1*	CND	H	NUT	Short primary root and long lateral roots under limited phosphate	Yes
AD045	2	At3g07740, At4g16420	*ADA2a, ADA2b*	MRP	V	IST, ARC, SRF	Multiple primary inflorescences; Complete sterility	Yes
AD046	2	At3g08720, At3g08730	*S6K2, S6K1*	ESN	G	GAM	Male gametophyte defective	No
AD047	2	At3g12990, At3g60500	*RRP45a, CER7*	ESN	G	GAM	Male and female gametophyte defective	Yes
AD048	2	At3g13730, At4g36380	*CYP90D1, CYP90C1*	MRP	V	NLS, GRS, LIT	Short hypocotyl; Short, epinastic cotyledons; Dwarf; Very short hypocotyl and open cotyledons in the dark	No
AD049	2	At3g23580, At3g27060	*RNR2A, TSO2*	ESN	L	SRL, TCM	Seedling lethal; SAM terminates with callus-like cells	Yes
AD050	2	At3g27280, At5g40770	*PHB4, PHB3*	ESN	L	NHM	No homozygous double mutant plants recovered	No
AD051	2	At3g30180, At5g38970	*CYP85A2, CYP85A1*	MRP	V	GRS	Severe dwarf	No
AD052	2	At3g47460, At5g62410	*AtCAP-E2, AtCAP-E1*	ESN	G	EMG	Embryo defective; Male and female gametophyte defective	No
AD053	2	At3g48190, At5g40820	*ATM, AtATR*	MRP	R	SRF	complete sterility	No
AD054	2	At3g48870, At5g50920	*HSP93-III, HSP93-V*	ESN	G	GEM	Male and female gametophyte defective; Very early embryo defective	No
AD055	2	At4g11260, At4g23570	*SGT1b, SGT1a*	ESN	S	EMB	Embryo defective	Yes

AD056	2	At4g11660, At4g36990	*HsfB2b, HsfB1*	CND	I	PTH	Resistant to disease	No
AD057	2	At4g16760, At5g65110	*ACX1, ACX2*	ESN	L	SRL, GER	Seedling lethal without exogenous sucrose; Low germination rate	No
AD058	2	At4g18480, At5g45930	*CHLI1, CHLI2*	ESN	L	SRL, PIG	Seedling lethal; Albino	No
AD059	2	At4g24280, At5g49910	*cpHsc70-1, cpHsc70-2*	ESN	G	GAM	Complete female gametophyte defective; Male gametophyte defective	No
AD060	2	At4g25230, At5g51450	*RIN2, RIN3*	CLB	B	CPR	Decreased ion leakage	Yes
AD061	2	At4g26690, At5g55480	*SHV3, SVL1*	MRP	V	NLS, ROT, STT, LIT	Brown hypocotyl and root endodermis; Incomplete penetrance of collapsed trichomes; Swollen guard cells; Short, thick hypocotyl in the dark	No
AD062	2	At4g26850, At5g55120	*VTC2, VTC5*	ESN	L	SRL	Very early seedling lethality	Yes
AD063	2	At4g27780, At5g53470	*ACBP2, ACBP1*	ESN	S	EMB	Embryo defective	Yes
AD064	2	At4g31700, At5g10360	*RPS6A, RPS6B*	ESN	G	MGD	Male and female gametophyte defective	Yes
AD065	2	At4g34840, At4g38800	*MTN2, MTN1*	MRP	R	SRF, FLT	Sterile; Late flowering	Yes
AD066	2	At4g36890, At5g67230	*IRX14, IRX14L*	MRP	V	GRS, IST, FLT	Dwarf; Very slow growth; Complete loss of bolting	Yes
AD067	2	At5g09790, At5g24330	*ATXR5, ATXR6*	MRP	V	LEF, CUL, LIT	Small leaves; Phenotype enhanced under short days; Partially decondensed heterochromatin	Yes
AD068	2	At5g09900, At5g64760	*RPN5A, RPN5B*	ESN	G	GAM	Complete male gametophyte defective	Yes
AD069	2	At5g10470, At5g65460	*KAC1, KAC2*	CLB	C	CUL	Complete loss of chloroplast photorelocation	No
AD070	2	At5g23730, At5g52250	*RUP2, RUP1*	CND	P	LIT	Sensitive to UV-B light; Resistant to UV-B light following acclimation	No

AT001	3	At1g13860, At1g78240, At2g03480	*QUL1*, *QUA2*, *QUL2*	MRP	V	IST, LIT	Thin inflorescence stems; Short hypocotyl in the dark	No
AT002	3	At1g27390, At3g27080, At5g40930	*TOM20-2*, *TOM20-3*, *TOM20-4*	MRP	V	GRS	Slow growth	No
AT003	3	At1g68050, At2g18915, At5g57360	*FKF1*, *LKP2*, *ZTL*	MRP	T	CDR	Abnormal circadian rhythms	Yes
AT004	3	At2g35930, At3g11840, At3g52450	*PUB23*, *PUB24*, *PUB22*	CND	I	PTH	Resistant to bacterial and fungal infection	No
AT005	3	At2g40300, At3g56090, At5g01600	*AtFER4*, *AtFER3*, *AtFER1*	CND	H	NUT	Sensitive to elevated iron	No
AP001	5	At2g14820, At2g23050, At4g31820, At4g37590, At5g67440	*NPY2*, *NPY4*, *NPY1*, *NPY5*, *NPY3*	MRP	V	ROT	Complete loss of root gravitropism	No
SD001	2	At1g01460, At4g01190	*PIPK11*, *PIPK10*	ESN	G	MGD, CHS	Slight reduction in pollen tube growth; No effect on fertility; Pollen tube growth sensitive to latrunculin B (inhibitor of actin polymerization)	No
SD002	2	At1g02280, At5g05000	*TOC33*, *TOC34*	ESN	S	EMB	Embryo defective	Yes
SD003	2	At1g22920, At1g71230	*CSN5A*, *CSN5B*	ESN	L	SRL	Seedling lethal	No
SD004	2	At1g26670, At5g39510	*VTI12*, *VTI11*	ESN	S	EMB	Embryo defective	No
SD005	2	At1g30330, At5g37020	*ARF6*, *ARF8*	MRP	V	GRS, LEF, FSM	Dwarf; Uneven; twisted leaves; Flowers arrest as infertile closed buds	No
SD006	2	At1g30400, At2g34660	*ABCC1*, *ABCC2*	CND	H	MCH	Sensitive to arsenic	No
SD007	2	At1g32230, At2g35510	*RCD1*, *SRO1*	ESN	S	EMB, GRS, OVP	Embryo defective; Homozygotes are viable: Dwarf; Abnormal integument morphology	No
SD008	2	At1g35720, At2g38750	*AnnAt1*, *AnnAt4*	CND	P	WAT, CHS	Resistant to drought and salt stress	No
SD009	2	At1g48410, At5g43810	*AGO1*, *PNH*	ESN	S	EMB, SRL	Embryo defective; Seedling lethal	No

