

Supplementary materials**Title:**

Cucumber strigolactone receptor CsDAD2 and GA₃ interact to regulate shoot branching in *Arabidopsis thaliana* L.

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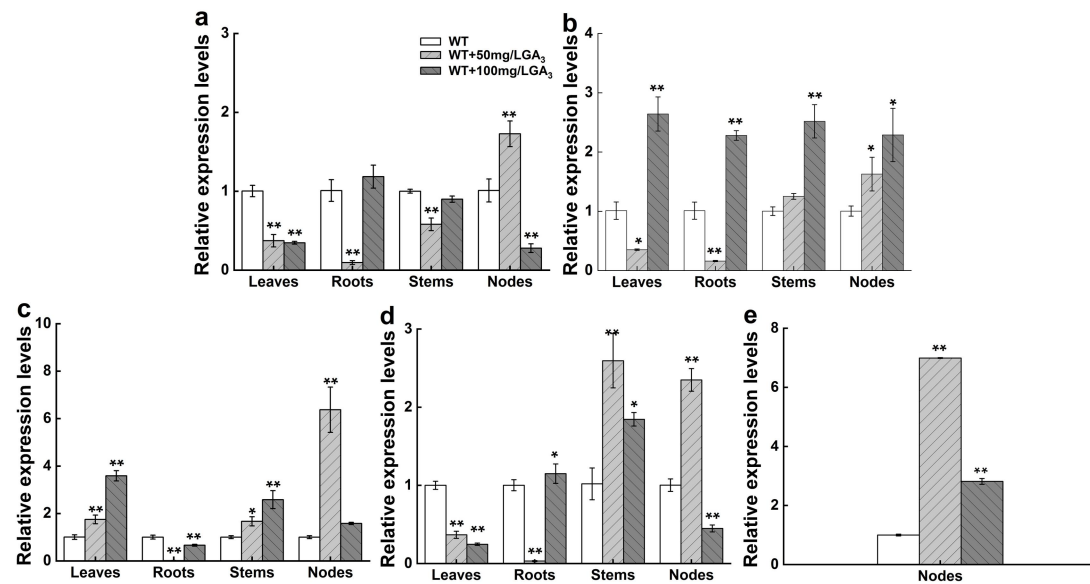


Figure S1. The expression of strigolactone genes and TCP transcription factors in the cucumber plants after GA₃ treatment. Cucumber seedlings at the five-leaf stage were treated with 0, 50 and 100 mg/L of GA₃ solution for 12 hours, before analyzing gene expression levels in the roots, leaves, nodes and stems. (a) SL biosynthesis gene *CsCCD7*, (b) SL receptor gene *CsD14*, (c) SL receptor gene *CsDAD2*, (d) *CsTCP2*, (e) *CsTCP18 (CsBRC1)*. Data represent the mean \pm SD of three biological replicates (Student's t test: * P < 0.05, ** P < 0.01)

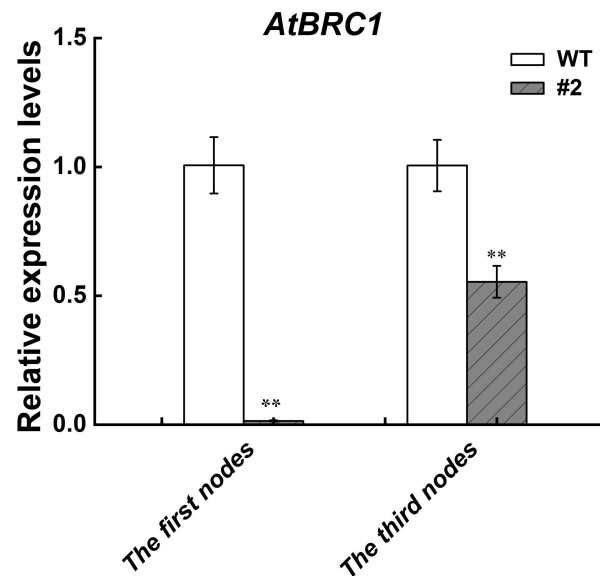


Figure S2. Expression of *CsBRC1* in WT and the overexpression of *CsDAD2* in the first and third nodes of *Arabidopsis*. Analysis of the expression of *CsBRC1* in the first nodes and the third nodes of WT and #2. The data represent the mean \pm SD of three biological replicates (Student's t test: ** P < 0.01)

