Title: Transcriptome and metabolome reveal distinct carbon allocation patterns during internode sugar accumulation in different sorghum genotypes.

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Running head: transcriptome and metabolome in sorghum internode

TableS9. Analysis of the TPS and Haloacid Dehalogenase (HAD) domains and conserved amino acids required for TPS activities in the deduced TPS proteins from E.coli, yeast, Arabidopsis, rice, maize and sorghum.																								
Domain	TPS domain																					HAD domai n		
substrate/motif	UDPG													G6P								T6P		
substrate/motif	Uracil	Ribose	Ribose	Phosphate	Phosphate	Phosphate	Phosphate	Phosphate	Glucose	Glucose	Glucose	Glucose	Glucose	Glucose	Glucose	Glucose	Glucose	Phosphate	Phosphate	Phosphate	Phosphate	Motif I	Motif M II II	otif I
otsA	F340	G22	E370	R263	K268	N365	L366	V367	H155	Q186	D362	M364	N365	R10	W86	D131	1156	R10	¥77	H133	R301	n	n	n
ScTPS1	I	G	Е	R	K	N	L	V	Н	Н	D	М	N	R	W	D	T262	R	Y	Н	R	n	n	n
ScTPS2	I	A	E	R	R	N	T	T	H	Q	D	M	N	Q	W	D	A	Q	W	Y	A	у	y	y
AtTPS2	V	G120	E470	R	K3/4	N	L4/2	V4/3	H	H292	D408	M	N N	R	W	D237	S	R	Y	H259	R	n	n	n
AtTPS3	I	G	E	R	K	N	L	V	Н	Н	D	М	N	S	W	D	T	S	Y	Н	R	n	n	n
AtTPS4	V	G	E	R	K	N	L	V	H	H	D	L	N	R	W	D	S	R	Y	H	R	n	n	n
AtTPS5 AtTPS6	L	S	E	D	K	N	L	I	Н	н	D	M	N	E	W	D	S	E	Y	Н	R	n v	y n	y v
AtTPS7	V	S	E	D	K	N	L	T	Н	Н	D	M	N	R	W	D	S	R	Y	Н	R	y	y I	y
AtTPS8	v	S	K	D	K	N	L	V	Н	Н	D	М	N	М	W	D	S	М	Y	Н	R	У	у	у
AtTPS9	V	S	K	D	K	N	L	V	Н	Н	D	M	N	M F	W	D	S	M F	Y	Н	R	y	У	<u>у</u>
AtTPS11	v	S	K	D	K	N	L	v	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	n	y y	y y
OsTPS1	L	G	E	R	K	N	L	V	Н	Н	D	М	N	R	W	D	Т	R	Y	Н	R	n	у	n
OsTPS5	V	A	I	D	K	N	R	I	H	Н	D	L	N	R	W	D	S	R	Y	H	R	У	у	y
OsTPS8	M	A	F	D	K	N	R	I	Н	Н	D	L	N	R	W	D	S	R	Y	Н	R	y v	v	v
OsTPS2	v	S	Е	D	K	N	L	Т	Н	Н	D	М	N	Q	W	D	S	Q	Y	Н	R	у	y	y
OsTPS6	v	S	E	D	K	N	L	Т	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	у	у	у
OsTPS11 OsTPS3	L	Q	E	D	K	N	L	T	Н	Q H	D	M	N	F	W	D	S	F	Y	Н	G	y v	y v	n V
OsTPS4	L	S	E	D	K	N	L	I	Н	Н	D	M	N	H	W	D	S	Н	Y	Н	R	y	y	y
OsTPS9	v	Α	F	D	K	N	R	I	Н	Н	D	L	N	R	W	D	S	R	Y	Н	R	у	у	у
OsTPS10	L	S	E	D	K	N	L	I	H	H	D	M	N	Q	W	D	S	Q	Y	H	R	У	n	y
ZmTPS I 1.1 ZmTPS I 1.2	L	U	E	R	K	N	L	V	п	п	D	M	N	K	w		1	K	I	n	R	n	y v	n
ZmTPS II 2.1	L	S	Е	D	К	N	L	I	Н	Н	D	М	N	Q	W	D	S	Q	Y	Н	R	у	n	
ZmTPS II 2.2	L	S	E	D	K	N	L	I	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	у	у	у
ZmTPS II 3.1 ZmTPS II 3.2	v	S	F	D	K	N	L	T	Н	н	D	M	N	Q	W	D	8	0	Y V	н	R	y	y v	y
ZmTPS II 3.3	v	S	E	D	K	N	L	T	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	y	y	y
ZmTPS II 4.1	I	Q	E	D	K	N	L	I	Н	Q	D	М	N	F	W	D	S	F	Y	Н	R	у	у	n
ZmTPS II 4.2	I	A	E	D	K	N	L	V	Н	Q	D	M	N	F	W	D	S	F	Y	Н	R	y	y	n
ZmTPS II 5.1		5	L	D	ĸ		L			V V	D	141				D	5	1			K	n	n	y
ZmTPS II 5.2	L	Α	I	D	N	N	R	Т	Н	Q	D	L	N	R	W	D	S	R	Y	Н	R	у	у	у
ZmTPS II 5.3	V	T	I	D	K	N	R	I	Н	H	D	L	N	R	W	D	S	R	Y	H	R	У	у	у
SbTPS I	L	G	E	R	K	N	L	V	H	H	D	M	N	R	W	D	T	R	Y	H	R	n	v	n
SbTPS II 2.1	L	S	E	D	К	N	L	I	Н	Н	D	М	N	Q	W	D	S	Q	Y	Н	R	у	n	у
