

Figure S1. Number of QTLs for starch content identified via the SLM method sorted according to PVE value.

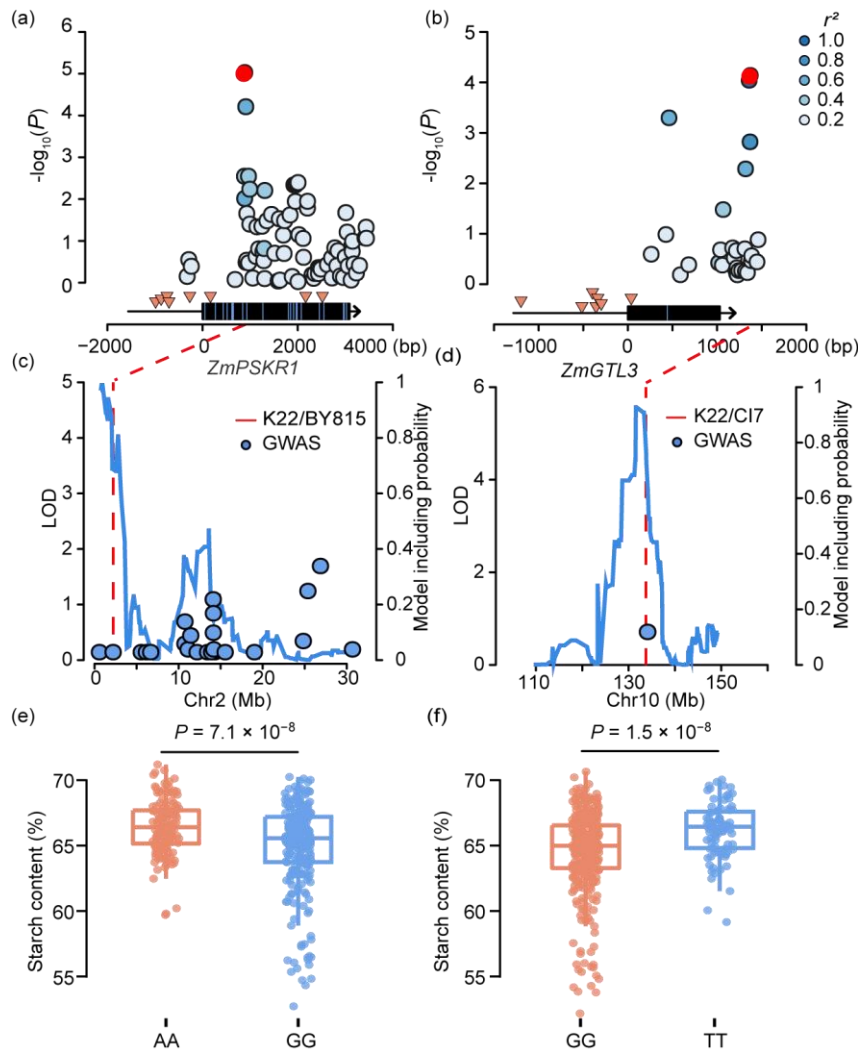


Figure S2 Associations between starch content and *ZmPSKR1* and *ZmGTL3*. (a,b)

Associations between the SNPs at the *ZmPSKR1* (a) and *ZmGTL3* (b) loci and starch content. The red dots show the lead SNP with the most significant association. Color coding of the remaining SNPs reflects the extent of their linkage disequilibrium (r^2) with the lead SNP. The black and gray boxes above the x axis represent exons and UTRs, respectively. The InDels (orange triangles) and nonsynonymous SNPs (blue vertical lines) in the promoter and exons are shown. (c, d) Co-localization between candidate genes and the QTL or SNPs identified via SLM and RIL-based GWAS for *ZmPSKR1* (c) and *ZmGTL3* (d). The blue line shows the LOD profile of the QTL identified via SLM for the indicated RILs, whereas the blue dots represent the results

of the RIL-GWAS. The red dashed lines indicate the position of candidate genes. (e, f)
The genetic effects of the lead SNPs at the *ZmPSKR1* (e) and *ZmGTL3* (f) loci on starch content. The *P*-values were calculated based on a two-tailed Student's *t*-test.

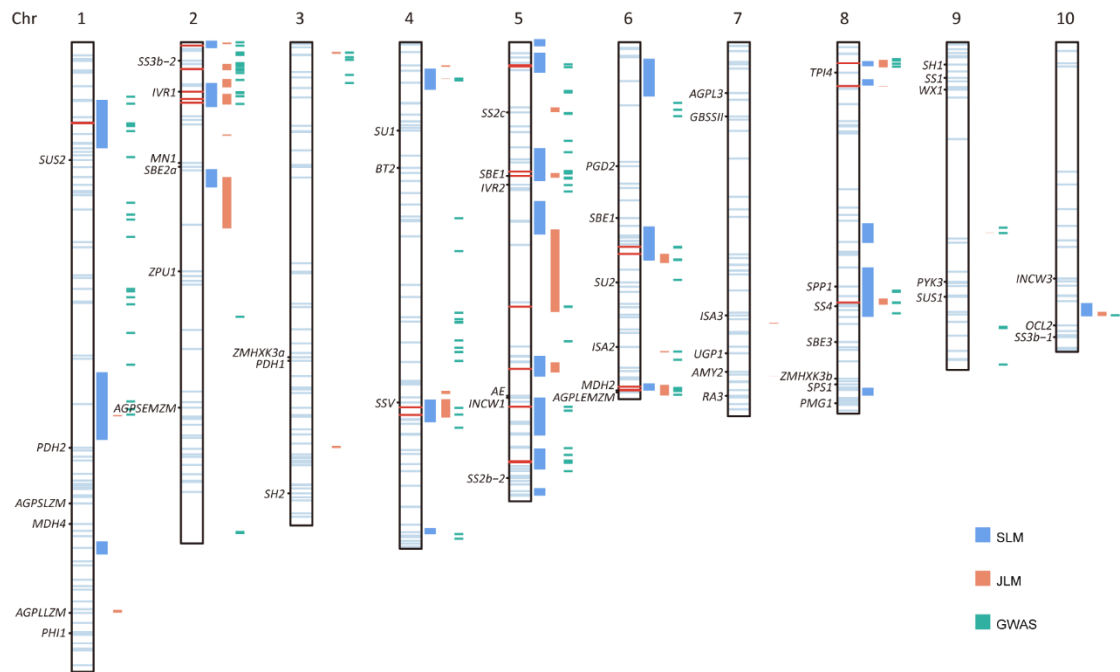


Figure S3. Co-localization of the identified QTLs and 471 genes involved in carbohydrate metabolism. The QTLs identified by SLM, JLM, and GWAS are represented as vertical rectangles of different colors next to each chromosome. The horizontal light blue lines on each chromosome show the positions of the 471 identified genes. The red horizontal lines denote those identified genes that co-localized with the QTLs identified by at least two methods.

