Plant Breed. Biotech. 2023 (March) 11(1):56~68
https://doi.org/10.9787/PBB.2023.11.1.56

Online ISSN: 2287-9366
Print ISSN: 2287-9358

Table S1. List of genes covering the *qAC11* on chromosome 11.

No.	Gene ID	Gene description
1	*Os11g0152700*	Similar to Transcription factor HBP-1b(C38) (Fragment)
2	*Os11g0153200*	Carbonic anhydrase, CAH1-like domain containing protein
3	*Os11g0153400*	Similar to Rac GTPase activating protein 3 (Fragment)
4	*Os11g0153500*	Protein of unknown function DUF3049 domain containing protein
5	*Os11g0153600*	Signal recognition particle 54 kDa (SRP54) protein, Chloroplast development
6	*Os11g0153700*	Similar to Signal recognition particle 54 kDa protein, chloroplast precursor (SRP54) (54 chloroplast protein) (54CP) (FFC)
7	*Os11g0153800*	Similar to Ribosomal protein S25 (40S ribosomal 25S subunit)
8	*Os11g0153900*	Ribonuclease HII/HIII family protein
9	*Os11g0154300*	Protein of unknown function DUF584 family protein
10	*Os11g0154500*	Blast disease-responsive transcription factor, Disease resistance
11	*Os11g0154700*	Similar to CBL-interacting protein kinase 14
12	*Os11g0154900*	Similar to DNA-binding factor of bZIP class (Fragment)
13	*Os11g0155000*	Dcp1-like decapping family protein
14	*Os11g0155100*	Similar to F-box domain containing protein
15	*Os11g0155500*	Similar to Amino acid permease family protein, expressed
16	*Os11g0155900*	Histone H3
17	*Os11g0156000*	Similar to AP2 domain containing protein RAP2.8 (Fragment)
18	*Os11g0156200*	Peptidase S28 family protein
19	*Os11g0156300*	Protein of unknown function DUF623, plant domain containing protein
20	*Os11g0156401*	Protein of unknown function DUF623, plant domain containing protein
21	*Os11g0156600*	Similar to H0622F05.7 protein
22	*Os11g0157000*	Putative 5-3 exonuclease domain containing protein
23	*Os11g0157100*	Similar to Cyclin T1 (Fragment)
24	*Os11g0157200*	Harpin-induced 1 domain containing protein
25	*Os11g0157300*	Harpin-induced 1 domain containing protein
26	*Os11g0157400*	Exo70 exocyst complex subunit family protein
27	*Os11g0157600*	Circadian-associated rice pseudo response regulator, Control of flowering time
28	*Os11g0158200*	FAD-dependent pyridine nucleotide-disulphide oxidoreductase domain containing protein
29	*Os11g0158300*	Pentatricopeptide repeat containing protein
30	*Os11g0158400*	Similar to Digalactosyldiacylglycerol synthase 1
31	*Os11g0158500*	Basic helix-loop-helix dimerisation region bHLH domain containing protein