SbTPS II 2.2	L	S	E	D	K	N	L	I	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	у	у	у
S01PS II 3.1 SbTPS II 3.2	v	5	E	D	K	N	L	T	Н	Н	D	M	N	Q	W	D	S	Q	Y	Н	R	y v	y v	y v
SbTPS II 3.3	L	S	E	D	K	N	L	T	Н	Н	D	M	N	Т	W	D	S	Т	Y	Н	G	y	y	y
SbTPS II 4.1	Ι	Q	Е	D	K	N	L	I	Н	Q	D	М	N	F	W	D	S	F	Y	Н	R	у	у	n
SbTPS II 4.2	I	A	E	D	K	N	L P	V	Н	Q H	D	M	N	F	W	D	S	F	Y	Н	R	У	y y	n
SbTPS II 5.3	V	T	I	D	K	N	R	I	Н	Н	D	L	N	R	W	D	S	R	Y	Н	R	y v	y y	y
SbTPS II 5.4	V	А	F	D	K	N	R	V			D	L	N	R	W	D		R	Y	Н	R	n	n	n
SbTPS II 5.5	D		K						F					R			S	R		Н	R	n	n	n
runctional AA Summary	F /I /V /L	G	Е	R	К	Ν	L	v	н	Q/H	D	M/L	N	R	w	D	I /S /T	R	Y	н	R			
Explanation:	1 11	1 1 1 7 7	EDG : A 111						12.1.1														+	
The domain ana	uysis table is c	otor-coded:	irs in Arabid	opsis, rice, m	are and sorghu	um are shown	i in green, blue	e, yellow and	white backgro	d probables e	on function-1		-	-	-					-			+-+	-+
For the TPS dor	nain function	amino acids	le is shown in	red otherwise	in black: An	v grev gride	uithout a amin	mani) are not	to lacking of t	he conserve	d motif		-											
For the HAD do	main whether	the motif is	conserved is i	indicated by h	etter (" y " = co	onserved: "n"	= not conserv	ed)															+	

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	Exnre										Corre	:1		Annotation of homologs in				50 170					located	
	ssion										with			Arabidopsis				hu					reported	
	levels										T6P		-	and rice				m			Su		QTLs	
geneID	RPK 1 M_RI 1 O_T1 0	RPK RI M_RI M D_T2 O	PK RPK _RI M_R _T3 O_T	RPK M_B 4 4 11 4 11	RPK T M_BT _ x406_ T2	RPK RP M_BT M_ x406_ x40 T3 T4	K RI BT M 6_ 18 1	PK RI I_R9 M 88_T 18 2	PK RP _R9 M_ 18_T 188 3	K RPK R9 M_R 8_T 188_ 4	9 Т6Р_ Г r_RI	T6P_0 r_BTx 06	0 T6P_0 4 r_R91 8	CO Arabidopsis_I LAST hits	Arabidopsis_BLAST hits_Annotation	Rice_BLAST hits	Rice_BLAST hits_Annotation	CV TF _ ^{su} bty pe	V CW 1 _tyj e	Ho Ho or rm or p on m e1 e2	ga r Te G P en	5 Transport	QTL_cho ck	^e Categories
																		Or			e			
																		ph an						
Sobic.001G225800	5	2	2	3	2 2	6	43	4	2	8	9 0.0	02 -0.79	2 -0.94	47 AT1G04500	CCT motif family protein	LOC_Os10g32900.1	CCT motif family protein, expressed	s na	na	na na	na na	na	1	Transcriptional/Post-transcriptional regulati
Sobic.004G186500	6	5	4	6	4 3	4	9	3	0	1	2 0.1	90 -0.80	2 -0.6	13 AT1G47480	protein	LOC_Os02g35940.1	expressed	na na	na	na na	na na	na	1	metabolism
															NAC domain containing protein		No anical meristem protein nutative	N A						
Sobic.004G191700	9	19	4 1	0	2 5	6	26	5	5	5 1	3 -0.6	83 -0.77	6 -0.72	27 AT5G61430	100	LOC_Os02g36880.3	expressed	C na	na	na na	na na	na	1	Transcriptional/Post-transcriptional regulati
Sobic.004G230900	3	2	2	3	4 3	5	12	3	2	4	6 -0.0	48 -0.86	9 -0.9	66 AT1G22330	RNA-binding (RRM/RBD/RNP motifs) family protein	LOC Os02g51890.1	RNA recognition motif containing protein, putative, expressed	na na	na	na na	na na	na	1	Transcriptional/Post-transcriptional regulati
G. 1.1. 00.4/30/5000	15	10				10		17	10		0.1				Phosphoribulokinase / Uridine	100.000 00000								