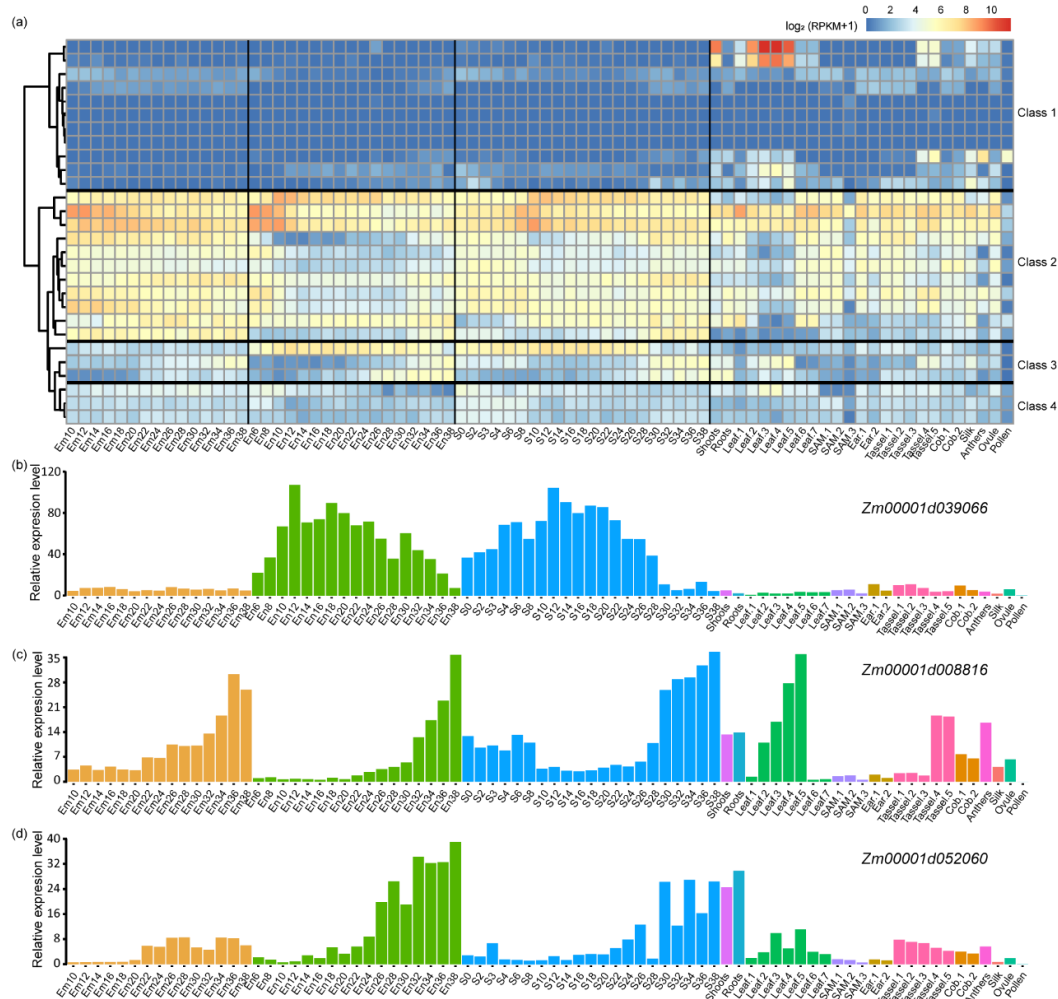


Figure S4. Expression patterns of 28 pathway genes co-localized with the detected QTLs. (a) Hierarchical clustering of 28 genes based on their expressional levels in different tissues from the public transcriptome data (**Dataset S3**; Chen *et al.*, 2014). The \log_2 -based values of one plus the normalized gene transcription level as reads per kilobase per million (RPKM) were used to build the heatmap. The rows in the heat map indicate the genes, and the columns indicate the tissues. Red represents high abundance, and blue represents low abundance. (b–d) Expression pattern of *Zm00001d039066* (b), *Zm00001d008816* (c), and *Zm00001d052060* (d) in various tissues at different stages of development. Em: embryo; En: endosperm; S: seed; SAM: shoot apical meristem.

			10	20	30	40	50	60															
ATTPS11_AT2G18700	1		MSPESW	KDQLS	LVSAD	DDYRIM	GRN--	RIPNAV	TKLS	GLE	TD	DD	PP	NGG	AWV	T	KPKR	I	VVS	NQ			
LOC_Os02g54820	1		MPSLS	CHNLL	DLVAA	ADDA	ASPAS	LPRVMS	AA	SPAS	PTSP	STPA	---	P	ARR	VVS	HR						
SORBI_3004G325900	1		MPSLS	CHNLL	DLAA	DEVPL	PSPT	LR	LPRVMS	VAS	SPAS	PTSP	SPA	---	P	RR	VIVS	HR					
TraesCS6D02G334000.2	1		MPSLS	CHNLL	DL--	ADEL	PLPP	SPL	R	LPRVM	AGAS	SPSS	ASPS	SPSG	---	P	RR	VIVS	HR				
TPS9_Zm00001d052060	1		MPSLS	CHNLL	DLAA	DEVPL	PSPT	LR	LPRVMS	VAS	SPAS	PTSP	SPPA	---	P	RR	VIVS	HR					
			70	80	90	100	110	120															
ATTPS11_AT2G18700	59		LPLRA	HRD	ISSN-	KWCF	FFD	NDSL	LYL	QLKDG	FP	PETE	V	VYVG	SL	NADV	LP	SE	QED	V	SQ	F	
LOC_Os02g54820	58		LPLRA	AA	DA	AS	PF	GF	FT	VD	S	DA	VAY	QL	RS	GL	PP	GAP	V	L	H	I	G
SORBI_3004G325900	58		LPLRA	S	P	DA	AP	F	G	F	N	S	V	D	S	G	T	V	A	Y	Q	L	R
TraesCS6D02G334000.2	56		LPLRA	S	P	DA	AP	F	G	F	K	F	T	V	D	A	G	T	V	A	Y	Q	L
TPS9_Zm00001d052060	58		LPLRA	S	P	DA	AP	F	G	F	R	F	S	V	D	A	G	T	V	A	Y	Q	L
			130	140	150	160	170	180															
ATTPS11_AT2G18700	118		LEKF	Q	C	V	P	T	F	L	P	S	D	L	N	K	Y	H	G	F	C	K	H
LOC_Os02g54820	118		L	A	N	F	S	C	L	P	V	Y	L	P	A	D	L	H	R	R	F	Y	H
SORBI_3004G325900	118		L	A	N	F	S	C	L	P	V	Y	L	P	T	D	L	H	R	R	F	Y	H
TraesCS6D02G334000.2	116		V	S	A	F	S	C	L	P	V	Y	L	P	A	D	L	H	R	R	F	Y	H
TPS9_Zm00001d052060	118		L	A	N	F	S	C	L	P	V	Y	L	P	T	D	L	H	R	R	F	Y	H
			190	200	210	220	230	240															
ATTPS11_AT2G18700	176		K	I	F	A	D	R	L	T	E	V	L	S	P	D	D	D	V	W	I	H	D
LOC_Os02g54820	178		R	A	F	A	D	R	L	T	E	V	L	S	P	D	D	D	V	W	I	H	D
SORBI_3004G325900	178		R	A	F	A	D	R	L	T	E	V	L	S	P	D	D	D	V	W	I	H	D
TraesCS6D02G334000.2	176		R	A	F	A	D	R	L	T	E	V	L	S	P	D	D	D	V	W	I	H	D
TPS9_Zm00001d052060	178		R	A	F	A	D	R	L	T	E	V	L	S	P	D	D	D	V	W	I	H	D
			250	260	270	280	290	300															
ATTPS11_AT2G18700	236		R	D	D	L	R	A	L	L	N	A	D	L	V	G	F	H	T	F	D	Y	
LOC_Os02g54820	238		R	D	D	L	R	A	L	L	N	A	D	L	V	G	F	H	T	F	D	Y	
SORBI_3004G325900	238		R	D	D	L	R	A	L	L	N	A	D	L	V	G	F	H	T	F	D	Y	
TraesCS6D02G334000.2	236		R	D	D	L	R	A	L	L	N	A	D	L	V	G	F	H	T	F	D	Y	
TPS9_Zm00001d052060	238		R	D	D	L	R	A	L	L	N	A	D	L	V	G	F	H	T	F	D	Y	
			310	320	330	340	350	360															
ATTPS11_AT2G18700	296		G	I	D	M	G	Q	L	R	S	V	V	S	A	P	E	T	A	D	V	V	
LOC_Os02g54820	298		G	I	D	M	G	Q	L	R	S	V	V	S	A	P	E	T	A	D	V	V	
SORBI_3004G325900	298		G	I	D	M	G	Q	L	R	S	V	V	S	A	P	E	T	A	D	V	V	
TraesCS6D02G334000.2	296		G	I	D	M	G	Q	L	R	S	V	V	S	A	P	E	T	A	D	V	V	
TPS9_Zm00001d052060	298		G	I	D	M	G	Q	L	R	S	V	V	S	A	P	E	T	A	D	V	V	
			370	380	390	400	410	420															
ATTPS11_AT2G18700	356		E	L	R	G	A	V	L	V	Q	I	A	N	P	A	R	S	E	G	R	D	
LOC_Os02g54820	358		E	L	R	G	A	V	L	V	Q	I	A	N	P	A	R	S	E	G	R	D	
SORBI_3004G325900	358		E	L	R	G	A	V	L	V	Q	I	A	N	P	A	R	S	E	G	R	D	
TraesCS6D02G334000.2	356		E	L	R	G	A	V	L	V	Q	I	A	N	P	A	R	S	E	G	R	D	
TPS9_Zm00001d052060	358		E	L	R	G	A	V	L	V	Q	I	A	N	P	A	R	S	E	G	R	D	
			430	440	450	460	470	480															
ATTPS11_AT2G18700	416		K	V	A	Y	A	A	I	S	E	C	V	V	N	A	V	R	D	G	M	N	
LOC_Os02g54820	417		K	A	A	Y	A	A	A	E	C	C	V	S	A	V	R	D	G	L	N	R	
SORBI_3004G325900	417		K	A	A	Y	A	A	A	E	C	C	V	S	A	V	R	D	G	L	N	R	
TraesCS6D02G334000.2	415		K	A	A	Y	A	A	A	E	C	C	V	S	A	V	R	D	G	L	N	R	
TPS9_Zm00001d052060	417		K	A	A	Y	A	A	A	E	C	C	V	S	A	V	R	D	G	L	N	R	
			490	500	510	520	530	540															
ATTPS11_AT2G18700	476		C	S	P	S	L	S	G	A	I	R	V	N	P	W	N	I	D	A	V	T	
LOC_Os02g54820	470		C	S	P	S	L	S	G	A	I	R	V	N	P	W	S	V	E	S	M	A	
SORBI_3004G325900	471		C	S	P	S	L	S	G	A	I	R	V	N	P	W	S	V	E	S	V	A	
TraesCS6D02G334000.2	468		C	S	P	S	L	S	G	A	I	R	V	N	P	W	S	V	E	S	V	A	
TPS9_Zm00001d052060	471		C	S	P	S	L	S	G	A	I	R	V	N	P	W	S	V	E	S	V	A	
			550	560	570	580	590	600															
ATTPS11_AT2G18700	536		L	Q	R	A	C	K	D	H	Y	N	K	R	F	W	G	V	G	F	L	F	
LOC_Os02g54820	530		L	Q	R	A	C	K	D	H	F	S	R	R	H	W	G	I	G	F	G	M	
SORBI_3004G325900	531		L	Q	R	A	C	K	D	H	F	S	R	R	H	W	G	I	G	F	G	M	
TraesCS6D02G334000.2	528		L	Q	R	A	C	K	D	H	F	S	R	R	H	W	G	I	G	F	G	M	
TPS9_Zm00001d052060	531		L	Q	R	A	C	K	D	H	F	S	R	R	H	W	G	I	G	F	G	M	

