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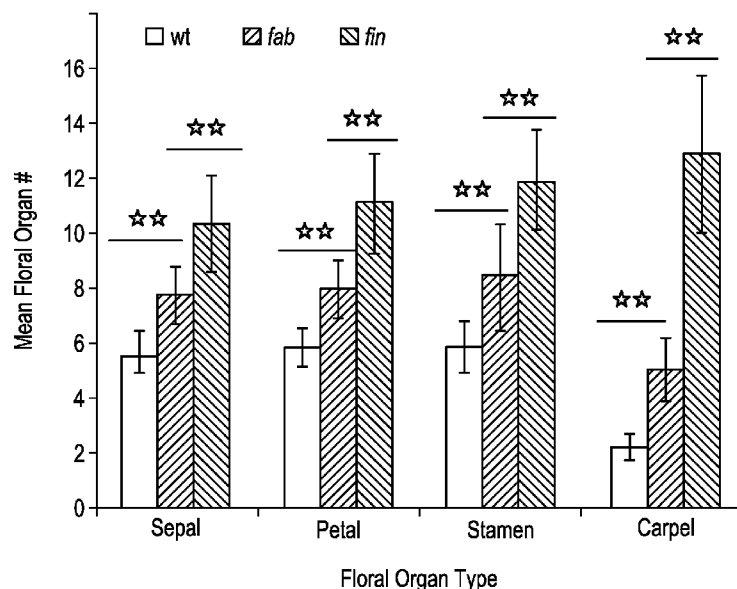
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[Continued on next page]

(54) Title: FASCIATED INFLORESCENCE (FIN) SEQUENCES AND METHODS OF USE

**FIG. 1A**(57) Abstract: Methods and compositions for modulating shoot apical meristem size are provided. Methods are provided for modulating the expression of *fin* sequence in a host plant or plant cell to modulate agronomic characteristics such as size and number of organs, including plant fruits and seeds.



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TITLE

FASCIATED INFLORESCENCE (FIN) SEQUENCES AND METHODS OF USE

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No.
5 61/881888, filed September 24, 2013, the entire content of which is herein
incorporated by reference.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

The official copy of the sequence listing is submitted electronically via EFS-
Web as an ASCII formatted sequence listing with a file named
10 “20140921_BB1934PCT_SequenceListing” created on September 21, 2014 and
having a size of 172 kilobytes and is filed concurrently with the specification. The
sequence listing contained in this ASCII formatted document is part of the
specification and is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

15 The invention relates to the field of the genetic manipulation of plants,
particularly the modulation of gene activity and development in plants.

BACKGROUND OF THE INVENTION

Flower production and crop yields are highly influenced by the architecture of
inflorescences.

20 The regulation of floral organ number is closely associated with floral
meristem size. Leaves and the axillary meristems that generate branches and
flowers are initiated in regular patterns from the shoot apical meristem (SAM). The
vegetative SAM forms new leaves, whereas the reproductive SAM, called the
inflorescence meristem, produces flowers that form seeds after fertilization. The
25 cells of the shoot apical meristem summit serve as stem cells that divide to
continuously displace daughter cells to the surrounding regions, where they are
incorporated into differentiated leaf or flower primordia. The meristems are thus
capable of regulating their size during development by balancing cell proliferation
with the incorporation of cells into new primordia. The SAM provides all aerial parts
30 of plant body. A major pathway of stem cells regulation is known by the signal
pathway of CLAVATA/WUSCHEL (CLV/WUS) genes. Loss of CLV1, CLV2, or
CLV3 activity in *Arabidopsis* causes accumulation of undifferentiated cells in the

shoot apex, indicating that CLV genes together promote the timely transition of stem cells into differentiation pathways, or repress stem cell division, or both (Fletcher et al. (1999) *Science* 283:1911-1914; Taguchi-Shiobara et al. (2001) *Genes and Development* 15:2755-5766; Trotochaud et al. (1999) *Plant Cell* 11:393-405; Merton et al. (1954) *Am. J. Bot.* 41:726-32; Szymkowiak et al. (1992) *Plant Cell* 4:1089-100; Yamamoto et al. (2000) *Biochim. Biophys. Acta.* 1491:333-40). It is desirable to be able to control the size and appearance of shoot and floral meristems, to give increased yields of leaves, flowers, and fruit.

The activity of the reproductive SAM is one of the most important parameters determining seed and fruit yield. Yield is a complex trait that is governed by many genes (quantitative trait loci), each contributing only a small portion to the total yield. Consequently, it is difficult to achieve large increases in seed yield by altering single or only a few genes.

Accordingly, it is an object of the invention to provide novel methods and compositions for the regulation of meristem function, and plant architecture.

SUMMARY OF THE INVENTION

In one embodiment, the current invention provides a method of producing a transgenic plant with decreased expression of endogenous *FIN* gene, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant construct comprising a polynucleotide sequence operably linked to a promoter, wherein the expression of the polynucleotide sequence reduces endogenous *FIN* gene expression; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a decrease in expression of *FIN* gene, when compared to a control plant not comprising the recombinant DNA construct.

In another embodiment, the current invention provides a method of producing a transgenic plant with decreased expression of endogenous *FIN* gene, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked, in sense or antisense orientation, to a promoter functional in a plant, wherein the polynucleotide comprises: (i) the nucleotide sequence 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, 45, 47 or 49; (ii) a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49; (iii) a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49; (iv) a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or (v) a modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a decrease in expression of *FIN* gene, when compared to a control plant not comprising the recombinant DNA construct.

One embodiment of the invention is a method of producing a transgenic plant with alteration of an agronomic characteristic, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked to at least one regulatory sequence, wherein the polynucleotide encodes a fragment or a variant of a polypeptide having an amino acid sequence of at least 80% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, wherein the fragment or the variant confers a dominant-negative phenotype in the regenerable plant cell; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within the inflorescence, flower number, fruit number, fruit size,

seed number, root branching, root biomass, root lodging, biomass and yield, when compared to a control plant not comprising the recombinant DNA construct.

Another embodiment of the current invention is the above method wherein expression of the polypeptide of part (a) in a plant line having the *fin* mutant

5 genotype is capable of partially or fully restoring the wild-type phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) performing a genetic screen on a population of mutant plants (b) identifying one or more mutant plants that exhibit weak *fin* phenotype than a *fin* null plant; and (c) identifying the weak *fin* allele from
10 the mutant plant with weaker *fin* phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) performing a genetic screen on a population of mutant maize plants (b) identifying one or more mutant maize plants that exhibit weak *fin* phenotype than a *fin* null plant; and (c) identifying the weak *fin*
15 allele from the mutant maize plant with weaker *fin* phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) gene shuffling using one or more nucleotide sequences encoding 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, 46, 48, 50, 51-65, or 66, or a protein
20 that is at least 70% identical to 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, 46, 48, 50, 51-65, or 66, or a fragment thereof; (b) transforming the shuffled sequences from step (a) into a population of regenerable plant cells; (c) regenerating a population of transformed plants from the population of transformed regenerable plant cells of step (b); (d) screening the
25 population of transformed plants from step (c) for weak *fin* phenotype; and (e) identifying the weak *fin* allele from the transformed plant exhibiting weak *fin* phenotype.

One embodiment of the invention is a plant in which expression of the endogenous *FIN* gene is reduced relative to a control plant. Another embodiment of
30 the current invention is a method of making said plant, the method comprising the steps of: (a) introducing a mutation into the endogenous *FIN* gene; and (b) detecting the mutation, wherein the mutation is effective in inhibiting the expression of the endogenous *FIN* gene. In one embodiment, the steps (a) and (b) are done using

Targeting Induced Local Lesions IN Genomics (TILLING) method. In embodiment, the mutation is a site-specific mutation.

One embodiment of the invention is a plant that exhibits weaker *fin* phenotype relative to a wild-type plant. Another embodiment is a method of making said plant wherein the method comprises the steps of: (a) introducing a transposon into a germplasm containing an endogenous *FIN* gene; (b) obtaining progeny of the germplasm of step (a); and (c) identifying a plant of the progeny of step (b) in which the transposon has inserted into the endogenous *FIN* gene and a reduction of expression of *FIN* gene is observed. Step (a) may further comprise introduction of the transposon into a regenerable plant cell of the germplasm by transformation and regeneration of a transgenic plant from the regenerable plant cell, wherein the transgenic plant comprises in its genome the transposon.

In one embodiment, the methods described above wherein the method further comprises the steps of (a) introducing into a regenerable plant cell a recombinant construct comprising the weak *fin* allele identified by the methods described above; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a weak *fin* phenotype, when compared to a control plant not comprising the recombinant DNA construct.

Another embodiment is a method of producing a transgenic plant with an alteration in agronomic characteristic, the method comprising: (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked, in sense or antisense orientation, to a promoter functional in a plant, wherein the polynucleotide comprises: (i) the nucleotide sequence 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, 45, 47 or 49; (ii) a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49; (iii) a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49; (iv) a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or (v) a modified plant

miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration in at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant not comprising the recombinant DNA construct. Another embodiment is the plant produced by this method. Another embodiment is the seed obtained from the plant produced by this method.

Another embodiment is a recombinant DNA construct comprising a polynucleotide that encodes a polypeptide having an amino acid sequence with at least 95% sequence identity, based on Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, and wherein the polypeptide has shoot meristem function altering activity. In another embodiment the polynucleotide encodes a polypeptide that has an amino acid sequence comprising 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, 46, 48, 50, 51-65, or 66, and wherein the polypeptide has shoot meristem function altering activity. In another embodiment, a plant and a seed comprising this recombinant construct is encompassed in the current invention. Another embodiment encompasses a transgenic microorganism comprising this recombinant construct.

Another embodiment is a plant comprising this recombinant construct, wherein the plant exhibits an alteration in at least one of the agronomic characteristics selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield.

Another embodiment is a method of identifying a first plant or a first plant germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first plant or the first plant germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to 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, 46, 48, 50, 51-65, or 66, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising 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, 46, 48, 50, 51-65, or 66.

Another embodiment is a method of identifying a first maize plant or a first maize germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first maize plant or the first maize germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to SEQ ID NO:4, 6 or 8, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising SEQ ID NO:4, 6 or 8.

Another embodiment is a method of increasing WUS expression in a plant or plant cell, wherein the method comprises the steps of: (a) altering a plant or plant cell to decrease endogenous expression of *FIN* gene in the plant or plant cell; (b) determining WUS protein expression in the altered plant or plant cell of step (a); and (c) selecting the altered plant or plant cell of step (b) with increased WUS

expression. Another embodiment of the invention is an altered plant or plant cell produced by this method, wherein the altered plant or plant cell has increased expression of WUS protein, and decreased expression of *FIN* gene.

Another embodiment of the current invention is a method of altering meristem function in a plant, wherein the method comprises the steps of: (a) altering a plant or plant cell to decrease endogenous expression of *FIN* gene in the plant or plant cell; (b) determining meristem function in the altered plant or plant cell; and (c) selecting the altered plant or plant cell of step (a) with altered meristem function.

Another embodiment of this invention is the altered plant or plant cell produced by the above method, wherein the altered plant or plant cell has altered meristem function, and decreased expression of *FIN* gene.

The invention includes a recombinant DNA construct comprising an isolated polynucleotide of the current invention operably linked, in sense or antisense orientation, to a promoter that is shoot apical meristem specific or shoot apical meristem preferred.

This invention includes a vector, cell, microorganism, plant, or seed comprising any of the recombinant DNA constructs described in the present invention.

The invention encompasses plants produced by the methods described herein.

The invention also encompasses regenerated, mature and fertile transgenic plants comprising the recombinant DNA constructs described above, transgenic seeds produced therefrom, T1 and subsequent generations. The transgenic plant cells, tissues, plants, and seeds may comprise at least one recombinant DNA construct of interest.

In one embodiment, the plant is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

In one embodiment, the plant comprising the recombinant constructs described in the present invention is a dicotyledonous plant. In another embodiment, the plant comprising the recombinant constructs described in the present invention is a tomato plant.

In one embodiment, the plant comprising the recombinant constructs described in the present invention is a monocotyledonous plant. In another embodiment, the plant comprising the recombinant constructs described in the present invention is a maize plant.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE LISTINGS

The invention can be more fully understood from the following detailed description and the accompanying drawings and Sequence Listing which form a part of this application. The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in Nucleic Acids Research 13:3021-3030 (1985) and in the Biochemical Journal 219 (No. 2): 345-373 (1984), which are herein incorporated by reference in their entirety. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. § 1.822.

FIG. 1A shows the quantification of floral organ number. Bars represent the mean values $\pm$ SD. Asterisks indicate statistical difference between genotypes; students t-test, $p < 0.01$. For each floral organ, wild-type is the left bar, *fab* is the middle bar, and *fin* is the right bar.

FIG. 1B and FIG. 1C show quantification of the meristem size at EVM and TM stages. Both mutants have significantly larger meristems as early as the EVM stage. Bars represent the mean values $\pm$ SD of meristem height and width at the EVM stage (FIG. 1B) and TM stage (FIG. 1C) for both mutants and wild type. Asterisks indicate statistical difference between genotypes; students t-test, * $p < 0.05$, ** $p < 0.01$. In each group of three bars, wild-type is the left bar, *fab* is the middle bar, and *fin* is the right bar.

FIG. 1D shows that *fin* tomato mutants show increased height and fewer side branches (right) relative to the wild type background genotype M82 (left).

FIG. 1E shows increased fruit size in *fin* (right) relative to M82 (left) (scale bar = 1cm.)

FIG. 2A shows the mapping interval of *FAB*. Vertical red lines show the positions of the closest mapping markers used with the number of recombinants (rec) listed below. *FAB* is boxed in red and a gene model is shown below indicating

characteristic domains and motifs. A red asterisk marks the site of the point mutation found in *fab-e0497*; the amino acid substitution at this position for both tomato and the identical substitution for *Arabidopsis thaliana clv1-9 mutant* are also indicated.

5 FIG. 2B shows the phylogenetic tree including tomato and *Arabidopsis* CLV1 and CLV2 and related proteins demonstrating that tomato FAB is the closest ortholog to *Arabidopsis* CLV1 (boxed in red).

10 FIG. 3A shows the mapping interval of *FIN*. Red lines show the positions of the mapping markers with the number of recombinants (rec) listed below. *FIN* is boxed in red and a gene model is displayed below with characteristic motifs indicated. Asterisks mark the two identified point mutations. Horizontal red lines above the map indicate the deletion mutants, with dashed lines marking the approximate borders of the deletions.

15 FIG. 3B shows a phylogenetic tree of the full tomato and *Arabidopsis* FIN protein family. Tomato FIN is boxed in red. Bootstrap values are indicated at each node.

20 FIG. 4 shows the quantitative phenotyping reveals weak semi-dominance for floral organ numbers in *fab/+* heterozygotes. The mean number of sepal, petal, stamen and carpel number for wild type, *fab/+* heterozygotes and *fab* homozygous mutants are represented in the bar graph with standard deviations (n>29 flowers for each genotype). Significant differences between means were tested by a Student's t-test and significant values are indicated with an asterisks (p<0.01). n.s.=not significant. For each floral organ, wild-type is the left bar, *fab/+* is the middle bar, and *fab* is the right bar.

25 FIG. 5A-5F show the multiple alignment of the amino acid sequences of the FIN polypeptides 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 and 44. Residues that are identical to the residues of SEQ ID NO:2 at a given position are enclosed in a box.

30 FIG. 6 shows the percent sequence identity and the divergence values for each pair of amino acids sequences of FIN polypeptides displayed in FIG. 5A-5F.

The sequence descriptions (Table 1) and Sequence Listing attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825. The Sequence Listing

contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in *Nucleic Acids Res.* 13:3021-3030 (1985) and in the *Biochemical J.* 219 (2):345-373 (1984) which are herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

SEQ ID NO:1 is the nucleotide sequence of the *FIN* wt gene (Solyc11g064850.1.1).

SEQ ID NO:2 is the amino acid sequence of wt FIN protein.

TABLE 1

cDNAs Encoding FIN Polypeptides

Plant	Clone Designation	SEQ ID NO: (Nucleotide)	SEQ ID NO: (Amino Acid)
Corn	dpzm09g005990.1.1 (GRMZM2G072550)	3	4
Corn	dpzm08g001240.1.1 (GRMZM2G035595)	5	6
Corn	dpzm06g044300.1.1 (GRMZM2G055020)	7	8
<i>Sesbania bispinosa</i>	sesgr1n.pk195.i23	9	10
<i>Sesbania bispinosa</i>	sesgr1n.pk090.p7	11	12
<i>Amaranthus hypochondriacus</i>	ahgr1c.pk049.i17	13	14
<i>Amaranthus hypochondriacus</i>	ahgr1c.pk014.i11	15	16
<i>Artemisia tridentata</i>	arttr1n.pk078.j9	17	18
<i>Lamium amplexicaule</i>	hengr1n.pk015.p2	19	20
<i>Lamium amplexicaule</i>	hengr1n.pk239.l13	21	22

<i>Lamium amplexicaule</i>	hengr1n.pk102.j7	23	24
<i>Lamium amplexicaule</i>	hengr1n.pk256.a19	25	26
<i>Delosperma nubigenum</i>	icegr1n.pk149.j10	27	28
<i>Peperomia caperata</i>	pepgr1n.pk256.h2	29	30
<i>Eschscholzia californica</i>	ecalgr1n.pk091.k19	31	32
<i>Eschscholzia californica</i>	ecalgr1n.pk071.k4	33	34
<i>Eschscholzia californica</i>	ecalgr1n.pk103.b5	35	36
<i>Eschscholzia californica</i>	ecalgr1n.pk098.a18	37	38
<i>Peperomia caperata</i>	pepgr1n.pk212.k4.r	39	40
<i>Lamium amplexicaule</i>	hengr1n.pk252.d9_edit	41	42
<i>Linum perenne</i>	lpgr1n.pk056.g15	43	44

SEQ ID NO:45 is the cDNA sequence corresponding to the locus Solyc07g021170.1.1 (*Lycopersicon esculentum*).

SEQ ID NO:46 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus Solyc07g021170.1.1 (*Lycopersicon esculentum*).

SEQ ID NO:47 is the cDNA sequence corresponding to the locus Solyc12g044760.1.1 (*Lycopersicon esculentum*).

SEQ ID NO:48 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus Solyc12g044760.1.1 (*Lycopersicon esculentum*).

SEQ ID NO:49 is the cDNA sequence corresponding to the locus Solyc08g041770.2.1 (*Lycopersicon esculentum*).

SEQ ID NO:50 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus Solyc08g041770.2.1 (*Lycopersicon esculentum*).

5 SEQ ID NO:51 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus At5g25265.1 (*Arabidopsis thaliana*).

SEQ ID NO:52 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus At5g13500.1 (*Arabidopsis thaliana*).

SEQ ID NO:53 is the amino acid sequence encoded by the nucleotide sequence corresponding to the locus At2g25260.1 (*Arabidopsis thaliana*).

10 SEQ ID NO:54 is the amino acid sequence corresponding to the locus LOC_Os05g32060.1, a rice (japonica) predicted protein from the Michigan State University Rice Genome Annotation Project Osa1 release 6 (January 2009).

SEQ ID NO:55 is the amino acid sequence corresponding to the locus LOC_Os01g16600.1, a rice (japonica) predicted protein from the Michigan State
15 University Rice Genome Annotation Project Osa1 release 6 (January 2009).

SEQ ID NO:56 is the amino acid sequence corresponding to the locus LOC_Os06g08180.1, a rice (japonica) predicted protein from the Michigan State University Rice Genome Annotation Project Osa1 release 6 (January 2009).

20 SEQ ID NO:57 is the amino acid sequence corresponding to Sb09g019030.1, a sorghum (*Sorghum bicolor*) predicted protein from the Sorghum JGI genomic sequence version 1.4 from the US Department of energy Joint Genome Institute.

SEQ ID NO:58 is the amino acid sequence corresponding to Sb03g010840.1, a sorghum (*Sorghum bicolor*) predicted protein from the Sorghum JGI genomic sequence version 1.4 from the US Department of energy Joint Genome Institute.

25 SEQ ID NO:59 is the amino acid sequence corresponding to Sb10g005440.1, a sorghum (*Sorghum bicolor*) predicted protein from the Sorghum JGI genomic sequence version 1.4 from the US Department of energy Joint Genome Institute.