Sobic.004G265800	17	10	9 1	3	/ 16	18	23	17	12	33 3	9 0.1	45 -0.72	5 -0.89	97 ATIG26190	kinase family Plant VAMP (vesicle-associated	LOC_Os02g47860.2	uridine kinase, putative, expressed	na na	na	na na	na na	na	1	metabolism
Sobic.004G293000	7	5	3	3	5 2	4	7	5	4	5	8 -0.6	54 -0.76	2 -0.84	40 AT4G00170	membrane protein) family protein	LOC_Os02g44300.1	MSP domain containing protein, expressed	na na	na	na na	na na	na	1	signaling transduction
																		D-						
Sobic 004G300300	51	19	17 4		6 11	10	16	2	0	1	5 02	72 -0.65	0 -0.8	39 AT2G46680	homeobox 7	LOC Os02#43330.1	homeobox associated leucine zipper, putative, expressed	ZI P na	na	na na	na na	na		Transcriptional/Post-transcriptional regulati
Sobic.002G271600	8	10	3	5	5 19	56	123	4	10	33 3	0 -0.8	24 -0.90	2 -0.7	18 AT1G01200	RAB GTPase homolog A3	LOC_Os09g35860.1	ras-related protein, putative, expressed	na na	na	na na	na na	na	1	signaling transduction
																		R W						
															DI A LA DIVID DIVIC 1			P-						
Sobic.002G287400	7	7	6	7	3 5	6	7	3	4	6	8 -0.1	51 -0.68	1 -0.83	21 AT1G76350	Plant regulator RWP-RK family protein	LOC_Os09g37710.1	NIN, putative, expressed	R K na	na	na na	na na	na	1	Transcriptional/Post-transcriptional regulati
															Haloacid dehalogenase-like		CBuOPE?? concerned pentide uOPE				т	,		
Sobic.002G303900	0	0	0	0	0 1	2	9	0	1	2	4	0 -0.82	3 -0.6	61 AT5G51460	protein	LOC_Os02g44230	containing transcript, expressed	na na	na	na na	na P	na	1	metabolism
Sobic.002G304000	55	84	73 8	32 4	1 153	257	408	92	114 2	243 31	2 0.1	28 -0.85	8 -0.83	34 AT5G64370	beta-ureidopropionase	LOC_Os07g30170.1	nitrilase, putative, expressed	na na	na	na na	na na	na	1	metabolism
Sobic.002G322000	570	1225	1653 99	4 7	3 225	85	43	89 1	1209 6	688 22	7 0.0	96 0.77	9 0.70	07 AT1G61800	glucose-6-phosphate/phosphate translocator 2	LOC Os07g34006.1	transporter family protein, putative, expressed	na na	na	na na	na na	glucose-6-phosphate/phosphate translocator 2	1	transport
S-hi- 002(220(00	224	220	141 4	2 10	7 60		80	122	14	40	6 07	0 0.20		22 AT4C05180	abatamatan II sebuait O 2	100.0-07-26080.1	oxygen evolving enhancer protein 3							an at the lines
S00ic.002G329000	324	230	141 0	55 19	/ 00	0.5	80	132	14	40 2	5 -0.7	80 0.28	5 -0.0.	55 A14005180	photosystem it subunit Q-2	LOC_050/g56080.1	TKL_IRAK_CR4L.3 - The CR4L	па па	па	па па	па па	112		metabolism
Sobic 006G087900	13	8	10	7	7 8	3	4	7	6	1	2 -0.2	18 0.93	2 0.76	65 AT5G47850	CRINKLY4 related 4	LOC Os04#35890.1	subfamily has homology with Crinkly4, expressed	na na	na	na na	na na	na	0	signaling transduction
Sobic.006G144600	20	6	7	7 2	1 12	3	1	15	10	3	2 -0.1	93 0.81	7 0.64	41 AT2G33385	actin-related protein C2B	LOC_Os04g43290.1	ARPC2B, putative, expressed	na na	na	na na	na na	na	0	others: cytoskeleton
																		1.2	I.Pe I. lysa	D 1				
																		1. CS	cch:	a				
																		_G	T_sy	n				
