



**Supplemental Table S2. RNA-Seq analysis of differentially expressed genes involved in organ development in the *mf* mutant compared with the wild-type**

<b>Gene ID</b>	<b>log<sub>2</sub>FC</b>	<b>FDR</b>	<b>Putative functions</b>
Csa3G895620	-1.19	6.59E-06	Leucine-rich receptor-like protein kinase family
Csa4G043850	-1.57	4.21 E-03	Homeobox-leucine zipper protein family
Csa6G095280	-5.02	3.14 E-02	Agamous-like MADS-box protein
Csa5G341040	-1.43	2.51 E-04	Myb-like transcription factor REVEILLE 1-like
Csa4G043850	-1.57	4.21 E-03	homeobox-leucine zipper protein ATHB-21-like
Csa5G630820	1.05	3.28 E-02	homeobox-leucine zipper protein HAT5-like
Csa2G352950	1.18	4.17E-05	transcription factor RAX3-like
Csa3G183960	1.09	1.62E-07	transcription factor ASG4-like
Csa7G168060	2.5	8.37 E-03	transcription factor RADIALIS-like

**Supplemental Table S3. Cucumber genes analyzed in this study and their putative functions**

Name in this study	Gene ID	Annotation in CuGenDB ( <a href="https://cucurbitgenomics.org/">https://cucurbitgenomics.org/</a> )
CsWOX1	Csa1G042780	WUSCHEL-related homeobox; contains IPR009057 (Homeodomain-like)
CsPID1	Csa1G537400	Protein kinase; contains IPR011009 (Protein kinase-like domain)
CsPID2	Csa2G006100	Kinase family protein; contains IPR011009 (Protein kinase-like domain)
CsPID2-like	Csa4G064100	Serine/threonine protein kinase, putative; contains IPR011009 (Protein kinase-like domain)
CsPIN1	Csa1G042820	Auxin efflux carrier; contains IPR004776 (Auxin efflux carrier)
CsPIN2	Csa5G284520	Auxin efflux carrier; contains IPR004776 (Auxin efflux carrier)
CsPIN3	Csa1G025070	Auxin efflux carrier; contains IPR004776 (Auxin efflux carrier)
CsPIN4	Csa4G430820	Auxin efflux carrier; contains IPR004776 (Auxin efflux carrier)
CsPIN5	Csa1G427480	Auxin efflux carrier protein; contains IPR004776 (Auxin efflux carrier)
CsPIN6	Csa5G576590	Auxin efflux carrier; contains IPR004776 (Auxin efflux carrier)
CsAUX1	Csa4G308640	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX1	Csa3G731880	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX2	Csa7G010800	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX3	Csa5G374730	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX4	Csa2G264590	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX5	Csa5G201310	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsLAX6	Csa6G011040	Auxin transporter-like protein; contains IPR013057 (Amino acid transporter, transmembrane)
CsTCP2a	Csa6G524000	TCP transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP2b	Csa1G025920	TB1-like TCP family transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP4a	Csa4G088720	Transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP4b	Csa6G156050	Transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP4c	Csa4G628330	Transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP4d	Csa1G077150	Transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP5a	Csa4G132680	TB1-like TCP family transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP5b	Csa1G014310	Transcription factor; contains IPR005333 (Transcription factor, TCP)
CsTCP5c	Csa1G039270	TCP transcription factor; contains IPR005333 (Transcription factor, TCP)