32	*Os11g0158600*	Homeodomain-like domain containing protein
33	*Os11g0158832*	Similar to Associated with HOX family protein, expressed
34	*Os11g0159000*	Phox-associated domain domain containing protein
35	*Os11g0159900*	Protein of unknown function DUF241, plant domain containing protein
36	*Os11g0160000*	Protein of unknown function DUF241, plant domain containing protein
37	*Os11g0160100*	Zinc finger, RING/FYVE/PHD-type domain containing protein
38	*Os11g0160300*	Protein kinase, core domain containing protein
39	*Os11g0160500*	Similar to BZIP transcriptional activator RSG-related
40	*Os11g0160550*	Similar to GRAS family transcription factor containing protein
41	*Os11g0160600*	Similar to GRAS family transcription factor containing protein
42	*Os11g0160700*	Zinc finger, RING/FYVE/PHD-type domain containing protein
43	*Os11g0160900*	NB-ARC domain containing protein
44	*Os11g0161000*	NB-ARC domain containing protein
45	*Os11g0161100*	NB-ARC domain containing protein
46	*Os11g0161133*	Similar to NB-ARC domain containing protein
47	*Os11g0161200*	Similar to ATOZI1
48	*Os11g0161900*	Similar to Integral membrane protein
49	*Os11g0162000*	Autophagy-related protein 13 domain containing protein
50	*Os11g0162200*	Similar to Ubiquinol-cytochrome c reductase complex 7.8 kDa protein (EC 1.10.2.2) (Mitochondrial hinge protein) (CR7)
51	*Os11g0163100*	Similar to Actin 7 (Actin 2)
52	*Os11g0163500*	Homeodomain-like containing protein
53	*Os11g0163600*	Similar to Tubby-like F-box protein 13
54	*Os11g0163800*	Protein of unknown function DUF793 family protein
55	*Os11g0164200*	Similar to Ribosome inactivating protein
56	*Os11g0165700*	Mannose-binding lectin domain containing protein
57	*Os11g0166100*	Cyclin-like F-box domain containing protein
58	*Os11g0166201*	Similar to BZIP transcription factor family protein, expressed
59	*Os11g0166800*	Transcription elongation factor, TFIIS/CRSP70, N-terminal domain containing protein
60	*Os11g0167200*	Similar to predicted protein
61	*Os11g0167300*	Protein of unknown function DUF537 family protein
62	*Os11g0167500*	Similar to Serine esterase family protein, expressed
63	*Os11g0167600*	Similar to Exo70 exocyst complex subunit family protein, expressed
64	*Os11g0167800*	Similar to Anth (Pollen-specific desiccation-associated LLA23 protein)
65	*Os11g0168000*	Protein of unknown function DUF1278 family protein
66	*Os11g0168100*	Similar to Syntaxin 61 (AtSYP61)
67	*Os11g0168200*	Ribosomal large subunit protein L3B, Regulation of leaf morphology and plant architecture
68	*Os11g0168300*	Alba, DNA/RNA-binding protein family protein

69	*Os11g0168600*	Protein kinase, core domain containing protein
70	*Os11g0169100*	Sec1-like protein family protein
71	*Os11g0169200*	Amino acid transporter, transmembrane domain containing protein
72	*Os11g0169400*	Similar to Zinc finger, C2H2 type family protein, expressed
73	*Os11g0169600*	Hyccin domain containing protein
74	*Os11g0169700*	Galactose oxidase/kelch, beta-propeller domain containing protein
75	*Os11g0169800*	Similar to Long-chain-fatty-acid--CoA ligase 4 (EC 6.2.1.3) (Long-chain acyl-CoA synthetase 4) (LACS 4)
76	*Os11g0169900*	Similar to Vacuolar ATP synthase 16 kDa proteolipid subunit (EC 3.6.3.14) (V- ATPase 16 kDa proteolipid subunit) (Fragment)
77	*Os11g0170000*	Similar to Amidase family protein, expressed
78	*Os11g0170100*	Similar to 6-aminohexanoate-cyclic-dimer hydrolase (EC 3.5.2.12)
79	*Os11g0170200*	Protein of unknown function DUF869, plant family protein
80	*Os11g0170300*	Similar to CBS domain containing protein
81	*Os11g0170900*	Similar to BURP domain-containing protein 17
82	*Os11g0171300*	Fructose-bisphosphate aldolase, chloroplast precursor (EC 4.1.2.13) (ALDP)
83	*Os11g0171400*	Integrator complex, subunit 3 domain containing protein
84	*Os11g0171500*	Calcium-dependent protein kinase
85	*Os11g0171700*	Forkhead-associated domain containing protein
86	*Os11g0171800*	Protein kinase, core domain containing protein
87	*Os11g0172100*	Similar to Pectinesterase
88	*Os11g0172150*	Similar to Leucine Rich Repeat family protein, expressed
89	*Os11g0172300*	Leucine-rich repeat domain containing protein
90	*Os11g0172350*	Similar to Protein kinase domain containing protein
91	*Os11g0172400*	Similar to Protein kinase domain containing protein
92	*Os11g0173432*	Protein kinase, catalytic domain domain containing protein
93	*Os11g0173500*	Leucine-rich repeat, typical subtype domain containing protein
94	*Os11g0173750*	Similar to Leucine Rich Repeat family protein, expressed
95	*Os11g0173800*	Serine/threonine protein kinase-related domain containing protein
96	*Os11g0173900*	Similar to Leucine Rich Repeat family protein, expressed
97	*Os11g0174000*	Coatomer, beta subunit domain containing protein
98	*Os11g0175000*	Domain of unknown function DUF1618 domain containing protein
99	*Os11g0175300*	Domain of unknown function DUF1618 domain containing protein
100	*Os11g0175400*	Plant neutral invertase family protein
101	*Os11g0175500*	RING finger E3 ligase, Negative regulator in response to salinit
102	*Os11g0175700*	Similar to Transcription factor PCF3
103	*Os11g0175900*	Similar to TPLATE; binding
104	*Os11g0176000*	Similar to nucleotide binding protein
105	*Os11g0176100*	Nucleotide-binding, alpha-beta plait domain containing protein

