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(54) **Title:** MATERIALS AND METHODS FOR CONTROLLING BUNDLE SHEATH CELL FATE AND FUNCTION IN PLANTS

(57) **Abstract:** The subject invention concerns materials and methods for increasing and/or improving photosynthetic efficiency in plants, and in particular, C3 plants. In particular, the subject invention provides for means to increase the number of bundle sheath (BS) cells in plants, to improve the efficiency of photosynthesis in BS cells, and to increase channels between BS and mesophyll (M) cells. In one embodiment, a method of the invention concerns altering the expression level or pattern of one or more of SHR, SCR, and/or SCL23 in a plant. The subject invention also pertains to genetically modified plants, and in particular, C3 plants, that exhibit increased expression of one or more of SHR, SCR, and/or SCL23. Transformed and transgenic plants are contemplated within the scope of the invention. The subject invention also concerns methods for increasing expression of photosynthetically important genes in a plant, wherein one or more genes of interest are operably linked with a plant SHR, SCR or SCL23 promoter sequence and expressed in a plant.



DESCRIPTION

MATERIALS AND METHODS FOR CONTROLLING BUNDLE SHEATH CELL
FATE AND FUNCTION IN PLANTS

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CROSS-REFERENCE TO RELATED APPLICATION

The present application claims the benefit of U.S. Provisional Application No. 61/833,771, filed June 11, 2013, which is hereby incorporated by reference herein in its entirety, including any figures, tables, nucleic acid sequences, amino acid sequences, or drawings.

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BACKGROUND OF THE INVENTION

With a rapidly growing world population and dwindling natural resources, we are facing an enormous challenge of increasing crop yields while simultaneously improving the efficiency of resource utilization. In C3 plants, a 3-carbon molecule is the first product of carbon fixation, whereas in C4 plants, a 4-carbon molecule is the first product. Because C4 plants are much more efficient than C3 plants in photosynthesis as well as water and nitrogen usage, particularly in hot climates (Langdale (2011)), tremendous efforts are being taken to introduce C4 photosynthesis into economically important C3 crops (Sage and Zhu (2011)), such as rice (Hibberd *et al.* (2008)). It is estimated that yields can be increased by 50% if rice is transformed into a C4 plant (Hibberd *et al.* (2008)).

Evidence indicates that C4 plants have evolved multiple times from C3 plants (Brown *et al.* (2011)), but all C4 plants share some common features that make them perform better. A critical innovation is the deployment of phosphoenolpyruvate (PEP) carboxylase as the enzyme for the initial fixation of CO₂ in C4 plants. Unlike RUBISCO, the enzyme used for the initial fixation of CO₂ in C3 plants, PEP carboxylase does not have an oxygenase activity and therefore can maintain a high rate of photosynthesis even under conditions of low CO₂ (stomates partially closed) and high temperature (RUBISCO's oxygenase activity is stimulated at high temperatures (Spreitzer *et al.* (2002))). Another critical feature of C4 plants is the separation of the two phases of

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photosynthesis, namely CO₂ fixation and carbohydrate biosynthesis, into the mesophyll and bundle sheath cells, respectively. To sustain a high rate of photosynthesis, C₄ plants also have numerous plasmodesmata and various types of nutrient transporters distributed along the cell wall between the mesophyll and bundle sheath cells (Haritatos *et al.* (2000);
5 Takahashi *et al.* (2000)), which ensure efficient transport of the primary products from the CO₂ fixation process. In the bundle sheath cells, CO₂ is released from the primary photosynthetic product and is then utilized in a standard C₃-type photosynthesis involving RUBISCO. RUBISCO is expressed only in the bundle sheath cells, whereas PEP carboxylase is mesophyll cell specific. Due to the spatial separation of the
10 photosynthetic processes along with the active transport system, CO₂ is effectively concentrated in the bundle sheath cells, which in turn leads to the repression of the oxygenase activity of RUBISCO. Last but not least, each bundle sheath cell layer is associated with a central cylinder of vascular tissue, which provides water and inorganic nutrients, and is surrounded by a single layer of mesophyll cells, a feature characteristic
15 of C₄ plants called the Kranz anatomy (Wang *et al.* (2011)).

Attempts to increase yield by expressing PEP carboxylase in both mesophyll and bundle sheath cells in rice have failed (Taniguchi *et al.* (2008)), suggesting that the mesophyll and bundle sheath cells must be engineered separately (Kajala *et al.* (2011)).

Despite the pivotal role of bundle sheath cells in C₄ photosynthesis, the
20 mechanisms that determine their cell identity and patterning are still unknown. Extensive mutant screening efforts in the past decades have identified several maize and Arabidopsis mutants defective in chloroplast development in the bundle sheath cells (Nelson (2011); Brutnell *et al.* (1999); Hall *et al.* (1998); Kinsman and Pyke (1998); Petricka *et al.* (2008); Rossini *et al.* (2001)), but none of these mutants affects bundle
25 sheath cell identity.

Bundle sheath cells are a leaf cell type that forms a single cell layer between the mesophyll cells and the central vascular tissue. In C₃ plants, both the mesophyll cells and BS cells are photosynthetic, but the BS cells are small with fewer chloroplasts. In contrast, the BS cells are the major sites of photosynthesis in most C₄ plants, whereas the
30 mesophyll cells are involved in CO₂ fixation only. Accordingly, the BS cells are much larger in size. The spatial separation of the two phases of photosynthesis into mesophyll and BS cells is one of the features that make C₄ plants significantly more efficient

photosynthetically. Another feature that improves the photosynthetic efficiency in C4 plants is the Kranz anatomy, characterized by an approximately 1:1 ratio between mesophyll and BS cells. The close association between the two cell types facilitates metabolite transport, which is critical for the C4 mechanism. In C3 plants, this ratio is greater than 2:1.

Many important crops, such as rice (*Oryza sativa*) and wheat (*Triticum aestivum*), are C3 plants. To meet the needs for food of a rapidly growing population, tremendous efforts are being undertaken to introduce the C4 mechanism into C3 crops (Langdale, 2011). For example, millions of dollars have been invested at the C4 rice consortium to convert this important crop into a C4 plant (von Caemmerer *et al.*, 2012). Although the input is huge and the risk is high, the potential reward is enormous. It is estimated that a 10% increase in the photosynthetic efficiency would increase the yield by 50% (Langdale, 2011). However, to achieve C4 photosynthesis in C3 plants requires engineering of the BS and mesophyll cells at many levels, including an increase in the density of BS cells and modification of the physiology in the BS and mesophyll cells. This in turn demands a good understanding of the mechanisms that control BS and mesophyll cell fate. However, at present, the molecular basis of BS cell-fate specification is still unclear (Nelson, 2011).

There is evidence that the development of BS cells is determined by a signal from the vascular tissue (Langdale *et al.*, 1988; Langdale *et al.*, 1991; Jankovsky *et al.*, 2001), but nothing is known about the nature of this positional information. Although several factors with a role in chloroplast development in BS cells have been reported, none of these appears to control BS cell fate. In maize (*Zea mays*), for example, mutations in the genes encoding GOLDEN2 and related transcription factors (Hall *et al.*, 1998; Rossini *et al.*, 2001), as well as BSD2 (BUNDLE SHEATH DEFECTIVE 2), a DnaJ-like protein (Brutnell *et al.*, 1999), disrupt chloroplast development in the BS cells but do not affect BS cell fate. Mutants defective in chloroplast development in BS cells (Kinsman and Pyke, 1998) and vein patterning (Petricka *et al.*, 2008) have also been isolated in *Arabidopsis*, but these mutants have a normal layer of BS cells.

SCARECROW (SCR, AT3G54220) and SHORT-ROOT (SHR, AT4G37650) are key regulators of radial patterning in the *Arabidopsis* root (Di Laurenzio *et al.*, 1996; Helariutta *et al.*, 2000). In the *scr* and *shr* mutants, the cortex/endodermis initial fails to

divide longitudinally, resulting in loss of one cell layer (Di Laurenzio *et al.*, 1996). Unlike SCR, which is expressed specifically in the endodermis and cortex/endodermis initial cells (Di Laurenzio *et al.*, 1996), SHR is expressed exclusively in the central vascular tissue (Helariutta *et al.*, 2000). However, the SHR protein moves into the adjacent cell layer (Nakajima *et al.*, 2001), where it activates transcription of SCR (Levesque *et al.*, 2006). SCR in turn restricts SHR movement by physical interaction and nuclear sequestration, thus defining a single layer of endodermis (Cui *et al.*, 2007).

SHR and SCR are also expressed in the shoot (Wysocka-Diller *et al.*, 2000; Dhondt *et al.*, 2010; Gardiner *et al.*, 2010). In addition to the shoot apical meristem and young leaf primordia, SCR is also expressed in BS cells (Wysocka-Diller *et al.*, 2000). Although BS cells and the endodermis are produced from different groups of stem cells (the shoot apical meristem and the root apical meristem, respectively), and at different stages of plant development (during and after embryogenesis, respectively) (Kangasjarvi *et al.*, 2009), they are considered as analogous cell types (Bosabalidis *et al.*, 1984).

BRIEF SUMMARY OF THE INVENTION

The subject invention concerns materials and methods for increasing and/or improving photosynthetic efficiency in plants. In particular, the subject invention provides for means to increase the number of bundle sheath (BS) cells in plants, to improve the efficiency of photosynthesis in BS cells, to improve carbohydrate biosynthesis, and to increase channels between BS and mesophyll (M) cells. In one embodiment, a method of the invention concerns increasing expression of one or more of SHR (Short-Root), SCR (Scarecrow), and/or SCL23 (Scarecrow-like 23) polypeptides in a plant. In one embodiment, one or more of SHR, SCR, and/or SCL23 are expressed in mesophyll cells wherein a cell-type specific promoter is operably linked with a polynucleotide encoding the SHR, SCR, and/or SCL23 polypeptide. Any method that can be used to increase expression is contemplated within the scope of the present invention. In one embodiment, a polynucleotide encoding for one or more of a SHR, SCR, and/or SCL23 polypeptide is incorporated into a plant. For example, a plant can be transformed with a polynucleotide encoding one or more of a SHR, SCR, and/or SCL23 and subsequently screened for increased expression of SHR, SCR, and/or SCL23. In one embodiment, the plant is a C3 plant. In one embodiment, the polynucleotide can be

provided in an expression construct that provides for expression of the polynucleotide in a plant. In one embodiment, the expression construct provides for cell-type specific expression in the plant. In a further embodiment, the expression construct provides for leaf-specific expression of the polynucleotide. In a more specific embodiment, the expression construct provides for mesophyll-specific expression. In a preferred embodiment, the polynucleotide is stably incorporated into the plant genome.

The subject invention also pertains to modified plants that exhibit increased expression of one or more of SHR, SCR, and/or SCL23 polypeptides, as well as plants that comprise an SHR, SCR, or SCL23 promoter sequence operably linked with a gene of interest. In one embodiment, the plant is a C3 plant. In a specific embodiment, the plant is a rice, soybean, tobacco, wheat, barley, tomato, cotton, or potato plant. Transformed and transgenic plants are contemplated within the scope of the invention. In one embodiment, the plant expresses higher levels of one or more of SHR, SCR, and/or SCL23 relative to a corresponding wild type plant.

The subject invention also concerns methods for increasing expression of photosynthetically important genes in a plant. In one embodiment, one or more genes of interest are operably linked with an SHR, SCR or SCL23 promoter sequence and expressed in a plant. In one embodiment, the genes are expressed in BS cells in order to modify the morphology, anatomy, and/or physiology of BS cells.

Herein we show that three GRAS (Gibberallic-acid insensitive (GAI), Repressor of GAI (RGA), and Scarecrow (SCR)) family transcriptional factors, namely SHORT-ROOT (SHR), SCARECROW (SCR) and SCARECROW-like 23, constitute a developmental pathway that regulates bundle sheath cell fate, positioning and function in the leaves of C3 plants.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Patent and Trademark Office upon request and payment of the necessary fee.

Figures 1A, 1A-1, 1B, 1B-1, 1C, 1C-1, 1D, 1D-1, 1E, 1E-1, 1F, 1F-1. Semi-thin sectioning and toluidine blue staining, showing leaf anatomy. (1A, 1A-1) Ws, (1B, 1B-1)

Col-0, (1C, 1C-1) *shr-2*, (1D, 1D-1) *scr-1*, (1E, 1E-1) *scl23-2*, (1F, 1F-1) *scr-1 scl23-2*. Figures 1A, 1B, 1C, 1D, 1E, and 1F show paradermal sectioning, whereas Figures 1A-1, 1B-1, 1C-1, 1D-1, 1E-1, and 1F-1 show cross-sectioning. The numbers at the bottom left-hand corners are the cross-sectional area of the BS cells (μm^2 , mean $\pm$ standard deviation), as measured using ImageJ (imagej.nih.gov/ij). Arrows indicate the position of BS cells; diamonds indicate the location of mesophyll cells; asterisks indicate cells in the mutant cell layer. BS, bundle sheath cells; v, vascular tissue; x, xylem; p, phloem. Scale bars = 50 μm .

Figures 2A-2H. GUS staining showing the cell type-specific expression pattern of SHR, SCR and SCL23. (Figures 2A, 2D, 2G) SCRpro:GUS, (Figures 2B, 2E, 2H) SCL23pro:GUS, (Figures 2C, 2F) SHRpro:GUS; Figures 2A-2C are longitudinal views of small veins; Figures 2D-2F are cross-sectional views after semi-thin sectioning; Figures 2G and 2H are cross-sections of major veins. The dashed lines indicate the boundary between the BS cells and mesophyll cells; BS, bundle sheath cells; V, vascular bundle; x, xylem; p, phloem. Scale bars = 50 μm .

Figures 3A-3E. SCL23 is regulated by SHR and SCR in leaves. (Figures 3A and 3B) SCRpro:GUS and SCL23pro:GUS expression in wild-type (WT) or *shr* leaves. (Figure 3C) ChIP-PCR assay showing binding of SHR to the SCR promoter in leaves. (Figure 3D) ChIP-PCR assay showing SHR and SCR binding to the SCL23 promoter in leaves. In Figures 3C and 3D, the numbers on the x axis represent the distance from the first codon (kb); the y axis shows the fold enrichment. (Figure 3E) SCL23pro:GUS expression in WT, *scr-1*, *scl23-2* and *scr-1 scl23-2* leaves.

Figures 4A-4E. SHR, SCR and SCL23 play a role in sugar homeostasis. (Figures 4A and 4B) Starch level in wild-type (Ws and Col-0 ecotypes), *scr-1* and *shr-2* mutants at the end of the day (Figure 4A) or morning (Figure 4B). (Figure 4C) Starch level in *scr-1*, *scl23-2* and *scr-1 scl23-2* mutants at the end of the day (PM) or morning (AM). (Figure 4D) Free sugar concentration (mg g^{-1} fresh weight) in leaves of 1-month-old plants. (Figure 4E) Size of plants grown in soil at 4 weeks after germination.

Figures 5A and 5B. Characterization of T-DNA insertional mutants for SCL23. (Figure 5A) Diagram showing the position of the T-DNA insert in *scl23-1* (Salk_054051) and *scl23-2* (GT_5_16303). (Figure 5B) Quantitative RT-PCR assay of SCL23 transcript in leaves of one-month-old plants, using primers SCL23_FW,

TCATTGGATGCAGCACCGGTTA (SEQ ID NO:50), and SCL23_RV, TCCGTGCGCCACAATGTTTCTT (SEQ ID NO:51). For each line, two plants were analyzed. The error bars represent standard deviations from triplicate experiments.

Figures 6A-6D. Thin sectioning showing leaf anatomy. (Figure 6A) Col. (Figure 6B) *scr-1*. (Figure 6C) *scl23-1*. (Figure 6D) *scr-1 scl23-1*. Arrows mark the position of bundle sheath cells. Bars = 50 μ m.

Figures 7A and 7B. SCL23pro:GUS expression pattern in primary roots of one-week-old seedlings. (Figure 7A) Root apical meristem. (Figure 7B) Maturation zone. Bars = 50 μ m.

Figure 8. Venn diagram showing the common and distinct targets of SHR, SCR and SCL23 as identified by the ChIP–chip technique.

BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NO:1 is an amino acid sequence of an *Arabidopsis* SCR protein [AAB06318.1].

SEQ ID NO:2 is a nucleotide sequence comprising a coding sequence of an *Arabidopsis* SCR protein [U62798.1].

SEQ ID NO:3 is an amino acid sequence of a rice SCR protein [BAD22576].

SEQ ID NO:4 is a nucleotide sequence comprising a coding sequence of a rice SCR protein [AB180961.1].

SEQ ID NO:5 is an amino acid sequence of a maize SCR protein [AAG13663].

SEQ ID NO:6 is a nucleotide sequence comprising a coding sequence of a maize SCR protein [AF263457.1].

SEQ ID NO:7 is an amino acid sequence of an *Arabidopsis* SHR protein [AEE86820].

SEQ ID NO:8 is a nucleotide sequence comprising a coding sequence of an *Arabidopsis* SHR protein [AF233752.1].

SEQ ID NO:9 is an amino acid sequence of a rice SHR protein [Q8H2X8.2].

SEQ ID NO:10 is a nucleotide sequence comprising a coding sequence of a rice SHR protein [NM_001066668].

SEQ ID NO:11 is an amino acid sequence of an apple SHR protein [ADL36816].

SEQ ID NO:12 is a nucleotide sequence comprising a coding sequence of an apple SHR protein [HM122677].

SEQ ID NO:13 is an amino acid sequence of a rice SCL23 protein [Os07g38030.1].

5 **SEQ ID NO:14** is a nucleotide sequence comprising a coding sequence of a rice SCL23 protein [Os07g38030.1].

SEQ ID NO:15 is an amino acid sequence of a rice SCR protein [Os11g03110.1].

SEQ ID NO:16 is a nucleotide sequence comprising a coding sequence of a rice SCR protein [Os11g03110.1].

10 **SEQ ID NO:17** is an amino acid sequence of a rice SCR protein [Os12g02870.1].

SEQ ID NO:18 is a nucleotide sequence comprising a coding sequence of a rice SCR protein [Os12g02870.1].

SEQ ID NO:19 is an amino acid sequence of a rice SHR protein [Os07g39820.1].

15 **SEQ ID NO:20** is a nucleotide sequence comprising a coding sequence of a rice SHR protein [Os07g39820.1].

SEQ ID NO:21 is an amino acid sequence of a rice SHR protein [Os03g31880.1].

SEQ ID NO:22 is a nucleotide sequence comprising a coding sequence of a rice SHR protein [Os03g31880.1].

20 **SEQ ID NO:23** is an amino acid sequence of a maize SCR protein [GRMZM2G131516].

SEQ ID NO:24 is a nucleotide sequence comprising a coding sequence of a maize SCR protein [GRMZM2G131516].

SEQ ID NO:25 is an amino acid sequence of a maize SCR protein [GRMZM2G015080].

25 **SEQ ID NO:26** is a nucleotide sequence comprising a coding sequence of a maize SCR protein [GRMZM2G015080].

SEQ ID NO:27 is an amino acid sequence of a maize SHR protein [GRMZM2G172657].

30 **SEQ ID NO:28** is a nucleotide sequence comprising a coding sequence of a maize SHR protein [GRMZM2G172657].

SEQ ID NO:29 is an amino acid sequence of a maize SHR protein [GRMZM2G019060].

SEQ ID NO:30 is a nucleotide sequence comprising a coding sequence of a maize SHR protein [GRMZM2G019060].

SEQ ID NO:31 is an amino acid sequence of a maize SHR protein [GRMZM2G132794].

5 SEQ ID NO:32 is a nucleotide sequence comprising a coding sequence of a maize SHR protein [GRMZM2G132794].

SEQ ID NO:33 is an amino acid sequence of a maize SCL23 protein [GRMZM2G106548].

10 SEQ ID NO:34 is a nucleotide sequence comprising a coding sequence of a maize SCL23 protein [GRMZM2G106548].

SEQ ID NO:35 is an amino acid sequence of a Brachypodium SCR protein [Bradi4g44090.1].

SEQ ID NO:36 is a nucleotide sequence comprising a coding sequence of a Brachypodium SCR protein [Bradi4g44090.1].

15 SEQ ID NO:37 is an amino acid sequence of a Brachypodium SHR protein [Bradi1g23060.1].

SEQ ID NO:38 is a nucleotide sequence comprising a coding sequence of a Brachypodium SHR protein [Bradi1g23060.1].

20 SEQ ID NO:39 is an amino acid sequence of a Brachypodium SCL23 protein [Bradi4g44090].

SEQ ID NO:40 is a nucleotide sequence comprising a coding sequence of a Brachypodium SCL23 protein [Bradi4g44090].

SEQ ID NO:41 is an amino acid sequence of an *Arabidopsis* SCR protein [AT3G54220].

25 SEQ ID NO:42 is a nucleotide sequence comprising a coding sequence of an *Arabidopsis* SCR protein [AT3G54220].

SEQ ID NO:43 is an amino acid sequence of an *Arabidopsis* SHR protein [AT4G37650].

30 SEQ ID NO:44 is a nucleotide sequence comprising a coding sequence of an *Arabidopsis* SHR protein [AT4G37650].

SEQ ID NO:45 is an amino acid sequence of an *Arabidopsis* SCL23 protein [AT5G41920].

SEQ ID NO:46 is a nucleotide sequence comprising a coding sequence of an *Arabidopsis* SCL23 protein [AT5G41920].

SEQ ID NO:47 is an *Arabidopsis* SCR promoter sequence.

SEQ ID NO:48 is an *Arabidopsis* SCL23 promoter sequence.

5 SEQ ID NO:49 is an *Arabidopsis* SHR promoter sequence.

SEQ ID NOs:50-77 are oligonucleotide primers.

DETAILED DESCRIPTION OF THE INVENTION

The subject invention concerns materials and methods for increasing and/or
10 improving photosynthetic efficiency in plants. In particular, the subject invention provides for means to increase the number of bundle sheath (BS) cells in plants, to improve the efficiency of photosynthesis in BS cells, to improve carbohydrate biosynthesis, and to increase channels between BS and mesophyll (M) cells. The methods of the invention can also be used to increase the number of BS cells relative to
15 mesophyll cells in a plant, for example, increasing the ratio of BS cells to M cells close to about 1:1. In one embodiment, a method of the invention concerns ectopically expressing or increasing expression of one or more of SHR, SCR, and/or SCL23 polypeptides in a plant (non-limiting examples of each are shown in SEQ ID NOs:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, and 45, or an amino acid sequence
20 that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.). Any method that can be used to increase expression or altered expression pattern is contemplated within the scope of the present invention. In one embodiment, one or more polynucleotide encoding for one or more of a SHR, SCR, and/or SCL23 polypeptide is incorporated into a plant. For example, a plant
25 can be transformed with a polynucleotide encoding one or more of a SHR, SCR, and/or SCL23 and subsequently screened for increased expression or ectopic expression or altered expression pattern of SHR, SCR, and/or SCL23. In one embodiment, the polynucleotide comprises the protein coding sequence of a *SHR*, *SCR*, and/or *SCL23* gene. In one embodiment, the plant is a C3 plant. Examples of contemplated C3 plants
30 include, but are not limited to, rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In a specific embodiment, the plant is a rice, soybean,

tobacco, wheat, barley, tomato, cotton, or potato plant. In one embodiment, the polynucleotide is heterologous to the plant. In one embodiment, the polynucleotide can be provided in an expression construct that provides for expression of the polynucleotide in a plant. In one embodiment, the expression construct provides for cell-type specific expression in the plant. In a further embodiment, the expression construct provides for leaf-specific expression of the polynucleotide. In a more specific embodiment, the expression construct provides for mesophyll-specific expression, or BS cell-specific expression, or vascular bundle-specific expression. In one embodiment, an expression construct comprises a lysine histidine transporter (LHT1) promoter, a PEPC promoter, or ribulose-1,5-biphosphate carboxylase small subunit (rbcS) promoter, or a functional fragment or variant of any of these that is able to promote expression. In a preferred embodiment, the polynucleotide is stably incorporated into the plant genome. Examples of polynucleotides encoding an SHR, SCR, or SCL23 polypeptide contemplated within the scope of the invention include, but are not limited to, those in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, and 46, or the polypeptide coding region thereof, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO. In one embodiment, the SHR, SCR, or SCL23 and/or the expression construct is heterologous to the plant. In one embodiment, the polynucleotide and/or expression construct can comprise cDNA. In one embodiment, a plant ectopically expressing or having increased expression of one or more of SHR, SCR, and/or SCL23 using the subject method exhibits a cell pattern similar to Kranz anatomy.

The subject invention also pertains to modified plants that exhibit increased expression or ectopic expression or altered expression pattern of one or more of SHR, SCR, and/or SCL23. The subject invention also concerns plants that comprise an SHR, SCR, or SCL23 promoter sequence operably linked with a gene of interest. In one embodiment, one or more polynucleotide coding for one or more of a SHR, SCR, and/or SCL23 polypeptide is incorporated into a plant. In one embodiment, the polynucleotide is heterologous to the plant. In one embodiment, the polynucleotide can be provided in an expression construct that provides for expression of the polynucleotide in a plant. In one embodiment, the expression construct provides for cell-type specific expression in the plant. In a further embodiment, the expression construct provides for leaf-specific

expression of the polynucleotide. In a more specific embodiment, the expression construct provides for mesophyll-specific expression, or BS cell-specific expression, or vascular bundle-specific expression. In one embodiment, an expression construct comprises a lysine histidine transporter (LHT1) promoter, a PEPC promoter, or ribulose-
5 1,5-biphoshate carboxylase small subunit (rbcS) promoter, or a functional fragment or variant of any of these that is able to promote expression. In a preferred embodiment, the polynucleotide is stably incorporated into the plant genome. In one embodiment, the plant is a C3 plant. In a specific embodiment, the plant is a rice plant. Transformed and transgenic plants are contemplated within the scope of the invention. In one embodiment,
10 the plant expresses higher levels of one or more of SHR, SCR, and/or SCL23 relative to a corresponding wild type plant. C3 plants are contemplated within the scope of the invention. Examples of contemplated C3 plants include, but are not limited to, rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In one
15 embodiment, the SHR, SCR, and/or SCL23, or the promoter sequence thereof, is heterologous to the plant. In one embodiment, the polynucleotide and/or expression construct can comprise cDNA. In one embodiment, the modified plant exhibits a cell pattern similar to Kranz anatomy.

The subject invention also concerns plant SHR, SCR, and SCL23 promoters and
20 methods for increasing expression of genes or polypeptides of interest, such as photosynthetically important genes or polypeptides, in a plant. In one embodiment, one or more polynucleotides or genes of interest are operably linked with a promoter sequence of a plant SHR, SCR or SCL23 gene, or a functional homolog or fragment or
25 variant of the promoter sequence that is able to promote expression of the operably linked polynucleotide or gene of interest, and the operably linked polynucleotide or gene of interest and the promoter are incorporated into and expressed in a plant, plant tissue, or plant cell. The polynucleotide comprising the polynucleotide or gene of interest and promoter can be incorporated in the plant using any suitable method in the art. The plant,
30 plant tissue, or plant cell can be screened for expression of the polynucleotide or gene of interest. In one embodiment, the promoter and polynucleotide or gene of interest is provided in an expression construct of the invention. In one embodiment, the promoter, polynucleotide, and/or gene of interest is heterologous to the plant. The polynucleotide

and/or gene of interest can comprise cDNA. In one embodiment, any plant gene whose product is associated with photosynthesis is contemplated for use in the present invention, such as phosphoenolpyruvate carboxylase (PEPC), or pyruvate phosphate dikinase (PPDK). In one embodiment, the photosynthesis-associated genes are expressed in BS
5 cells in order to modify the morphology, anatomy, and/or physiology of BS cells. The SHR, SCR, and SCL23 promoter sequences can be from any plant. SHR, SCR, and SCL23 promoters can be readily identified in other plants using information provided herein and techniques known in the art. In one embodiment, the promoter is from a C3
10 plant, such as rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In a specific embodiment, a promoter of the invention comprises the nucleotide sequence of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment or variant thereof that is able to promote expression of the operably
15 linked gene of interest in a plant cell, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO. In one embodiment, a method of the invention comprises transforming a plant, plant tissue, or plant cell with one or more genes of interest operably linked with one or more promoter sequence of a plant SHR, SCR, or SCL23 gene, or a functional
20 fragment or variant thereof that is able to promote expression of the operably linked gene of interest in a plant cell, and generating from the plant, plant tissue, or plant cell a transgenic plant expressing the one or more genes of interest. In one embodiment, the plant is a C3 plant, such as rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In a specific embodiment, the plant is a rice, soybean, tobacco,
25 wheat, barley, tomato, cotton, or potato plant. Agronomic genes and polypeptides of interest include, but are not limited to, those involved in carbohydrate (starch, sucrose, *etc.*) synthesis, resistance to disease and pathogens (fungus, nematode, virus, bacteria, insects, *etc.*), herbicide resistance, increased yield, oil production, and resistance to stress conditions.

30 Sequences of numerous plant SHR, SCR, and SCL23 proteins (and nucleic acid encoding the same) are known in the art and are all contemplated within the scope of the present invention. Examples of SCR include those having Genbank accession numbers

AAB06318.1 and U62798.1 (*Arabidopsis*) (SEQ ID NOs:1 and 2); BAD22576 and AB180961.1 (rice) (SEQ ID NOs:3 and 4); and AAG13663 and AF263457.1 (maize) (SEQ ID NOs:5 and 6); Arabidopsis Information Resource locus AT3G54220 (SEQ ID NOs:41 and 42). Examples of SHR include Genbank accession numbers AEE86820 and AF233752.1 (*Arabidopsis*) (SEQ ID NOs:7 and 8); and Q8H2X8.2 and NM_001066668 (rice) (SEQ ID NOs:9 and 10); maizesequence.org gene ID GRM2M2G172657, GRMZM2G019060, and GRMZM2G132794 (SEQ ID NOs:27-32, respectively); PlantGDB.org ID Si29296m and Si034653m (*Setaria viridis*); Arabidopsis Information Resource locus AT4G37650 (SEQ ID NOs: 43 and 44). Examples of SCL23 include those having Genbank accession numbers ADL36816 and HM122677 (apple) (SEQ ID NOs:11 and 12); maizesequence.org gene ID GRMZM2G106548 (SEQ ID NOs:33 and 34); PlantGDB.org ID Si032551m (*Setaria viridis*); Arabidopsis Information Resource locus AT5G41920 (SEQ ID NOs:45 and 46). Additional sequences of rice SHR, SCR, and SCL23 polynucleotides and the polypeptides encoded are shown in SEQ ID NOs:13-22.

In one embodiment, a method of the invention comprises producing a transgenic plant with increased expression and/or ectopic expression of one or more of SHR, SCR, and/or SCL23 polypeptides relative to a wild type variety of the plant, wherein the method comprises transforming a plant, plant tissue, or plant cell with a polynucleotide (e.g., in an expression construct) encoding one or more of a plant SHR, SCR, and/or SCL23 polypeptide, or a biologically active fragment or variant thereof; and generating from the plant, plant tissue, or plant cell a transgenic plant that exhibits one or more of the following: increased number of BS cells, improved photosynthetic efficiency of BS cells, and/or increased number of channels and improved nutrient exchange between BS and M cells. In one embodiment, the transgenic plant exhibits a cell pattern similar to Kranz anatomy. The polynucleotide can be incorporated in the plant, plant tissue, or plant cell using any suitable method in the art. In one embodiment, the plant is a C3 plant, such as rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In a specific embodiment, the plant is a rice, soybean, tobacco, wheat, barley, tomato, cotton, or potato plant. Transformed and transgenic plants are contemplated within the scope of the invention. In one embodiment, the plant expresses one or more of SHR,

SCR, and/or SCL23 at higher levels or in other cell types relative to a corresponding wild type plant or a non-transformed or non-transgenic plant. In one embodiment, the polynucleotide encodes a polypeptide comprising the amino acid sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, or 45, or a biologically active fragment or variant thereof. In a specific embodiment, the polynucleotide encodes a rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, or spinach SHR, SCR, or SCL23 polypeptide. Examples of polynucleotides contemplated within the scope of the invention include, but are not limited to, those in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, and 46, or the polypeptide coding region thereof.

The subject invention also concerns plants, plant tissue, and plant cells of the invention that comprise or express a polynucleotide of the invention or a SHR, SCR, and/or SCL23 protein encoded by a polynucleotide of the invention, or a biologically active fragment or variant thereof. Plant tissue includes, but is not limited to, seed, scion, leaf, and rootstock. Plants within the scope of the present invention include monocotyledonous plants, such as, for example, rice, wheat, barley, oats, rye, sorghum, maize, sugarcane, pineapple, onion, bananas, coconut, lilies, turfgrasses, and millet. Plants within the scope of the present invention also include dicotyledonous plants, such as, for example, tomato, cucumber, squash, peas, alfalfa, melon, chickpea, chicory, clover, kale, lentil, soybean, beans, tobacco, potato, sweet potato, yams, cassava, radish, broccoli, spinach, cabbage, rape, apple trees, citrus (including oranges, mandarins, grapefruit, lemons, limes and the like), grape, cotton, sunflower, strawberry, lettuce, and hop. Herb plants containing a polynucleotide of the invention are also contemplated within the scope of the invention. Herb plants include parsley, sage, rosemary, thyme, and the like. In one embodiment, the plant is a C3 plant, such as rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, spinach, and most trees. In a specific embodiment, the plant is a rice, soybean, tobacco, wheat, barley, tomato, cotton, or potato plant. In one embodiment, a plant, plant tissue, or plant cell is a transgenic plant, plant tissue, or plant cell. Specifically contemplated within the scope of the invention are plant seeds produced

by a transgenic plant of the invention. In another embodiment, a plant, plant tissue, or plant cell is one that has been obtained through a breeding program.

Polynucleotides encoding a SHR, SCR, and/or SCL23 polypeptide and/or a polynucleotide comprising a SHR, SCR, and/or SCL23 gene promoter sequence of the present invention can be provided in an expression construct. Expression constructs of the invention generally include regulatory elements that are functional in the intended host cell in which the expression construct is to be expressed. Thus, a person of ordinary skill in the art can select regulatory elements for use in bacterial host cells, yeast host cells, plant host cells, insect host cells, mammalian host cells, and human host cells.

Regulatory elements include, for example, promoters, transcription termination sequences, translation termination sequences, enhancers, and polyadenylation elements. As used herein, the term “expression construct” refers to a combination of nucleic acid sequences that provides for transcription of an operably linked nucleic acid sequence. As used herein, the term “operably linked” refers to a juxtaposition of the components described wherein the components are in a relationship that permits them to function in their intended manner. In general, operably linked components are in contiguous relation. In one embodiment, an expression construct comprises a polynucleotide encoding an amino acid sequence of any of SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, or 45, or a biologically active fragment or variant thereof.

Polynucleotides that can be used in an expression construct include, but are not limited to, any of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, or 46, or the protein coding region thereof, and/or any of SEQ ID NOs:47, 48, or 49, or a functional fragment or variant thereof that is able to promote expression of the operably linked gene of interest.