Sobic 007G050600	163	215	307 18	7 6	1 37	8	5	58	63	22 2	0 01	180 081	5 0.85	88 AT3G03050	cellulose synthase-like D3	LOC Ox08x06380 1	CSLF6 - cellulose synthase-like family F; betal 3:14 alucan synthase expressed	2	thes	si na na	na na	na	0	metabolism
500000000000000000000000000000000000000	100														centrose syntalse nice by	1000_0300800300.1	OsAPx4 - Peroxisomal Ascorbate							
Sobic.007G177000	64	89	77 7	78 4	6 98	148	158	69	100 1	132 15	0 -0.2	53 -0.79	9 -0.6:	55 AT4G35000	ascorbate peroxidase 3	LOC_Os08g43560.1	Peroxidase encoding gene 5,8,9, expressed	na na M	na	na na	na na	na	0	metabolism
S-hi- 007(1178200	20	10		0 1		10	e	12	10	0	7 0.2	77 0.01		RR AT4C12250	muh damain mutain 42	100 0-00-26260 1	MYB family transcription factor, putative,	Y D						Terreristica - 1/Dent terreristica - 1 errelati
Sobie:00/G1/8500	28	10	11	9 1.	5 24	10	5	15	18	0	/ -0.2	75 0.91	5 0.94	88 A14012550	GroES-like zinc-binding alcohol	LOC_0509g56250.1	expressed	ь па	па	па па	па па	112	0	transcriptional Post-transcriptional regulati
Sobic.007G181600	20	14	8	8 1	1 15	32	55	9	8	17 1	7 -0.6	63 -0.92	6 -0.8	73 AT5G51970	dehydrogenase family protein	LOC_Os08g43190.2	dehydrogenase, putative, expressed nodulin MtN3 family protein putative	na na	na	na na	na na	na	0	metabolism
Sobic.007G191200	4	1	2	2 1	5 11	5	2	7	5	3	2 0.0	33 0.88	9 0.63	75 AT5G13170	senescence-associated gene 29	LOC_Os08g42350.1	expressed	na na	na	na na	na na	SWEET family	0	transport
Sobic.008G111300	3	4	2	4	6 4	6	12	3	2	4	6 0.1	08 -0.81	2 -0.9	60 AT3G18830	polyol/monosaccharide transporter 5	LOC_Os12g32940.1	transporter family protein, putative, expressed	na na	na	na na	na na	polyol transporter (PLT)	0	transport
S-hi- 008C157100	12	21	-			12	76			20 6		12 0.76	0.00	ATEC 28770	bZIP transcription factor family	100.0-12-40020.1	bZIP transcription factor domain	bZ						Tononistional/Best tononistional constati
30010.008(1157100	12	21	'	,	5 8	12	15		0	20 .	2 -0.8	45 -0.70	o -0.o.	25 A15028/70	methylcrotonyl-CoA carboxylase	1000_0312940320.1	containing protein, expressed	ппа	na	па па	на на	- ita	0	Transcriptional Fost-transcriptional regulati
															alpha chain, mitochondrial / 3- methylcrotonyl-CoA carboxylase 1		methylcrotonoyl-CoA carboxylase subunit alpha mitochondrial precursor putative							
Sobic.008G160700	13	16	14 1	6 1	1 23	25	33	17	11	27 4	5 0.1	22 -0.69	6 -0.9	17 AT1G03090	(MCCA)	LOC_Os12g41250.1	expressed	na na	na	na na	na na	na	0	metabolism
															NAC (No Apical Meristem) domai transcriptional regulator	n	No apical meristem protein, putative,	N A						
Sobic.009G142200	6	4	3	4	1 6	12	27	0	0	4	5 -0.2	31 -0.85	0 -0.8	73 AT1G01720	superfamily protein	LOC_Os05g34830.1	expressed	C na	na	na na	na na	na	0	Transcriptional/Post-transcriptional regulati
															Lung seven transmembrane		domain containing protein, putative,							
Sobic.009G165500	20	15	18 1	6 3	0 17	10	11	26	17	10	6 0.0	08 0.63	1 0.6	10 AT5G18520	receptor family protein	LOC_Os05g38720.1	expressed serine/threonine-protein kinase SNT7	na na	na	na na	na na	na	0	signaling transduction