Glycosyl transferase

Mutation site

Phosphatase box A

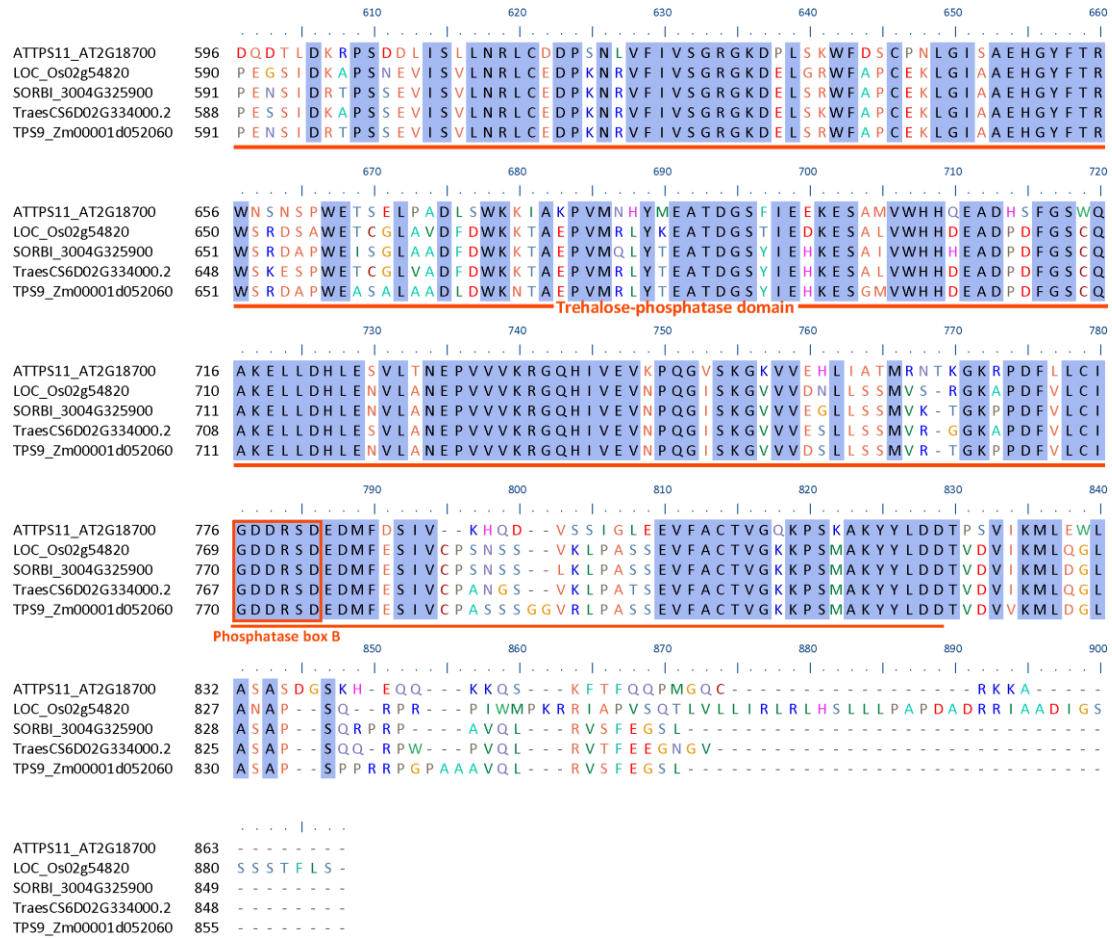


Figure S5. The amino acid sequence alignment of TPS proteins from *Arabidopsis thaliana*, *Oryza sativa*, *Sorghum bicolor*, *Triticum aestivum*, and *Zea mays*. Identical residues are highlighted in blue. The orange lines indicate the glycosyltransferase domain and trehalose-6-phosphate phosphatase-like domain. The trehalose-6-phosphate phosphatase-like domain contains conserved phosphatase consensus sequence boxes A and B, depicted in orange boxes. The scale above indicates the sequence position of amino acids after alignment. The orange star indicates the mutation position of *tps9*.

