Avrb6

5'-MDPIRSRTPSPARELLPGPQPDGVQPTADRGVSPPAGGPLDGLPARRTMSRTRLPSPPAPSPAFSAGSFS DLLRQFDPSLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPTMRVAVTAARPPRAKPAPRRR AAQPSDASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKY QDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRN ALTGAPLNLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGKQALETVQRLLPVLC LCQAHGLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGKQALETVQRLLPVLC QAHGLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGKQALETVQRLLPVLCQAHG LTPQQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGKQALETVQRLLPVLCQAHG LTPQQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGKQALETVQRLLPVLCQAHG LTPQQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPA QVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPA QVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPA QVVAIAS<u>HD</u>GGKQALETVQRLLPVLCQAHGLTPEQVVAIAS<u>NI</u>GGRPALESIVAQLSRPDPALAALTNDH LVALACLGGRPALDAVKKGLPHAPALIKRTNRRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMT QFGMSRHGLVQLFRRVGVTELEARSGTLPPASQRWDRILQASGMKRAKPSPTSTQTPDQASLHAFADSLE RDLDAPSPMHEGDQTRASSRKRSRSDRAVTGPSAQQSFEVRVPEQRDALHLPLSWRVKRPRTSIGGGLPD PGTPTAADLAASSTVMREQDEDPFAGAADDFPAFNEEELAWLMELLPQ-3'

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Supplementary Figure 1. Avrb6 amino acid sequence. The first amino acid of each TAL
effector repeat is highlighted in blue. The RVD of each repeat is underlined.





Supplementary Figure 2. Cycloheximide (CHX) suppresses Avrb6 protein synthesis in a cotton transient assay. Cotyledons from two-week-old Ac44E cotton were infiltrated with Agrobacterium carrying 35S::avrb6-HA at $OD_{600} = 0.6$ with or without 50μ M CHX. Tissues were harvested 4 dpi and subjected to immunoblotting with α -HA antibody (top panel). Ponceau S staining (Ponc) for RuBisCo (RBC) served as the protein loading control (bottom panel).

EBE

pGhSWEET10D	TTGTCGTTTCCTCATCCCCAGCCCGTTCTCCTCGGC
pGh067700	TATCTCCTCCCTCCCCCCCCCCCACCCCATAATTTCTTAA
pGhKBS1	GTCATTTTCAATCACCCACCACCATAAATGGAAAA
pGhMDR1	CTCTTTCAGCATCATCCCCATCCCCTACTTTTTATT
pGhHLH1	ATCCATGAAACTCATCCACATCACAT TTCTTTCTCC

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43	Supplementary Figure 3. Avrb6 EBEs of candidate genes. Avrb6 EBE of each candidate gene
44	is underlined. The sequenced EBE of Gh067700 bears a deleted nucleotide (indicated with the
45	"C" highlighted in blue) when compared to the predicted Avrb6 EBE.
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c	C
σ	σ