An expression construct of the invention can comprise a promoter sequence (including, for example, an SHR, SCR, or SCL23 promoter of the invention) operably linked to one or more polynucleotide sequences, for example a sequence encoding a polypeptide of the invention, or to one or more genes or polynucleotides of interest. The expression construct can be a chimeric or recombinant expression construct. Promoters can be incorporated into a polynucleotide using standard techniques known in the art. Multiple copies of promoters or multiple promoters can be used in an expression construct of the invention. In a preferred embodiment, a promoter can be positioned

about the same distance from the transcription start site in the expression construct as it is from the transcription start site in its natural genetic environment. Some variation in this distance is permitted without substantial decrease in promoter activity. A transcription start site is typically included in the expression construct.

5 If the expression construct is to be provided in or introduced into a plant cell, then plant viral promoters, such as, for example, a cauliflower mosaic virus (CaMV) 35S (including the enhanced CaMV 35S promoter (see, for example U.S. Patent No. 5,106,739)) or a CaMV 19S promoter or a cassava vein mosaic can be used. Other promoters that can be used for expression constructs in plants include, for example, 10 prolifera promoter, Ap3 promoter, heat shock promoters, T-DNA 1'- or 2'-promoter of *A. tumefaciens*, polygalacturonase promoter, chalcone synthase A (CHS-A) promoter from petunia, tobacco PR-1a promoter, ubiquitin promoter, actin promoter, alcA gene promoter, pin2 promoter (Xu *et al.*, 1993), maize WipI promoter, maize trpA gene promoter (U.S. Patent No. 5,625,136), maize CDPK gene promoter, and RUBISCO SSU 15 promoter (U.S. Patent Nos. 5,034,322 and 4,962,028) can also be used. Leaf-specific promoters include, for example, light harvest chlorophyll a/b binding protein (CAB) promoter of rice (Sakamoto *et al.* (1991)). The LHT1 promoter (Hirner *et al.* (2006)), or a functional fragment or variant thereof, which is mesophyll specific, can also be used. Other mesophyll-specific promoters that are contemplated for use within the scope of the 20 invention include, but are not limited to, the phosphoenolpyruvate carboxylase (PEPC) (Stockhaus *et al.* (1997); Kausch *et al.* (2001)), or a functional fragment or variant thereof, and rbcS promoter (Schäffner and Sheen (1991); Nomura *et al.* (2000)), or a functional fragment or variant thereof. U.S. Patent No. 6,610,840 also describes mesophyll-specific promoters. Other tissue-specific promoters include, for example, 25 fruit-specific promoters, such as the E8 promoter of tomato (accession number: AF515784; Good *et al.* (1994)) can be used. Fruit-specific promoters such as flower organ-specific promoters can be used with an expression construct of the present invention for expressing a polynucleotide of the invention in the flower organ of a plant. Examples of flower organ-specific promoters include any of the promoter sequences 30 described in U.S. Patent Nos. 6,462,185; 5,639,948; and 5,589,610. Seed-specific promoters such as the promoter from a β -phaseolin gene (for example, of kidney bean) or a glycinin gene (for example, of soybean), and others, can also be used. Endosperm-

specific promoters include, but are not limited to, MEG1 (EPO application No. EP1528104) and those described by Wu *et al.* (1998), Furtado *et al.* (2002), and Hwang *et al.* (2002). Root-specific promoters, such as any of the promoter sequences described in U.S. Patent No. 6,455,760 or U.S. Patent No. 6,696,623, or in published U.S. patent application Nos. 20040078841; 20040067506; 20040019934; 20030177536; 20030084486; or 20040123349, can be used with an expression construct of the invention. Constitutive promoters (such as the CaMV, ubiquitin, actin, or NOS promoter), developmentally-regulated promoters, and inducible promoters (such as those promoters that can be induced by heat, light, hormones, or chemicals) are also contemplated for use with polynucleotide expression constructs of the invention. Expression constructs of the invention can also comprise one or more plant SHR, SCR, and/or SCL23 promoter sequences. The SHR, SCR, and SCL23 promoter sequences can be from any plant. SHR, SCR, and SCL23 promoters can be readily identified in other plants using information provided herein and techniques known in the art. In one embodiment, the promoter is from a C3 plant. In a specific embodiment, a promoter of the invention comprises the nucleotide sequence of SEQ ID NO:47, SEQ ID NO:48, and SEQ ID NO:49, or a functional fragment or variant thereof that is able to promote expression of the operably linked gene of interest in a plant cell.

Expression constructs of the invention may optionally contain a transcription termination sequence, a translation termination sequence, a sequence encoding a signal peptide, and/or enhancer elements. Transcription termination regions can typically be obtained from the 3' untranslated region of a eukaryotic or viral gene sequence. Transcription termination sequences can be positioned downstream of a coding sequence to provide for efficient termination. A signal peptide sequence is a short amino acid sequence typically present at the amino terminus of a protein that is responsible for the relocation of an operably linked mature polypeptide to a wide range of post-translational cellular destinations, ranging from a specific organelle compartment to sites of protein action and the extracellular environment. Targeting gene products to an intended cellular and/or extracellular destination through the use of an operably linked signal peptide sequence is contemplated for use with the polypeptides of the invention. Classical enhancers are cis-acting elements that increase gene transcription and can also be included in the expression construct. Classical enhancer elements are known in the art,

and include, but are not limited to, the CaMV 35S enhancer element, cytomegalovirus (CMV) early promoter enhancer element, and the SV40 enhancer element. Intron-mediated enhancer elements that enhance gene expression are also known in the art. These elements must be present within the transcribed region and are orientation
5 dependent. Examples include the maize *shrunk-1* enhancer element (Clancy and Hannah, 2002).

DNA sequences which direct polyadenylation of mRNA transcribed from the expression construct can also be included in the expression construct, and include, but are not limited to, an octopine synthase or nopaline synthase signal. The expression
10 constructs of the invention can also include a polynucleotide sequence that directs transposition of other genes, *i.e.*, a transposon.

Polynucleotides of the present invention can be composed of either RNA or DNA. Preferably, the polynucleotides are composed of DNA. In one embodiment, the DNA is complementary DNA (cDNA) prepared from or based on a messenger RNA (mRNA)
15 template sequence. The subject invention encompasses those polynucleotides that are complementary in sequence to the polynucleotides disclosed herein. Polynucleotides and polypeptides of the invention can be provided in purified or isolated form.

Because of the degeneracy of the genetic code, a variety of different polynucleotide sequences can encode polypeptides of the present invention. A table
20 showing all possible triplet codons (and where U also stands for T) and the amino acid encoded by each codon is described in Lewin (1985). In addition, it is well within the skill of a person trained in the art to create alternative polynucleotide sequences encoding the same, or essentially the same, polypeptides of the subject invention. These variant or alternative polynucleotide sequences are within the scope of the subject invention. As
25 used herein, references to “essentially the same” sequence refers to sequences which encode amino acid substitutions, deletions, additions, or insertions which do not materially alter the functional activity of the polypeptide encoded by the polynucleotides of the present invention. Allelic variants of the nucleotide sequences encoding a wild type polypeptide of the invention are also encompassed within the scope of the invention.

30 Substitution of amino acids other than those specifically exemplified or naturally present in a wild type polypeptide of the invention are also contemplated within the scope of the present invention. For example, non-natural amino acids can be substituted for the

amino acids of a polypeptide, so long as the polypeptide having the substituted amino acids retains substantially the same biological or functional activity as the polypeptide in which amino acids have not been substituted. Examples of non-natural amino acids include, but are not limited to, ornithine, citrulline, hydroxyproline, homoserine, 5 phenylglycine, taurine, iodotyrosine, 2,4-diaminobutyric acid, α -amino isobutyric acid, 4-aminobutyric acid, 2-amino butyric acid, γ -amino butyric acid, ϵ -amino hexanoic acid, 6-amino hexanoic acid, 2-amino isobutyric acid, 3-amino propionic acid, norleucine, norvaline, sarcosine, homocitrulline, cysteic acid, τ -butylglycine, τ -butylalanine, phenylglycine, cyclohexylalanine, β -alanine, fluoro-amino acids, designer amino acids 10 such as β -methyl amino acids, C-methyl amino acids, N-methyl amino acids, and amino acid analogues in general. Non-natural amino acids also include amino acids having derivatized side groups. Furthermore, any of the amino acids in the protein can be of the D (dextrorotary) form or L (levorotary) form. Allelic variants of a protein sequence of a wild type polypeptide of the present invention are also encompassed within the scope of 15 the invention.

Amino acids can be generally categorized in the following classes: non-polar, uncharged polar, basic, and acidic. Conservative substitutions whereby a polypeptide of the present invention having an amino acid of one class is replaced with another amino acid of the same class fall within the scope of the subject invention so long as the 20 polypeptide having the substitution still retains substantially the same biological or functional activity (*e.g.*, enzymatic) as the polypeptide that does not have the substitution. Polynucleotides encoding a polypeptide having one or more amino acid substitutions in the sequence are contemplated within the scope of the present invention. Table 1 below provides a listing of examples of amino acids belonging to each class.

Table 1.	
Class of Amino Acid	Examples of Amino Acids
Nonpolar	Ala, Val, Leu, Ile, Pro, Met, Phe, Trp
Uncharged Polar	Gly, Ser, Thr, Cys, Tyr, Asn, Gln
Acidic	Asp, Glu
Basic	Lys, Arg, His

The subject invention also concerns variants of the polynucleotides of the present invention that retain biological activity (*e.g.*, promoter activity) or that encode functional polypeptides of the invention. Variant sequences include those sequences wherein one or more nucleotides of the sequence have been substituted, deleted, and/or inserted. The nucleotides that can be substituted for natural nucleotides of DNA have a base moiety that can include, but is not limited to, inosine, 5-fluorouracil, 5-bromouracil, hypoxanthine, 1-methylguanine, 5-methylcytosine, and tritylated bases. The sugar moiety of the nucleotide in a sequence can also be modified and includes, but is not limited to, arabinose, xylulose, and hexose. In addition, the adenine, cytosine, guanine, thymine, and uracil bases of the nucleotides can be modified with acetyl, methyl, and/or thio groups. Sequences containing nucleotide substitutions, deletions, and/or insertions can be prepared and tested using standard techniques known in the art.

Fragments and variants of a polypeptide of the present invention can be generated as described herein and tested for the presence of biological function using standard techniques known in the art. Thus, an ordinarily skilled artisan can readily prepare and test fragments and variants of a polypeptide of the invention and determine whether the fragment or variant retains functional or biological activity relative to full-length or a non-variant polypeptide.

Polynucleotides and polypeptides contemplated within the scope of the subject invention can also be defined in terms of more particular identity and/or similarity ranges with those sequences of the invention specifically exemplified herein. The sequence identity will typically be greater than 60%, preferably greater than 75%, more preferably greater than 80%, even more preferably greater than 90%, and can be greater than 95%.

The identity and/or similarity of a sequence can be 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, or 99% as compared to a sequence exemplified herein. Unless otherwise specified, as used herein percent sequence identity and/or similarity of two sequences can be determined using the algorithm of Karlin and Altschul (1990), modified as in Karlin and Altschul (1993). Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990). BLAST searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain sequences with the desired percent sequence identity. To obtain gapped alignments for comparison purposes, Gapped BLAST can be used as described in Altschul *et al.* (1997). When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (NBLAST and XBLAST) can be used. See NCBI/NIH website.

As used herein, the terms “nucleic acid” and “polynucleotide” refer to a deoxyribonucleotide, ribonucleotide, or a mixed deoxyribonucleotide and ribonucleotide polymer in either single- or double-stranded form, and unless otherwise limited, would encompass known analogs of natural nucleotides that can function in a similar manner as naturally-occurring nucleotides. The polynucleotide sequences include the DNA strand sequence that is transcribed into RNA and the strand sequence that is complementary to the DNA strand that is transcribed. The polynucleotide sequences also include both full-length sequences as well as shorter sequences derived from the full-length sequences. Allelic variations of the exemplified sequences also fall within the scope of the subject invention. The polynucleotide sequence includes both the sense and antisense strands either as individual strands or in the duplex.

Techniques for transforming plant cells with a polynucleotide or gene are known in the art and include, for example, *Agrobacterium* infection, transient uptake and gene expression in plant seedlings, biolistic methods, electroporation, calcium phosphate or calcium chloride treatment, lipofection, DEAE-dextran mediated transfection, PEG-mediated transformation, *etc.* U.S. Patent No. 5,661,017 teaches methods and materials for transforming an algal cell with a heterologous polynucleotide. Transformed cells can be selected, redifferentiated, and grown into plants that contain and express a polynucleotide of the invention using standard methods known in the art. The seeds and

other plant tissue and progeny of any transformed or transgenic plant cells or plants of the invention are also included within the scope of the present invention. In one embodiment, the cell is transformed with a polynucleotide sequence comprising a sequence encoding the amino acid sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, or 45, or a biologically active fragment or variant thereof. In one embodiment, the polynucleotide comprises a nucleotide sequence of any of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, or 46, or the protein coding region thereof, and/or any of SEQ ID NOs:47, 48, or 49, or a functional fragment or variant thereof that is able to promote expression of the operably linked gene of interest.

Transgenic plants of the invention can be self-pollinated, or they can be pollinated with pollen from a non-transgenic plant, such as an inbred plant line. Pollen from transgenic plants of the invention can be used to pollinate a non-transgenic plant, such as an inbred plant line.

The subject invention also concerns cells transformed with a polynucleotide of the present invention, such as a polynucleotide comprising a plant SHR, SCR, or SCL23 gene promoter sequence, or a polynucleotide encoding a polypeptide of the invention. In one embodiment, the cell is transformed with a polynucleotide sequence comprising a sequence encoding the amino acid sequence shown in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, or 45, or a biologically active fragment or variant thereof. In one embodiment, the polynucleotide comprises a nucleotide sequence of any of SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, or 46, or the protein coding region thereof, and/or any of SEQ ID NOs:47, 48, or 49, or a functional fragment or variant thereof that is able to promote expression of the operably linked gene of interest in a cell. In one embodiment, the polynucleotide sequence of the invention is provided in an expression construct of the invention. The transformed cell can be a prokaryotic cell, for example, a bacterial cell such as *E. coli* or *B. subtilis*, or the transformed cell can be a eukaryotic cell, for example, a plant cell, including protoplasts, or an animal cell. Plant cells include, but are not limited to, dicotyledonous, monocotyledonous, and conifer cells. In one embodiment, the cell is an embryonic cell. In one embodiment, the plant cell is a cell of a C3 plant. In another embodiment, the plant cell is a cell of a C4 plant. In a specific embodiment, the

plant cell is a rice, barley, thale cress (*Arabidopsis*), wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybeans, or spinach plant cell. Animal cells include human cells, mammalian cells, avian cells, and insect cells. Mammalian cells include, but are not limited to, COS, 3T3, and CHO cells. Transgenic cells comprising a polynucleotide of the present invention are also contemplated within the scope of the invention.

Single letter amino acid abbreviations are defined in Table 2.

Table 2.			
Letter Symbol	Amino Acid	Letter Symbol	Amino Acid
A	Alanine	M	Methionine
B	Asparagine or aspartic acid	N	Asparagine
C	Cysteine	P	Proline
D	Aspartic Acid	Q	Glutamine
E	Glutamic Acid	R	Arginine
F	Phenylalanine	S	Serine
G	Glycine	T	Threonine
H	Histidine	V	Valine
I	Isoleucine	W	Tryptophan
K	Lysine	Y	Tyrosine
L	Leucine	Z	Glutamine or glutamic acid

10

MATERIALS AND METHODS

Plant materials

The plants used in this study were in the WS or Col-0 backgrounds, and were grown at 22°C and 50% humidity with 16 h daily illumination in a controlled-environment growth room. The scl23-2 mutant (GT_5_16303), which is in the Ler background, was introduced into the Ws background by genetic crossing. All transgenic plants were generated in the Col-0 ecotype by the flower-dip method (Clough and Bent, 1998).

Molecular cloning

All the constructs described here were cloned using the multi-site Gateway system (Invitrogen). The SCR promoter (2 kb) and the SCL23 promoter (1.3 kb) were first PCR-

20

amplified from genomic DNA using Phusion DNA polymerase (NEB). Both promoters were then cloned into pDONR-P4-P1R (Invitrogen), yielding the entry clones pENTR-SCRpro and pENTR-SCL23pro. The SCL23 cDNA was amplified by RT-PCR and cloned into pDONR221 (Invitrogen), resulting in the entry clone pENTR-SCL23. The entry clone for SHRpro has been described previously (Nakajima *et al.*, 2001). To clone the SCRpro:GUS, SCL23pro:GUS and SHRpro:GUS constructs, the entry clones for the SCR, SCL23 and SHR promoters were cloned into binary vector dpGreenBarT (Levesque *et al.*, 2006), together with the entry clones for the GUS gene and the Nos terminator. To clone the SCL23pro:SCL23-GFP construct, the entry clones for the promoter and cDNA of SCL23 as well as the GFP gene were cloned into binary vector dpGreen-BarT. The primers used for the cloning were

B4_pSCR_F (5'-ggggacaactttgtatagaaaagttgCCAAACAGATATTTGCATTTGGGC-3') (SEQ ID NO:52) and B1_pSCR_R (5'-ggggactgctttttgtacaaacttgGAGATTGAAGGGTTGTTGGTCG-3') (SEQ ID NO:53) for the SCR promoter, attB4_pSCL23_FW (5'-ggggacaactttgtatagaaaagttgATTTCACCAATTCCGGC-3') (SEQ ID NO:54) and attB1_pSCL23_RV (5'-ggggactgctttttgtacaaacttgTCGATACGGCGTTTAGCGGAG-3') (SEQ ID NO:55) for the SCL23 promoter, and attB1_SCL23_FW (5'-ggggacaagttgtacaaaaaagcaggctCCATGACTACAAAACGCA-3') (SEQ ID NO:56) and attB2_SCL23_RV (5'-ggggaccactttgtacaagaaagctgggtACGGCTGAGATTTCCAGGC-3') (SEQ ID NO:57) for the SCL23 cDNA. The uppercase letters in the primers are gene-specific sequences, whereas the lowercase letters are adaptor sequences used for the gateway cloning method.

Genotyping

Genotyping of the T-DNA insertional mutant for SCL23 was performed by PCR using RedTaq DNA polymerase (Sigma). For *scl23-1* (Salk_054051), primers SCL23_LP1 (5'-TAATAATGCAAAGCCTCCACG-3') (SEQ ID NO:58) and SCL23_RP1 (5'-TTTTCAAGAACTGATCCATCC-3') (SEQ ID NO:59) were used to amplify the wild-type gene, and primers SCL23_RP1 and LBb1 (5'-GCGTGGACCGCTTGCTGCAACT-3') (SEQ ID NO:60) were used for the T-DNA insert. For *scl23-2* (GT_5_16303), primers SCL23_LP2 (5'-

GGTGGAGATGGTTCTGAATCTC-3') (SEQ ID NO:61) and SCL23_RP2 (5'-CAGTTGAAGCGAGTAGATCGG-3') (SEQ ID NO:62) were used for amplification of the wild-type gene, and primers SCL23_RP2 and Ds3-1 (5'-ACCCGACCGGATCGTATCGGT-3') (SEQ ID NO:63) were used for the T-DNA
 5 insert.

ChIP-PCR and ChIP-chip assay

ChIP was performed as previously described (Cui *et al.*, 2011), using a GFP antibody (Ab290, Abcam), except that 0.5 g of leaves of 3-week-old plants was used for
 10 each experiment. A transgenic line with a functional SHR-GFP fusion protein expressed under the control of the SHR promoter in the *shr-2* background (SHRpro:SHR-GFP/*shr-2*) (Nakajima *et al.*, 2001) was used for ChIP with SHR, whereas transgenic line SCRpro:GFPSCR/*scr-4* (Cui and Benfey, 2009) was used for SCR. To identify direct targets of SCL23, we generated transgenic plants expressing a SCL23-GFP fusion protein
 15 in the *scl23* mutant background.

The primers used for the ChIP assay were SCR_F2 (5'-CTCTACGTCTTGTCCAATTCC-3') (SEQ ID NO:64), SCR_R2 (5'-CAAAGTGTGGTACGATGTGCT-3') (SEQ ID NO:65), SCR_F1 (5'-AGAAACGAAATGGATCGGCAAACG-3') (SEQ ID NO:66), SCR_R1 (5'-
 20 ATTTGGAAGGATGTGGGTTGGAGA-3') (SEQ ID NO:67), SCR_FW (5'-ACTTCTTCCGGTAGTAGCAGCA-3') (SEQ ID NO:68), and SCR_RV (5'-AGAGACGGTGGTTGTTGTGGT-3') (SEQ ID NO:69) for the SCR promoter, SCL23_F2 (5'-TCCGGCGATTGTGTTCTGTGT-3') (SEQ ID NO:70), SCL23_R2 (5'-CTTCTTCTTCGTCGGTGGTCCT-3') (SEQ ID NO:71), SCL23_F1 (5'-
 25 CTGGTTAAGTATCAATCCATGA-3') (SEQ ID NO:72), SCL23_R1 (5'-ACCAACGAAACCAAGTGAACA-3') (SEQ ID NO:73), SCL23_FW (5'-TGCTGCCGCAATCAAACCTCCT-3') (SEQ ID NO:74), and SCL23_RV (5'-AGCTGATCACGCGCGTTTGTA-3') (SEQ ID NO:75) for the SCL23 promoter, and 18S-5 (5'-TACCGTCCTAGTCTCAACCA-3') (SEQ ID NO:76) and 18S-3 (5'-
 30 AACATCTAAGGGCATCACAG-3') (SEQ ID NO:77) for 18S (used as an internal control).

To identify genome-wide targets by the ChIP–chip technique, the DNA from the ChIP experiments as well as mock ChIP experiments (ChIP with extract from the wildtype) was first amplified using a GENOMEPLEX complete WGA kit (WGA2, Sigma) and then re-amplified using a GENOMEPLEX WGA re-amplification kit (WGA3, Sigma). DNA (1 µg) from re-amplification of each pair of mock and ChIP samples was labeled with Cy3 and Cy5 nucleotides using a NimbleGen dual-color DNA labeling kit (06370250001, NimbleGen), and, after mixing, both samples were hybridized to a custom Arabidopsis whole-genome microarray containing 720 K probes. This microarray has been validated previously (Gendrel *et al.*, 2005). For each protein, two biological replicates were performed, and promoters with at least two probes that had a Cy5/Cy3 ratio >2 in all biological replicates were identified as target genes. For data analysis, we used the method described previously (Cui *et al.*, 2011). Briefly, probes with greater than twofold enrichment and $P < 0.001$ were identified from each replicate, and target genes were defined as those whose promoters have at least one probe meeting these criteria in at least two of the three replicates.

Other methods

Starch staining and sugar measurement were performed as previously described (Cui *et al.*, 2012). GUS staining and thin sectioning were performed according to the standard procedure (Weigel and Glazebrook, 2002). Leaves from 2–4-week-old plants grown in soil were incubated for 4 h in GUS staining buffer (50 mM sodium phosphate buffer, pH 7.2, containing 0.2% Triton X–100, 2 mM potassium ferrocyanide, 2 mM potassium ferricyanide and 2 mM X–Gluc). For microscopy, the leaves were fixed in FAA (50% ethanol, 10% Glacial acetic acid and 5% formaldehyde), and cleared using chloral hydrate solution for microscopy. For sectioning, the leaves were first fixed for 12 h with 4% glutaraldehyde, embedded in TECHNOVIT 7100 resin (Heraeus Kulzer), sectioned using a microtome (Bausch & Lomb Optical Co.), and stained with 1% toluidine blue solution for 1 min followed by de-staining for 2 min under running water.

All patents, patent applications, provisional applications, and publications referred to or cited herein are incorporated by reference in their entirety, including all figures and

tables, to the extent they are not inconsistent with the explicit teachings of this specification.

Following are examples that illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and
5 all solvent mixture proportions are by volume unless otherwise noted.

Example 1—SHR, SCR and SCL23 are essential for BS cell-fate specification

To determine whether SCR and SHR play a role in BS cell fate specification, we examined the leaf anatomy in *scr-1* and *shr-2* mutants by thin sectioning. In the wild-
10 type (Ws and Col-0), BS cells may be easily recognized by their rectangular cell shape, ordered organization and intermediate cell size relative to the vascular cells and mesophyll cells, which are large and irregularly shaped (Bosabalidis *et al.*, 1984) (Figures 1A and 1B). As expected, the BS cell layer appeared to be missing in the *shr* mutant (Figure 1C). Surprisingly, we found that the *scr* mutant has a normal cell pattern (Figure
15 1D). However, the cells surrounding the vascular tissue became slightly enlarged, suggesting that SCR may play a role in BS cell-fate specification but that additional factors are involved (Figure 1D).

Among the GRAS family of transcriptional regulators (Bolle, 2004), to which both SHR and SCR belong (Pysh *et al.*, 1999), SCL23 is the closest paralog to SCR
20 (Bolle, 2004), and therefore may also play a role in BS cell-fate specification. To test this hypothesis, we obtained two T-DNA insertion lines from the Arabidopsis Biological Resource Center (SALK_054051 and GT_5_16303), both of which harbor a T-DNA insertion in the 5' end of the coding region, and thus are likely to be null mutants. Quantitative RT-PCR analysis showed that levels of the SCL23 transcript were
25 dramatically reduced in both lines (Figure 5). However, neither mutant showed any obvious defects in BS cells (Figure 1E and Figure 6). We therefore generated a double mutant for SCR and SCL23. Interestingly, the cells surrounding the vascular tissue in the *scr scl23* double mutant were large and irregular in shape, similarly to what was observed in the *shr* mutant (Figure 1F and Figure 6).

30 To determine whether the BS cell layer is lost in the *shr* and *scr scl23* mutants, we examined the cell pattern by cross-sectioning. Interestingly, in both mutants, there was still a cell layer tightly associated with the vascular tissue (Figure 1C-1 and 1F-1).

However, compared to the BS cells in the wild-type (Figure 1A-1, 1B-1), the BS cells in the mutants were larger and some also became less regular in shape. This result suggests that, although the BS cell layer is not lost, the cells have become more mesophyll-like. A similar but less significant expansion of the BS cells was observed in *scr* leaves (Figure 1D-1). As expected, the BS cell layer in the *scl23* mutant was apparently normal (Figure 1E-1). Together, these results suggest that all three proteins are required to maintain BS cell fate, and that, although SCR and SCL23 act redundantly, SCR appears to play a more important role.

10 Example 2—SCR and SCL23 are expressed specifically in BS cells

The observation that SCR and SCL23 function redundantly in BS cell-fate specification suggests that SCL23, like SCR, may also be expressed in this cell type. To investigate this possibility, we created transgenic plants that express the GUS reporter gene under the control of the promoters of SCR and SCL23 (SCRpro:GUS and SCL23pro:GUS, respectively), and examined the GUS expression pattern. This histological analysis confirmed that both SCR and SCL23 were expressed specifically in BS cells (Figures 2A, 2B, 2D, and 2E). However, the similar expression pattern of SCR and SCL23 was observed only in small veins during early stages of leaf development. In major veins or later developmental stages, SCR expression became restricted to BS cells on the lower side of the leaf blade (Figure 2G), where the phloem is located. In contrast, SCL23 was preferentially expressed in BS cells associated with the xylem on the upper side of the leaf (Figure 2H). Hence, although SCR and SCL23 act redundantly in BS cell-fate specification, they function differently at later stage of leaf development.

25 Example 3—SCR and SCL23 act downstream of SHR

Previous studies have shown that, in leaves, SHR is expressed exclusively in the vascular tissue (Gardiner *et al.*, 2010). However, it has also been reported that SHR is expressed in other leaf cell types as well, including BS cells (Dhondt *et al.*, 2010). Due to this discrepancy, we also examined the GUS staining pattern in transgenic plants expressing the SHRpro:GUS construct (Helariutta *et al.*, 2000). Our results clearly show that SHR is expressed only in the vascular tissue (Figure 2C). Furthermore, by cross-sectioning, we found that SHR expression was xylem-specific (Figure 2F).

The distinct expression domains of SHR, SCR and SCL23 suggest that SHR must act non-cell-autonomously, similarly to its mode of action in the root (Nakajima *et al.*, 2001). This is indeed the case, because a recent study showed that the SHR promoter confers gene expression only in the vascular tissue, but an SHR–GFP protein expressed under the control of this promoter is present in BS cells (Gardiner *et al.*, 2010). In other words, the SHR protein must have moved from the vascular tissue into the adjacent cells to control BS cell-fate specification.

The cell type-specific expression patterns of SHR, SCR and SCL23, as well as their respective mutant phenotypes, suggest that both SCR and SCL23 are under the control of SHR. To determine whether this is the case, we introduced the SCRpro:GUS and SCL23pro:GUS constructs into the *shr* background by genetic crossing. As shown in Figures 3A and 3B, GUS activity from either construct was no longer detectable in the *shr* mutant, lending support to the possibility that SCR and SCL23 are regulated by SHR.

To determine whether SHR regulates SCR and SCL23 expression directly, we performed ChIP assays using a functional SHR–GFP fusion protein expressed in the *shr* mutant background (Cui *et al.*, 2007). As SHR and SCR control a common set of genes in the root, we predicted that SCL23 is also a direct target of SCR. We therefore also performed a ChIP–PCR assay using a GFP–SCR fusion protein expressed in the *scr* mutant background (Cui *et al.*, 2012). This experiment showed that SHR and SCR bind to the promoters of SCR and SCL23 (Figures 3C and 3D). Intriguingly, although no GUS staining was detectable in most *scr* mutant leaves, the SCRpro:GUS and SCL23pro:GUS reporters were still expressed in approximately 20% of the leaves (Figure 3E). This result suggests that, similarly to the situation in the root, factors other than SHR are involved in regulation of SCR and SCL23 expression in the leaves.

Example 4—Genome-wide identification of SHR, SCR and SCL23 direct targets

To understand how SCR and SCL23 control BS cell fate, and whether they function differently in leaves, we identified their direct targets at the genome scale by the ChIP–chip technique. Using the same criteria for both proteins (twofold enrichment and $P < 0.001$, see also Materials and Methods), we identified 1566 and 391 genes as direct targets of SCR and SCL23, respectively (Tables 4 and 5, and Figure 8), of which 93 are common targets. The small number of common targets and larger number of SCR direct

targets lend support to the possibility that SCR and SCL23 function differently but SCR plays a major role in BS cells. To determine the extent of functional overlap between SHR, SCR and SCL23, we also performed a ChIP–chip assay with SHR in leaves, and identified 1133 direct targets (Table 6). Consistent with our recent finding that SCR has both SHR-dependent and -independent functions (Cui *et al.*, 2012), the SHR and SCR direct targets are only partially overlapping (266 genes, *i.e.*, 23 and 17% of all SHR and SCR targets, respectively). Surprisingly, we found that SHR shared a larger number of targets with SCL23 than with SCR (261 and 93 genes, respectively). Only 74 genes were regulated by SHR, SCR and SCL23. Because SCR and SCL23 diverged in their expression patterns during late stages of leaf development, it is likely that SCR and SHR determine the expression of SCL23 in phloem-associated BS cells, whereas additional factors are involved in specification of SCL23 expression in xylem-associated BS cells.

Example 5—The expression pattern and function of SCR and SCL23 diverge at later stages of leaf development

In most C3 plants, a major role for the BS cells is metabolite transport between mesophyll cells and the vascular tissue (Leegood, 2008). Because of their preferential association with phloem and xylem, which are involved in uploading of sugar and unloading of minerals, respectively, SCR and SCL23 may regulate different aspects of metabolite and nutrient transport in BS cells. To test this hypothesis, we focused our analysis on genes involved in metabolite and mineral transport. This analysis showed indeed that, relative to SCL23, SCR had a much larger number of direct targets that encode transporter proteins (Table 3). Particularly interesting is that a number of genes involved in sugar transport are among the list of SCR direct targets, but none appear to be a target of SCL23 (Table 3). Intriguingly, there is little overlap between the transporter genes identified as SHR and SCR direct targets, but most SCR targets that are sugar transporter genes appear also to be SHR direct targets.

Our ChIP–chip data provide an explanation for our recent finding that SCR plays an important role in sugar homeostasis (Cui *et al.*, 2012). To assess the role of SCL23 in BS cells, we next measured sugar content in the *scl23* single mutant and the *scr scl23* double mutant. Both free sugars and starch were accumulated to a slightly higher level in the *scr scl23* mutant than in the *scr* mutant, but the *scl23* single mutation did not seem to

affect sugar homeostasis (Figures 4C and 4D). Consistent with these results, the *scr scl23* mutant also had a slightly smaller stature (Figure 4E). These results are consistent with the notion that SCR and SCL23 are both required for normal plant growth and development, but they function differently in BS cells.

5

Example 6

Taken together, the results shown here demonstrate that SHR, SCR and SCL23 constitute a developmental pathway controlling BS cell fate in the leaves of *Arabidopsis thaliana*. Although a role for SHR and SCR in bundle sheath cell-fate specification had been predicted (Nelson, 2011), they appear to regulate cell patterning differently in the root and shoot. In the root, mutation in either gene causes loss of a cell layer, whereas in *shr* and *scr* mutant leaves, the cell pattern is normal. However, we do not consider that the cells surrounding the vascular tissue in the *shr* and *scr* mutants are the same cell type as in the wild-type for the following reasons. First, these cells were expanded in size, and some were even irregular in shape, suggesting that they have become more mesophyll cell-like. Second, these cells do not express the SCR_{pro}:GUS and SCL23_{pro}:GUS constructs, which may be considered as BS cell typespecific markers. Third, because SHR and SCR control a number of genes directly many additional genes should be affected in the mutant cell layer in the *shr* and *scr* mutants. Inevitably, this will result in a change in physiology in these cells, even though they are still associated with the vascular tissue.

The finding that SCL23 is required for BS cell-fate specification and function is unexpected, because SCL23 does not have an N-terminal domain, which has been shown to be critical for the function of other GRAS family transcriptional regulators (Sun *et al.*, 2011). The GRAS family transcriptional regulators typically have a variable N-terminal domain and a conserved C-terminal GRAS domain (Pysh *et al.*, 1999). In SCR, the GRAS domain is required for physical interaction with SHR (Cui *et al.*, 2007), and the N-terminal domain is also a protein-protein interaction domain, through which a number of proteins interact with SCR (Cui and Benfey, 2009; Cruz-Ramirez *et al.*, 2012). The N-terminal domain of SCR also confers nuclear localization, and nuclear localization of SCR is important for its function in root radial patterning (Cui and Benfey, 2009). Truncated SCR protein without the N-terminal domain is still localized in the nucleus,

probably by forming a multiprotein complex (Welch *et al.*, 2007), but the ability of SCR to block SHR movement is compromised, as an additional ground tissue cell layer is formed in plants expressing the truncated protein in the *scr* background (Cui and Benfey, 2009). As no additional layers of BS cells are produced in the *scr* mutant, SCL23 must be
5 sufficient to block SHR movement. Nevertheless, SCL23 does not appear to have the same spectrum of functions as SCR, because SCR controls much a larger set of genes and the *scr* mutation causes much more serious defects in the morphology and function of the BS cells. In addition, SCL23 does not appear to play an important role in other organs, as the *scr* mutation alone causes loss of the endodermis in the root or starch sheath cells in
10 the inflorescence stem (Di Laurenzio *et al.*, 1996; Fukaki *et al.*, 1998).