▼Promoter

K22 1 CCGTAGCGTAAGCCACCGATGACTGAAAGTAGGGGACGTTCTGCATCACTGCATGAACGAGTATAAACCTTACGCCTC--TGCAAACCT
 CI7 1 CCGTAGCGTAAGCCACCGATGACTGAAAGTAGGGGACGTT-----CTGCATGAACGAGTATAAACCTTATGCCCTCCGGCAAACCT

K22 89 CCGGAGCCCAACACGTATACTAAATTTACTTGTGAGCGATGTATGAAACACCAACAATAAGAATAAAAAATTTACTTATCCCCTGT
 CI7 83 CCGGAGCCCAACACGTATAATAAATTTACTTGTGAGCGATGTATGAAACACCAACAATAAGAATAAAAAATTTACCATCCCCTGT

K22 179 CAATTTATAATGTGCTTGACTTTTTTACTAAATTTGATTGGTTCGTCTTAATAAAGAGTCTATAAAAAAT---AAAAATCCAATGGCG
 CI7 173 CAATTTATAATTTGCTTGACTTTTTTACTAAGTTAATTGGTTCGTCTTAATAAAGAGTCTATAAAAAATAAAAAAAATCCAATGTCA

K22 266 TACTTAAA-----GTAAATAGTATTGCAATAAAAAATTAATAATAATTATAAAA-TTTTTTAATAAGATGTACCGATCAACATA
 CI7 263 TACTTAAAGCATATTATGCTAAATACTATCAAAATAAAAAATTAATAATAATTATAAAA-TTTTTTAATAAGATGAACCGATCAACATA

K22 344 TGATAAAAAATATCAAAGGGAACATAGATTGGTCCCGATATCGAGGGTAACAAGTGGTATTGTGGGTATTTTTATTAACTTGAACCTGG
 CI7 353 TGATAAAAAATATCAAAGGGAACATAGATTGGTCCCGATATCGAGGGTAACAAGTGGTATTGTGGGTATTTTTATTAACTTGAACCTGG

K22 434 TAAAGTATACTTTGGAATGATC---TATTAAATTTGTTGAATATAGAGTATAGATTTAGCGGATTAGTTAAATCTCAATCTGATTCCGTG
 CI7 443 TAAAGTATACTTTGGAATGATCAGTATTAAATTTGTTGAATATAGAGTATAGATTTAGCGGATTAGTTAAATCTCAATCTGATTCCGTG

K22 521 TACCAAGATCTGGTCAAACGGGCCATGAACCACCGTTAGCCGACCGGACACTGATGCACCAACCATCCCACATCCCACGTGGGG
 CI7 533 TACCAAGATCTGGTCAAACGGGCCGTGAACCACCGTTAGCCGACCGGACACTGATGCACCAACCATCCCACATCCCACGTGGGG

K22 611 AAGAGCGGGCAATGCCGTCAATTCGCGGGCGAACGTTGTGGAAGAGGCGATGTACAGTGGTGTCTTAAGTTGTCTTAGAGTGTGT
 CI7 623 AAGAGCGGGCAGTGGCCGTCAATTCGCGGGCGAACGATGTGGA-----

K22 701 CTAGGGGGGTGAATGTAAAAATCTCAAGCATGTATCTTGACGAAGACACAGTGTCTTAGCTCTATATTCGAGACAGGAGACTATCTGA
 CI7 666

InDel283
 K22 791 TTGGTCACTTTAATTTATTGAATGTTCTGATTGGTACAAATGAATATGGTAAGACACATGTTTAGACATGACCACTGTATTATGTTGTG
 CI7 666

K22 881 TTTAGCTGTGTCTTACTTGGAGTACCGTGCAGCTGTATCTAGGTTGTACATGCCCTAAGACTAGAGGCCAAGCCATGCGCCATGC
 CI7 666 TAAAGTGTAGAGGCCAAGCCATGCGCCATGC

▼5'UTR

K22 971 CGTCACACCTCCTACTCTGACCTCCGGTTCGCCCCGTCCGTTCTTCTTCTCCTCGCCGCTCAGACACGCACACGCATATCCAGCTTGCCAT
 CI7 700 CGTCACACCTCCTACTCTGACCTCCGGTTCGCCCCGTCCGTTCTTCTTCTCCTCGCCGCTCAGACACGCACACGCATATCCAGCTTGCCAT

K22 1061 ATTTGTACCACCTGTCTCCTCCGTGCCGAGACCCACCTCGGCGTTCTTATCCCAGAAACTTCGGCAAAAGTGATCGATCCGTCTCC
 CI7 790 ATTTGTACCACCTGTCTCCTCCGTGCCGAGACCCACCTCGGCGTTCTTATCCCAGAAACTTCGGCAAAAGTGATCGATCCGTCTCC

K22 1151 CACTCCCACCCCGACCGACCGACCGCCGAAACGAAACCGGTACACCTCGTCCGCTCGCGGCGCTTCTCTTCTTCTCATGCGCTATCGCCGC
 CI7 880 CACTCCCACCCCGACCGACCGCCGAAACGAAACCGGTACACCTCGTCCGCTCGCGGCGCTTCTCTTCTTCTCATGCGCTATCGCCGC

▼Exon1

K22 1241 CGCCTCCACCTCTGCGACGCCACAGATAGGCAAGAGGAGGACGAGGAGGCGATGCGCTTCCGCTCTCCTGCCAACCTCCTCGACCTCGC
 CI7 970 CGCCTCCACCTCTGCGACGCCACAGATAGGCAAGAGGAGGACGAGGAGGCGATGCGCTTCCGCTCTCCTGCCAACCTCCTCGACCTCGC

K22 1331 CGCTGCCGACGAGGTGCCCTGCCGTGCCGACGCCGCTCCGCTCCCGCGCTCATGTCCGTCCGCTCCCGGCTCGCCACCTCGCC
 CI7 1060 CGCTGCCGACGAGGTGCCCTGCCGTGCCGACGCCGCTCCGCTCCCGCGCTCATGTCCGTCCGCTCCCGGCTCGCCACCTCGCC

K22 1421 GTCCCGCCCGCCCGCCGCGCGCTCATCGTCTCCACCGTCTGCCGCTCCGCGCTCGCCGACCCCTCCGCGCCCTTCGGATTCA
 CI7 1150 GTCCCGCCCGCCCGCCGCGCGCTCATCGTCTCCACCGTCTGCCGCTCCGCGCTCGCCGACCCCTCCGCGCCCTTCGGATTCA

K22 1511 GTTCTCCGTGACGCGCGCCGCTCGGCTACCGTCCGCTCGGGCTGCCACCAACGCGCCGCTCCTCCACATCGGCACCTCCAGC
 CI7 1240 GTTCTCCGTGACGCGCGCCGCTCGGCTACCGTCCGCTCGGGCTGCCACCAACGCGCCGCTCCTCCACATCGGCACCTCCAGC

K22 1601 GGCCGCGCGGAGGCGCCCTCAGATGAGTTGTCCAACCTACCTGCTGGCAATTTCTCGTGCCTGCCGGTGTACCTTCCACCGACCTCCA
 CI7 1330 GGCCGCGCGGAGGCGCCCTCAGATGAGTTGTCCAACCTACCTGCTGGCAATTTCTCGTGCCTGCCGGTGTACCTTCCACCGACCTCCA

K22 1691 CCACCGCTTACACCGGATTCTGCAAGCACTACCTCTGGCCGCTCCTCCACTACCTCCTCCGCTGACGCCCTCCTCGCTCGGTGGCT
 CI7 1420 CCACCGCTTACACCGGATTCTGCAAGCACTACCTCTGGCCGCTCCTCCACTACCTCCTCCGCTGACGCCCTCCTCGCTCGGTGGCT

K22 1781 CCCTTTCAGCGAACGCTTACCACCTCCTCTCGGCCAACAGGGCGTTGCGGACCGCCTCACCAGGTTGCTTCCCCGACGAGGA
 CI7 1510 CCCTTTCAGCGAACGCTTACCACCTCCTCTCGGCCAACAGGGCGTTGCGGACCGCCTCACCAGGTTGCTTCCCCGACGAGGA

K22 1871 CCTCGTCTGGATCCACGATTACCACCTCCTCGCGCTCCGACCTTCTCCGCAAGCGCTTCCCGCGCCAAAGGTCGGATTCTTCTCCA
 CI7 1600 CCTCGTCTGGATCCACGATTACCACCTCCTCGCGCTCCGACCTTCTCCGCAAGCGCTTCCCGCGCCAAAGGTCGGATTCTTCTCCA