SEQ ID NO:60 is the amino acid sequence corresponding to Glyma13g26610.1, a soybean (*Glycine max*) predicted protein from predicted
30 coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:61 is the amino acid sequence corresponding to Glyma15g37490.1, a soybean (*Glycine max*) predicted protein from predicted

coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:62 is the amino acid sequence corresponding to Glyma14g03930.1, a soybean (*Glycine max*) predicted protein from predicted coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:63 is the amino acid sequence corresponding to Glyma20g08020.1, a soybean (*Glycine max*) predicted protein from predicted coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:64 is the amino acid sequence corresponding to Glyma14g13780.1, a soybean (*Glycine max*) predicted protein from predicted coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:65 is the amino acid sequence corresponding to Glyma17g32910.1, a soybean (*Glycine max*) predicted protein from predicted coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:66 is the amino acid sequence corresponding to Glyma02g44810.1, a soybean (*Glycine max*) predicted protein from predicted coding sequences from Soybean JGI Glyma1.01 genomic sequence from the US Department of energy Joint Genome Institute.

SEQ ID NO:67 is the sequence of the EMS *FIN* allele e4489.

SEQ ID NO:68 is the sequence of the EMS *FIN* allele e4632.

The sequence descriptions and Sequence Listing attached hereto comply with the rules governing nucleotide and/or amino acid sequence disclosures in patent applications as set forth in 37 C.F.R. §1.821-1.825.

The Sequence Listing contains the one letter code for nucleotide sequence characters and the three letter codes for amino acids as defined in conformity with the IUPAC-IUBMB standards described in *Nucleic Acids Res.* 13:3021-3030 (1985) and in the *Biochemical J.* 219 (No. 2):345-373 (1984) which are herein incorporated by reference. The symbols and format used for nucleotide and amino acid sequence data comply with the rules set forth in 37 C.F.R. §1.822.

DETAILED DESCRIPTION OF THE INVENTION

The disclosure of each reference set forth herein is hereby incorporated by reference in its entirety.

As used herein and in the appended claims, the singular forms "a", "an", and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, reference to "a plant" includes a plurality of such plants, reference to "a cell" includes one or more cells and equivalents thereof known to those skilled in the art, and so forth.

As used herein:

The terms "monocot" and "monocotyledonous plant" are used interchangeably herein. A monocot of the current invention includes the *Gramineae*.

The terms "dicot" and "dicotyledonous plant" are used interchangeably herein. A dicot of the current invention includes the following families: *Brassicaceae*, *Leguminosae*, and *Solanaceae*.

The terms "full complement" and "full-length complement" are used interchangeably herein, and refer to a complement of a given nucleotide sequence, wherein the complement and the nucleotide sequence consist of the same number of nucleotides and are 100% complementary.

"Transgenic" refers to any cell, cell line, callus, tissue, plant part or plant, the genome of which has been altered by the presence of a heterologous nucleic acid, such as a recombinant DNA construct, including those initial transgenic events as well as those created by sexual crosses or asexual propagation from the initial transgenic event. The term "transgenic" as used herein does not encompass the alteration of the genome (chromosomal or extra-chromosomal) by conventional plant breeding methods or by naturally occurring events such as random cross-fertilization, non-recombinant viral infection, non-recombinant bacterial transformation, non-recombinant transposition, or spontaneous mutation.

"Genome" as it applies to plant cells encompasses not only chromosomal DNA found within the nucleus, but organelle DNA found within subcellular components (e.g., mitochondrial, plastid) of the cell.

"Plant" includes reference to whole plants, plant organs, plant tissues, seeds and plant cells and progeny of same. Plant cells include, without limitation, cells

from seeds, suspension cultures, embryos, meristematic regions, callus tissue, leaves, roots, shoots, gametophytes, sporophytes, pollen, and microspores.

"Progeny" comprises any subsequent generation of a plant.

"Transgenic plant" includes reference to a plant which comprises within its
5 genome a heterologous polynucleotide. For example, the heterologous polynucleotide is stably integrated within the genome such that the polynucleotide is passed on to successive generations. The heterologous polynucleotide may be integrated into the genome alone or as part of a recombinant DNA construct.

A "trait" refers to a physiological, morphological, biochemical, or physical
10 characteristic of a plant or particular plant material or cell. In some instances, this characteristic is visible to the human eye, such as seed or plant size, or can be measured by biochemical techniques, such as detecting the protein, starch, or oil content of seed or leaves, or by observation of a metabolic or physiological process, e.g. by measuring tolerance to water deprivation or particular salt or sugar
15 concentrations, or by the observation of the expression level of a gene or genes, or by agricultural observations such as osmotic stress tolerance or yield.

"Agronomic characteristic" is a measurable parameter including but not limited to, ear meristem size, tassel size, greenness, yield, growth rate, biomass, fresh weight at maturation, dry weight at maturation, fruit size, fruit yield, seed yield,
20 total plant nitrogen content, fruit nitrogen content, seed nitrogen content, nitrogen content in a vegetative tissue, total plant free amino acid content, fruit free amino acid content, seed free amino acid content, free amino acid content in a vegetative tissue, total plant protein content, fruit protein content, seed protein content, protein content in a vegetative tissue, drought tolerance, nitrogen uptake, root lodging,
25 harvest index, stalk lodging, plant height, ear height, ear length, salt tolerance, early seedling vigor and seedling emergence under low temperature stress.

"Heterologous" with respect to sequence means a sequence that originates from a foreign species, or, if from the same species, is substantially modified from its native form in composition and/or genomic locus by deliberate human
30 intervention.

"Polynucleotide", "nucleic acid sequence", "nucleotide sequence", or "nucleic acid fragment" are used interchangeably to refer to a polymer of RNA or DNA that is single- or double-stranded, optionally containing synthetic, non-natural or altered

nucleotide bases. Nucleotides (usually found in their 5'-monophosphate form) are referred to by their single letter designation as follows: "A" for adenylate or deoxyadenylate (for RNA or DNA, respectively), "C" for cytidylate or deoxycytidylate, "G" for guanylate or deoxyguanylate, "U" for uridylate, "T" for deoxythymidylate, "R" for purines (A or G), "Y" for pyrimidines (C or T), "K" for G or T, "H" for A or C or T, "I" for inosine, and "N" for any nucleotide.

"Polypeptide", "peptide", "amino acid sequence" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical analogue of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers. The terms "polypeptide", "peptide", "amino acid sequence", and "protein" are also inclusive of modifications including, but not limited to, glycosylation, lipid attachment, sulfation, gamma-carboxylation of glutamic acid residues, hydroxylation and ADP-ribosylation.

"Messenger RNA (mRNA)" refers to the RNA that is without introns and that can be translated into protein by the cell.

"cDNA" refers to a DNA that is complementary to and synthesized from an mRNA template using the enzyme reverse transcriptase. The cDNA can be single-stranded or converted into the double-stranded form using the Klenow fragment of DNA polymerase I.

"Coding region" refers to a polynucleotide sequence that when transcribed, processed, and/or translated results in the production of a polypeptide sequence.

An "Expressed Sequence Tag" ("EST") is a DNA sequence derived from a cDNA library and therefore is a sequence which has been transcribed. An EST is typically obtained by a single sequencing pass of a cDNA insert. The sequence of an entire cDNA insert is termed the "Full-Insert Sequence" ("FIS"). A "Contig" sequence is a sequence assembled from two or more sequences that can be selected from, but not limited to, the group consisting of an EST, FIS and PCR sequence. A sequence encoding an entire or functional protein is termed a "Complete Gene Sequence" ("CGS") and can be derived from an FIS or a contig.

"Mature" protein refers to a post-translationally processed polypeptide; i.e., one from which any pre- or pro-peptides present in the primary translation product have been removed.

“Precursor” protein refers to the primary product of translation of mRNA; i.e., with pre- and pro-peptides still present. Pre- and pro-peptides may be and are not limited to intracellular localization signals.

5 “Isolated” refers to materials, such as nucleic acid molecules and/or proteins, which are substantially free or otherwise removed from components that normally accompany or interact with the materials in a naturally occurring environment. Isolated polynucleotides may be purified from a host cell in which they naturally occur. Conventional nucleic acid purification methods known to skilled artisans may be used to obtain isolated polynucleotides. The term also embraces recombinant
10 polynucleotides and chemically synthesized polynucleotides.

“Recombinant” refers to an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis or by the manipulation of isolated segments of nucleic acids by genetic engineering techniques.

“Recombinant” also includes reference to a cell or vector, that has been modified by
15 the introduction of a heterologous nucleic acid or a cell derived from a cell so modified, but does not encompass the alteration of the cell or vector by naturally occurring events (e.g., spontaneous mutation, natural transformation/transduction/transposition) such as those occurring without deliberate human intervention.

20 “Recombinant DNA construct” refers to a combination of nucleic acid fragments that are not normally found together in nature. Accordingly, a recombinant DNA construct may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different
25 than that normally found in nature.

The terms “entry clone” and “entry vector” are used interchangeably herein.

“Regulatory sequences” or “regulatory elements” are used interchangeably and refer to nucleotide sequences located upstream (5' non-coding sequences), within, or downstream (3' non-coding sequences) of a coding sequence, and which
30 influence the transcription, RNA processing or stability, or translation of the associated coding sequence. Regulatory sequences may include, but are not limited to, promoters, translation leader sequences, introns, and polyadenylation

recognition sequences. The terms "regulatory sequence" and "regulatory element" are used interchangeably herein.

"Promoter" refers to a nucleic acid fragment capable of controlling transcription of another nucleic acid fragment.

5 "Promoter functional in a plant" is a promoter capable of controlling transcription in plant cells whether or not its origin is from a plant cell.

"Tissue-specific promoter" and "tissue-preferred promoter" are used interchangeably to refer to a promoter that is expressed predominantly but not necessarily exclusively in one tissue or organ, but that may also be expressed in
10 one specific cell.

"Developmentally regulated promoter" refers to a promoter whose activity is determined by developmental events.

"Operably linked" refers to the association of nucleic acid fragments in a single fragment so that the function of one is regulated by the other. For example, a
15 promoter is operably linked with a nucleic acid fragment when it is capable of regulating the transcription of that nucleic acid fragment.

"Expression" refers to the production of a functional product. For example, expression of a nucleic acid fragment may refer to transcription of the nucleic acid fragment (e.g., transcription resulting in mRNA or functional RNA) and/or translation
20 of mRNA into a precursor or mature protein.

"Overexpression" refers to the production of a gene product in transgenic organisms that exceeds levels of production in a null segregating (or non-transgenic) organism from the same experiment.

"Phenotype" means the detectable characteristics of a cell or organism.

25 "Introduced" in the context of inserting a nucleic acid fragment (e.g., a recombinant DNA construct) into a cell, means "transfection" or "transformation" or "transduction" and includes reference to the incorporation of a nucleic acid fragment into a eukaryotic or prokaryotic cell where the nucleic acid fragment may be incorporated into the genome of the cell (e.g., chromosome, plasmid, plastid or
30 mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

A "transformed cell" is any cell into which a nucleic acid fragment (e.g., a recombinant DNA construct) has been introduced.

“Transformation” as used herein refers to both stable transformation and transient transformation.

“Stable transformation” refers to the introduction of a nucleic acid fragment into a genome of a host organism resulting in genetically stable inheritance. Once stably transformed, the nucleic acid fragment is stably integrated in the genome of the host organism and any subsequent generation.

“Transient transformation” refers to the introduction of a nucleic acid fragment into the nucleus, or DNA-containing organelle, of a host organism resulting in gene expression without genetically stable inheritance.

The term “crossed” or “cross” means the fusion of gametes via pollination to produce progeny (e.g., cells, seeds or plants). The term encompasses both sexual crosses (the pollination of one plant by another) and selfing (self-pollination, e.g., when the pollen and ovule are from the same plant). The term “crossing” refers to the act of fusing gametes via pollination to produce progeny.

A “favorable allele” is the allele at a particular locus that confers, or contributes to, a desirable phenotype, e.g., increased cell wall digestibility, or alternatively, is an allele that allows the identification of plants with decreased cell wall digestibility that can be removed from a breeding program or planting (“counterselection”). A favorable allele of a marker is a marker allele that segregates with the favorable phenotype, or alternatively, segregates with the unfavorable plant phenotype, therefore providing the benefit of identifying plants.

The term “introduced” means providing a nucleic acid (e.g., expression construct) or protein into a cell. Introduced includes reference to the incorporation of a nucleic acid into a eukaryotic or prokaryotic cell where the nucleic acid may be incorporated into the genome of the cell, and includes reference to the transient provision of a nucleic acid or protein to the cell. Introduced includes reference to stable or transient transformation methods, as well as sexually crossing. Thus, “introduced” in the context of inserting a nucleic acid fragment (e.g., a recombinant DNA construct/expression construct) into a cell, means “transfection” or “transformation” or “transduction” and includes reference to the incorporation of a nucleic acid fragment into a eukaryotic or prokaryotic cell where the nucleic acid fragment may be incorporated into the genome of the cell (e.g., chromosome,

plasmid, plastid or mitochondrial DNA), converted into an autonomous replicon, or transiently expressed (e.g., transfected mRNA).

“Suppression DNA construct” is a recombinant DNA construct which when transformed or stably integrated into the genome of the plant, results in “silencing” of a target gene in the plant. The target gene may be endogenous or transgenic to the plant. “Silencing,” as used herein with respect to the target gene, refers generally to the suppression of levels of mRNA or protein/enzyme expressed by the target gene, and/or the level of the enzyme activity or protein functionality. The terms “suppression”, “suppressing” and “silencing”, used interchangeably herein, include lowering, reducing, declining, decreasing, inhibiting, eliminating or preventing. “Silencing” or “gene silencing” does not specify mechanism and is inclusive, and not limited to, anti-sense, cosuppression, viral-suppression, hairpin suppression, stem-loop suppression, RNAi-based approaches, and small RNA-based approaches. Silencing may be targeted to coding regions or non-coding regions, e.g., introns, 5'-UTRs and 3'-UTRs, or both.

A suppression DNA construct may comprise a region derived from a target gene of interest and may comprise all or part of the nucleic acid sequence of the sense strand (or antisense strand) of the target gene of interest. Depending upon the approach to be utilized, the region may be 100% identical or less than 100% identical (e.g., at least 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% identical) to all or part of the sense strand (or antisense strand) of the gene of interest.

Suppression DNA constructs are well-known in the art, are readily constructed once the target gene of interest is selected, and include, without limitation, cosuppression constructs, antisense constructs, viral-suppression constructs, hairpin suppression constructs, stem-loop suppression constructs, double-stranded RNA-producing constructs, and more generally, RNAi (RNA interference) constructs and small RNA constructs such as siRNA (short interfering RNA) constructs and miRNA (microRNA) constructs.

“Antisense inhibition” refers to the production of antisense RNA transcripts capable of suppressing the expression of the target gene or gene product.

“Antisense RNA” refers to an RNA transcript that is complementary to all or part of a target primary transcript or mRNA and that blocks the expression of a target isolated nucleic acid fragment (U.S. Patent No. 5,107,065). The complementarity of an antisense RNA may be with any part of the specific gene transcript, i.e., at the 5' non-coding sequence, 3' non-coding sequence, introns, or the coding sequence.

“Cosuppression” refers to the production of sense RNA transcripts capable of suppressing the expression of the target gene or gene product. “Sense” RNA refers to RNA transcript that includes the mRNA and can be translated into protein within a cell or *in vitro*. Cosuppression constructs in plants have been previously designed by focusing on overexpression of a nucleic acid sequence having homology to a native mRNA, in the sense orientation, which results in the reduction of all RNA having homology to the overexpressed sequence (see Vaucheret et al., *Plant J.* 16:651-659 (1998); and Gura, *Nature* 404:804-808 (2000)). Cosuppression constructs may contain sequences from coding regions or non-coding regions, e.g., introns, 5'-UTRs and 3'-UTRs, or both.

Another variation describes the use of plant viral sequences to direct the suppression of proximal mRNA encoding sequences (PCT Publication No. WO 98/36083 published on August 20, 1998).

RNA interference refers to the process of sequence-specific post-transcriptional gene silencing in animals mediated by short interfering RNAs (siRNAs) (Fire et al., *Nature* 391:806 (1998)). The corresponding process in plants is commonly referred to as post-transcriptional gene silencing (PTGS) or RNA silencing and is also referred to as quelling in fungi. The process of post-transcriptional gene silencing is thought to be an evolutionarily-conserved cellular defense mechanism used to prevent the expression of foreign genes and is commonly shared by diverse flora and phyla (Fire et al., *Trends Genet.* 15:358 (1999)).

Small RNAs play an important role in controlling gene expression. Regulation of many developmental processes, including flowering, is controlled by small RNAs. It is now possible to engineer changes in gene expression of plant genes by using transgenic constructs which produce small RNAs in the plant.

Small RNAs appear to function by base-pairing to complementary RNA or DNA target sequences. When bound to RNA, small RNAs trigger either RNA

cleavage or translational inhibition of the target sequence. When bound to DNA target sequences, it is thought that small RNAs can mediate DNA methylation of the target sequence. The consequence of these events, regardless of the specific mechanism, is that gene expression is inhibited.

5 MicroRNAs (miRNAs) are noncoding RNAs of about 19 to about 24 nucleotides (nt) in length that have been identified in both animals and plants (Lagos-Quintana et al., *Science* 294:853-858 (2001), Lagos-Quintana et al., *Curr. Biol.* 12:735-739 (2002); Lau et al., *Science* 294:858-862 (2001); Lee and Ambros, *Science* 294:862-864 (2001); Llave et al., *Plant Cell* 14:1605-1619 (2002);
10 Mourelatos et al., *Genes. Dev.* 16:720-728 (2002); Park et al., *Curr. Biol.* 12:1484-1495 (2002); Reinhart et al., *Genes. Dev.* 16:1616-1626 (2002)). They are processed from longer precursor transcripts that range in size from approximately 70 to 200 nt, and these precursor transcripts have the ability to form stable hairpin structures.

15 MicroRNAs (miRNAs) appear to regulate target genes by binding to complementary sequences located in the transcripts produced by these genes. It seems likely that miRNAs can enter at least two pathways of target gene regulation: (1) translational inhibition; and (2) RNA cleavage. MicroRNAs entering the RNA cleavage pathway are analogous to the 21-25 nt short interfering RNAs (siRNAs)
20 generated during RNA interference (RNAi) in animals and posttranscriptional gene silencing (PTGS) in plants, and likely are incorporated into an RNA-induced silencing complex (RISC) that is similar or identical to that seen for RNAi.

 The term "locus" generally refers to a genetically defined region of a chromosome carrying a gene or, possibly, two or more genes so closely linked that
25 genetically they behave as a single locus responsible for a phenotype. When used herein with respect to *FIN*, the "*FIN* locus" shall refer to the defined region of the chromosome carrying the *FIN* gene including its associated regulatory sequences.

 A "gene" shall refer to a specific genetic coding region within a locus, including its associated regulatory sequences. One of ordinary skill in the art would
30 understand that the associated regulatory sequences will be within a distance of about 4 kb from the *FIN* coding sequence, with the promoter located upstream.

 "Germplasm" refers to genetic material of or from an individual (e.g., a plant), a group of individuals (e.g., a plant line, variety or family), or a clone derived from a

line, variety, species, or culture. The germplasm can be part of an organism or cell, or can be separate from the organism or cell. In general, germplasm provides genetic material with a specific molecular makeup that provides a physical foundation for some or all of the hereditary qualities of an organism or cell culture.

5 As used herein, germplasm includes cells, seed or tissues from which new plants may be grown, or plant parts, such as leaves, stems, pollen, or cells, that can be cultured into a whole plant.

Sequence alignments and percent identity calculations may be determined using a variety of comparison methods designed to detect homologous sequences
10 including, but not limited to, the Megalign® program of the LASERGENE® bioinformatics computing suite (DNASTAR® Inc., Madison, WI). Unless stated otherwise, multiple alignment of the sequences provided herein were performed using the Clustal W method of alignment.

The Clustal W method of alignment (described by Higgins and Sharp,
15 CABIOS. 5:151-153 (1989); Higgins, D. G. et al., Comput. Appl. Biosci. 8:189-191 (1992)) can be found in the MegAlign™ v6.1 program of the LASERGENE® bioinformatics computing suite (DNASTAR® Inc., Madison, Wis.). Default parameters for multiple alignment correspond to GAP PENALTY=10, GAP LENGTH PENALTY=0.2, Delay Divergent Sequences=30%, DNA Transition Weight=0.5,
20 Protein Weight Matrix=Gonnet Series, DNA Weight Matrix=IUB. For pairwise alignments the default parameters are Alignment=Slow-Accurate, Gap Penalty=10.0, Gap Length=0.10, Protein Weight Matrix=Gonnet 250 and DNA Weight Matrix=IUB.

After alignment of the sequences, using the Clustal W program, it is possible
25 to obtain “percent identity” and “divergence” values by viewing the “sequence distances” table on the same program; unless stated otherwise, percent identities and divergences provided and claimed herein were calculated in this manner.