Another unexpected finding is that, despite their redundant roles in BS cell-fate specification, SCL23 and SCR function distinctly in later stages of leaf development. This is suggested by the observation that SCR is preferentially expressed in phloem-associated BS cells but SCL23 is more strongly expressed in xylem-associated BS cells. Consistent
15 with this complementary expression pattern, we found that SCR directly controls genes involved in sugar and amino acid transport, whereas SCL23 direct target genes are involved in the transport of inorganic compounds. Compared to the *scf23* mutant, the *scr* mutant also shows a much more severe defect in sugar homeostasis. Although the *scf23* mutation alone does not result in obvious plant growth defects, the *scr scf23* double
20 mutant has smaller leaves, which indicates that SCL23 is important for normal plant growth and development. Interestingly, we found that SCL23 is also expressed in the root, albeit with a different expression pattern to that of SCR (Figures 7A and 7B).

Although the expression pattern of SHR in leaves has been described previously (Dhondt *et al.*, 2010; Gardiner *et al.*, 2010), how SHR regulates BS cell fate has been
25 unclear due to inconsistency in the results from previous studies. According to Gardiner *et al.* (2010), SHR is specifically expressed in the vascular tissue. In contrast, Dhondt *et al.* (2010) showed that SHR is expressed in both the vascular tissue and BS cells. This discrepancy may be due to the use of different reporter genes. Gardiner *et al.* used GFP, which may not be able to reveal SHR expression in mesophyll cells because of its relative
30 low sensitivity, whereas Dhondt *et al.* used the GUS gene, which may cause non-specific staining after an extended period of staining when GUS activity is strong and the stringency of the staining conditions is low. The SHR promoter is strong, so the broader

expression domain of SHR revealed by GUS staining may be an artifact. To resolve this issue, we re-examined the SHR expression pattern in the same transgenic plants containing the SHRpro:GUS construct as used by Dhondt *et al.* but under more stringent conditions (2 mM potassium ferrocyanide and 2 mM potassium ferricyanide in this study versus 2 mM potassium ferricyanide in the study by Dhondt *et al.*) and a shorter incubation time (4 h in this study versus 12–24 h in the previous study). Strikingly, we observed strong GUS activity in the vascular tissue but no activity in the BS cells. Moreover, by cross-sectioning, we showed that the SHRpro:GUS reporter gene is expressed specifically in the xylem. These results, together with the studies by Gardiner *et al.* (2010) suggest that, in the leaves, SHR is expressed in the vascular tissue but the protein moves into the adjacent cell layer, where it controls SCR and SCL23 expression and BS cell fate. The non-cell-autonomous action of SHR suggests that it is an important component of the positional information that is derived from the vascular tissue and determines the position of the BS cell layer. Homologs of SHR and SCR have been identified in many plants (Lim *et al.*, 2000; Sassa *et al.*, 2001; Kamiya *et al.*, 2003; Cui *et al.*, 2007; Laajanen *et al.*, 2007; Sole *et al.*, 2008; Cermak *et al.*, 2011). This suggests that the mechanism for BS cell-fate specification revealed in this study is likely to be evolutionarily conserved. In support of this possibility, an abnormal number of BS cell layers were produced in the maize *scr* mutant (Slewiniski *et al.*, 2012).

Table 3. Direct targets of SHR, SCR and SCL23 involved in nutrient transport, as identified by ChIP-chip.

Arabidopsis Genome Initiative (AGI) identification number	SHR target	SCR target	SCL23 target	Gene function
AT2G28070	Yes	Yes	Yes	ABC-2 type transporter family protein
AT1G59870	Yes		Yes	ABC-type transporter family protein
AT2G27240	Yes		Yes	Aluminium activated malate transporter
AT2G30070	Yes		Yes	K transporter
AT4G16370	Yes	Yes		Oligopeptide transporter
AT1G11260	Yes	Yes		Sugar transporter 1
AT1G71880	Yes	Yes		Sucrose transporter 1
AT5G26340		Yes		STP13, glucose transporter
AT1G50310		Yes		Sugar transporter 9
AT2G02810		Yes		UDP-galactose transporter 1
AT4G32390		Yes		Nucleotide-sugar transporter
AT5G55950		Yes		Nucleotide/sugar transporter
AT4G27970		Yes		Malic acid transport family protein
AT5G64560		Yes		Mg transporter

AT3G58970		Yes		Mg transporter 6
AT2G46800		Yes		Zn transporter
AT3G46900		Yes		Copper transporter
AT5G52860		Yes		ABC-2 type transporter family protein
AT1G12940		Yes		Nitrate transporter
AT3G45060		Yes		High affinity nitrate transporter 2.6
AT5G43360		Yes		Phosphate transporter
AT1G23090		Yes		Sulfite transporter
AT2G41190		Yes		Transmembrane amino acid transporter
AT5G01180		Yes		Peptide transporter 5
AT5G07630		Yes		Lipid transporters
AT3G21090		Yes		ABC-2 type transporter family protein
AT3G55110		Yes		ABC-2 type transporter family protein
AT4G27420		Yes		ABC-2 type transporter family protein
AT3G18830	Yes			Polyol/monosaccharide transporter 5
AT1G12110	Yes			Nitrate transporter 1.1
AT1G69850	Yes			Nitrate transporter 1:2
AT1G69870	Yes			Nitrate transporter 1.7
AT4G21680	Yes			Nitrate transporter 1.8
AT5G14570	Yes			High affinity nitrate transporter 2.7
AT1G80310	Yes			Sulfate transmembrane transporters
AT1G60160	Yes			Potassium transporter family protein
AT5G43810	Yes			Stabilizer of iron transporter SufD
AT2G38120	Yes			Transmembrane amino acid transporter
AT2G36590	Yes			Proline transporter 3
AT5G04770	Yes			Cationic amino acid transporter 6
AT4G27730	Yes			Oligopeptide transporter 1
AT1G80300	Yes			Nucleotide transporter 1
AT5G45370	Yes			Nodulin MtN21 /EamA-like transporter
AT1G70610	Yes			Transporter activity

Table 4. SCL23 direct targets identified by ChIP-chip

Arabidopsis Genome Initiative (AGI) identification number	Short description
AT2G40008	other RNA
AT1G78090	trehalose-6-phosphate phosphatase
AT2G22520	unknown protein
AT4G29780	unknown protein
AT2G25480	TPX2 (targeting protein for Xklp2) protein family
AT3G19030	unknown protein
AT2G23140	RING/U-box superfamily protein with ARM repeat domain
AT5G64370	beta-ureidopropionase
AT3G19020	Leucine-rich repeat (LRR) family protein
AT5G42110	unknown protein
AT1G61890	MATE efflux family protein
AT2G22510	hydroxyproline-rich glycoprotein family protein
AT1G32920	unknown protein, LOCATED IN: endomembrane system
AT1G32928	unknown protein
AT2G30040	mitogen-activated protein kinase kinase kinase 14
AT1G09070	soybean gene regulated by cold-2
AT3G62280	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G67350	unknown protein
AT2G23142	Plant self-incompatibility protein S1 family
AT2G29490	glutathione S-transferase TAU 1
AT1G76620	Protein of unknown function, DUF547
AT5G59770	Protein-tyrosine phosphatase-like, PTPLA
AT5G59880	actin depolymerizing factor 3

AT2G30070	potassium transporter 1
AT4G13395	ROTUNDIFOLIA like 12
AT3G30320	unknown protein
AT3G24670	Pectin lyase-like superfamily protein
AT5G11750	Ribosomal protein L19 family protein
AT4G01250	WRKY family transcription factor
AT1G79130	SAUR-like auxin-responsive protein family
AT5G57020	myristoyl-CoA:protein N-myristoyltransferase
AT1G76660	unknown protein, LOCATED IN: plasma membrane
AT1G22190	Integrase-type DNA-binding superfamily protein
AT4G27654	unknown protein
AT1G18740	Protein of unknown function (DUF793)
AT5G51490	Plant invertase/pectin methylesterase inhibitor superfamily
AT4G36920	Integrase-type DNA-binding superfamily protein
AT1G58037	Cysteine/Histidine-rich C1 domain family protein
AT5G59780	myb domain protein 59
AT3G56010	unknown protein
AT4G39800	myo-inositol-1-phosphate synthase 1
AT4G27270	Quinone reductase family protein
AT5G64360	Chaperone DnaJ-domain superfamily protein
AT4G15610	Uncharacterised protein family (UPF0497)
AT2G30380	Plant protein of unknown function (DUF641)
AT5G53420	CCT motif family protein
AT4G20362	other RNA
AT2G35960	NDR1/HIN1-like 12
AT1G27730	salt tolerance zinc finger
AT3G07360	plant U-box 9
AT4G25490	C-repeat/DRE binding factor 1
AT1G20823	RING/U-box superfamily protein
AT5G11530	embryonic flower 1 (EMF1)
AT3G04732	unknown protein
AT1G29920	chlorophyll A/B-binding protein 2
AT2G41140	CDPK-related kinase 1
AT1G60130	Mannose-binding lectin superfamily protein
AT5G44090	Calcium-binding EF-hand family protein
AT2G46530	auxin response factor 11
AT5G25220	KNOTTED1-like homeobox gene 3
AT1G64385	unknown protein, LOCATED IN: endomembrane
AT5G47940	unknown protein
AT4G01720	WRKY family transcription factor
AT4G37610	BTB and TAZ domain protein 5
AT4G27280	Calcium-binding EF-hand family protein
AT1G07135	glycine-rich protein
AT5G06320	NDR1/HIN1-like 3
AT4G25470	C-repeat/DRE binding factor 2
AT1G35560	TCP family transcription factor
AT4G27657	unknown protein
AT2G22460	Protein of unknown function, DUF617
AT2G28070	ABC-2 type transporter family protein
AT5G11060	KNOTTED1-like homeobox gene 4
AT1G20330	sterol methyltransferase 2
AT5G63170	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G65340	Protein of unknown function, DUF617
AT1G25550	myb-like transcription factor family protein
AT5G23280	TCP family transcription factor
AT1G15750	Transducin family protein / WD-40 repeat family protein
AT1G17420	lipxygenase 3
AT4G32020	unknown protein
AT1G19180	jasmonate-zim-domain protein 1
AT4G28230	unknown protein
AT4G28240	Wound-responsive family protein

AT4G17453	This gene encodes a small protein and has either evidence of transcription or purifying selection
AT3G53450	Putative lysine decarboxylase family protein
AT5G08139	RING/U-box superfamily protein
AT4G19700	SBP (S-ribonuclease binding protein) family protein
AT5G11740	arabinogalactan protein 15
AT4G15800	ralf-like 33
AT1G68450	VQ motif-containing protein
AT1G35750	pumilio 10
AT4G26690	PLC-like phosphodiesterase family protein
AT1G27290	unknown protein
AT3G12320	unknown protein
AT4G11280	1-aminocyclopropane-1-carboxylic acid (acc) synthase 6
AT5G01850	Protein kinase superfamily protein
AT5G34830	unknown protein
AT1G01490	Heavy metal transport/detoxification superfamily protein
AT2G23340	DREB and EAR motif protein 3
AT3G23810	S-adenosyl-l-homocysteine (SAH) hydrolase 2
AT3G56000	cellulose synthase like A14
AT1G78030	unknown protein
AT1G01470	Late embryogenesis abundant protein
AT5G59613	unknown protein
AT5G67290	FAD-dependent oxidoreductase family protein
AT3G44610	Protein kinase superfamily protein
AT3G15210	ethylene responsive element binding factor 4
AT4G37260	myb domain protein 73
AT5G63580	flavonol synthase 2
AT5G21940	unknown protein
AT5G67440	Phototropic-responsive NPH3 family protein
AT3G16830	TOPLESS-related 2
AT4G05320	polyubiquitin 10
AT4G32030	unknown protein
AT3G17860	jasmonate-zim-domain protein 3
AT4G24120	YELLOW STRIPE like 1
AT1G70550	Protein of Unknown Function (DUF239)
AT1G02350	protoporphyrinogen oxidase-related
AT1G09390	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G65700	Leucine-rich receptor-like protein kinase family protein
AT3G28340	galacturonosyltransferase-like 10
AT4G01960	unknown protein
AT1G05710	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT2G23148	Plant self-incompatibility protein S1 family
AT3G22380	time for coffee
AT1G73550	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G50770	calmodulin-like 41
AT5G20190	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G13730	sigma factor 4
AT2G27240	Aluminium activated malate transporter family protein
AT2G45970	cytochrome P450, family 86, subfamily A, polypeptide 8
AT1G55230	Family of unknown function (DUF716)
AT4G13340	Leucine-rich repeat (LRR) family protein
AT4G17500	ethylene responsive element binding factor 1
AT3G11700	FASCICLIN-like arabinogalactan protein 18 precursor
AT1G03730	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03600.1); Has 50 Blast hits to 50 prot....
AT5G13740	zinc induced facilitator 1
AT1G20340	Cupredoxin superfamily protein
AT5G61990	Pentatricopeptide repeat (PPR) superfamily protein
AT4G20830	FAD-binding Berberine family protein
AT5G45470	Protein of unknown function (DUF594)
AT5G65207	unknown protein
AT3G14450	CTC-interacting domain 9

AT3G63006	pre-tRNA
AT1G02065	squamosa promoter binding protein-like 8
AT1G19050	response regulator 7
AT1G70370	polygalacturonase 2
AT5G65210	bZIP transcription factor family protein
AT1G64380	Integrase-type DNA-binding superfamily protein
AT3G52490	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
AT3G17120	unknown protein
AT5G08790	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT4G22980	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
AT3G44730	kinesin-like protein 1
AT3G16570	rapid alkalization factor 23
AT4G13830	DNAJ-like 20
AT2G41340	RNA polymerase II fifth largest subunit, D
AT1G07580	pre-tRNA
AT3G16860	COBRA-like protein 8 precursor
AT3G52840	beta-galactosidase 2
AT1G22180	Sec14p-like phosphatidylinositol transfer family protein
AT3G06070	unknown protein
AT1G02340	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G27510	unknown protein
AT3G13310	Chaperone DnaJ-domain superfamily protein
AT3G50660	Cytochrome P450 superfamily protein
AT4G01540	NAC with transmembrane motif1
AT5G15410	Cyclic nucleotide-regulated ion channel family protein
AT3G15200	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G73600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G73602	conserved peptide upstream open reading frame 32
AT1G04130	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G46730	glycine-rich protein
AT5G43030	Cysteine/Histidine-rich C1 domain family protein
AT1G13240	pre-tRNA
AT5G64690	neurofilament triplet H protein-related
AT1G01550	Protein of unknown function (DUF793)
AT3G02150	plastid transcription factor 1
AT3G04730	indoleacetic acid-induced protein 16
AT5G67450	zinc-finger protein 1
AT1G21810	Plant protein of unknown function (DUF869)
AT1G73560	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT2G27320	Protein of Unknown Function (DUF239)
AT2G46380	Protein of unknown function (DUF3133)
AT3G19380	plant U-box 25
AT3G20340	Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress.
AT5G35750	histidine kinase 2
AT3G26511	unknown protein
AT1G18300	nudix hydrolase homolog 4
AT3G63050	unknown protein
AT5G64310	arabinogalactan protein 1
AT2G23700	Protein of unknown function, DUF547
AT5G45120	Eukaryotic aspartyl protease family protein
AT1G23710	Protein of unknown function (DUF1645)
AT1G13260	related to ABI3/VP1 1
AT1G07000	exocyst subunit exo70 family protein B2
AT4G38520	Protein phosphatase 2C family protein
AT5G17300	Homeodomain-like superfamily protein
AT3G22104	Phototropic-responsive NPH3 family protein
AT5G67240	small RNA degrading nuclease 3
AT1G76190	SAUR-like auxin-responsive protein family
AT3G13080	multidrug resistance-associated protein 3
AT5G60890	myb domain protein 34

AT5G13100	unknown protein
AT3G11410	protein phosphatase 2CA
AT3G11660	NDR1/HIN1-like 1
AT1G24150	formin homologue 4
AT1G14740	Protein of unknown function (DUF1423)
AT2G41200	unknown protein
AT2G41430	dehydration-induced protein (ERD15)
AT1G12610	Integrase-type DNA-binding superfamily protein
AT3G48530	SNF1-related protein kinase regulatory subunit gamma 1
AT4G32410	cellulose synthase 1
AT3G05800	AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1
AT1G25560	AP2/B3 transcription factor family protein
AT1G80450	VQ motif-containing protein
AT1G13360	unknown protein
AT5G15420	unknown protein
AT4G34410	redox responsive transcription factor 1
AT4G08950	Phosphate-responsive 1 family protein
AT4G36040	Chaperone DnaJ-domain superfamily protein
AT1G79120	Ubiquitin carboxyl-terminal hydrolase family protein
AT5G57690	diacylglycerol kinase 4
AT1G32640	Basic helix-loop-helix (bHLH) DNA-binding family protein
AT4G27310	B-box type zinc finger family protein
AT2G41910	Protein kinase superfamily protein
AT5G62060	F-box and associated interaction domains-containing protein
AT5G62065	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G21960	Integrase-type DNA-binding superfamily protein
AT1G64470	Ubiquitin-like superfamily protein
AT1G15820	light harvesting complex photosystem II subunit 6
AT3G10720	Plant invertase/pectin methylesterase inhibitor superfamily
AT3G15630	unknown protein
AT5G06865	other RNA
AT4G33920	Protein phosphatase 2C family protein
AT1G78080	related to AP2 4
AT3G24050	GATA transcription factor 1
AT1G01720	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT5G11090	serine-rich protein-related
AT3G23920	beta-amylase 1
AT1G30360	Early-responsive to dehydration stress protein (ERD4)
AT3G07790	DGCR14-related
AT2G47090	zinc ion binding;nucleic acid binding
AT1G20440	cold-regulated 47
AT3G11420	Protein of unknown function (DUF604)
AT3G59090	tobamovirus multiplication 1
AT1G72520	PLAT/LH2 domain-containing lipoxygenase family protein
AT3G19580	zinc-finger protein 2
AT3G22968	conserved peptide upstream open reading frame 59
AT3G22970	Protein of unknown function (DUF506)
AT5G62050	homolog of yeast oxidase assembly 1 (OXA1)
AT5G61670	unknown protein
AT3G15810	Protein of unknown function (DUF567)
AT4G39840	unknown protein
AT1G53850	20S proteasome alpha subunit E1
AT3G46660	UDP-glucosyl transferase 76E12
AT2G29980	fatty acid desaturase 3
AT5G06390	FASCICLIN-like arabinogalactan protein 17 precursor
AT5G20230	blue-copper-binding protein
AT5G47260	ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases
AT5G67330	natural resistance associated macrophage protein 4
AT4G22780	ACT domain repeat 7
AT3G10930	unknown protein
AT2G20585	nuclear fusion defective 6

AT4G27652	unknown protein
AT1G02660	alpha/beta-Hydrolases superfamily protein
AT1G51710	ubiquitin-specific protease 6
AT2G01670	nudix hydrolase homolog 17
AT1G04000	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44060.1); Has 62 Blast hits to 62 prot....
AT1G05370	Sec14p-like phosphatidylinositol transfer family protein
AT1G19210	Integrase-type DNA-binding superfamily protein
AT1G20450	Dehydrin family protein
AT1G20510	OPC-8:0 CoA ligase1
AT1G25400	unknown protein
AT1G27100	Actin cross-linking protein
AT1G31130	unknown protein
AT1G32930	Galactosyltransferase family protein
AT1G45150	unknown protein
AT1G49100	Leucine-rich repeat protein kinase family protein
AT1G50300	TBP-associated factor 15
AT1G50430	Ergosterol biosynthesis ERG4/ERG24 family
AT1G55680	Transducin/WD40 repeat-like superfamily protein
AT1G59870	ABC-2 and Plant PDR ABC-type transporter family protein
AT1G60110	Mannose-binding lectin superfamily protein
AT1G60200	splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein
AT1G66730	DNA LIGASE 6
AT1G68850	Peroxidase superfamily protein
AT1G70300	K ⁺ uptake permease 6
AT1G70710	glycosyl hydrolase 9B1
AT1G72180	Leucine-rich receptor-like protein kinase family protein
AT1G72460	Leucine-rich repeat protein kinase family protein
AT1G73480	alpha/beta-Hydrolases superfamily protein
AT1G73490	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G74950	TIFY domain/Divergent CCT motif family protein
AT1G76050	Pseudouridine synthase family protein
AT1G76610	Protein of unknown function, DUF617
AT1G77460	Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein
AT1G80500	SNARE-like superfamily protein
AT2G05940	Protein kinase superfamily protein
AT2G06050	oxophytodienoate-reductase 3
AT2G06520	photosystem II subunit X
AT2G23830	PapD-like superfamily protein
AT2G24810	Pathogenesis-related thaumatin superfamily protein
AT2G25270	unknown protein; LOCATED IN: plasma membrane
AT2G25470	receptor like protein 21
AT2G27100	C2H2 zinc-finger protein SERRATE (SE)
AT2G28350	auxin response factor 10
AT2G30580	DREB2A-interacting protein 2
AT2G32170	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G34460	NAD(P)-binding Rossmann-fold superfamily protein
AT2G34470	urease accessory protein G
AT2G36070	translocase inner membrane subunit 44-2
AT2G40010	Ribosomal protein L10 family protein
AT2G41040	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G41945	unknown protein
AT2G42790	citrate synthase 3
AT2G43040	tetratricopeptide repeat (TPR)-containing protein
AT2G43360	Radical SAM superfamily protein
AT2G45500	AAA-type ATPase family protein
AT2G45620	Nucleotidyltransferase family protein
AT2G45700	sterile alpha motif (SAM) domain-containing protein
AT2G46520	cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative
AT3G03990	alpha/beta-Hydrolases superfamily protein
AT3G05200	RING/U-box superfamily protein

AT3G07350	Protein of unknown function (DUF506)
AT3G07390	auxin-responsive family protein
AT3G11170	fatty acid desaturase 7
AT3G14440	nine-cis-epoxycarotenoid dioxygenase 3
AT3G20310	ethylene response factor 7
AT3G20600	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT3G23820	UDP-D-glucuronate 4-epimerase 6
AT3G24518	other RNA
AT3G24520	heat shock transcription factor C1
AT3G46658	other RNA
AT3G47990	SUGAR-INSENSITIVE 3
AT3G50370	unknown protein
AT3G54230	suppressor of abi3-5
AT3G55460	SC35-like splicing factor 30
AT3G56408	other RNA
AT3G56410	Protein of unknown function (DUF3133)
AT3G56750	unknown protein
AT3G56920	DHHC-type zinc finger family protein
AT3G57060	binding
AT3G57470	Insulinase (Peptidase family M16) family protein
AT3G58120	Basic-leucine zipper (bZIP) transcription factor family protein
AT3G60440	Phosphoglycerate mutase family protein
AT3G61480	Quinoprotein amine dehydrogenase, beta chain-like; RIC1-like guanyl-nucleotide exchange factor
AT3G63460	transducin family protein / WD-40 repeat family protein
AT3G62660	galacturonosyltransferase-like 7
AT4G00360	cytochrome P450, family 86, subfamily A, polypeptide 2
AT4G02330	Plant invertase/pectin methylesterase inhibitor superfamily
AT4G05050	ubiquitin 11
AT4G05070	Wound-responsive family protein
AT4G21740	unknown protein
AT4G24240	WRKY DNA-binding protein 7
AT4G27410	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT4G27520	early nodulin-like protein 2
AT4G30440	UDP-D-glucuronate 4-epimerase 1
AT4G31500	cytochrome P450, family 83, subfamily B, polypeptide 1
AT4G32060	calcium-binding EF hand family protein
AT4G36648	other RNA
AT4G36500	unknown protein
AT4G36988	conserved peptide upstream open reading frame 49
AT4G36990	heat shock factor 4
AT5G06310	Nucleic acid-binding, OB-fold-like protein
AT5G06860	polygalacturonase inhibiting protein 1
AT5G09760	Plant invertase/pectin methylesterase inhibitor superfamily
AT5G11000	Plant protein of unknown function (DUF868)
AT5G20110	Dynein light chain type 1 family protein
AT5G22630	arogenate dehydratase 5
AT5G24590	TCV-interacting protein
AT5G24930	CONSTANS-like 4
AT5G27420	carbon/nitrogen insensitive 1
AT5G42120	Concanavalin A-like lectin protein kinase family protein
AT5G42690	Protein of unknown function, DUF547
AT5G45110	NPR1-like protein 3
AT5G49410	unknown protein
AT5G51500	Plant invertase/pectin methylesterase inhibitor superfamily
AT5G57015	casein kinase I-like 12
AT5G57700	BNR/Asp-box repeat family protein
AT5G57770	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AT5G58690	phosphatidylinositol-specific phospholipase C5
AT5G60690	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein
AT5G61000	Replication factor-A protein 1-related
AT5G62600	ARM repeat superfamily protein

AT5G63180	Pectin lyase-like superfamily protein
AT5G63470	nuclear factor Y, subunit C4
AT5G67360	Subtilase family protein
AT5G67460	O-Glycosyl hydrolases family 17 protein
AT1G01300	Eukaryotic aspartyl protease family protein

Table 5. SCR direct targets identified by ChIP-chip

Arabidopsis Genome Initiative (AGI) identification number	Description
AT2G29220	Concanavalin A-like lectin protein kinase family protein
AT5G26340	STP13
AT1G13260	EDF4, RAV1. AP2/B3 domain transcription factor which is upregulated in response to low temperature
AT3G32260	Nucleic acid-binding proteins superfamily;
AT1G27290	unknown protein;
AT1G47570	RING/U-box superfamily protein
AT5G24660	RESPONSE TO LOW SULFUR 2 (LSU2)
AT3G02170	LONGIFOLIA2 (LNG2). Regulates leaf morphology by promoting cell expansion in the leaf-length direction
AT4G08700	ATPUP13. Likely involved in purine transport
AT5G24655	RESPONSE TO LOW SULFUR 4 (LSU4)
AT4G16780	ATHB-2; light & auxin response & development. Encodes a homeodomain-leucine zipper protein that is rapidly and strongly induced by changes in the ratio of red to far-red light. It is also involved in cell expansion and cell proliferation and in the response to auxin
AT3G42950	Pectin lyase-like superfamily protein
AT2G07280	unknown protein
AT5G43820	Pentatricopeptide repeat (PPR) superfamily protein
AT1G70550	expressed protein, similar to putative putative carboxyl-terminal peptidase
AT3G07360	AtPUB9, ARABIDOPSIS THALIANA PLANT U-BOX 9
AT1G03840	MGP
AT3G42060	myosin heavy chain-related
AT4G36920	AP2, FL1, FLO1
AT2G15420	myosin heavy chain-related
AT1G69530	expansin, ATEXP1.
AT2G21340	MATE efflux family protein
AT1G19850	MP, IAA24, ARF5
AT2G45190	YABBY1 / abnormal floral organs protein (AFO) / filamentous flower protein (FIL)
AT3G45000	ESCRT III complex, vesicle-mediated transport; SNF7 family protein.
AT2G23320	WRKY15, H2O2 responsive
AT3G06070	unknown protein
AT1G31910	GHMP kinase family protein
AT2G21330	FBA1, fructose-bisphosphate aldolase 1
AT4G27430	COP1-interacting protein 7
AT1G71880	SUC1, sucrose-proton symporter
AT3G19380	plant U-box 25
AT3G23810	SAHH2, S-adenosyl-l-homocysteine (SAH) hydrolase 2
AT5G53420	CCT motif family protein
AT1G47820	unknown protein
AT4G16447	unknown protein
AT1G23100	GroES-like family protein
AT2G19980	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein)
AT3G66656	AGL91
AT5G24670	EMB2820, CAP (Cysteine-rich secretory proteins, Antigen 5
AT3G54240	alpha/beta-Hydrolases superfamily protein
AT1G47810	F-box and associated interaction domains-containing protein
AT1G45976	S-ribonuclease binding protein 1 (SBP1)
AT1G09970	RLK7, Leucine-rich receptor-like protein kinase family protein

AT4G39800	myo-inositol-1-phosphate synthase 1
AT4G34760	SAUR-like auxin-responsive protein family
AT2G36410	Family of unknown function (DUF662)
AT3G06080	TBL10, TRICHOME BIREFRINGENCE-LIKE 10 (2nd cell wall synthesis)
AT5G38030	MATE efflux family protein, similar to ripening regulated protein DDTFR18 (<i>Lycopersicon esculentum</i>) GI:12231296;
AT3G23820	GAE6, UDP-D-glucuronate 4-epimerase
AT5G40930	TRANSLOCASE OF OUTER MEMBRANE 20-4 (component of the TOM complex involved in transport of nuclear-encoded mitochondrial proteins)
AT5G25220	KNAT3, KNOTTED1-like homeobox gene 3
AT5G62430	CDF1, CYCLING DOF FACTOR 1
AT1G30950	UFO (weak allele specifically affects petal -transformation into carpel or stamen)
AT5G24830	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G33080	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein
AT1G33590	Leucine-rich repeat (LRR) family protein
AT3G11590	unknown protein;
AT4G01690	PPOX1, HEMG1, protoporphyrinogen oxidase
AT2G46530	ARF11
AT1G07090	LSH6, LIGHT SENSITIVE HYPOCOTYLS 6 (LSH6)
AT3G03770	Leucine-rich repeat protein kinase family protein
AT1G23010	LPR1, LOW PHOSPHATE ROOT1. Encodes a protein with multicopper oxidase activity
AT3G19390	Granulin repeat cysteine protease family protein;
AT4G28703	RmlC-like cupins superfamily protein
AT3G61460	BRH1, BRASSINOSTEROID-RESPONSIVE RING-H2; zinc finger (C3HC4-type RING finger) family protein (BRH1)
AT5G67350	unknown protein
AT1G47660	unknown protein
AT5G42790	proteasome alpha subunit F1
AT4G25480	encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF3).
AT5G08330	TCP family transcription factor
AT1G72310	RING/U-box superfamily protein
AT5G67450	ZINC-FINGER PROTEIN 1, Zinc finger (C2H2 type) protein 1 (AZF1),
AT4G01960	unknown protein;
AT1G01650	SIGNAL PEPTIDE PEPTIDASE-LIKE 4
AT3G57860	OSD1, OMISSION OF SECOND DIVISION (2nd in meiosis); UVI4-LIKE
AT5G25190	encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family
AT5G03140	Concanavalin A-like lectin protein kinase family protein
AT1G76890	GT-2 factor (GT2), trihelix DNA-binding protein
AT5G55230	MICROTUBULE-ASSOCIATED PROTEINS 65-1; microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (<i>Homo sapiens</i>)
AT3G23040	unknown protein
AT1G29195	expressed protein
AT4G36860	LIM domain-containing protein
AT2G44500	O-fucosyltransferase family protein
AT5G51490	Plant invertase/pectin methylesterase inhibitor superfamily
AT1G04240	IAA3, SHY2, regulates multiple auxin responses in roots.
AT1G25390	Protein kinase superfamily protein
AT2G33710	encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family.
AT1G53180	unknown protein;
AT1G05710	bHLH family protein
AT2G38120	AUX1
AT3G27020	YELLOW STRIPE like 6
AT4G35490	MRPL11, mitochondrial ribosomal protein L11
AT1G19040	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT4G14770	AtTCX2, TESMIN/TSO1-like CXC 2
AT1G47870	ATE2F2, Member of the E2F transcription factors
AT3G02140	TMAC2, ABI FIVE BINDING PROTEIN 4
AT1G30825	ACTIN-RELATED PROTEIN C2A, ARPC2A, DIS2DISTORTED TRICHOMES 2 (mutant display enlarge trichomes)
AT1G72630	ELF4-like 2

AT3G23220	ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family.
AT3G53450	Putative lysine decarboxylase family protein
AT2G04550	IBR5, indole-3-butyric acid response 5
AT2G21140	proline-rich protein 2
AT1G33860	unknown protein
AT5G59270	Concanavalin A-like lectin protein kinase family protein
AT1G68450	PIGMENT DEFECTIVE 337; VQ motif-containing protein, contains PF05678: VQ motif
AT5G67240	small RNA degrading nuclease 3
AT5G44250	Protein of unknown function DUF829, transmembrane 53
AT1G28360	ERF domain protein 12
AT3G27170	chloride channel B
AT2G35960	NDR1/HIN1-like 12
AT3G25905	CLE27, CLAVATA3/ESR-RELATED 27
AT1G26920	
AT1G19410	FBD / Leucine Rich Repeat domains containing protein
AT1G29060	Target SNARE coiled-coil domain protein
AT4G16770	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT4G40050	Protein of unknown function (DUF3550/UPF0682)
AT1G31290	ARGONAUTE 3
AT5G28770	bZIP transcription factor family protein
AT3G06500	Plant neutral invertase family protein
AT1G20620	catalase 3
AT1G12330	
AT1G78240	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT4G37840	hexokinase-like 3
AT4G35780	ACT-like protein tyrosine kinase family protein
AT3G12130	KH domain-containing protein / zinc finger (CCCH type) family protein
AT1G15670	Galactose oxidase/kelch repeat superfamily protein
AT1G31350	KAR-UP F-box 1
AT1G02270	Calcium-binding endonuclease/exonuclease/phosphatase family
AT3G28930	AIG2-like (avirulence induced gene) family protein
AT1G13300	myb-like transcription factor family protein
AT4G30140	GDSL-like Lipase/Acylhydrolase superfamily protein
AT4G17670	Protein of unknown function (DUF581)
AT3G24550	proline extensin-like receptor kinase 1
AT4G01680	myb domain protein 55
AT2G40750	WRKY DNA-binding protein 54
AT4G28290	
AT2G01150	RING-H2 finger protein 2B
AT5G17300	Homeodomain-like superfamily protein
AT4G01250	WRKY family transcription factor
AT3G05110	Domain of unknown function (DUF3444)
AT2G46800	zinc transporter of Arabidopsis thaliana
AT2G44350	Citrate synthase family protein
AT5G16190	cellulose synthase like A11
AT5G53550	YELLOW STRIPE like 3
AT2G01830	CHASE domain containing histidine kinase protein
AT1G68480	C2H2 and C2HC zinc fingers superfamily protein
AT5G14800	pyrroline-5- carboxylate (P5C) reductase
AT1G19180	jasmonate-zim-domain protein 1
AT1G50490	ubiquitin-conjugating enzyme 20
AT3G18280	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G44730	kinesin-like protein 1
AT1G23000	Heavy metal transport/detoxification superfamily protein
AT2G15790	peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase
AT1G22520	Domain of unknown function (DUF543)
AT2G01850	endoxyloglucan transferase A3
AT1G53170	ethylene response factor 8
AT3G50690	Leucine-rich repeat (LRR) family protein
AT4G31800	WRKY DNA-binding protein 18
AT5G17840	DnaJ/Hsp40 cysteine-rich domain superfamily protein