106	*Os11g0176200*	Similar to HUA enhancer 2
107	*Os11g0176300*	GDP-fucose protein O-fucosyltransferase domain containing protein
108	*Os11g0177400*	Similar to ATPase, coupled to transmembrane movement of substances
109	*Os11g0178800*	Plant disease resistance response protein family protein
110	*Os11g0179000*	Plant disease resistance response protein family protein
111	*Os11g0179400*	Similar to Dirigent-like protein
112	*Os11g0179500*	Similar to dirigent-like protein pDIR9
113	*Os11g0179700*	Similar to Dirigent-like protein
114	*Os11g0180000*	Plant disease resistance response protein family protein
115	*Os11g0180200*	Similar to Protein tyrosine phosphatase 1
116	*Os11g0180600*	Similar to Type III restriction enzyme, res subunit family protein, expressed
117	*Os11g0180900*	Myb transcription factor domain containing protein
118	*Os11g0181100*	Similar to Transmembrane protein TM9SF3 (Fragment)
119	*Os11g0181400*	Similar to barley mlo defense gene homolog4
120	*Os11g0181500*	Similar to Nitrogen fixation like protein
121	*Os11g0181700*	Similar to retinol dehydrogenase 12
122	*Os11g0181800*	Similar to Short-chain dehydrogenase Tic32
123	*Os11g0181900*	Prefoldin domain containing protein
124	*Os11g0182100*	Protein of unknown function DUF688 domain containing protein
125	*Os11g0182200*	Transferase family protein
126	*Os11g0182400*	WD40/YVTN repeat-like domain containing protein
127	*Os11g0182500*	Ankyrin repeat-containing protein, Regulator in basal defense
128	*Os11g0182900*	Ankyrin repeat domain containing protein
129	*Os11g0183150*	Ankyrin repeat domain containing protein
130	*Os11g0183700*	Myb, DNA-binding domain containing protein
131	*Os11g0183800*	Similar to Armadillo/beta-catenin-like repeat family protein, expressed
132	*Os11g0183900*	Similar to Aspartic proteinase Asp1 precursor (EC 3.4.23.-) (OsAsp1) (Nucellin- like protein)
133	*Os11g0184100*	3-oxo-5-alpha-steroid 4-dehydrogenase, C-terminal domain containing protein
134	*Os11g0184300*	Beta-glucosidase 30
135	*Os11g0184600*	Similar to Aspartic proteinase Asp1
136	*Os11g0184800*	Nucellin-like protein
137	*Os11g0184900*	Similar to OsNAC5 protein [imported]-rice
138	*Os11g0186200*	Similar to Aldehyde dehydrogenase (EC 1.2.1.3)
139	*Os11g0186300*	Similar to Ankyrin-like protein
140	*Os11g0186400*	Similar to DNA polymerase delta catalytic subunit (EC 2.7.7.7)
141	*Os11g0186500*	Similar to GH3 auxin-responsive promoter family protein
142	*Os11g0186600*	Tetratricopeptide-like helical domain containing protein