SD010	2	At1g49430, At2g47240	*LACS2*, *LACS1*	MRP	V	GER, LEF, FSM, SRF	Low germination rate; Fused leaves and flower buds; Indehiscent sepals and petals; Reduced fertility	No
SD011	2	At1g64060, At5g47910	*RbohF*, *RbohD*	ESN	L	SRL, GRS, MSL, PTH	Low penetrance of rosette lethality; Semi-dwarf; Necrotic lesions; Resistant to fungal infection	No
SD012	2	At1g69270, At3g02130	*RPK1*, *RPK2*	ESN	S	MSD	Embryo defective; 50% defective seeds	No
SD013	2	At2g14120, At4g33650	*DRP3B, DRP3A*	MRP	V	GRS, LEF, CUL	Dwarf; Slow growth; Abnormal leaf morphology; Very long mitochondria with abnormal morphology	No
SD014	2	At2g22780, At5g09660	*PMDH1, PMDH2*	ESN	L	SRL	Seedling lethal without exogenous sucrose	No
SD015	2	At2g25490, At5g25350	*EBF1, EBF2*	MRP	V	NLS, ROT	Short hypocotyl; Short roots; Exaggerated apical hook	No
SD016	2	At2g32700, At4g32551	*LUH, LUG*	ESN	S	EMB	Embryo defective	Yes
SD017	2	At2g35350, At2g46920	*PLL1, POL*	ESN	S	EMB, SRL	Embryo defective; Abnormal stem cell specification; Seedling lethal	No
SD018	2	At2g36910, At3g28860	*AtPGP1, PGP19*	MRP	V	NLS, LEF, LIT	Downward-bending cotyledons; Curled leaves; Short, wavy hypocotyl in the dark	No
SD019	2	At2g38170, At3g51860	*CAX1, CAX3*	MRP	V	GRS, MSL, FSM, SRF, NUT	Slow growth; Dwarf; Necrotic leaves and flowers; Reduced fertility; Sensitive to calcium and other ions; Resistant to magnesium	No
SD020	2	At2g38230, At5g01410	*PDX1.1, PDX1.3*	ESN	S	EMB	Embryo defective	No
SD021	2	At2g43790, At3g45640	*AtMPK6, AtMPK3*	ESN	S	EMB	Embryo defective	No
SD022	2	At2g46790, At5g02810	*APRR9, PRR7*	MRP	T	CDR	Long circadian rhythms in cotyledon movements	No
SD023	2	At3g02470, At5g18930	*SAMDC, SAMDC4*	ESN	S	EMB	Embryo defective	No

SD024	2	At3g04240, At3g11540	*SEC, SPY*	ESN	G	EMG	Embryo defective; Male gametophyte defective	Yes
SD025	2	At3g14270, At4g33240	*FAB1B, FAB1A*	ESN	G	GAM	Male gametophyte defective	No
SD026	2	At3g15170, At5g53950	*CUC1, CUC2*	ESN	S	EMB, SRL, NLS	Embryo defective; Cupped cotyledons; Seedling lethal	No
SD027	2	At3g18660, At4g33330	*GUX1, GUX2*	CLB	B	PRA	Low α(1;2)-linked D-glucuronyl levels	No
SD028	2	At3g45780, At5g58140	*PHOT1, PHOT2*	CLB	C	CUL	Abnormal chloroplast positioning	No
SD029	2	At3g50500, At5g66880	*SnRK2.2, SnRK2.3*	MRP	V	GER, HRM	Decreased seed dormancy; Germination and seedling growth insensitive to ABA	No
SD030	2	At4g25420, At5g51810	*GA20ox1, GA20ox2*	MRP	V	GER, NLS, GRS, LEF, ARC, FSM, SRF, FLT	Early germination; Dwarf; Very short hypocotyl; Downward-bending rosette leaves; Increased branching; Sterile early flowers with short, indehiscent anthers; Reduced fertility; Late flowering	No
SD031	2	At5g07440, At5g18170	*GDH2, GDH1*	CND	P	LIT, NUT	Sensitive to darkness and limited carbon	No
CT001.01	2	At1g01030, At2g46870	*NGA3, NGA1*	MRP	R	FSM	Abnormal pistil morphology	No
CT001.02	2	At1g01030, At3g61970	*NGA3, NGA2*	MRP	R	FSM	Abnormal pistil morphology	No
CT002.01	2	At1g04580, At2g27150	*AAO4, AAO3*	CLB	B	PRA	Low ABA levels	No
CT002.02	2	At2g27150, At5g20960	*AAO3, AAO1*	CLB	B	PRA	Low ABA levels	No
CT003.01	2	At1g06390, At2g30980	*BIL2, BIL1*	CND	H	HRM	Root and hypocotyl growth insensitive to brassinosteroids	No
CT003.02	3	At1g06390, At2g30980, At4g18710	*BIL2, BIL1, BIN2*	MRP	V	LEF	Long, wavy petioles; Narrow, twisted rosette leaves	No
CT004.01	2	At1g08860, At5g61900	*BON3, BON1*	ESN	L	SRL, LEF	Seedling lethal; Very small leaves; Phenotype rescued at high temperature	No

CT004.02	2	At5g07300, At5g61900	*BON2*, *BON1*	ESN	L	SRL, LEF	Seedling lethal; Very small leaves; Phenotype rescued at high temperature	No
CT004.03	3	At1g08860, At5g07300, At5g61900	*BON3*, *BON2*, *BON1*	ESN	L	SRL	Seedling lethal immediately following germination regardless of temperature	Yes
CT005.01	2	At1g09000, At1g54960	*ANP1*, *ANP2*	MRP	V	NLS	Short hypocotyl	No
CT005.02	2	At1g54960, At3g06030	*ANP2*, *ANP3*	MRP	V	GRS, LIT	Dwarf; Short hypocotyl in the dark	No
CT005.03	3	At1g09000, At1g54960, At3g06030	*ANP1*, *ANP2*, *ANP3*	ESN	G	MGD	Male gametophyte defective	No
CT006.01	2	At1g11310, At1g61560	*MLO2*, *MLO6*	CND	I	PTH	Resistant to powdery mildew	No
CT006.02	2	At1g11310, At2g39200	*MLO2*, *MLO12*	CND	I	PTH	Resistant to powdery mildew	No
CT007.01	2	At1g12820, At3g62980	*AFB3*, *TIR1*	CND	H	CHS	Resistant to oxidative stress	No
CT007.02	2	At3g26810, At3g62980	*AFB2*, *TIR1*	CND	H	CHS	Resistant to oxidative stress	No
CT008.01	2	At1g13320, At1g25490	*PP2AA3*, *RCN1*	MRP	V	NLS, GRS, ROT, LEF, SRF	Incomplete penetrance of abnormal cotyledon number and morphology; Short, thick hypocotyl and roots; Slow growth; Dwarf; Small rosette; Reduced fertility	No
CT008.02	2	At1g13320, At3g25800	*PP2AA3*, *PP2AA2*	CND	P	LIT	Short roots in the dark	No
CT008.03	2	At1g25490, At3g25800	*RCN1*, *PP2AA2*	MRP	V	NLS, GRS, ROT, LEF, IST, FSM, SRF	Incomplete penetrance of abnormal cotyledon number and morphology; Short, thick hypocotyl and roots; Slow growth; Dwarf; Small rosette; Thick inflorescence stems; Sterile; Short stigmas	No
CT009.01	2	At1g14400, At2g02760	*AtUBC1*, *AtUBC2*	MRP	V	LEF, FLT, TCM	Large leaves; Decreased rosette leaf number; Early flowering; Reduced leaf vasculature	No
CT009.02	3	At1g14400, At2g02760, At5g62540	*AtUBC1*, *AtUBC2*, *AtUBC3*	MRP	V	GRS, ARC, SRF	Dwarf; Increased branching; Sterile	No

