

**Supplemental Table 1****Primer sequences used for quantitative real-time RT-PCR**

Acc. NO.	Forward Sequence (5'→3')	Reverse Sequence (5'→3')	Description
AK108254	TGCAGTATTTCCACCAACA	ACATGAACATGGCTGTGGAG	10 kDa prolamin
AK121775	CACCAAACCCGATCTTCAGT	CGGAACAGCTTCTCCATCTC	11S globulin
AK242306	CACAGCGCAGTTTGATGTTT	GCTTGCCGCAATGCTATACT	13 kDa prolamin
AK242322	TTGATGCTTGCACCTATGG	GCAGCTGCTCAGTTTATGCC	17 kDa prolamin
AK287940	GCCAGTAATTGCAGGGGATA	AGGTCACCACCAACGTAAGC	19 kDa globulin precursor ( $\alpha$ -globulin)
AK100910	CATCAAGGACGGGAAGGTCA	ACTTCACTCGGGGAGCTTA	ADP-glucose pyrophosphorylase large subunit 1
AK071497	CTGAGGAAGAGGTGCTTTGG	TCTTTCGGGAGGATTGTGTC	ADP-glucose pyrophosphorylase large subunit 2
AK069296	GACCATTTGCGGCAGGAATA	TGGAACAACCAATACCCAGA	ADP-glucose pyrophosphorylase large subunit 3
AK121036	TCCCTTCTGGTTTGTGCATTT	CCAAAACGTTCTTGCCATGC	ADP-glucose pyrophosphorylase large subunit 4
AK073146	AGAATGCTCGTATTGGAGAAAATG	GGCAGCATGGAATAAACCCAC	ADP-glucose pyrophosphorylase small subunit 1
AK071826	AGTAGTGGGACTCCGGTCCT	ATGCCACCTTTTTACCAAG	ADP-glucose pyrophosphorylase small subunit 2a
AK103906	AACAATCGAAGCGCGAGAAA	GCCTGTAGTTGGCACCCAGA	ADP-glucose pyrophosphorylase small subunit 2b
AK102488	CCATTTCTCGAGCAACAACA	ATTTGCAGGGTATCCGTCAC	Alanine aminotransferase
*Os02g0255700	TGAAGTCAAAGAGAATGGAACG	TACGGCTTAAGGTGTTACCTG	FLL1
*Os07g0422000	TCAGCATCATCTGAGCAACC	GCAGCCGATTTAGGTCTTTG	FLL2
*Os04g0645100	CACACCCTCCAGCAATATCA	CCTTCTGCGACTGCTTTTCT	FLO2
AK068061	TCAGCATGCCTACATTACAGC	TGCAACATCCCGAACAAATA	Glucose-6-phosphate isomerase A
AK068236	GTTGCACGAAGCATCAAAGA	ATGTTTCGCAACAGCATCAG	Glucose-6-phosphate isomerase, cytosolic B
AK107343	GCCAAAGTCAGAGCCAAAAG	GAACCAATGTGCAACACCAG	Glutelin B1
AK243000	TGGCGACCATAGCTTTCTCT	GGGTTGTGCCATGGATTTAC	Glutelin $\lambda$ -RG21
AK242245	CATTGAGCCAATTCGGAGT	GGCCTGATTGTTGAACTGT	Glutelin A1
AK107314	GCAAGAGCAGGAACAAGGAC	CCTCATGGTGAAAAGGTCT	Glutelin A2
AK107271	TGAAAACCAACCCTGACTCC	ACTCATCTCCCCTGTTGTGC	Glutelin A3
AK242872	GCGACCAGAAGGCTACAAAAG	TTGCTTGTGATCGTTGCTC	Glutelin B4
AK070431	TCCGAGAGGTTTCAGGTCATC	ATGAGCTCCTCGGCGTAGTA	Granule-bound starch synthase I
AK067654	AAACGGGCTCTGAAGCAGTA	CTCCTCCACTTCTTTGCAG	Granule-bound starch synthase II
AK105347	ATCGAGAACGGCGAGAAGT	GGACGGAGATGGTATGGAGA	Homologue to maize globulin 1
AK121667	CGACGAGGTGTTCTACGTCA	GTGTTGGCGGAGTAGACGAT	Homologue to maize globulin 2
AB093426	TGCTCAGCTACTCCTCCATCATC	AGGACCGCACAACTTCAACATA	Isoamylase I
AC132483	TAGAGGTCTCTTGGAGG	AATCAGCTTCTGAGTCACCG	Isoamylase II
AP005574	ACAGCTTGAGACTGGGTTGAG	GCATCAAGAGGACAACCATCTG	Isoamylase III
AK068268	ACCAGGGCAAGAACATTCAG	TTGCGTCTTCTGGTACTTG	Protein disulfide-isomerase precursor
AB012915	ACTTTCTTCCATGCTGG	CAAAGGTCTGAAAGATGGG	Pullulanase
AK103898	CATGCACTGTTTCGAGGAGAA	GGGAAATGGCTCTCCCTTAG	Pyruvate, phosphate dikinase 1(OsPPDKB)
AK100267	CCCTCTGAAAGGAAGTACAGTGT	GTCCGAAGAATTAGAAGCATTTC	Actin 1
AK242298	AGGTAGTGATCTCGGCGTTG	CCGATTCTGGCTGACATAG	allergen protein RA16
AK242340	TTCTCGGTATTGCTCCTCGT	CTTATTCTGGCCGACATTG	allergen protein RA17
AK242333	TGGCTTCCAACAAGGTAGTG	ACCTGGTCTTGGTGGTGGTA	allergen protein RA5B
AK107328	AGGTAGTGTCTCGGCGTTG	GTACATCGGGTAGCCCATTTC	Seed allergen RAG2 (RA14b)
AK119436	GGCATTGCACTCCAAAAGAT	GCTCCAGTTGTTGCCTTCTC	Starch branching enzyme I
AB023498	GCCAATGCCAGGAAGATGA	GCGCAACATAGGATGGGTTT	Starch branching enzyme IIa
D16201	ATGCTAGAGTTTGACCGC	AGTGTGATGGATCCTGCC	Starch branching enzyme IIb