Table S1 Primer name and sequence

Gene Name	Primer Name	Primer Sequence (5'-3')
<i>CsDAD2</i>	<i>CsDAD2</i> -CQF	CGGGGTACCATCATCAGTAATAAGAAGAAGAAG
	<i>CsDAD2</i> -CQR	AACTGCAGCCTAACCCAAGATTTCCT

Note: The *CsDAD2*-CQF transverse line is an *KpnI* enzyme cut site; the *CsDAD2*-CQR transverse line is an *PstI* enzyme cut site

Table S2 Species and accession numbers of DAD2 and its homologous proteins

Organism	Accession Numbers
<i>Cucumis sativus</i>	XP_004148713.1
<i>Benincasa hispida</i>	XP_038879267.1
<i>Erythranthe guttata</i>	XP_012846483.1
<i>Tarenaya hassleriana</i>	XP_010532830.1
<i>Medicago truncatula</i>	XP_013459502.1
<i>Glycine max</i>	NP_001304372.2
<i>Oryza sativa</i>	XP_015631400.1
<i>Pisum sativum</i>	XP_050892745.1
<i>Petunia hybrida</i>	QSV51912.1
<i>Arabidopsis thaliana</i>	NP_566220

Note: *CsDAD2* and its homologous proteins from other species were selected to generate a phylogenetic tree with the MEGA 6.0 software, based on the Neighbor-Joining (NJ) method with 1000 bootstrap replication. The accession numbers of DAD2 were listed. Multiple sequence alignment was carried out with the DNAMAN software

Table S3 Primer sequences used for real-time quantitative PCR

Gene Name	Description	Primer Name	Primer Sequence (5'-3')
<i>β-Actin</i>	multifunctional proteins that form microfilaments	<i>β-Actin</i> -F	AGAAACGGCTACACATC
		<i>β-Actin</i> -R	CCAAGGTCCAACCTACGAG
<i>CsDAD2</i>	Strigolactones receptor	<i>CsDAD2</i> -F	AGCGATGGTTCTGGGTCA
		<i>CsDAD2</i> -R	GCAAGGCAGCCAATAAGG
<i>CsD14</i>	Strigolactones receptor	<i>CsD14</i> -F	GATTTCTCCCGTTACACCACT
		<i>CsD14</i> -R	GGCAAACCCGTTGACCC
<i>CsCCD7</i>	carotenoid cleavage dioxygenase 7	<i>CsCCD7</i> -F	TTCTGGCACATACTACCT
		<i>CsCCD7</i> -R	TTTCTTCCCTCCCTTC
<i>CsTCP2</i>	TEOSINTE BRANCHED 1, cycloidein and PCF transcription factor 2	<i>CsTCP2</i> -F	TTTCATTGGCGAGGTCTGC
		<i>CsTCP2</i> -R	TCGTCCGATTGGTGGTGTTA
<i>CsTCP18</i>	TCP family transcription factor	<i>CsTCP18</i> -F	CATTCCATCTTCCCATCTC
		<i>CsTCP18</i> -R	CTACCTTTATCAACACCCAAC

Note: *CsDAD2* is an SL receptor gene; *CsCCD7* is an SL synthetic gene; *CsTCP2* and *CsTCP18* are TCP family genes