143	*Os11g0186800*	Similar to inorganic phosphate cotransporter
144	*Os11g0186900*	ACC oxidase, Ethylene biosynthesis
145	*Os11g0187100*	WD40 repeat domain containing protein
146	*Os11g0187200*	GATA zinc finger family protein, Control of heading date, plant height and panicle length
147	*Os11g0187500*	Similar to Heat shock protein 70
148	*Os11g0187600*	Similar to Heat shock protein 70
149	*Os11g0187700*	Similar to Heat shock protein 70
150	*Os11g0188100*	Similar to inositol or phosphatidylinositol kinase/ phosphotransferase, alcohol group as acceptor
151	*Os11g0189600*	2,3-oxidosqualene cyclase, Triterpene synthase, Parkeol synthase
152	*Os11g0191300*	Similar to MEI1 protein
153	*Os11g0191400*	ATP-NAD kinase, PpnK-type, all-beta domain containing protein
154	*Os11g0191500*	Pectinesterase inhibitor domain containing protein
155	*Os11g0191800*	Similar to Pectinesterase family protein
156	*Os11g0192400*	Pectin lyase fold/virulence factor domain containing protein
157	*Os11g0192500*	Similar to Pectinesterase family protein
158	*Os11g0193800*	Similar to Pectinesterase family protein
159	*Os11g0194000*	Similar to Pectinesterase
160	*Os11g0194200*	Similar to pectinesterase family protein
161	*Os11g0194400*	Similar to Pectinesterase family protein
162	*Os11g0194600*	Pectinesterase inhibitor domain containing protein
163	*Os11g0194800*	Similar to DNA-directed RNA polymerase II 7.6 kDa polypeptide (EC 2.7.7.6) (RPB10) (RPB7.6)
164	*Os11g0194900*	Protein kinase, core domain containing protein
165	*Os11g0195000*	Similar to J033060E19, full insert sequence
166	*Os11g0195100*	Similar to Protein translocase subunit secA
167	*Os11g0195600*	Similar to Amino acid carrier (Fragment)
168	*Os11g0197400*	Protein of unknown function DUF803 domain containing protein
169	*Os11g0197600*	Transcriptional factor B3 family protein
170	*Os11g0198100*	Similar to EMB2756
171	*Os11g0199000*	Similar to cDNA, clone: J065168H08, full insert sequence
172	*Os11g0199200*	Protein disulfide isomerase-like enzyme, Starch synthesis, Maturation of proglutelin in endosperm
173	*Os11g0199600*	Zinc finger, CCHC-type domain containing protein
174	*Os11g0199700*	Similar to VHS and GAT domain protein
175	*Os11g0199900*	Similar to F-box domain containing protein
176	*Os11g0200000*	Histone deacetylase family protein
177	*Os11g0200600*	Cyclin-like F-box domain containing protein
178	*Os11g0201400*	Similar to Histone deacetylase
179	*Os11g0201175*	Similar to H0315A08.1 protein

180	*Os11g0200950*	F-box domain, cyclin-like domain containing protein
181	*Os11g0201299*	Similar to F-box domain containing protein
182	*Os11g0201360*	Cyclin-like F-box domain containing protein
183	*Os11g0201900*	Similar to F-box domain containing protein
184	*Os11g0202000*	F-box domain, cyclin-like domain containing protein
185	*Os11g0202200*	Cyclin-like F-box domain containing protein
186	*Os11g0202300*	Cyclin-like F-box domain containing protein
187	*Os11g0202400*	Similar to F-box domain containing protein
188	*Os11g0202500*	UDP-glucuronosyl/UDP-glucosyltransferase domain containing protein
189	*Os11g0202600*	Similar to OSIGBa0126J24.2 protein

Legend:

🟨 - highly potential candidate gene

Table S2. List of japonica accessions from the KRICE_CORE set at PDIL1-1 locus and their amylose content (AC).