The present invention includes the following isolated polynucleotides and polypeptides:

30 An isolated polynucleotide comprising: (i) a nucleic acid sequence encoding a polypeptide having an amino acid sequence of at least 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%, 99%, or 100% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66; or (ii) a full

5 complement of the nucleic acid sequence of (i), wherein the full complement and the nucleic acid sequence of (i) consist of the same number of nucleotides and are 100% complementary. Any of the foregoing isolated polynucleotides may be utilized in any recombinant DNA constructs (including suppression DNA constructs) of the present invention. The polypeptide is preferably a FIN polypeptide. The
10 polypeptide preferably has FIN activity.

An isolated polypeptide having an amino acid sequence of at least 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%,
15 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66. The polypeptide is preferably a FIN polypeptide. The polypeptide preferably has FIN activity.

20 An isolated polynucleotide comprising (i) a nucleic acid sequence of at least 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%, 99%, or 100% sequence identity, based on
25 the Clustal W method of alignment, when compared to 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, 45, 47 or 49; or (ii) a full complement of the nucleic acid sequence of (i). Any of the foregoing isolated polynucleotides may be utilized in any recombinant DNA constructs (including suppression DNA constructs) of the present invention. The polynucleotide
30 preferably encodes a FIN polypeptide. The polypeptide preferably has FIN activity.

An isolated polynucleotide comprising a nucleotide sequence, wherein the nucleotide sequence is hybridizable under stringent conditions with a DNA molecule comprising the full complement 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, 45, 47 or 49. The polynucleotide preferably encodes a FIN polypeptide. The polypeptide preferably has FIN activity.

An isolated polynucleotide comprising a nucleotide sequence, wherein the nucleotide sequence is derived from 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, 45, 47 or 49 by alteration of one or more nucleotides by at least one method selected from the group consisting of: deletion, substitution, addition and insertion. The polynucleotide preferably encodes a FIN polypeptide. The polypeptide preferably has FIN activity.

An isolated polynucleotide comprising a nucleotide sequence, wherein the nucleotide sequence corresponds to an allele 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, 45, 47 or 49.

In one embodiment, the present invention includes recombinant DNA constructs (including suppression DNA constructs). The recombinant DNA construct (including suppression DNA constructs) may comprise a polynucleotide of the present invention operably linked, in sense or antisense orientation, to at least one regulatory sequence (e.g., a promoter functional in a plant). The polynucleotide may comprise 100, 200, 300, 400, 500, 600, 700, 800, 900 or 1000 contiguous nucleotides 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, 45, 47 or 49. The polynucleotide may encode a polypeptide of the present invention.

Standard recombinant DNA and molecular cloning techniques used herein are well known in the art and are described more fully in Sambrook, J., Fritsch, E.F. and Maniatis, T. *Molecular Cloning: A Laboratory Manual*; Cold Spring Harbor Laboratory Press: Cold Spring Harbor, 1989 (hereinafter "Sambrook").

It is well understood by those skilled in the art that different promoters may direct the expression of a gene in different tissues or cell types, or at different stages of development, or in response to different environmental conditions.

Promoters that can be used for this invention include, but are not limited to, shoot apical meristem specific promoters and shoot apical meristem preferred promoters.

Maize *knotted 1* promoter, and promoters from genes that are known to be expressed in maize SAM can be used for expressing the polynucleotides disclosed in the current invention. Examples of such genes include, but are not limited to Zm

phabulosa, *terminal ear1*, *rough sheath2*, *rolled leaf1*, *zyb14*, *narrow sheath* (Ohtsu, K. et al (2007) *Plant Journal* 52, 391–404). Promoters from orthologs of these genes from other species can be also be used for the current invention.

Examples of *Arabidopsis* promoters from genes with SAM-preferred expression include, but are not limited to, *clv3*, *aintegumenta-like (ail5, ail6, and ail7)* and *terminal ear like1*, *clavata1*, *wus*, *shootmeristemless*, *terminal flower1* (Yadav et al (2009) *Proc Natl Acad Sci U S A*. March 24).

Tomato promoters can also be used for the recombinant constructs described in this invention. Tomato promoters with shoot meristem-specific expression can be used for this invention. Examples of tomato promoters from genes with SAM-preferred expression include, but are not limited to, *KNAT6*, *WUSCHEL (WUS)*, *LBD1 (LATERAL ORGAN BOUNDARIES DOMAIN 1)*, *BLH1 (BELL-like homeodomain protein 1)* (Wang et al. Plos one, 2013 (8) Issue 2 e55238).

PCT Publication No. WO 2004/071467 and US Patent No. 7,129,089 describe the synthesis of multiple promoter/gene/terminator cassette combinations by ligating individual promoters, genes, and transcription terminators together in unique combinations. Generally, a *NotI* site flanked by the suitable promoter is used to clone the desired gene. *NotI* sites can be added to a gene of interest using PCR amplification with oligonucleotides designed to introduce *NotI* sites at the 5' and 3' ends of the gene. The resulting PCR product is then digested with *NotI* and cloned into a suitable promoter/*NotI*/terminator cassette. Although gene cloning into expression cassettes is often done using the *NotI* restriction enzyme, one skilled in the art can appreciate that a number of restriction enzymes can be utilized to achieve the desired cassette. Further, one skilled in the art will appreciate that other cloning techniques including, but not limited to, PCR-based or recombination-based techniques can be used to generate suitable expression cassettes.

In addition, WO 2004/071467 and US Patent No. 7,129,089 describe the further linking together of individual promoter/gene/transcription terminator cassettes in unique combinations and orientations, along with suitable selectable marker cassettes, in order to obtain the desired phenotypic expression. Although this is done mainly using different restriction enzymes sites, one skilled in the art can appreciate that a number of techniques can be utilized to achieve the desired

promoter/gene/transcription terminator combination or orientations. In so doing, any combination and orientation of shoot apical meristem-specific promoter/gene/transcription terminator cassettes can be achieved. One skilled in the art can also appreciate that these cassettes can be located on individual DNA fragments or on multiple fragments where co-expression of genes is the outcome of co-transformation of multiple DNA fragments.

The wild-type *FIN* gene or “fasciated inflorescence” gene encodes the “FIN protein” that is a novel regulator of meristem function in plants. “*FIN* gene” as described herein refers to the gene from the tomato plant locus Solyc11g064850, and homologs of this gene. “FIN protein” as described herein refers to the tomato FIN protein encoded by the locus Solyc11g064850, and its homologs from tomato and other organisms. “FIN proteins” would include proteins from plants such as *Lycopersicon esculentum*, *Arabidopsis thaliana*, *Zea mays*, *Glycine max*, *Glycine tabacina*, *Glycine soja*, *Glycine tomentella*, *Oryza sativa*, *Brassica napus*, *Sorghum bicolor*, *Paspalum notatum*, *Eragrostis nindensis*, *Saccharum officinarum*, or *Triticum aestivum*. These are examples of plant species from which “FIN protein” can be isolated, and are not meant to be limiting.

The “tomato FIN protein” described herein is encoded by the locus Solyc11g064850, and is a 373 amino acid protein, is predicted to have an N-terminal signal peptide in the first 25 amino acids and a single transmembrane domain. It has been found to regulate meristem function and fruit size in tomato.

As used herein, a polypeptide (or polynucleotide) with “FIN activity” refers to a polypeptide (or polynucleotide), that when expressed in a “*fin* mutant line” that exhibits the “*fin* mutant phenotype”, is capable of partially or fully rescuing the *fin* mutant phenotype.

A polypeptide with “FIN activity” also has shoot meristem function altering activity.

Our analysis of *fin/fab* double mutants indicates that FIN and FAB proteins act in independent pathways. Our analysis of *fin/s* double mutants indicates that FIN and S proteins act in independent pathways.

Our analysis of *fin/an* double mutants indicates that FIN and AN proteins act in independent pathways.

The term fasciation, from the Latin *fascis*, meaning bundle, describes variations in plant form resulting from proliferative growth.

Plants with *FIN* loss of function mutations, wherein the mutation results in a loss of *fin* function or loss of *fin* expression are also called “*fin* plants” or “*fin* null plants”. “*fin* null plants” exhibit the “*fin* phenotype” or the “*fin* null phenotype”.

FIN loss of function mutations in tomato result in increased inflorescence branches, flowers, locule number and fruit size due to the progressive over-proliferation of plant stem cells in shoot meristems, suggesting that *FIN* protein is a regulator of meristem function and normally acts to limit the growth of these meristems. Our analysis shows that *FIN* is a member of a small, but well conserved, plant specific unknown gene family that has not been previously characterized, and is therefore a novel regulator of meristem function. Plants with weak *fin* mutations, wherein the mutation results in a partial loss of *fin* function or partial loss of *fin* expression are also called “*fin* plants with weak *fin* phenotype”. “weak *fin* plants” exhibit the “weak *fin* phenotype”. *fin* plants with weak *fin* alleles exhibit similar phenotype as the *fin* null plants, but to a lesser extent. *fin* plants with weak *fin* alleles may also exhibit partial *fin* null phenotype, that is may not exhibit all the *fin* null characteristics. “Weak *fin* alleles” as referred to herein are *fin* variants or variants 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, 45, 47 or 49, which confer weak *fin* phenotype on the plant.

Plants with *fin* mutations that exhibit “null *fin* phenotype” or “weak *fin* phenotype” are referred to herein as plants with “mutant *fin* phenotype”.

The term “dominant negative mutation” as used herein refers to a mutation that has an altered gene product that acts antagonistically to the wild-type allele. These mutations usually result in an altered molecular function (often inactive) and are characterized by a “dominant negative” phenotype. A gene variant, a mutated gene or an allele that confers “dominant negative phenotype” would confer a “null” or a “mutated” phenotype on the host cell even in the presence of a wild-type allele.

The terms “gene shuffling” and “directed evolution” are used interchangeably herein. The method of “gene shuffling” consists of iterations of DNA shuffling followed by appropriate screening and/or selection to generate variants of *FIN* nucleic acids or portions thereof having a modified biological activity (Castle et al., (2004) Science 304(5674):1151-4; U.S. Patent Nos. 5,811,238 and 6,395,547).

“TILLING” or “Targeting Induced Local Lesions IN Genomics” refers to a mutagenesis technology useful to generate and/or identify, and to eventually isolate mutagenised variants of a particular nucleic acid with modulated expression and/or activity (McCallum et al., (2000), *Plant Physiology* 123:439-442; McCallum et al., (2000) *Nature Biotechnology* 18:455-457; and, Colbert et al., (2001) *Plant Physiology* 126:480-484).

TILLING combines high density point mutations with rapid sensitive detection of the mutations. Typically, ethylmethanesulfonate (EMS) is used to mutagenize plant seed. EMS alkylates guanine, which typically leads to mispairing. For example, seeds are soaked in an about 10-20 mM solution of EMS for about 10 to 20 hours; the seeds are washed and then sown. The plants of this generation are known as M1. M1 plants are then self-fertilized. Mutations that are present in cells that form the reproductive tissues are inherited by the next generation (M2). Typically, M2 plants are screened for mutation in the desired gene and/or for specific phenotypes.

TILLING also allows selection of plants carrying mutant variants. These mutant variants may exhibit modified expression, either in strength or in location or in timing (if the mutations affect the promoter for example). These mutant variants may even exhibit lower *FIN* activity than that exhibited by the gene in its natural form. TILLING combines high-density mutagenesis with high-throughput screening methods. The steps typically followed in TILLING are: (a) EMS mutagenesis (Redei G P and Koncz C (1992) In *Methods in Arabidopsis Research*, Koncz C, Chua N H, Schell J, eds. Singapore, World Scientific Publishing Co, pp. 16-82; Feldmann et al., (1994) In Meyerowitz E M, Somerville C R, eds, *Arabidopsis*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., pp 137-172; Lightner J and Caspar T (1998) In J Martinez-Zapater, J Salinas, eds, *Methods on Molecular Biology*, Vol. 82. Humana Press, Totowa, N.J., pp 91-104); (b) DNA preparation and pooling of individuals; (c) PCR amplification of a region of interest; (d) denaturation and annealing to allow formation of heteroduplexes; (e) DHPLC, where the presence of a heteroduplex in a pool is detected as an extra peak in the chromatogram; (f) identification of the mutant individual; and (g) sequencing of the mutant PCR product. Methods for TILLING are well known in the art (US Patent No. 8,071,840).

Other mutagenic methods can also be employed to introduce mutations in the *FIN* gene. Methods for introducing genetic mutations into plant genes and

selecting plants with desired traits are well known. For instance, seeds or other plant material can be treated with a mutagenic chemical substance, according to standard techniques. Such chemical substances include, but are not limited to, the following: diethyl sulfate, ethylene imine, and N-nitroso-N-ethylurea. Alternatively, ionizing radiation from sources such as X-rays or gamma rays can be used.

Other detection methods for detecting mutations in the *FIN* gene can be employed, e.g., capillary electrophoresis (e.g., constant denaturant capillary electrophoresis and single-stranded conformational polymorphism). In another example, heteroduplexes can be detected by using mismatch repair enzymology (e.g., CELI endonuclease from celery). CELI recognizes a mismatch and cleaves exactly at the 3' side of the mismatch. The precise base position of the mismatch can be determined by cutting with the mismatch repair enzyme followed by, e.g., denaturing gel electrophoresis. See, e.g., Oleykowski et al., (1998) "Mutation detection using a novel plant endonuclease" *Nucleic Acid Res.* 26:4597-4602; and, Colbert et al., (2001) "High-Throughput Screening for Induced Point Mutations" *Plant Physiology* 126:480-484.

The plant containing the mutated *FIN* gene can be crossed with other plants to introduce the mutation into another plant. This can be done using standard breeding techniques.

Homologous recombination allows introduction in a genome of a selected nucleic acid at a defined selected position. Homologous recombination has been demonstrated in plants. See, e.g., Puchta et al. (1994), *Experientia* 50: 277-284; Swoboda et al. (1994), *EMBO J.* 13: 484-489; Offringa et al. (1993), *Proc. Natl. Acad. Sci. USA* 90: 7346-7350; Kempin et al. (1997) *Nature* 389:802-803; and, Terada et al., (2002) *Nature Biotechnology*, 20(10):1030-1034).

Methods for performing homologous recombination in plants have been described not only for model plants (Offringa et al. (1990) *EMBO J.* October; 9(10):3077-84) but also for crop plants, for example rice (Terada R, Urawa H, Inagaki Y, Tsugane K, Iida S. *Nat Biotechnol.* 2002 20(10):1030-4; Iida and Terada: *Curr Opin Biotechnol.* 2004 April; 15(2):1328). The nucleic acid to be introduced (which may be *FIN* nucleic acid or a variant thereof as hereinbefore defined) need not be targeted to the locus of the *FIN* gene, but may be introduced into, for example, regions of high expression. The nucleic acid to be introduced may be a

weak *fin* allele or a dominant negative allele used to replace the endogenous gene or may be introduced in addition to the endogenous gene.

Transposable elements can be categorized into two broad classes based on their mode of transposition. These are designated Class I and Class II; both have applications as mutagens and as delivery vectors. Class I transposable elements transpose by an RNA intermediate and use reverse transcriptases, i.e., they are retroelements. There are at least three types of Class I transposable elements, e.g., retrotransposons, retroposons, SINE-like elements. Retrotransposons typically contain LTRs, and genes encoding viral coat proteins (*gag*) and reverse transcriptase, *RnaseH*, integrase and polymerase (*pol*) genes. Numerous retrotransposons have been described in plant species. Such retrotransposons mobilize and translocate via a RNA intermediate in a reaction catalyzed by reverse transcriptase and *RNase H* encoded by the transposon. Examples fall into the *Tyl*-*copia* and *Ty3*-*gypsy* groups as well as into the SINE-like and LINE-like classifications(Kumar and Bennetzen (1999) *Annual Review of Genetics* 33:479). In addition, DNA transposable elements such as *Ac*, *Taml* and *En/Spm* are also found in a wide variety of plant species, and can be utilized in the invention. Transposons (and IS elements) are common tools for introducing mutations in plant cells.

The term “meristem” as used herein means the formative plant tissue usually made up of undifferentiated cells capable of dividing and giving rise to similar cells or to cells that differentiate to produce the tissues and organs. Meristems are characterized by active cell division. Meristems are plant tissues composed of dividing cells and giving rise to organs such as leaves, flowers, xylem, phloem, roots. Meristems are regions of a plant in which cells are not fully differentiated and which are capable of repeated mitotic divisions. Most plants have apical meristems which give rise to the primary tissues of plants. The main meristematic areas within the plant are the apical meristems of the terminal and lateral shoots, the vascular cambium, the root apex, and the marginal meristems (active during the growth of leaves). Lateral meristems exist near root and shoot tips causing vertical plant growth. Higher plants produce most organs post-embryonically, including stems, leaves and roots. These organs develop from meristems at the tip of the stem and the root that are called the shoot apical meristem (SAM) and the root apical meristem, respectively.

While the shoot apical meristem appears as a mound of cells lacking distinct morphological features, it is in fact a very heterogeneous and highly organized structure. As genes affecting meristem function have successively been identified and their domains of expression determined, it is clear that regions of the meristem have distinct transcriptional profiles. Improvements in technology have allowed researchers to identify regional transcriptional differences on a more global scale. The *Arabidopsis* meristem is made up of three distinct cell layers. The two outermost layers (L1 and L2) grow as two-dimensional sheets of cells with cell divisions (mitotic spindles) oriented parallel to the meristem surface. The third and innermost layer (L3) contains cells that divide in all orientations. The meristems of the monocots maize and rice are similarly organized but tend to be taller and more finger-shaped. Although three is the most common, the number of layers within the meristem can vary. Maize, for instance, has only two meristem layers with a single sheet-like layer (L1) overlaying the L2 layer with its less regularly oriented cell divisions. Stem cells reside in the center of the meristem in the central zone. Surrounding the central zone is the peripheral zone. As the stem cells in the central zone divide, their descendants are pushed outward into the peripheral zone. It is in the peripheral zone that leaves are generated. Subtending the central zone is the rib zone. Stem cell descendants pushed downward into the rib zone generate stem tissues.

Shoot meristem would encompass all stages of shoot meristem, examples include but are not limited to, vegetative meristem, transitional meristem, inflorescence meristem.

Each type of meristem contains a small mass of stem cells that divide to produce new cells to be used in the constant formation of new organs.

The terms “meristem function”, “Shoot meristem function” or “shoot apical meristem function (SAM function)” are used interchangeably herein, and are defined herein as the ability of the shoot meristem to proliferate and renew itself, and its ability to provide cells for formation of new organs such as leaf, stem and flower.

An alteration of meristem function would include an alteration of the size of the SAM, a change in its mitotic activity, a change in its ability to proliferate and renew itself, a change in its ability to provide cells for formation of new organs such

as leaf, stem and flower, or a change in the type, number or size of new organs forming from the shoot meristem.

An alteration of "meristem function" encompasses a change in the number or activity of stem cells. This can encompass an increase in the size of the central zone comprising the undifferentiated stem cells, the rate at which the stem cells divide to renew themselves, or the rate at which the stem cells initiate formation of new organs, the number of organs initiated by the stem cells, or the size of the organs initiated.

The function of the SAM is regulated by many factors, including transcriptional regulators, receptor kinases, and plant hormones (Tucker and Laux, 2007 *Trends Cell Biol* 17:403-410).

The shoot apical meristem (SAM) regulates its size during development by balancing stem cell proliferation and the incorporation of daughter cells into primordia. Several "fasciated" mutants with enlarged meristems have been identified in maize, and can be used to study the genetic basis of meristem size regulation. Two maize genes, *thick tassel dwarf1* (*td1*; Bommert et al. (2005) *Development* 132:1235-1245) and *fasciated ear2* (*fea2*; Taguchi-Shiobara et al. (2001) *Genes Dev.* 15:2755-2766), are homologous to the *Arabidopsis* leucine-rich-repeat (LRR) receptor-genes CLAVATA1 (CLV1) and CLAVATA2 (CLV2), respectively. CLV1 and CLV2 were predicted to form a receptor complex that is activated by the CLV3 ligand and represses the stem cell promoting transcription factor WUSCHEL. Recent analysis in *Arabidopsis* revealed that the separate action of three major receptor complexes (CLV1-BAM1 (BARELY ANY MERISTEM1), CLV2-CRN (CORYNE), and RPK2/TOAD2 (RECEPTOR-LIKE PROTEIN KINASE2/TOADTOOL2)) is necessary for proper meristem size control in *Arabidopsis*. Here we present a phenotypic and molecular characterization of the tomato *fin* mutant that exhibits increased inflorescence branches, flowers, locule number and fruit size due to the progressive over-proliferation of plant stem cells in shoot meristems. The *FIN* gene is one of only a very small number of known tomato genes with a role in flower number and fruit size regulation. In addition to the observed increases in fruit size, *fin* mutants also exhibit a more up-right growth habit. We also found that *FIN* mutation has a similar effect in both processing tomatoes (variety M82) and the small fruited currant tomato *S. pimpinellifolium*.