a		b		
GaSWEET10	MALHLSWVFVFGILGNAVSFMVSLAPLPTFYQIFKKKTSE			-822
GhSWEET10A	MALHLSWVFVFGILGNAVSFMVSLAPLPTFYQIFKKKTSE	G.rai G.arb	mondii	CTTATTT6GAA6TTTAATTACAAAA6CTCTTTTT6CCTATTAACACCTTTT6TATTTCTA CTTATTT6GAA6TTTAATTACAAAA6CTCTTTTTACCTATTGACACCTTTT6TATTTCTA
GrSWEET10	MALHLSWVFVFGILGNAVSFMVSLAPLPTFYQIYKKKTSE	Acb6 Ac44E	66 44E	CTTATITOGAAGTITAATTACAAAAGCTCTTTTTACCTATTGACACCTTTTGATATTCTA CTTATTTGGAAGTTTAATTACAAAAGCTCTTTTTACCTATTGACACCTTTTGTATTTCTA
GhSWEET10D	MALHLSWVFVFGILGNAVSFMVSLAPLPTFYQIYKKKTSE	G.rai	mondii	-762 АЛАССТСАСТОСССАЛБАЛАЛАЛАЛАЛАЛАТТАЛТАСТСТТТТАЛТОСАТОССАСАСАТТСА
	**********	G.arb Acb6	oneum	AAAGCTCACTGCCCAAGAAAAAAACAAATTAATACTCTTTTAATGCATACCACACATTCA AAAGCTCACTGCCCAAGAAAAAAACAAATTAATACTCTTTTTAATGCATACCACACATTCA
GaSWEET10	GFQSIPYVVSLFSAMLWIYYALLKKDAIFLITINTFCVFI	Ac448		-702
GhSWEET10A	GFQSIPYVVSLFSAMLWIYYALLKKDAIFLITINTFCVFI	G.rai G.arb	mondii	ΑΑΑΑΑΤΑΑΤΑΑΤΑΑΤΤΑΑΤΤΑΑGTAGACTGGTTAAATCATGATTTATTTAGAATGACAAAATCA ΑΑΑΑΑΤΑΑΤΤΑΤΤΤΑΑGTAGACTGGTTAAATGATGATTTATTTAGAATGACAAAATCA
GrSWEET10	GFQSIPYVVSLFSAMLWIYYALLKKDAIFLITINTFCVFI	Acb6 Ac44E		AAAAATAATATTAATTAAGTAGACTGGTTAAATGATGATTATTTAGAATGACAAAAT AAAAATAATATTAATTAAGTAGACTGGTTAAATGATGATTATTTAGAATGACAAAAT
GhSWEET10D	GFQSIPYVVSLFSAMLWIYYALLKKDAIFLITINTFCVFI	G.rai	mondii	-642
	*********	G.arb Acb6	oneum	TTTATCAATTGAATGGTTTTATGATTTTTTTTATTTTTTGCTAGAATTGTGATTTTATATA TTTATCAATTGCAATGGTTTTATGATTTTTTTTTT
GaSWEET10	QTFYIVTYFYYGPKKEKIVTVKLMLLFNVFGFGVIFLATY	Ac44E		-582
GhSWEET10A	QTFYIVTYFYYGPKKEKIVTVKLMLLFNVFGFGVIFLATY	G.rai G.arb	mondii	TATTTTTTAATCTTCATTTATAAATTAATGATATGTTATTCTTTAATCATTGAGTTTTAT TTTTTTT-TATTTTTAGCTATAAATTAATGATATGTTATTCTTTAATTATTGAGATTTAT
GrSWEET10	QTFYIVTYFYYGPKKEKIVTVKLMLLFNVFGFGVIFLATY	Acb6 Ac448		TATTITT-TATTITTAGCTATAATTAATGATATGTTATTCTTTAATTATTGAGATTTAT TATTITT-TATTITTAGCTATAATTAATGATATGTTATTCTTTAATTATTGAGATTTAT
GhSWEET10D	QTFYIVTYFYYGPKKEKIVTVKLMLLFNVFGFGVIFLATY	G. rai	mondii	-522 GITABATTITTATACTAGAATTACAGITTITTABATTATGTABATTATTITATTABACAAT
	************	G.arb Acb6	oreum	GTTAAATTTTTATACTAGAATTACAGTTTTTTTAAATATATAT
GaSWEET10	FLKNPSLRLLILGYICMAFALAVFVAPLAIVRKVIKTKSV	Ac448		GTTAAATTTTATACTAGAATTACAGTTTTTTAAATATATAT
GhSWEET10A	FLKNPSLRLLILGYICMAFALAVFVAPLAIVRKVIKTKSV	G.rai G.arb	mondii	AAATTTAGGGTGAATTCAGAATTACAATTTTTTAGGTATATATA
GrSWEET10	FLKNPSLRLLILGYICMAFALAVFVAPLAIVRKVIKTKSV	Acb6 Ac44E		GAATTCAGAATTACAATTTTTAAATATATTGTACTACAG GAATTCAGAATTACAATTTTTTAAATATATTGTACTACAG