**Supplemental Table S4. The parameters of vein pattern in cucumber leaves of Fig. 5B**

Leaf	$\alpha$ Angle (°)	$\beta$ Angle (°)	Total length of primary vein	primary vein density (cm / cm <sup>2</sup> )	Total length of secondary vein	Number of secondary vein	Average length of secondary vein	Secondary vein density (cm / cm <sup>2</sup> )	Leaf area (cm <sup>2</sup> )
AM218	57.7±1.2	91.8±1.3	40.2±1.8	0.62±0.04	71.4±2.8	26±0	2.75±0.11	1.11±0.05	64.5±3.6
<i>rl</i>	31.8±0.8**	96.7±1.5**	29.2±1.6**	0.44±0.02**	97.5±4.5**	18±0**	5.42±0.25**	1.46±0.10**	66.8±3.7
<i>mf</i>	30.0±0.9**	67.2±1.6**	38.9±1.9	1.14±0.09**	55.2±3.1**	27±1**	2.03±0.12**	1.62±0.10**	34.2±2.5**
<i>CsWOX1</i> -OE	41.2±0.8**	87.9±1.3**	19.6±1.2**	0.76±0.07**	34.8±2.2**	22±0**	1.58±0.10**	0.76±0.07**	25.9±2.5**

Asterisks indicate a significant difference (t test, P < 0.01).