AT4G16444	
AT1G52180	Aquaporin-like superfamily protein
AT4G05090	Inositol monophosphatase family protein
AT4G22120	ERD (early-responsive to dehydration stress) family protein
AT3G63020	Protein of unknown function (DUF3049)
AT3G15200	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G21430	Zinc finger, RING-type;Transcription factor jumonji/aspartyl beta-hydroxylase
AT1G14920	GRAS family transcription factor family protein
AT5G17760	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G57360	Galactose oxidase/kelch repeat superfamily protein
AT1G21010	
AT5G67340	ARM repeat superfamily protein
AT1G24625	zinc finger protein 7
AT2G41310	response regulator 3
AT2G36970	UDP-Glycosyltransferase superfamily protein
AT5G13820	telomeric DNA binding protein 1
AT5G53120	spermidine synthase 3
AT3G18060	transducin family protein / WD-40 repeat family protein
AT2G03240	EXS (ERD1/XPR1/SYG1) family protein
AT5G14080	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G63040	expressed protein
AT5G67360	Subtilase family protein
AT2G28570	unknown protein;
AT5G35450	Disease resistance protein (CC-NBS-LRR class) family
AT1G48330	
AT4G19710	aspartate kinase-homoserine dehydrogenase ii
AT5G03210	unknown protein;
AT3G05320	O-fucosyltransferase family protein
AT5G53590	SAUR-like auxin-responsive protein family
AT1G59790	Cullin family protein
AT5G22950	SNF7 family protein
AT1G17380	jasmonate-zim-domain protein 5
AT3G16800	Protein phosphatase 2C family protein
AT5G26680	5'-3' exonuclease family protein
AT4G27970	SLAC1 homologue 2, C4-dicarboxylate transporter/malic acid transport family protein
AT3G10870	methyl esterase 17
AT5G51580	unknown protein;
AT1G69430	unknown protein;
AT2G05710	ACO3, aconitase 3
AT3G23920	beta-amylase 1
AT5G41080	PLC-like phosphodiesterases superfamily protein
AT4G32620	Enhancer of polycomb-like transcription factor protein
AT5G24930	CONSTANS-like 4
AT1G43730	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT5G22570	WRKY DNA-binding protein 38
AT2G17620	Cyclin B2;1
AT4G30720	FAD/NAD(P)-binding oxidoreductase family protein
AT2G39180	CRINKLY4 related 2
AT1G80450	VQ motif-containing protein
AT3G03990	alpha/beta-Hydrolases superfamily protein
AT1G76100	plastocyanin 1
AT5G42150	Glutathione S-transferase family protein
AT5G01830	ARM repeat superfamily protein
AT4G38550	Arabidopsis phospholipase-like protein (PEARLI 4) family
AT5G50450	HCP-like superfamily protein with MYND-type zinc finger
AT5G62040	PEBP (phosphatidylethanolamine-binding protein) family protein
AT1G05860	
AT5G44700	Leucine-rich repeat transmembrane protein kinase
AT5G04030	
AT3G02580	sterol 1
AT3G46500	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein

AT1G21590	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
AT1G36070	Transducin/WD40 repeat-like superfamily protein
AT1G48260	CBL-interacting protein kinase 17
AT4G35090	catalase 2
AT5G38790	
AT1G50300	TBP-associated factor 15
AT3G55110	ABC-2 type transporter family protein
AT5G51590	AT hook motif DNA-binding family protein
AT4G39950	cytochrome P450, family 79, subfamily B, polypeptide 2
AT1G47780	alpha/beta-Hydrolases superfamily protein
AT5G14920	Gibberellin-regulated family protein
AT3G50780	
AT5G16520	
AT4G26540	Leucine-rich repeat receptor-like protein kinase family protein
AT5G61660	glycine-rich protein
AT1G30610	pentatricopeptide (PPR) repeat-containing protein
AT1G30610	pentatricopeptide (PPR) repeat-containing protein
AT2G19810	CCCH-type zinc finger family protein
AT1G75540	salt tolerance homolog2
AT5G22390	Protein of unknown function (DUF3049)
AT3G05840	Protein kinase superfamily protein
AT2G22430	homeobox protein 6
AT2G30550	alpha/beta-Hydrolases superfamily protein
AT4G27420	ABC-2 type transporter family protein
AT2G39190	Protein kinase superfamily protein
AT3G13110	serine acetyltransferase 2;2
AT3G24770	CLAVATA3/ESR-RELATED 41
AT5G03320	Protein kinase superfamily protein
AT4G11440	Mitochondrial substrate carrier family protein
AT3G21220	MAP kinase kinase 5
AT5G24500	
AT1G35614	
AT3G50660	Cytochrome P450 superfamily protein
AT1G70300	K ⁺ uptake permease 6
AT5G44080	Basic-leucine zipper (bZIP) transcription factor family protein
AT5G66960	Prolyl oligopeptidase family protein
AT2G01890	purple acid phosphatase 8
AT1G35500	
AT3G17860	jasmonate-zim-domain protein 3
AT1G50280	Phototropic-responsive NPH3 family protein
AT5G55950	Nucleotide/sugar transporter family protein
AT3G23050	indole-3-acetic acid 7
AT2G46420	Plant protein 1589 of unknown function
AT2G01910	Microtubule associated protein (MAP65/ASE1) family protein
AT1G19360	Nucleotide-diphospho-sugar transferase family protein
AT5G25460	Protein of unknown function, DUF642
AT1G23020	ferric reduction oxidase 3
AT4G15920	Nodulin MtN3 family protein
AT3G19680	Protein of unknown function (DUF1005)
AT3G16500	phytochrome-associated protein 1
AT5G22860	Serine carboxypeptidase S28 family protein
AT3G10530	Transducin/WD40 repeat-like superfamily protein
AT1G52200	PLAC8 family protein
AT1G69170	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein
AT3G53670	
AT1G65420	Protein of unknown function (DUF565)
AT3G54570	Plant calmodulin-binding protein-related
AT5G04560	HhH-GPD base excision DNA repair family protein
AT2G26040	PYR1-like 2
AT1G71400	receptor like protein 12
AT4G20790	Leucine-rich repeat protein kinase family protein

AT1G28230	purine permease 1
AT4G04750	Major facilitator superfamily protein
AT3G13750	beta galactosidase 1
AT3G25805	
AT4G25835	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G69080	Adenine nucleotide alpha hydrolases-like superfamily protein
AT3G56070	rotamase cyclophilin 2
AT2G15640	F-box family protein
AT5G15160	BANQUO 2
AT2G44940	Integrase-type DNA-binding superfamily protein
AT4G20240	cytochrome P450, family 71, subfamily A, polypeptide 27
AT2G18050	histone H1-3
AT2G23340	DREB and EAR motif protein 3
AT5G49570	peptide-N-glycanase 1
AT1G21340	Dof-type zinc finger DNA-binding family protein
AT2G17110	Protein of unknown function (DUF630 and DUF632)
AT2G13840	Polymerase/histidinol phosphatase-like
AT4G25470	C-repeat/DRE binding factor 2
AT5G36260	Eukaryotic aspartyl protease family protein
AT1G20900	Predicted AT-hook DNA-binding family protein
AT1G70420	Protein of unknown function (DUF1645)
AT4G27440	protochlorophyllide oxidoreductase B
AT5G07590	Transducin/WD40 repeat-like superfamily protein
AT1G07280	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G47390	cytidine/deoxycytidylate deaminase family protein
AT1G55370	NDH-dependent cyclic electron flow 5
AT1G61667	Protein of unknown function, DUF538
AT3G43700	BTB-POZ and MATH domain 6
AT1G59980	ARG1-like 2
AT3G46900	copper transporter 2
AT5G61420	myb domain protein 28
AT5G45830	delay of germination 1
AT3G54190	Transducin/WD40 repeat-like superfamily protein
AT4G36910	Cystathionine beta-synthase (CBS) family protein
AT4G39780	Integrase-type DNA-binding superfamily protein
AT5G52860	ABC-2 type transporter family protein
AT2G14910	unknown protein
AT3G23750	Leucine-rich repeat protein kinase family protein
AT4G39410	WRKY DNA-binding protein 13
AT3G52890	KCBP-interacting protein kinase
AT1G69580	Homeodomain-like superfamily protein
AT5G57070	hydroxyproline-rich glycoprotein family protein
AT1G33770	Protein kinase superfamily protein
AT2G23470	Protein of unknown function, DUF647
AT5G05440	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT3G16860	COBRA-like protein 8 precursor
AT2G10020	unknown protein
AT5G45280	Pectinacetylsterase family protein
AT1G71970	unknown protein
AT5G18270	Arabidopsis NAC domain containing protein 87
AT1G78090	trehalose-6-phosphate phosphatase
AT5G07440	glutamate dehydrogenase 2
AT2G22860	phytosulfokine 2 precursor
AT3G45260	C2H2-like zinc finger protein
AT3G56050	Protein kinase family protein
AT2G01670	nudix hydrolase homolog 17
AT1G46696	Protein of unknown function, DUF601
AT3G06130	Heavy metal transport/detoxification superfamily protein
AT5G08139	RING/U-box superfamily protein
AT1G22640	myb domain protein 3
AT1G07570	Protein kinase superfamily protein

AT5G44170	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G70710	glycosyl hydrolase 9B1
AT5G47240	nudix hydrolase homolog 8
AT4G23690	Disease resistance-responsive (dirigent-like protein) family protein
AT4G26210	Mitochondrial ATP synthase subunit G protein
AT1G44350	IAA-leucine resistant (ILR)-like gene 6
AT4G38940	Galactose oxidase/kelch repeat superfamily protein
AT3G12920	SBP (S-ribonuclease binding protein) family protein
AT3G61590	Galactose oxidase/kelch repeat superfamily protein
AT3G61590	Galactose oxidase/kelch repeat superfamily protein
AT5G44190	GOLDEN2-like 2
AT1G69560	myb domain protein 105
AT2G40110	Yippee family putative zinc-binding protein
AT4G08960	phosphotyrosyl phosphatase activator (PTPA) family protein
AT2G24330	Protein of unknown function (DUF2296)
AT3G11410	protein phosphatase 2CA
AT1G52320	unknown protein
AT1G25560	AP2/B3 transcription factor family protein
AT1G01360	regulatory component of ABA receptor 1
AT5G10780	unknown protein
AT5G59820	C2H2-type zinc finger family protein
AT2G40470	LOB domain-containing protein 15
AT1G30110	nudix hydrolase homolog 25
AT3G08660	Phototropic-responsive NPH3 family protein
AT4G11380	Adaptin family protein
AT5G47940	unknown protein
AT1G21080	DNAJ heat shock N-terminal domain-containing protein
AT2G32980	unknown protein
AT3G55980	salt-inducible zinc finger 1
AT1G02620	Ras-related small GTP-binding family protein
AT3G57550	guanylate kinase
AT1G12940	nitrate transporter2
AT4G37790	Homeobox-leucine zipper protein family
AT5G28620	protein kinase C-related
AT5G08130	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G65230	myb domain protein 53
AT2G45770	signal recognition particle receptor protein, chloroplast (FTSY)
AT3G27570	Sucrase/ferredoxin-like family protein
AT1G15550	gibberellin 3-oxidase 1
AT3G30820	Arabidopsis retrotransposon ORF-1 protein
AT1G01140	CBL-interacting protein kinase 9
AT5G28020	cysteine synthase D2
AT1G07540	TRF-like 2
AT5G36870	glucan synthase-like 9
AT2G47190	myb domain protein 2
AT4G14500	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT5G18610	Protein kinase superfamily protein
AT2G39380	exocyst subunit exo70 family protein H2
AT5G25930	Protein kinase family protein with leucine-rich repeat domain
AT1G43890	RAB GTPASE HOMOLOG B18
AT3G14450	CTC-interacting domain 9
AT1G02450	NIM1-interacting 1
AT1G35350	EXS (ERD1/XPR1/SYG1) family protein
AT1G47128	Granulin repeat cysteine protease family protein
AT4G16110	response regulator 2
AT2G15695	Protein of unknown function DUF829, transmembrane 53
AT3G49590	Autophagy-related protein 13
AT4G13810	receptor like protein 47
AT2G26260	3beta-hydroxysteroid-dehydrogenase/decarboxylase isoform 2
AT1G01260	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G12430	armadillo repeat kinesin 3

AT1G60060	Serine/threonine-protein kinase WNK (With No Lysine)-related
AT3G57950	unknown protein
AT3G27260	global transcription factor group E8
AT2G40690	NAD-dependent glycerol-3-phosphate dehydrogenase family protein
AT5G27700	Ribosomal protein S21e
AT5G04590	sulfite reductase
AT2G24740	SET domain group 21
AT4G35930	F-box family protein
AT5G12990	CLAVATA3/ESR-RELATED 40
AT5G02640	unknown protein
AT3G61470	photosystem I light harvesting complex gene 2
AT3G13890	myb domain protein 26
AT1G19835	Plant protein of unknown function (DUF869)
AT2G14110	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT2G45970	cytochrome P450, family 86, subfamily A, polypeptide 8
AT4G04210	plant UBX domain containing protein 4
AT5G59650	Leucine-rich repeat protein kinase family protein
AT2G28690	Protein of unknown function (DUF1635)
AT2G18960	H(+)-ATPase 1
AT3G21670	Major facilitator superfamily protein
AT1G06400	Ras-related small GTP-binding family protein
AT2G29670	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G20250	Raffinose synthase family protein
AT1G18710	myb domain protein 47
AT4G38950	ATP binding microtubule motor family protein
AT4G14230	CBS domain-containing protein with a domain of unknown function (DUF21)
AT4G11330	MAP kinase 5
AT2G39950	unknown protein
AT3G63010	alpha/beta-Hydrolases superfamily protein
AT4G39400	Leucine-rich receptor-like protein kinase family protein
AT5G43680	unknown protein
AT3G44330	unknown protein
AT5G37790	Protein kinase superfamily protein
AT3G29780	ralf-like 27
AT3G23240	ethylene response factor 1
AT2G34720	nuclear factor Y, subunit A4
AT2G17120	lysm domain GPI-anchored protein 2 precursor
AT1G10180	unknown protein
AT4G30020	PA-domain containing subtilase family protein
AT1G30360	Early-responsive to dehydration stress protein (ERD4)
AT2G14060	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G23300	Leucine-rich repeat protein kinase family protein
AT4G37470	alpha/beta-Hydrolases superfamily protein
AT3G47500	cycling DOF factor 3
AT4G35920	PLAC8 family protein
AT5G63580	flavonol synthase 2
AT1G76420	NAC (No Apical Meristem) domain transcriptional regulator superfamily protein
AT2G33320	Calcium-dependent lipid-binding (CaLB domain) family protein
AT4G37630	cyclin d5;1
AT1G50310	sugar transporter 9
AT4G12480	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT4G20010	plastid transcriptionally active 9
AT4G27980	Domain of unknown function (DUF3444)
AT5G51770	Protein kinase superfamily protein
AT3G50300	HXXXD-type acyl-transferase family protein
AT1G36000	LOB domain-containing protein 5
AT2G22490	Cyclin D2;1
AT1G50730	unknown protein
AT1G77750	Ribosomal protein S13/S18 family
AT3G14050	RELA/SPOT homolog 2
AT1G76510	ARID/BRIGHT DNA-binding domain-containing protein

AT2G13810	AGD2-like defense response protein 1
AT1G23860	RS-containing zinc finger protein 21
AT5G47280	ADR1-like 3
AT3G07190	B-cell receptor-associated protein 31-like
AT3G52780	Purple acid phosphatases superfamily protein
AT5G05690	Cytochrome P450 superfamily protein
AT3G26130	Cellulase (glycosyl hydrolase family 5) protein
AT1G43810	unknown protein
AT5G55120	galactose-1-phosphate guanylyltransferase (GDP)s;GDP-D-glucose phosphorylases;quercetin 4'-O-glucosyltransferases
AT5G67440	Phototropic-responsive NPH3 family protein
AT3G20370	TRAF-like family protein
AT5G35460	unknown protein
AT1G41830	SKU5-similar 6
AT3G57940	Domain of unknown function (DUF1726) ;Putative ATPase (DUF699)
AT3G14440	nine-cis-epoxycarotenoid dioxygenase 3
AT4G19440	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G15090	3-ketoacyl-CoA synthase 8
AT3G47370	Ribosomal protein S10p/S20e family protein
AT1G26620	Plant protein of unknown function (DUF863)
AT4G14490	SMAD/FHA domain-containing protein
AT3G11980	Jojoba acyl CoA reductase-related male sterility protein
AT2G31820	Ankyrin repeat family protein
AT2G22560	Kinase interacting (KIP1-like) family protein
AT3G52480	unknown protein
AT3G12840	unknown protein
AT5G25830	GATA transcription factor 12
AT2G01900	DNase I-like superfamily protein
AT4G12990	unknown protein
AT4G27400	Late embryogenesis abundant (LEA) protein-related
AT2G36960	TSL-kinase interacting protein 1
AT1G69420	DHHC-type zinc finger family protein
AT3G57370	Cyclin family protein
AT1G30140	unknown protein
AT5G51500	Plant invertase/pectin methylesterase inhibitor superfamily
AT2G45700	sterile alpha motif (SAM) domain-containing protein
AT3G48640	unknown protein
AT2G36090	F-box family protein
AT1G76620	Protein of unknown function, DUF547
AT2G46620	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G27380	succinate dehydrogenase 2-1
AT4G36520	Chaperone DnaJ-domain superfamily protein
AT3G05800	AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1
AT3G58890	RNI-like superfamily protein
AT5G66390	Peroxidase superfamily protein
AT1G07795	unknown protein
AT4G39000	glycosyl hydrolase 9B17
AT1G78260	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G51110	Plastid-lipid associated protein PAP / fibrillin family protein
AT5G28040	DNA-binding storekeeper protein-related transcriptional regulator
AT3G27360	Histone superfamily protein
AT1G72700	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT3G06200	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G33770	Inositol 1,3,4-trisphosphate 5/6-kinase family protein
AT3G61910	NAC domain protein 66
AT3G51430	Calcium-dependent phosphotriesterase superfamily protein
AT2G25270	unknown protein
AT4G35730	Regulator of Vps4 activity in the MVB pathway protein
AT5G23610	unknown protein
AT5G40480	embryo defective 3012
AT4G36110	SAUR-like auxin-responsive protein family

AT1G69750	cytochrome c oxidase 19-2
AT2G20110	Tesmin/TSO1-like CXC domain-containing protein
AT1G24490	OxaA/YidC-like membrane insertion protein
AT3G13810	indeterminate(ID)-domain 11
AT5G41180	leucine-rich repeat transmembrane protein kinase family protein
AT5G10140	K-box region and MADS-box transcription factor family protein
AT1G53325	F-box associated ubiquitination effector family protein
AT5G01020	Protein kinase superfamily protein
AT4G39680	SAP domain-containing protein
AT2G37210	lysine decarboxylase family protein
AT5G11040	TRS120
AT2G44830	Protein kinase superfamily protein
AT1G61900	unknown protein
AT3G63050	unknown protein
AT4G28080	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G02520	RNA-directed DNA polymerase (reverse transcriptase)-related family protein
AT1G71890	Major facilitator superfamily protein
AT3G48000	aldehyde dehydrogenase 2B4
AT1G77870	membrane-anchored ubiquitin-fold protein 5 precursor
AT2G42610	Protein of unknown function (DUF640)
AT4G24780	Pectin lyase-like superfamily protein
AT4G34138	UDP-glucosyl transferase 73B1
AT5G54510	Auxin-responsive GH3 family protein
AT1G79430	Homeodomain-like superfamily protein
AT1G54130	RELA/SPOT homolog 3
AT1G23440	Peptidase C15, pyroglutamyl peptidase I-like
AT5G55970	RING/U-box superfamily protein
AT1G59780	NB-ARC domain-containing disease resistance protein
AT3G50770	calmodulin-like 41
AT3G63210	Protein of unknown function (DUF581)
AT2G46610	RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G22640	MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein
AT5G64980	unknown protein
AT1G56160	myb domain protein 72
AT5G21100	Plant L-ascorbate oxidase
AT3G46570	Glycosyl hydrolase superfamily protein
AT1G49490	Leucine-rich repeat (LRR) family protein
AT1G23090	sulfate transporter 91
AT3G50500	SNF1-related protein kinase 2
AT3G20980	Gag-Pol-related retrotransposon family protein
AT2G41190	Transmembrane amino acid transporter family protein
AT1G17420	lipxygenase 3
AT4G12330	cytochrome P450, family 706, subfamily A, polypeptide 7
AT2G36950	Heavy metal transport/detoxification superfamily protein
AT3G05050	Protein kinase superfamily protein
AT3G08620	RNA-binding KH domain-containing protein
AT1G20580	Small nuclear ribonucleoprotein family protein
AT4G29810	MAP kinase kinase 2
AT3G27660	oleosin 4
AT1G73490	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G44835	YbaK/aminoacyl-tRNA synthetase-associated domain
AT5G15960	stress-responsive protein (KIN1) / stress-induced protein (KIN1)
AT5G13560	unknown protein
AT4G32760	ENTH/VHS/GAT family protein
AT4G23890	unknown protein
AT1G18190	golgin candidate 2
AT2G35230	VQ motif-containing protein
AT1G73050	Glucose-methanol-choline (GMC) oxidoreductase family protein
AT1G71330	non-intrinsic ABC protein 5
AT2G27090	Protein of unknown function (DUF630 and DUF632)
AT5G03690	Aldolase superfamily protein

AT5G47820	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT5G10020	Leucine-rich receptor-like protein kinase family protein
AT1G27000	Protein of unknown function (DUF1664)
AT2G21390	Coatomer, alpha subunit
AT5G50400	purple acid phosphatase 27
AT1G02300	Cysteine proteinases superfamily protein
AT5G12330	Lateral root primordium (LRP) protein-related
AT5G46250	RNA-binding protein
AT1G06225	CLAVATA3/ESR-RELATED 3
AT1G75460	ATP-dependent protease La (LON) domain protein
AT5G62940	Dof-type zinc finger DNA-binding family protein
AT5G24470	pseudo-response regulator 5
AT1G53050	Protein kinase superfamily protein
AT4G33560	Wound-responsive family protein
AT1G14690	microtubule-associated protein 65-7
AT1G49940	unknown protein
AT1G02330	unknown protein
AT1G51100	unknown protein
AT3G30350	unknown protein
AT1G76880	Duplicated homeodomain-like superfamily protein
AT2G17390	ankyrin repeat-containing 2B
AT4G36010	Pathogenesis-related thaumatin superfamily protein
AT1G65580	Endonuclease/exonuclease/phosphatase family protein
AT1G23870	trehalose-phosphatase/synthase 9
AT4G12360	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G56070	unknown protein
AT5G53540	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G41330	Glutaredoxin family protein
AT1G52690	Late embryogenesis abundant protein (LEA) family protein
AT5G02590	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G67720	Leucine-rich repeat protein kinase family protein
AT5G01190	laccase 10
AT2G41660	Protein of unknown function, DUF617
AT1G76520	Auxin efflux carrier family protein
AT3G04060	NAC domain containing protein 46
AT1G31300	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein
AT2G17260	glutamate receptor 2
AT2G41760	unknown protein
AT4G22010	SKU5 similar 4
AT3G20810	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT1G70430	Protein kinase superfamily protein
AT5G52110	Protein of unknown function (DUF2930)
AT4G08850	Leucine-rich repeat receptor-like protein kinase family protein
AT2G30020	Protein phosphatase 2C family protein
AT1G27980	dihydrosphingosine phosphate lyase
AT5G08590	SNF1-related protein kinase 2.1
AT3G09920	phosphatidyl inositol monophosphate 5 kinase
AT2G07050	cycloartenol synthase 1
AT1G48470	glutamine synthetase 1;5
AT1G70060	SIN3-like 4
AT3G20340	unknown protein
AT2G28360	SIT4 phosphatase-associated family protein
AT2G20970	unknown protein
AT1G09160	Protein phosphatase 2C family protein
AT2G34710	Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein
AT1G66860	Class I glutamine amidotransferase-like superfamily protein
AT5G45390	CLP protease P4
AT5G18130	unknown protein
AT5G18130	unknown protein
AT2G16950	transportin 1
AT2G02070	indeterminate(ID)-domain 5

AT5G18490	Plant protein of unknown function (DUF946)
AT1G09390	GDSL-like Lipase/Acylhydrolase superfamily protein
AT2G47410	WD40/YVTN repeat-like-containing domain;Bromodomain
AT2G34700	Pollen Ole e l allergen and extensin family protein
AT1G68530	3-ketoacyl-CoA synthase 6
AT4G34590	G-box binding factor 6
AT2G26880	AGAMOUS-like 41
AT2G32540	cellulose synthase-like B4
AT4G36810	geranylgeranyl pyrophosphate synthase 1
AT3G51830	SAC domain-containing protein 8
AT2G46690	SAUR-like auxin-responsive protein family
AT3G12290	Amino acid dehydrogenase family protein
AT3G27110	Peptidase family M48 family protein
AT3G56100	meristematic receptor-like kinase
AT3G53460	chloroplast RNA-binding protein 29
AT1G07870	Protein kinase superfamily protein
AT3G51860	cation exchanger 3
AT2G26510	Xanthine/uracil permease family protein
AT5G03290	isocitrate dehydrogenase V
AT1G04620	coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family
AT3G28480	Oxoglutarate/iron-dependent oxygenase
AT1G17700	prenylated RAB acceptor 1.F1
AT1G35560	TCP family transcription factor
AT2G35075	unknown protein
AT5G60750	CAAX amino terminal protease family protein
AT3G14067	Subtilase family protein
AT2G33380	Caleosin-related family protein
AT2G33380	Caleosin-related family protein
AT5G41100	unknown protein
AT1G22530	PATELLIN 2
AT5G43360	phosphate transporter 1;3
AT4G08920	cryptochrome 1
AT1G78080	related to AP2 4
AT5G24530	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT1G20330	sterol methyltransferase 2
AT3G44990	xyloglucan endo-transglycosylase-related 8
AT5G66570	PS II oxygen-evolving complex 1
AT3G24590	plastidic type i signal peptidase 1
AT2G19190	FLG22-induced receptor-like kinase 1
AT1G23780	F-box family protein
AT5G44230	Pentatricopeptide repeat (PPR) superfamily protein
AT3G10550	Myotubularin-like phosphatases II superfamily
AT1G68680	unknown protein
AT2G39230	LATERAL ORGAN JUNCTION
AT4G14000	Putative methyltransferase family protein
AT5G09760	Plant invertase/pectin methylesterase inhibitor superfamily
AT1G53645	hydroxyproline-rich glycoprotein family protein
AT4G11980	nudix hydrolase homolog 14
AT1G79080	Pentatricopeptide repeat (PPR) superfamily protein
AT1G43000	PLATZ transcription factor family protein
AT1G58370	glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein
AT3G15150	RING/U-box superfamily protein
AT5G10290	leucine-rich repeat transmembrane protein kinase family protein
AT5G16640	Pentatricopeptide repeat (PPR) superfamily protein
AT1G73500	MAP kinase kinase 9
AT3G51120	DNA binding;zinc ion binding;nucleic acid binding;nucleic acid binding
AT1G62800	aspartate aminotransferase 4
AT3G15880	WUS-interacting protein 2
AT5G64560	magnesium transporter 9
AT1G62830	LSD1-like 1
AT1G69920	glutathione S-transferase TAU 12

AT2G17600	Cysteine/Histidine-rich C1 domain family protein
AT4G00630	K ⁺ efflux antiporter 2
AT4G32390	Nucleotide-sugar transporter family protein
AT3G60510	ATP-dependent caseinolytic (Clp) protease/crotonase family protein
AT2G24810	Pathogenesis-related thaumatin superfamily protein
AT3G49560	Mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein
AT3G14670	unknown protein
AT1G07890	ascorbate peroxidase 1
AT4G38760	Protein of unknown function (DUF3414)
AT2G30210	laccase 3
AT1G73910	actin-related proteins 4A
AT3G57380	Glycosyltransferase family 61 protein
AT4G20800	FAD-binding Berberine family protein
AT1G29400	MEI2-like protein 5
AT5G53290	cytokinin response factor 3
AT1G71010	FORMS APLOID AND BINUCLEATE CELLS 1C
AT4G32750	unknown protein
AT2G23360	Plant protein of unknown function (DUF869)
AT5G08580	Calcium-binding EF hand family protein
AT5G61340	unknown protein
AT1G05850	Chitinase family protein
AT2G02810	UDP-galactose transporter 1
AT1G13950	eukaryotic elongation factor 5A-1
AT2G02950	phytochrome kinase substrate 1
AT1G63850	BTB/POZ domain-containing protein
AT2G28070	ABC-2 type transporter family protein
AT1G42470	Patched family protein
AT1G45616	receptor like protein 6
AT1G61500	S-locus lectin protein kinase family protein
AT3G23090	TPX2 (targeting protein for Xklp2) protein family
AT4G01730	DHHC-type zinc finger family protein
AT5G35730	EXS (ERD1/XPR1/SYG1) family protein
AT4G18600	SCAR family protein
AT4G18610	Protein of unknown function (DUF640)
AT5G07010	sulfotransferase 2A
AT5G65210	bZIP transcription factor family protein
AT3G24503	aldehyde dehydrogenase 2C4
AT3G16850	Pectin lyase-like superfamily protein
AT4G13450	Adenine nucleotide alpha hydrolases-like superfamily protein
AT3G04230	Ribosomal protein S5 domain 2-like superfamily protein
AT4G29700	Alkaline-phosphatase-like family protein
AT5G67190	DREB and EAR motif protein 2
AT5G65310	homeobox protein 5
AT4G01120	G-box binding factor 2
AT5G04400	NAC domain containing protein 77
AT5G49400	zinc knuckle (CCHC-type) family protein
AT3G51680	NAD(P)-binding Rossmann-fold superfamily protein
AT2G46370	Auxin-responsive GH3 family protein
AT3G08600	Protein of unknown function (DUF1191)
AT1G74670	Gibberellin-regulated family protein
AT5G06700	Plant protein of unknown function (DUF828)
AT5G45070	phloem protein 2-A8
AT1G26730	EXS (ERD1/XPR1/SYG1) family protein
AT3G12110	actin-11
AT3G15530	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G03680	Duplicated homeodomain-like superfamily protein
AT3G25480	Rhodanese/Cell cycle control phosphatase superfamily protein
AT3G05630	phospholipase D P2
AT3G11670	UDP-Glycosyltransferase superfamily protein
AT2G16710	Iron-sulphur cluster biosynthesis family protein
AT3G60570	expansin B5

AT3G21090	ABC-2 type transporter family protein
AT5G03880	Thioredoxin family protein
AT4G29010	Enoyl-CoA hydratase/isomerase family
AT5G17570	TatD related DNase
AT5G66730	C2H2-like zinc finger protein
AT4G39840	unknown protein
AT1G71720	Nucleic acid-binding proteins superfamily
AT2G06850	xyloglucan endotransglucosylase/hydrolase 4
AT1G08180	unknown protein
AT5G53410	unknown protein
AT5G07630	lipid transporters
AT1G58340	MATE efflux family protein
AT3G21770	Peroxidase superfamily protein
AT1G10030	homolog of yeast ergosterol28
AT2G03020	Heat shock protein HSP20/alpha crystallin family
AT2G19760	profilin 1
AT4G15310	cytochrome P450, family 702, subfamily A, polypeptide 3
AT2G43510	trypsin inhibitor protein 1
AT1G13250	galacturonosyltransferase-like 3
AT1G34130	staurosporin and temperature sensitive 3-like b
AT3G22630	20S proteasome beta subunit D1
AT4G20740	Pentatricopeptide repeat (PPR-like) superfamily protein
AT1G19090	receptor-like serine/threonine kinase 2
AT4G37870	phosphoenolpyruvate carboxykinase 1
AT2G20240	Protein of unknown function (DUF3741)
AT3G52960	Thioredoxin superfamily protein
AT1G27320	histidine kinase 3
AT5G28560	unknown protein
AT4G25630	fibrillarin 2
AT4G37550	Acetamidase/Formamidase family protein
AT1G07680	unknown protein
AT5G15540	PHD finger family protein
AT5G51830	pfkB-like carbohydrate kinase family protein
AT2G33500	B-box type zinc finger protein with CCT domain
AT3G12640	RNA binding (RRM/RBD/RNP motifs) family protein
AT3G13320	cation exchanger 2
AT5G42110	unknown protein
AT2G34180	CBL-interacting protein kinase 13
AT5G56870	beta-galactosidase 4
AT1G26960	homeobox protein 23
AT5G30520	unknown protein
AT1G30250	unknown protein
AT5G11160	adenine phosphoribosyltransferase 5
AT3G06520	agenet domain-containing protein
AT2G05600	F-box associated ubiquitination effector family protein
AT4G01130	GDSL-like Lipase/Acylhydrolase superfamily protein
AT1G21410	F-box/RNI-like superfamily protein
AT1G20980	squamosa promoter binding protein-like 14
AT1G69780	Homeobox-leucine zipper protein family
AT4G03510	RING membrane-anchor 1
AT4G25380	stress-associated protein 10
AT4G31720	TBP-associated factor II 15
AT4G04730	unknown protein
AT4G20270	Leucine-rich receptor-like protein kinase family protein
AT5G35410	Protein kinase superfamily protein
AT1G61890	MATE efflux family protein
AT1G12270	stress-inducible protein, putative
AT2G24550	unknown protein
AT4G22570	adenine phosphoribosyl transferase 3
AT1G70490	Ras-related small GTP-binding family protein
AT5G09800	ARM repeat superfamily protein

AT5G62620	Galactosyltransferase family protein
AT2G23410	cis-prenyltransferase
AT1G56210	Heavy metal transport/detoxification superfamily protein
AT2G32740	galactosyltransferase 13
AT3G05860	MADS-box transcription factor family protein
AT3G45620	Transducin/WD40 repeat-like superfamily protein
AT1G21060	Protein of unknown function, DUF547
AT1G66390	myb domain protein 90
AT2G34555	gibberellin 2-oxidase 3
AT1G01630	Sec14p-like phosphatidylinositol transfer family protein
AT2G46360	unknown protein
AT3G01480	cyclophilin 38
AT3G62790	NADH-ubiquinone oxidoreductase-related
AT1G09250	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G10150	Carbohydrate-binding protein
AT3G07310	Protein of unknown function (DUF760)
AT2G27590	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G06010	unknown protein
AT3G22530	unknown protein
AT4G25350	EXS (ERD1/XPR1/SYG1) family protein
AT1G28050	B-box type zinc finger protein with CCT domain
AT5G05060	Cystatin/monellin superfamily protein
AT3G15220	Protein kinase superfamily protein
AT4G05100	myb domain protein 74
AT1G26770	expansin A10
AT2G35900	unknown protein
AT2G43150	Proline-rich extensin-like family protein
AT4G12300	cytochrome P450, family 706, subfamily A, polypeptide 4
AT1G20693	high mobility group B2
AT5G51940	RNA polymerase Rpb6
AT5G66360	Ribosomal RNA adenine dimethylase family protein
AT5G06320	NDR1/HIN1-like 3
AT5G57800	Fatty acid hydroxylase superfamily
AT5G55680	glycine-rich protein
AT4G25560	myb domain protein 18
AT2G40800	unknown protein
AT3G61920	unknown protein
AT5G16720	Protein of unknown function, DUF593
AT2G16810	F-box and associated interaction domains-containing protein
AT1G26970	Protein kinase superfamily protein
AT1G32930	Galactosyltransferase family protein
AT1G65920	Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain
AT5G43270	squamosa promoter binding protein-like 2
AT1G67210	Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein
AT1G76040	calcium-dependent protein kinase 29
AT4G31860	Protein phosphatase 2C family protein
AT5G46900	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G56600	profilin 3
AT1G62850	Class I peptide chain release factor
AT4G38680	glycine rich protein 2
AT5G09810	actin 7
AT2G43160	ENTH/VHS family protein
AT3G12360	Ankyrin repeat family protein
AT1G70750	Protein of unknown function, DUF593
AT1G64290	F-box protein-related
AT1G21090	Cupredoxin superfamily protein
AT4G11000	Ankyrin repeat family protein
AT5G64310	arabinogalactan protein 1
AT2G37820	Cysteine/Histidine-rich C1 domain family protein
AT1G26270	Phosphatidylinositol 3- and 4-kinase family protein
AT1G62570	flavin-monooxygenase glucosinolate S-oxygenase 4