GhSWEET10D	FLKNPSLRLLILGYICMAFALAVFVAPLAIVRKVIKTKSV	G.rai	mondii	-402 TATGTAATCTCACCGTCATCATTACTTTTTACACTAATTACAAATAAACTAACCTTTAATA
	***********	G.arb Acb6	oneum	TATTTAATTTTATCGTCATTGTTATTTTTACACTAATTATAAATAA
GaSWEET10	EYMPFTLSVFLTLGAVMWFFYGLCLKDMNVAVPNILGFIF	Ac44E		TATTTAATTTTATCGTCATTGTTATTTTTACACTAATTATAGATAAACCCACCTTTAATA -342
GhSWEET10A	EYMPFTLSVFLTLGAVMWFFYGLCLKDMNVAVPNILGFIF	G.rai G.arb	mondii	TTAAATTATAAAA-AATACAATTAAATTCAACATGAATTAGAGGTGTGATTTOTTAA TTAAATTATAAAAAAATACAATTAAATTGAACATGAATTAGAGGTGTGATTTGTTTTTT
GrSWEET10	EYMPFTLSVFLTLGAVMWFFYGLCLKDMNVAVPNILGFIF	Acb6 Ac448		TTAAATTATAAAAAAATACAATTAAATTGAACATGAATTAGAGGTGTGATTTGTTTTT TTAAATTATAAAAAAATACAATTAAATTGAACATGAATTAGAGGTGTGATTTGTTTTT
GhSWEET10D	EYMPFTLSVFLTLGAVMWFFYGLCLKDMNVAVPNILGFIF	G.rai	imondii	-282
	*******	G.art Acb6 Ac448	l	ΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΤΟΤΤCACAGCAATAATCAGATTTAAAAAGTAAGGAGAATTAAAAATTC TTTTTTTTGTTCACAGCAATAATCAGATTTAAAAAGTAAGGAAGAATTAAAAATTC TTTTTTTTGTTCACAGCAATAATCAGATTTAAAAAGTAAGGAGAATTAAAAATTC
GaSWEET10	GVLQMILYAVYKNHPKKTVEESDPKLQLSDHPVVVVDVAK	0.001	modil	-222
GhSWEET10A	GVLQMILYAVYKNHPKKTVEESDPKLQLSDHPVVVVDVAK	G.art Acb6	oreum	AAATATTGCATATGATAAAAAAAAACTTGACCTTCCTTGTCGTTTCTTCATCCCCA AAATATTGCATATGATAAAAATAAAACTTGACCTTCCTTGTCGTTTCTTCATCCCCA
GrSWEET10	GVLQMILYAVYKNHPKKTVEESDPKLQLSDHPVVVVDVAK			-162
GhSWEET10D	GVLQMILYAVYKNHPKKTVEESDPKLQLSDHPVVVVDVAK	G.arb Acb6	boneum	OCCCOTTCTCCTCOOCTATAAATATAAACCTTOAGAATOCTTCACAGATCOTGGAAGTAA GCCCCTTCTCCTCGGCTATAAATATAAACCTTOCTCACAGATCOTGGAAGTAA GCCCCTTCTCCCCGGCTATAAATATAAACCTTOCACAGATCOTGGAAGTAA
	******	Ac448		-102
GaSWEET10	LGSNVNAIIPNSTNSNNGGNNGGRTEGNAFSKV	G.rai G.art Acb6	lmond11	GAGGTAGAAAGAGCTTCTTCACTTTGACAACAAATACTCACTTTCTCTTACAGAGATTGA GAGATAGAAAGAGCTTCTTCACTTTGACAAC-AATACTCACTTTCTCTTACAGAGATGA AGGATAGAAAGAGCTTCTTCACTTTGACAAC-AATACTCACTTTCTCTTACAGAGATTGA
GhSWEET10A	LGSNVNAI I PNSTNSNNGGNNGGRTEGNAFSKV	Ac448		
GrSWEET10	LGSDVNAVIPNSTKSNNGGRTEGNANSKV	G.rai G.art	G.raimondii G.arboreum Acb6 Ac44E	GAGAAAATCACAAACACCACAATTATATAGCACAGTGATCATGATG GAGAAAATCACAAACACCACTTATATAGCACAGTGATCATCATG GAGAAAATCACAAACACCACTTATATAGCACAGTGATCATCATG
GhSWEET10D	LGSDVNAVIPNSTKSNNGGRTEGNANSKV	Ac44(GAGAAAATCACAAAACACACATTTATATATAGCACAGTGATCATCATG
	*** *** **** ***			