Supplemental Table S5. Primer sequences used in this study

Primers	Gene ID <sup>a</sup>	Forward primer (5' to 3')	Reverse primer (5' to 3')
I305.4-CsWOX1	Csa1G042780	ACGGGGGACTCTAGAGGATCCATGTGGATGATGGGTTACAAT	CTGGTCACCAATTCACACGTGTTAGTGGTGGTGGTGGTGGTATTCTTCAATGGTAGGAATTC
BD-CsWOX1	Csa1G042780	ATGGCCATGGAGGCCGAATTCATGTGGATGATGGGTTACAATGAC	ATGCGGCCCTGCAGGTCGACTCAATCTTCAATGGTAGGAATTC
BD-CsWOX1N	Csa1G042780	ATGGCCATGGAGGCCGAATTCATGTGGATGATGGGTTACAATGAC	ATGCGGCCCTGCAGGTCGACACCACCACGGAGAGCAGCG
NE-CsWOX1	Csa1G042780	CCCAGGCCTACTAGTGGATCCATGTGGATGATGGGTTACAATGAC	CCCAGGAGCGGTACCCCTCGAGTCAATCTTCAATGGTAGGAATTC
NE-CsWOX1N	Csa1G042780	CCCAGGCCTACTAGTGGATCCATGTGGATGATGGGTTACAATGAC	CCCAGGAGCGGTACCCCTCGAGACCACCACGGAGAGCAGCG
AD-CSTCP4a	Csa4G088720	GTGGGCATCGATACGGGATCCATATGGGAGAGAGCCACCGC	ACGATTCTATCGAGCTCGAGTCAATGGCGAGAATCAGAGGA
AD-CsAP2	Csa6G491020	GTGGGCATCGATACGGGATCCATATGGGAGAGAGCCACCGC	ACGATTCTATCGAGCTCGAGTCAAGAGGGTCTCATAAGACAATGA
CRISPR-AiWOX1, 3	At3G18010, AT2G28610	TCGAAGTAGTGATTGGCGCAGATTCCCTCAACGGGTTTATAGAGCTAGAAATAG	TTCTAGCTCTAAAACCGTTGAAGCCACAGGACTCCAATCTTCTAGTCTACTAC
pGREEN-P35-CsWOX1	Csa1G042780	GCCCAAGCTACGCTCTCGAGATGTGGATGATGGGTTACAATGAC	TCCCCCGGGCTCGAGGAATTCATTCTTCAATGGTAGGAATTCAAAAG
Check-HYG517	--	TCGTTATGTTTATCGGCACCTT	GATGTTGGCGACCTCGTATT
Check-eGFP427	--	TCCAGGAGCGCACCATCTT	TCGTCCATGCCGTGAGTGA
qCsActin2	Csa6G484600	ATTCTTGCATCTCTAAGTACCTTCC	CCAACATAAGGGAAATAACTCACC
qCsWOX1	Csa1G042780	GGGGCAACAGATTGCAGGAC	GGGCAATGTTTCATCATTAGTTGG
qCsCLE5	Csa4G627800	ATGGCTAATTGTAGTGTAAAGCTG	GATAAACTTCAACATTTCTTCCG
qCsCLE6	Csa6G518900	CTTAGCTTGTGGGTATGCCTGA	CCCTCGTTGAGGAATGCTTC
qCsPID1	Csa1G537400	TCATCCGTTTTGCTACACT	ACTTCCGCTGCATAAAAACCT
qCsPID2	Csa2G006100	CACGCTCCGACTCCATCTA	GTCACCAATCCACTCCGC
qCsPID2-like	Csa4G064100	GAGATTCTGGCTTCTTTGGACC	GCAACAGAGAAGCGGCTACC
qCsPIN1	Csa1G042820	GCTACAACAGGGGCAATG	TCCTCTGTTTTCCCATTTGGC
qCsPIN2	Csa5G284520	CTTTCAACTTTGCCGAATACG	CAGAATCTTCGCTCCACGAT
qCsPIN3	Csa1G025070	ATCATCGTTCGGTGTGCT	TGAACCTTAAGTGCACAGA
qCsPIN4	Csa4G430820	GAATGTACGGGACTCCACT	ACAATCTCCCTGCAGTATCC
qCsPIN5	Csa1G427480	GAGCTTCGAATCTACCCGGA	CGTCGCTTGAAAACCTATTGG
qCsPIN6	Csa5G576590	TCATTTCAATCCGGTGGCAT	GGCAAAAGTAGCAACAGAGTTCC
qCsAUX1	Csa4G308640	GGAAAGGAGGAAGGGGAAGA	AGGCAGAGTCAAAAACCTG
qCsLAX1	Csa3G731880	TTGTTAAAGGGCTATTGCGAG	CAGCATATGAGCCATAGCAGG
qCsLAX2	Csa7G010800	TTTGGTGTGGTGTGTTGGC	GCCGTAGCATTGAACGATTG
qCsLAX3	Csa5G374730	TTGGACCGATCAACTCGACA	TTCACTGAGTACAGCCCTGCC
qCsLAX4	Csa2G264590	GTCTACATCATCCCGCCC	CACCAAGCCAAACCTACA
qCsLAX5	Csa5G201310	GGGCTTGTGTGCCACTACT	GAATGCTTCAACCCCTCGAC
qCsLAX6	Csa6G011040	TCCCAACTGGGTATGCTCTC	ACCCATCCAGCACTTCAAAC
qCsTCP2a	Csa6G524000	TCCAGAACTCCGAAACAGC	CGCGAAAGAGACAAACCTGA
qCsTCP2b	Csa1G025920	CATCGGTGGAGTGTGGCTA	AGCGACAGAAAGCCGAATC
qCsTCP4a	Csa4G088720	AGGAGGCCACATTGTTCTGTT	CAGCTTTACTGGGTCGGTCA
qCsTCP4b	Csa6G156050	CACCAACTACCAATGGGAA	TGAGCGGATAAACGAACAGC
qCsTCP4c	Csa4G628330	GCTGGAGTGTGGATGGAGA	GCGTGTAACTGGACTGAAGGG
qCsTCP4d	Csa1G077150	CACAGTTCAGCTTACCCTTCC	TCCCACATCGGAAAGAAAGG
qCsTCP5a	Csa4G132680	TTCTCAGCCCTTTGAATAATGT	TGAGATGATTGAAGGATGAAGGT
qCsTCP5b	Csa1G014310	CCCTACCTCCTCCGTTTATGC	TCAATCCACTTCCCTTTCGTC
qCsTCP5c	Csa1G039270	CATTCTGATATTGGAGATGCTGC	GGGGCTGAATTAGTCTGATCG
CsWOX1-sp6	Csa1G042780	GATTTAGGTGACACTATAGaatGCTGTCGACAAATGGAATCTTCAGC	--
CsWOX1-T7	Csa1G042780	TGTAATACGACTACTATAGGGGAAAACAATGCAACAATTGCAAAA	--

<sup>a</sup> The gene ID is based on 9930 V2.0.