AT3G46480	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT5G14700	NAD(P)-binding Rossmann-fold superfamily protein
AT2G25080	glutathione peroxidase 1
AT3G28910	myb domain protein 30
AT2G04038	basic leucine-zipper 48
AT1G22275	Myosin heavy chain-related protein
AT2G36750	UDP-glucosyl transferase 73C1
AT1G19390	Wall-associated kinase family protein
AT3G08940	light harvesting complex photosystem II
AT5G18870	Inosine-uridine preferring nucleoside hydrolase family protein
AT1G18070	Translation elongation factor EF1A/initiation factor IF2gamma family protein
AT3G04920	Ribosomal protein S24e family protein
AT2G07760	Zinc knuckle (CCHC-type) family protein
AT4G24960	HVA22 homologue D
AT2G27860	UDP-D-apirose/UDP-D-xylose synthase 1
AT5G43920	transducin family protein / WD-40 repeat family protein
AT1G49430	long-chain acyl-CoA synthetase 2
AT1G53300	tetratricopeptide-repeat thioredoxin-like 1
AT3G26110	Anther-specific protein agp1-like
AT4G25450	non-intrinsic ABC protein 8
AT3G14060	unknown protein
AT3G47620	TEOSINTE BRANCHED, cycloidea and PCF (TCP) 14
AT5G03840	PEBP (phosphatidylethanolamine-binding protein) family protein
AT1G67090	ribulose biphosphate carboxylase small chain 1A
AT1G10710	poor homologous synapsis 1
AT3G11650	NDR1/HIN1-like 2
AT3G22970	Protein of unknown function (DUF506)
AT5G22510	alkaline/neutral invertase
AT5G06250	AP2/B3-like transcriptional factor family protein
AT5G20730	Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related
AT3G45160	Putative membrane lipoprotein
AT4G17460	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein
AT3G59190	F-box/RNI-like superfamily protein
AT4G23060	IQ-domain 22
AT1G72140	Major facilitator superfamily protein
AT1G22030	unknown protein
AT1G64970	gamma-tocopherol methyltransferase
AT5G27810	MADS-box transcription factor family protein
AT1G71000	Chaperone DnaJ-domain superfamily protein
AT5G58590	RAN binding protein 1
AT4G18710	Protein kinase superfamily protein
AT3G55880	Alpha/beta hydrolase related protein
AT4G11890	Protein kinase superfamily protein
AT4G34200	D-3-phosphoglycerate dehydrogenase
AT5G17610	unknown protein
AT1G49710	fucosyltransferase 12
AT2G39980	HXXXXD-type acyl-transferase family protein
AT2G20580	26S proteasome regulatory subunit S2 1A
AT4G29900	autoinhibited Ca(2+)-ATPase 10
AT1G47720	Primosome PriB/single-strand DNA-binding
AT4G37480	Chaperone DnaJ-domain superfamily protein
AT3G15850	fatty acid desaturase 5
AT3G61490	Pectin lyase-like superfamily protein
AT3G03040	F-box/RNI-like superfamily protein
AT1G66090	Disease resistance protein (TIR-NBS class)
AT2G01540	Calcium-dependent lipid-binding (CaLB domain) family protein
AT2G17730	NEP-interacting protein 2
AT4G29190	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT2G35750	unknown protein
AT2G27760	tRNAisopentenyltransferase 2
AT4G18840	Pentatricopeptide repeat (PPR-like) superfamily protein

AT1G68050	flavin-binding, kelch repeat, f box 1
AT2G39030	Acyl-CoA N-acyltransferases (NAT) superfamily protein
AT3G54990	Integrase-type DNA-binding superfamily protein
AT2G38800	Plant calmodulin-binding protein-related
AT3G47050	Glycosyl hydrolase family protein
AT4G22370	unknown protein
AT1G28490	syntaxin of plants 61
AT5G07830	glucuronidase 2
AT1G59650	Protein of unknown function (DUF1336)
AT3G60580	C2H2-like zinc finger protein
AT5G28910	unknown protein
AT4G15930	Dynein light chain type 1 family protein
AT1G78110	unknown protein
AT1G04250	AUX/IAA transcriptional regulator family protein
AT4G14930	Survival protein SurE-like phosphatase/nucleotidase
AT4G14940	amine oxidase 1
AT3G13682	LSD1-like2
AT5G62220	glycosyltransferase 18
AT4G01720	WRKY family transcription factor
AT4G14680	Pseudouridine synthase/archaeosine transglycosylase-like family protein
AT4G18290	potassium channel in Arabidopsis thaliana 2
AT1G55120	beta-fructofuranosidase 5
AT4G13460	SU(VAR)3-9 homolog 9
AT4G37610	BTB and TAZ domain protein 5
AT5G54530	Protein of unknown function, DUF538
AT5G24810	ABC1 family protein
AT5G54250	cyclic nucleotide-gated cation channel 4
AT2G27750	Surfeit locus protein 6
AT4G02320	Plant invertase/pectin methylesterase inhibitor superfamily
AT2G05160	CCCH-type zinc fingerfamily protein with RNA-binding domain
AT3G25640	Protein of unknown function, DUF617
AT1G31940	unknown protein
AT1G48095	unknown protein
AT2G01180	phosphatidic acid phosphatase 1
AT1G23390	Kelch repeat-containing F-box family protein
AT1G27990	unknown protein
AT1G66140	zinc finger protein 4
AT1G77510	PDI-like 1-2
AT4G35410	Clathrin adaptor complex small chain family protein
AT3G23540	alpha/beta-Hydrolases superfamily protein
AT3G62170	VANGUARD 1 homolog 2
AT4G16563	Eukaryotic aspartyl protease family protein
AT5G12460	Protein of unknown function (DUF604)
AT5G65100	Ethylene insensitive 3 family protein
AT5G65070	K-box region and MADS-box transcription factor family protein
AT5G67420	LOB domain-containing protein 37
AT3G07160	glucan synthase-like 10
AT5G06710	homeobox from Arabidopsis thaliana
AT5G27600	long-chain acyl-CoA synthetase 7
AT2G24150	heptahelical protein 3
AT1G51990	O-methyltransferase family protein
AT5G05780	RP non-ATPase subunit 8A
AT5G18690	arabinogalactan protein 25
AT5G43880	Protein of unknown function (DUF3741)
AT5G64790	O-Glycosyl hydrolases family 17 protein
AT4G12860	EF hand calcium-binding protein family
AT2G41390	Pollen Ole e 1 allergen and extensin family protein
AT5G43030	Cysteine/Histidine-rich C1 domain family protein
AT3G14310	pectin methylesterase 3
AT2G32510	mitogen-activated protein kinase kinase kinase 17
AT3G62010	unknown protein

AT4G17910	transferases, transferring acyl groups
AT1G11720	starch synthase 3
AT2G01820	Leucine-rich repeat protein kinase family protein
AT3G57610	adenylosuccinate synthase
AT5G24140	squalene monooxygenase 2
AT1G33790	jacalin lectin family protein
AT4G25360	TRICHOME BIREFRINGENCE-LIKE 18
AT3G21970	Domain of unknown function (DUF26)
AT4G33010	glycine decarboxylase P-protein 1
AT4G12690	Plant protein of unknown function (DUF868)
AT4G28250	expansin B3
AT5G07560	glycine-rich protein 20
AT2G31470	F-box and associated interaction domains-containing protein
AT5G62150	peptidoglycan-binding LysM domain-containing protein
AT2G45900	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related
AT5G18310	unknown protein
AT5G17860	calcium exchanger 7
AT5G52680	Copper transport protein family
AT5G49520	WRKY DNA-binding protein 48
AT1G44478	Cyclophilin
AT3G24190	Protein kinase superfamily protein
AT5G37560	RING/U-box superfamily protein
AT3G17120	unknown protein
AT4G24010	cellulose synthase like G1
AT4G36960	RNA-binding (RRM/RBD/RNP motifs) family protein
AT2G04690	Pyridoxamine 5'-phosphate oxidase family protein
AT4G37750	Integrase-type DNA-binding superfamily protein
AT3G13800	Metallo-hydrolase/oxidoreductase superfamily protein
AT3G07570	Cytochrome b561/ferric reductase transmembrane with DOMON related domain
AT1G32090	early-responsive to dehydration stress protein (ERD4)
AT2G02620	Cysteine/Histidine-rich C1 domain family protein
AT4G23960	F-box family protein
AT3G15160	unknown protein
AT3G12560	TRF-like 9
AT4G25990	CCT motif family protein
AT3G12820	myb domain protein 10
AT1G34370	C2H2 and C2HC zinc fingers superfamily protein
AT1G65190	Protein kinase superfamily protein
AT2G31400	genomes uncoupled 1
AT4G07380	unknown protein
AT2G41140	CDPK-related kinase 1
AT3G53040	late embryogenesis abundant protein, putative / LEA protein, putative
AT5G67480	BTB and TAZ domain protein 4
AT4G00810	60S acidic ribosomal protein family
AT1G33950	Avirulence induced gene (AIG1) family protein
AT2G20610	Tyrosine transaminase family protein
AT1G02580	SET domain-containing protein
AT5G55620	unknown protein
AT2G30860	glutathione S-transferase PHI 9
AT5G53370	pectin methylesterase PCR fragment F
AT3G59580	Plant regulator RWP-RK family protein
AT1G16500	unknown protein
AT2G28170	Cation/hydrogen exchanger family protein
AT1G75810	unknown protein
AT5G40420	oleosin 2
AT3G53410	RING/U-box superfamily protein
AT3G45130	lanosterol synthase 1
AT3G51370	Protein phosphatase 2C family protein
AT5G07580	Integrase-type DNA-binding superfamily protein
AT5G52160	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G48140	B12D protein

AT1G54210	Ubiquitin-like superfamily protein
AT5G57620	myb domain protein 36
AT1G36640	unknown protein
AT4G32800	Integrase-type DNA-binding superfamily protein
AT4G34110	poly(A) binding protein 2
AT3G45700	Major facilitator superfamily protein
AT1G48760	delta-adaptin
AT4G21910	MATE efflux family protein
AT1G20400	Protein of unknown function (DUF1204)
AT4G35830	aconitase 1
AT5G24030	SLAC1 homologue 3
AT2G03890	phosphoinositide 4-kinase gamma 7
AT2G23290	myb domain protein 70
AT2G41890	curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein
AT5G22600	FBD / Leucine Rich Repeat domains containing protein
AT4G32190	Myosin heavy chain-related protein
AT1G66450	Cysteine/Histidine-rich C1 domain family protein
AT1G28375	unknown protein
AT1G13680	PLC-like phosphodiesterases superfamily protein
AT1G34640	peptidases
AT1G30620	NAD(P)-binding Rossmann-fold superfamily protein
AT5G47530	Auxin-responsive family protein
AT1G54040	epithiospecifier protein
AT2G16500	arginine decarboxylase 1
AT5G07250	RHOMBOID-like protein 3
AT1G08340	Rho GTPase activating protein with PAK-box/P21-Rho-binding domain
AT1G71980	Protease-associated (PA) RING/U-box zinc finger family protein
AT1G60940	SNF1-related protein kinase 2.10
AT2G03500	Homeodomain-like superfamily protein
AT3G62550	Adenine nucleotide alpha hydrolases-like superfamily protein
AT2G46140	Late embryogenesis abundant protein
AT4G08840	pumilio 11
AT3G19140	RING/U-box superfamily protein
AT3G29010	Biotin/lipoate A/B protein ligase family
AT3G44550	fatty acid reductase 5
AT3G44100	MD-2-related lipid recognition domain-containing protein
AT4G26620	Sucrase/ferredoxin-like family protein
AT5G04020	calmodulin binding
AT1G13940	Plant protein of unknown function (DUF863)
AT1G23030	ARM repeat superfamily protein
AT3G43270	Plant invertase/pectin methylesterase inhibitor superfamily
AT1G69310	WRKY DNA-binding protein 57
AT3G23130	C2H2 and C2HC zinc fingers superfamily protein
AT4G37250	Leucine-rich repeat protein kinase family protein
AT2G26490	Transducin/WD40 repeat-like superfamily protein
AT1G77690	like AUX1 3
AT3G55000	tonneau family protein
AT1G18740	Protein of unknown function (DUF793)
AT3G12280	retinoblastoma-related 1
AT3G56720	unknown protein
AT1G43970	unknown protein
AT3G57040	response regulator 9
AT3G47510	unknown protein
AT1G16750	Protein of unknown function, DUF547
AT1G47370	Toll-Interleukin-Resistance (TIR) domain family protein
AT1G56040	HEAT/U-box domain-containing protein
AT4G18140	SCP1-like small phosphatase 4b
AT1G04120	multidrug resistance-associated protein 5
AT3G03680	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AT1G34510	Peroxidase superfamily protein
AT2G30750	cytochrome P450, family 71, subfamily A, polypeptide 12

AT5G01180	peptide transporter 5
AT3G44735	PHYTOSULFOKINE 3 PRECURSOR
AT1G17230	Leucine-rich receptor-like protein kinase family protein
AT2G38970	Zinc finger (C3HC4-type RING finger) family protein
AT1G29660	GDSL-like Lipase/Acylhydrolase superfamily protein
AT5G22850	Eukaryotic aspartyl protease family protein
AT5G54800	glucose 6-phosphate/phosphate translocator 1
AT1G13590	phytosulfokine 1 precursor
AT5G46830	NACL-inducible gene 1
AT5G28630	glycine-rich protein
AT4G30530	Class I glutamine amidotransferase-like superfamily protein
AT1G78360	glutathione S-transferase TAU 21
AT4G28100	unknown protein
AT5G25290	F-box family protein with a domain of unknown function (DUF295)
AT1G75390	basic leucine-zipper 44
AT3G58970	magnesium transporter 6
AT2G17550	unknown protein
AT3G03380	DegP protease 7
AT1G64260	MuDR family transposase
AT1G43900	Protein phosphatase 2C family protein
AT3G44370	Membrane insertion protein, OxaA/YidC with tetratricopeptide repeat domain
AT3G28920	homeobox protein 34
AT1G58100	TCP family transcription factor
AT1G09940	Glutamyl-tRNA reductase family protein
AT1G31240	Bromodomain transcription factor
AT5G11960	Protein of unknown function (DUF803)
AT2G28560	DNA repair (Rad51) family protein
AT4G14730	Bax inhibitor-1 family protein
AT1G76990	ACT domain repeat 3
AT4G17150	alpha/beta-Hydrolases superfamily protein
AT4G36050	endonuclease/exonuclease/phosphatase family protein
AT3G45430	Concanavalin A-like lectin protein kinase family protein
AT5G62070	IQ-domain 23
AT1G16530	ASYMMETRIC LEAVES 2-like 9
AT2G04220	Plant protein of unknown function (DUF868)
AT1G49620	Cyclin-dependent kinase inhibitor family protein
AT4G37540	LOB domain-containing protein 39
AT3G17730	NAC domain containing protein 57
AT4G31250	Leucine-rich repeat protein kinase family protein
AT4G13610	DNA (cytosine-5-)-methyltransferase family protein
AT1G31220	Formyl transferase
AT2G40440	BTB/POZ domain-containing protein
AT1G35670	calcium-dependent protein kinase 2
AT5G24010	Protein kinase superfamily protein
AT5G49660	Leucine-rich repeat transmembrane protein kinase family protein
AT4G04900	ROP-interactive CRIB motif-containing protein 10
AT1G67350	unknown protein
AT5G47990	cytochrome P450, family 705, subfamily A, polypeptide 5
AT1G59600	ZCW7
AT2G23700	Protein of unknown function, DUF547
AT5G42170	SGNH hydrolase-type esterase superfamily protein
AT2G17710	unknown protein
AT4G23180	cysteine-rich RLK (RECEPTOR-like protein kinase) 10
AT2G26760	Cyclin B1;4
AT5G10190	Major facilitator superfamily protein
AT3G27240	Cytochrome C1 family
AT5G46680	Pentatricopeptide repeat (PPR-like) superfamily protein
AT5G01600	ferretin 1
AT2G28890	poltergeist like 4
AT4G36550	ARM repeat superfamily protein
AT5G39950	thioredoxin 2

AT4G32020	unknown protein
AT3G08020	PHD finger family protein
AT4G35040	Basic-leucine zipper (bZIP) transcription factor family protein
AT5G59760	Protein of unknown function (DUF1635)
AT1G44830	Integrase-type DNA-binding superfamily protein
AT4G26940	Galactosyltransferase family protein
AT5G53190	Nodulin MtN3 family protein
AT1G51950	indole-3-acetic acid inducible 18
AT2G46940	unknown protein
AT5G55050	GDSL-like Lipase/Acylhydrolase superfamily protein
AT3G04810	NIMA-related kinase 2
AT3G18560	unknown protein
AT1G07430	highly ABA-induced PP2C gene 2
AT5G03870	Glutaredoxin family protein
AT1G30780	F-box associated ubiquitination effector family protein
AT4G12430	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT4G38570	probable CDP-diacylglycerol--inositol 3-phosphatidyltransferase 2
AT3G48510	unknown protein
AT3G52000	serine carboxypeptidase-like 36
AT1G52990	thioredoxin family protein
AT4G13520	small acidic protein 1
AT1G75830	low-molecular-weight cysteine-rich 67
AT5G27730	Protein of unknown function (DUF1624)
AT1G33110	MATE efflux family protein
AT1G02670	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G24480	Leucine-rich repeat (LRR) family protein
AT3G60560	unknown protein
AT5G13870	xyloglucan endotransglucosylase/hydrolase 5
AT4G34135	UDP-glucosyltransferase 73B2
AT4G31460	Ribosomal L28 family
AT5G38780	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G38195	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT1G73680	alpha dioxygenase
AT1G75450	cytokinin oxidase 5
AT1G51310	transferases;tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferases
AT3G15730	phospholipase D alpha 1
AT5G11900	Translation initiation factor SUI1 family protein
AT1G77790	Glycosyl hydrolase superfamily protein
AT1G31650	RHO guanyl-nucleotide exchange factor 14
AT1G02060	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G63840	RING/U-box superfamily protein
AT1G31120	K ⁺ uptake permease 10
AT4G38900	Basic-leucine zipper (bZIP) transcription factor family protein
AT2G18520	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G57810	tetraspanin15
AT3G13880	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G58680	ARM repeat superfamily protein
AT4G35620	Cyclin B2;2
AT1G67060	unknown protein
AT1G68190	B-box zinc finger family protein
AT5G43700	AUX/IAA transcriptional regulator family protein
AT3G02180	SPIRAL1-like3
AT2G14850	unknown protein
AT1G10740	alpha/beta-Hydrolases superfamily protein
AT5G03040	IQ-domain 2
AT3G25870	unknown protein
AT4G25030	unknown protein
AT1G28610	GDSL-like Lipase/Acylhydrolase superfamily protein
AT4G24970	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein
AT1G20640	Plant regulator RWP-RK family protein
AT1G49380	cytochrome c biogenesis protein family

AT1G68720	tRNA arginine adenosine deaminase
AT5G47370	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein
AT5G56980	unknown protein
AT3G61010	Ferritin/ribonucleotide reductase-like family protein
AT4G30580	Phospholipid/glycerol acyltransferase family protein
AT5G09450	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G38310	PYR1-like 4
AT4G11790	Pleckstrin homology (PH) domain superfamily protein
AT1G31230	aspartate kinase-homoserine dehydrogenase i
AT5G39250	F-box family protein
AT1G10640	Pectin lyase-like superfamily protein
AT3G19450	GroES-like zinc-binding alcohol dehydrogenase family protein
AT1G10490	Domain of unknown function (DUF1726) ;Putative ATPase (DUF699)
AT1G68510	LOB domain-containing protein 42
AT5G25810	Integrase-type DNA-binding superfamily protein
AT1G33560	Disease resistance protein (CC-NBS-LRR class) family
AT1G32540	lsd one like 1
AT4G26140	beta-galactosidase 12
AT2G02180	tobamovirus multiplication protein 3
AT1G23310	glutamate:glyoxylate aminotransferase
AT5G25560	CHY-type/CTCHY-type/RING-type Zinc finger protein
AT2G45340	Leucine-rich repeat protein kinase family protein
AT1G51300	alpha/beta-Hydrolases superfamily protein
AT3G12670	CTP synthase family protein
AT1G10560	plant U-box 18
AT5G02580	Plant protein 1589 of unknown function
AT1G25550	myb-like transcription factor family protein
AT5G51460	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT5G29050	Protein of unknown function (DUF3287)
AT1G04130	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G28760	Uncharacterized conserved protein (DUF2215)
AT1G04150	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AT5G10130	Pollen Ole e 1 allergen and extensin family protein
AT1G65480	PEBP (phosphatidylethanolamine-binding protein) family protein
AT3G04110	glutamate receptor 1.1
AT1G76550	Phosphofructokinase family protein
AT2G21870	copper ion binding;cobalt ion binding;zinc ion binding
AT4G05370	BCS1 AAA-type ATPase
AT3G03270	Adenine nucleotide alpha hydrolases-like superfamily protein
AT1G13270	methionine aminopeptidase 1B
AT3G19860	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G37140	MEI2 C-terminal RRM only like 1
AT3G30210	myb domain protein 121
AT3G50080	VIER F-box proteine 2
AT2G04795	unknown protein
AT1G76410	RING/U-box superfamily protein
AT2G21910	cytochrome P450, family 96, subfamily A, polypeptide 5
AT5G40750	FBD / Leucine Rich Repeat domains containing protein
AT1G45110	Tetrapyrrole (Corrin/Porphyrin) Methylases
AT5G39910	Pectin lyase-like superfamily protein
AT3G23730	xyloglucan endotransglucosylase/hydrolase 16
AT1G31360	RECQ helicase L2
AT2G24070	Family of unknown function (DUF566)
AT4G11160	Translation initiation factor 2, small GTP-binding protein
AT5G02730	CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein
AT1G01110	IQ-domain 18
AT3G43840	3-oxo-5-alpha-steroid 4-dehydrogenase family protein
AT2G30540	Thioredoxin superfamily protein
AT4G11310	Papain family cysteine protease
AT3G14200	Chaperone DnaJ-domain superfamily protein

AT1G11260	sugar transporter 1
AT5G35750	histidine kinase 2
AT1G53460	unknown protein
AT2G30520	Phototropic-responsive NPH3 family protein
AT4G13550	triglyceride lipases;triglyceride lipases
AT1G79780	Uncharacterised protein family (UPF0497)
AT2G28740	histone H4
AT4G14130	xyloglucan endotransglucosylase/hydrolase 15
AT5G02220	unknown protein
AT4G09000	general regulatory factor 1
AT5G53160	regulatory components of ABA receptor 3
AT5G38260	Protein kinase superfamily protein
AT1G28327	unknown protein
AT5G24580	Heavy metal transport/detoxification superfamily protein
AT1G10550	xyloglucan:xyloglucosyl transferase 33
AT2G28950	expansin A6
AT4G16970	Protein kinase superfamily protein
AT4G16980	arabinogalactan-protein family
AT2G32350	Ubiquitin-like superfamily protein
AT3G57930	unknown protein
AT2G14890	arabinogalactan protein 9
AT3G02875	Peptidase M20/M25/M40 family protein
AT1G05010	ethylene-forming enzyme
AT5G61650	CYCLIN P4;2
AT2G20930	SNARE-like superfamily protein
AT5G02030	POX (plant homeobox) family protein
AT1G64060	respiratory burst oxidase protein F
AT1G63420	Arabidopsis thaliana protein of unknown function (DUF821)
AT4G23580	Galactose oxidase/kelch repeat superfamily protein
AT5G60910	AGAMOUS-like 8
AT5G59380	methyl-CPG-binding domain 6
AT1G62750	Translation elongation factor EFG/EF2 protein
AT1G23340	Protein of Unknown Function (DUF239)
AT1G20440	cold-regulated 47
AT3G45060	high affinity nitrate transporter 2.6
AT5G63520	unknown protein
AT2G38530	lipid transfer protein 2
AT4G29100	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G11150	vacuolar ATP synthase subunit E1
AT5G28010	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT3G27280	prohibitin 4
AT2G17480	Seven transmembrane MLO family protein
AT3G62000	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G50760	galacturonosyltransferase-like 2
AT2G05840	20S proteasome subunit PAA2
AT4G17010	unknown protein
AT1G80330	gibberellin 3-oxidase 4
AT1G03090	methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA)
AT5G07760	formin homology 2 domain-containing protein / FH2 domain-containing protein
AT3G23290	Protein of unknown function (DUF640)
AT5G38760	Late embryogenesis abundant protein (LEA) family protein
AT5G58960	Plant protein of unknown function (DUF641)
AT5G06790	unknown protein
AT5G15750	Alpha-L RNA-binding motif/Ribosomal protein S4 family protein
AT3G51610	unknown protein
AT4G13030	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT1G76930	extensin 4
AT2G32580	Protein of unknown function (DUF1068)
AT3G23000	CBL-interacting protein kinase 7
AT5G62350	Plant invertase/pectin methylesterase inhibitor superfamily protein

AT1G35515	high response to osmotic stress 10
AT5G14210	Leucine-rich repeat protein kinase family protein
AT5G16990	Zinc-binding dehydrogenase family protein
AT2G29450	glutathione S-transferase tau 5
AT2G04070	MATE efflux family protein
AT3G46130	myb domain protein 48
AT4G18010	myo-inositol polyphosphate 5-phosphatase 2
AT2G23040	unknown protein
AT5G18650	CHY-type/CTCHY-type/RING-type Zinc finger protein
AT2G28830	PLANT U-BOX 12
AT1G44000	unknown protein
AT3G24100	Uncharacterised protein family SERF
AT1G30840	purine permease 4
AT3G03900	adenosine-5'-phosphosulfate (APS) kinase 3
AT1G17500	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT3G10210	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
AT2G17770	basic region/leucine zipper motif 27
AT5G24165	unknown protein
AT1G04160	myosin XI B
AT5G44610	microtubule-associated protein 18
AT1G14840	microtubule-associated proteins 70-4
AT4G37780	myb domain protein 87
AT3G11820	syntaxin of plants 121
AT3G05220	Heavy metal transport/detoxification superfamily protein
AT5G27920	F-box family protein
AT3G28860	ATP binding cassette subfamily B19
AT5G50130	NAD(P)-binding Rossmann-fold superfamily protein
AT5G18940	Mo25 family protein
AT2G46060	transmembrane protein-related
AT5G49060	Heat shock protein DnaJ, N-terminal with domain of unknown function (DUF1977)
AT3G21420	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT1G75880	SGNH hydrolase-type esterase superfamily protein
AT5G17240	SET domain group 40
AT1G18470	Transmembrane Fragile-X-F-associated protein
AT5G26230	unknown protein
AT5G04820	ovate family protein 13
AT4G22070	WRKY DNA-binding protein 31
AT3G07910	unknown protein
AT5G62420	NAD(P)-linked oxidoreductase superfamily protein
AT4G29940	pathogenesis related homeodomain protein A
AT4G38170	FAR1-related sequence 9
AT5G24050	Domain of unknown function (DUF313)
AT2G39710	Eukaryotic aspartyl protease family protein
AT3G28940	AIG2-like (avirulence induced gene) family protein
AT3G03840	SAUR-like auxin-responsive protein family
AT4G36930	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G60620	glycerol-3-phosphate acyltransferase 9
AT5G04600	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G17130	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT5G59880	actin depolymerizing factor 3
AT1G52300	Zinc-binding ribosomal protein family protein
AT3G11420	Protein of unknown function (DUF604)
AT4G02860	Phenazine biosynthesis PhzC/PhzF protein
AT4G34970	actin depolymerizing factor 9
AT5G48240	unknown protein
AT4G22650	unknown protein
AT1G05500	Calcium-dependent lipid-binding (CaLB domain) family protein
AT2G15860	unknown protein
AT5G06800	myb-like HTH transcriptional regulator family protein
AT5G58650	plant peptide containing sulfated tyrosine 1
AT1G67820	Protein phosphatase 2C family protein

AT2G28160	FER-like regulator of iron uptake
AT3G21070	NAD kinase 1
AT2G43880	Pectin lyase-like superfamily protein
AT2G33540	C-terminal domain phosphatase-like 3
AT4G22960	Protein of unknown function (DUF544)
AT4G17810	C2H2 and C2HC zinc fingers superfamily protein
AT1G56500	haloacid dehalogenase-like hydrolase family protein
AT1G61740	Sulfite exporter TauE/SafE family protein
AT4G26680	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G63200	Cystatin/monellin superfamily protein
AT5G21170	5'-AMP-activated protein kinase beta-2 subunit protein
AT4G14920	Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger protein
AT4G16370	oligopeptide transporter
AT5G05180	unknown protein
AT1G30090	Galactose oxidase/kelch repeat superfamily protein
AT2G02450	NAC domain containing protein 35
AT1G68570	Major facilitator superfamily protein
AT3G24650	AP2/B3-like transcriptional factor family protein
AT4G16640	Matrixin family protein
AT5G19870	Family of unknown function (DUF716)
AT1G63870	Disease resistance protein (TIR-NBS-LRR class) family
AT3G29370	unknown protein
AT4G18820	AAA-type ATPase family protein
AT2G13570	nuclear factor Y, subunit B7
AT4G22770	AT hook motif DNA-binding family protein
AT5G47060	Protein of unknown function (DUF581)
AT1G80050	adenine phosphoribosyl transferase 2
AT1G35470	SP1a/Ryanodine receptor (SPRY) domain-containing protein
AT3G29796	unknown protein
AT4G40040	Histone superfamily protein
AT5G19130	GPI transamidase component family protein / Gaa1-like family protein
AT1G31530	DNase I-like superfamily protein
AT2G19380	RNA recognition motif (RRM)-containing protein
AT3G15770	unknown protein
AT3G30380	alpha/beta-Hydrolases superfamily protein
AT5G25350	EIN3-binding F box protein 2
AT3G15630	unknown protein
AT4G34770	SAUR-like auxin-responsive protein family
AT4G30520	Leucine-rich repeat protein kinase family protein
AT1G26630	Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) protein
AT4G22190	unknown protein
AT3G43810	calmodulin 7
AT1G48880	TRICHOME BIREFRINGENCE-LIKE 7
AT5G44290	Protein kinase superfamily protein
AT3G26230	cytochrome P450, family 71, subfamily B, polypeptide 24
AT2G02820	myb domain protein 88
AT5G49540	Rab5-interacting family protein
AT1G13410	Tetratricopeptide repeat (TPR)-like superfamily protein
AT2G20750	expansin B1
AT2G30100	pentatricopeptide (PPR) repeat-containing protein
AT5G24270	Calcium-binding EF-hand family protein
AT2G44210	Protein of Unknown Function (DUF239)
AT3G47020	F-box and associated interaction domains-containing protein
AT1G22480	Cupredoxin superfamily protein
AT1G14890	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT3G15790	methyl-CPG-binding domain 11
AT5G15950	Adenosylmethionine decarboxylase family protein
AT1G48870	Transducin/WD40 repeat-like superfamily protein
AT5G44820	Nucleotide-diphospho-sugar transferase family protein
AT5G12440	CCCH-type zinc fingerfamily protein with RNA-binding domain
AT2G24762	glutamine dumper 4

AT3G61880	cytochrome p450 78a9
AT1G20960	U5 small nuclear ribonucleoprotein helicase, putative
AT1G58270	TRAF-like family protein
AT1G18540	Ribosomal protein L6 family protein
AT3G19050	phragmoplast orienting kinesin 2
AT1G55360	Protein of Unknown Function (DUF239)
AT5G65370	ENTH/ANTH/VHS superfamily protein
AT2G03040	emp24/gp25L/p24 family/GOLD family protein
AT5G13220	jasmonate-zim-domain protein 10
AT5G11060	KNOTTED1-like homeobox gene 4
AT3G18850	lysophosphatidyl acyltransferase 5
AT1G06410	trehalose-phosphatase/synthase 7
AT1G05470	DNase I-like superfamily protein
AT1G34670	myb domain protein 93
AT1G34540	cytochrome P450, family 94, subfamily D, polypeptide 1
AT3G25660	Amidase family protein
AT1G47610	Transducin/WD40 repeat-like superfamily protein
AT4G39900	unknown protein
AT3G29400	exocyst subunit exo70 family protein E1
AT4G39040	RNA-binding CRS1 / YhbY (CRM) domain protein
AT2G18840	Integral membrane Yip1 family protein
AT4G16990	disease resistance protein (TIR-NBS class), putative
AT1G47840	hexokinase 3
AT4G07515	Protein of unknown function (DUF784)
AT1G56230	Protein of unknown function (DUF1399)
AT3G13620	Amino acid permease family protein
AT3G13240	unknown protein
AT2G18160	basic leucine-zipper 2
AT5G20790	unknown protein
AT1G50620	RING/FYVE/PHD zinc finger superfamily protein
AT3G20830	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein
AT5G10650	RING/U-box superfamily protein
AT1G62660	Glycosyl hydrolases family 32 protein
AT1G47410	unknown protein
AT1G22430	GroES-like zinc-binding dehydrogenase family protein
AT4G10170	SNARE-like superfamily protein
AT3G44830	Lecithin:cholesterol acyltransferase family protein
AT2G39970	Mitochondrial substrate carrier family protein
AT3G61220	NAD(P)-binding Rossmann-fold superfamily protein
AT1G69970	CLAVATA3/ESR-RELATED 26
AT1G30820	CTP synthase family protein
AT5G14430	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G63410	Leucine-rich repeat protein kinase family protein
AT1G74650	myb domain protein 31
AT4G15050	Protein of Unknown Function (DUF239)
AT3G15260	Protein phosphatase 2C family protein
AT1G80580	Integrase-type DNA-binding superfamily protein
AT3G44380	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT2G18120	SHI-related sequence 4
AT4G05340	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G27820	beta glucosidase 9
AT3G23300	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G36510	Nucleic acid-binding proteins superfamily
AT1G49780	plant U-box 26
AT5G05140	Transcription elongation factor (TFIIS) family protein
AT5G16490	ROP-interactive CRIB motif-containing protein 4
AT1G73780	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT3G07270	GTP cyclohydrolase I
AT1G30210	TEOSINTE BRANCHED 1, cycloidea, and PCF family 24
AT5G26650	AGAMOUS-like 36
AT3G62620	sucrose-phosphatase-related

AT3G57850	unknown protein
AT3G25810	Terpenoid cyclases/Protein prenyltransferases superfamily protein
AT1G26090	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT3G57520	seed imbibition 2
AT5G28530	FAR1-related sequence 10