Therefore, our analysis shows that modulation of FIN function and/or expression leads to alteration of meristem function and plant architectures, and this can lead to the creation of high yielding crop plants, since the activity of the reproductive SAM is an important parameter determining seed and fruit yield.

5 The Wuschel protein, also designated herein as WUS, is a homeodomain transcription factor that is both necessary and sufficient for stem cell specification (Laux et al. (1996) *Development* 122, 87–96.). WUS protein plays a key role in the initiation and maintenance of the apical meristem, which contains a pool of pluripotent stem cells (Endrizzi et al., (1996) *Plant Journal* 10:967-979; Laux et al.,
10 (1996) *Development* 122:87-96; and Mayer et al., (1998) *Cell* 95:805-815).

WUS is expressed in the organizing centre (a group of cells abutting the stem cells) and induces stem cell fate in the overlaying cells, and is required to maintain the stem cells undifferentiated state. The stem cells in turn express CLV3, a small secreted peptide that is thought to act as ligand for the CLV1–CLV2 heteromeric
15 receptor complex. Activation of the CLV1–CLV2 receptor leads to the suppression of WUS expression, creating a negative feedback loop that controls the size of the stem cell pool (Tucker and Laux (2007) *Trends Cell Biol.* Vol.17 (8)).

In *wuschel* mutants, the central zone of the SAM (shoot apical meristem) is not maintained. *Arabidopsis* plants mutant for the WUS gene contain stem cells that
20 are misspecified and that appear to undergo differentiation. (Mayer et al., (1998) *Cell* 95:805-815). The stem cell population of *Arabidopsis* shoot meristems is believed to be maintained by a regulatory loop between the CLAVATA (CLV) genes which promote organ initiation and the WUS gene which is required for stem cell identity, with the CLV genes repressing WUS at the transcript level, and WUS
25 expression being sufficient to induce meristem cell identity and the expression of the stem cell marker CLV3 (Brand et al., (2000) *Science* 289:617-619; Schoof et al., (2000) *Cell* 100:635-644). CLAVATA3 acts to limit the size of the WUSCHEL-expressing zone. Constitutive expression of WUS in *Arabidopsis* has been shown to lead to adventitious shoot proliferation from leaves (in planta) (US Patent No.
30 8383891).

Increasing WUS expression can lead to increased number of stem cells. Increased WUS expression as described herein includes an increase in the expression levels of WUS protein in the meristem. An increase in WUS expression

levels can include a spatial increase that would include an increase in the size of the zone expressing WUS in the SAM; temporal increase that would lead to a prolonged expression of WUS in any of the stem cells and/or a change in the timing of WUS expression, or an increase in the intensity of WUS expression.

5 We cloned the *FIN* gene using a map-based cloning approach. FIN protein is predicted to be localized in the plasma membrane. Double mutants of *fin/fab*, *fin/s* and *fin/an* have additive and synergistic fasciated phenotypes in tomato, indicating that they act in independent pathways that converge on the same downstream target to control meristem size. Consequently, the function of FIN as a regulator of
10 meristem function is in a new pathway distinct from that of S and AN.

Embodiments:

In one embodiment, the *FIN* gene variant that can be used in the methods of the current invention is one or more of the following *FIN* nucleic acid variants: (i) a portion of a *FIN* nucleic acid sequence (SEQ ID NO:1, 3, 5, 7, 9, 11, 13, 15, 17, 19,
15 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47 or 49); (ii) a nucleic acid sequence capable of hybridizing with a *FIN* nucleic acid sequence (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, 45, 47 or 49); (iii) a splice variant of a *FIN* nucleic acid sequence (SEQ ID NO:1, 2 or 4); (iv) a naturally occurring allelic variant of a *FIN* nucleic acid sequence (SEQ ID NO:1, 3, 5,
20 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47 or 49); (v) a *FIN* nucleic acid sequence obtained by gene shuffling; (vi) a *FIN* nucleic acid sequence obtained by site-directed mutagenesis; (vii) a *FIN* gene variant obtained and identified by the method of TILLING.

In one embodiment, the levels of endogenous *FIN* gene expression can be
25 decreased in a plant cell by antisense constructs, sense constructs, RNA silencing constructs, RNA interference, artificial microRNAs and genomic disruptions. Examples of genomic disruption include, but are not limited to, disruptions induced by transposons, tilling, homologous recombination.

In one embodiment, a modified plant miRNA precursor may be used, wherein
30 the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to *FIN* gene. The precursor is also modified in the star strand sequence to correspond to changes in the miRNA encoding region.

In one embodiment, a nucleic acid variant of *FIN* useful in the methods of the invention is a nucleic acid variant obtained by gene shuffling.

In one embodiment, a genetic modification may also be introduced in the locus of a tomato *FIN* gene using the technique of TILLING (Targeted Induced Local
5 Lesions In Genomes).

In one embodiment, a genetic modification may also be introduced in the locus of a maize *FIN* gene using the technique of TILLING (Targeted Induced Local Lesions In Genomes).

In one embodiment, site-directed mutagenesis may be used to generate
10 variants of *FIN* nucleic acids. Several methods are available to achieve site-directed mutagenesis; the most common being PCR based methods (US Patent No. 7956240).

In one embodiment homologous recombination can also be used to inactivate or reduce the expression of endogenous *FIN* gene in a plant.

15 Homologous recombination can be used to induce targeted gene modifications by specifically targeting the *FIN* gene *in vivo*. Mutations in selected portions of the *FIN* gene sequence (including 5' upstream, 3' downstream, and intragenic regions) such as those provided herein are made *in vitro* and introduced into the desired plant using standard techniques. Homologous recombination
20 between the introduced mutated *FIN* gene and the target endogenous *FIN* gene would lead to targeted replacement of the wild-type gene in transgenic plants, resulting in suppression of *FIN* expression or activity.

In one embodiment, catalytic RNA molecules or ribozymes can also be used to inhibit expression of *FIN* gene. It is possible to design ribozymes that specifically
25 pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage, the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of
30 the constructs. A number of classes of ribozymes have been identified. For example, one class of ribozymes is derived from a number of small circular RNAs that are capable of self-cleavage and replication in plants. The RNAs can replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples of RNAs

include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and subterranean clover mottle virus. The design and use of target RNA-specific ribozymes has been described. See, e.g., Haseloff et al. (1988)

5 *Nature*, 334:585-591.

Another method to inactivate the *FIN* gene is by inhibiting expression is by sense suppression. Introduction of expression cassettes in which a nucleic acid is configured in the sense orientation with respect to the promoter has been shown to be an effective means by which to block the transcription of a desired target gene.

10 (Napoli et al. (1990), *The Plant Cell* 2:279-289, and U.S. Pat. Nos. 5,034,323, 5,231,020, and 5,283,184).

In one embodiment, the *FIN* gene can also be inactivated by, e.g., transposon based gene inactivation.

In one embodiment, the inactivating step comprises producing one or more mutations in the *FIN* gene sequence, where the one or more mutations in the *FIN* gene sequence comprise one or more transposon insertions, thereby inactivating the *FIN* gene compared to a corresponding control plant. For example, the mutation may comprise a homozygous disruption in the *FIN* gene or the one or more mutations comprise a heterozygous disruption in the *FIN* gene.

20 These mobile genetic elements are delivered to cells, e.g., through a sexual cross, transposition is selected for and the resulting insertion mutants are screened, e.g., for a phenotype of interest. Plants comprising disrupted *FIN* genes can be crossed with a wt plant. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. The location of a TN (transposon) within a genome of an isolated or recombinant plant can be determined by known methods, e.g., sequencing of flanking regions as described herein. For example, a PCR reaction from the plant can be used to amplify the sequence, which can then be diagnostically sequenced to confirm its origin. Optionally, the insertion mutants are screened for a desired phenotype, such as the inhibition of expression or activity of *FIN* protein, or alteration of an agronomic characteristic.

30 In one embodiment, the *FIN* protein has shoot meristem function altering activity.

One embodiment of the current invention is a method of increasing WUS expression in a plant or plant cell by decreasing endogenous expression of the *FIN* gene in the plant or plant cell.

The agronomic characteristics that can be altered by alteration of *FIN* gene expression, or by alteration of FIN protein expression or activity include, but are not limited to the following: ear meristem size, kernel row number, leaf number, inflorescence number, branching within the inflorescence, flower number, fruit number, fruit size, seed number, root branching, root biomass, root lodging, biomass and yield. In one embodiment, the agronomic characteristic is increased resistance to abiotic stress. In one embodiment, the agronomic characteristic is increased resistance to biotic stress.

In one embodiment, the current invention provides a method of producing a transgenic plant with decreased expression of endogenous *FIN* gene, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant construct comprising a polynucleotide sequence operably linked to a promoter, wherein the expression of the polynucleotide sequence reduces endogenous *FIN* gene expression; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a decrease in expression of *FIN* gene, when compared to a control plant not comprising the recombinant DNA construct.

In another embodiment, the current invention provides a method of producing a transgenic plant with decreased expression of endogenous *FIN* gene, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked, in sense or antisense orientation, to a promoter functional in a plant, wherein the polynucleotide comprises: (i) the nucleotide sequence 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, 45, 47 or 49; (ii) a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49; (iii) a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49; (iv) a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or (v) a modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a decrease in expression of *FIN* gene, when compared to a control plant not comprising the recombinant DNA construct.

One embodiment of the invention is a method of producing a transgenic plant with alteration of an agronomic characteristic, the method comprising the steps of: (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked to at least one regulatory sequence, wherein the polynucleotide encodes a fragment or a variant of a polypeptide having an amino acid sequence of at least 80% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, wherein the fragment or the variant confers a dominant-negative phenotype in the regenerable plant cell; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within the inflorescence, flower number, fruit number, fruit size, seed number, root branching, root biomass, root lodging, biomass and yield, when compared to a control plant not comprising the recombinant DNA construct.

Another embodiment of the current invention is the above method wherein expression of the polypeptide of part (a) in a plant line having the *fin* mutant genotype is capable of partially or fully restoring the wild-type phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of (a) performing a genetic screen on a population of mutant plants (b) identifying one or more mutant plants that exhibit weak *fin* phenotype than a *fin* null plant; and (c) identifying the weak *fin* allele from the mutant plant with weaker *fin* phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) performing a genetic screen on a population of mutant maize plants (b) identifying one or more mutant maize plants that exhibit weak *fin* phenotype than a *fin* null plant; and (c) identifying the weak *fin* allele from the mutant maize plant with weaker *fin* phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) performing a genetic screen on a population of mutant tomato plants (b) identifying one or more mutant tomato plants that exhibit weak *fin* phenotype than a *fin* null plant; and (c) identifying the weak *fin* allele from the mutant tomato plant with weaker *fin* phenotype.

One embodiment of the current invention is a method of identifying a weaker allele of *fin*, the method comprising the steps of: (a) gene shuffling using one or more nucleotide sequences encoding 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, 46, 48, 50, 51-65, or 66, or a protein that is at least 70% identical to 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, 46, 48, 50, 51-65, or 66, or a fragment thereof; (b) transforming the shuffled sequences from step (a) into a population of regenerable plant cells; (c) regenerating a population of transformed plants from the population of transformed regenerable plant cells of step (b); (d) screening the population of transformed plants from step (c) for weak *fin* phenotype; and (e) identifying the weak *fin* allele from the transformed plant exhibiting weak *fin* phenotype.

One embodiment of the invention is a plant in which expression of the endogenous *FIN* gene is reduced relative to a control plant. Another embodiment of the current invention is a method of making said plant, the method comprising the steps of: (a) introducing a mutation into the endogenous *FIN* gene; and (b) detecting the mutation, wherein the mutation is effective in inhibiting the expression of the endogenous *FIN* gene. In one embodiment, the steps (a) and (b) are done using

Targeting Induced Local Lesions IN Genomics (TILLING) method. In one embodiment, the mutation is a site-specific mutation.

One embodiment of the invention is a plant that exhibits weaker *fin* phenotype relative to a wild-type plant. Another embodiment is a method of making said plant wherein the method comprises the steps of: (a) introducing a transposon into a germplasm containing an endogenous *FIN* gene; (b) obtaining progeny of the germplasm of step (a); and (c) identifying a plant of the progeny of step (b) in which the transposon has inserted into the endogenous *FIN* gene and a reduction of expression of *FIN* gene is observed. Step (a) may further comprise introduction of the transposon into a regenerable plant cell of the germplasm by transformation and regeneration of a transgenic plant from the regenerable plant cell, wherein the transgenic plant comprises in its genome the transposon.

In one embodiment, the methods described above wherein the method further comprises the steps of: (a) introducing into a regenerable plant cell a recombinant construct comprising the weak *fin* allele identified by the methods described above; (b) regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a weak *fin* phenotype, when compared to a control plant not comprising the recombinant DNA construct.

Another embodiment is a method of producing a transgenic plant with an alteration in at least one agronomic characteristic, the method comprising (a) introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked, in sense or antisense orientation, to a promoter functional in a plant, wherein the polynucleotide comprises: (i) the nucleotide sequence 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, 45, 47 or 49; (ii) a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49; (iii) a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49; (iv) a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or (v) a

modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49; (b) regenerating a transgenic plant from the
5 regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and (c) selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration in at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence
10 number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant not comprising the recombinant DNA construct. Another embodiment is the plant produced by this method. Another embodiment is the seed obtained from the plant produced by this method.

15 Another embodiment is a recombinant DNA construct comprising a polynucleotide that encodes a polypeptide having an amino acid sequence with at least 95% sequence identity, based on Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, and wherein the polypeptide has shoot
20 meristem function altering activity. In another embodiment the polynucleotide encodes a polypeptide that has an amino acid sequence comprising 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, 46, 48, 50, 51-65, or 66, and wherein the polypeptide has shoot meristem function altering activity. In another embodiment, a plant and a seed comprising this recombinant
25 construct is encompassed in the current invention. Another embodiment encompasses a transgenic microorganism comprising this recombinant construct. The transgenic microorganism may be a bacterial or a yeast cell. The bacterial cell may be *Agrobacterium*, e.g., *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*.

30 Another embodiment is a plant comprising this recombinant construct, wherein the plant exhibits an alteration in at least one of the agronomic characteristics selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower

number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield.

Another embodiment is a method of identifying a first plant or a first plant germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first plant or the first plant germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to 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, 46, 48, 50, 51-65, or 66, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising 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, 46, 48, 50, 51-65, or 66.

Another embodiment is a method of identifying a first maize plant or a first maize germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first maize plant or the first maize germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to SEQ ID NO:4, 6 or 8, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising SEQ ID NO:4, 6 or 8.

Another embodiment is a method of identifying a first tomato plant or a first tomato germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first tomato plant or the first tomato

germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to SEQ ID NO:2, 46, 48 or 50, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising SEQ ID NO:2, 46, 48 or 50.

Another embodiment is the above method wherein said marker locus encodes a polypeptide that comprises the sequence set forth in SEQ ID NO:67 or 68.

Another embodiment is a method of increasing WUS expression in a plant or plant cell, wherein the method comprises the steps of: (a) altering a plant or plant cell to decrease endogenous expression of *FIN* gene in the plant or plant cell; (b) determining WUS protein expression in the altered plant or plant cell of step (a); and (c) selecting the altered plant or plant cell of step (b) with increased WUS expression. Another embodiment of the invention is an altered plant or plant cell produced by this method, wherein the altered plant or plant cell has increased expression of WUS protein, and decreased expression of *FIN* gene.

To increase WUS expression, *FIN* gene expression can be decreased by using any of the methods described herein. To increase WUS expression, the levels of endogenous *FIN* gene expression can be decreased in a plant cell by antisense constructs, sense constructs, RNA silencing constructs, RNA interference, artificial microRNAs and genomic disruptions. Examples of genomic disruption include, but are not limited to, disruptions induced by transposons, tilling, homologous recombination.

Another embodiment of the current invention is a method of altering meristem function in a plant, wherein the method comprises the steps of: (a) altering a plant or plant cell to decrease endogenous expression of *FIN* gene in the plant or plant cell; (b) determining meristem function in the altered plant or plant cell; and (c) selecting the altered plant or plant cell of step (a) with altered meristem function.

Another embodiment of this invention is the altered plant or plant cell produced by the above method, wherein the altered plant or plant cell has altered meristem function, and decreased expression of *FIN* gene.

The invention includes a recombinant DNA construct comprising an isolated polynucleotide of the current invention operably linked, in sense or antisense orientation, to a promoter that is shoot apical meristem specific or shoot apical meristem preferred.

This invention includes a vector, microorganism, cell, plant, or seed comprising any of the recombinant DNA constructs described in the present invention.

The invention encompasses plants produced by the methods described herein.

The invention also encompasses regenerated, mature and fertile transgenic plants comprising the recombinant DNA constructs described above, transgenic seeds produced therefrom, T1 and subsequent generations. The transgenic plant cells, tissues, plants, and seeds may comprise at least one recombinant DNA construct of interest.

In one embodiment, the plant is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

In one embodiment, the plant comprising the recombinant constructs described in the present invention is a dicotyledonous plant. In another embodiment, the plant comprising the recombinant constructs described in the present invention is a tomato plant.

In one embodiment, the plant comprising the recombinant constructs described in the present invention is a monocotyledonous plant. In another embodiment, the plant comprising the recombinant constructs described in the present invention is a maize plant.

EXAMPLES

The present invention is further illustrated in the following Examples, in which parts and percentages are by weight and degrees are Celsius, unless otherwise stated. It should be understood that these examples, while indicating embodiments of the invention, are given by way of illustration only. From the above discussion

and these Examples, one skilled in the art can ascertain the essential characteristics of this invention, and without departing from the spirit and scope thereof, can make various changes and modifications of the invention to adapt it to various usages and conditions. Furthermore, various modifications of the invention in addition to those shown and described herein will be apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims.

EXAMPLE 1

Isolation and Characterization of Tomato Inflorescence Mutants

Showing Both Branching and Fasciation

To explore mechanisms controlling inflorescence and flower production in tomato in relation to meristem size we isolated several mutants that exhibited both branched inflorescences and fasciated stems and flowers. Six such mutants were identified in a screen of 13,000 ethyl methane sulfonate (EMS) and fast-neutron (FN) mutant M2 lines in the standard processing 'M82' cultivar (Menda et al., 2004 *Plant J* 38, 861-872). These mutants formed two complementation groups with one EMS allele for a mutant that we designated *fasciated and branched (fab)* and 5 alleles (3 EMS and 2 FN) for a mutant designated *fasciated inflorescence (fin)*. Complementation tests demonstrated neither mutant was allelic to the only other known fasciated mutant *fas* or to the inflorescence branching mutant *s* (Cong et al., 2008 *Nat. Gen.* 40, 800-804; Lippman et al., 2008, *PLoS Biol.* 6, e288). While both mutants showed similarly branched inflorescences and fasciated flowers and fruits, the *fin* mutant was more severe than *fab* for all affected traits. In particular, unlike *fab*, *fin* mutants showed extremely fasciated vegetative shoots and a grossly enlarged first flower. We found that floral organ numbers in all four whorls were significantly increased in both mutants, with the most organs in *fin* (FIG. 1A). Whereas all *fin* inflorescences were branched compared to the typical unbranched multi-flowered inflorescences of wild type (WT) tomatoes, the first inflorescence of *fab* was often unbranched, although all later inflorescences showed mild to moderate branching.

To pinpoint the developmental origins of the striking morphological phenotypes of *fab* and *fin*, we took advantage of the large and readily accessible tomato SAM to measure morphological changes over time (Park et al., 2012 *Proc*

Natl Acad. Sci. 109, 639-644). Soon after germination, the tomato vegetative SAM can be observed under a stereomicroscope as a small dome. Gradually, this dome grows taller and broader and leaves are formed around its flanks in a spiral phyllotaxy until the transition to reproductive growth, at which point the SAM is consumed in the formation of the first flower of the first multi-flowered inflorescence (Lippman et al., 2008 *PLoS Biol.* 6, e288; Park et al., 2012 *Proc Natl Acad. Sci.* 109, 639-644). To precisely compare size differences in *fab*, *fin*, and WT meristems during the transition from vegetative to reproductive growth, we used our previously defined meristem stages and measured the early vegetative meristem (EVM; 5th leaf initiated) and the transition meristem (TM; 8th and last leaf initiated prior to flowering) from all three genotypes. Both mutants appear larger than WT at the EVM stage, but the fasciation phenotype is most pronounced in *fin*, particularly in the TM stage, and this difference was reflected in a quantification of meristem size (FIG. 1B). Notably, in *fin* mutants the meristem grows both taller and wider throughout the transition to flowering, whereas in *fab* excess growth is mostly confined to an increase in meristem height. This perhaps explains the more dramatic shoot and flower fasciation in *fin* mutants compared to *fab* mutants. Thus, both the *FAB* and *FIN* genes regulate meristem size in tomato, with *FIN* potentially functioning very early in the vegetative phase to restrict overproliferation of the stem cell population.

fin mutants show increased height and fewer side branches relative to the wild type background genotype M82 (FIG. 1D). Increased fruit size in *fin* relative to M82 tomato plants can be seen in FIG. 1E.