CT010.01	2	At1g18080, At1g48630	*RACK1A*, *RACK1B*	MRP	V	ROT, LEF	Short roots; Few rosette leaves and lateral roots	No
CT010.02	2	At1g18080, At3g18130	*RACK1A*, *RACK1C*	MRP	V	ROT, LEF	Short roots; Few rosette leaves and lateral roots	No
CT011.01	2	At1g20840, At4g35300	*TMT1*, *TMT2*	CLB	B	PRA, TMP	Low fructose levels; Very low fructose and glucose levels at low temperature	No
CT011.02	3	At1g20840, At3g51490, At4g35300	*TMT1*, *TMT3*, *TMT2*	CLB	B	PRA, TMP	Low fructose and glucose levels; Very low fructose and glucose levels at low temperature	No
CT012.01	2	At1g27320, At5g35750	*AHK3*, *AHK2*	MRP	V	GRS, LEF, FLT	Dwarf; Small rosette; Slightly late flowering	No
CT012.02	3	At1g27320, At2g01830, At5g35750	*AHK3*, *AHK4*, *AHK2*	MRP	V	NLS, ROT, LEF, IST, FSM, SRF, FLT	Short hypocotyl and roots; Small cotyledons, rosette, and flowers; Short, thin inflorescence stems; Sterile; Late flowering	No
CT013.01	2	At1g51590, At3g21160	*MNS1*, *MNS2*	CND	H	NUT	Short roots, increased lateral root formation, and abnormal cell wall composition in response to glucose	No
CT013.02	3	At1g30000, At1g51590, At3g21160	*MNS3*, *MNS1*, *MNS2*	MRP	V	LEF, FLT, NUT	Small rosette; Late flowering; Very short, thick roots and abnormal cell wall composition in response to glucose	No
CT014.01	2	At1g33280, At4g10350	*BRN1*, *BRN2*	CLB	C	TCM	Complete loss of columella cell detachment	No
CT014.02	3	At1g33280, At1g79580, At4g10350	*BRN1*, *SMB*, *BRN2*	CLB	C	TCM	Mass of cells forms at the root tip	No
CT015.01	2	At1g43850, At4g25520	*SEU*, *SLK1*	MRP	V	GRS, FSM, SRF	Dwarf; Abnormal flower morphology; Sterile	No

CT015.02	2	At1g43850, At5g62090	*SEU, SLK2*	ESN	S	EMB, W:GRS, W:FSM, W:FLT	Embryo defective; Abnormal cotyledon development; Knockdown: Dwarf; Homeotic floral transformations; Very late flowering	No
CT016.01	2	At1g49760, At4g34110	*PAB8, PAB2*	MRP	V	GRS, PTH	Dwarf; Susceptible to viral infection	No
CT016.02	2	At2g23350, At4g34110	*PAB4, PAB2*	MRP	V	GRS, LEF, PTH	Dwarf; Small rosette; Susceptible to viral infection	No
CT016.03	3	At1g49760, At2g23350, At4g34110	*PAB8, PAB4, PAB2*	ESN	L	NHM	No homozygous triple mutant plants recovered	No
CT017.01	2	At1g57820, At5g39550	*VIM1, VIM3*	CLB	B	CPR	Decreased DNA methylation in heterochromatic regions	No
CT017.02	3	At1g57820, At1g66050, At5g39550	*VIM1, VIM2, VIM3*	MRP	V	IST, ARC, FLT	Aerial rosettes; Late flowering	No
CT018.01	2	At1g58300, At2g26670	*HO4, HY1*	MRP	V	MSL, FLT, LIT	Chlorotic leaves; Early flowering; Slow growth and small, chlorotic leaves under continuous light	No
CT018.02	2	At1g69720, At2g26670	*HO3, HY1*	MRP	V	MSL, FLT, LIT	Chlorotic leaves; Early flowering; Slow growth and small, chlorotic leaves under continuous light	No
CT018.03	3	At1g58300, At1g69720, At2g26670	*HO4, HO3, HY1*	MRP	V	PIG, MSL, FLT, LIT	Pale yellow-green; Chlorotic leaves; Early flowering; Slow growth and small, chlorotic leaves under continuous light	No
CT019.01	2	At1g80840, At4g31800	*WRKY40, WRKY18*	CND	I	PTH	Resistant to bacterial infection; Susceptible to fungal infection	No
CT019.02	2	At2g25000, At4g31800	*WRKY60, WRKY18*	CND	I	PTH	Resistant to bacterial infection; Susceptible to fungal infection	No
CT019.03	3	At1g80840, At2g25000, At4g31800	*WRKY40, WRKY60, WRKY18*	CND	I	PTH	Resistant to bacterial infection; Susceptible to fungal infection	Yes
CT020.01	2	At2g26330, At5g07180	*ER, ERL2*	MRP	R	FSM	Short, blunt siliques; Short pedicels	No

CT020.02	2	At2g26330, At5g62230	*ER, ERL1*	MRP	V	GRS	Dwarf	No
CT021.01	2	At2g32370, At4g21750	*HDG3, AtML1*	MRP	V	NLS	Upward-bending cotyledons	No
CT021.02	2	At4g04890, At4g21750	*PDF2, AtML1*	ESN	L	SRL	Seedling lethal without exogenous sucrose; With exogenous sucrose: Glossy, pointed leaves lacking an epidermis; Complete loss of flowering	No
CT022.01	2	At3g05120, At3g63010	*GID1a, GID1b*	MRP	V	IST, FSM, SRF	Tall inflorescence stems; Reduced fertility due to short filaments	No
CT022.02	2	At3g05120, At5g27320	*GID1a, GID1c*	MRP	V	GRS, SRF	Semi-dwarf; Slightly reduced fertility	No
CT022.03	3	At3g05120, At3g63010, At5g27320	*GID1a, GID1b, GID1c*	MRP	V	GER	Complete loss of germination; Germination proceeds after removal of seed coat: Extreme dwarf; Small rosettes; Short leaves; Late flowering; Abnormal floral morphology; complete sterility	No
CT023.01	2	At3g06490, At5g61420	*MYB108, MYB28*	MRP	R	SRF, SEN	Reduced fertility due to delayed anther dehiscence; Delayed floral organ senescence	No
CT023.02	2	At5g07690, At5g61420	*AtMYB29, MYB28*	MRP	V	GER, GRS, OBI	Delayed germination and growth; Complete loss of glucosinolates; Increased susceptibility to herbivory	No
CT024.01	2	At3g10160, At3g55630	*FPGS2, FPGS3*	ESN	L	SRL	Seedling lethal without exogenous sucrose	No
CT024.02	2	At3g10160, At5g05980	*FPGS2, FPGS1*	ESN	S	EMB	Embryo defective	No
CT024.03	2	At3g55630, At5g05980	*FPGS3, FPGS1*	ESN	G	MGD, LEF, SRF, FLT, SEN	Male and female gametophyte defective; Homozygotes viable: Small leaves; Reduced fertility; Late flowering; Delayed senescence	No
CT025.01	2	At3g23920, At4g17090	*BAM1, BAM3*	CLB	B	PRA	Elevated starch levels	No

CT025.02	2	At4g17090, At5g55700	*BAM3*, *BAM4*	CLB	B	PRA	Elevated starch levels	No
CT025.03	3	At3g23920, At4g17090, At5g55700	*BAM1*, *BAM3*, *BAM4*	CLB	B	PRA	Severely elevated starch levels	No
CT026.01	2	At3g49670, At5g65700	*BAM2*, *BAM1*	MRP	V	GRS, LEF, ARC, FSM, SRF, FLT, SEN, TCM	Slow growth; Increased branching; Abnormal rosette leaf and flower morphology; Severely reduced fertility; Delayed senescence; Late flowering; Few leaf veins; Small shoot meristems	No
CT026.02	3	At3g49670, At4g20270, At5g65700	*BAM2*, *BAM3*, *BAM1*	MRP	V	LEF, IST, ARC, FSM, SRF, TCM	Complete loss of primary inflorescence stem; Short secondary inflorescence stems; Few, ruffled, serrated leaves; Reduced stamen and carpel number; Abnormal flower morphology; Complete sterility; Few leaf veins; Early shoot meristem termination	No
CQ001.01	2	At3g29350, At5g39340	*AHP2*, *AHP3*	CND	H	HRM	Root growth insensitive to cytokinin	No
CQ001.02	3	At1g03430, At3g29350, At5g39340	*AHP5*, *AHP2*, *AHP3*	MRP	V	ROT, TCM, HRM	Short, narrow primary root; Reduced root xylem development; Hypocotyl growth insensitive to cytokinin	No
CQ001.03	3	At3g21510, At3g29350, At5g39340	*AHP1*, *AHP2*, *AHP3*	CND	H	HRM	Root, hypocotyl, and vegetative growth insensitive to exogenous cytokinin	No
CQ001.04	4	At1g03430, At3g21510, At3g29350, At5g39340	*AHP5*, *AHP1*, *AHP2*, *AHP3*	MRP	V	NLS, ROT	Long hypocotyl; Short, narrow primary root	No
CQ002.01	2	At1g06430, At2g30950	*FTSH8*, *FTSH2*	ESN	S	EMB, SRL, PIG	Embryo defective; Low penetrance of abnormal embryo morphology; Seedling lethal without exogenous sucrose; Albino; With exogenous sucrose: Pale flowers; Sterile	No