Table 6. SHR direct targets identified by ChIP-chip

Arabidopsis Genome Initiative (AGI) identification number	Short description
AT1G78090	trehalose-6-phosphate phosphatase
AT4G01960	unknown protein
AT2G40008	other RNA
AT3G19020	Leucine-rich repeat (LRR) family protein
AT2G45190	Plant-specific transcription factor YABBY family protein
AT3G19030	unknown protein
AT4G36040	Chaperone DnaJ-domain superfamily protein
AT5G35698	Plant thionin family protein
AT4G01720	WRKY family transcription factor
AT4G01120	G-box binding factor 2
AT3G61460	brassinosteroid-responsive RING-H2
AT4G39800	myo-inositol-1-phosphate synthase 1
AT3G63052	This gene encodes a small protein and has either evidence of transcription or purifying selection.
AT3G49960	Peroxidase superfamily protein
AT2G23140	RING/U-box superfamily protein with ARM repeat domain
AT5G49750	Leucine-rich repeat (LRR) family protein
AT1G67195	MIR414 (MICRORNA 414)
AT1G20320	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT1G23010	Cupredoxin superfamily protein
AT1G29920	chlorophyll A/B-binding protein 2
AT3G30775	Methylenetetrahydrofolate reductase family protein
AT5G64310	arabinogalactan protein 1
AT1G68680	unknown protein, LOCATED IN: chloroplast
AT2G23148	Plant self-incompatibility protein S1 family
AT1G49510	embryo defective 1273
AT1G61740	Sulfite exporter TauE/SafE family protein
AT2G30070	potassium transporter 1
AT3G49820	unknown protein
AT1G71880	sucrose-proton symporter 1
AT1G21590	Protein kinase protein with adenine nucleotide alpha hydrolases-like domain
AT5G03210	Encodes a small polypeptide contributing to resistance to potyvirus
AT5G13740	zinc induced facilitator 1
AT5G62060	F-box and associated interaction domains-containing protein
AT1G70550	Protein of Unknown Function (DUF239)
AT4G16447	unknown protein
AT4G08950	Phosphate-responsive 1 family protein
AT2G23142	Plant self-incompatibility protein S1 family
AT5G01810	CBL-interacting protein kinase 15
AT4G19700	SBP (S-ribonuclease binding protein) family protein
AT1G77765	unknown protein
AT2G29490	glutathione S-transferase TAU 1
AT5G54300	Protein of unknown function (DUF761)
AT4G32480	Protein of unknown function (DUF506)
AT2G23300	Leucine-rich repeat protein kinase family protein
AT5G14920	Gibberellin-regulated family protein
AT3G13000	Protein of unknown function, DUF547
AT3G03770	Leucine-rich repeat protein kinase family protein

AT5G51490	Plant invertase/pectin methylesterase inhibitor superfamily
AT5G11740	arabinogalactan protein 15
AT2G46530	auxin response factor 11
AT1G64380	Integrase-type DNA-binding superfamily protein
AT3G07360	plant U-box 9
AT2G28570	unknown protein
AT1G70370	polygalacturonase 2
AT3G19380	plant U-box 25
AT1G13260	related to ABI3/VP1 1
AT5G14120	Major facilitator superfamily protein
AT5G20250	Raffinose synthase family protein
AT2G28070	ABC-2 type transporter family protein
AT5G47940	unknown protein
AT3G52490	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
AT5G53420	CCT motif family protein
AT1G11260	sugar transporter 1
AT4G34131	UDP-glucosyl transferase 73B3
AT5G67350	
AT1G13245	ROTUNDIFOLIA like 17
AT3G50660	Cytochrome P450 superfamily protein
AT3G19390	Granulin repeat cysteine protease family protein
AT4G16444	molecular function unknown
AT1G25560	AP2/B3 transcription factor family protein
AT1G72630	ELF4-like 2
AT1G66170	RING/FYVE/PHD zinc finger superfamily protein
AT2G26740	soluble epoxide hydrolase
AT2G38120	Transmembrane amino acid transporter family protein
AT3G02580	sterol 1
AT5G59780	myb domain protein 59
AT5G57020	myristoyl-CoA:protein N-myristoyltransferase
AT3G50770	calmodulin-like 41
AT5G65340	Protein of unknown function, DUF617
AT4G36920	Integrase-type DNA-binding superfamily protein
AT5G11750	Ribosomal protein L19 family protein
AT1G32928	unknown protein
AT3G61470	photosystem I light harvesting complex gene 2
AT5G21940	unknown protein
AT3G23000	CBL-interacting protein kinase 7
AT3G15200	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G79130	SAUR-like auxin-responsive protein family
AT2G22520	unknown protein
AT1G30110	nudix hydrolase homolog 25
AT1G03840	C2H2 and C2HC zinc fingers superfamily protein
AT5G25280	serine-rich protein-related
AT4G31550	WRKY DNA-binding protein 11
AT4G13830	DNAJ-like 20
AT5G56610	Phosphotyrosine protein phosphatases superfamily protein
AT4G01250	WRKY family transcription factor
AT1G03610	Protein of unknown function (DUF789)
AT1G05010	ethylene-forming enzyme
AT1G15750	Transducin family protein / WD-40 repeat family protein
AT4G16370	oligopeptide transporter
AT1G03457	RNA-binding (RRM/RBD/RNP motifs) family protein
AT3G20340	Expression of the gene is downregulated in the presence of paraquat, an inducer of photooxidative stress.
AT5G27030	TOPELESS-related 3
AT5G25290	F-box family protein with a domain of unknown function (DUF295)
AT5G62410	structural maintenance of chromosomes 2
AT3G02150	plastid transcription factor 1
AT3G02140	AFP2 (ABI five-binding protein 2) family protein
AT5G39620	RAB GTPase homolog G1
AT2G31750	UDP-glucosyl transferase 74D1

AT3G06080	Plant protein of unknown function (DUF828)
AT1G05710	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G69760	unknown protein
AT3G16240	delta tonoplast integral protein
AT1G13210	autoinhibited Ca ²⁺ /ATPase II
AT1G13950	eukaryotic elongation factor 5A-1
AT1G19180	jasmonate-zim-domain protein 1
AT1G01550	Protein of unknown function (DUF793)
AT3G48630	unknown protein
AT3G19850	Phototropic-responsive NPH3 family protein
AT1G15670	Galactose oxidase/kelch repeat superfamily protein
AT5G52690	Copper transport protein family
AT1G13250	galacturonosyltransferase-like 3
AT1G06400	Ras-related small GTP-binding family protein
AT1G21000	PLATZ transcription factor family protein
AT1G32920	unknown protein, LOCATED IN: endomembrane system
AT4G37780	myb domain protein 87
AT4G30490	AFG1-like ATPase family protein
AT3G06070	unknown protein
AT5G62400	unknown protein
AT3G53450	Putative lysine decarboxylase family protein
AT2G45970	cytochrome P450, family 86, subfamily A, polypeptide 8
AT3G17120	unknown protein
AT1G21835	Plant thionin family protein
AT3G25717	ROTUNDIFOLIA like 16
AT3G05690	nuclear factor Y, subunit A2
AT3G04732	unknown protein
AT1G21810	Plant protein of unknown function (DUF869)
AT4G29700	Alkaline-phosphatase-like family protein
AT4G27740	Yippee family putative zinc-binding protein
AT1G30590	RNA polymerase I specific transcription initiation factor RRN3 protein
AT3G16830	TOPLESS-related 2
AT4G33080	AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein
AT5G11530	embryonic flower 1 (EMF1)
AT5G67070	ralf-like 34
AT4G32020	unknown protein
AT3G13810	indeterminate(ID)-domain 11
AT3G03990	alpha/beta-Hydrolases superfamily protein
AT3G47660	Regulator of chromosome condensation (RCC1) family protein
AT5G56075	Domain of unknown function (DUF2431)
AT3G15095	Encodes HCF243 (high chlorophyll fluorescence), a chloroplast-localized protein involved in the D1 protein stability of the photosystem II complex1
AT1G78050	phosphoglycerate/bisphosphoglycerate mutase
AT1G53170	ethylene response factor 8
AT4G38470	ACT-like protein tyrosine kinase family protein
AT4G37260	myb domain protein 73
AT1G80450	VQ motif-containing protein
AT5G13181	This gene encodes a small protein and has either evidence of transcription or purifying selection.
AT1G78240	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G20330	sterol methyltransferase 2
AT1G18075	MIR159/MIR159B; miRNA
AT3G05490	ralf-like 22
AT1G62510	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G13730	sigma factor 4
AT1G18740	Protein of unknown function (DUF793)
AT2G36420	unknown protein
AT1G02350	protoporphyrinogen oxidase-related
AT4G36870	BEL1-like homeodomain 2
AT5G52930	Protein of unknown function (DUF295)
AT3G56850	ABA-responsive element binding protein 3
AT4G36030	armadillo repeat only 3

AT5G42110	unknown protein
AT2G25480	TPX2 (targeting protein for Xklp2) protein family
AT1G67740	photosystem II BY
AT3G03773	HSP20-like chaperones superfamily protein
AT3G23030	indole-3-acetic acid inducible 2
AT5G62050	homolog of yeast oxidase assembly 1 (OXA1)
AT3G16800	Protein phosphatase 2C family protein
AT2G31620	Receptor-like protein kinase-related family protein
AT1G55120	beta-fructofuranosidase 5
AT3G02550	LOB domain-containing protein 41
AT2G20680	Glycosyl hydrolase superfamily protein
AT2G28060	5'-AMP-activated protein kinase beta-2 subunit protein
AT3G23020	Tetratricopeptide repeat (TPR)-like superfamily protein
AT3G05110	Domain of unknown function (DUF3444)
AT4G36860	LIM domain-containing protein
AT3G14310	pectin methylesterase 3
AT3G02570	Mannose-6-phosphate isomerase, type I
AT5G40440	mitogen-activated protein kinase kinase 3
AT1G12440	A20/AN1-like zinc finger family protein
AT4G24120	YELLOW STRIPE like 1
AT5G67450	zinc-finger protein 1
AT1G22400	UDP-Glycosyltransferase superfamily protein
AT3G63050	unknown protein
AT2G20613	DNA-binding storekeeper protein-related transcriptional regulator
AT2G35960	NDR1/HIN1-like 12
AT3G18080	B-S glucosidase 44
AT1G75500	Walls Are Thin 1
AT4G27730	oligopeptide transporter 1
AT1G02420	Pentatricopeptide repeat (PPR) superfamily protein
AT1G23030	ARM repeat superfamily protein
AT3G25770	allene oxide cyclase 2
AT3G04730	indoleacetic acid-induced protein 16
AT5G03290	isocitrate dehydrogenase V
AT2G30550	alpha/beta-Hydrolases superfamily protein
AT1G02065	squamosa promoter binding protein-like 8
AT4G13340	Leucine-rich repeat (LRR) family protein
AT1G78020	Protein of unknown function (DUF581)
AT4G25500	arginine/serine-rich splicing factor 35
AT5G05440	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT1G22190	Integrase-type DNA-binding superfamily protein
AT5G01720	RNI-like superfamily protein
AT1G02340	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT5G64690	neurofilament triplet H protein-related
AT1G68530	3-ketoacyl-CoA synthase 6
AT5G67460	O-Glycosyl hydrolases family 17 protein
AT1G01140	CBL-interacting protein kinase 9
AT3G06760	Drought-responsive family protein
AT1G22180	Sec14p-like phosphatidylinositol transfer family protein
AT3G22380	time for coffee
AT3G07460	Protein of unknown function, DUF538
AT4G32410	cellulose synthase 1
AT5G05590	phosphoribosylanthranilate isomerase 2
AT3G50820	photosystem II subunit O-2
AT2G27240	Aluminium activated malate transporter family protein
AT1G68450	VQ motif-containing protein
AT5G65207	unknown protein
AT4G27260	Auxin-responsive GH3 family protein
AT1G30330	auxin response factor 6
AT3G45230	hydroxyproline-rich glycoprotein family protein
AT4G15430	ERD (early-responsive to dehydration stress) family protein
AT5G43060	Granulin repeat cysteine protease family protein

AT5G03140	Concanavalin A-like lectin protein kinase family protein
AT1G04120	multidrug resistance-associated protein 5
AT3G12920	SBP (S-ribonuclease binding protein) family protein
AT1G19835	Plant protein of unknown function (DUF869)
AT1G45976	S-ribonuclease binding protein 1
AT5G01850	Protein kinase superfamily protein
AT3G48350	Cysteine proteinases superfamily protein
AT1G71980	Protease-associated (PA) RING/U-box zinc finger family protein
AT2G45340	Leucine-rich repeat protein kinase family protein
AT5G62390	BCL-2-associated athanogene 7
AT2G34720	nuclear factor Y, subunit A4
AT4G36850	PQ-loop repeat family protein / transmembrane family protein
AT4G30270	xyloglucan endotransglucosylase/hydrolase 24
AT5G25190	Integrase-type DNA-binding superfamily protein
AT3G14205	Phosphoinositide phosphatase family protein
AT3G19580	zinc-finger protein 2
AT3G11700	FASCI-LIN-like arabinogalactan protein 18 precursor
AT4G22980	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein
AT1G24170	Nucleotide-diphospho-sugar transferases superfamily protein
AT1G24540	cytochrome P450, family 86, subfamily C, polypeptide 1
AT3G04120	glyceraldehyde-3-phosphate dehydrogenase C subunit 1
AT4G37608	unknown protein
AT1G19490	Basic-leucine zipper (bZIP) transcription factor family protein
AT3G04000	NAD(P)-binding Rossmann-fold superfamily protein
AT5G09490	Ribosomal protein S19 family protein
AT4G38670	Pathogenesis-related thaumatin superfamily protein
AT1G17380	jasmonate-zim-domain protein 5
AT4G23060	IQ-domain 22
AT4G18710	Protein kinase superfamily protein
AT2G22460	Protein of unknown function, DUF617
AT5G40430	myb domain protein 22
AT1G51300	alpha/beta-Hydrolases superfamily protein
AT5G65210	bZIP transcription factor family protein
AT4G17453	This gene encodes a small protein and has either evidence of transcription or purifying selection
AT1G30410	multidrug resistance-associated protein 13
AT1G51950	indole-3-acetic acid inducible 18
AT1G23100	GroES-like family protein
AT2G27510	ferredoxin 3
AT2G37200	Uncharacterised protein family (UPF0497)
AT3G12560	TRF-like 9
AT3G23750	Leucine-rich repeat protein kinase family protein
AT2G35980	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT5G42170	SGNH hydrolase-type esterase superfamily protein
AT1G68550	Integrase-type DNA-binding superfamily protein
AT1G68552	conserved peptide upstream open reading frame 53
AT2G40750	WRKY DNA-binding protein 54
AT1G47870	winged-helix DNA-binding transcription factor family protein
AT1G44350	IAA-leucine resistant (ILR)-like gene 6
AT5G10310	unknown protein
AT4G26690	PLC-like phosphodiesterase family protein
AT4G37550	Acetamidase/Formamidase family protein
AT1G16510	SAUR-like auxin-responsive protein family
AT5G14820	Pentatricopeptide repeat (PPR) superfamily protein
AT5G19190	unknown protein
AT4G17500	ethylene responsive element binding factor 1
AT3G48640	unknown protein
AT1G27290	unknown protein
AT1G77510	PDI-like 1-2
AT5G16030	unknown protein
AT1G19350	Brassinosteroid signalling positive regulator (BZR1) family protein
AT4G40050	Protein of unknown function (DUF3550/UPF0682)

AT1G20440	cold-regulated 47
AT3G63040	unknown protein
AT4G30020	PA-domain containing subtilase family protein
AT2G15640	F-box family protein
AT4G29905	unknown protein
AT1G20340	Cupredoxin superfamily protein
AT5G62430	cycling DOF factor 1
AT5G07580	Integrase-type DNA-binding superfamily protein
AT4G15800	ralf-like 33
AT2G29980	fatty acid desaturase 3
AT2G28755	UDP-D-glucuronate carboxy-lyase-related
AT5G09440	EXORDIUM like 4
AT3G12320	unknown protein
AT3G52480	unknown protein
AT3G48390	MA3 domain-containing protein
AT4G18010	myo-inositol polyphosphate 5-phosphatase 2
AT3G28920	homeobox protein 34
AT1G64385	unknown protein, LOCATED IN: endomembrane
AT2G01850	endoxyloglucan transferase A3
AT3G57840	Plant self-incompatibility protein S1 family
AT4G37590	Phototropic-responsive NPH3 family protein
AT4G37250	Leucine-rich repeat protein kinase family protein
AT4G18890	BES1/BZR1 homolog 3
AT5G19900	PRLI-interacting factor, putative
AT5G54365	pre-tRNA
AT4G17900	PLATZ transcription factor family protein
AT5G39630	Vesicle transport v-SNARE family protein
AT4G00630	K ⁺ efflux antiporter 2
AT1G76190	SAUR-like auxin-responsive protein family
AT1G04400	cryptochrome 2
AT5G45470	Protein of unknown function (DUF594)
AT1G04130	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G42790	proteasome alpha subunit F1
AT5G17847	unknown protein
AT4G03210	xyloglucan endotransglucosylase/hydrolase 9
AT1G09260	Chaperone DnaJ-domain superfamily protein
AT1G28310	Dof-type zinc finger DNA-binding family protein
AT5G46730	glycine-rich protein
AT5G44160	C2H2-like zinc finger protein
AT4G20930	6-phosphogluconate dehydrogenase family protein
AT2G39180	CRINKLY4 related 2
AT1G01040	dicer-like 1
AT1G01046	MIR838a; miRNA
AT5G11090	serine-rich protein-related
AT3G13080	multidrug resistance-associated protein 3
AT5G54200	Transducin/WD40 repeat-like superfamily protein
AT4G13395	ROTUNDIFOLIA like 12
AT1G14770	RING/FYVE/PHD zinc finger superfamily protein
AT1G07010	Calcineurin-like metallo-phosphoesterase superfamily protein
AT4G14730	Bax inhibitor-1 family protein
AT5G03370	acylphosphatase family
AT1G72520	PLAT/LH2 domain-containing lipoxygenase family protein
AT4G01080	TRICHOME BIREFRINGENCE-LIKE 26
AT5G59880	actin depolymerizing factor 3
AT5G49740	ferric reduction oxidase 7
AT5G49540	Rab5-interacting family protein
AT1G14720	xyloglucan endotransglucosylase/hydrolase 28
AT2G42885	Defensin-like (DEFL) family protein
AT4G00140	Calcium-binding EF-hand family protein
AT5G67340	ARM repeat superfamily protein
AT1G25540	phytochrome and flowering time regulatory protein (PFT1)

AT1G76900	tubby like protein 1
AT5G10550	global transcription factor group E2
AT3G26511	unknown protein
AT5G56100	glycine-rich protein / oleosin
AT5G49410	unknown protein
AT4G20780	calmodulin like 42
AT5G01710	methyltransferases
AT5G01712	conserved peptide upstream open reading frame 48
AT1G61260	Protein of unknown function (DUF761)
AT4G32160	Phox (PX) domain-containing protein
AT2G35490	Plastid-lipid associated protein PAP / fibrillin family protein
AT2G35500	shikimate kinase like 2
AT1G21830	unknown protein
AT3G60570	expansin B5
AT1G73600	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G73602	conserved peptide upstream open reading frame 32
AT1G14330	Galactose oxidase/kelch repeat superfamily protein
AT2G45900	Phosphatidylinositol N-acetylglucosaminyltransferase subunit P-related
AT5G03380	Heavy metal transport/detoxification superfamily protein
AT1G63430	Leucine-rich repeat protein kinase family protein
AT1G30825	Arp2/3 complex, 34 kD subunit p34-Arc
AT1G01580	ferric reduction oxidase 2
AT2G38325	MIR390A; miRNA
AT1G78080	related to AP2 4
AT5G03520	RAB GTPase homolog 8C
AT5G46140	Protein of unknown function (DUF295)
AT1G80470	F-box/RNI-like/FBD-like domains-containing protein
AT5G65683	Zinc finger (C3HC4-type RING finger) family protein
AT4G28230	unknown protein
AT4G28240	Wound-responsive family protein
AT4G08949	This gene encodes a small protein and has either evidence of transcription or purifying selection.
AT2G36090	F-box family protein
AT5G07710	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
AT1G61890	MATE efflux family protein
AT1G32190	alpha/beta-Hydrolases superfamily protein
AT5G41460	Protein of unknown function (DUF604)
AT1G67510	Leucine-rich repeat protein kinase family protein
AT2G46330	arabinogalactan protein 16
AT5G53910	RING/U-box superfamily protein
AT4G39403	polaris
AT1G18710	myb domain protein 47
AT1G63090	phloem protein 2-A11
AT1G72060	serine-type endopeptidase inhibitors
AT1G10410	Protein of unknown function (DUF1336)
AT3G50080	VIER F-box proteine 2
AT5G19120	Eukaryotic aspartyl protease family protein
AT3G05120	alpha/beta-Hydrolases superfamily protein
AT1G32230	WWE protein-protein interaction domain protein family
AT5G49520	WRKY DNA-binding protein 48
AT5G24890	unknown protein
AT1G17620	Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family
AT1G14920	GRAS family transcription factor family protein
AT4G38520	Protein phosphatase 2C family protein
AT4G39404	other RNA
AT5G01849	This gene encodes a small protein and has either evidence of transcription or purifying selection.
AT1G76880	Duplicated homeodomain-like superfamily protein
AT2G27850	pre-tRNA
AT4G37790	Homeobox-leucine zipper protein family
AT1G67210	Proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein
AT3G27960	Tetratricopeptide repeat (TPR)-like superfamily protein
AT1G07090	Protein of unknown function (DUF640)

AT2G28950	expansin A6
AT4G38860	SAUR-like auxin-responsive protein family
AT5G41470	Nuclear transport factor 2 (NTF2) family protein
AT5G65700	Leucine-rich receptor-like protein kinase family protein
AT4G34760	SAUR-like auxin-responsive protein family
AT3G50760	galacturonosyltransferase-like 2
AT5G18610	Protein kinase superfamily protein
AT2G18750	Calmodulin-binding protein
AT5G16010	3-oxo-5-alpha-steroid 4-dehydrogenase family protein
AT4G28720	Flavin-binding monooxygenase family protein
AT3G19590	Transducin/WD40 repeat-like superfamily protein
AT3G05840	Protein kinase superfamily protein
AT1G64625	Serine/threonine-protein kinase WNK (With No Lysine)-related
AT1G36060	Integrase-type DNA-binding superfamily protein
AT4G23190	cysteine-rich RLK (RECEPTOR-like protein kinase) 11
AT1G01490	Heavy metal transport/detoxification superfamily protein
AT4G25640	detoxifying efflux carrier 35
AT4G21680	NITRATE TRANSPORTER 1.8
AT2G01570	GRAS family transcription factor family protein
AT5G58680	ARM repeat superfamily protein
AT3G16860	COBRA-like protein 8 precursor
AT5G40930	translocase of outer membrane 20-4
AT3G18485	iaa-leucine resistant 2
AT5G66816	unknown protein
AT3G13750	beta galactosidase 1
AT5G17300	Homeodomain-like superfamily protein
AT2G39675	TAS1C; other RNA
AT5G10290	leucine-rich repeat transmembrane protein kinase family protein
AT5G57510	unknown protein
AT2G16630	Pollen Ole e 1 allergen and extensin family protein
AT2G34355	Major facilitator superfamily protein
AT5G07290	MEI2-like 4
AT5G05860	UDP-glucosyl transferase 76C2
AT5G08330	TCP family transcription factor
AT5G10840	Endomembrane protein 70 protein family
AT3G02315	pre-tRNA
AT1G72200	RING/U-box superfamily protein
AT5G14110	Protein of unknown function (DUF 3339)
AT5G04560	HhH-GPD base excision DNA repair family protein
AT2G46630	unknown protein; LOCATED IN: chloroplast
AT4G36770	UDP-Glycosyltransferase superfamily protein
AT2G25470	receptor like protein 21
AT4G23760	Cox19-like CHCH family protein
AT1G13350	Protein kinase superfamily protein
AT2G31751	unknown gene
AT5G67440	Phototropic-responsive NPH3 family protein
AT2G41340	RNA polymerase II fifth largest subunit, D
AT4G27510	unknown protein
AT3G17230	invertase/pectin methylesterase inhibitor family protein
AT5G64770	unknown protein
AT3G50920	Phosphatidic acid phosphatase (PAP2) family protein
AT5G24870	RING/U-box superfamily protein
AT1G01260	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT2G22770	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G05060	PapD-like superfamily protein
AT3G11590	unknown protein
AT2G39030	Acyl-CoA N-acyltransferases (NAT) superfamily protein
AT1G21010	unknown protein
AT3G10530	Transducin/WD40 repeat-like superfamily protein
AT2G30040	mitogen-activated protein kinase kinase kinase 14
AT5G15160	BANQUO 2

AT3G48425	DNAse I-like superfamily protein
AT1G30810	Transcription factor jumonji (jmi) family protein / zinc finger (C5HC2 type) family protein
AT2G45620	Nucleotidyltransferase family protein
AT4G17615	calcineurin B-like protein 1
AT5G66780	unknown protein
AT1G74950	TIFY domain/Divergent CCT motif family protein
AT5G56080	nicotianamine synthase 2
AT1G09520	BEST Arabidopsis thaliana protein match is: PHD finger family protein (TAIR:AT3G17460.1)
AT4G00650	FRIGIDA-like protein
AT3G54826	Zim17-type zinc finger protein
AT1G28330	dormancy-associated protein-like 1
AT2G42880	MAP kinase 20
AT4G00440	Protein of unknown function (DUF3741)
AT5G12010	unknown protein
AT3G51990	Protein kinase superfamily protein
AT2G23700	Protein of unknown function, DUF547
AT4G25470	C-repeat/DRE binding factor 2
AT5G58950	Protein kinase superfamily protein
AT4G25480	dehydration response element B1A
AT5G56840	myb-like transcription factor family protein
AT4G35940	unknown protein
AT4G20010	plastid transcriptionally active 9
AT3G04855	unknown protein
AT2G36590	proline transporter 3
AT5G18670	beta-amylase 3
AT1G24120	ARG1-like 1
AT1G72180	Leucine-rich receptor-like protein kinase family protein
AT1G68570	Major facilitator superfamily protein
AT5G15350	early nodulin-like protein 17
AT1G76580	Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein
AT5G56090	cytochrome c oxidase 15
AT5G02020	Encodes a protein involved in salt tolerance, names SIS (Salt Induced Serine rich).
AT1G73560	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT4G23920	UDP-D-glucose/UDP-D-galactose 4-epimerase 2
AT1G24265	Protein of unknown function (DUF1664)
AT1G03870	FASCICLIN-like arabinogalactan 9
AT2G44500	O-fucosyltransferase family protein
AT1G21050	Protein of unknown function, DUF617
AT4G37080	Protein of unknown function, DUF547
AT2G22510	hydroxyproline-rich glycoprotein family protein
AT3G05800	AtBS1(activation-tagged BRI1 suppressor 1)-interacting factor 1
AT1G23710	Protein of unknown function (DUF1645)
AT3G19100	Protein kinase superfamily protein
AT5G24030	SLAC1 homologue 3
AT4G37320	cytochrome P450, family 81, subfamily D, polypeptide 5
AT1G12380	unknown protein
AT3G02170	longifolia2
AT2G01680	Ankyrin repeat family protein
AT4G17460	Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein
AT4G05071	This gene encodes a small protein and has either evidence of transcription or purifying selection.
AT4G18900	Transducin/WD40 repeat-like superfamily protein
AT5G45360	F-box family protein
AT1G09070	soybean gene regulated by cold-2
AT1G73840	hydroxyproline-rich glycoprotein family protein
AT5G23280	TCP family transcription factor
AT5G13100	unknown protein
AT3G07350	Protein of unknown function (DUF506)
AT5G43810	Stabilizer of iron transporter SufD / Polynucleotidyl transferase
AT3G56000	cellulose synthase like A14
AT1G66140	zinc finger protein 4
AT3G27170	chloride channel B

AT1G71890	Major facilitator superfamily protein
AT4G23750	cytokinin response factor 2
AT5G52260	myb domain protein 19
AT5G44090	Calcium-binding EF-hand family protein
AT4G40060	homeobox protein 16
AT3G24050	GATA transcription factor 1
AT5G06865	other RNA
AT5G06870	polygalacturonase inhibiting protein 2
AT3G15770	unknown protein
AT4G36780	BES1/BZR1 homolog 2
AT1G72430	SAUR-like auxin-responsive protein family
AT5G15210	homeobox protein 30
AT1G30380	photosystem I subunit K
AT1G13360	unknown protein
AT5G46740	ubiquitin-specific protease 21
AT5G06390	FASCICLIN-like arabinogalactan protein 17 precursor
AT5G56010	heat shock protein 81-3
AT2G35940	BEL1-like homeodomain 1
AT1G03860	prohibitin 2
AT1G04000	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44060.1); Has 62 Blast hits to 62 prot....
AT1G68845	unknown protein
AT2G34450	HMG-box (high mobility group) DNA-binding family protein
AT4G37610	BTB and TAZ domain protein 5
AT3G62200	Putative endonuclease or glycosyl hydrolase
AT4G38680	glycine rich protein 2
AT5G57690	diacylglycerol kinase 4
AT4G27310	B-box type zinc finger family protein
AT3G61480	Quinoprotein amine dehydrogenase, beta chain-like; RIC1-like guanyl-nucleotide exchange factor
AT2G02070	indeterminate(ID)-domain 5
AT3G02910	AIG2-like (avirulence induced gene) family protein
AT1G35560	TCP family transcription factor
AT1G70710	glycosyl hydrolase 9B1
AT3G19680	Protein of unknown function (DUF1005)
AT4G03400	Auxin-responsive GH3 family protein
AT1G30360	Early-responsive to dehydration stress protein (ERD4)
AT3G05200	RING/U-box superfamily protein
AT5G67240	small RNA degrading nuclease 3
AT5G66815	unknown protein
AT2G06520	photosystem II subunit X
AT3G48530	SNF1-related protein kinase regulatory subunit gamma 1
AT3G49970	Phototropic-responsive NPH3 family protein
AT5G09620	Octicosapeptide/Phox/Bem1p family protein
AT3G52740	unknown protein
AT4G17250	unknown protein
AT4G39100	PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein
AT1G70100	unknown protein
AT5G25220	KNOTTED1-like homeobox gene 3
AT5G25350	EIN3-binding F box protein 2
AT4G36648	other RNA
AT3G25905	CLAVATA3/ESR-RELATED 27
AT4G16780	homeobox protein 2
AT5G13180	NAC domain containing protein 83
AT1G03040	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT4G00310	Putative membrane lipoprotein
AT3G15210	ethylene responsive element binding factor 4
AT1G32640	Basic helix-loop-helix (bHLH) DNA-binding family protein
AT4G16980	arabinogalactan-protein family
AT3G14067	Subtilase family protein
AT4G35800	RNA polymerase II large subunit
AT2G48030	DNAse I-like superfamily protein

AT4G08920	cryptochrome 1
AT5G51590	AT hook motif DNA-binding family protein
AT1G80460	Actin-like ATPase superfamily protein
AT5G52940	Protein of unknown function (DUF295)
AT5G05250	unknown protein
AT5G65660	hydroxyproline-rich glycoprotein family protein
AT3G05910	Pectinacetylase family protein
AT2G43360	Radical SAM superfamily protein
AT2G43370	RNA-binding (RRM/RBD/RNP motifs) family protein
AT5G58690	phosphatidylinositol-specific phospholipase C5
AT3G12700	Eukaryotic aspartyl protease family protein
AT5G15340	Pentatricopeptide repeat (PPR) superfamily protein
AT3G24480	Leucine-rich repeat (LRR) family protein
AT5G45370	nodulin MtN21 /EamA-like transporter family protein
AT4G29190	Zinc finger C-x8-C-x5-C-x3-H type family protein
AT1G02640	beta-xylosidase 2
AT4G29780	unknown protein
AT1G59750	auxin response factor 1
AT2G23350	poly(A) binding protein 4
AT1G10020	Protein of unknown function (DUF1005)
AT3G46660	UDP-glucosyl transferase 76E12
AT5G54360	C2H2-like zinc finger protein
AT3G47500	cycling DOF factor 3
AT3G21890	B-box type zinc finger family protein
AT2G39880	myb domain protein 25
AT5G60890	myb domain protein 34
AT4G04640	ATPase, F1 complex, gamma subunit protein
AT4G25490	C-repeat/DRE binding factor 1
AT5G23850	Arabidopsis thaliana protein of unknown function (DUF821)
AT1G75820	Leucine-rich receptor-like protein kinase family protein
AT4G39070	B-box zinc finger family protein
AT4G11300	Protein of unknown function (DUF793)
AT3G23820	UDP-D-glucuronate 4-epimerase 6
AT2G36020	HVA22-like protein J
AT2G47180	galactinol synthase 1
AT4G30960	SOS3-interacting protein 3
AT4G38620	myb domain protein 4
AT5G55970	RING/U-box superfamily protein
AT5G57700	BNR/Asp-box repeat family protein
AT5G59490	Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
AT5G01820	serine/threonine protein kinase 1
AT1G70944	unknown protein
AT3G60410	Protein of unknown function (DUF1639)
AT1G10150	Carbohydrate-binding protein
AT2G01490	phytanoyl-CoA dioxygenase (PhyH) family protein
AT2G35610	xyloglucanase 113
AT1G10470	response regulator 4
AT3G57785	unknown protein
AT1G06070	Basic-leucine zipper (bZIP) transcription factor family protein
AT1G19380	Protein of unknown function (DUF1195)
AT1G06680	photosystem II subunit P-1
AT5G21960	Integrase-type DNA-binding superfamily protein
AT1G69850	nitrate transporter 1:2
AT1G33240	GT-2-like 1
AT5G62040	PEBP (phosphatidylethanolamine-binding protein) family protein
AT4G16380	Heavy metal transport/detoxification superfamily protein
AT5G12050	unknown protein
AT3G05220	Heavy metal transport/detoxification superfamily protein
AT1G11330	S-locus lectin protein kinase family protein
AT1G02080	transcription regulators
AT1G09940	Glutamyl-tRNA reductase family protein