EXAMPLE 2

FAB and *FIN* Likely Function in Separate Pathways

As *fab* and *fin* have similar fasciated and branched inflorescence phenotypes, we wondered whether they were a part of the same pathway. To test, we generated *fab fin* double mutants and found a remarkable synergistic double mutant phenotype, suggesting separate pathways. The double mutants develop grossly enlarged and fasciated meristems that produce an excessive amount of leaves prior to flowering (30+ leaves compared to 8 in wild type, data not shown). No viable flowers ever formed in *fab fin* double mutants and the shoot stalls at the transition to flowering to give rise to an excessively large fascinated meristem. Simultaneously, basal axillary meristems are released from dormancy to give rise to shoots that can

produce flowers and immature fruits that lack seeds.

EXAMPLE 3

Double Mutant Analysis with Known Inflorescence and Fasciated Mutants

To determine whether *FAB* and *FIN* are part of the inflorescence branching pathways of genes that affect meristem maturation like *S*, we examined a suite of double mutants. The vast majority of inflorescence branching in domesticated tomato traces back to mutations in *s*, which is defective in the ortholog of *Arabidopsis WOX9* (Lippman et al., 2008 *PLoS Biol.* 6, e288)). Mutations in *s* can yield inflorescences with dozens to hundreds of flowers arranged in complex branching patterns. Similar to *s*, a second mutant called *anantha (an)*, which is defective in an F-box protein, also bears highly branched inflorescences, however, *an* flowers are not viable and extreme mutant inflorescences resemble cauliflower (Lippman et al., 2008 *PLoS Biol.* 6, e288)). *S* and *AN* have been found to act in sequence to modulate the timing of meristem maturation from an inflorescence to a flower (Lippman et al., 2008 *PLoS Biol.* 6, e288; Park et al., 2012 *Proc.Natl Acad.Sci, USA*, 109:639-644). We asked if the inflorescence branching in *fab* and *fin* was due to a defect in the same pathway by making double mutants with *s* and *an*. All of these double mutants showed either additive or synergistic phenotypes, indicating that *FIN* and *FAB* are not functioning in meristem maturation to control branching. We also generated double mutants with *fas* and found a synergistic effect on meristem size and inflorescence branching, again implying *FAB* and *FIN* are not in any of the known classical branching or fasciation pathways (Cong et al., 2008 *Nature genetics* 40, 800-804, Eshed et al., 2001; *Curr Biol* 11, 1251-1260.; Goldshmidt et al., 2008 *Plant cell* 20, 1217-1230; Sarojam et al., 2010 *Plant Cell* 22, 2113-2130)

EXAMPLE 4

Isolation of *FAB*

To determine the genetic basis underlying the *fab* and *fin* mutant phenotypes, we cloned the underlying genes. Recent genome sequencing of domesticated tomato (*S. lycopersicum*) and a closely related, cross-compatible wild relative (*S. pimpinellifolium*) has improved our ability to generate both insertion-deletion (InDel) and single-nucleotide polymorphism (SNP) mapping markers (Consortium, 2012 *Nature* 485, 635-641), which has helped facilitate rapid mapping of tomato mutants.

Using a bulk-segregant mapping approach, *fab* was roughly positioned to the bottom of chromosome 4, and further fine-mapping narrowed the region to 326kb, encompassing 45 genes (FIG. 2A). Reviewing the gene annotations revealed the predicted closest tomato homolog of *CLAVATA1* (FIG. 2B). Sanger sequencing of Solyc04g081590 from our single *fab* allele revealed a missense mutation causing an Alanine to a Valine substitution (position 841 of 986aa) at a highly conserved residue within the kinase domain. Remarkably, this exact amino acid substitution was previously reported in the *A. thaliana clv1-9* allele (FIG. 2A), which is described as having a dominant negative effect (Dievart et al., 2003 *Plant Cell* 15, 1198-1211). Our F2 mapping population segregated one-quarter mutant for plants with both inflorescence branching and fasciation in the flowers and fruits, suggesting a single-recessive gene underlying the *fab* mutant phenotype. In light of the dominant negative nature of the *Arabidopsis* allele, we went back and performed a detailed phenotypic analysis of *fab/+* heterozygotes compared to WT and *fab* mutants from a segregating F2 population, which revealed weak semi-dominant effects on sepal, petal, and stamen number (FIG. 4). That carpel number in *fab/+* heterozygotes is not significantly different from wild type and branched inflorescences are absent made it easy to overlook the dominant negative nature of this mutant allele without quantitative examination.

As we only isolated one *fab* allele from the screen, we designed a transgenic experiment to provide further evidence that this mutation underlies the *fab* phenotype. Transgenic constructs of the full genomic sequences for both the wild type (p35S::g*CLV1*) and mutant (p35S::g*fab*) forms of the putative tomato *CLV1* gene were transformed into plants. Not surprisingly, as our detailed phenotyping of *fab/+* plants revealed that this allele acts in a weak dominant negative fashion, the p35S::g*CLV1* construct failed to complement *fab* mutant phenotypes. Importantly, however, the dominant negative phenotype was recapitulated in WT plants transformed with p35S::g*fab*, providing strong support that a dominant negative form of tomato *CLV1/FAB* underlies the *fab* mutant phenotype. In total, greater than 20% of T1 generation plants showed an increase in sepal, petal and stamen number that phenocopied *fab* heterozygotes. In about 10% of these plants (3 out of ~30 independent events), the phenotype was skewed towards *fab* homozygous mutants, with a greater increase in floral organ number and inflorescence branching.

Surprisingly, in two transgenic lines carrying the *Sl-gCLV1* transgene in a *fab* mutant background, the floral fasciation and inflorescence branching was even more severe than in untransformed *fab* homozygous mutants. One explanation is a co-suppression of *FAB*, although semi-quantitative RT-PCR ruled this possibility out.

5 Notably, the strongest predicted molecular alleles of *clv1* in *Arabidopsis* tend to have the weakest phenotypes (Dievart et al., 2003 *Plant Cell* 15, 1198-1211), and CLV1 is known to act as a homodimer and in heterodimer complexes with other transmembrane proteins such as CLV2 (Katsir et al., 2011 *Curr Biol* 21, R356-364; Miwa et al., 2009 *J Plant Res* 122, 31-39). Thus, another possibility is that

10 overexpressing the transgene provides more FAB protein complexes to poison in a dominant negative fashion, perhaps explaining the more severe phenotype.

Regardless of the mechanism, the transgenic experiments demonstrate that *FAB* is tomato *CLV1*, providing the first evidence of a functional role for the CLV pathway in regulating meristem maintenance in tomato.

15 EXAMPLE 5

Isolation of *FIN*

As with *fab*, a bulk-segregant analysis enabled us to roughly position *fin* to a 1Mb region of chromosome 11, which includes 71 annotated genes (FIG. 3A).

Further fine-mapping was hindered by a lack of recombination, which led us to

20 adopt a cloning-by-sequencing approach. Fortunately, five *fin* alleles were uncovered from the EMS and FN mutagenesis screening, allowing us to combine meristem-enriched mRNA from four alleles (*fin-e4489*, *fin-e4643*, *fin-e9501* and *fin-n2326*) for Illumina paired-end 100bp (PE100) sequencing. A total of 42M reads

were aligned to the genes in the 1Mb interval and two mutations were found within

25 the coding sequence Solyc11g064850. PCR amplification and Sanger sequencing confirmed mutations in this gene for all five alleles. One mutant, *fin-e4489* (SEQ ID NO:67), harbored a nonsense mutation causing a truncated protein, which we

designated as the reference allele. A second EMS mutant, *fin-e4632* (SEQ ID NO:68) harbored a missense mutation resulting in a Proline to Serine change. We

30 were unable to PCR-amplify *FIN* from the remaining three alleles (*fin-e9501*, *fin-n2326*, *fin-n5644*), nor were we able to amplify fragments of the flanking genomic regions, indicating complete deletions, which we confirmed by RT-PCR (FIG. 3A).

FIN encodes a 373 amino acid protein belonging to a small, highly conserved gene family (FIG. 3B). Four additional *FIN* homologs were found in tomato, and four members were found in *Arabidopsis*. *FIN* is predicted to have an N-terminal signal peptide in the first 25 amino acids and a single transmembrane domain from amino acids 13-35 (Tusnady and Simon, 1998 *J Mol Biol* 283, 489-506, Tusnady and Simon 2001 *Bioinformatics* 17, 849-850). Thus, *FIN* defines a new gene in tomato development whose primary role is to repress meristem overproliferation and based on our double mutant analysis, *FIN* appears to function separately from *CLV1-WUS*.

EXAMPLE 6

FIN Localizes To the Plasma Membrane

The *FIN* protein family members are predicted to have a transmembrane domain (FIG. 3B) (Tusnady and Simon, 1998 *J Mol Biol* 283, 489-506, Tusnady and Simon 2001 *Bioinformatics* 17, 849-850). Moreover, in a screen for membrane-associated protein interactors, an *Arabidopsis* *FIN*-like protein was found to localize to the membrane (Jaquinod et al., 2007 *Mol Cell Proteomics* 6, 394-412; Marmagne et al., 2007 *Mol Cell Proteomics* 6, 1980-1996.; Mitra et al., 2009 *J Proteome Res* 8, 2752-2767). Therefore, we sought test whether tomato *FIN* likewise localized to the membrane. *FIN*-YFP tagged proteins were introduced into onion cells by particle bombardment and imaged by confocal microscopy. To differentiate between cell wall and plasma membrane localization, imaging was completed on cells counterstained with cell wall (fluorescent brightener) and plasma membrane (FM4-64) markers followed by plasmolysis to detach the plasma membrane from the cell wall. This enabled us to visualize *FIN* specifically at the plasma membrane, but curiously in a punctate pattern. Such puncta could reflect either processing steps or transport in vesicles or potentially an artifact of the transient expression causing YFP aggregation or processing steps. We observed the same pattern in multiple transient expression experiments with both YFP-*FIN* and *FIN*-YFP constructs in both bombarded onion cells and *Agrobacterium*-mediated transfected tobacco leaves (data not shown). Thus, while the punctate pattern may not completely reflect the full functional distribution of *FIN*, our results clearly show membrane localization.

EXAMPLE 7

FAB and *FIN* Are Expressed Broadly and Stably Throughout Development

To assess how *FAB* and *FIN* are expressed throughout development, we performed RT-PCR on a panel of tomato tissue types and found both genes are expressed broadly. We also took advantage of our recent tomato meristem maturation transcriptome atlas (Park et al., 2012 *Proc. Natl. Acad. Sci., USA*, 109:639-644)) and found that *FAB* and *FIN* are expressed broadly and stably in all meristem stages, although *FIN* is expressed at a lower level compared to *FAB*. Previous studies uncovered specific spatial expression for the *CLV* genes within the SAM relevant to its role in meristem (Katsir et al., 2011 *Curr Biol* 21, R356-364; Miwa et al., 2009 *J Plant Res* 122, 31-39). Thus, we performed RNA *in situ* hybridization on WT EVMs using *FAB* full-length RNA probes, and as expected, expression mirrored that of *Arabidopsis CLV1*; *FAB* was expressed broadly in the SAM throughout the central zone and peripheral zones, but as in *Arabidopsis*, transcripts were absent from L1 and L2 layers. *FAB* was also expressed in the transition meristem and floral meristem. Notably, in *fab* and *fin* mutants, the *FAB* expression pattern is not altered from WT.

As *fin* mutant meristems are grossly enlarged, we hypothesized that *FIN* may also be spatially regulated within the SAM to regulate meristem maintenance in parallel to the *CLV* pathway. We attempted *in situ* hybridizations with both a full-length probe and a short N-terminal probe, and in three separate experiments, we failed to detect signal, which could be a reflection of lower transcript levels compared to *FAB* (~10-fold lower).

EXAMPLE 8

The *WUSCHEL* Domain Is Dramatically Expanded in *fin* Mutants

In *Arabidopsis*, signaling through a feedback loop involving *CLV1* restricts the expression of *WUS* to a small number of cells just underlying the stem cell niche in a zone called the organizing center (OC). In *Arabidopsis clv1* mutants, the *WUS* expression domain is expanded in vegetative meristems. To determine if tomato *fab* mutants experience a similar expansion of *WUS*, we probed WT and *fab* mutant meristems with a tomato *WUS* probe. Indeed, as expected, in WT meristems, *WUSCHEL* is specifically expressed in the OC of vegetative meristems and in the floral meristems. *WUS* expression is slightly expanded in *fab* vegetative SAMs; however, we observed a much greater expansion in *fab* flowers.

Our genetics suggested that *FIN* acts in a parallel meristem maintenance pathway to *FAB*. Therefore, we were curious to determine if the stem cell promoting region is also expanded in *fin* mutants. Strikingly, we observed a dramatic expansion of *WUS* in *fin* mutants, extending laterally towards the flanks of the meristem. In addition, we observed strong foci of *WUS* expression in *fin* TMs. These foci likely mark the sites of ectopic meristems that allow for the outgrowth of additional branches seen in *fin* inflorescences. Importantly, these results fail to inform if there is a functional signaling connection between *FIN* and *WUS* as has been demonstrated for *CLV1* and *WUS*, nor does it demonstrate whether the number of stem cells *per se* are increased in *fin* mutants, which will require probing with meristem-specific markers. However, the drastic expansion of the stem cell-promoting cells marked by *WUS* indicates a dramatic loss of stem cell control in *fin* meristems.

EXAMPLE 9

Transcriptome Profiling in *fab* and *fin* Mutants

Double mutant analysis revealed a remarkable synergistic interaction between *FAB* and *FIN*, suggesting separate pathways are at work to control tomato meristem size. *clv1* mutants have been investigated in other systems and the role of *CLV1* in shoot apical meristem maintenance via the *CLV/WUS* feedback loop is well established (Katsir et al., 2011 *Curr Biol* 21, R356-364; Miwa et al., 2009 *J Plant Res* 122, 31-39; Pautler et al., 2013 *Plant Cell Physiol* 54, 302-312); however, aside from a single report of a *FIN* homolog that is implicated in root nodulation in *Medicago truncatula* (Schnabel et al., 2011 *Plant Mol Biol* 58, 809-822), nothing is known about the role of *FIN* family genes and in what developmental pathway(s) they might function. To further characterize tomato *fab* and *fin* mutants and to begin to tease apart their roles from one another in meristem maintenance and other developmental processes we subjected mutant SAMs to transcriptome profiling. The mutant phenotype for *fab* and *fin* are evident as early as 8 d.a.g. in the Early Vegetative Meristems (EVMs). Thus, we compared the transcriptome profile of *fab* and *fin* mutant EVMs to wild type matched stages to determine the major genes and gene classes that are differentially expressed (DE).

If *FIN* is acting in a separate pathway from the *FAB/CLV-WUS* pathway, we would expect that a majority of the genes that are DE in *fin* mutants compared to

wild type would be different from those DE in *fab* mutants compared to WT – these genes and/or gene classes may give us a clue as to the role of *FIN* in meristem maintenance. However, as both *FAB* and *FIN* act to regulate meristem size, we also expected to see some overlap in the types of DE genes – these genes could be

5 universally important for meristem growth and maintenance, such as genes involved in the cell cycle, cell membrane formation or degradation. Thus, we first took an unbiased approach and asked how many of these genes are unique to each mutant versus how many overlap between the two mutants. We found that *fin* mutants,

10 which manifest a more severe mutant phenotype, had 1194 DE genes at the EVM stage, whereas *fab* only had 679 DE genes. As expected, a majority of genes, 77% of *fin* DE genes and 60% of *fab* DE genes were unique to *fin* and *fab*, respectfully, with limited overlap. We reasoned that these genes might fall into particular gene classes that could further help us to define the roles of *FIN* versus *FAB*. Thus we grouped the genes into functional categories using MapMan classification and

15 asked if particular categories were overrepresented in either of the mutants. We first looked at broad MapMan categories, and found that very few classes were significantly altered in *fab*, but that several classes were changed in *fin*. When informative, these broad categories were split into sub-categories to further distinguish between the effects of the two mutants on the global gene expression

20 profile.

When looking at global categories alone, only two major classes, “biotic stress” and “transport”, were significantly altered in both *fab* and *fin* mutants. The most significantly overrepresented category for both mutants was the transport category, which includes transport of ions, lipids, proteins and other metabolites that

25 are essential during development. Both mutants see a particular enrichment in DE genes in the “p- and v-Type ATPase” category, which includes proteins involved in transport of ions, heavy metals and lipids. Similarly, in *fin* mutants, “metal transport” and “ABC transport” genes are enriched. ABC transporters are known to be important for many developmental processes including organ development and

30 reaction to abiotic stresses (Kang et al., 2011 *Arabidopsis Book* 9, e0153). Likewise, genes in the “abiotic stress” category are also enriched in *fin* mutants. *fin* mutant meristems expand rapidly compared to wild type and develop ectopic leaves and a highly fasciated shoot, which likely increases the mechanical stress suffered by

these young mutant meristems. In *fab* mutants, which do not undergo the same dramatic overproliferation and fasciation, these stress-related categories are not enriched. However, intriguingly, aside from the ATPase transporters, the only transport categories that are slightly enriched are the “amino acid transport” and “peptide and oligopeptide transport” categories. The transport of peptides is particularly interesting as perception of the CLV3 peptide by CLV1 and other receptor protein complexes is essential for proper meristem maintenance.

Several categories involved in the “regulation of transcription” are also highly over represented in *fin* mutants. Among these, the most highly overrepresented are YABBY-like transcription factors and Homeobox transcription factors. YABBY transcription factors are involved in defining boundaries between the meristem and organ primordia (Eshed et al., 2001; *Curr Biol* 11, 1251-1260.; Goldshmidt et al., 2008 *Plant cell* 20, 1217-1230; Sarojam et al., 2010 *Plant Cell* 22, 2113-2130) and homeobox transcription factors are universally important in development, especially the roles of WUSCHEL-related homeobox containing transcription factors (WOXs) for tissue patterning and meristem maintenance (Breuninger et al., 2008 *Dev Cell* 14, 867-876.; Haecker, 2004 *Development* 131, 657-668; Wu et al., 2007 *Developmental biology* 309, 306-316). Overexpression of both classes is consistent with the *fin* meristem showing extreme enlargement with ectopic organ formation early in development. In *fab*, we do not see overrepresentation of either of these categories; rather, the CONSTANS-like (CO-like) transcription factors, many members of which are implicated in regulating flowering time, is the only transcription factor family significantly changed in *fab* mutants.

Looking at the MapMan findings provides an overview of the global functional expression changes occurring in the mutants compared to WT. However, this analysis only looks at the number of genes in each category that have altered gene expression, but does not maintain information about the direction of change (under or overexpressed), nor does it reflect the level of expression change. Therefore, we searched the expression data for genes most highly downregulated or upregulated in each mutant. A few genes known to be involved in meristem maintenance immediately caught our attention. Most strikingly, *CLV3* was highly upregulated in *fin* mutants (logFC >5 or ~40-fold increase according to normalized counts). *CLV3* is also overexpressed in *fab* mutants, but to a much lesser extent (logFC ~2.3,

normalized fold change ~5). A slight increase in *CLV3* expression could simply be a consequence of increased meristem size; however, at the vegetative stage, *fab* meristems are only about twice the size of WT, and *fin* meristems are only about three times larger. Assuming a linear relationship between the size of the meristem/number of stem cells and *CLV3* expression, the dramatic increase of *CLV3* expression in *fin* mutants could not be strictly due to the change in the number of cells. With overexpression of *CLV3*, we would expect to see a decrease in *WUS* expression; however, *WUSCHEL* is 2-fold higher in *fin* mutants compared to wild type, consistent with *in situ* hybridization. Although the increase in *CLV3* transcripts may be within the physiological range (Muller et al., 2006), high *CLV3* levels typically cause loss of *WUS* expression and meristem termination, which is opposite from what is observed in *fin* mutants. It is possible that the *CLV3* transcripts are not properly localized or that the *CLV3p* is either not processed properly or properly localized to the apoplast to be perceived by CLV receptor complexes. Also notable in *fin* mutants are changes in expression of genes involved in cell wall modifications, particularly cell wall-associated proteins. Interestingly, several of these proteins are in the top downregulated genes in *fin* mutants, including a number of pectinesterases, which are known to help facilitate modifications at the cell wall and cellulose synthesis genes are also altered. Curiously, the ortholog of *Arabidopsis* *TAPETUM DETERMINANT1*, which was identified in a male sterile screen and is known to interact with the LRR kinase EMS1, is not normally expressed in the tomato vegetative meristem, but was detected in *fin* mutants. Similarly, *GAMETE EXPRESSED PROTEIN1* a transmembrane domain protein that has a role in gametophyte development in *Arabidopsis* is also ectopically expressed. Finally, the tomato ortholog of *DVL*, a gene that encodes a small polypeptide, which when overexpressed in *Arabidopsis* are known to cause short plants with clustered inflorescences is ectopically expressed in the *fin* vegetative meristem. Altogether, the expression profiling, in combination with our genetics analysis, suggests that *FIN* functions separately from *FAB* and the LRR kinases in the CLV-WUS pathway to control meristem maintenance, but has a role in the perception of CLV3 by WUS.