CQ002.02	2	At1g50250, At2g30950	*FTSH1*, *FTSH2*	MRP	V	PIG, GRS	Dwarf; Variegated leaves	No
CQ002.03	2	At1g50250, At5g42270	*FTSH1*, *FTSH5*	ESN	L	SRL	Seedling lethal without exogenous sucrose; With exogenous sucrose: Severe dwarf; Albino cotyledons and leaves	No
CQ002.04	2	At2g30950, At5g42270	*FTSH2*, *FTSH5*	MRP	V	PIG	Variegated leaves	No
CQ003.01	2	At1g15550, At1g80330	*GA3ox1*, *GA3ox4*	MRP	V	GRS, LEF, FLT	Semi-dwarf; Small rosette; Late flowering	No
CQ003.02	2	At1g15550, At1g80340	*GA3ox1*, *GA3ox2*	MRP	V	GER, GRS, ROT, LEF, FLT	Very low germination rate; Dwarf; Small rosette; Short roots; Late flowering	No
CQ003.03	2	At1g15550, At4g21690	*GA3ox1*, *GA3ox3*	MRP	R	FSM, SRF	Small petals; Sterile early flowers	No
CQ003.04	3	At1g15550, At1g80330, At4g21690	*GA3ox1*, *GA3ox4*, *GA3ox3*	MRP	V	GRS, LEF, SRF, FLT	Semi-dwarf; Small rosette; Severely reduced fertility; Late flowering	No
CQ003.05	3	At1g15550, At1g80340, At4g21690	*GA3ox1*, *GA3ox2*, *GA3ox3*	MRP	R	SRF	Severely reduced fertility	No
CQ004.01	3	At1g16190, At1g79650, At3g02540	*RAD23A*, *RAD23B*, *RAD23C*	ESN	L	NHM	No homozygous triple mutant plants recovered	No
CQ004.02	3	At1g16190, At3g02540, At5g38470	*RAD23A*, *RAD23C*, *RAD23D*	ESN	L	NHM	No homozygous triple mutant plants recovered	No
CQ005.01	2	At2g38440, At5g01730	*SCAR2*, *SCAR4*	CLB	C	STT	Abnormal trichome morphology	No
CQ005.02	3	At1g29170, At2g34150, At2g38440	*SCAR3*, *SCAR1*, *SCAR2*	CLB	C	STT, LIT	Short trichome branches; Short hypocotyl in the dark	No
CQ005.03	4	At1g29170, At2g34150, At2g38440, At5g01730	*SCAR3*, *SCAR1*, *SCAR2*, *SCAR4*	CLB	C	TCM	Altered cotyledon pavement cell morphology	No
CQ006.01	2	At2g14750, At4g39940	*APK1*, *APK2*	MRP	V	GRS, FLT	Semi-dwarf; Late flowering; Low glucosinolate levels	No
CQ006.02	2	At2g14750, At5g67520	*APK1*, *APK4*	CLB	B	PRA	Elevated glucosinolate levels	No
CQ006.03	3	At2g14750, At3g03900, At4g39940	*APK1*, *APK3*, *APK2*	CND	P	LIT	Slow growth under short days	No

CQ006.04	3	At2g14750, At3g03900, At5g67520	*APK1*, *APK3*, *APK4*	ESN	G	GAM	Male gametophyte defective	No
CQ006.05	3	At2g14750, At4g39940, At5g67520	*APK1*, *APK2*, *APK4*	CND	P	LIT	Slow growth under short days	No
CQ007.01	2	At4g39350, At5g64740	*CESA2*, *CESA6*	MRP	V	GRS, ROT, LIT	Dwarf; Short, thick roots; Short, thick hypocotyl in the dark	No
CQ007.02	2	At5g09870, At5g64740	*CESA5*, *CESA6*	ESN	L	SRL	Seedling lethal	No
CQ007.03	3	At2g21770, At4g39350, At5g64740	*CESA9*, *CESA2*, *CESA6*	ESN	G	GAM	Complete male gametophyte defective; Deformed pollen grains	No
CQ008.01	3	At2g38310, At4g17870, At5g46790	*PYL4*, *PYR1*, *PYL1*	CND	H	HRM	Insensitive to ABA	No
CQ008.02	4	At2g26040, At2g38310, At4g17870, At5g46790	*PYL2*, *PYL4*, *PYR1*, *PYL1*	CND	H	HRM	Insensitive to ABA	No
CQ009.01	2	At2g28550, At5g60120	*TOE1*, *TOE2*	MRP	T	FLT	Early flowering	No
CQ009.02	4	At2g28550, At2g39250, At3g54990, At5g60120	*TOE1*, *SNZ*, *SMZ*, *TOE2*	MRP	T	FLT	Early flowering	No
CQ010.01	2	At2g35990, At5g06300	*LOG2*, *LOG7*	CND	H	HRM	Lateral root growth insensitive to cytokinin	No
CQ010.02	3	At2g37210, At3g53450, At5g06300	*LOG3*, *LOG4*, *LOG7*	MRP	V	GRS, ROT, SRF, HRM	Dwarf; Increased adventitious root number; Few flowers; Lateral root growth insensitive to cytokinin	No
CQ011.01	2	At4g13260, At5g25620	*YUC2*, *YUC6*	MRP	V	GRS, LEF, ARC, FSM, SRF	Semi-dwarf; Abnormal rosette leaf morphology; Increased branching; Severely reduced fertility; Short stamens	No
CQ011.02	2	At4g32540, At5g11320	*YUC1*, *YUC4*	MRP	V	GRS, LEF, ARC, FSM, SRF, TCM	Semi-dwarf; Abnormal rosette leaf morphology; Increased branching; complete sterility due to anther defects; Abnormal floral organ morphology; Abnormal leaf and flower vasculature	No

CQ011.03	3	At4g13260, At4g32540, At5g11320	*YUC2*, *YUC1*, *YUC4*	MRP	V	GRS, LEF, ARC, FSM, SRF, TCM	Dwarf; Increased branching; Abnormal rosette leaf and flower morphology; Few, small flowers; Abnormal leaf and flower vasculature	No
CQ011.04	3	At4g32540, At5g11320, At5g25620	*YUC1*, *YUC4*, *YUC6*	MRP	V	GRS, LEF, ARC, FSM, SRF, TCM	Dwarf; Increased branching; Abnormal rosette leaf and flower morphology; Few, small flowers; Abnormal leaf and flower vasculature	No
CQ011.05	4	At4g13260, At4g32540, At5g11320, At5g25620	*YUC2*, *YUC1*, *YUC4*, *YUC6*	MRP	V	GRS, LEF, ARC, FSM, TCM	Severe dwarf; Small rosette leaves with abnormal morphology; Increased branching; Small flowers with abnormal morphology; Abnormal to complete loss of leaf and flower vasculature	No
CP001.01	2	At1g12780, At4g23920	*UGE1*, *UGE2*	MRP	V	LEF, MSL	Small rosette; Chlorotic young leaves	No
CP001.02	2	At1g63180, At4g23920	*UGE3*, *UGE2*	MRP	R	SRF	Severely reduced fertility	No
CP001.03	2	At1g64440, At4g23920	*UGE4*, *UGE2*	MRP	V	NLS, PIG, ROT, LEF, MSL, FSM, SRF, LIT	Thin hypocotyl; Very small rosette; Chlorotic leaves; Pale green; Short roots; Abnormal flower morphology; Reduced fertility; Short hypocotyl in the dark	No
CP001.04	3	At1g12780, At1g63180, At1g64440	*UGE1*, *UGE3*, *UGE4*	MRP	V	ROT, LIT	Short roots; Short hypocotyl in the dark	No
CP001.05	3	At1g12780, At1g64440, At4g23920	*UGE1*, *UGE4*, *UGE2*	MRP	V	NLS, PIG, GRS, FSM, SRF, LIT	Thin hypocotyl; Dwarf; Pale green; Slow growth; complete sterility; Small floral organs with abnormal morphology; Short hypocotyl in the dark	No