AT5G60700	glycosyltransferase family protein 2
AT5G15850	CONSTANS-like 1
AT1G15820	light harvesting complex photosystem II subunit 6
AT5G18310	unknown protein
AT3G18830	polyol/monosaccharide transporter 5
AT2G43040	tetratricopeptide repeat (TPR)-containing protein
AT3G11410	protein phosphatase 2CA
AT5G67360	Subtilase family protein
AT2G47090	zinc ion binding;nucleic acid binding
AT5G56070	unknown protein
AT1G29930	chlorophyll A/B binding protein 1
AT5G67330	natural resistance associated macrophage protein 4
AT2G03240	EXS (ERD1/XPR1/SYG1) family protein
AT3G25910	Protein of unknown function (DUF1644)
AT4G38550	Arabidopsis phospholipase-like protein (PEARLI 4) family
AT3G04470	Ankyrin repeat family protein
AT2G41910	Protein kinase superfamily protein
AT3G15530	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G08940	light harvesting complex photosystem II
AT5G11970	Protein of unknown function (DUF3511)
AT1G01430	TRICHOME BIREFRINGENCE-LIKE 25
AT4G05320	polyubiquitin 10
AT1G75540	salt tolerance homolog2
AT5G40480	embryo defective 3012
AT1G31835	unknown protein
AT5G61670	unknown protein
AT4G32030	unknown protein
AT5G04830	Nuclear transport factor 2 (NTF2) family protein
AT2G27710	60S acidic ribosomal protein family
AT1G03600	photosystem II family protein
AT5G52050	MATE efflux family protein
AT5G21280	hydroxyproline-rich glycoprotein family protein
AT5G52100	Dihydrodipicolinate reductase, bacterial/plant
AT5G05140	Transcription elongation factor (TFIIS) family protein
AT1G68585	unknown protein
AT1G28190	unknown protein
AT1G20980	squamosa promoter binding protein-like 14
AT1G03730	unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G03600.1); Has 50 Blast hits to 50 prot....
AT3G16610	pentatricopeptide (PPR) repeat-containing protein
AT1G50020	unknown protein
AT5G40380	cysteine-rich RLK (RECEPTOR-like protein kinase) 42
AT1G80930	MIF4G domain-containing protein / MA3 domain-containing protein
AT3G51690	PIF1 helicase
AT1G26580	molecular function unknown
AT1G58110	Basic-leucine zipper (bZIP) transcription factor family protein
AT1G80200	unknown protein, LOCATED IN: endomembrane
AT4G24570	dicarboxylate carrier 2
AT1G72700	ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein
AT3G11690	unknown protein
AT5G25360	unknown protein
AT4G34050	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G07870	Protein kinase superfamily protein
AT5G15780	Pollen Ole e 1 allergen and extensin family protein
AT3G59090	tobamovirus multiplication 1
AT4G17870	Polyketide cyclase/dehydrase and lipid transport superfamily protein
AT4G24960	HVA22 homologue D
AT1G66260	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G30200	F-box family protein
AT4G03010	RNI-like superfamily protein
AT3G13110	serine acetyltransferase 2;2

AT3G13784	cell wall invertase 5
AT1G01620	plasma membrane intrinsic protein 1C
AT1G15810	S15/NS1, RNA-binding protein
AT4G39840	unknown protein
AT1G29910	chlorophyll A/B binding protein 3
AT1G62390	Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein
AT4G29890	choline monooxygenase, putative (CMO-like)
AT1G27730	salt tolerance zinc finger
AT2G45630	D-isomer specific 2-hydroxyacid dehydrogenase family protein
AT3G19970	alpha/beta-Hydrolases superfamily protein
AT4G16563	Eukaryotic aspartyl protease family protein
AT5G10980	Histone superfamily protein
AT1G08315	ARM repeat superfamily protein
AT3G22968	conserved peptide upstream open reading frame 59
AT3G22970	Protein of unknown function (DUF506)
AT5G03285	other RNA
AT4G28750	Photosystem I reaction centre subunit IV / PsaE protein
AT3G08610	unknown protein
AT1G34000	one-helix protein 2
AT3G17040	high chlorophyll fluorescent 107
AT4G03110	RNA-binding protein-defense related 1
AT1G37130	nitrate reductase 2
AT3G28860	ATP binding cassette subfamily B19
AT3G14440	nine-cis-epoxycarotenoid dioxygenase 3
AT4G20860	FAD-binding Berberine family protein
AT1G12240	Glycosyl hydrolases family 32 protein
AT1G71040	Cupredoxin superfamily protein
AT4G31800	WRKY DNA-binding protein 18
AT3G49290	ABL interactor-like protein 2
AT5G03890	unknown protein
AT2G44798	other RNA
AT1G46264	heat shock transcription factor B4
AT1G12110	nitrate transporter 1.1
AT1G70530	cysteine-rich RLK (RECEPTOR-like protein kinase) 3
AT4G04850	K ⁺ efflux antiporter 3
AT2G45850	AT hook motif DNA-binding family protein
AT1G78110	unknown protein, LOCATED IN: plasma membrane
AT5G05600	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT5G45113	mitochondrial transcription termination factor-related / mTERF-related
AT4G29735	unknown protein
AT2G26750	alpha/beta-Hydrolases superfamily protein
AT4G30350	Double Clp-N motif-containing P-loop nucleoside triphosphate hydrolases superfamily protein
AT4G30190	H(+)-ATPase 2
AT3G17130	Plant invertase/pectin methylesterase inhibitor superfamily protein
AT5G42150	Glutathione S-transferase family protein
AT4G39780	Integrase-type DNA-binding superfamily protein
AT5G17760	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT4G23740	Leucine-rich repeat protein kinase family protein
AT3G57790	Pectin lyase-like superfamily protein
AT1G01120	3-ketoacyl-CoA synthase 1
AT1G01180	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT1G01570	Protein of unknown function (DUF604)
AT1G02090	Proteasome component (PCI) domain protein
AT1G02110	Protein of unknown function (DUF630 and DUF632)
AT1G02360	Chitinase family protein
AT1G02660	alpha/beta-Hydrolases superfamily protein
AT1G04830	Ypt/Rab-GAP domain of gyp1p superfamily protein
AT1G05370	Sec14p-like phosphatidylinositol transfer family protein
AT1G05805	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G06040	B-box zinc finger family protein

AT1G07250	UDP-glucosyl transferase 71C4
AT1G08510	fatty acyl-ACP thioesterases B
AT1G09250	basic helix-loop-helix (bHLH) DNA-binding superfamily protein
AT1G12090	extensin-like protein
AT1G13080	cytochrome P450, family 71, subfamily B, polypeptide 2
AT1G13700	6-phosphogluconolactonase 1
AT1G13880	ELM2 domain-containing protein
AT1G14280	phytochrome kinase substrate 2
AT1G14540	Peroxidase superfamily protein
AT1G14780	MAC/Perforin domain-containing protein
AT1G15700	ATPase, F1 complex, gamma subunit protein
AT1G15800	unknown protein
AT1G17420	lipoxygenase 3
AT1G18010	Major facilitator superfamily protein
AT1G19210	Integrase-type DNA-binding superfamily protein
AT1G19720	Pentatricopeptide repeat (PPR-like) superfamily protein
AT1G21400	Thiamin diphosphate-binding fold (THDP-binding) superfamily protein
AT1G21600	plastid transcriptionally active 6
AT1G21920	Histone H3 K4-specific methyltransferase SET7/9 family protein
AT1G22360	UDP-glucosyl transferase 85A2
AT1G27200	Domain of unknown function (DUF23)
AT1G27930	Protein of unknown function (DUF579)
AT1G28280	VQ motif-containing protein
AT1G29300	Plant protein of unknown function (DUF641)
AT1G34010	unknown protein
AT1G48970	NagB/RpiA/CoA transferase-like superfamily protein
AT1G49790	F-box associated ubiquitination effector family protein
AT1G50300	TBP-associated factor 15
AT1G50430	Ergosterol biosynthesis ERG4/ERG24 family
AT1G50640	ethylene responsive element binding factor 3
AT1G51690	protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform
AT1G51710	ubiquitin-specific protease 6
AT1G52240	RHO guanyl-nucleotide exchange factor 11
AT1G53530	Peptidase S24/S26A/S26B/S26C family protein
AT1G53850	20S proteasome alpha subunit E1
AT1G54080	oligouridylate-binding protein 1A
AT1G55230	Family of unknown function (DUF716)
AT1G55340	Protein of unknown function (DUF1639)
AT1G55680	Transducin/WD40 repeat-like superfamily protein
AT1G56230	Protein of unknown function (DUF1399)
AT1G56290	CwJ1-like family protein
AT1G56590	Clathrin adaptor complexes medium subunit family protein
AT1G60110	Mannose-binding lectin superfamily protein
AT1G60160	Potassium transporter family protein
AT1G60970	SNARE-like superfamily protein
AT1G61750	Receptor-like protein kinase-related family protein
AT1G62050	Ankyrin repeat family protein
AT1G63020	nuclear RNA polymerase D1A
AT1G65410	non-intrinsic ABC protein 11
AT1G66150	transmembrane kinase 1
AT1G66950	pleiotropic drug resistance 11
AT1G67855	unknown protein
AT1G67856	RING/U-box superfamily protein
AT1G67900	Phototropic-responsive NPH3 family protein
AT1G67950	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G68850	Peroxidase superfamily protein
AT1G69870	nitrate transporter 1.7
AT1G70250	receptor serine/threonine kinase, putative
AT1G70290	trehalose-6-phosphatase synthase S8
AT1G70300	K ⁺ uptake permease 6
AT1G70610	transporter associated with antigen processing protein 1

AT1G71528	other RNA
AT1G71530	Protein kinase superfamily protein
AT1G72440	CCAAT-binding factor
AT1G72460	Leucine-rich repeat protein kinase family protein
AT1G72510	Protein of unknown function (DUF1677)
AT1G72640	NAD(P)-binding Rossmann-fold superfamily protein
AT1G72760	Protein kinase superfamily protein
AT1G73480	alpha/beta-Hydrolases superfamily protein
AT1G73530	RNA-binding (RRM/RBD/RNP motifs) family protein
AT1G74960	fatty acid biosynthesis 1
AT1G75470	purine permease 15
AT1G76170	2-thiocytidine tRNA biosynthesis protein, TtcA
AT1G76400	Ribophorin I
AT1G77460	Armadillo/beta-catenin-like repeat ; C2 calcium/lipid-binding domain (CaLB) protein
AT1G78280	transferases, transferring glycosyl groups
AT1G78580	trehalose-6-phosphate synthase
AT1G79080	Pentatricopeptide repeat (PPR) superfamily protein
AT1G79350	RING/FYVE/PHD zinc finger superfamily protein
AT1G79430	Homeodomain-like superfamily protein
AT1G79890	RAD3-like DNA-binding helicase protein
AT1G80190	partner of SLD five 1
AT1G80300	nucleotide transporter 1
AT1G80310	sulfate transmembrane transporters
AT1G80325	other RNA
AT2G01420	Auxin efflux carrier family protein
AT2G01670	nudix hydrolase homolog 17
AT2G01735	RING-finger protein for embryogenesis
AT2G05790	O-Glycosyl hydrolases family 17 protein
AT2G08986	unknown protein
AT2G18100	Protein of unknown function (DUF726)
AT2G18800	xyloglucan endotransglucosylase/hydrolase 21
AT2G18969	Encodes a atypical member of the bHLH (basic helix-loop-helix) family transcriptional factors
AT2G18970	unknown protein
AT2G19830	SNF7 family protein
AT2G20550	HSP40/DnaJ peptide-binding protein
AT2G20616	Family of unknown function (DUF566)
AT2G21540	SEC14-like 3
AT2G22120	RING/FYVE/PHD zinc finger superfamily protein
AT2G22480	phosphofructokinase 5
AT2G22870	P-loop containing nucleoside triphosphate hydrolases superfamily protein
AT2G24390	AIG2-like (avirulence induced gene) family protein
AT2G24810	Pathogenesis-related thaumatin superfamily protein
AT2G25270	unknown protein; LOCATED IN: plasma membrane
AT2G26130	RING/U-box protein with C6HC-type zinc finger
AT2G26550	heme oxygenase 2
AT2G28350	auxin response factor 10
AT2G28900	outer plastid envelope protein 16-1
AT2G30250	WRKY DNA-binding protein 25
AT2G30520	Phototropic-responsive NPH3 family protein
AT2G30580	DREB2A-interacting protein 2
AT2G30890	Cytochrome b561/ferric reductase transmembrane protein family
AT2G31350	glyoxalase 2-5
AT2G32170	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT2G32730	26S proteasome regulatory complex, non-ATPase subcomplex, Rpn2/Psmd1 subunit
AT2G34090	maternal effect embryo arrest 18
AT2G34110	forkhead-associated (FHA) domain-containing protein
AT2G34460	NAD(P)-binding Rossmann-fold superfamily protein
AT2G34470	urease accessory protein G
AT2G35880	TPX2 (targeting protein for Xklp2) protein family
AT2G36060	MMS ZWEI homologue 3
AT2G36250	Tubulin/FtsZ family protein

AT2G36340	DNA-binding storekeeper protein-related transcriptional regulator
AT2G36840	ACT-like superfamily protein
AT2G37210	lysine decarboxylase family protein
AT2G38320	TRICHOME BIREFRINGENCE-LIKE 34
AT2G39020	Acyl-CoA N-acyltransferases (NAT) superfamily protein
AT2G39040	Peroxidase superfamily protein
AT2G39380	exocyst subunit exo70 family protein H2
AT2G40010	Ribosomal protein L10 family protein
AT2G40160	Plant protein of unknown function (DUF828)
AT2G40990	DHHC-type zinc finger family protein
AT2G41330	Glutaredoxin family protein
AT2G41590	unknown protein
AT2G41945	unknown protein
AT2G42710	Ribosomal protein L1p/L10e family
AT2G42780	molecular function unknow
AT2G42790	citrate synthase 3
AT2G42980	Eukaryotic aspartyl protease family protein
AT2G43070	SIGNAL PEPTIDE PEPTIDASE-LIKE 3
AT2G43080	P4H isoform 1
AT2G44520	cytochrome c oxidase 10
AT2G44950	histone mono-ubiquitination 1
AT2G45180	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT2G45500	AAA-type ATPase family protein
AT2G45700	sterile alpha motif (SAM) domain-containing protein
AT2G45880	beta-amylase 7
AT2G45980	unknown protein
AT2G46290	Transducin/WD40 repeat-like superfamily protein
AT2G46430	cyclic nucleotide gated channel 3
AT2G46840	DOMAIN OF UNKNOWN FUNCTION 724 4
AT2G48060	unknown protein
AT3G01430	NHL domain-containing protein
AT3G01640	glucuronokinase G
AT3G02880	Leucine-rich repeat protein kinase family protein
AT3G03470	cytochrome P450, family 87, subfamily A, polypeptide 9
AT3G03980	NAD(P)-binding Rossmann-fold superfamily protein
AT3G05670	RING/U-box protein
AT3G07390	auxin-responsive family protein
AT3G07470	Protein of unknown function, DUF538
AT3G08580	ADP/ATP carrier 1
AT3G09630	Ribosomal protein L4/L1 family
AT3G10985	senescence associated gene 20
AT3G11850	Protein of unknown function, DUF593
AT3G13790	Glycosyl hydrolases family 32 protein
AT3G14840	Leucine-rich repeat transmembrane protein kinase
AT3G14870	Plant protein of unknown function (DUF641)
AT3G17100	sequence-specific DNA binding transcription factors
AT3G17800	Protein of unknown function (DUF760)
AT3G18050	unknown protein
AT3G20310	ethylene response factor 7
AT3G23450	unknown protein
AT3G24520	heat shock transcription factor C1
AT3G25700	Eukaryotic aspartyl protease family protein
AT3G25760	allene oxide cyclase 1
AT3G27831	Gamma-thionin family protein
AT3G45300	isovaleryl-CoA-dehydrogenase
AT3G46658	other RNA
AT3G46668	other RNA
AT3G46670	UDP-glucosyl transferase 76E11
AT3G47360	hydroxysteroid dehydrogenase 3
AT3G47460	Structural maintenance of chromosomes (SMC) family protein
AT3G47675	Protein of unknown function

AT3G47680	DNA binding
AT3G47990	SUGAR-INSENSITIVE 3
AT3G49810	ARM repeat superfamily protein
AT3G51070	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT3G51075	other RNA
AT3G51580	unknown protein
AT3G51700	PIF1 helicase
AT3G51860	cation exchanger 3
AT3G53280	cytochrome p450 71b5
AT3G54060	unknown protein
AT3G54230	suppressor of abi3-5
AT3G54440	glycoside hydrolase family 2 protein
AT3G54950	patatin-like protein 6
AT3G55590	Glucose-1-phosphate adenylyltransferase family protein
AT3G56920	DHHC-type zinc finger family protein
AT3G57060	binding
AT3G57110	unknown protein
AT3G57470	Insulinase (Peptidase family M16) family protein
AT3G58640	Mitogen activated protein kinase kinase kinase-related
AT3G58840	Tropomyosin-related
AT3G58890	RNI-like superfamily protein
AT3G59420	crinkly4
AT3G59970	methylenetetrahydrofolate reductase 1
AT3G59980	Nucleic acid-binding, OB-fold-like protein
AT3G60140	Glycosyl hydrolase superfamily protein
AT3G60440	Phosphoglycerate mutase family protein
AT3G60660	unknown protein
AT3G60800	DHHC-type zinc finger family protein
AT3G61780	embryo defective 1703
AT3G62660	galacturonosyltransferase-like 7
AT3G63060	EID1-like 3
AT3G63070	Tudor/PWWP/MBT domain-containing protein
AT3G63460	transducin family protein / WD-40 repeat family protein
AT4G00150	GRAS family transcription factor
AT4G00335	RING-H2 finger B1A
AT4G00430	plasma membrane intrinsic protein 1;4
AT4G01400	Pentatricopeptide repeat (PPR) superfamily protein (
AT4G01970	stachyose synthase
AT4G02100	Heat shock protein DnaJ with tetratricopeptide repeat
AT4G02770	photosystem I subunit D-1
AT4G05018	unknown protein
AT4G05070	Wound-responsive family protein
AT4G05150	Octicosapeptide/Phox/Bem1p family protein
AT4G08850	Leucine-rich repeat receptor-like protein kinase family protein
AT4G09000	general regulatory factor 1
AT4G09010	ascorbate peroxidase 4
AT4G12230	alpha/beta-Hydrolases superfamily protein
AT4G12730	FASCICLIN-like arabinogalactan 2
AT4G14620	Protein of unknown function (DUF506)
AT4G14622	conserved peptide upstream open reading frame 60
AT4G15560	Deoxyxylulose-5-phosphate synthase
AT4G15920	Nodulin MtN3 family protein
AT4G16140	proline-rich family protein
AT4G16490	ARM repeat superfamily protein
AT4G17090	chloroplast beta-amylase
AT4G17430	O-fucosyltransferase family protein
AT4G17895	ubiquitin-specific protease 20
AT4G18020	CheY-like two-component responsive regulator family protein
AT4G18570	Tetratricopeptide repeat (TPR)-like superfamily protein
AT4G18670	Leucine-rich repeat (LRR) family protein
AT4G19160	unknown protein

AT4G19190	zinc knuckle (CCHC-type) family protein
AT4G20830	FAD-binding Berberine family protein
AT4G21210	PPDK regulatory protein
AT4G22010	SKU5 similar 4
AT4G22360	SWIB complex BAF60b domain-containing protein
AT4G23205	other RNA
AT4G23630	VIRB2-interacting protein 1
AT4G23810	WRKY family transcription factor
AT4G24240	WRKY DNA-binding protein 7
AT4G24805	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT4G24920	secE/sec61-gamma protein transport protein
AT4G26400	RING/U-box superfamily protein
AT4G26850	mannose-1-phosphate guanylyltransferase (GDP)s;GDP-galactose:mannose-1-phosphate guanylyltransferases;GDP-galactose:glucose-1-phosphate guanylyltransferases;GDP-galactose:myo-inositol-1-phosphate guanylyltransferases;glucose-1-phosphate guanylyltransferase
AT4G27280	Calcium-binding EF-hand family protein
AT4G27500	proton pump interactor 1
AT4G27520	early nodulin-like protein 2
AT4G27700	Rhodanese/Cell cycle control phosphatase superfamily protein
AT4G28290	unknown protein
AT4G28760	Protein of unknown function (DUF3741)
AT4G29840	Pyridoxal-5'-phosphate-dependent enzyme family protein
AT4G30440	UDP-D-glucuronate 4-epimerase 1
AT4G31500	cytochrome P450, family 83, subfamily B, polypeptide 1
AT4G32290	Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein
AT4G33670	NAD(P)-linked oxidoreductase superfamily protein
AT4G34135	UDP-glucosyltransferase 73B2
AT4G35750	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
AT4G36500	unknown protein
AT4G36970	Remorin family protein
AT4G36988	conserved peptide upstream open reading frame 49
AT4G36990	heat shock factor 4
AT4G37040	methionine aminopeptidase 1D
AT4G39270	Leucine-rich repeat protein kinase family protein
AT5G01210	HXXXD-type acyl-transferase family protein
AT5G01215	other RNA
AT5G01530	light harvesting complex photosystem II
AT5G01750	Protein of unknown function (DUF567)
AT5G01790	unknown protein
AT5G02190	Eukaryotic aspartyl protease family protein
AT5G03230	Protein of unknown function, DUF584
AT5G03730	Protein kinase superfamily protein
AT5G03760	Nucleotide-diphospho-sugar transferases superfamily protein
AT5G04170	Calcium-binding EF-hand family protein
AT5G04610	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AT5G04770	cationic amino acid transporter 6
AT5G06320	NDR1/HIN1-like 3
AT5G06860	polygalacturonase inhibiting protein 1
AT5G09850	Transcription elongation factor (TFIIS) family protein
AT5G11000	Plant protein of unknown function (DUF868)
AT5G14565	MIR398C; miRNA
AT5G14570	high affinity nitrate transporter 2.7
AT5G15845	other RNA
AT5G15970	stress-responsive protein (KIN2) / stress-induced protein (KIN2) / cold-responsive protein (COR6.6) / cold-regulated protein (COR6.6)
AT5G17490	RGA-like protein 3
AT5G17980	C2 calcium/lipid-binding plant phosphoribosyltransferase family protein
AT5G19140	Aluminium induced protein with YGL and LRDR motifs
AT5G19150	plkB-like carbohydrate kinase family protein
AT5G20110	Dynein light chain type 1 family protein
AT5G21482	cytokinin oxidase 7

AT5G23100	Protein of unknown function, DUF617
AT5G23240	DNAJ heat shock N-terminal domain-containing protein
AT5G24530	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
AT5G24930	CONSTANS-like 4
AT5G35695	unknown protein
AT5G37590	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G38910	RmlC-like cupins superfamily protein
AT5G39710	Tetratricopeptide repeat (TPR)-like superfamily protein
AT5G40820	Ataxia telangiectasia-mutated and RAD3-related
AT5G42120	Concanavalin A-like lectin protein kinase family protein
AT5G44180	Homeodomain-like transcriptional regulator
AT5G44230	Pentatricopeptide repeat (PPR) superfamily protein
AT5G44310	Late embryogenesis abundant protein (LEA) family protein
AT5G45110	NPR1-like protein 3
AT5G45840	Leucine-rich repeat protein kinase family protein
AT5G47260	ATP binding;GTP binding;nucleotide binding;nucleoside-triphosphatases
AT5G47300	F-box and associated interaction domains-containing protein
AT5G47430	DWNN domain, a CCHC-type zinc finger
AT5G47440	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AT5G47690	binding
AT5G47700	60S acidic ribosomal protein family
AT5G49400	zinc knuckle (CCHC-type) family protein
AT5G49470	PAS domain-containing protein tyrosine kinase family protein
AT5G49550	Putative homolog of mammalian BLOC-1 Subunit 2. Protein - protein interaction with BLOS1.
AT5G49555	FAD/NAD(P)-binding oxidoreductase family protein
AT5G51500	Plant invertase/pectin methylesterase inhibitor superfamily
AT5G51600	Microtubule associated protein (MAP65/ASE1) family protein
AT5G53310	myosin heavy chain-related
AT5G54510	Auxin-responsive GH3 family protein
AT5G55070	Dihydrolipoamide succinyltransferase
AT5G56270	WRKY DNA-binding protein 2
AT5G56510	pumilio 12
AT5G56690	FBD, F-box and Leucine Rich Repeat domains containing protein
AT5G56880	unknown protein
AT5G57015	casein kinase I-like 12
AT5G57770	Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region
AT5G57970	DNA glycosylase superfamily protein
AT5G58170	SHV3-like 5
AT5G59120	subtilase 4.13
AT5G59830	unknown protein
AT5G60530	late embryogenesis abundant protein-related / LEA protein-related
AT5G60900	receptor-like protein kinase 1
AT5G61000	Replication factor-A protein 1-related
AT5G61140	U5 small nuclear ribonucleoprotein helicase
AT5G62600	ARM repeat superfamily protein
AT5G63200	tetratricopeptide repeat (TPR)-containing protein
AT5G63470	nuclear factor Y, subunit C4
AT5G63580	flavonol synthase 2
AT5G64080	Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein
AT5G64670	Ribosomal protein L18e/L15 superfamily protein
AT5G65200	plant U-box 38
AT5G65950	unknown protein
AT5G66610	DA1-related protein 7
AT5G66620	DA1-related protein 6
AT5G66770	GRAS family transcription factor
AT5G67385	Phototropic-responsive NPH3 family protein

It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims. In addition, any
5 elements or limitations of any invention or embodiment thereof disclosed herein can be combined with any and/or all other elements or limitations (individually or in any combination) or any other invention or embodiment thereof disclosed herein, and all such combinations are contemplated with the scope of the invention without limitation thereto.

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CLAIMS

We claim:

1. A method for increasing photosynthetic efficiency in a plant, comprising ectopically expressing or increasing expression of one or more of SHORT-ROOT (SHR), SCARECROW (SCR), or SCARECROW-LIKE 23 (SCL23) in the plant.
2. The method according to claim 1, wherein the plant is a C3 plant.
3. The method according to claim 1, wherein the plant is rice, barley, thale cress, wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybean, spinach, or a tree.
4. The method according to claim 1, comprising incorporating a polynucleotide encoding one or more of SHR, SCR, or SCL23, or a functional fragment thereof, into a plant, plant tissue, or plant cell and optionally screening for expression of the one or more SHR, SCR, or SCL23 in the plant, plant tissue, or plant cell.
5. The method according to claim 4, wherein the polynucleotide is provided in an expression construct that can be expressed in the plant.
6. The method according to claim 4, wherein the polynucleotide is stably incorporated into the genome of the plant.
7. The method according to claim 4, wherein the polynucleotide comprises cDNA.
8. The method according to claim 5, wherein the expression construct provides for cell-type specific expression in the plant.
9. The method according to claim 5, wherein the expression construct provides for leaf-specific expression in the plant.

10. The method according to claim 5, wherein the expression construct provides for mesophyll-specific expression, or bundle sheath (BS) cell-specific expression, or vascular bundle-specific expression.

11. The method according to claim 4, wherein the expressed SHR, SCR, or SCL23 is heterologous to the plant.

12. The method according to any of claims 1-11, wherein the number of BS cells in the plant is increased relative to the number of BS cells in a wild type or non-modified plant.

13. The method according to any of claims 1-11, wherein the number of BS cells in the plant is increased relative to the number of mesophyll cells in the plant.

14. The method according to claim 13, wherein the ratio of BS cells to mesophyll cells in the plant is about 1:1.

15. The method according to claim 4, wherein the SHR comprises the amino acid sequence shown in SEQ ID NO: 7, 9, 11, 19, 21, 27, 29, 31, 37, or 43, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

16. The method according to claim 4, wherein the SCR comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 15, 17, 23, 25, 35, or 41, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

17. The method according to claim 4, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 8, 10, 12, 20, 22, 28, 30, 32, 38, or 44, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

18. The method according to claim 4, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 2, 4, 6, 16, 18, 24, 26, 36, or 42, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

19. The method according to claim 4, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 14, 34, 40, or 46, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

20. The method according to claim 4, wherein the SCL23 comprises the amino acid sequence shown in SEQ ID NO: 13, 33, 39, or 45, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

21. The method according to any of claims 1-11, wherein the number of channels between BS cells and mesophyll cells is increased in the plant.

22. The method according to any of claims 1-11, wherein a cell pattern similar to Kranz anatomy is produced in the plant.

23. A plant that exhibits increased expression or ectopic expression or altered expression of one or more of SHR, SCR, or SCL23.

24. The plant according to claim 23, wherein the plant is a C3 plant.

25. The plant according to claim 23, wherein the plant is a transformed or transgenic plant.

26. The plant according to claim 23, wherein the plant is rice, barley, thale cress, wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybean, spinach, or a tree.

27. The plant according to claim 23, wherein the expression of SHR, SCR, or SCL23 is increased or altered relative to expression in a corresponding wild type plant or non-modified plant.

28. The plant according to claim 23, wherein the SHR comprises the amino acid sequence shown in SEQ ID NO: 7, 9, 11, 19, 21, 27, 29, 31, 37, or 43, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

29. The plant according to claim 23, wherein the SCR comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 15, 17, 23, 25, 35, or 41, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

30. The plant according to claim 23, wherein the SCL23 comprises the amino acid sequence shown in SEQ ID NO: 13, 33, 39, or 45, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

31. The plant according to claim 23, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 8, 10, 12, 20, 22, 28, 30, 32, 38, or 44, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

32. The plant according to claim 23, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 2, 4, 6, 16, 18, 24, 26, 36, or 42, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

33. The plant according to claim 23, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 14, 34, 40, or 46, or a nucleotide sequence that

has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

34. The plant according to claim 23, wherein the expressed SHR, SCR, or SCL23 is heterologous to the plant.

35. The plant according to claim 23, wherein a polynucleotide encoding one or more of SHR, SCR, or SCL23, or a functional fragment thereof, is incorporated into the plant and wherein the one or more SHR, SCR, or SCL23 is expressed in the plant.

36. The plant according to claim 35, wherein the polynucleotide is provided in an expression construct that can be expressed in the plant.

37. The plant according to claim 35, wherein the polynucleotide is stably incorporated into the genome of the plant.

38. The plant according to claim 35, wherein the polynucleotide comprises cDNA.

39. The plant according to claim 36, wherein the expression construct provides for cell-type specific expression in the plant.

40. The plant according to claim 36, wherein the expression construct provides for leaf-specific expression in the plant.

41. The plant according to claim 36, wherein the expression construct provides for mesophyll-specific expression, or bundle sheath (BS) cell-specific expression, or vascular bundle-specific expression.

42. The plant according to claim 35, wherein the SHR, SCR, or SCL23 is heterologous to the plant.

43. The plant according to claim 35, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 8, 10, 12, 20, 22, 28, 30, 32, 38, or 44, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

44. The plant according to claim 35, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 2, 4, 6, 16, 18, 24, 26, 36, or 42, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

45. The plant according to claim 35, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 14, 34, 40, or 46, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

46. The plant according claim 35, wherein the SHR comprises the amino acid sequence shown in SEQ ID NO: 7, 9, 11, 19, 21, 27, 29, 31, 37, or 43, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

47. The plant according claim 35, wherein the SCR comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 15, 17, 23, 25, 35, or 41, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

48. The plant according claim 35, wherein the SCL23 comprises the amino acid sequence shown in SEQ ID NO: 13, 33, 39, or 45, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

49. The plant according to claim 23, wherein a cell pattern similar to Kranz anatomy is produced in the plant.

50. An isolated polynucleotide promoter sequence of a plant *SHR*, *SCR*, or *SCL23* gene, or a functional fragment thereof that exhibits promoter activity.

51. The polynucleotide promoter sequence according to claim 50, wherein the promoter sequence is from a C3 plant.

52. The polynucleotide promoter sequence according to claim 50, wherein the promoter sequence comprises the nucleotide sequence of any of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment thereof that exhibits promoter activity, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

53. A polynucleotide comprising a promoter sequence of a plant *SHR*, *SCR*, or *SCL23* gene, or a functional fragment thereof that exhibits promoter activity, operably linked to a polynucleotide of interest or gene of interest.

54. The polynucleotide according to claim 53, wherein the polynucleotide of interest or gene of interest is heterologous to the *SHR*, *SCR*, or *SCK23* promoter sequence.

55. The polynucleotide according to claim 53, wherein the promoter sequence is from a C3 plant.

56. The polynucleotide according to claim 53, wherein the promoter sequence comprises the nucleotide sequence of any of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment thereof that exhibits promoter activity, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

57. The polynucleotide according to claim 53, wherein the polynucleotide is provided in an expression construct.

58. An expression construct comprising i) a polynucleotide comprising a promoter sequence of any of claims 50 to 57, or ii) a polynucleotide encoding one or more of SHR, SCR, or SCL23.

59. The expression construct according to claim 58, wherein the expression construct further comprises a polynucleotide operably linked to the promoter sequence, wherein the polynucleotide comprises a polynucleotide of interest or gene of interest.

60. The expression construct according to claim 59, wherein the SHR comprises the amino acid sequence shown in SEQ ID NO: 7, 9, 11, 19, 21, 27, 29, 31, 37, or 43, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

61. The expression construct according to claim 59, wherein the SCR comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 15, 17, 23, 25, 35, or 41, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

62. The expression construct according to claim 59, wherein the SCL23 comprises the amino acid sequence shown in SEQ ID NO: 13, 33, 39, or 45, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

63. The expression construct according to claim 59, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 8, 10, 12, 20, 22, 28, 30, 32, 38, or 44, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

64. The expression construct according to claim 59, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 2, 4, 6, 16, 18, 24, 26, 36, or 42, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

65. The expression construct according to claim 59, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 14, 34, 40, or 46, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

66. The expression construct according to claim 58, wherein the promoter sequence comprises the nucleotide sequence of any of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment thereof exhibiting promoter activity, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

67. The expression construct according to claim 59, wherein the polynucleotide of interest or gene of interest encodes a protein associated with photosynthesis.

68. The expression construct according to claim 59, wherein the polynucleotide of interest or gene of interest encodes a phosphoenolpyruvate carboxylase or pyruvate phosphate dikinase (PPDK).

69. A cell transformed with i) a polynucleotide comprising a promoter sequence of any of claims 50 to 57, operably linked to a polynucleotide of interest or gene of interest, or ii) a polynucleotide encoding one or more of SHR, SCR, or SCL23.

70. The cell according to claim 69, wherein the cell is a plant cell.

71. The cell according to claim 70, wherein the plant cell is a cell of a C3 plant.

72. The cell according to claim 70, wherein the plant cell is a cell from rice, barley, thale cress, wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybean, spinach, or a tree.

73. The cell according to claim 69, wherein the polynucleotide is an expression construct.

74. The cell according to claim 69, wherein the promoter sequence comprises the nucleotide sequence of any of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment thereof exhibiting promoter activity, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

75. The cell according to claim 69, wherein the polynucleotide of interest or gene of interest is heterologous to the cell.

76. The cell according to claim 69, wherein the polynucleotide of interest or gene of interest comprises cDNA.

77. The cell according to claim 69, wherein the polynucleotide of interest or gene of interest encodes a phosphoenolpyruvate carboxylase or pyruvate phosphate dikinase (PPDK).

78. A method for increasing expression of a polynucleotide in a plant, comprising incorporating in a plant, plant tissue, or plant cell said polynucleotide operably linked to a polynucleotide comprising a promoter sequence of a plant *SHR*, *SCR*, or *SCL23* gene of any of claims 50 to 57, and optionally screening for expression of said polynucleotide in the plant, plant tissue, or plant cell.

79. The method according to claim 78, wherein the plant is a C3 plant.

80. The method according to claim 78, wherein the plant is rice, barley, thale cress, wheat, rye, oat, fescue, sunflower, tomato, cucumber, potato, peanut, cotton, sugar beet, tobacco, soybean, spinach, or a tree.

81. The method according to claim 78, wherein said polynucleotide encodes one or more of *SHR*, *SCR*, or *SCL23*, or a functional fragment thereof.

82. The method according to claim 78, wherein the polynucleotide is provided in an expression construct that can be expressed in the plant.

83. The method according to claim 78, wherein the polynucleotide is stably incorporated into the genome of the plant.

84. The method according to claim 78, wherein the polynucleotide comprises cDNA.

85. The method according to claim 82, wherein the expression construct provides for cell-type specific expression in the plant.

86. The method according to claim 82, wherein the expression construct provides for leaf-specific expression in the plant.