CLAIMS

What is claimed is:

1. A plant in which expression of an endogenous *FIN* gene is reduced relative to a control plant.

2. A method of producing the plant of claim 1, the method comprising:

a. introducing into a regenerable plant cell a recombinant construct comprising a polynucleotide operably linked to a heterologous promoter, wherein the expression of the polynucleotide sequence reduces endogenous *FIN* gene expression;

b. regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and

c. selecting the transgenic plant of (b), wherein the transgenic plant comprises the recombinant construct and exhibits a decrease in expression of *FIN* gene, when compared to a control plant not comprising the recombinant DNA construct.

3. The method of claim 2, wherein the polynucleotide is operably linked, in sense or antisense orientation, to a promoter functional in a plant, further wherein the polynucleotide comprises:

a. the nucleotide sequence 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, 45, 47 or 49;

b. a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49;

c. a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49;

d. a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or

e. a modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence

designed to produce an miRNA directed to 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, 45, 47 or 49.

4. A method of producing a transgenic plant with alteration of an agronomic characteristic, the method comprising:
 - a. introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked to at least one heterologous regulatory sequence, wherein the polynucleotide encodes a fragment or a variant of a polypeptide having an amino acid sequence of at least 80% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, wherein the fragment or the variant confers a dominant-negative phenotype in the regenerable plant cell;
 - b. regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and
 - c. selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within the inflorescence, flower number, fruit number, fruit size, seed number, root branching, root biomass, root lodging, biomass and yield, when compared to a control plant not comprising the recombinant DNA construct.
5. A plant that exhibits a weak *fin* phenotype relative to a wild-type plant.
6. A method of isolating the plant of claim 5 and identifying a weak *fin* allele in the plant, the method comprising the steps of:
 - a. performing a genetic screen on a population of mutant plants;
 - b. identifying one or more mutant plants that exhibit a weak *fin* phenotype than a *fin* null plant; and

- c. identifying the weak *fin* allele from the mutant plant with weaker *fin* phenotype.

7. The method of claim 6, wherein the method comprising the steps of:

- a. performing a genetic screen on a population of mutant maize plants;
- b. identifying one or more mutant maize plants that exhibit a weak *fin* phenotype than a *fin* null plant; and
- c. identifying the weak *fin* allele from the mutant maize plant with weaker *fin* phenotype.

8. A method of identifying a weak allele of *fin*, the method comprising the steps of:

- a. gene shuffling using one or more nucleotide sequences encoding 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, 46, 48, 50, 51-65, or 66, or a protein that is at least 70% identical to 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, 46, 48, 50, 51-65, or 66, or a fragment thereof;
- b. transforming the shuffled sequences from step (a) into a population of regenerable plant cells;
- c. regenerating a population of transformed plants from the population of transformed regenerable plant cells of step (b);
- d. screening the population of transformed plants from step (c) for weak *fin* phenotype; and
- e. identifying the weak *fin* allele from the transformed plant exhibiting weak *fin* phenotype.

9. A method of making the plant of claim 1, the method comprising the steps of

- a. introducing a mutation into the endogenous *FIN* gene; and
- b. detecting the mutation.

10. The method of claim 9 wherein using the steps (a) and (b) are done using a Targeting Induced Local Lesions IN Genomics (TILLING) method and wherein the mutation is effective in reducing the expression of the endogenous *FIN* gene or its activity.

11. The method of claim 9 or 10 wherein the mutation is a site-specific mutation.

12. A method of making the plant of claim 1, wherein the method comprises the steps of:

- 5 a. introducing a transposon into a germplasm containing an endogenous *fin* gene;
- b. obtaining progeny of the germplasm of step (a); and
- c. identifying a plant of the progeny of step (b) in which the transposon has inserted into the endogenous *FIN* gene and a reduction of
- 10 expression of *fin* is observed.

13. The method of claim 12, in which step (a) further comprises introduction of the transposon into a regenerable plant cell of the germplasm by transformation and regeneration of a transgenic plant from the regenerable plant cell, wherein the transgenic plant comprises in its genome the transposon.

15 14. The method of claim 6 or 7 wherein the method further comprises the steps of:

- i. introducing into a regenerable plant cell a recombinant construct comprising the weak *fin* allele identified by the method of claim 6 or 7;
- 20 ii. regenerating a transgenic plant from the regenerable plant cell after step (i), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and
- iii. selecting a transgenic plant of (ii), wherein the transgenic plant comprises the recombinant DNA construct and exhibits a weak *fin*
- 25 phenotype, when compared to a control plant not comprising the recombinant DNA construct.

15. The method of claim 3 or 4 wherein expression of the polypeptide of part (a) in a plant line having the *fin* mutant genotype is capable of partially or fully restoring the wild-type phenotype.

30 16. A method of producing a transgenic plant with an alteration in agronomic characteristic, the method comprising the steps of:

- a. introducing into a regenerable plant cell a recombinant DNA construct comprising an isolated polynucleotide operably linked, in

sense or antisense orientation, to a heterologous promoter functional in a plant, wherein the polynucleotide comprises:

- i. the nucleotide sequence 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, 45, 47 or 49;
- ii. a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49;
- iii. a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49;
- iv. a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (i); or
- v. a modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49;

- b. regenerating a transgenic plant from the regenerable plant cell after step (a), wherein the transgenic plant comprises in its genome the recombinant DNA construct; and
- c. selecting a transgenic plant of (b), wherein the transgenic plant comprises the recombinant DNA construct and exhibits an alteration in at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, seed number, fruit number, fruit size, root branching, root biomass, root lodging, biomass, and yield, when compared to a control plant not comprising the recombinant DNA construct.

17. The method of any of the claims 2-4 or 6-16, wherein said plant is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean,

sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

18. A plant or a seed comprising in its genome a recombinant DNA construct comprising an isolated polynucleotide operably linked, in sense or antisense orientation or both, to a heterologous promoter functional in a plant, wherein the polynucleotide comprises:

- a. the nucleotide sequence 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, 45, 47 or 49;
- b. a nucleotide sequence with at least 90% sequence identity, based on the Clustal W method of alignment, when compared to 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, 45, 47 or 49;
- c. a nucleotide sequence of at least 100 contiguous nucleotides 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, 45, 47 or 49;
- d. a nucleotide sequence that can hybridize under stringent conditions with the nucleotide sequence of (a); or
- e. a modified plant miRNA precursor, wherein the precursor has been modified to replace the miRNA encoding region with a sequence designed to produce a miRNA directed to 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, 45, 47 or 49; and

wherein the plant exhibits an alteration in at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, seed number, root branching, root biomass, root lodging, biomass, fruit number, fruit size and yield, when compared to a control plant not comprising the recombinant DNA construct.

19. The plant or seed of claim 18, wherein said plant or seed is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

20. A recombinant DNA construct comprising a polynucleotide operably linked to at least one heterologous regulatory element, wherein the polynucleotide encodes a polypeptide having an amino acid sequence with at least 95% sequence

identity, based on Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, and wherein the polypeptide has shoot meristem function altering activity.

21. The recombinant DNA construct of claim 20, wherein the polynucleotide encodes a polypeptide having an amino acid sequence comprising 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, 46, 48, 50, 51-65, or 66.

22. A plant or seed comprising the recombinant construct of claim 20 or 21.

23. The plant or seed of Claim 22, wherein said plant or seed is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

24. A transgenic microorganism comprising the recombinant construct of claim 20 or 21.

25. A plant or seed comprising in its genome a recombinant DNA construct comprising a polynucleotide operably linked to at least one heterologous regulatory element, wherein said polynucleotide encodes a polypeptide having an amino acid sequence of at least 95% sequence identity, based on the Clustal W method of alignment, when compared to 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, 46, 48, 50, 51-65, or 66, and wherein said plant exhibits an alteration in at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, seed number, root branching, root biomass, root lodging, biomass, fruit number, fruit size and yield, when compared to a control plant not comprising the recombinant DNA construct.

26. The plant or seed of claim 25, wherein said polynucleotide encodes a polypeptide having an amino acid sequence comprising 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, 46, 48, 50, 51-65, or 66.

27. The plant or seed of claim 25 or 26, wherein said plant or seed is selected from the group consisting of: *Arabidopsis*, tomato, maize, soybean, sunflower, sorghum, canola, wheat, alfalfa, cotton, rice, barley, millet, sugar cane and switchgrass.

28. A method of identifying a first plant or a first plant germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first plant or the first plant germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to 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, 46, 48, 50, 51-65, or 66, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, fruit number, fruit size, seed number, root branching, root biomass, root lodging, biomass and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising 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, 46, 48, 50, 51-65, or 66.

29. A method of identifying a first maize plant or a first maize germplasm that has an alteration of at least one agronomic characteristic, the method comprising detecting in the first maize plant or the first maize germplasm at least one polymorphism of a marker locus that is associated with said phenotype, wherein the marker locus encodes a polypeptide comprising an amino acid sequence having at least 90% and less than 100% sequence identity to SEQ ID NO:4, 6 or 8, wherein expression of said polypeptide in a plant or plant part thereof results in an alteration of at least one agronomic characteristic selected from the group consisting of: ear meristem size, kernel row number, leaf number, inflorescence number, branching within inflorescence, flower number, fruit number, fruit size, seed number, root branching, root biomass, root lodging, biomass and yield, when compared to a control plant, wherein the control plant comprises a polynucleotide that encodes a polypeptide comprising SEQ ID NO:4, 6 or 8.

30. A method of increasing WUS expression in a plant or plant cell, wherein the method comprises the steps of:

- a. altering a plant or plant cell to decrease endogenous expression of a *FIN* gene in the plant or plant cell;

- b. determining WUS protein expression in the altered plant or plant cell of step (a); and
- c. selecting the altered plant or plant cell of step (b) with increased WUS expression.

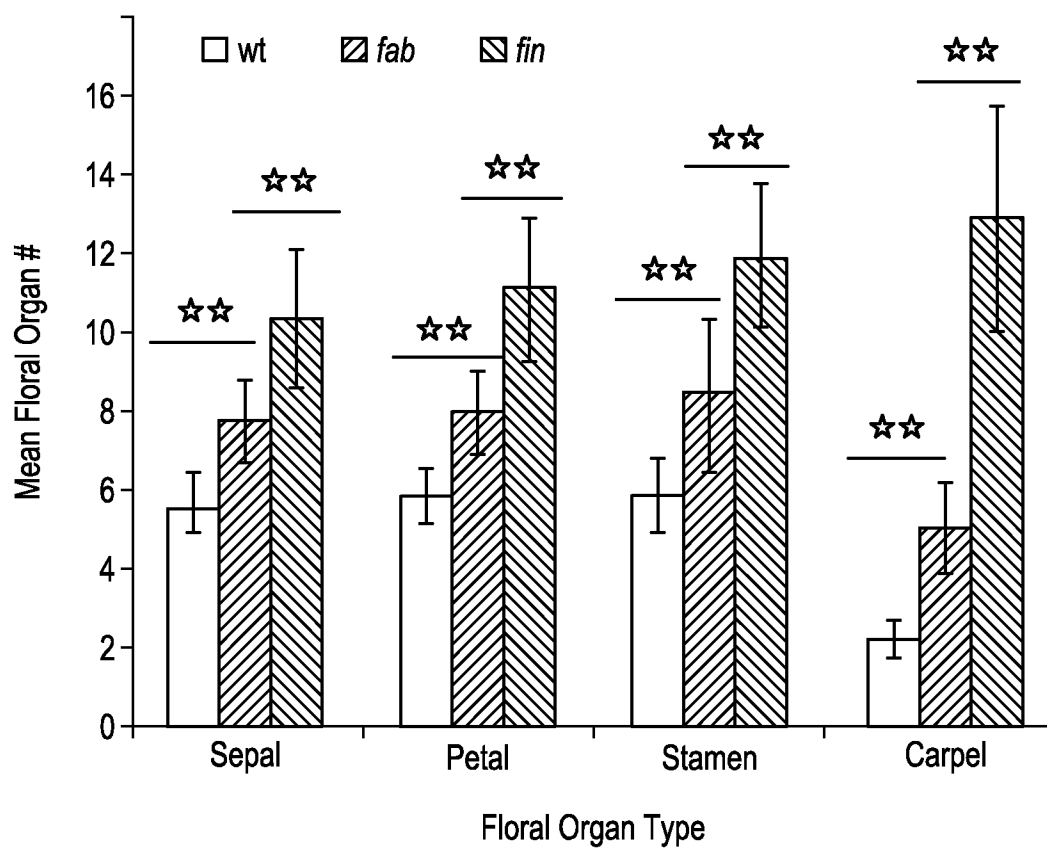
5 31. An altered plant or plant cell produced by the method of claim 30, wherein the altered plant or plant cell has increased expression of WUS protein, and decreased expression of *FIN* gene.

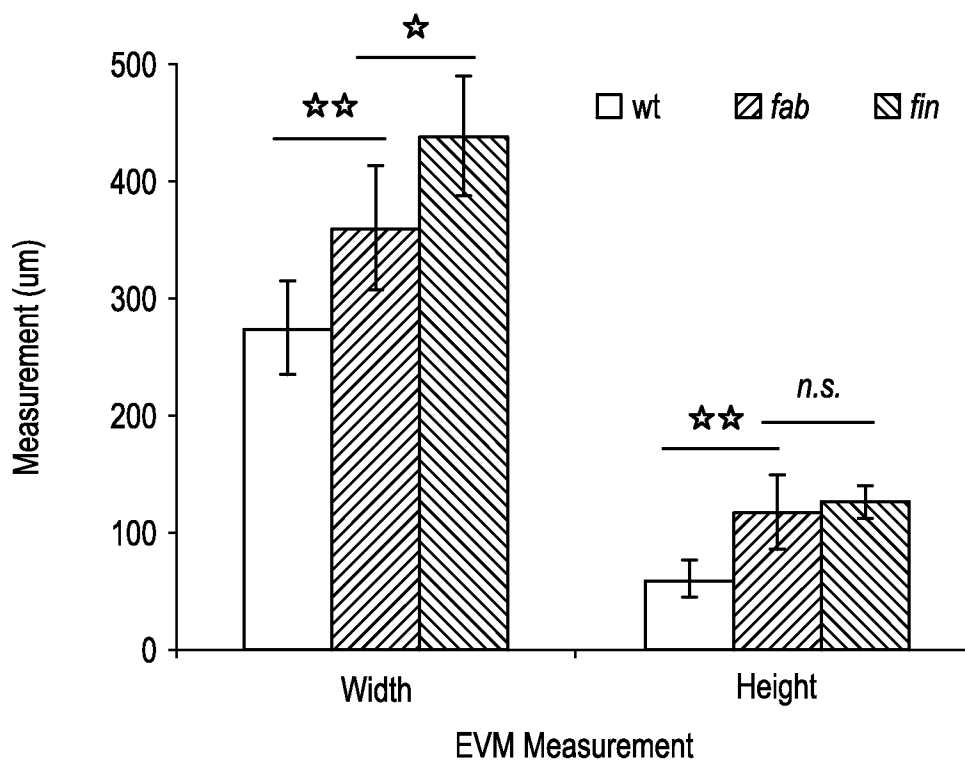
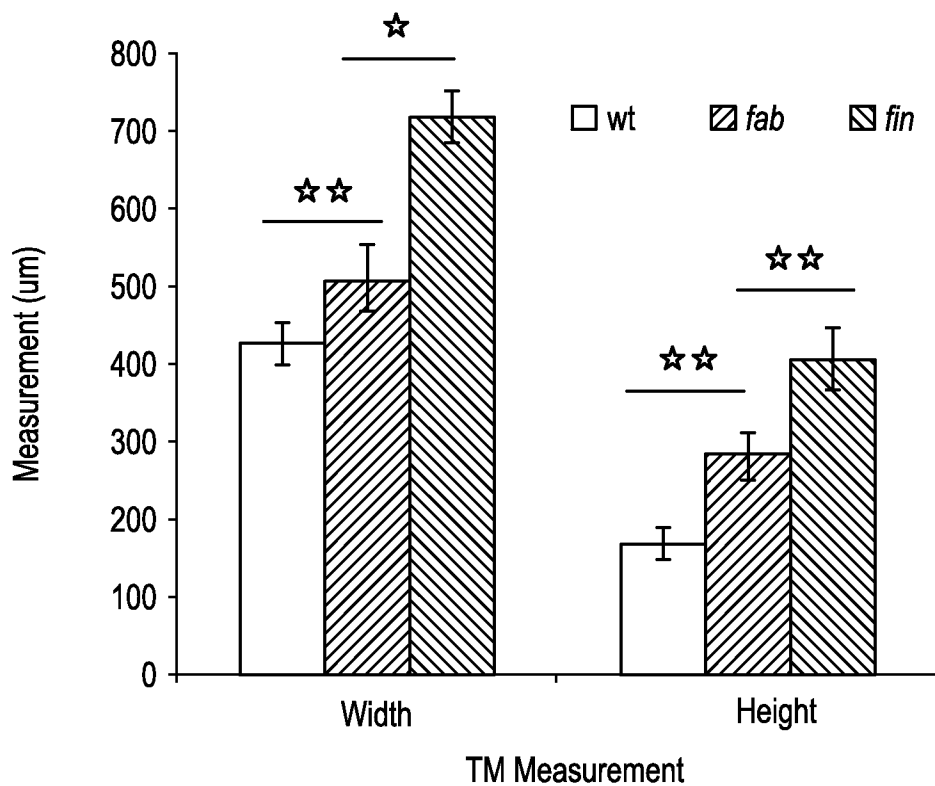
 32. A method of altering meristem function in a plant, wherein the method comprises the steps of:

- 10 a. altering a plant or plant cell to decrease endogenous expression of a *FIN* gene in the plant or plant cell;
- b. determining meristem function in the altered plant or plant cell; and
- c. selecting the altered plant or plant cell of step (a) with altered meristem function.

15 33. An altered plant or plant cell produced by the method of claim 32, wherein the altered plant or plant cell has altered meristem function, and decreased expression of *FIN* gene.