K22 1961 CTCACCTTTCCCCTCGTGGAGATCTTCCGTACGATCCCCTGCGGGATGACCTCGTCCGCGACTCCTCAACGCCGACCTCGTGGCTT
 CI7 1690 CTCACCTTTCCCCTCGTGGAGATCTTCCGTACGATCCCCTGCGGGATGACCTCGTCCGCGACTCCTCAACGCCGACCTCGTGGCTT

K22 2051 CCACACCTTCGACTACGCGGCCACTTCTGTCCGCGTGTGCGGGTGTGCTCGGCCTCGACTACCAAGCGCGGTACATCGGCAT
 CI7 1780 CCACACCTTCGACTACGCGGCCACTTCTGTCCGCGTGTGCGGGTGTGCTCGGCCTGACTACCAAGCGCGGTACATCGGCAT

K22 2141 CGAGTATTACGGCCGACCGTACTGTCAAGATACTCCCGTGGGATCGACATGGGGCAGCTCAGATCGGTGGTCTCGGCGCGGAGAC
 CI7 1870 CGAGTATTACGGCCGACCGTACTGTCAAGATACTCCCGTGGGATCGACATGGGGCAGCTCAGATCGGTGGTCTCGGCGCGGAGAC

K22 2231 GGAGGACGCGGTGCGGCGGGTACAGAGGCGTACAAGGGGAGGCGCCTCATGGTAGGCGTGCAGACGCTCGATCTGTTCAAGGGGATCGG
 CI7 1960 GGAGGACGCGGTGCGGCGGGTACAGAGGCGTACAAGGGGAGGCGCCTCATGGTAGGCGTGCAGACGCTCGATCTGTTCAAGGGGATCGG

K22 2321 GCTCAAGTTCTGGCGATGGAGCACTGCTCGTGGAGCACCGGAGCTCCGCGCGCGCCGCTGCTGGTGCAGATCGCCAAACCTGCCCG
 CI7 2050 GCTCAAGTTCTGGCGATGGAGCACTGCTCGTGGAGCACCGGAGCTCCGCGCGCGCCGCTGCTGGTGCAGATCGCCAAACCTGCCCG

K22 2411 CAGCGAAGGGCGGACGTCGAAGCGTGCAGGACGAGGCCAGGGCCATCAGCGCCGGGTCAATGCGCGCTTCCGACCCCCGGGTACAC
 CI7 2140 CAGCGAAGGGCGGACGTCGAAGCGTGCAGGACGAGGCCAGGGCCATCAGCGCTGGGTCAATGCGCGCTTCCGACCCCCGGGTACAC

GAC (Asp)

K22 2501 GCCGATCGTGTCTCATCGACGACCCGGTACGCGCAGGAGAAAGCCGCTACTACGCGCGCCGAGTGTGCTGCTGAGCGCCGTGCG
 CI7 2230 GCCGATCGTGTCTCATCGACGACCCGGTACGCGCAGGAGAAAGCCGCTACTACGCGCGCCGAGTGTGCTGCTGAGCGCCGTGCG

GGC (Gly)

K22 2591 CGACGGGCTCAACCGGATCCCGTACATCTATACGGTGTGCCGCGAGGAGACCCGCTCGGAGACGACGCGCCAAAGCGGAGCCCAT
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K22 2681 CGTGCTCTCAAGGTTCTGCGTTGCTCCCGTCCCTCAGCGGCGGATCCGCGTGAACCCGTGGAGCGTGGAGTCCGTGGCGGAGCCAT
 CI7 2410 CGTGCTCTCAAGGTTCTGCGTTGTTCCCGTCCCTCAGCGGCGGATCCGCGTGAACCCGTGGAGCGTGGAGTCCGTGGCGGAGCCAT

K22 2771 GAAACCGCGCTGCGGATGCCGAGGCCGAGCAGCGGCTGCGGCACGAGAAGCACTACAAGTACGTGAGCACCCACGACGTGCCTACTG
 CI7 2500 GAAACCGCGCTGCGGATGCCGAGGCCGAGCAGCGGCTGCGGCACGAGAAGCACTACAAGTACGTGAGCACCCACGACGTGCCTACTG