No.	Code a)	Name	SNP/InDel (Physical position, bp)									HAPLOTYPE	AC (%) d)
			-4974915 b) G/C	-4974161 c) ATTCG/G	-4973583 b) A/G	-4973456 b) G/C	-4973180 b) G/A	-4972773 b) A/C	-4972611b) G/T	-4972553 b) G/C	-4972037 b) A/G		
1	RWG-140	Hopyung	G	ATTCG	A	G	G	A	G	G	A	HAP1	14.84
2	RWG-142	Gopum	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.73
3	RWG-143	Unkwang	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.90
4	RWG-144	Haiami	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.29
5	RWG-146	Hopum	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.23
6	RWG-147	Chilbo	G	ATTCG	A	G	G	A	G	G	A	HAP1	14.46
7	RWG-150	Junam Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.39
8	RWG-151	Shindongjin Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.12
9	RWG-156	Hwaeyong Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.15
10	RWG-157	Dongjin Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.87
11	RWG-161	Jopyeong	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.20
12	RWG-162	Chinnong	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.47
13	RWG-170	Sinunbon Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.02
14	RWG-171	Sambaek byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.40
15	RWG-173	Geuru Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.49
16	RWG-176	Geumo Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.60
17	RWG-178	Jinmi Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.78
18	RWG-181	Naepung Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.51
19	RWG-183	Seoan Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.19
20	RWG-186	Yeonghae Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.59
21	RWG-194	Gyehwa Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.45
22	RWG-212	Goun	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.40
23	RWG-213	Pungmi	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.11
24	RWG-215	Hanmaeum	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.72
25	RWG-217	Onnuri	G	ATTCG	A	G	G	A	G	G	A	HAP1	15.64
26	RWG-218	Ganbaek	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.97
27	RWG-219	Hwangkeummnuri	G	ATTCG	A	G	G	A	G	G	A	HAP1	14.59
28	RWG-220	Dami	G	ATTCG	A	G	G	A	G	G	A	HAP1	14.99
29	RWG-221	Hongjinju	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.10
30	RWG-227	Younghojinmi	G	ATTCG	A	G	G	A	G	G	A	HAP1	19.90
31	RWG-232	Shinbaeg	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.89
32	RWG-234	Sodami	G	ATTCG	A	G	G	A	G	G	A	HAP1	19.27
33	RWG-235	Sukwang	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.92
34	RWG-237	Pungok	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.30
35	RWG-239	Palgoeong	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.35
36	RWG-258	Taebong Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.41
37	RWG-260	Saesangju	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.52
38	RWG-261	Manchu Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.42
39	RWG-263	Sura Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.40
40	RWG-267	Daesan Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.50
41	RWG-268	Nongho Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	20.63
42	RWG-269	Manguem Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.18
43	RWG-270	Saegyehwa	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.05

44	RWG-271	Manweol Byeo	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.65
45	RWG-274	Cheonga	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.50
46	RWG-277	Saenuri	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.52
47	RWG-279	Cheongan	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.03
48	RWG-281	Jinbaek	G	ATTCG	A	G	G	A	G	G	A	HAP1	16.47
49	RWG-282	Cheongnam	G	ATTCG	A	G	G	A	G	G	A	HAP1	19.68
50	RWG-284	Dongbo	G	ATTCG	A	G	G	A	G	G	A	HAP1	18.20
51	RWG-285	Seolemi	G	ATTCG	A	G	G	A	G	G	A	HAP1	17.03
52	RWG-139	Palgong Byeo	G	G	G	G	G	A	T	C	G	HAP2	18.35
53	RWG-154	Hwaseong Byeo	G	G	G	G	G	A	T	C	G	HAP2	19.48
54	RWG-160	Hwacheong	G	G	G	G	G	A	T	C	G	HAP2	19.27
55	RWG-175	Sangmi Byeo	G	G	G	G	G	A	T	C	G	HAP2	19.43
56	RWG-184	Gancheok Byeo	G	G	G	G	G	A	T	C	G	HAP2	19.57
57	RWG-187	Sobi Byeo	G	G	G	G	G	A	T	C	G	HAP2	17.34
58	RWG-190	Daelip Byeo 1	G	G	G	G	G	A	T	C	G	HAP2	20.25
59	RWG-192	Ilmi Byeo	G	G	G	G	G	A	T	C	G	HAP2	17.89
60	RWG-195	Yeongnam Byeo	G	G	G	G	G	A	T	C	G	HAP2	18.24
61	RWG-228	Honong	G	G	G	G	G	A	T	C	G	HAP2	19.07
62	RWG-231	Gangchan	G	G	G	G	G	A	T	C	G	HAP2	19.54
63	RWG-248	Seomjin Byeo	G	G	G	G	G	A	T	C	G	HAP2	18.61
64	RWG-266	Dongan Byeo	G	G	G	G	G	A	T	C	G	HAP2	18.64
65	RWG-283	Suan	G	G	G	G	G	A	T	C	G	HAP2	19.29
66	RWG-148	Ilpum Byeo	G	G	G	G	A	A	T	C	G	HAP3	18.08
67	RWG-159	Giho Byeo	G	G	G	G	A	A	T	C	G	HAP3	18.47
68	RWG-169	Unbong Byeo	G	G	G	G	A	A	T	C	G	HAP3	16.03
69	RWG-179	Heugjinju Byeo	G	G	G	G	A	A	T	C	G	HAP3	15.84
70	RWG-185	Juan Byeo	G	G	G	G	A	A	T	C	G	HAP3	16.92
71	RWG-188	Haepyeong Byeo	G	G	G	G	A	A	T	C	G	HAP3	14.88
72	RWG-224	Heugseol	G	G	G	G	A	A	T	C	G	HAP3	16.47
73	RWG-247	Samnam Byeo	G	G	G	G	A	A	T	C	G	HAP3	17.27
74	RWG-250	Seohae	G	G	G	G	A	A	T	C	G	HAP3	20.60
75	RWG-254	Sobaeg Byeo	G	G	G	G	A	A	T	C	G	HAP3	16.77
76	RWG-255	Sangju Byeo	G	G	G	G	A	A	T	C	G	HAP3	16.72
77	RWG-256	Samcheon Byeo	G	G	G	G	A	A	T	C	G	HAP3	17.25
78	RWG-273	Hwangkeumbora	G	G	G	G	A	A	T	C	G	HAP3	18.06
79	RWG-275	Cheongdam	G	G	G	G	A	A	T	C	G	HAP3	18.59