20

1/15*FIG. 1A*

2/15*FIG. 1B**FIG. 1C*

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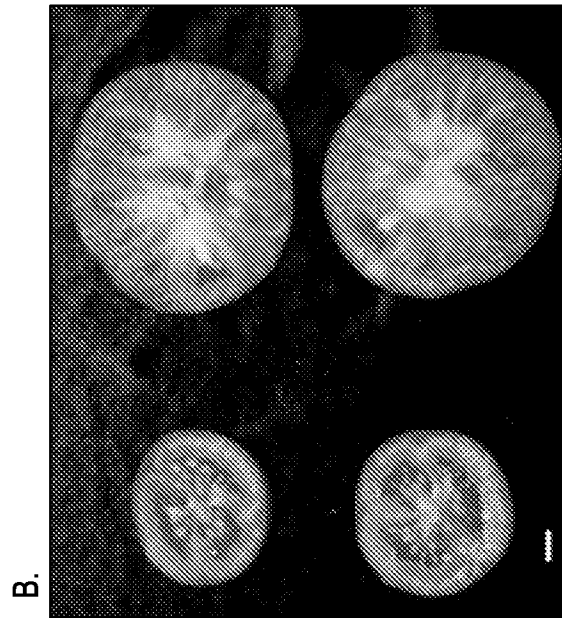


FIG. 1E

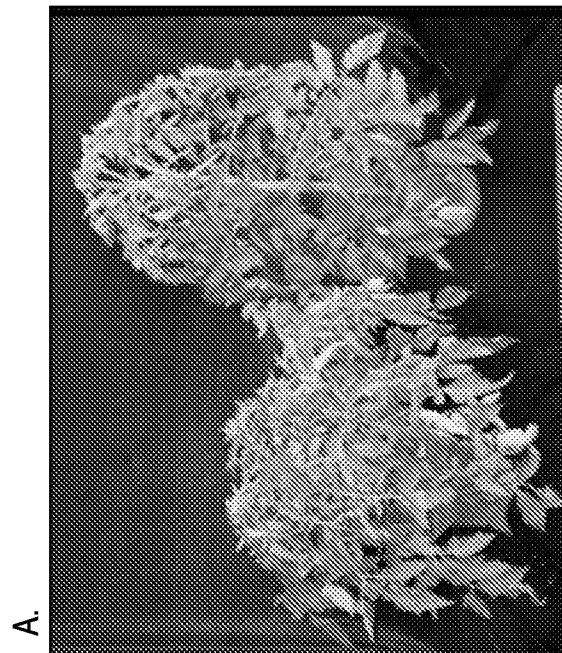


FIG. 1D

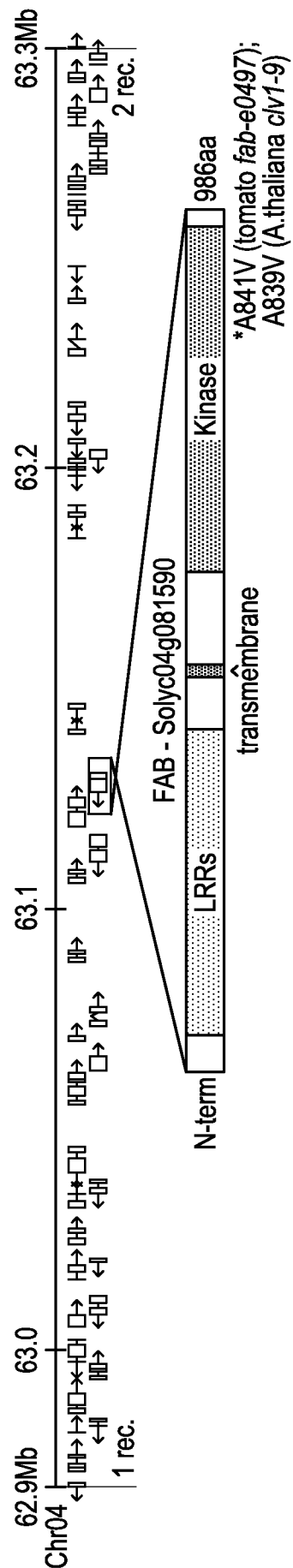


FIG. 2A

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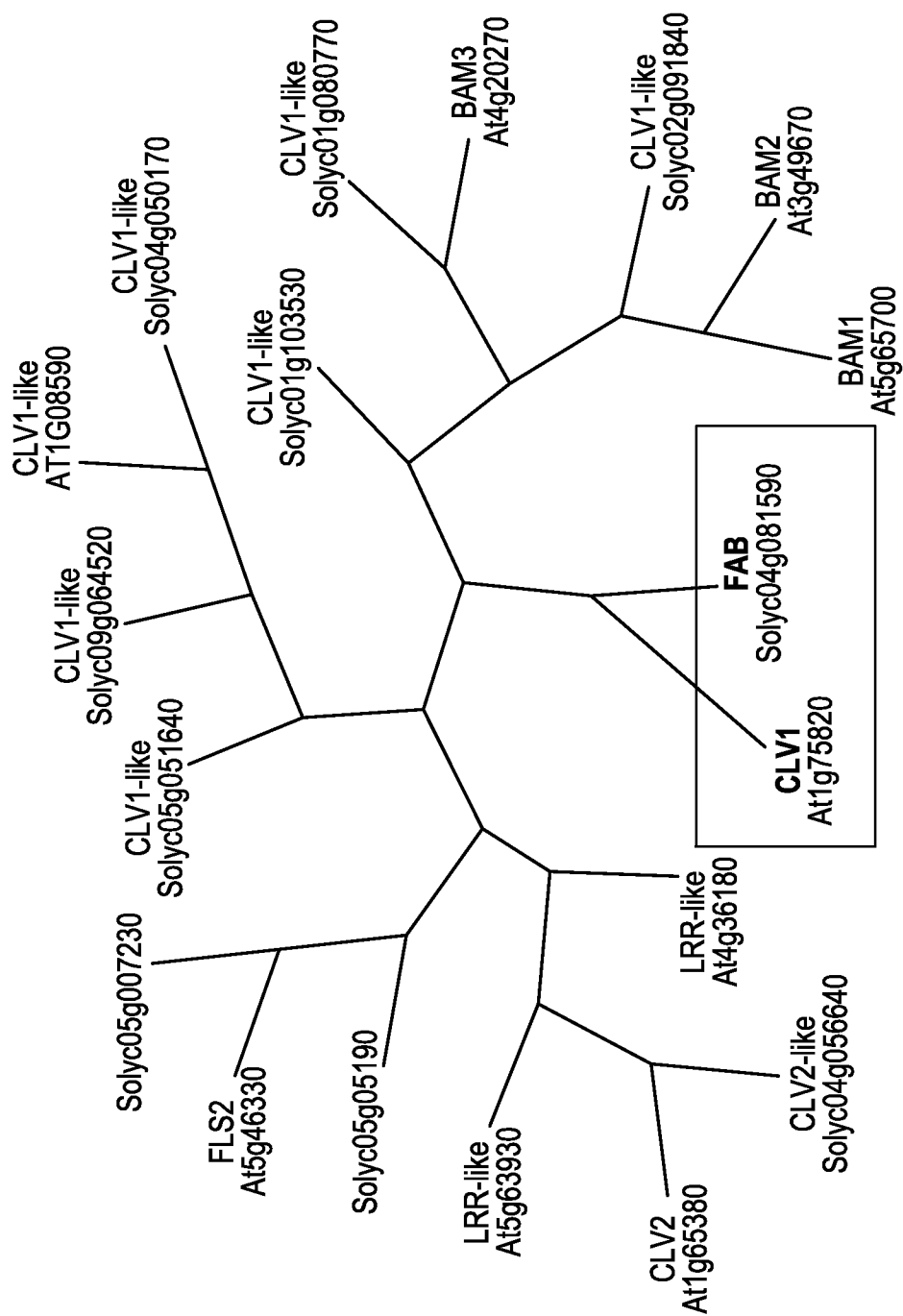


FIG. 2B

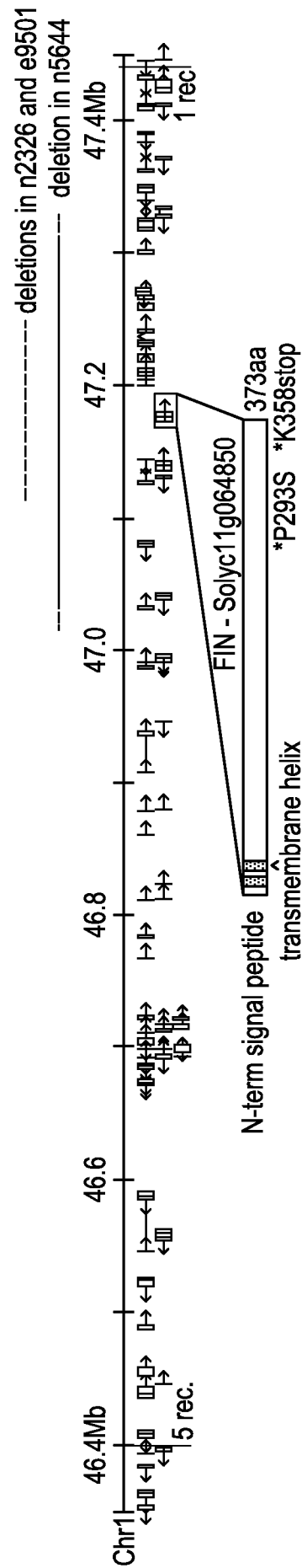


FIG. 3A

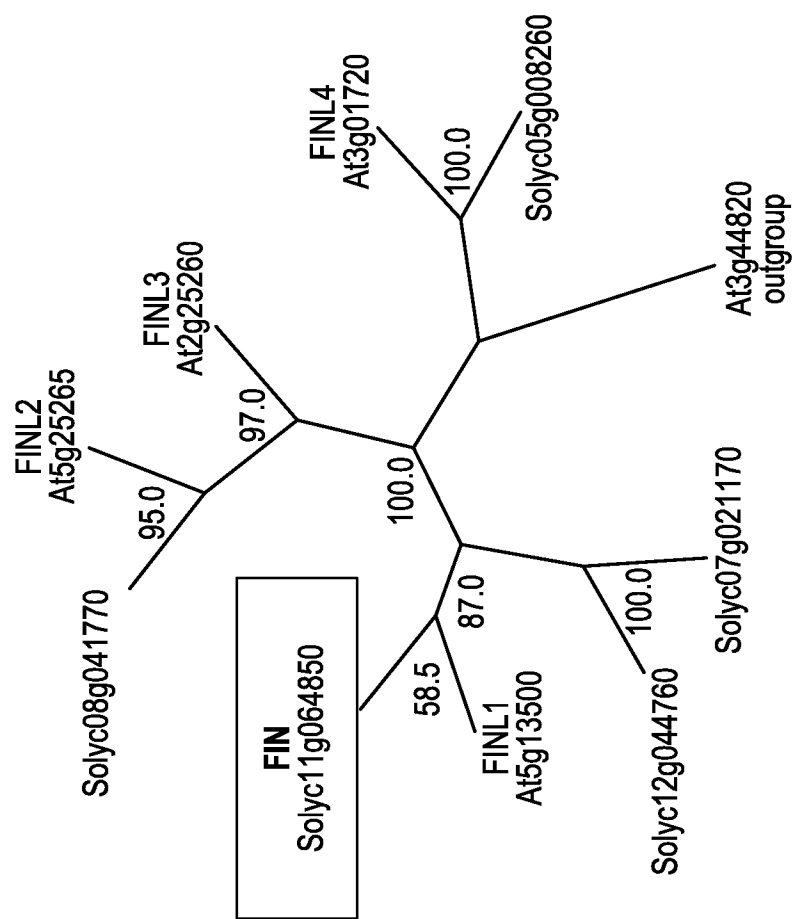


FIG. 3B

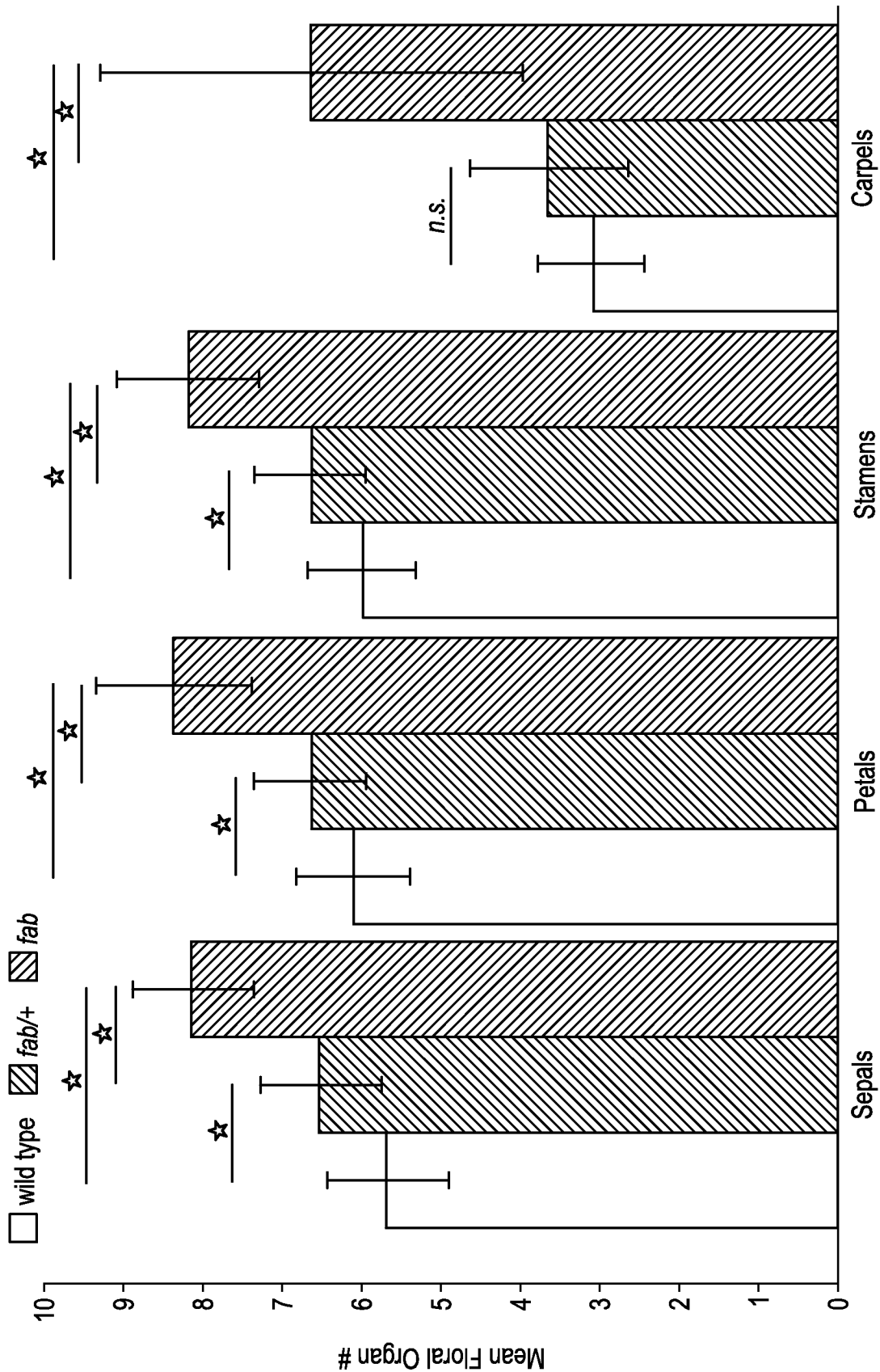


FIG. 4

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	10	20	30	40	50	60	70	
1	MIPRKNMG	PLLLILLALGFFFA	TYNLV	TLIIHYR	ATSSSF	ISTSGSSN	GGG	SEQ ID 2
1	MAAP	CGRGGT	TLVLMA	SAAF	LTYNV	LISFHSS	QPLP	SEQ ID 4
1	MDAAVRKAAG	AGIARAP	ALVLALMA	GAFLIS	YNEFT	MLFHGG	GGIGAAV	SEQ ID 6
1	MSCRKNAG	KVS	PWLLVLIC	GCFFVT	YNLLIT	MPSRGR	DGPRKFL	SEQ ID 8
1	MG	RAS	PLLIIFL	VLGS	FEATYN	LVMIIRYG	SSENVAT	SEQ ID 10
1	MG	CGN	LFFTLLIT	FTSVAL	ITYNII	ISGNAPL	KQDFPGP	SEQ ID 12
1	MIGGKNMG	RTS	PLLLILLALG	FFFA	TYNLLIT	MVIHNR	FSSWVPNN	SEQ ID 14
1	MGMG	YGL	FCCKTLLIS	FSAA	ITYNII	ISSNAP	FP	SEQ ID 16
1	MG	CGN	IFFTLLIT	FSVSL	ITYNII	ISANAPL	KQELPG	SEQ ID 18
1	MIGRKNAG	RAS	PSLLVLLAF	GFFLA	TYNLLIL	VHK	NSGNDT	SEQ ID 20
1	MG	WGN	IFFTLLIT	FSAA	ITYNII	ISANASL	RQDFPGN	SEQ ID 22
1	MG	WGN	IFFTLLIT	FSAA	ITYNII	ISANASL	RQDFPGN	SEQ ID 24
1	MG	CGK	LFFTLLIT	CSAIL	ITYSII	ISSNAPL	KQDFPG	SEQ ID 26
1	MGLNLGLS	FGN	LFKTLLIIF	SVAVV	TYNVIV	SANSPL	KLDFPGPKDQ	SEQ ID 28
1	MG	WQS	VFYLLILLIT	LSVAL	ITYNAIV	SSTAPL	SPSFPGSDAG	SEQ ID 30
1	MIGRKSG	RAS	SLLILLVA	GIGFFV	TYNLLIT	MIIQN	RSGDNL	SEQ ID 32
1	MG	CES	IFYTLLIT	FTSVAL	ITYNVII	ISANAPL	RQDFPG	SEQ ID 34
1	MG	CES	YFYTLLIT	FTSVAL	ITYNVII	ISSNTPL	KQDFPGY	SEQ ID 36
1	MG	CGS	YFYTLLIT	FTSVAL	ITYNVII	AANSPLN	RHDLPE	SEQ ID 38
1	MIGGKNMG	RAS	PFFLLILLIT	VG	FIVTYN	LVSF	LVSESEKNSL	SEQ ID 40
1	MS	KAL	PFLVLLS	IGAF	VLLTYN	FVTMTI	THYQVKWLS	SEQ ID 42
1	MIERRNMG	KVS	PLLLMLLIT	FGFA	TYNLLIT	LIINH	KSATNSV	SEQ ID 44

FIG. 5A

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	80	90	100	110	120	130	140																											
58	G	---	SEWFD	PVKE	---	SNLVK	SGDR	---	KFH	VAL	TAT	DAP	YSK	WQCR	IMYY	WYKK	MKE	---	RDGS	---	EMG	SEQ	ID	2										
42	S	---	FPTAS	RRF	-GA	AGS	---	ARRR	A	FHT	AVT	ASG	SA	YNT	WQCR	VMY	HHW	FKE	ARR	---	APG	DEM	SEQ	ID	4									
54	---	TRDP	V	VAMP	WRAA	ADTE	ARRR	PE	FH	VAL	TAT	DAP	YSR	WQCR	VMY	F	WYKR	MQA	---	RPG	GEAM	SEQ	ID	6										
48	---	GDR	H	STAS	---	LGSG	SDS	DPA	KR	---	FH	VAL	TAT	DAL	YSQ	WQSR	IMH	YWK	EMRD	---	RPGS	-DMG	SEQ	ID	8									
42	---	ALF	FDP	PI	EM	---	PAH	V	KNR	KTS	KAP	FH	VAL	TAT	DAP	YNK	WQCR	IMYY	WYKR	QRS	---	LPGS	---	SEQ	ID	10								
45	---	LDPI	I	KMPL	-NRR	SSS	SS	---	SSK	L	FHT	AVT	ASD	SV	YNT	WQCR	IMYY	W	EKK	FKD	---	SPDS	-AMG	SEQ	ID	12								
50	---	SIL	IDPI	TEM	---	PGQ	LKR	QGV	KE	PE	FH	VAL	TAT	DAP	YSK	WQCR	IMYY	WYKK	QKS	---	LPGS	-DEG	SEQ	ID	14									
38	---	SFDR	S	DPV	I	KLPS	-DRK	FKI	G	SAQ	KRL	FHT	AVT	ASD	SV	YNT	WQCR	VMYY	W	EKK	FKQ	---	QPN	---	SEQ	ID	16							
42	S	-SQ	PV	FLND	PI	IKMPE	-NKK	STLT	-QK	RLL	FHT	AVT	ASNS	SV	YNT	WQTR	VMYY	W	EKK	MKE	NGD	EC	---	EMG	SEQ	ID	18							
44	---	ELY	DP	PI	IRR	---	PEAM	REG	DAL	---	KFH	VAL	TAT	DAP	YSK	WQCR	VMYY	WYKK	MKD	---	MPGS	-DMG	SEQ	ID	20									
45	S	-SSK	-LAV	DP	II	QMPT	-DLP	SSSK	-KTK	RLL	FHT	AVT	SSD	SV	YNT	WQCR	VMYY	W	EKK	QKN	---	LPNS	---	EMG	SEQ	ID	22							
45	S	-AK	-LAV	DP	II	QMPT	-DLP	SSSK	-KTK	RLL	FHT	AVT	SSD	SV	YNT	WQCR	VMYY	W	EKK	QKN	---	LPNS	---	EMG	SEQ	ID	24							
44	G	---	---	---	---	FSV	VKMPT	-D	SPS	---	KPK	RL	FHT	AVT	ATD	SV	YSA	WQCR	VMYY	W	FQK	QKK	---	NPNS	---	DMG	SEQ	ID	26					
52	R	FET	F	DTL	ID	PV	IRLPT	-DRK	SKL	G	LARK	RL	FHT	AVT	ASD	SV	YNT	WQCR	VMYY	W	EKK	FKQD	---	GPGS	---	EMG	SEQ	ID	28					
46	L	P	STAR	L	R	F	DPV	V	KMPA	-Q	RASAK	---	TKK	R	P	FHT	AVT	ASD	SV	YNT	WQCR	VMYY	W	FNK	FKQ	---	EPGS	---	EMG	SEQ	ID	30		
46	---	---	---	---	---	SKY	DP	II	QM	---	PDN	V	RK	F	G	NK	MPE	FH	VAL	TAT	DAP	YSK	WQCR	IMYY	WYKK	TKF	---	MPGS	---	EMG	SEQ	ID	32	
44	---	---	---	---	---	ID	PI	I	TMPT	---	EKS	KLK	-SQ	KRL	FHT	AVT	SSD	SV	YNT	WQCR	F	IMYY	W	EKK	FKQ	---	GPNS	---	EMG	SEQ	ID	34		
45	S	-SSS	S	F	S	DP	LI	HMPN	-EGR	PKI	I	R	SQ	KRL	FHT	AVT	ASD	SV	YNT	WQCR	IMYY	W	EKK	FKQ	---	EPGS	---	EMG	SEQ	ID	36			
45	S	-SL	---	I	S	DP	VI	KMPN	---	GRS	KPK	-TE	KRL	FHT	AVT	SSD	SV	YNT	WQCR	IMYY	W	EKK	FKQ	---	GPNS	---	EMG	SEQ	ID	38				
52	---	---	---	---	---	LLS	DP	V	VGM	---	PRN	V	KKN	D	G	T	KLL	FH	VAL	TAT	DAP	YSK	WQCR	IMYY	WYKK	V	RD	---	MPGS	---	EMG	SEQ	ID	40
41	N	---	QVA	ID	P	L	VE	---	PEY	V	K	T	M	DEK	Q	P	FHT	AVT	SSD	SV	YNT	WQCR	IMYY	WYKK	MKD	---	LDGS	---	NMG	SEQ	ID	42		
47	---	SAF	P	DP	PI	ATM	---	PQR	V	R	K	L	G	K	P	KL	FHT	AVT	DAP	YSK	WQCR	IMYY	WYRR	MKD	---	APGS	---	DMG	SEQ	ID	44			

