Supplemental Data

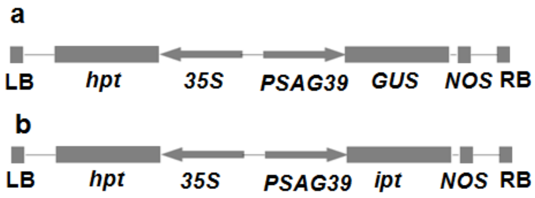

Figure S1. The native promoter constructs of P_{SAG39}. a, Diagram of the P_{SAG39}:*GUS* construct; b, Diagram of the P_{SAG39}:*ipt* construct.

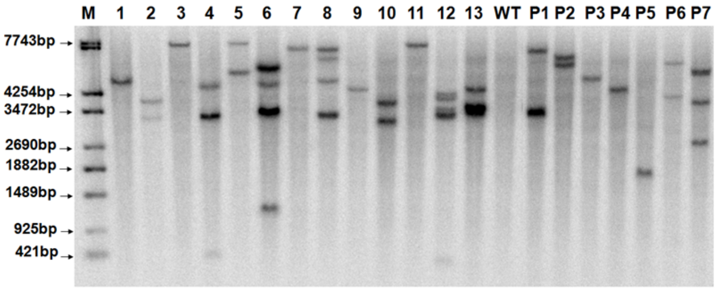

Figure S2. The copy number of T_0 transformants determined by Southern blot analysis. M, λ-ECoT14 Ⅰ; Lanes 1to 13, transgenic plants harboring P_{SAG39}:*GUS*; P1 to P7, transgenic plants harboring P_{SAG39}:*ipt*; WT, wild-type plants.

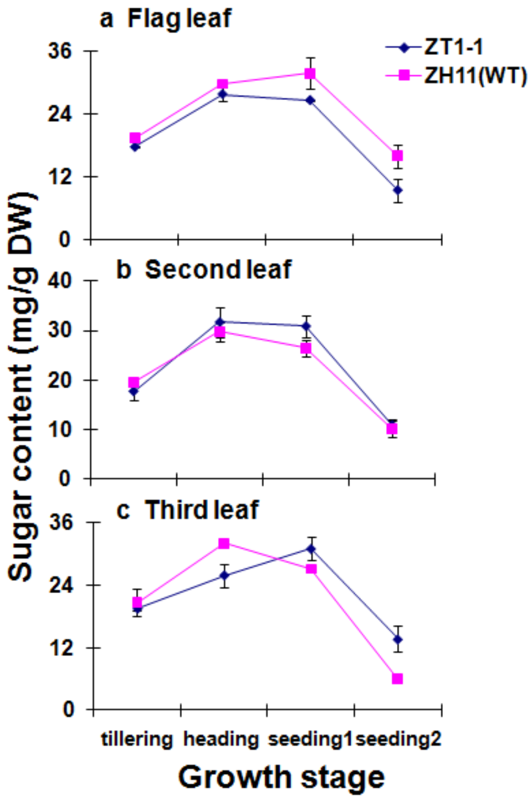

Figure S3. Analysis of sugar content in wild-type and transgenic plants. a, Flag leaf; b, Second leaf; c, Third leaf. Error bars refer to ± SEM of three replicates, with each replicate including 10 plants.

Table S1 Primers for P_{SAG39} and a series of truncated promoters

Vector	truncated promoter	Primer	Forward primer (5'-3')[1]	Reverse primer (5'-3')[2]
P_{SAG39}:GUS	P39	P39-F/R	ggctctagaattcataagagagggaggcacacg	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-62}$:GUS	Pf06	Pf06-F/R	ggctctagaattcaacatcgtacacgcaccgta	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-239}$:GUS	Pf2	Pf2-F/R	ggctctagaattcacttcacggctacgcagact	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-493}$:GUS	Pf5	Pf5-F/R	ggctctagaattcccaatgtgcaaaactctcca	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-719}$:GUS	Pf7	Pf7-F/R	ggctctagaattccgcacatatacacccaacctt	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-1100}$:GUS	Pf10	Pf10-F/R	ggctctagaattcgatgagatgggaggaggtga	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-1300}$:GUS	Pf13	Pf13-F/R	ggctctagaattcggagagagcgtcggatatga	gcagatctaccatgaggatggcgaagagcagag
$P_{SAG39-1600}$:GUS	Pf16	Pf16-F/R	ggctctagaattccgtggggaattttgtgagtt	gcagatctaccatgaggatggcgaagagcagag