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Supplementary Figure 4. Sequence alignment of SWEET10 coding sequences and promoters from *G. raimondii*, *G. arboreum*, and *G. hirsutum*. Alignment was performed with the protein coding sequences (A) and with the promoters using the Clustal Omega website ((<u>http://www.ebi.ac.uk/Tools/msa/clustalo/</u>) (B) with a hierarchical clustering approach. In (B), Avrb6 EBE is highlighted with a black bracket. ATG is highlighted with a blue box. The promoter sequences of *pGhSWEET10A* from A-subgenome in Ac44E and Acb6 are shown here.



79	Supplementary Figure 5. VIGS-GhSWEET10 did not affect cotton seedling growth. Pictures	
80	were taken at three weeks after inoculation. VIGS-GhCLA1 is a visual marker for VIGS	
81	efficiency.	
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Supplementary Figure 6. GhSWEET10D sugar transport activity in N. benthamiana and **yeast.** (A) Expression of *GhSWEET10D* resulted in higher sucrose concentration in apoplasts of N. benthamiana leaves. Agrobacterium strain carrying 35S::GhSWEET10D or an empty vector control (EV) was inoculated into N. benthamiana leaves. The sucrose content was normalized to a ratio relative to the EV. Error bar is SD and asterisk indicates significant difference using twotailed t-test (p<0.05). The experiment was repeated twice. (B) GhSWEET10D does not complement yeast EBY4000 mutant, a hexose transport-deficient strain. The yeast was grown on the medium supplemented with 2% glucose or 2% fructose as the sole carbon source or 2% maltose as control. HXT5 from yeast and AtSWEET1 from Arabidopsis served as positive controls and empty vector served as a negative control.

Clade I		Clad	le II	Clade III		Clade IV	
Gene ID	Gene Name	Gene ID	Gene Name	Gene ID	Gene Name	Gene ID	Gene Name
Gh_A02G0694	GhSWEET1aA	Gh_A05G3128	GhSWEET4A	Gh_A08G0663	GhSWEET9aA	Gh_A11G2442	GhSWEET16aA
Gh_D02G0740	GhSWEET1aD	Gh_D04G0509	GhSWEET4D	Gh_D08G2730	GhSWEET9aD	Gh_D11G2760	GhSWEET16aD
Gh_A02G1806	GhSWEET1bA	Gh_A05G3127	GhSWEET5aA	Gh_A07G0421	GhSWEET9bA	Gh_A13G1540	GhSWEET16bA
Gh_D03G1717	GhSWEET1bD	Gh_D04G0510	GhSWEET5aD	Gh_D07G0486	GhSWEET9bD	Gh_D13G1875	GhSWEET16bD
Gh_A11G3285	GhSWEET2aA	Gh_A07G0535	GhSWEET5bA	Gh_A12G1747	GhSWEET10A	Gh_A10G1468	GhSWEET17aA
Gh_D11G2975	GhSWEET2aD	Gh_D07G0604	GhSWEET5bD	Gh_D12G1898	GhSWEET10D	Gh_D10G1709	GhSWEET17aD
Gh_D10G0303	GhSWEET2bD	Gh_A12G2152	GhSWEET6A	Gh_A03G0461	GhSWEET11A	Gh_D02G0542	GhSWEET17bD
Gh_A11G2655	GhSWEET3A	Gh_D12G2328	GhSWEET6D	Gh_D03G1078	GhSWEET11D	Gh_D13G1146	GhSWEET17cD
Gh_D12G2692	GhSWEET3D	Gh_A02G0950	GhSWEET7A	Gh_A07G0423	GhSWEET12aA	Gh_A13G1434	GhSWEET18A
		Gh_D03G0812	GhSWEET7D	Gh_D07G0487	GhSWEET12aD	Gh_D13G1763	GhSWEET18D
		Gh_A13G0907	GhSWEET8aA	Gh_A07G0422	GhSWEET12bA		
		Gh_D13G1148	GhSWEET8aD	Gh_A11G0347	GhSWEET13A		
		Gh_A11G2446	GhSWEET8bA	Gh_D11G0404	GhSWEET13D		
		Gh_D11G2763	GhSWEET8bD	Gh_A04G0861	GhSWEET14aA		
				Gh_D04G1360	GhSWEET14aD		
				Gh_D02G1767	GhSWEET14bD		
				Gh_A01G0160	GhSWEET15A		
				Gh_D01G0202	GhSWEET15D		