Supplemental Data. She et al. (2010). Plant Cell 10.1105/tpc.109.070821

AK109458	TCATGGATGTGAAGGAGCAA	TGGCAGTGAACCACAAACAT	Starch synthase I
AK101978	GATCGACCAGGATGACGATT	GGGTAAAGCACCTGCAACAT	Starch synthase IIa
AK066446	CGGAACTACAAGGAGAGCTGGA	GTGCCGCCGTCTCAGCAG	Starch synthase IIb
AK072339	CGTGGCCCATTAGATGACTT	CAGTAAGCAAACGGTCAGCA	Starch synthase IIc
AK061604	GCCTGCCTGGACTACATTG	GCAAACATATGTACACGGTTCTGG	Starch synthase IIIa
AK122098	ATCCGCTCGCAAGAACTGA	CAACCGCAGGATAACGGAAA	Starch synthase IIIb
AK103906	GGGAGCGGCTCAAACATAAAA	CCGTGCACTGACTGCAAAAT	Starch synthase IVa
AK067577	GAGCTGCTCCTGCTCAAGAT	ACACAATTGCACCCTTGACA	Starch synthase IVb
AK100546	AATGGTATCCTCCGCAAGTG	GGCTTGCAATTTCCCTCATAA	Sucrose synthase 1
AK100334	GCTGAAGGACAGGAACAAGC	CACCACAGACAACCACAAGG	Sucrose synthase 2
AK289078	CATGTACCCCCTGCTCAACT	GTCAGCTGTAATGCCTGCAA	Sucrose synthase 3
AK099330	CCCAGGAGTACCATGCATCT	CTTGGTGATGACCCTCTCGT	$\alpha$ -amylase 3A
AK241191	TCCTTATCGCCTTGCTCTGT	GAAGCGTCCAGGTCGTAGAG	$\alpha$ -amylase 3B
AK101358	CTGGCTCCACACAGAACTCA	CGTAGACATCTCCGTCAGCA	$\alpha$ -amylase 3C
AK119761	GTCGACGAGAAGGTCATGGT	CCTTCTCCAGACGCTGTAG	$\alpha$ -amylase 3D
AK064300	ACAAGGTCATGCAGGGCTAC	GTTCTTGACCGGATTTCAG	$\alpha$ -amylase 3E

Acc. NOs (accession numbers) show the cDNAs registered in the full-length cDNA database. Forward sequences and Reverse sequences show the primer sequence sets to amplify the corresponding genes. Description indicates the annotated names in the database. \*The genes investigated in this study.