[1] The underlined sites are the sites for the digestion of restriction enzymes *Eco*RI

[2] The underlined sites are the sites for the digestion of restriction enzymes *Bgl* II

Table S2 The sequence of probes for electrophoretic mobility shift assay

Probe	Sequence (5'-3')	Position
E1	ACATACACCCATATAAACGCACATATAC	-701 to -674
E2	TAATTAGCCGTAAATACGAGTACT	-562 to -539
E3	GCAAAACTCTCCATAGGATAAA	-451 to -430
E4	TCAACAAACCCCCACAGCATAATTTAAAATGTAGGCGTCTGTGTT	-299 to -255
E5	AAGAGAGGGAGGCACACGGCTGGGAGGCCTAGCTGCTGAGTC	-2018 to -1977
E6	CTTGACCACCGTGGCTCGACGGG	-1899 to -1877
E7	GGAGGAGTGAGGAGGCGAGGAGGAGGAGAGGGGGAGCGAAGC	-1420 to -1379
E8	AGGGAGGAGCGAGGAGGCGAGGAGGACCG	-1349 to -1321
E3.1	GCAAAACT	-451 to -444
E3.2	CTCTCCAT	-445 to -438
E3.3	TAGGATAAA	-438 to -430
E6.1	TCGACGGG	-1884 to -1877
E6.2	ACCGTGGCT	-1892 to -1884
E6.3	CTTGACCA	-1899 to -1892

Table S3 The sequence of primers for RT-PCR or probes for Northern bloting

Gene locus id or accession number	Primer	Forward primer (5'-3')	Reverse primer (5'-3')
AB025109	ipt-F/R	gcctctggtgaagggtatcat	gcgatcccatgaatcaactta
AF372831	Oshxk1-F/R	agcttgaatcctggagagca	accaccgaagacgagacatc
AY220486	Osinv4-F/R	aagatgaacgcggaggagta	tgcagcctccaaatttatcc
AY342320	Oscin3-F/R	ccaagcacgtcaatgtcact	tactcctccgcgttcatctt
NM_001074422	Osnadh-F/R	cagaacatggtgcagcagac	tgatcaccgagttcacgttc
AF276703	Osinv2-F/R	cgctaaagatttgggagctg	gccctaaatttgtggcattg
EF122480	Oss2-F/R	gagagcctctacccccttgct	ggcaacagcctggttacaat
NM_001074422	Osht-F/R	acgtggagaccaagaacgag	tgtagtagagcacgccgttg
L34271	osmads1-F/R	tccatatgtcctggcaagat	aagagagcacgcacgtactt
AF058697	osmads14-F/R	tcctatgcagaaaaggtcctt	ggacgaagccaaaatatacac
AF091458	osmads18-F/R	ccaaactggatgcacttcag	atcaatatcgctggaagatg
AB003328	osmads50-F/R	aaagctgacgctgatggtttg	gagatccagcttattcctgg
NM_001063913	Hd1-F/R	ttctcctctccaaagattcc	catacgcctttcttgtttca
NM_001063395	Hd3a-F/R	atggccggaagtggcagggac	atcgatcgggatcatcgttag
NM_001048755	OSGI-F/R	tggagaaaggttgtggatgc	gatagacggcacttcagcagat
AL606590	sag39i-F/R	acaatgaggctgcccttatg	aaaggctcacttgctcatgg
AF234297.1	gus-F/R	gggcgaacagttcctgatta	cgaaatattcccgtgcactt
NM_001053188	actin-F/R	ccttaccgacaaccttatga	atggagttgtatgtggcttc