Table S4 Primer sequences used for real-time quantitative PCR analysis

Gene name	Description	Primer name	Primer sequence (5'-3')
<i>Actin</i>	multifunctional proteins that form microfilaments	<i>Actin</i> -F	GAAGATGGCAGACGCTGAGGAT
		<i>Actin</i> -R	ACGACCTACAATGCTGGGTAACA C
<i>AtGA2ox2</i>	gibberellin 2-oxidase 2	<i>AtGA2ox2</i> -F	CCTCCTCAATGCTAATCCTCAG
		<i>AtGA2ox2</i> -R	TCGGCAACCATCTCCAACA
<i>AtGA2ox6</i>	gibberellin 2-oxidase 6	<i>AtGA2ox6</i> -F	CGGCGACGAATGATTACA
		<i>AtGA2ox6</i> -R	TACGGTGCTGGTGGATAG
<i>AtGA3ox2</i>	gibberellin 3-oxidase 2	<i>AtGA3ox2</i> -F	GTGGTTTCGCATTAGGTTCA
		<i>AtGA3ox2</i> -R	TGGCTCTGTCTGGTTCTG
<i>AtGA20ox1</i>	Fe(II)-dependent oxygenase superfamily protein	<i>AtGA20ox1</i> -F	GGTGAGAGTGTTGGCTAC
		<i>AtGA20ox1</i> -R	ACGCATCGCAGAAGTAAT
<i>AtGA20ox2</i>	Fe(II)-dependent oxygenase superfamily protein	<i>AtGA20ox2</i> -F	TCTTCCTCGTCGTCAATCA
		<i>AtGA20ox2</i> -R	GCATAGCCACAACCTCTCAC
<i>AtGID1a</i>	gibberellin receptor GID1A	<i>AtGID1a</i> -F	AGCATCCAGCGTGTAATCC
		<i>AtGID1a</i> -R	GCCAACTGCCAATCTCTAATC
<i>AtRGA1</i>	VHIID/DELLA regulatory family gene	<i>AtRGA1</i> -F	GATTGGTGGAGTCATAGGAA
		<i>AtRGA1</i> -R	TCTGCTGGATTGCTTCTG
<i>AtRGL1</i>	VHIID/DELLA regulatory family gene	<i>AtRGL1</i> -F	GAGTGATGTCGGAGTTATTC
		<i>AtRGL1</i> -R	ATGCTTGCTTGCTTATACG
<i>AtSLY1</i>	F-box family protein	<i>AtSLY1</i> -F	TCTAGTGTACGAGGTGTTGAA
		<i>AtSLY1</i> -R	GCCGATGTTAGTCCAGTGA
<i>AtBRC1</i>	TCP family transcription factor.	<i>AtBRC1</i> -F	CCGTTGAATGGTTGCTTACA
		<i>AtBRC1</i> -R	GTTAGTATTGCTGCCTCTATCG
<i>AtCCD7</i>	carotenoid cleavage dioxygenase 7	<i>AtCCD7</i> -F	TGGCGACGACAACTACTCC
		<i>AtCCD7</i> -R	TGTTCCACCCGTTTAGAGGC
<i>AtCCD8</i>	carotenoid cleavage dioxygenase 8	<i>AtCCD8</i> -F	TGATGCTGCACATATCCATCG
		<i>AtCCD8</i> -R	GTTTTACCCGATGCTAGGATC
<i>AtD14</i>	Strigolactones receptor	<i>AtD14</i> -F	ACGGCGAAGGATGTTTCTGT
		<i>AtD14</i> -R	CTAAGCTGCGCAAATGTCC

Note: *AtGA2ox2* and *AtGA2ox6* are GA degradation genes; *AtGA20ox1*, *AtGA20ox2* and *AtGA3ox2* are GA synthetic genes; *AtGID1a*, *AtRGA1*, *AtRGL1* and *AtSLY1* are GA signaling genes; *AtBRC1* is a branch inhibitory gene; *AtCCD7* and *AtCCD8* are SL biosynthesis gene; *AtD14* is an SL receptor gene