Sobic.009G219100	33	49	48 4	16 1	7 37	46	53	16	22	33 3	9 0.0	70 -0.72	3 -0.74	46 AT1G68830	STT7 homolog STN7	LOC_Os05g47560.1	chloroplast precursor, putative, expressed	na na	na	na na	na na	na	0	signaling transduction
															2-oxoglutarate (20G) and Fe(II)- dependent oxygenase superfamily									
Sobic.009G226300	16	26	24 2	27	6 20	54	97	13	16	46 7	2 0.2	66 -0.91	7 -0.84	48 AT4G13400	protein	LOC_Os05g48230.1	expressed protein	na na	na	na na	na na	na	0	metabolism
Sobic.009G232200	269	161	290 18	30	4 130	23	7	197	142	22 1	9 0.1	58 0.71	9 0.70	01 AT2G20520	FASCICLIN-like arabinogalactan	5 LOC_Os05g48900.1	expressed	na na	na	na na	na na	na	0	metabolism
Sobic.010G033000	6	10	10	9	6 4	3	1	8	7	3	3 0.0	70 0.69	0 0.64	96 AT5G23310	Fe superoxide dismutase 3	LOC Os062051101	superoxide dismutase, chloroplast, putative expressed	na na	na	na na	na pa	na	0	metabolism
												2.07										2	-	
na = not applicable																								

TableS10. Details of twenty-nine differentially-expressed candidate genes that were associated with T6P and located in the introgression region of R9188.

na = not applicable

Year of								
reference	QTL name	chromosome	Left coordinate	Right coordinate	TYPE	Traits	Reference	
2015	FD1	Chr02	8,031,702	20,388,713	double markers	flowering date	Anne Mocoeur, et al. 2015	
2015	FD2	Chr04	61,178,557	62,286,897	double markers	flowering date	Anne Mocoeur, et al. 2015	
2015	FD3	Chr08	9,515,032	46,796,389	double markers	flowering date	Anne Mocoeur, et al. 2015	
2010	GLUC1	Chr01	68,494,074	69,632,980	double markers	glucose content	Amukelani Lacrecia Shiringani, et al. 2010	
2010	GLUC2	Chr03	7,489,898	55,404,530	double markers	glucose content	Amukelani Lacrecia Shiringani, et al. 2010	
2011	JW1	Chr01	16,624,307	50,203,705	double markers	juice weight	Yan-an Guan, et al. 2011	
2011	JW2	Chr01	50,068,342	50,645,315	double markers	juice weight	Yan-an Guan, et al. 2011	
2011	JW4	Chr07	57,780,614	59,111,746	double markers	juice weight	Yan-an Guan, et al. 2011	
2011	JW5	Chr09	57,312,365	58,975,869	double markers	juice weight	Yan-an Guan, et al. 2011	
2010	PHT1	Chr01	23,702,809	61,146,468	double markers	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2010	PHT10	Chr08	46,039,745	48,122,969	double markers	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2015	PHT11	Chr09	16,146	2,589,508	double markers	plant height	Anne Mocoeur, et al. 2015	
2015	PHT2	Chr01	62,704,567	66,681,750	double markers	plant height	Anne Mocoeur, et al. 2015	
2010	PHT3	Chr10	11,029,735	11,037,083	single marker	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2015	PHT4	Chr10	3,630,327	4,593,432	double markers	plant height	Anne Mocoeur, et al. 2015	
2010	PHT5	Chr04	48,757,775	51,234,749	double markers	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2010	PHT6	Chr04	58,537,697	61,178,168	double markers	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2015	PHT7	Chr04	57,538,106	58,537,974	double markers	plant height	Anne Mocoeur, et al. 2015	