FIG. 5B

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114	GFTRVLHSGKPDNLMEEIPTFVVDP	150	160	170	180	190	200	210	SEQ ID 2
98	GFTRVLHSGKPDNLMEEIPTFVADP	150	160	170	180	190	200	210	SEQ ID 4
115	GFTRVLHSGKPDGLMDEIPTFVVDPL	150	160	170	180	190	200	210	SEQ ID 6
104	GFTRVLHSGKPDGLMDEIPTMVVDPL	150	160	170	180	190	200	210	SEQ ID 8
101	GFTRVLHSGKPDNLMDEIPTMVVDPL	150	160	170	180	190	200	210	SEQ ID 10
102	GFTRVLHSGKPDQFMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 12
109	GFTRVLHSGRTDDLMEEIPTFVVDPL	150	160	170	180	190	200	210	SEQ ID 14
101	GFTRVLHSGVDPDKHMDIPTFVVQPL	150	160	170	180	190	200	210	SEQ ID 16
108	GFTRVLHSGKSDKFMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 18
100	GFTRVLHSGKSDNLMEEIPTFVVDP	150	160	170	180	190	200	210	SEQ ID 20
108	GFTRVLHSGKSDKFMDEIPTFVAKPL	150	160	170	180	190	200	210	SEQ ID 22
107	GFTRVLHSGKSDKFMDEIPTFVAKPL	150	160	170	180	190	200	210	SEQ ID 24
98	GFTRVLHSGKSDKFMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 26
118	GFTRVLHSGKPDGLMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 28
110	GFTRVLHSGKPDGFMDEIPTFVADPL	150	160	170	180	190	200	210	SEQ ID 30
104	GFTRVLHSGSPDNLMDEIPTFVVDP	150	160	170	180	190	200	210	SEQ ID 32
100	GFTRVLHSGKPDKYMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 34
110	GFTRVLHSGKPDKYMDEIPTFLAQPL	150	160	170	180	190	200	210	SEQ ID 36
106	GFTRVLHSGRDKYMDEIPTFVAQPL	150	160	170	180	190	200	210	SEQ ID 38
110	GFTRVLHSGKADNLMEEIPTLVVDPL	150	160	170	180	190	200	210	SEQ ID 40
101	RFTRVLHSGRPDDLMNEIPTFVVDPL	150	160	170	180	190	200	210	SEQ ID 42
106	KFTRVLHSGKADNLMDEIPTFIVDPL	150	160	170	180	190	200	210	SEQ ID 44

FIG. 5C

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	220	230	240	250	260	270	280					
1184	PNLARGDLPA	AFPPFFYIK	PAEHEGVIR	KYYPEELGP	VTNVDPI	GNSPV	IIKKSILEK	IAPTWMNVSLRMK				
1167	PNLSRDGQAA	AFPPFYIE	PKKYENVL	RKFFPE	DKGPI	TKIDPI	GNSPV	IIKESLGR	IAPTWMNVSLAMK			
1185	PNLAHDD	DPAAFPFFYI	TSEHEKII	RKYYAKER	GPVTDD	PIGNSPV	IIKKTI	LEK	IAPTWMNVSLQMK			
1174	PNLSHGDE	PAAFPPFFYIK	PTENEKIL	RKFFPEEK	GPI	SNDDPI	GNSPV	IIKKAQLEK	IAPTWMNVSLKMK			
1171	PNLAYGEH	PAAFPPFFYIK	PDQNEKIV	RKFYPEENG	GPVTNVD	PIGNSPV	IIRRDLIA	K	IAPTWMNVSLKMK			
1172	PNLAREGM	GAAFPPFFYIE	PKKYEAVL	RKYFFPEENG	GPI	TNDDPI	GNSPV	IVGKEYLKK	IAPTWMNVSLAMK			
1179	PNLALGGR	PAAYPPFFYIK	PAEHENIV	RKFYPEENG	GPI	TNVDPI	GNSPV	IIKKELLAD	IAPTWMNVSLKMK			
1171	PNLSRDGH	GAAFPPFFYIE	PKKYESVL	RKFFPESK	GPI	TEIDPI	GNSPV	IVAKESL	RK	IAPTWMNVSL	EMK	
1178	PNLSRDGL	GAAFPPFFYIE	PKKYEPVL	RKFFPEDK	GPI	TNIDPI	GNSPV	IVGKESL	KK	IAPTWMNVSLAMK		
1170	PNLAHGDN	PAAFPPFFYIK	PTDNEKVV	RKYYPEENG	GPVTNID	PIGNSPV	IIKKS	LEK	IAPTWMNVSLRMK			
1178	PNLSKDG	LAAAFPPFFYIE	PKKYEKVL	RKFFPEEK	GPI	TNIDPI	GNSPV	IVGKEDL	KK	IAPTWMNVSLAMK		
1177	PNLSKDG	LAAAFPPFFYIE	PKKYEKVL	RKFFPEEK	GPI	TNIDPI	GNSPV	IVGKEDL	KK	IAPTWMNVSLAMK		
1168	PNLSINGR	GAAFHFFFYIE	PEKYE	TTLRKFFPEEM	GPI	TKIDPI	GNSPV	IVGKDAL	KL	IAPTWMNVSLAMH		
1188	PNLSRNL	GAAFPPFFYIE	PKKYESTL	RKFFPEDK	GPI	TNIDPI	GNSPV	IVGKESL	QK	IAPTWMN	ISLAMK	
1180	PNLSKDNF	GAAFPPFFYIE	PKKFE	SVLRKFFPEDK	GPI	TNIDPI	GNSPV	IVGKESL	KK	IAPTWMNVSLAMK		
1174	PNLARGGF	PAAFPPFFYIK	PTEHENI	RKYYPEEK	GPVTNVD	PIGNSPV	IIKKS	MLEK	IAPTWMNVSLSMK			
1170	PNLSRDGL	GAAFPPFFYIE	PKKYEATL	RKFFPEDK	GPI	TNIDPI	GNSPV	IVGKESL	RK	IAPTWMNVSLAMK		
1180	PNLSRDGH	GAAYHFSYIE	PEKYE	GQLRKFFPEK	GPI	TNIDPI	GNSPV	IVGKESL	KK	IAPTWMNVSLAMK		
1176	PNLSKDL	GAAFPPFFYIE	PKKYETTL	RKFFPEDK	GPI	TNIDPI	GNSPV	IVGKESL	KK	IAPTWMNVSLAMK		
1180	PNLARE	DYPAAFPFFYIK	PSDNEKII	RKFYPEEV	GPVTDD	PIGNSPV	IIKKAQLEK	IAPT	R	MN	ISL	KMK
1171	PNLVYGDY	PAFPFFYIK	PAENENV	RKFFPEEM	GPVTS	IDPI	GNSPV	IIKRD	LLEK	IAPTWMNVSLRMK		
1176	PNLSHGDN	PAAFPPFFYIK	PTDHE	DMVRKFFPEK	GPVTNVD	PIGNSPV	IIKKTI	LEE	ISPTW	MNVSLRMK		

FIG. 5D

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290										300										310										320										330										340										350									
2254	DDPETDKAF	GWVLEMYG	YAVASALHGV	RHILRKDF	MLQPPWD	LEVGGKFI	IHYTYG	CDYNMKGELTYGKI	SEQ	ID	2																																																										
2237	KDPDADKSF	GWVLEMYA	YAVASALHGV	GNILRKDF	MIQPPWD	LEVGD	SFIHYTYG	CDYDMTGKLT	YGKI	SEQ	ID	4																																																									
2255	EDEETDKV	FGWVLEMYA	YAVASALHGV	HHILRKDF	MIQPPF	DTKLQNT	FIHF	TYGCDYS	IKGELTYGKV	SEQ	ID	6																																																									
2244	EDQETDKA	FGWVLEMYA	YAVASALHGV	HHSHLHKDF	MIQPPWD	LKTDNT	FIHYTYG	CDYS	SMKGQLTYGKI	SEQ	ID	8																																																									
2241	EDPETDKA	FGWVLEMYA	YAVASALHGV	RHILRKDF	MLQPPWD	LETYNKFI	IHYTYG	CDYN	IKGELTYGKI	SEQ	ID	10																																																									
2242	KDPETDKA	FGWVLEMYA	YAVASALHGV	RNIILYKEF	MIQPPWD	KEIGKTYI	IHYTYG	CDYS	SMKGELTYGKI	SEQ	ID	12																																																									
2249	EDPETDKA	FGWVLEMYA	YAVASALHGV	KHILRNDF	MLQPPWD	LSTKDKFI	LHYTYG	CDYNMKGELTYGKI	SEQ	ID	14																																																										
2241	QDPETDKA	FGWVLEMYA	YAVASALHGV	KNIILYKDF	MIQPPWD	TEVGA	KYIHYTYG	CDYDMKGKLT	YGKI	SEQ	ID	16																																																									
2248	KDPEADKA	FGWVLEM	CAYAVASALHGV	NIILHKDF	MLQPPWD	TEIGNKF	IHYTYG	CDYDMQCKLT	YGKI	SEQ	ID	18																																																									
2240	DDPETDKA	FGWVLEMYG	YAVASALHGV	RHILRKDF	MLQPPWD	QEI	GKFIHYTYG	CDYNMKGELTYGKI	SEQ	ID	20																																																										
2248	KDPEADKA	FGWVLEMYA	YAVASALHGV	GNILYKEF	MIQPPWD	TKIGKSYI	IHYTYG	CDYN	LQGMTPGKI	SEQ	ID	22																																																									
2247	KDPEADKA	FGWVLEMYA	YAVASALHGV	GNILYKEF	MIQPPWD	AKIGKSYI	IHYTYG	CDYN	LQGMTPGKI	SEQ	ID	24																																																									
2238	KDPEARKAF	DWVLEMYA	YAVASALHGV	GNGLHEEF	MIQPPWD	TEIDKAYI	IHYTYG	CFD	SKGKPAKGEA	SEQ	ID	26																																																									
2258	KDPEADKA	FGWVLEMYA	YAVASALHGV	KNIILYKDF	MIQPPWD	TEVGGK	KYIHYTYG	CDYDMKGKLT	YGKI	SEQ	ID	28																																																									
2250	NDSEADKA	FGWVLEMYA	YAVSSALHGV	SNILRKDF	MIQPPWD	LEV	RDKFIHYTYG	CDYNMKGNLT	YGKI	SEQ	ID	30																																																									
2244	DDPETDKA	FGWVLEMYA	YAVASALHGV	QHILRKDF	MLQPPWD	LEVGGKRF	IHYTYG	CDYS	IKGELTYGKI	SEQ	ID	32																																																									
2240	KDPEADKA	FGWVLEMYA	YAVASALHGV	GNILYKDF	MLQPPWD	TEIGK	KFIHYTYG	CDYDMKGKMT	YGKI	SEQ	ID	34																																																									
2250	KDPEADKA	FGWVLEMYA	YGVASALHGV	NIILQDD	MLQPPWD	TEIGK	KFIHYTYG	CDYDMKGKMT	YGKI	SEQ	ID	36																																																									
2246	KDPEADKA	FGWVLEMYA	YAVASALHGV	NIILYKDF	MLQPPWD	TEIGK	KYIHYTYG	CDYDMKGRS	TYGKI	SEQ	ID	38																																																									
2250	DYPETDKA	FGWVLEMYA	YAVASALHGV	QVHILRKDF	MIQPPWD	HN	VGKSF	IHF	TYGCDYS	IKGELTYGKI	SEQ	ID	40																																																								
2241	NDAFADAT	FGWVLEMYG	YAVASALHGV	QVHILRKDF	MLQPPWD	LPT	TRDKFI	LHYTYG	CDYDLQGLTYGKI	SEQ	ID	42																																																									
2246	DDPETDKA	FGWVLEMYA	YAVASALHGV	RHILRKDF	MIQPPWD	AEVGGKTF	IHYTYG	CDYN	IKGELTYGKM	SEQ	ID	44																																																									

FIG. 5E

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324	GEWRFDKRSYLRGPPPKNLSLPPPGVPESVVR	360	370	380	390	400	SEQ ID 2
307	GEWRFDKRSYTDKPPPRNLP	360	370	380	390	400	SEQ ID 4
325	GEWRFDKRSFDPDRPPPRNLT	360	370	380	390	400	SEQ ID 6
314	GEWRFDKRSYIQSPPRNLSLPPPGVPESVVR	360	370	380	390	400	SEQ ID 8
311	GEWRFDKRSYLRGPPPKNLT	360	370	380	390	400	SEQ ID 10
312	GEWRFDKRSYLDHVA	360	370	380	390	400	SEQ ID 12
319	GEWRFDKRSYLRGPPPKNLT	360	370	380	390	400	SEQ ID 14
311	GEWRFDKRSYTKVP	360	370	380	390	400	SEQ ID 16
318	GEWRFDKRSFDNVY	360	370	380	390	400	SEQ ID 18
310	GEWRFDKRSYHLSGPPPRNLT	360	370	380	390	400	SEQ ID 20
318	GEWRFDKRSYDNVW	360	370	380	390	400	SEQ ID 22
317	GEWRFDE	360	370	380	390	400	SEQ ID 24
308	SEW	360	370	380	390	400	SEQ ID 26
328	GEWRFDKRSYDKV	360	370	380	390	400	SEQ ID 28
320	GEWRFDKRSYTYT	360	370	380	390	400	SEQ ID 30
314	GEWRFDKRSYLRGPPPKNLSLPPPGVPESVVR	360	370	380	390	400	SEQ ID 32
310	GEWRFDKRSYDQT	360	370	380	390	400	SEQ ID 34
320	GEWRFDKRSYTRA	360	370	380	390	400	SEQ ID 36
316	GEWRFDKRSYGT	360	370	380	390	400	SEQ ID 38
320	GEWRFDKRSYLRGPPPKNLT	360	370	380	390	400	SEQ ID 40
311	GEW	360	370	380	390	400	SEQ ID 42
316	GEWRFDKRTY	360	370	380	390	400	SEQ ID 44

FIG. 5F

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Percent Identity																					
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
1	63.6	69.2	73.3	77.5	66.1	76.9	64.7	61.3	84.0	60.8	60.8	55.9	62.4	66.1	82.5	64.8	62.4	62.9	77.8	73.6	80.1
2	49.5	63.2	65.9	63.1	72.7	62.5	74.9	74.2	63.9	72.0	71.4	65.5	75.2	75.1	65.4	75.8	73.1	73.6	62.3	61.0	62.1
3	39.7	50.3	69.8	68.2	61.6	64.8	63.7	59.1	69.8	58.8	58.5	56.0	59.5	63.9	70.5	60.0	57.9	59.0	68.2	65.1	65.7
4	33.1	45.3	38.6	70.3	64.7	69.1	64.8	61.3	72.5	61.0	61.0	57.9	63.0	65.5	72.4	64.5	62.1	62.9	70.1	66.9	70.2
5	26.8	50.4	41.4	37.8	63.9	78.3	63.7	61.1	75.6	60.6	60.6	55.4	61.3	65.8	77.7	63.7	61.3	62.0	74.4	70.2	72.7
6	44.9	34.0	53.3	47.5	48.9	63.7	80.9	81.5	66.2	81.9	81.4	73.8	80.8	76.6	67.2	83.2	80.0	81.3	66.8	60.2	65.0
7	27.6	51.7	47.2	39.7	25.6	49.4	63.7	60.2	74.4	60.6	60.6	56.9	61.4	65.0	76.0	63.7	62.4	63.2	71.9	69.6	71.5
8	47.5	30.6	49.4	47.3	49.2	22.1	49.4	78.7	64.6	77.5	76.3	72.9	83.8	77.2	65.7	83.4	79.3	80.7	64.7	61.5	62.3
9	54.0	31.6	58.4	54.0	54.4	21.3	56.1	25.2	63.2	81.0	80.1	73.4	79.4	75.5	62.3	84.8	79.4	80.9	61.5	59.4	59.6
10	18.0	49.0	38.5	34.2	29.5	44.8	31.4	47.7	50.2	61.9	61.4	56.8	62.8	64.3	79.9	65.5	62.2	62.3	76.9	70.0	78.0
11	54.9	35.1	59.1	54.6	55.3	20.7	55.3	26.9	22.0	52.7	98.9	75.6	76.5	74.0	62.7	83.0	76.8	79.6	63.1	58.4	61.6
12	54.9	36.0	59.7	54.6	55.3	21.4	55.3	28.5	23.2	53.8	1.1	74.7	76.2	73.6	62.7	82.1	75.6	78.7	62.8	58.4	61.9
13	65.4	46.0	65.2	61.0	66.4	32.3	63.2	33.6	32.8	63.3	29.6	30.9	71.9	69.7	57.0	74.0	72.8	72.1	57.7	56.9	57.6
14	51.7	30.1	57.7	50.7	54.0	22.2	53.8	18.2	24.1	50.9	28.2	28.7	35.2	75.8	63.8	85.8	78.0	82.1	63.7	60.7	61.0
15	44.9	30.3	49.0	45.9	45.4	28.1	46.9	27.3	29.7	48.2	32.0	32.5	38.8	66.5	79.0	74.9	76.8	76.8	66.3	64.4	64.9
16	20.0	46.1	37.4	34.5	26.6	42.9	28.9	45.6	52.1	23.5	51.1	51.1	62.9	44.3	66.5	63.6	64.4	78.3	70.4	77.0	16
17	47.4	29.3	56.6	47.9	49.2	19.0	49.2	18.8	17.0	46.0	19.4	20.5	31.9	15.8	24.7	44.3	89.1	91.1	64.6	61.6	63.4
18	51.9	33.4	60.9	52.4	54.0	23.3	51.8	24.3	24.1	52.2	27.8	29.5	33.9	26.1	30.7	49.5	11.8	85.7	63.1	58.5	62.0
19	50.9	32.6	58.7	50.9	52.6	21.6	50.3	22.3	22.1	52.0	23.8	25.1	34.9	20.5	27.8	48.0	9.5	15.9	62.9	60.6	61.3
20	26.4	52.0	41.3	38.2	31.4	43.8	35.2	47.5	53.5	27.7	50.4	50.9	61.4	49.3	44.6	25.7	47.7	50.4	50.8	69.9	74.0
21	32.6	54.6	46.8	43.4	38.0	56.2	38.9	53.6	57.8	38.3	59.9	59.9	63.2	55.1	48.0	37.7	53.3	59.7	55.4	38.4	68.0
22	23.2	52.4	45.7	37.9	34.0	47.0	35.8	52.1	57.5	26.1	53.3	52.8	61.6	54.6	47.1	27.4	50.0	52.6	54.0	32.0	41.7
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22

Divergence

FIG. 6

SEQ ID 2
SEQ ID 4
SEQ ID 6
SEQ ID 8
SEQ ID 10
SEQ ID 12
SEQ ID 14
SEQ ID 16
SEQ ID 18
SEQ ID 20
SEQ ID 22
SEQ ID 24
SEQ ID 26
SEQ ID 28
SEQ ID 30
SEQ ID 32
SEQ ID 34
SEQ ID 36
SEQ ID 38
SEQ ID 40
SEQ ID 42
SEQ ID 44