CP001.06	3	At1g12780, At4g10960, At4g23920	*UGE1*, *UGE5*, *UGE2*	MRP	V	LEF, MSL, SRF, LIT	Small rosette; Curled leaves; Necrotic lesions; Reduced fertility; Short hypocotyl in the dark	No
CP001.07	3	At4g10960, At1g64440, At4g23920	*UGE5*, *UGE4*, *UGE2*	MRP	V	PIG, ROT, SRF	Pale green; Short roots; complete sterility	No
CP001.08	4	At1g12780, At1g63180, At1g64440, At4g10960	*UGE1*, *UGE3*, *UGE4*, *UGE5*	MRP	V	ROT, LIT	Short roots; Short hypocotyl in the dark	No
CP001.09	4	At1g12780, At1g64440, At4g10960, At4g23920	*UGE1*, *UGE4*, *UGE5*, *UGE2*	MRP	V	GER	Complete loss of germination without exogenous galactose; With exogenous galactose: Very low germination; Extremely disorganized seedling	No
CP002.01	2	At1g15750, At1g80490	*TPL*, *TPR1*	CND	I	PTH	Susceptible to *Pseudomonas syringae*	No
CP002.02	3	At1g15750, At1g80490, At3g15880	*TPL*, *TPR1*, *TPR4*	CND	I	PTH	Susceptible to *Pseudomonas syringae*	No
CP002.03	5	At1g15750, At1g80490, At3g15880, At3g16830, At5g27030	*TPL*, *TPR1*, *TPR4*, *TPR2*, *TPR3*	ESN	L	SRL, TMP	Seedling lethal; Cotyledon-fusion and pin-shaped seedling defects; Shoot develops as a root at high temperature	No
CP003.01	3	At3g23630, At3g63110, At5g19040	*AtIPT7*, *AtIPT3*, *AtIPT5*	MRP	V	ROT, LEF, IST, SRF, SSC, TCM	Short; thin inflorescence stems; Long roots; Few rosette leaves; Reduced fertility; Large seeds; Small SAM	No
CP003.02	4	At1g25410, At3g23630, At3g63110, At5g19040	*AtIPT6*, *AtIPT7*, *AtIPT3*, *AtIPT5*	MRP	V	ROT, LEF, IST, SRF, SSC, TCM	Short; thin inflorescence stems; Long roots; Few rosette leaves; Reduced fertility; Large seeds; Small SAM	No
CP003.03	4	At1g68460, At3g23630, At3g63110, At5g19040	*AtIPT1*, *AtIPT7*, *AtIPT3*, *AtIPT5*	MRP	V	ROT, LEF, IST, SRF, SSC, TCM	Short; thin inflorescence stems; Long roots; Few rosette leaves; Reduced fertility; Large seeds; Small SAM	No

CP003.04	5	At1g25410, At1g68460, At3g23630, At3g63110, At5g19040	*AtIPT6*, *AtIPT1*, *AtIPT7*, *AtIPT3*, *AtIPT5*	MRP	V	ROT, LEF, IST, SRF, SSC, TCM	Short; thin inflorescence stems; Long roots; Few rosette leaves; Reduced fertility; Large seeds; Small SAM	No
CP004.01	2	At5g07290, At5g61960	*AML4*, *AML1*	ESN	L	SRL, ROT	Incomplete penetrance of seedling lethality and abnormal root growth	No
CP004.02	3	At2g42890, At5g07290, At5g61960	*AML2*, *AML4*, *AML1*	ESN	L	SRL, SRF	Incomplete penetrance of seedling lethality; Reduced fertility due to defects in meiosis	No
CP004.03	5	At1g29400, At2g42890, At4g18120, At5g07290, At5g61960	*AML5*, *AML2*, *AML3*, *AML4*, *AML1*	MRP	V	ARC, SRF	Increased branching; Sterile due to defects in meiosis	No
CP005.01	2	At1g30490, At5g60690	*PHV*, *REV*	MRP	V	GRS, LEF, FSM	Dwarf; Low penetrance of trumpet-shaped leaves; Flowers develop as small filamentous structures	No
CP005.02	2	At1g52150, At2g34710	*CNA*, *PHB*	MRP	V	GRS, FSM	Dwarf; Incomplete penetrance of increased carpel number	No
CP005.03	2	At2g34710, At5g60690	*PHB*, *REV*	ESN	L	SRL, TCM	Seedling lethal; Radially symmetric organ forms instead of the shoot meristem	No
CP005.04	3	At1g30490, At1g52150, At2g34710	*PHV*, *CNA*, *PHB*	MRP	V	NLS, IST, ARC, FSM, OVP, SRF, TCM	Increased cotyledon number; Fasciated stems and inflorescences; Increased floral organ number; Reduced fertility; Abnormal ovule morphology; Large SAM; Abnormal vascular tissue	No
CP005.05	3	At1g30490, At2g34710, At5g60690	*PHV*, *PHB*, *REV*	ESN	S	EMB, SRL	Embryo defective; Apical portion of embryo replaced by radially symmetric cotyledon-like structure; Seedling lethal	No

CP005.06	3	At1g52150, At2g34710, At5g60690	*CNA*, *PHB*, *REV*	ESN	S	EMB, SRL	Embryo defective; Apical portion of embryo replaced by radially symmetric cotyledon-like structure; Seedling lethal	No
CP005.07	4	At1g30490, At1g52150, At2g34710, At4g32880	*PHV*, *CNA*, *PHB*, *AtHB8*	MRP	V	GRS, LEF	Dwarf; Small rosettes	No
CP006.01	2	At5g12080, At5g19520	*MSL10*, *MSL9*	CLB	B	CPR	Abnormal stretch-activated channel activity	No
CP006.02	5	At1g53470, At1g78610, At3g14810, At5g12080, At5g19520	*MSL4*, *MSL6*, *MSL5*, *MSL10*, *MSL9*	CLB	B	CPR	Complete loss of stretch-activated channel activity	No
CS001.01	2	At1g10470, At1g59940	*ARR4*, *ARR3*	CND	P	LIT, HRM	Long petioles under short days; Short hypocotyl under red light; Lateral root formation sensitive to cytokinin	No
CS001.02	2	At1g10470, At3g48100	*ARR4*, *ARR5*	CND	P	LIT, HRM	Short hypocotyl under red light; Lateral root formation sensitive to cytokinin	No
CS001.03	2	At1g10470, At5g62920	*ARR4*, *ARR6*	CND	P	LIT	Short hypocotyl under red light	No
CS001.04	2	At2g41310, At3g57040	*ARR8*, *ARR9*	MRP	V	ROT	Slightly fewer lateral roots	No
CS001.05	2	At3g48100, At5g62920	*ARR5*, *ARR6*	CND	P	LIT	Short hypocotyl under red light	No
CS001.06	3	At1g10470, At1g59940, At5g62920	*ARR4*, *ARR3*, *ARR6*	CND	H	HRM	Short roots in response to cytokinin	No
CS001.07	4	At1g10470, At1g59940, At2g41310, At3g57040	*ARR4*, *ARR3*, *ARR8*, *ARR9*	MRP	V	ROT, HRM	Few lateral roots; Lateral root growth sensitive to cytokinin	No
CS001.08	4	At1g10470, At1g59940, At3g48100, At5g62920	*ARR4*, *ARR3*, *ARR5*, *ARR6*	CND	P	LIT, HRM	Long petioles under short days; Delayed senescence in the dark; Pale green, short roots, and decreased lateral root formation in response to cytokinin	No
CS001.09	4	At2g41310, At3g48100, At3g57040, At5g62920	*ARR8*, *ARR5*, *ARR9*, *ARR6*	CND	H	HRM	Lateral root formation sensitive to cytokinin	No