2010	PHT8	Chr06	58,217,493	58,217,656	single marker	plant height	Amukelani Lacrecia Shiringani, et al. 2010	
2015	PHT9	Chr07	50,339,917	56,155,869	double markers	plant height	Anne Mocoeur, et al. 2015	
2008	SUG1	Chr01	50,203,535	55,065,768	double markers	sugar	Kimberley B. Ritter, et al. 2008	
2011	SUG10	Chr03	7,489,898	52,308,712	double markers	sugar	Yan-an Guan, et al. 2011	
2002	SUG11	Chr04	51,234,586	67,894,310	double markers	sugar	A. Natoli, et al. 2002	
2010	SUG12	Chr04	58,537,697	58,537,974	single marker	sugar	Amukelani Lacrecia Shiringani, et al. 2010	
2015	SUG13	Chr04	51,875,816	55,385,999	double markers	sugar	Anne Mocoeur, et al. 2015	
2002	SUG14	Chr05	5,686,170	11,099,019	double markers	sugar	A. Natoli, et al. 2002	
2008	SUG15	Chr05	1,907,420	11,099,019	double markers	sugar	Kimberley B. Ritter, et al. 2008	
2010	SUG16	Chr06	58,217,493	58,217,656	single marker	sugar	Amukelani Lacrecia Shiringani, et al. 2010	
2015	SUG17	Chr06	1,822,330	1,908,756	double markers	sugar	Anne Mocoeur, et al. 2015	
2011	SUG18	Chr07	57,780,614	59,111,746	double markers	sugar	Yan-an Guan, et al. 2011	
2008	SUG19	Chr08	45,992,122	50,413,945	double markers	sugar	Kimberley B. Ritter, et al. 2008	
2010	SUG2	Chr01	50,608,251	50,608,477	single marker	sugar	Amukelani Lacrecia Shiringani, et al. 2010	
2010	SUG20	Chr08	48,122,810	50,414,003	double markers	sugar	Amukelani Lacrecia Shiringani, et al. 2010	
2010	SUG21	Chr08	46,039,745	48,122,969	double markers	sugar	Amukelani Lacrecia Shiringani, et al. 2010	
2015	SUG22	Chr08	1,553,582	1,9/1,5//	double markers	sugar	Anne Mocoeur, et al. 2015	
2011	SUG3	Chr01	50,068,342	50,645,315	double markers	sugar	Yan-an Guan, et al. 2011	
2011	SUG4	Chr01	55,/21,520	58,/12,/96	double markers	sugar	Yan-an Guan, et al. 2011	
2010	SUGS	Chr10 Chr02	11,036,814	4/,161,323	double markers	sugar	Amukeiani Lacrecia Shiringani, et al. 2010	
2002	5000	Chr02	5,700,035	01,503,893	double markers	sugar	A. Natoli, et al. 2002	
2010	SUG/	Chr02	61,887,961	61,888,140	single marker	sugar	Amukeiani Lacrecia Shiringani, et al. 2010	
2010	SUG8	Chr02	5,076,675	13,161,221	double markers	sugar	Amukeiani Lacrecia Shiringani, et al. 2010	
2011	SUU9	Chr02	40,504,003	00,421,807	double markers	sugar	r an-an Guan, et al. 2011	
2016	NFC1_2016_chr04	Chr04	63,201,409	63,401,429	GWAS	n-norous carbohydrates (NF)	Brenton et al. 2016	
2016	NFC2_2016_cnr04	Chr04	03,247,013	03,447,023	GWAS	n-norous carbonydrates (NF)	Brenton et al. 2016	
2015	JV_2015_chr06	Chr06	51,666,559	51,901,476	GWAS	Juice volume	Burks et al. 2015	
2016	NFC3_2016_cnr06	Chr06	4,220,818	4,430,900	GWAS	n-norous carbonydrates (NF)	Brenton et al. 2016	
2016	NFC4_2016_chr06	Chr06	49,6/3,083	49,884,457	GWAS	n-norous carbohydrates (NF)	Brenton et al. 2016	

TableS11. Information about QTLs associated with plant height, flowering time, glucose concentration, juice volume, juice weight, non-fibrous carbohydrates and sugar contents, which were identified by previous studies.