87. The method according to claim 82, wherein the expression construct provides for mesophyll-specific expression, or bundle sheath (BS) cell-specific expression, or vascular bundle-specific expression.

88. The method according to claim 81, wherein the SHR comprises the amino acid sequence shown in SEQ ID NO: 7, 9, 11, 19, 21, 27, 29, 31, 37, or 43, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

89. The method according to claim 81, wherein the SCR comprises the amino acid sequence shown in SEQ ID NO: 1, 3, 5, 15, 17, 23, 25, 35, or 41, or an amino acid sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

90. The method according to claim 81, wherein the SCL23 comprises the amino acid sequence shown in SEQ ID NO: 13, 33, 39, or 45, or an amino acid sequence that has at least

60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

91. The method according to claim 81, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 8, 10, 12, 20, 22, 28, 30, 32, 38, or 44, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

92. The method according to claim 81, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 2, 4, 6, 16, 18, 24, 26, 36, or 42, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

93. The method according to claim 81, wherein the polynucleotide comprises the nucleotide sequence shown in SEQ ID NO: 14, 34, 40, or 46, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

94. The method according to claim 78, wherein said polynucleotide is heterologous to the plant.

95. The method according to claim 78, wherein the polynucleotide encodes a protein associated with photosynthesis.

96. The method according to claim 78, wherein the polynucleotide encodes a phosphoenolpyruvate carboxylase or a pyruvate phosphate dikinase (PPDK).

97. The method according to claim 78, wherein the promoter sequence comprises the nucleotide sequence of any of SEQ ID NO:47, SEQ ID NO:48, or SEQ ID NO:49, or a functional fragment thereof that exhibits promoter activity, or a nucleotide sequence that has at least 60%, or at least 70%, or at least 80%, or at least 90%, or at least 95% sequence identity with the SEQ ID NO.

FIG. 1A

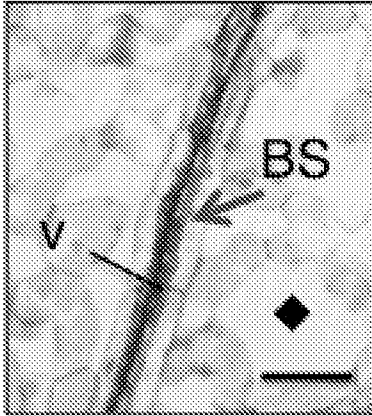


FIG. 1C

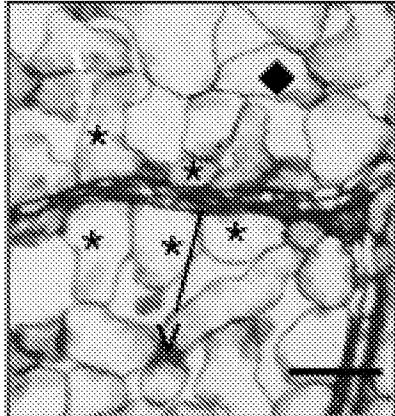


FIG. 1E

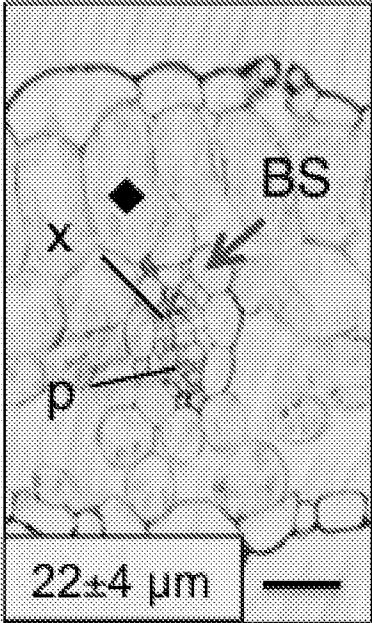
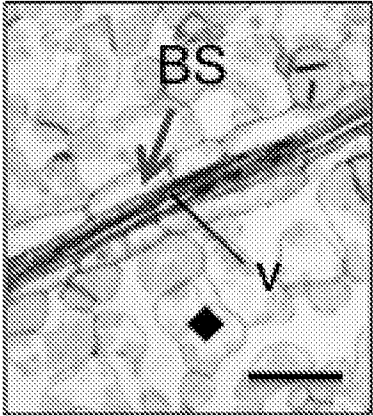


FIG. 1A-1

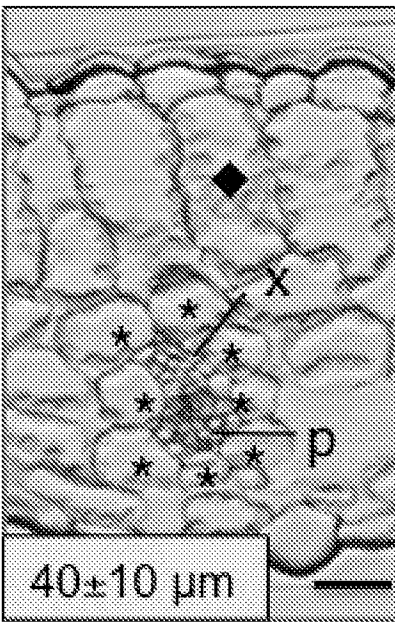


FIG. 1C-1

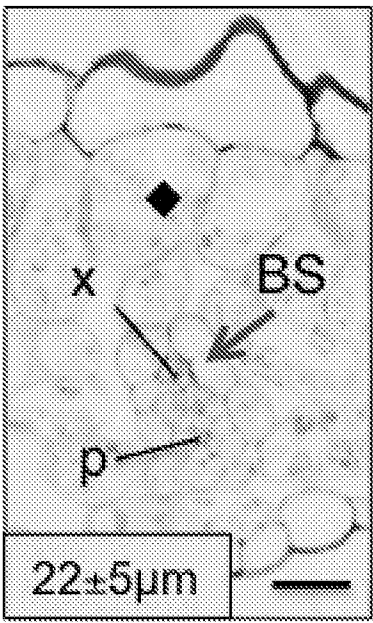


FIG. 1E-1

FIG. 1B

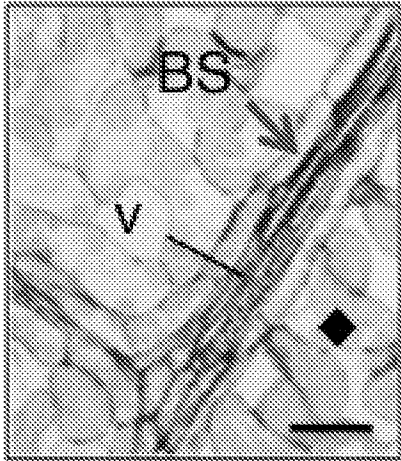


FIG. 1D

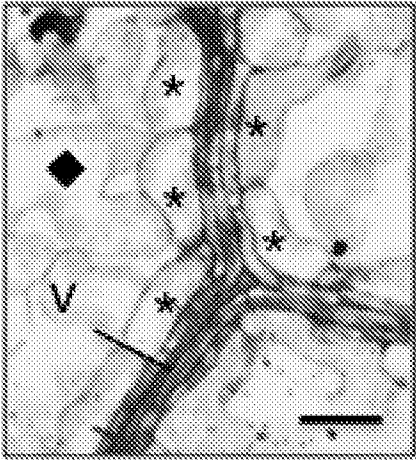
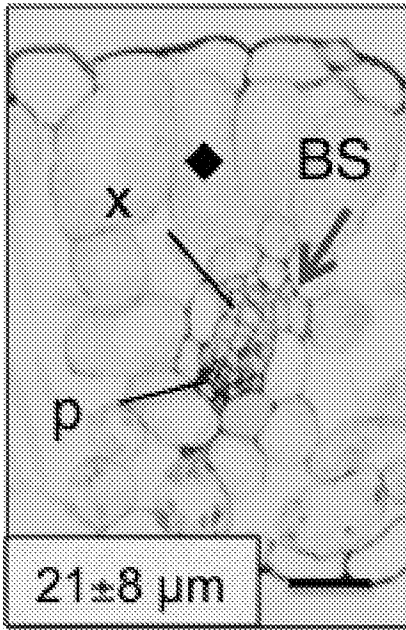
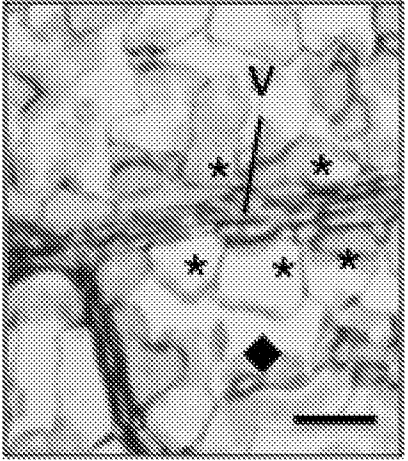
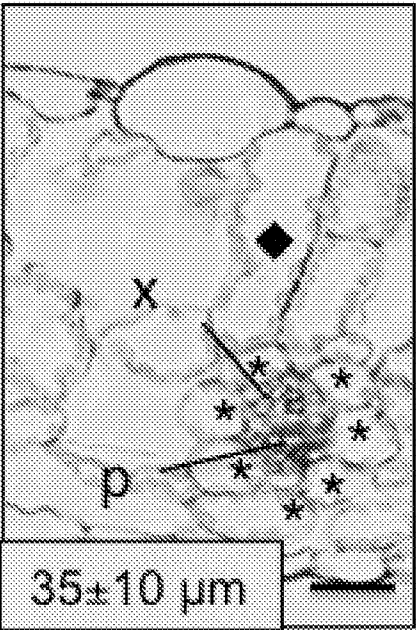


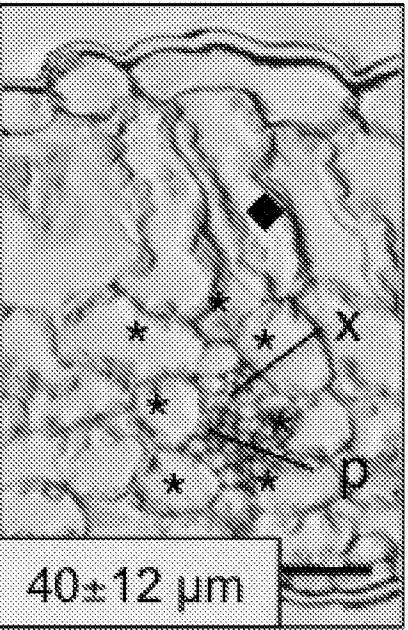
FIG. 1F



$21 \pm 8 \mu\text{m}$



$35 \pm 10 \mu\text{m}$



$40 \pm 12 \mu\text{m}$

FIG. 1B-1

FIG. 1D-1

FIG. 1F-1

FIG. 2A

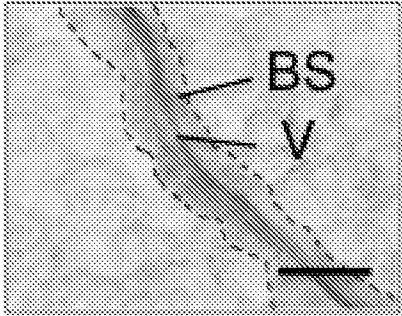


FIG. 2B

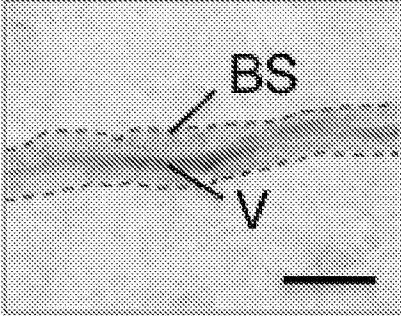


FIG. 2C

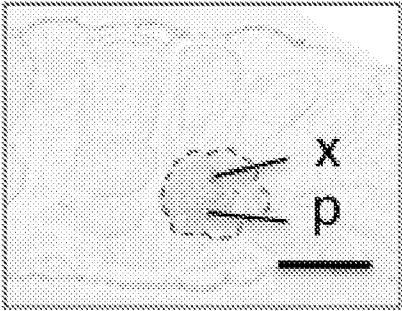
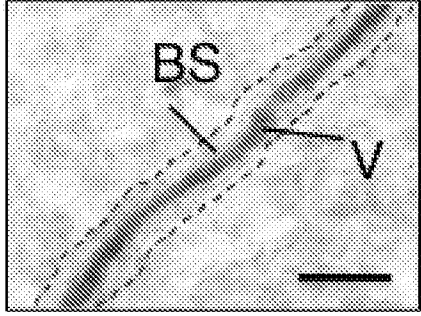


FIG. 2D

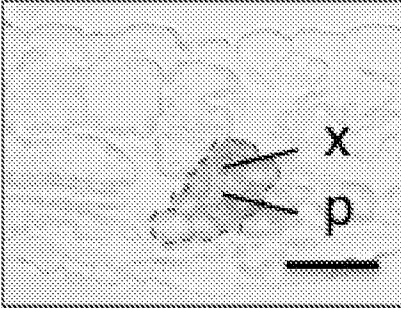


FIG. 2E

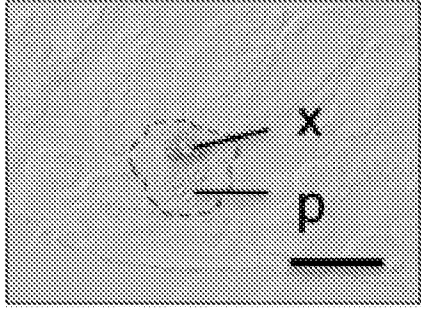


FIG. 2F

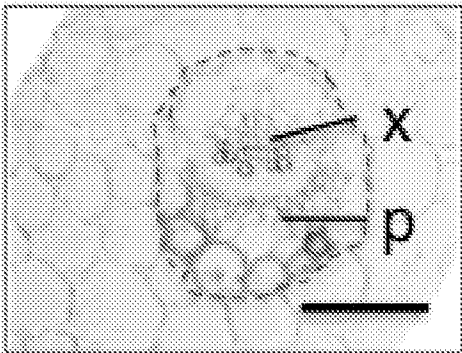


FIG. 2G

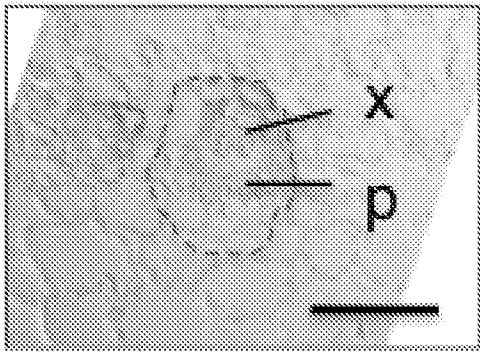
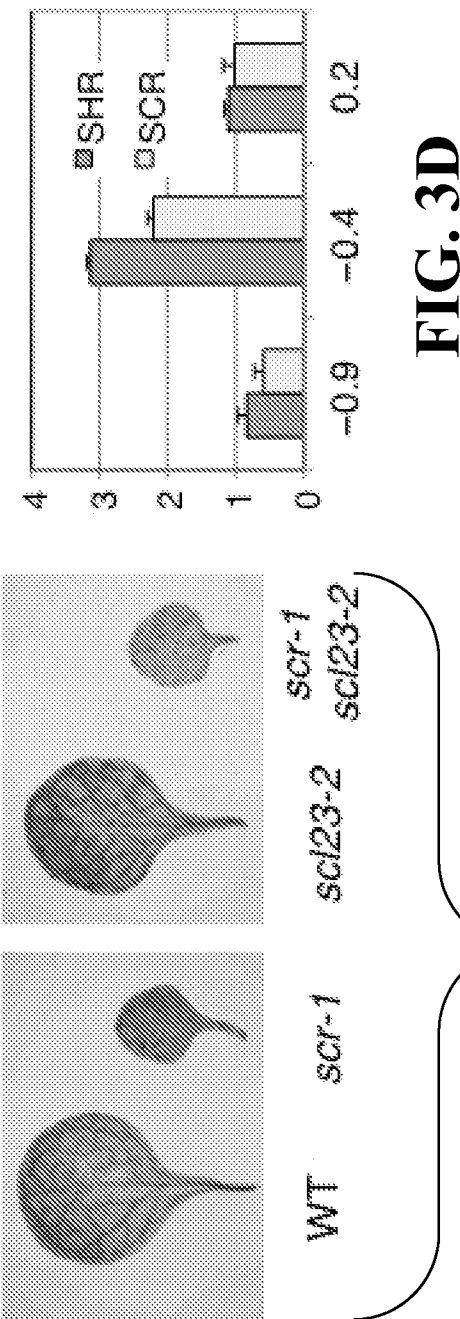
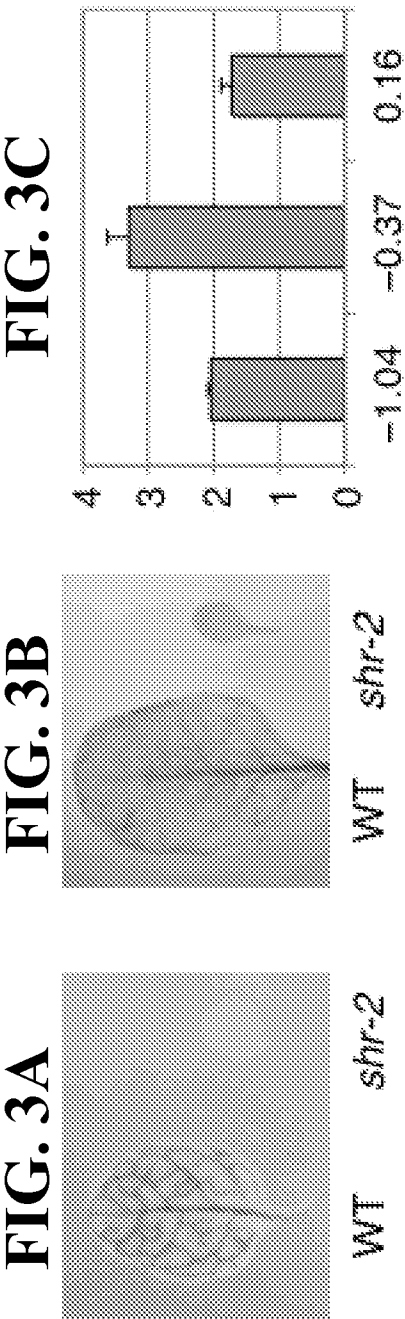


FIG. 2H



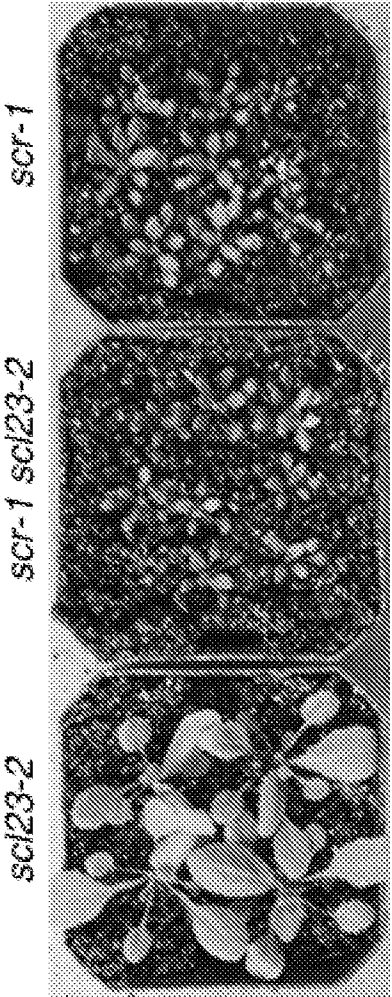


FIG. 4E

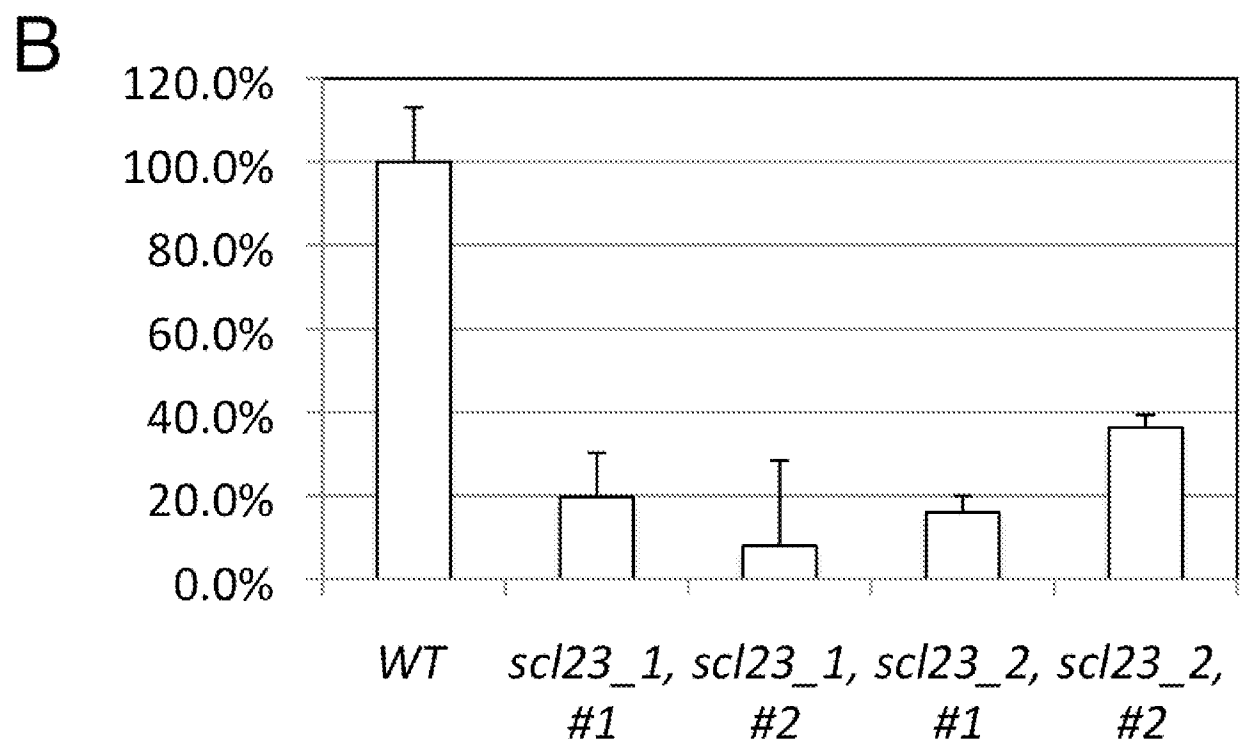
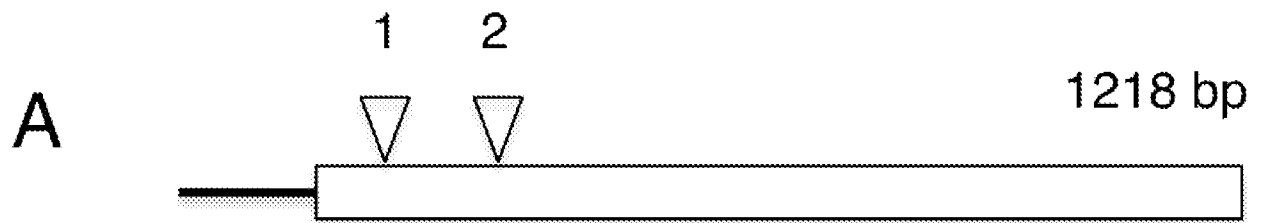
FIG. 5A**FIG. 5B**

FIG. 6A

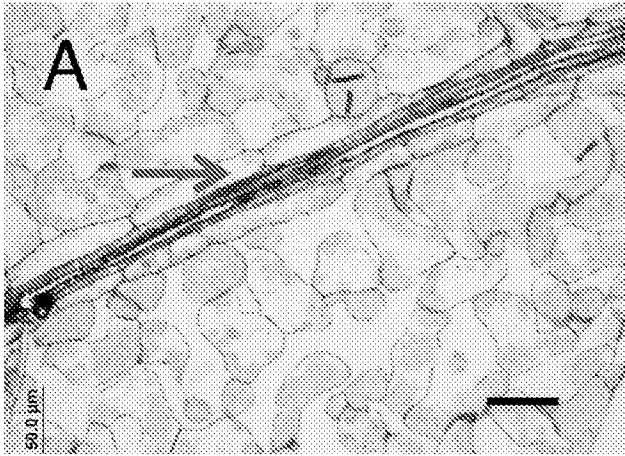


FIG. 6C

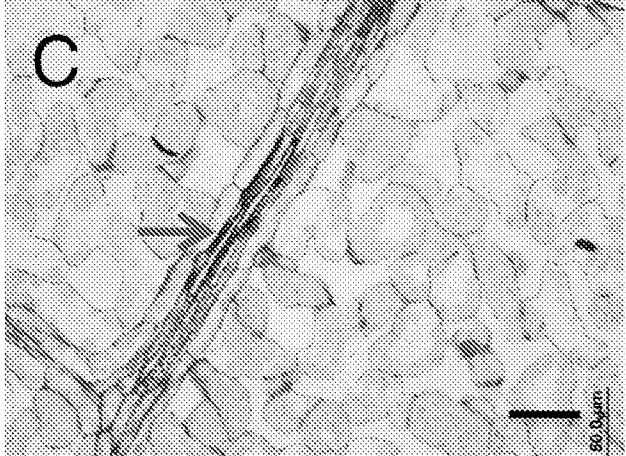


FIG. 6B

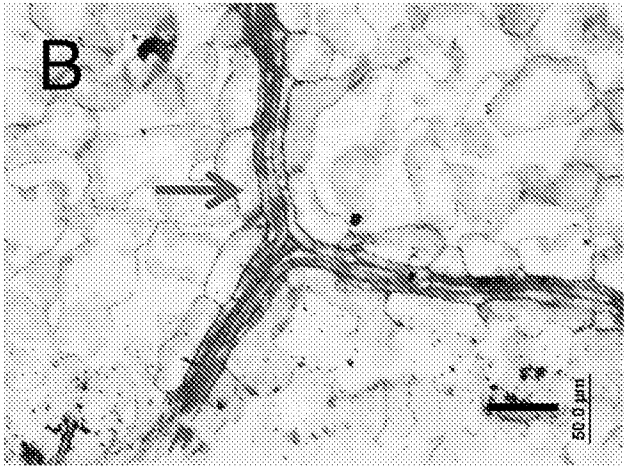
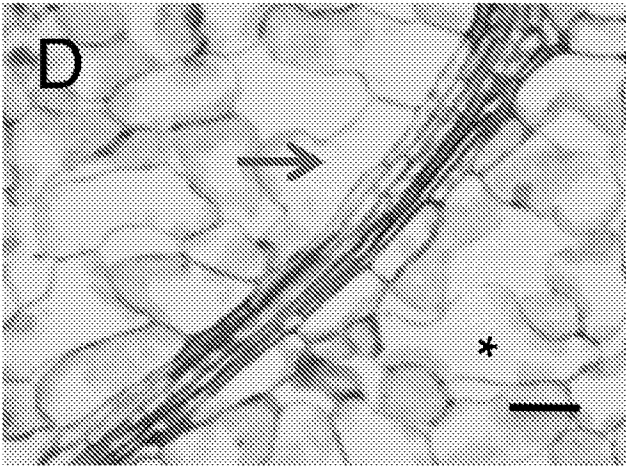


FIG. 6D



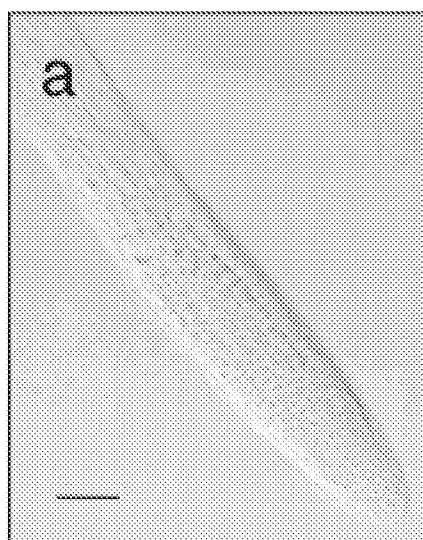


FIG. 7A

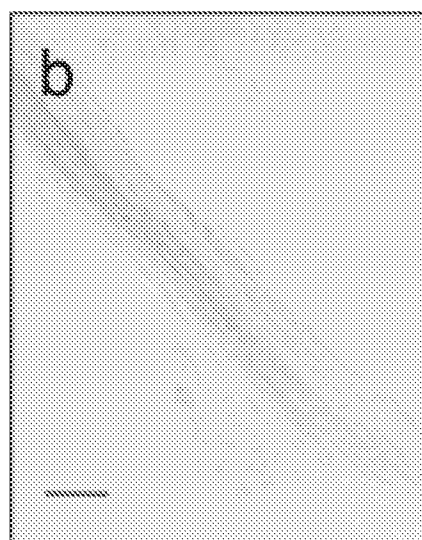
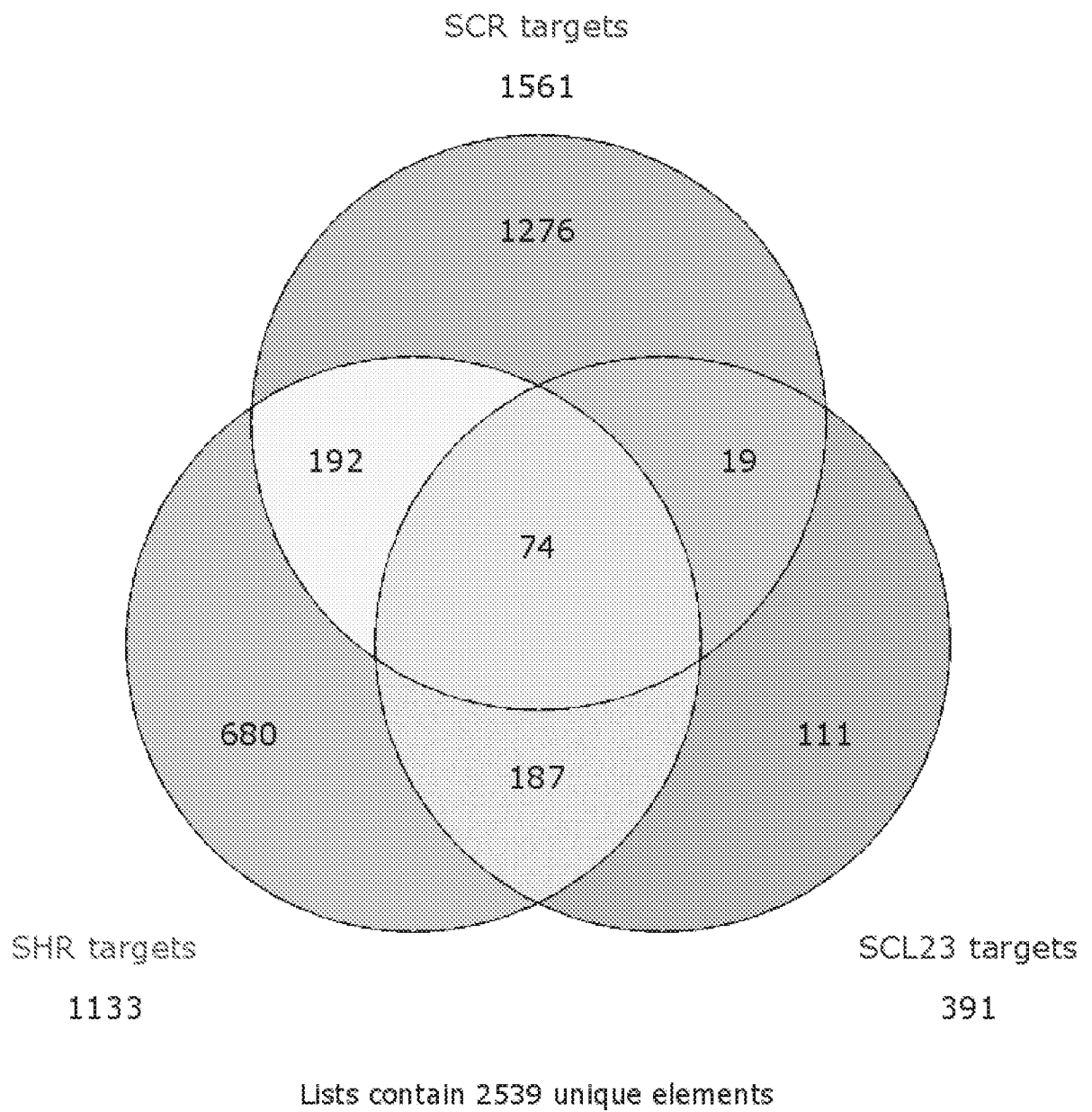


FIG. 7B

10/10

**FIG. 8**

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US2014/041975**A. CLASSIFICATION OF SUBJECT MATTER****C12N 15/29(2006.01)i, C12N 15/63(2006.01)i**

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

C12N 15/29; C07K 14/415; C12N 5/04; C12N 15/63

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Korean utility models and applications for utility models

Japanese utility models and applications for utility models

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

eKOMPASS(KIPO internal) & keywords: SHORT-ROOT(SHR), SCARECROW(SCR), SCARECROW-LIKE 23(SCL23),
photosynthesis, plant, expression, vascular bundle, bundle sheath**C. DOCUMENTS CONSIDERED TO BE RELEVANT**

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 2003-0088073 A1 (BENFEY, P. N. et al.) 8 May 2003	1-11, 23-27, 34-42
Y	See abstract; paragraphs [0003], [0018]-[0020], [0059], [0060], [0136] and [0140]; claims 1, 7-12 and 17-28.	, 50-51, 53-55, 57-59, 67-73, 75-87, 94-96
A		16, 18, 29, 32, 44, 47, 52, 56, 61, 64, 66, 74, 89, 92, 97
		12-15, 17, 19-22, 28, 30-31, 33, 43, 45-46, 48-49, 60, 62-63, 65, 88, 90-91, 93
Y	NCBI, GenBank Accession No. AAB06318.1, 'SCARECROW [Arabidopsis thaliana]', 6 November 2000 See the whole document.	16, 29, 47, 61, 89
Y	NCBI, GenBank Accession No. U62798.1, 'Arabidopsis thaliana SCARECROW (SCARECROW1) gene, complete cds', 6 November 2000 See the whole document.	18, 32, 44, 64, 92
Y	NCBI, GenBank Accession No. EF104556.1, 'Arabidopsis suecica clone scr_24 genomic sequence', 26 August 2007 See the whole document.	52, 56, 66, 74, 97



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

27 October 2014 (27.10.2014)

Date of mailing of the international search report

27 October 2014 (27.10.2014)

Name and mailing address of the ISA/KR

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US2014/041975

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	DHONDT, S. et al., 'SHORT-ROOT and SCARECROW regulate leaf growth in Arabidopsis by stimulating S-phase progression of the cell cycle', Plant Physiol., 25 August 2010, Vol. 154, No. 3, pp. 1183-1195 See abstract; figures 1-2.	1-97
A	LEE, M. H. et al., 'Large-scale analysis of the GRAS gene family in Arabidopsis thaliana', Plant Mol. Biol., 26 May 2008, Vol. 67, No. 6, pp. 659-670 See abstract; figures 1-6.	1-97

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No.

PCT/US2014/041975Patent document
cited in search reportPublication
datePatent family
member(s)Publication
date

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