CS001.10	6	At1g10470, At1g59940, At2g41310, At3g48100, At3g57040, At5g62920	*ARR4*, *ARR3*, *ARR8*, *ARR5*, *ARR9*, *ARR6*	MRP	V	ROT, LIT, HRM	Short roots; Few lateral roots; Long hypocotyl under red light; Root growth sensitive to cytokinin	No
CO001.01	2	At1g01480, At2g22810	*ACS2*, *ACS4*	MRP	V	IST	Tall inflorescence stems	No
CO001.02	2	At1g01480, At3g49700	*ACS2*, *ACS9*	MRP	V	IST	Tall inflorescence stems	No
CO001.03	2	At2g22810, At3g49700	*ACS4*, *ACS9*	MRP	V	IST	Tall inflorescence stems	No
CO001.04	2	At3g49700, At4g11280	*ACS9*, *ACS6*	MRP	V	IST	Tall inflorescence stems	No
CO001.05	2	At3g49700, At5g65800	*ACS9*, *ACS5*	MRP	V	IST	Tall inflorescence stems	No
CO001.06	2	At4g11280, At4g26200	*ACS6*, *ACS7*	MRP	V	LEF, FLT	Increased rosette leaf number; Late flowering; Low ethylene levels	No
CO001.07	5	At1g01480, At2g22810, At3g49700, At4g11280, At5g65800	*ACS2*, *ACS4*, *ACS9*, *ACS6*, *ACS5*	MRP	V	NLS, IST, FLT	Tall inflorescence stems; Long hypocotyl; Early flowering; Low ethylene levels	No
CO001.08	8	At1g01480, At2g22810, At3g49700, At4g08040, At4g11280, At4g26200, At4g37770, At5g65800	*ACS2*, *ACS4*, *ACS9*, *ACS11*, *ACS6*, *ACS7*, *ACS8*, *ACS5*	ESN	S	EMB, W:NLS, W:GRS, W:IST, W:ARC, W:FLT, W:SEN	Null: Embryo defective; Knockdown: Short hypocotyl; Complete loss of apical hook formation; Slow growth; Tall inflorescence stems; Reduced branching; Delayed senescence; Slightly early flowering	No

APPENDIX I: Phenotypes of Putative Orthologs

This appendix includes a truncated version of the dataset describing phenotypes of putatively orthologous genes in Arabidopsis, rice, tomato, and maize. Included data are gene symbols, locus numbers (where available), phenotype groups and classes, mutant phenotype descriptions, and a subjective comparison of phenotype similarity of the two genes being compared. The full putative ortholog phenotype dataset is available as a spreadsheet appended to the *Plant Physiology* publication describing its construction and analysis (Lloyd and Meinke, 2012; Table S7).

Footnotes for the title row of the following table are described below:

[a] Refer to Appendix B for explanations of phenotype group, class, and subset abbreviations.

[b] Based on a subjective comparison of described mutant phenotypes. See text (Chapter 5; Phenotypes of Putative Orthologs) for more information.

[c] NA, Not available, based on current annotation of the maize genome.

Ortholog Plant	**Arabidopsis Locus**	**Arabidopsis Gene Symbol**	**Ortholog Gene Symbol**	**Phenotype Group *Ath*/Other[a]**	**Phenotype Class *Ath*/Other[a]**	**Phenotype Similarity[b]**	**Arabidopsis Phenotype**	**Other Plant Phenotype**	**Ortholog Locus Number[c]**
Rice	At1g02205	*CER1*	*WDA1*	MRP / MRP	V / V	Moderate High	Glossy inflorescence stems and siliques; Male sterile in low humidity	Semi-dwarf; Male sterile; Altered wax composition	LOC_Os10g33250
Tomato	At1g10760	*SEX1*	*GWD*	CLB / ESN	B / G	Moderate	Elevated starch in leaves after prolonged darkness	Male gametophyte defective (GAM); Increased starch levels in pollen	Solyc05g005020
Rice	At1g14920	*GAI*	*SLR*	CND / MRP	H / V	Low	Resistant to paclobutrazol (inhibitor of GA synthesis)	Fast growth; Elongated shoots; Reduced roots; Sterile	LOC_Os03g49990
Tomato	At1g14920	*GAI*	*GAI*	CND / MRP	H / V	Low	Resistant to paclobutrazol (inhibitor of GA synthesis)	Elongated stems; Altered branching architecture	Solyc11g011260
Tomato	At1g16540	*ABA3*	*FLC*	MRP / MRP	V / V	Moderate High	Reduced seed dormancy; Wilty; Low ABA levels; Altered response to low temperature and osmotic stress	Slow growth; Downward-bending leaves; Wilty; Excessive transpiration due to loss of stomatal control; Low ABA levels	Solyc07g066480
Rice	At1g22770	*GI*	*GI*	MRP / CND	T / P	High	Late flowering	Late flowering under short days	LOC_Os01g08700

Tomato	At1g30950	*UFO*	*AN*	MRP / MRP	R / V	Moderate	Homeotic floral transformations	Leaves are small and highly suppressed with a cauliflower-like appearance; No flowers form; Determinate floral meristems replaced by indeterminate proliferous shoot	Solyc02g081670
Rice	At1g30950	*UFO*	*APO1*	MRP / MRP	R / V	Moderate High	Homeotic floral transformations	Increased leaf number; Abnormal panicle phyllotaxy; Decreased panicle branching; Homeotic floral transformations; Reduced fertility	LOC_Os06g45460
Rice	At1g55580	*LAS*	*MOC1*	MRP / MRP	V / V	High	Decreased branching	Complete loss of tiller formation	LOC_Os06g40780
Tomato	At1g55580	*LAS*	*LS*	MRP / MRP	V / V	Moderate High	Decreased branching	Few or no axillary branches; Corolla suppressed; Partially male sterile	Solyc07g066250
Maize	At1g63650	*EGL3*	*R1*	CLB / MRP	C / V	Low	Slightly increased root hair density in upper region of root	Modified aleurone and plant pigmentation	NA

Maize	At1g65380	*CLV2*	*FEA2*	MRP / MRP	R / R	High	Abnormal pistil, pedicel, and stamen development; Large shoot and floral meristems; Fasciated stems and inflorescences, early flowering, and rescued floral phenotypes under short days	Fasciated ear with irregular rows; Ear broadened and flattened at tip; Meristem overproliferation	NA
Rice	At1g67370	*ASY1*	*PAIR2*	MRP / MRP	R / R	High	Severely reduced fertility due to defects in meiosis	Sterile; Loss of homologous chromosome pairing	LOC_Os09g32930
Rice	At1g67940	*STAR1*	*STAR1*	CND / CND	H / H	High	Sensitive to aluminum	Sensitive to aluminum	LOC_Os06g48060
Rice	At1g69180	*CRC*	*DL*	MRP / MRP	R / V	Moderate High	Abnormal carpel development	Drooping leaves due to loss of leaf midrib formation; Abnormal carpel development	LOC_Os03g11600
Rice	At1g72560	*PSD*	*PSD*	MRP / MRP	V / V	Moderate High	Delayed leaf growth; Few lateral roots; Abnormal phyllotaxy; Reduced fertility	Slow growth; Delayed panicle heading; Reduced fertility	LOC_Os07g42180