120 Supplementary Figure 7. Gene IDs and corresponding names of the cotton GhSWEET

- **family.** Tables are separated by different clades of GhSWEET family.







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Supplementary Figure 9. Differential responses of Avrb6 in Ac44E and Acb6. (A) Avrb6 150 causes water-soaking on Ac44E, but HR on Acb6. Cotyledons of two-week-old plants were 151 syringe-inoculated with XcmHM2.2S (placZ:avrb6) at OD₆₀₀ = 0.1. Pictures were taken at 4 dpi. 152 (B) Strains carrying avrb6, XcmH1005 and HM2.2S+avrb6 cause HR in Acb6. (C) Sequence 153 alignment of the GhSWEET10D promoter in Ac44E and Acb6. Alignment was performed using 154 the Clustal Omega website (http://www.ebi.ac.uk/Tools/msa/clustalo/) with a hierarchical 155 clustering approach. Avrb6 EBE is highlighted with a black box. ATG is highlighted with a blue 156 box. (D) dTALE2 causes water-soaking on Acb6. Cotyledons of two-week-old plants were 157 syringe-inoculated with XcmH1005 Aavrb6 carrying dTALE2 or pKEB1 (empty vector) at OD₆₀₀ 158 = 0.1. Pictures were taken at 4 dpi. 159

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pXcmH_left end	pXcmH_right end	pXcmN_left end	pXcmN_right end
79681	79764	9909	9992
-3939	-7800	10470	14331
-3463	-3935	14391	14877
16064	25400	16064	25399
25467	25611	25473	25616
59530	63360	35092	38921
7801	16063	0	0
25401	25466	0	0
25612	59529	0	0
63361	79680	0	0
0	0	9993	10469
0	0	14332	14390
0	0	14878	16063
0	0	25400	25472
0	0	25617	35091

175 Supplementary Table 1. Progressive MAUVE on pXcmH and pXcmN

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177 Supplementary Table 2. RVD sequences and AnnoTALE names of XcmH1005 and 178 NamN1003 TAL affectors

178 XcmN1003 TAL effectors.

Annotated	Gene coordinates	RVD Sequence	AnnoTALE Name	Comments on
Name		1 2 3 4 5 6 7 8 9 10		coding
		11 12 13 14 15 16 17 18 19		sequence
		20 21 22 23		_
XcmH1005 ch	romosome			
AvrB5	193705196791	NI NS HD NI NS NS NS NS HD	TalDZ1	
		NI NS HD HD HD	XcmH1005	
AvrB104	197283200771	NI HD HD NS HD NG HD HD HD	TalDX1	
		NI NI NI NN NI NG NG N* NG	XcmH1005	
PthN2	228643231927	NI NG NI NI NS NI NN NI N* NN	TalEG1	
		HD NN NS NG N* NN	XcmH1005	
AvrBn	27208142723696	NI NG NI HD HD HD HD NG HD	TalEE1	
		HD NG NG	XcmH1005	
AvrB103	27482152751499	HD NI NG NI NI NI NG NG NS	TalEB2	
		NG HD HD NI HD N* NN	XcmH1005	
Tal6 _{XcmH1005}	49796484982734	NI NG NI NI NI NG HD HD NG	TalED1	
		NI HD NI NG NG	XcmH1005	
XcmH1005 pl	asmid (pXcmH)			
AvrB4	805611649	NI NG NI NI NS NG NI HD NI NS	TalDY1	
		NS HD HD HD NI NI HD HD NG	XcmH1005	