Legend:
SNP, Single nucleotide polymorphism
InDel, Insertion-Deletion
[a], KNU number is a serial number used in Kongju National University to define germplasm identity.
[b], SNPs are located in the coding region
[c], SNP/InDel is located in the non-coding region
[d], Data for estimated amylose content (AC) were obtained from the Department of Southern Area Crop Science, National Institute of Crop Science, Rural Development Adminitration (RDA), Miryang.

Table S3. Genotype of japonica cultivars at GBSS1 and PDIL1-1 loci and their amylose content (AC), protein content (PC), and days to heading.

No.	Varieties [a)]	AC (%)	PC (%)	*GBSS1* (Physical position, bp) [b)]	*PDIL1-1* (Physical position, bp) [c)]		Days to heading	Remarks
				1765761 T/G	-4973180 G/A	-4974161 ATTCG/G		
1	Jinbuol	16.35	7.44	T	A	G	51	
2	Undoo	16.56	6.51	T	G	ATTCG	56	
3	Jopum	18.04	6.29	T	A	G	56	
4	Hanseol	18.20	6.60	T	G	G	57	
5	Joun	18.53	6.62	T	G	G	57	
6	Goun	16.62	6.24	T	G	ATTCG	58	
7	Jinok	17.85	6.45	T	G	ATTCG	58	
8	Unbong	16.46	6.52	T	A	G	59	
9	Obong	17.66	6.90	T	A	G	59	
10	Unjang	16.89	6.01	T	A	G	59	
11	Taebong	16.42	6.82	T	G	ATTCG	59	
12	Joan	16.56	6.45	T	G	ATTCG	59	
13	Manna	18.12	6.35	T	A	G	59	
14	Keumo3	18.82	6.40	T	G	ATTCG	59	
15	Manho	17.97	6.39	T	G	ATTCG	60	
16	Sinunbong1	18.02	6.75	T	G	G	60	
17	Jinhan	17.91	6.54	T	G	ATTCG	60	
18	Geumo	17.52	6.29	T	G	ATTCG	61	
19	Sinunbong	17.60	6.67	T	A	G	61	
20	Sangju	17.34	6.38	T	A	G	61	
21	Joryeong	18.61	6.65	T	G	ATTCG	61	
22	Samcheon	17.19	6.52	T	A	G	61	
23	Junghwa	16.58	6.37	T	G	ATTCG	61	
24	Jeogjinju	17.03	6.35	T	A	G	61	
25	Manchoo	17.47	6.45	T	G	ATTCG	61	
26	Unkwang	17.62	5.95	T	G	G	61	
27	Hwangkeumbora	18.98	5.98	T	A	G	61	