Rice	At1g75820	*CLV1*	*FON1*	MRP / MRP	V / R	Moderate High	Fasciated stems and inflorescences; Abnormal leaf phyllotaxy; Slightly rounded leaves; Incomplete penetrance of double leaf formation and increased floral organ number	Increased floral organ number; Enlarged floral meristem	LOC_Os06g50340
Maize	At1g78390	*NCED9*	*VP14*	CLB / MRP	B / V	Low	Low ABA levels; Germination resistant to paclobutrazol (inhibitor of GA synthesis)	Precocious germination; Yellow endosperm	NA
Rice	At1g79460	*GA2*	*KS1*	MRP / MRP	V / V	Moderate High	Very low germination rate; Severe dwarf; Dark green; Sterile	Severe dwarf; Does not flower; With exogenous GA: Male sterile	LOC_Os04g52230
Rice	At2g01110	*APG2*	*TATC*	ESN / ESN	L / L	High	Seedling lethal; Albino and pale green seedlings	Vegetative lethality; Pale green; Elevated ABA levels under drought	LOC_Os01g31680
Rice	At2g16910	*AMS*	*TDR*	MRP / MRP	R / R	High	Completely male sterile; Very short filaments	Male sterile; Abnormal stamen development	LOC_Os02g02820
Rice	At2g19810	*AtOZF1*	*DOS*	CND / MRP	H / T	Low	Sensitive to oxidative stress	Early senescence	LOC_Os01g09620

Rice	At2g22540	*SVP*	*MDP1*	MRP / CND	T / P	Low	Early flowering	Long coleoptile and short primary root in dark-grown seedlings; Seedlings sensitive to 24-epibrassinolide	LOC_Os03g08754
Tomato	At2g22540	*SVP*	*J*	MRP / MRP	T / R	Low	Early flowering	Inflorescence meristems revert to vegetative growth; Flowers fail to abscise	Solyc11g010570
Rice	At2g26300	*GPA1*	*D1*	ESN / MRP	G / V	Low	Low pollen germination rate; Short pollen tubes; Homozygotes are viable: Short hypocotyl; Large leaf cells; Short roots in response to auxin	Dwarf; Broad, dark green leaves; Compact panicles; Short, round grains; Insensitive to GA	LOC_Os05g26890
Rice	At2g26670	*HY6*	*SE5*	MRP / MRP	V / V	Moderate High	Dwarf; Pale green; Long hypocotyl; Slow growth and small, chlorotic leaves under continuous light	Semi-dwarf; Few stems; Yellow leaves; Early flowering	LOC_Os06g40080
Tomato	At2g28160	*FRU*	*FER*	ESN / ESN	L / L	High	Seedling lethal without exogenous iron	Seedling lethal without exogenous iron	Solyc06g051550

Tomato	At2g33880	*STIP*	*S*	ESN / MRP	L / R	Low	Seedling lethal; Small, upward-bending cotyledons; Incomplete penetrance of complete loss of primary root	Highly branched inflorescence; Multiple flowers	Solyc02g077390
Maize	At2g37630	*AS1*	*RS2*	MRP / MRP	V / V	Moderate High	Altered leaf morphology	Short plants; Disorganized ligule; Warty, distorted sheaths and leaves	NA
Tomato	At2g39940	*COI1*	*COI1*	MRP / MRP	R / R	High	Male sterile; Altered response to wounding; Insensitive to jasmonate	Almost completely sterile; Insensitive to jasmonate	Solyc05g052620
Rice	At2g42620	*ORE9*	*D3*	MRP / MRP	V / V	Moderate	Increased branching; Long hypocotyl and cotyledonary petioles; Delayed senescence; Resistant to oxidative stress	Dwarf; Excessive tillers	LOC_Os06g06050
Rice	At2g44990	*CCD7*	*HTD1*	MRP / MRP	V / V	High	Increased branching; Semi-dwarf; Short leaves and petioles	Dwarf; Excessive tillers	LOC_Os04g46470
Tomato	At3g09150	*HY2*	*AUREA*	MRP / MRP	V / V	Low	Long hypocotyl	Yellow-green leaves; Low phytochrome levels in dark grown seedlings	Solyc01g008930

Tomato	At3g14440	*NCED3*	*NOT*	CND / MRP	H / V	Low	Insensitive to potassium and calcium; Sensitive to lithium	Dainty and delicate yellow-green leaves; Wilty in dry or hot weather	Solyc07g056570
Maize	At3g24650	*ABI3*	*VP1*	MRP / MRP	V / V	High	Reduced seed dormancy; Insensitive to ABA	Precocious germination (normal chlorophyll and carotenoids); Reduced aleurone anthocyanin	NA
Rice	At3g30180	*BR6OX2*	*DWARF*	MRP / MRP	V / V	High	Slightly smaller seedlings; Slightly shorter inflorescence stems; Rounded, curled, dark green leaves; Short petioles; Abnormal cauline leaf and stamen formation; Reduced fertility	Semi-dwarf; Wide, dark green leaves	LOC_Os03g40540
Maize	At3g44880	*ACD1*	*LLS1*	MRP / MRP	V / V	High	Necrotic lesions	Chlorotic-necrotic leaf lesions; Early leaf senescence; Premature plant death	NA
Rice	At3g50660	*DWF4*	*DWARF4*	MRP / MRP	V / V	High	Dwarf	Dwarf; Insensitive to auxin	LOC_Os03g12660
Maize	At3g54340	*AP3*	*SI1*	MRP / MRP	R / R	High	Homeotic floral transformations	Homeotic floral defects; Male sterile	NA

Maize	At3g54720	*AMP1*	*VP8*	ESN / MRP	S / V	Low	Embryo and seedling defective	Precocious germination (normal chlorophyll and carotenoids); Small seedlings with pointed leaves	NA
Maize	At3g59420	*ACR4*	*CR4*	MRP / MRP	V / V	Low	Few lateral roots; Abnormal integuments; Increased lateral root meristem number	Crinkly leaves; Dwarf plants; Club-shaped tassels; Reduced pollen	NA
Rice	At4g02780	*GA1*	*CPS1*	MRP / MRP	V / V	Moderate	Complete loss of germination without exogenous GA	Dwarf; Phenotype rescued by exogenous GA	LOC_Os02g17780
Rice	At4g03560	*AtTPC1*	*TPC1*	CND / MRP	H / V	Low	Insensitive to ABA; Abnormal stomatal regulation in response to calcium	Semidwarf	LOC_Os01g48680
Tomato	At4g10180	*DET1*	*DET1*	MRP / MRP	V / V	Moderate	Dwarf; Red cotyledons and lower leaf surfaces; Green roots; Dark-grown seedlings are de-etiolated	Dwarf; Short hypocotyl; Dark green leaves and immature fruits; Elevated anthocyanin levels; No phenotype in dark-grown seedlings	Solyc01g056340