Annotated	Gene coordinates	RVD Sequence	AnnoTALE Name	Comments on
Name		1 2 3 4 5 6 7 8 9 10		coding
		11 12 13 14 15 16 17 18 19		sequence
		20 21 22 23		
Avrb6	1243015516	HD NI NG HD HD NI HD NI NS	TalEC1	
		HD HD HD NN NG	XcmH1005	
AvrB101	3263336637	HD NG NS NG NI NI NS NG HD	TalEA1	
		NS HD HD NS HD NG NI HD HD	XcmH1005	
		NG NS NG HD NG		
AvrBIn	3981743617	HD NI NG NI NI NI NG NG NS	TalEB1	
		NG HD HD NI HD NS NG NS NG	XcmH1005	
A 5100	50050 540 (5	NG NG NG	T IDIUI	
AvrB102	508/354367	NI NI NI NG HD NG NI HD NI	TalDWI	
. 17	((22) (0022	HD NG NS NG HD NG HD NS NG	XcmH1005	
Avrb/	6622669822	HD NI NG NI NI NI NS HD HD	I alEF I	
		HD N5 HD HD N5 N5 NG N5 NG	ACMH1005	
VomN1002 ol	romosomo	NO		
Tall?	10/000 106/50	НД	TolCD4	Only a last 57
1 all XcmN1003	194999190430	IID	YcmN1003	bn (19.22)
			Achiny1005	repeat: IS
				element in 3'
				end
Tal2' _{XcmN1003}	23544702355501	HD	TalCP5	Integrase
Xemitroos			XcmN1003	insertion in 2 nd
				repeat
AvrBn	23799392382821	NI NG NI HD HD HD HD NG HD	TalEE2	
		HD NG NG	XcmN1003	
Tal4' _{XcmN1003}	28307322832598	NI HD HD NG HD NG NI NS NS	TalCC4	Frameshift
		HD	XcmN1003	deletion at 11 th
				and 12 th repeats
Tal5' _{XcmN1003}	49883664990750	HD NG NI NI NG HD HD NG NI	TalEI1 XcmN1003	4 bp insertion in
		HD NI NG NG HD NI		last repeat
XcmN1003 pl	asmid (pXcmN)			
PthN'	2643629081	NI HD HD NI HD NI NG NI NN	TalEJ2	Frameshift in 3'
	10050 15105	HD NI NG N* NN	XcmN1003	end
Tal/ _{XcmN1003}	4225845437	NI HD HD NS NG HD HD N* NN	TalEHI	
DIN	51000 540(0	HD NN NS NG N* NN	XcmN1003	
PthN	5188954969	NI HD HD NI HD NI NG NI NN	TalEJI NamN1002	
D4hNIO	55205 59444	HD NI NG NI NI NG NI NINI NI NI NI NI	ACMIN1003	Dan atitizza
PthN2	5529558444	NI NG NI NI NS NI NN NI N* NN	TalEG2 NomN1002	Repetitive
			ACIMINIOUS	insertion in 2'
				end
				Cilu