**Supplemental Table 2****Markers used for FLO2 mapping****1. Cultivar Specific Markers**

Marker Name*	Forward Sequence (5'→3')	Reverse Sequence (5'→3')	Discription
72	ATGTGTGGTGTTTGAGCATC	TTCTCGAATGCAATAGCGCC	Kasalath specific 72cM
72	CTGTGTGGTGTTTGTGCACC	TTCTCGTACGCGATTGCGAC	Kinmaze specific 72cM
85	CCAGGATCTTGGGGCCTTCA	CTCCGGCTCTCTGTCGTAC	Kasalath specific 85cM
85	CCAGGATCTTGGGGCCTTGA	CTCCGGCTCTCTACCGTCGC	Kinmaze specific 85cM
105	TCAATCCTATGAAGGACTTT	ACCAAGTCAAATTAGCCACG	Kasalath specific 105cM
105	CTTGTGTTTTTCAATCCTTT	ACCAAATCAAATTAGCCAAG	Kinmaze specific 105cM
106	ACCGTTGACTTTTTAGCACA	TAAGACCGACGGACAAACGT	Kasalath specific 106cM
106	ACCGTTAACTTTTTAGCATA	CCGTGCTAACGTTTGACTGT	Kinmaze specific 106cM
109	TACTGGTGCAGTGGTGCT	ATGGGAGCCTGTCAGACA	Kasalath specific 109cM
109	ACCACGTGATGTGAAGAA	ATGGGAGCCTGTCAGAGA	Kinmaze specific 109cM

\*Numbers in primer name means approximate distance (cM) at chorosome 4

**2. Markers for Fine Mapping**

Marker Name	Forward Sequence (5'→3')	Reverse Sequence (5'→3')	Restriction Enzyme*
218187	GAACATCCCAGAAGCGAGTG	GCTCAAGCTCCTCGTCAACT	
218244	GGTCGAATGGTGGTGATAGG	GCGTATCGATCTGGGTTAGC	
217951	CTAGCATGCGAAACAGGACA	TGGATTTCAATGACACGTAGG	AvaII
218042	GGAAGGGTAAAGGGCAGAAG	CGCCAACCCTATCTCATCAC	HinfI
218345	TGACACTTATTAGTTGTCCCTGTGA	TGTTTGCCACAAATCAATCA	
218767	CTGGGCATACCTTCCAAAGA	CGTCTGGTCCACTTGGTTTT	AluI
218787	TGTGGACCCAGTCAAAACAA	TTGCATGTCGTAGGCTTGAG	RsaI
218801	TTCGCAATCTTATGAAACAAGG	GGATCGCTTTTCACGTTTTC	
218567	GCGTGTTGAATTGTTGATGG	CGAATCGAGCCAAGGATAAG	

\*Restriction enzyme that needed to distinguish polymorphism is showing aside

**Supplemental Table 3**

## Primer sequences used for yeast two-hybrid experiments

Primer Name	Sequence	Vector Constructed
FLO2-Head- BamHI	GGGATCCCTGTTGGGTTTGGAGCTTCA	Both
FLO2-Head- Sall	ATAGTCGACTTGATGATTCTAATAAGTTT	pGBKT7 (bait)
FLO2-Head- XhoI	GCTCGAGTTGATGATTCTAATAAGTTT	pGADT7 (prey)
FLO2-Middle-BamHI	AGGATCCTTGTCAACTCAGACATCGCT	Both
FLO2-Middle-Sall	ATAGTCGACGAGATCCTATGTCGTGCTCA	pGBKT7 (bait)
FLO2-Middle-XhoI	GCTCGAGGAGATCCTATGTCGTGCTCA	pGADT7 (prey)
FLO2-Tail-BamHI	AGGATCCAGATGGCTTTGGATAAAGGA	Both
FLO2-Tail-Sall	ATAGTCGACAGCTGACAGAAGTGCAAATT	pGBKT7 (bait)
FLO2-Tail-XhoI	GCTCGAGCGATACCTTTCTTCCAAA	pGADT7 (prey)
bHLH-A-Prey	TGAATTCATGTCGAGCTTGATGGACAA	pGADT7 (prey)
bHLH-B-Prey	CGGATCCTTAGAACATGTCCTTGAGTG	pGADT7 (prey)
LEA-A-Prey	GGTGAGGGTGGAAATTCATGGCGAAGGTGC	pGADT7 (prey)
LEA-B-Prey	CCCGGATCCTCACCTCTCCATCTCGGTCTC	pGADT7 (prey)
bHLH-A-Bait	TGAATTCATGCAGGTCAAGGCCATG	pGBKT7 (bait)
bHLH-B-Bait	ACCTAGGCCTCACCTCTCCATCTCGGT	pGBKT7 (bait)
LEA-A-Bait	TGAATTCATGTCGAGCTTGATGGACAA	pGBKT7 (bait)
LEA-B-Bait	CGGATCCTTAGAACATGTCCTTGAGTG	pGBKT7 (bait)