K22 2861 GGC GCGGT CCTT CGACT CGGACCT GCAGCGCGCTGCAAGGACCATTCTCGCGCCGGCATTGGGGGATCGGGTTCGGCATGAGCTTCAA
 CI7 2590 GGC GCGGT CCTT CGACT CGGACCT GCAGCGCGCTGCAAGGACCATTCTCGCGCCGGCATTGGGGGATCGGGTTCGGCATGAGCTTCAA
 K22 2951 GGTGGTGGCCCTTGGCCCGAACTTCCGGCGGCTCTCCGTGGAGCACATTGTCCCTTCTGATCGGAGGACGGAGAACC GGCTGATTCTCCT
 CI7 2680 GGTGGTGGCCCTTGGCCCGAACTTCCGGCGGCTCTCCGTGGAGCACATTGTCCCTTCTGATCGGAGGACGGAGAACC GGCTGATTCTCCT
 K22 3041 GGACTACGACGGCACCGTGATGCCGGAGAATTCGATCGACCGGACGCCGAGCAGTGAGGTCATCTCTGTGCTGAATCGTCTGTGCGAGGA
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 K22 3131 CCCC AAGAACAGAGTGTTCATCGTGAGCGGGCGTGGGAAGGACGAGCTGAGTAGGTGGTTCGCCCCCTGCGAGAAGCTGGGCATCGCGGC
 CI7 2860 CCCC AAGAACAGAGTGTTCATCGTGAGCGGGCGGGGAAGGACGAGCTGAGTAGGTGGTTCGCCCCCTGCGAGAAGCTGGGCATCGCGGC
 K22 3221 GGAGCA CGTTACTT CACAAGG TAAAAATCTTCGTACACTGTTCCACCGGCGAAGTTCGCTGGTAGTTCGTTTTGGTACCACCTTTGCT
 CI7 2950 GGAGCA TGGTACTT CACAAGG TAAAAATCTTCGTACAA TGTTCACCGGCGAAGTTCGCTGGTAGTTCGTTTTGGTACCACCTTTGCT
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 CI7 3040 TTGCTTGGATTGGGTTCTTATTA CTGCTCCAGATTCCGGCCACAGAA TAGAATGGTACGAATTAAGCAATGGTACC CGCAAATCTAG
 K22 3401 GAGGAGCGTT CATATTCTGATGCGTTGGT CAGTCACTTTTGGTTACA ACTAGTCCCACCGTCCGTCCACACAGAAAGAAGACTGCAATT
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 CI7 3220 GTCGTTTTCGTTTTTAAAGGAGTCCGAAGAGTCTGAACCTTCAACTTTGACCAATTTATTCGTATAAAAAGGTACCAACGTT CATAATATA
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 CI7 3308 AAATAACTATAATTTATAGTTATAGAATATGTTTTAAAATAAGTTTATTTGAAGTAAACATTTATTGATTATAAAAAATTA CTCAA
 K22 3671 CTTGTGCATTTCTTCGCGCGA CGGAGTTAAGTCCAGAGAGCGTTCTGTTCTA ACTTGTAAATGTAGTAGGGCGATACGTGACAACGGGT
 CI7 3398 CTTGTGCATTTCTTCGCGCGA TGGAGTTGAGTCCAGAGAGCA TCTGTTCTA ACTTGTAAATGTAGTAGG CCGATACGTGACAACGGGT
 K22 3761 CACCGACTCTTTTGTCTGCAGGTGGAGCAGGGACGCGCATGGGAGGCCTCAGCATTGGCCGCGACCTGGACTGGAAGAACACCGCGGA
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 K22 3941 TCCGGACTTCGGTTCCTGCCAGGCCAAGGAGCTGCTCGACCATCTCGAGAACGTGCTGGCCAAACGAACCCGTTGGTGGTGAAGAGAGGCCA
 CI7 3668 TCCGGACTTCGGTTCCTGCCAGGCCAAGGAGCTGCTCGACCATCTCGAGAACGTGCTGGCCAAACGAACCCGTTGGTGGTGAAGAGAGGCCA
 K22 4031 GCACATCGTGGAGGTGAACCCCAAGTGAAGT CATGAGCGGGCGAG ---- CCAGACGCGTGCATGC -TTTTTCTCTGCTCATTAAATTAT
 CI7 3758 GCACATCGTGGAGGTGAACCCCAAGTGAAGT CATGAGCGGGCGAG CCGAGCCAGACGCGTGCATGCTTTTTTCTCTGCTCATTAAATTAT
 K22 4115 TCCATACCTACTGCTTACTGCTCGTGGTTGTTGATTCAAAATTTCCCGGACGTGTATGAAACGTGCCGACCGAGTAGAGCTAGCTTTTC
 CI7 3848 TCCATACC-----TACTGCTCGTGGTTGTTCAATTCAAAATTTCCCGGACGTGTATGAAACGTGCCGACCGAGTAGAGCTAGCTTTTC
 K22 4205 AAACCAAAGGCATCGGATAAGTATTGATCTAATCCAGTCCAGTCTCATCCA CTATGCATGCCTGCGACAATCTGTTCCCTCTGCGCAA
 CI7 3931 AAACCAAAGGCATCGGATAAGGATTGATCTAATCCAGTCCAGTCTCATCCA CTATGCATGCCTGCGACAATCTGTTCCCTCTGCGCAA
 K22 4295 ATAGCGACGGGAAATCCCGGAGAACTGCCGCCCGCTCTGTGGATGTGGTCTCTTTTTTTTTTNNNNNNNNNNNNNNNNNNNNNNNN
 CI7 4021 ATAGCGACGGGAAATCCCGGAGAACTGCCGCCCGCTCTGTGGATGTGGTCTCTTTTTTTTTTNNNNNNNNNNNNNNNNNNNNNNNN
 K22 4385 NNN
 CI7 4111 NNN
 K22 4475 NNNNNNAAAAAATCTTGGTGTGTGGTGCAGGGCATCAGCAAAGGCGTGGTGGTGGACAGCCTGCTGTGCTCCATGGTCAGGACGG
 CI7 4201 NNNNNNAAAAAATCTTGGTGTGTGGTGCAGGGCATCAGCAAAGGCGTGGTGGTGGACAGCCTGCTGTGCTCCATGGTGGAGGACGG
 K22 4565 GGAAGCCGCGGACTTCTGCTGTGCATCGGCGACGACCGTCCGACGAGGACATGTTCCGAGAGCATCGTGTGCCCGGCTCCAGCAGCG
 CI7 4291 GGAAGCCGCGGACTTCTGCTGTGCATCGGCGACGACCGTCCGACGAGGACATGTTCCGAGAGCATCGTGTGCCCGGCTCCAGTAGCG
 K22 4655 GCGGCGTGAAGCTCCCGCCAGCAGCGAGGTGTTCCGCTGCACGGTGGGCAAGAAGCCGAGCATGGCCAAGTACTACCTGGACGACACGG
 CI7 4381 GCGGCGTGAAGCTCCCGCCAGCAGCGAGGTGTTCCGCTGCACGGTGGGCAAGAAGCCGAGCATGGCCAAGTACTACCTGGACGACACGG
 K22 4745 TGGACGTGGTCAAGATGCTGGACGGCTTGCCAGCGCGCCGTGCGCCGCGCAGCGCCGGGCGGCGGCGGCGTGCAGCTCCGGGTCT
 CI7 4471 TGGACGTGGTCAAGATGCTGGACGGCTTGCCAGCGCGCCGTGCGCCGCGCAGCGCCGGGCGGCGGCGGCGTGCAGCTCCGGGTCT
 K22 4835 CGTTCGAAGGCTCGCTCTGA - GGGGGAAGGGAAGTAAA - ACACAGCGCTAGCGGTAACAGCAAACGT CGAGCAAAGAAAGAA
 CI7 4561 CGTTCGAAGGCTCGCTCTGAGGGGGGAAGGGAAGTAAAACACACAGCGCTAGCGGTAACAGCAAACGT CGAGCAAAGAAAGAA

Figure S6. Sequence comparisons of *ZmTPS9* between CI7 and K22. The numbers on the left indicate the nucleotide positions in the full-length sequences. Polymorphic sites between K22 and CI7 are shown in different colors. The promoter, three exons, and UTRs of *ZmTPS9* are shaded in green, blue, and orange, respectively. The ATG start codon and TGA stop codon are shown with yellow shading. The red underlines highlighted in exon1 and exon3 indicate nonsynonymous SNPs.

Table S1 Statistical summary, broad-sense heritability, and variances associated with starch content in six RIL populations.

Founders		RIL populations								
Inbred line	Starch content (mean \pm SD)	Population	Population size	Starch content (mean \pm SD)	Range	Variance ^a			h^2 (%) ^b	CI (%) ^c
						σ_g^2	σ_e^2	σ_ε^2		
DE3	69.73 \pm 0.79	DE3/BY815	204	62.04 \pm 1.96	55.86–66.05	3.85**	1.58**	1.82	86.4	83.3–89.0
K22	67.90 \pm 1.02	K22/BY815	207	61.70 \pm 2.19	55.00–66.98	4.59**	3.11**	2.01	87.2	84.3–89.7
DAN340	63.77 \pm 1.04	BY815/KUI3	187	60.54 \pm 1.43	57.45–64.71	2.00**	2.14**	2.03	74.7	68.0–80.0
KUI3	62.85 \pm 0.41	K22/CI7	178	65.01 \pm 1.55	61.45–69.12	2.76**	0.44**	1.9	81.3	76.8–85.1
B77	62.72 \pm 0.34	DAN340/K22	189	66.11 \pm 1.02	63.17–68.60	1.29**	0.34**	1.57	71.2	64.4–76.9
CI7	61.96 \pm 0.04	KUI3/B77	176	65.25 \pm 1.36	61.92–68.40	1.85**	0.82**	1.55	78.1	72.4–82.7
BY815	53.99 \pm 0.01									

^a σ_g^2 is genetic variance, σ_e^2 is the environmental variance, and σ_ε^2 is the residual variance. **P < 0.01.

^bBroad-sense heritability of starch content.

^c95% confidence intervals for broad-sense heritability.

Table S2 Summary of polymorphisms of five candidate genes in seven parents via resequencing

Gene ID (Gene Name)	Promoter		5'UTR		Exon			Intron	
	SNPs	InDels	SNPs	InDels	Synonymous	Non-synonymous	InDels	SNPs	InDels
					SNPs	SNPs			
<i>Zm00001d029039 (ZmABCI6)</i>	NA	NA	NA	NA	16	0	2	111	8
<i>Zm00001d001877 (ZmPSKR1)</i>	44	5	0	0	36	22	3	0	0
<i>Zm00001d012818 (ZmACP3)</i>	26	0	0	1	3	1	0	5	2
<i>Zm00001d010607 (ZmCPR)</i>	54	2	0	0	38	12	0	0	0
<i>Zm00001d025917 (ZmGTL3)</i>	34	6	0	0	14	1	1	0	0

NA: None available

Table S3 Associations between the polymorphic sites at the *ZmTPS9* locus and starch content in maize kernels.