181 Supplementary Table 3. *Xcm* strains and plasmids used in this study.

Xcm strains

Strains	Relevant characteristics	Reference/Source
VamU1005	Spontaneous Dif ^r derivative of	Vong et al. 1004
Астп1005	<i>Xcm</i> H	1 ang <i>et ut</i> . 1994
<i>Xcm</i> N1003	Spc ^r , Rif ^r derivative of <i>Xcm</i> N	DeFeyter and Gabriel,
		1991
<i>Xcm</i> H1407 (H1005∆ <i>avrb6</i>)	<i>avrb6</i> ::Tn5- <i>gusA</i> , marker exchange	Yang <i>et al.</i> 1994
, , ,	mutant of <i>Xcm</i> H1005	
	(H1005 $\Delta avrb6$)	
H1005 (placZ::avrb6)	XcmH1005 with pUFR135	This study
HM2.2S	Mutant strain of H1005 lacking at	Chakrabarty et al. 1997
	least six <i>avr</i> genes	
HM2.2S (vector)	HM2.2S with pUFR042	This study
HM2.2S (avrb6)	HM2.2S with pUFR127	Yang et al. 1996
HM2.2S (placZ::avrb6)	HM2.2S with pUFR135	This study
HM2.2S+pKEB1	HM2.2S with pKEB1	This study
HM2.2S+dTALE1	HM2.2S with dTALE targeting	This study
	GhSWEET10D in pKEB1	
HM2.2S+dTALE2	HM2.2S with dTALE targeting	This study
	GhSWEET10 (A&D) in pKEB1	
HM2.2S+dTALE3	HM2.2S with dTALE targeting	This study
	<i>GhMDR1</i> in pKEB1	
HM2.2S+dTALE4	HM2.2S with dTALE targeting	This study
	<i>GhKBS1</i> in pKEB1	
<i>Xcm</i> H1005∆ <i>avrb6</i> +pKEB1	<i>Xcm</i> H1005∆ <i>avrb6</i> with pKEB1	This study
<i>Xcm</i> H1005∆ <i>avrb6</i> +dTALE1	<i>Xcm</i> H1005∆ <i>avrb6</i> with dTALE	This study
	targeting <i>GhSWEET10D</i> in pKEB1	
<i>Xcm</i> H1005∆ <i>avrb6</i> +dTALE2	<i>Xcm</i> H1005∆ <i>avrb6</i> with dTALE	This study
	targeting GhSWEET10 (A&D) in	
	pKEB1	
Xcm1	Field isolate from Plains, TX	This study
Xcm2	Field isolate from Plains, TX	This study
Xcm3	Field isolate from Plains, TX	This study
Xcm4	Field isolate from Plains, TX	This study
Xcm5	Field isolate from Plains, TX	This study
Хстб	Field isolate from Plains, TX	This study
Xcm7	Field isolate from Matagorda, TX	This study
Xcm8	Field isolate from Lubbock, TX	This study
Xcm9	Field isolate from Seminole, TX	This study

185 Plasmids

Plasmid	Relevant characteristics	Reference/Source
pKEB1	Low copy, gateway- compatible pUFR047	This study
pRK2073	pRK2013 derivative, npt::Tn7,Kms, Sp ^r , Tra ⁺ , helper plasmid	Leong <i>et al.</i> 1982
pUFR042	IncW, Km ^r , Gm ^r , Mob ⁺ , $lacZ\alpha^{+}$, Par ⁺	DeFeyter and Gabriel, 1991a
pUFR054	IncP, Tc ^r , Mob ⁺ , containing methylases <i>Xma</i> I and <i>Xma</i> II	DeFeyter and Gabriel, 1991b
pUFR127	5-kb fragment containing <i>avrb6</i> in pUFR042	DeFeyter and Gabriel, 1991a
pUFR135	2.9- + -0.5-kb <i>Bam</i> HI fragments from <i>Xcm</i> H containing intact <i>avrb6</i> in pUFR042; <i>lacZ</i> :: <i>avrb6</i>	DeFeyter et al. 1993
pTRV-RNA1	pTRV encoding replicase, movement and cysteine-rich protein	Gao <i>et al.</i> 2011
pYL156-RNA2	TRV-based VIGS vector, Km ^r	Gao <i>et al.</i> 2011

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187 Supplementary Table 4. Primers used in this study.