28	Pyeongwon	16.59	6.16	T	A	G	61
29	Unmi	16.89	6.25	T	A	G	61
30	Geumyoung	17.75	6.44	T	G	ATTCG	61
31	Joeunheukmi	16.88	6.13	T	G	G	61
32	Sanhomi	18.03	6.64	T	G	G	61
33	Shinpyeong	17.42	6.21	T	G	G	61
34	Guru	17.44	6.68	T	G	ATTCG	62
35	Manan	18.48	6.22	T	G	ATTCG	62
36	Saesangju	17.00	6.12	T	G	ATTCG	62
37	Sandeuljinmi	18.21	6.46	T	G	ATTCG	62
38	Junamjosaeng	18.63	6.40	T	G	G	62
39	Jogwang	18.11	6.22	T	G	ATTCG	62
40	Joami	17.65	6.27	T	G	ATTCG	62
41	Seolemi	17.47	6.65	T	G	ATTCG	62
42	Ondami	18.03	6.77	T	G	ATTCG	62
43	Danpyeong	19.00	7.17	T	G	ATTCG	62
44	Jinmi	16.60	6.40	T	G	ATTCG	63
45	Hwawang	17.59	6.54	T	G	G	63
46	Haedamssal	19.73	6.26	T	G	G	63
47	Joil	17.62	6.43	T	A	G	63
48	Jinkwang	17.14	6.42	T	G	ATTCG	63
49	Jungsan	18.13	6.27	T	G	ATTCG	64
50	Namil	18.10	6.38	T	A	G	64
51	Seongsan	18.59	6.39	T	G	ATTCG	64
52	CW92MR	17.24	7.06	T	A	G	64
53	Handeul	17.43	6.43	T	G	ATTCG	66
54	Jonong	19.20	6.72	T	G	ATTCG	66
55	Haedeul	17.41	6.70	T	G	ATTCG	67
56	Naepung	17.44	6.51	T	G	G	67
57	Pungmi1	16.70	6.46	T	G	ATTCG	67
58	Keumo1	17.94	6.28	T	A	G	68
59	Palgong	17.95	6.19	T	G	ATTCG	69
60	Janngan	18.33	6.27	T	G	ATTCG	69

61	Hwajung	19.76	6.31	T	G	ATTCG	69	
62	Haepyeong	17.22	5.70	T	A	G	69	
63	Pungmi	16.89	6.08	T	G	ATTCG	69	
64	Cheonga	18.41	6.28	T	G	ATTCG	69	
65	Manjong	19.21	6.56	T	G	ATTCG	70	
66	Seoan	17.18	7.20	T	G	ATTCG	70	
67	Gancheok	18.98	6.55	T	G	G	70	
68	Jinpum	19.17	6.86	T	G	ATTCG	70	
69	Yeongdeog	18.49	6.63	T	G	ATTCG	71	
70	Hwayeong	17.20	6.38	T	G	ATTCG	71	
71	Sangbo	19.15	6.23	T	G	ATTCG	71	
72	Keumo2	16.63	5.63	T	G	G	72	
73	Giho	17.72	6.44	T	A	G	72	
74	Hwajin	19.30	7.42	T	G	G	72	
75	Daeripbyeo1	20.12	7.44	T	G	G	72	
76	Sura	17.59	6.42	T	G	ATTCG	72	
77	Samdeog	18.34	6.13	T	G	ATTCG	72	
78	Cheongdam	19.33	6.07	T	A	G	72	
79	Cheongan	19.20	6.72	T	G	ATTCG	72	
80	Cheongnam	20.09	6.99	T	G	ATTCG	72	included in the analysis
81	Suryeojinmi	18.83	6.45	T	G	ATTCG	72	
82	Jungsaenggold	16.21	6.58	T	G	ATTCG	72	
83	Youngbo	17.55	6.67	T	G	ATTCG	72	
84	Hojin	20.24	6.63	T	G	ATTCG	72	
85	Keunpum	19.31	5.87	T	G	ATTCG	72	
86	Hwabong	18.09	6.71	T	G	G	73	
87	Manpung	19.38	6.25	T	G	ATTCG	73	
88	Manweol	18.90	6.00	T	G	ATTCG	73	
89	Gangbaek	18.73	6.49	T	G	ATTCG	73	
90	Hongjinju	17.85	6.69	T	G	ATTCG	73	
91	Heugseol	17.36	6.96	T	A	G	73	
92	Haeoreumi	17.79	6.23	T	G	ATTCG	73	
93	Samkwang1	17.24	6.84	T	G	ATTCG	73	