Location	Marker ^a	Allele ^b	MAF ^c	<i>P</i> -value	Type
Promoter	chr4.S_178024173	<u>C</u> / <u>T</u>	0.06	1.2×10^{-1}	Resequencing
Promoter	chr4.S_178024172	<u>C</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178024170	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178024134	<u>C</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178024116	<u>C</u> / <u>T</u>	0.22	3.2×10^{-1}	Resequencing
Promoter	chr4.S_178024115	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178024035	<u>C</u> / <u>T</u>	0.23	3.9×10^{-1}	Resequencing
Promoter	chr4.S_178024034	<u>A</u> / <u>G</u>	0.23	3.9×10^{-1}	Resequencing
Promoter	chr4.S_178023991	<u>1</u> / <u>0</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023990	<u>C</u> / <u>T</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023956	<u>A</u> / <u>G</u>	0.14	3.7×10^{-1}	Resequencing
Promoter	chr4.S_178023953	<u>C</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023950	<u>A</u> / <u>G</u> /-	0.04	2.2×10^{-1}	Resequencing
Promoter	chr4.S_178023910	<u>A</u> / <u>G</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023882	<u>2</u> / <u>0</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023881	<u>C</u> / <u>T</u>	0.22	8.9×10^{-1}	Resequencing
Promoter	chr4.S_178023866	<u>C</u> / <u>T</u>	0.2	9.2×10^{-2}	Resequencing
Promoter	chr4.S_178023863	<u>C</u> / <u>T</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023851	<u>A</u> / <u>C</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023836	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023798	<u>A</u> / <u>G</u> / <u>T</u>	0.04	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023771	<u>G</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023763	<u>C</u> / <u>T</u> /-	0.07	4.6×10^{-1}	Resequencing
Promoter	chr4.S_178023762	<u>1</u> / <u>0</u>	0.14	3.7×10^{-1}	Resequencing
Promoter	chr4.S_178023751	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023738	<u>A</u> / <u>G</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023727	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023724	<u>0</u> / <u>1</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023712	<u>0</u> / <u>1</u> / <u>2</u>	0.003	9.0×10^{-1}	Resequencing
Promoter	chr4.S_178023698	<u>G</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023696	<u>A</u> / <u>G</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023687	<u>11</u> / <u>0</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023663	<u>C</u> / <u>T</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023645	<u>0</u> / <u>1</u>	0.14	7.2×10^{-1}	Resequencing
Promoter	chr4.S_178023631	<u>A</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023620	<u>C</u> / <u>T</u>	0.13	4.4×10^{-1}	Resequencing
Promoter	chr4.S_178023598	<u>A</u> / <u>G</u>	0.41	9.8×10^{-1}	Resequencing

Location	Marker ^a	Allele ^b	MAF ^c	<i>P</i> -value	Type
Promoter	chr4.S_178023597	A/ <u>G</u>	0.49	8.1×10^{-1}	Resequencing
Promoter	chr4.S_178023596	A/ <u>C</u>	0.41	9.8×10^{-1}	Resequencing
Promoter	chr4.S_178023545	A/ <u>T</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023521	C/ <u>T</u>	0.09	6.1×10^{-1}	Resequencing
Promoter	chr4.S_178023298	0/ <u>283</u>	0.002	1.6×10^{-1}	Agarose
5'UTR	chr4.S_178023233	<u>C</u> /G	0.37	8.9×10^{-1}	0.56 million
5'UTR	chr4.S_178023232	<u>A</u> /G	0.37	8.9×10^{-1}	0.56 million
5'UTR	chr4.S_178023154	A/ <u>G</u>	0.12	6.0×10^{-1}	0.56 million
5'UTR	chr4.S_178023082	C/ <u>G</u>	0.12	8.1×10^{-1}	0.56 million
5'UTR	chr4.S_178022994	A/ <u>G</u>	0.45	7.4×10^{-2}	0.56 million
5'UTR	chr4.S_178022993	A/ <u>G</u>	0.32	9.1×10^{-1}	0.56 million
Exon1	chr4.S_178022711	A/ <u>G</u>	0.46	7.8×10^{-1}	0.56 million
Exon1	chr4.S_178022635	<u>A</u> /C	0.13	6.9×10^{-1}	0.56 million
Exon1	chr4.S_178022588	<u>A</u> /G	0.17	3.7×10^{-1}	0.56 million
Exon1	chr4.S_178022417	<u>G</u> /T	0.08	4.6×10^{-1}	0.56 million
Exon1	chr4.S_178022321	<u>A</u> /G	0.07	7.6×10^{-1}	0.56 million
Exon1	chr4.S_178022270	<u>A</u> /G	0.08	4.6×10^{-1}	0.56 million
Exon1	chr4.S_178022252	<u>G</u> /T	0.05	6.2×10^{-1}	0.56 million
Exon1	chr4.S_178022129	<u>A</u> /G	0.07	7.6×10^{-1}	0.56 million
Exon1	chr4.S_178022108	<u>C</u> /G	0.07	8.4×10^{-1}	0.56 million
Exon1	chr4.S_178022060	C/ <u>G</u>	0.07	8.2×10^{-1}	0.56 million
Exon1	chr4.S_178022054	<u>A</u> /G	0.07	8.2×10^{-1}	0.56 million
Exon1	chr4.S_178021967	<u>C</u> /T	0.08	4.6×10^{-1}	0.56 million
Exon1	chr4.S_178021892	C/ <u>T</u>	0.07	7.6×10^{-1}	0.56 million
Exon1	chr4.S_178021772	<u>A</u> /G	0.07	7.6×10^{-1}	0.56 million
Exon1	chr4.S_178021716	<u>C</u> /T	0.31	2.1×10^{-1}	0.56 million
Exon1	chr4.S_178021676	<u>A</u> /G	0.23	9.7×10^{-1}	0.56 million
Exon1	chr4.S_178021616	<u>A</u> /G	0.12	9.3×10^{-3}	0.56 million
Exon1	chr4.S_178021547	<u>A</u> /C	0.22	4.7×10^{-1}	0.56 million
Exon1	chr4.S_178021532	<u>A</u> /G	0.46	4.2×10^{-1}	0.56 million
Exon1	chr4.S_178021511	A/ <u>C</u>	0.08	1.9×10^{-1}	0.56 million
Exon1	chr4.S_178021478	<u>C</u> /G	0.08	1.9×10^{-1}	0.56 million
Exon1	chr4.S_178021211	A/ <u>G</u>	0.40	2.6×10^{-1}	0.56 million
Exon1	chr4.S_178021172	<u>C</u> /T	0.46	5.6×10^{-1}	0.56 million
Exon1	chr4.S_178021073	<u>A</u> /C	0.42	9.6×10^{-1}	0.56 million
Exon1	chr4.S_178021064	<u>A</u> /G	0.22	9.9×10^{-1}	0.56 million
Exon1	chr4.S_178021010	<u>A</u> /G	0.10	7.4×10^{-1}	0.56 million
Intron1	chr4.S_178020972	<u>G</u> /T	0.23	2.5×10^{-1}	0.56 million
Intron1	chr4.S_178020924	A/ <u>G</u>	0.11	4.6×10^{-1}	0.56 million
Intron1	chr4.S_178020909	A/ <u>G</u>	0.05	9.6×10^{-3}	0.56 million