188 **Cloning and mutation primers**

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Gene	Forward Primer	Reverse Primer
Avrb6	GG <u>ACTAGT</u> ATGGATCCCAT	GTCC <u>CCCGGG</u> CTGAGGCAATAGCT
	TCGTTCGCG	CCATC
PthN	GG <u>ACTAGT</u> ATGGATCCCAT	GTCC <u>CCCGGG</u> CTGAGGCAATAGCT
	TCGTTCGCG	CCCTC
GhSWEET10D	CG <u>GGATCC</u> ATGGCTCTTCA	GA <u>AGGCCT</u> AACTTTGTTGAAAGCA
	CTTGTCTTGGG	TTCCCTTC
pGhSWEET10D	CG <u>GGATCC</u> AAACCACATG	CATG <u>CCATGG</u> CTTCCACGATCTGT
	GTGGGTGACA	GAAGCA
pGh067700	CG <u>GGATCC</u> AGAGGGGCTG	CATG <u>CCATGG</u> TACGATCCGATCCC
	ACAGAGGCCCTA	CAGTAAAAACAAG
pGhKBS1	CG <u>GGATCC</u> TTCCTTCCAAG	CATG <u>CCATGG</u> AGAGATGTGAGCAG
	AGATGACAAGAGC	AGAGGGA
pGhMDR1	CG <u>GGATCC</u> TCGCTCCCAA	CATG <u>CCATGG</u> GGACAGGACAGTGT
	AAACAATATAAATCA	TGTGGT
pGhHLH1	CG <u>GGATCC</u> GTCATTCCAC	CATG <u>CCATGG</u> AAGGATGATTGGAT
	ATATCTCATCCCCA	GGTTTGATAGA
pGhSWEET10D	CGTTTCCTCATCCCGGGCC	GAGGAGAACGGGCCCGGGATGAG

-mEBE	CGTTCTCCTC	GAAACG
VIGS-	G <u>GAATTC</u> ACGGCCCAAAG	GG <u>GGTACC</u> AGGATGTTTGGAACGG
GhSWEET10	AAAGAAAAGAT	CGAC
pGaSWEET10	CG <u>GGATCC</u> AAACCACATG	CATG <u>CCATGG</u> CTTCCACGATCTGT
	GTGGGTGACA	GAAGCA

189 Note: The restriction enzyme sites are underlined and start codon is italicized. For point mutation

190 primers, the mutation sites are underlined.

RT-PCR Primers

Gene	Forward Primer	Reverse Primer
GhSWEET10	ACGGCCCAAAGAAAGAAAAGAT	AGGATGTTTGGAACGGCGAC
Gh067700	TCACCAACCCTTTGCCTCAAT	AAGGTCTTCATCACCGCCAA
GhKBS1	TCCAGCGAAGATCCCCAGTA	GAACCCTTGACGTTTCGTGC
GhMDR1	CACCCTGGGTACTACATTGTCA	AGTGGCATTATCGCCCACAA
GhHLH1	ACCAACCAACCAAGAAACACC	CCCACCTGCTTTGTTGGAGT
GhACTIN	CCTCCGTCTAGACCTTGCTG	TCATTCGGTCAGCAATACCA
GaACTIN	CCTCCGTCTAGACCTTGCTG	TCATTCGGTCAGCAATACCA

qRT-PCR Primers

Gene	Forward Primer	Reverse Primer
GhSWEET9a	CAGCCAGGATATACACGAC	AAACTGAGAAGATGGCAC
GhSWEET10	GCCATTGTGAGAAAAGTC	TGAAGTACTCCAAAGATG
GhSWEET11	GCATTCTGGGAAACGTTG	ATCCAAAGCATCGCACTG
GhSWEET12a	GCTATCGTGAGAAAGGTC	ACCCTAGTATGTTTGGTC
GhSWEET12b	CCTTGCCAACATTTTATC	AGTAGCATAGCATCCTTC
GhSWEET14a	ACCAGTGCCAACATTCTG	ATCAACGCGTAATACAGC
GhSWEET14b	GGTGTCTTAGGTAACATC	AGCTGAACAATGCCACCTG
GhUBQ1	CTGAATCTTCGCTTTCACGTTA	GGGATGCAAATCTTCGTGAAAA
	TC	C