Rice	At4g20910	*CRM2*	*WAF1*	MRP / ESN	V / S	Moderate	Corymb-like inflorescences; Increased cauline leaf number; Increased flower growth rate; Short stamens; Reduced fertility; Late flowering	Abnormal embryo development; Incomplete penetrance of seedling lethality; Abnormal leaf morphology; Short roots; Few lateral roots; Short panicle; Elongated bracts; Abnormal spikelet morphology; Reduced floral organ number; Sterile	LOC_Os07g06970
Tomato	At4g22260	*IM*	*PTOX*	ESN / ESN	L / L	High	Seedling lethal (inferred from pigment defect)	Albino	Solyc11g011990
Rice	At4g39400	*BRI1*	*D61*	MRP / MRP	V / V	Moderate High	Dwarf; Dark green; Increased branching; Completely male sterile; Late flowering; Delayed leaf senescence; Insensitive to brassinosteroids	Dwarf; Erect leaves; Reduced fertility	LOC_Os01g52050

Tomato	At4g39400	*BRI1*	*CU3*	MRP / MRP	V / V	Moderate High	Dwarf; Dark green; Increased branching; Completely male sterile; Late flowering; Delayed leaf senescence; Insensitive to brassinosteroids	Dwarf; Insensitive to brassinosteroids	Solyc04g051510
Tomato	At5g03840	*TFL1*	*SP*	MRP / MRP	V / V	Moderate High	Inflorescences terminate early with a single flower; Early flowering independent of photoperiod	Determinate inflorescence growth; Short plant	Solyc06g074350
Rice	At5g07280	*EXS*	*MSP1*	ESN / MRP	S / R	Moderate	Embryo defective; Cotyledon	Completely male sterile due to small, collapse anthers; Increased male and female sporocyte number	LOC_Os01g68870
Maize	At5g13930	*TT4*	*C2*	MRP / MRP	R / V	Moderate High	Yellow seed coat	Colorless aleurone; Reduced plant and cob color	NA

Maize	At5g16560	*KAN*	*MWP1*	MRP / MRP	V / V	Moderate	Cupped first true leaves; Rolled leaves that become flat over time; Abnormal pistil development; Ectopic ovules on outside of carpels; Abnormal trichome patterning	Rough surface of ear shoot husk; Longitudinal outgrowths; Altered polarity of sheath tissue	NA
Maize	At5g18580	*FS1*	*DCD1*	ESN / CLB	S / C	Moderate	Embryo and seedling defective	Altered asymmetric cell divisions in leaf epidermis; Abnormal stomata, cork cells, and silica cells	NA
Rice	At5g20910	*AIP2*	*DSG1*	CND / MRP	H / V	Low	Sensitive to ABA	Delayed germination; Dwarf; Tolerant to high salt and drought stress	LOC_Os09g26400
Maize	At5g23570	*SGS3*	*RGD1*	CND / MRP	I / V	Low	Susceptible to viral infection	Narrow, thread-like leaves; Severely reduced leaf blade	NA
Maize	At5g24520	*TTG1*	*PAC1*	MRP / MRP	R / V	Moderate	Yellow seed coat; Abnormal trichome and root hair development	Reduced kernel pigmentation	NA

Rice	At5g43810	*ZLL*	*PNH1*	ESN / MRP	L / V	Moderate	Complete loss of primary inflorescence; Fasciated adventitious stems and inflorescences; Arrested SAM development	Abnormal leaf morphology, vasculature, and SAM development	LOC_Os06g39640
Maize	At5g54160	*COMT1*	*BM3*	CND / MRP	I / V	Moderate	Susceptible to fungal infection	Modified lignin; Weak stalks; Reduced grain yield	NA
Tomato	At5g61850	*LFY*	*FA*	MRP / MRP	V / V	Moderate High	Increased branching; Flowers show some characteristics of secondary inflorescences; Flowers often subtended by leafy bracts	Increased branching; Leafy; No flowers form; Late flowering	Solyc03g118160
Rice	At5g64330	*NPH3*	*CPT1*	CND / CND	P / P	High	Reduced phototropism	Complete loss of coleoptile phototropism; Reduced root phototropism	LOC_Os02g35970
Rice	At5g67030	*ABA1*	*ZEP1*	MRP / MRP	V / V	High	Wilty; Low ABA levels	Wilty; Precocious germination; Low abscisic acid levels	LOC_Os04g37619

Tomato	At5g67030	*ABA1*	*ZEP1*	MRP / MRP	V / V	Moderate	Wilty; Low ABA levels	Decreased biomass; Wilty; Green leaves; Beige flowers; Intense red fruits; Increased carotenoids	Solyc02g090890

VITA

John Paul Lloyd, Jr.

Candidate for the Degree of

Master of Science

Thesis: A COMPREHENSIVE DATASET OF GENES WITH LOSS-OF-FUNCTION MUTANT PHENOTYPES IN *ARABIDOPSIS THALIANA*

Major Field: Botany

Biographical:

Personal: Born on April 16, 1983 in Minneapolis, Minnesota to parents John Lloyd, Sr. and Jeanine Landey.

Education: Graduated from Union High School, Tulsa, Oklahoma in May 2001; received Bachelor of Science degree in Microbiology from Oklahoma State University, Stillwater, Oklahoma in May 2009; completed the requirements for the Master of Science in Botany at Oklahoma State University in July, 2012.

Experience: Employed from August 2009 to May 2012 as a Teaching Assistant at Oklahoma State University, Stillwater, Oklahoma. In this role I served as a laboratory instructor for basic plant biology laboratory sections, graded all homework and exams and held review sessions and office hours for a general genetics lecture, and assisted with the teaching of a plant microtechniques course. Supervised over 400 students in total.

Cited as a lead author for a *Plant Physiology* publication (Lloyd and Meinke, 2012) and co-author on two additional publications (Bryant et al., 2011; Muralla et al., 2011).

Presented two research seminars hosted by the Botany Department at Oklahoma State University: February 2010 and March 2012. Presented four posters at international scientific conferences.

Name: John Paul Lloyd Date of Degree: July, 2012

Institution: Oklahoma State University Location: Stillwater, Oklahoma

Title of Study: A COMPREHENSIVE DATASET OF GENES WITH LOSS-OF-FUNCTION MUTANT PHENOTYPES IN *ARABIDOPSIS THALIANA*

Pages in Study: 482 Candidate for the Degree of Master of Science

Major Field: Botany

Scope and Method of Study: Mutant phenotypes of *Arabidopsis thaliana* have proven to be a powerful tool in the study of plant biology. However, genome-wide information on these mutant phenotypes and the altered genes that give rise to them remains difficult to obtain. This thesis describes the construction of a comprehensive, gene-based dataset of mutant phenotype information in Arabidopsis. The SeedGenes database of embryo-defective genes (www.seedgenes.org) and a preliminary phenotype dataset from a *Plant Physiology* paper published by the Meinke laboratory nine years ago established a foundation for this project. Additional genes and associated phenotypes were identified through manual literature curation focused on PubMed literature searches and a list of candidate phenotype genes provided by TAIR (www.arabidopsis.org). The final phenotype dataset contains information on 2,400 genes with a documented loss-of-function phenotype in Arabidopsis. A complementary dataset of phenotypes resulting from the disruption of more than one genetically redundant gene was also constructed. This multiple mutant dataset contains phenotype data for an additional 400 genes. The 2,800 total genes identified here represent over 10% of the Arabidopsis genome.

Findings and Conclusions: Information from this dataset assisted in evaluating Arabidopsis genes with gametophyte phenotypes and helped to address the curious survival of mutant gametophytes lacking basic cellular functions. The complete dataset was used to explore the relationship between mutant phenotype and protein function, subcellular localization, protein connectivity, and genetic redundancy. The degree of similarity in protein sequences and expression levels of fully- and partially-redundant genes was analyzed and the similarity in phenotypes of putative orthologs in rice, maize, and tomato was investigated. The thesis concludes with a discussion of Arabidopsis genes that display no apparent loss-of-function phenotype. Much of the work described here is available through several recent publications (Bryant et al., 2011; Muralla et al., 2011; Lloyd and Meinke, 2012).

ADVISER'S APPROVAL: David Meinke