Location	Marker ^a	Allele ^b	MAF ^c	<i>P</i> -value	Type
Intron1	chr4.S_178020888	<u>C</u> /T	0.12	2.5×10^{-1}	0.56 million
Intron1	chr4.S_178020886	<u>A</u> /T	0.13	1.2×10^{-1}	0.56 million
Intron1	chr4.S_178020880	<u>C</u> /G	0.06	1.6×10^{-1}	0.56 million
Intron1	chr4.S_178020872	<u>A</u> /T	0.13	3.2×10^{-1}	0.56 million
Intron1	chr4.S_178020842	<u>C</u> /G	0.12	4.6×10^{-1}	0.56 million
Intron1	chr4.S_178020478	<u>A</u> /C	0.21	8.5×10^{-1}	0.56 million
Intron1	chr4.S_178020477	C/ <u>G</u>	0.21	8.4×10^{-1}	0.56 million
Exon2	chr4.S_178020361	<u>C</u> /T	0.26	1.6×10^{-1}	0.56 million
Intron2	chr4.S_178020086	<u>C</u> /T	0.08	5.7×10^{-2}	0.56 million
Intron2	chr4.S_178020047	<u>C</u> /G	0.06	8.7×10^{-2}	0.56 million
Intron2	chr4.S_178020017	<u>A</u> /C	0.16	4.8×10^{-1}	0.56 million
Intron2	chr4.S_178019995	<u>C</u> /G	0.15	9.6×10^{-1}	0.56 million
Intron2	chr4.S_178019877	<u>A</u> /C	0.10	7.6×10^{-1}	0.56 million
Intron2	chr4.S_178019876	A/ <u>C</u>	0.36	4.3×10^{-1}	0.56 million
Exon3	chr4.S_178019687	A/ <u>C</u>	0.44	4.7×10^{-1}	0.56 million
Exon3	chr4.S_178019586	C/ <u>T</u>	0.47	1.2×10^{-1}	0.56 million
Exon3	chr4.S_178019585	<u>A</u> /G	0.47	1.2×10^{-1}	0.56 million
Exon3	chr4.S_178019462	<u>A</u> /C	0.19	2.1×10^{-1}	0.56 million
Exon3	chr4.S_178019441	C/ <u>T</u>	0.17	8.6×10^{-1}	0.56 million
3'UTR	chr4.S_178019332	C/ <u>T</u>	0.06	7.8×10^{-1}	0.56 million
3'UTR	chr4.S_178019319	C/ <u>T</u>	0.30	4.8×10^{-1}	0.56 million
3'UTR	chr4.S_178019237	<u>A</u> /C	0.21	6.3×10^{-2}	0.56 million
3'UTR	chr4.S_178019236	<u>A</u> /C	0.20	1.0×10^{-2}	0.56 million
3'UTR	chr4.S_178019234	A/ <u>C</u>	0.04	2.1×10^{-1}	0.56 million
3'UTR	chr4.S_178019233	A/ <u>C</u>	0.04	2.1×10^{-1}	0.56 million
3'UTR	chr4.S_178019232	<u>A</u> /G	0.10	5.9×10^{-1}	0.56 million
3'UTR	chr4.S_178019220	A/ <u>C</u>	0.09	3.8×10^{-1}	0.56 million
3'UTR	chr4.S_178019219	C/ <u>G</u>	0.09	3.5×10^{-1}	0.56 million
3'UTR	chr4.S_178019218	<u>A</u> /G	0.11	6.3×10^{-1}	0.56 million
3'UTR	chr4.S_178019216	<u>G</u> /T	0.14	4.7×10^{-1}	0.56 million
3'UTR	chr4.S_178019210	G/ <u>T</u>	0.15	2.9×10^{-2}	0.56 million
3'UTR	chr4.S_178019121	C/ <u>G</u>	0.14	5.2×10^{-1}	0.56 million
3'UTR	chr4.S_178019103	<u>C</u> /T	0.26	4.2×10^{-1}	0.56 million

^aThe sites were named based on the physical position according to the B73 reference genome Version 4; blue shading indicates markers that show polymorphism between K22 and CI7.

^bThe underlined nucleotide in a bold font is the favorable allele for each SNP.

^cMinor allele frequency

Table S4 Primers used in this study.

Type	Primer name	Forward Sequence (5' to 3')	Reverse Sequence (5' to 3')
EMS mutant identification	TPS9-EMS	GTCCAACCTACCTGCTGGCTAA	CCGCTCACGATGAACACTCT
AMP508-promoter	TPS9-AMseq	GCCTCATGGCAAGGGAAGAA	GGGCTTGGGCCTCTAGTCTT
AMP508-283InDel	TPS9-AMp283	ACTGATGCACCCAACCATCC	ATATGCGTGTGCGTGTCTGA
Promoter	TPS9-CI7p	TTCCAAACACCGACACCTCG	GCAAGCTGGATATGCGTGTG
	TPS9-K22p	TTTTACACATGCCTTGCGGC	GCAAGCTGGATATGCGTGTG
Gene body	TPS9-G1	CCATGAACCCACCGTTAGCC	GCGTAGTCGAAGGTGTGGAA
	TPS9-EMS	GTCCAACCTACCTGCTGGCTAA	CCGCTCACGATGAACACTCT
	TPS9-G2	GCCATCGTGCTCTCTGAGTT	GCTCATGACTCACCTGGGG
	TPS9-G3	GTGACAACGTCTCACCGACT	GCAGCTAATCCTACGCCACA
qRT-PCR	TPS9-qRT	CTGAATCGTCTGTGCGAGGA	GCGGTGTTCTTCCAGTCCAG
qRT-PCR	Actin	AATGCCAGCAATGTATGT	TTAGGTGGTCGGTGAGGT
Resequencing	ABCI-G1	CACCTTTGCCTTGCAGGTTT	ACCTGCTGCTTTTACGCTAT
	ABCI-G2	CAAACGTCATCCGAATCCGC	GAACCTGCAAGGCAAAGGTG
	ABCI-G3	ATTGGGACTGCAAGGGATCG	CTGTCCTCTGGCTCCATGTC

Type	Primer name	Forward Sequence (5' to 3')	Reverse Sequence (5' to 3')
Resequencing	ABCI-G4	AGCGAGCGTTAGAATCTGGG	TGCGGACCTACGTAGACAGA
	PSKR1-P1	GCCACAAATGTCGAGCTGTC	CCTGTTGGAGAGATCCAGCG
	PSKR1-G1	TCCTTGGGAGTTTCTGCGAC	AGGGTAAATGGGCCATGCAA
	ACP-P1	CAAGGTCCAGCAGGGACAAT	GACGACCGTCGATGGAATCA
	ACP-P2	GCGAGTGACCACAACAGAGA	CGGGCGCTTTGTTATTACGG
	ACP-P3	GGCTTCCACTTGTGCTTTGG	GGAAAGCTTGCTCTTTGCC
	ACP-G1	CCTTTGCCATTTTTGCGGGT	ACCAACGGCAGGTACAAGAG
	CPR-G1	AGGCGTCCCAAACAAATGC	ATCCTGGCAATCTCCTGTGC
	CPR-P1	TCATCCCCGCTGGAATCTCA	GATGTCCTGCTGCTCCCATC
	GTL-P1	TCGGATTCAAGCCAGCAACT	TCCCGGAGAATCTGATGGGT
	GTL-G1	ACCCAATAAAACCACAGGGA	GTGTCCAGGTGGGACTAATGT
Transient expression assays	TPS9-LUC (K22 and CI7)	ACTCACTATAGGGCGAATTGGGTACCGTA	GAACTAGTGGATCCCCCGGGCTGCAGCG
		GCGTAAGCCACCGATGA	CCTCCTCGTCCTCCTC
	TPS9-LUC-1 (K22 ^{-283bp})	ACTCACTATAGGGCGAATTGGGTACCGTA	GCTTGGGCCTCTAGTCTTATCCACAACG
		GCGTAAGCCACCGATGA	TTCGCCCGCG

Type	Primer name	Forward Sequence (5' to 3')	Reverse Sequence (5' to 3')
	TPS9-LUC-2 (K22 ^{-283bp})	CGCGGGCGAACGTTGTGGATAAGACTAG AGGCCCAAGC	GAACTAGTGGATCCCCGGGCTGCAGCG CCTCCTCGTCCTCCTC
	TPS9-LUC-1 (CI7 ^{+283bp})	ACTCACTATAGGGCGAATTGGGTACCGTA GCGTAAGCCACCGATGA	CCCACTGTACATGCCCTTATCCACATCG TTCGCCCCGCGG
	TPS9-LUC-2-indel (CI7 ^{+283bp})	CCGCGGGCGAACGATGTGGATAAGGGCA TGTACAGTGGG	GCTTGGGCCTCTAGTCTTAGGGCATGTA CAACCTAGATAC
	TPS9-LUC-3 (CI7 ^{+283bp})	GTATCTAGGTTGTACATGCCCTAAGACTA GAGGCCCAAGC	GAACTAGTGGATCCCCGGGCTGCAGCG CCTCCTCGTCCTCCTC