94	Hwanam	18.19	7.32	T	G	G	73
95	Cheongho	20.24	6.45	T	G	G	73
96	Hanmaeum	18.94	5.23	T	G	ATTCG	73
97	Jinbo	18.36	5.64	T	A	G	73
98	Daejin	18.64	6.05	T	G	ATTCG	74
99	Yeongan	19.09	6.26	T	G	G	74
100	Seoan1	19.38	6.64	T	G	G	74
101	Keunnun	16.52	6.14	T	A	G	74
102	Donghaejinmi	19.45	5.82	T	G	ATTCG	74
103	Suan	19.99	5.79	T	G	G	74
104	Dabo	17.99	6.57	T	G	ATTCG	74
105	Bodrami	19.65	7.08	T	G	G	74
106	Heugjinmi	17.93	6.58	T	A	G	74
107	Daecheong	19.04	7.01	T	G	ATTCG	74
108	Daean	18.67	7.65	T	G	G	74
109	Dongan	20.07	6.57	T	G	G	74
110	Gopum	18.80	6.02	T	G	ATTCG	74
111	Onnuri	19.31	6.16	T	G	ATTCG	74
112	Dongjin2	18.70	5.50	T	G	ATTCG	74
113	Hopum	18.45	5.54	T	G	ATTCG	74
114	Chilbo	18.37	5.84	T	G	ATTCG	74
115	Sukwang	18.72	5.49	T	G	ATTCG	74
116	Saegyehwa	18.94	6.93	T	G	ATTCG	75
117	Geuman	18.53	6.93	T	G	ATTCG	75
118	Daepyeong	18.19	6.18	T	G	ATTCG	75
119	Borami	20.43	6.82	T	G	G	75
120	Dongbo	18.31	6.55	T	G	ATTCG	75
121	Jeogjinju2	18.82	6.06	T	G	ATTCG	75
122	Ilpum	18.21	6.76	T	A	G	75
123	Ilmi	18.65	6.39	T	G	G	75
124	Hanam	18.34	5.60	T	G	ATTCG	75
125	Haiami	18.55	5.70	T	G	ATTCG	75
126	Seomyeong	19.57	6.23	T	G	G	75

127	Cheongun	19.39	6.85	T	G	ATTCG	75
128	Anbaek	19.51	6.31	T	G	ATTCG	75
129	Migwang	19.14	6.94	T	G	ATTCG	76
130	Gangchan	17.51	6.37	T	G	G	76
131	Sinbo	18.84	6.68	T	G	ATTCG	76
132	Dongjin	19.44	6.33	T	G	ATTCG	76
133	Samkwang	19.29	6.08	T	G	ATTCG	76
134	Dami	19.73	5.36	T	G	ATTCG	76
135	Malgeumi	19.21	5.59	T	G	ATTCG	76
136	Saenuri	20.24	5.73	T	G	ATTCG	76
137	Jinsumi	19.28	5.58	T	G	G	76
138	Misomi	18.78	6.42	T	G	ATTCG	76
139	Yechan	18.97	5.90	T	G	ATTCG	76
140	Shinbaeg	18.56	6.68	T	G	ATTCG	77
141	Kyehwa	17.52	6.53	T	G	ATTCG	77
142	Hwasin	20.68	6.67	T	G	G	77
143	Hwasam	18.27	7.05	T	G	ATTCG	77
144	Junam	19.33	6.07	T	G	ATTCG	77
145	Jinbaek	20.18	5.49	T	G	ATTCG	77
146	Chinnong	18.06	5.49	T	G	ATTCG	77
147	Sodami	18.76	5.64	T	G	G	77
148	Hyeonpum	20.55	6.54	T	G	G	77
149	Aromi	18.07	7.08	T	G	G	77
150	Tamjin	18.23	6.71	T	G	G	78
151	Daesan	19.36	6.50	T	G	ATTCG	78
152	Sujin	19.10	7.01	T	G	ATTCG	78
153	Honong	19.26	6.13	T	G	G	78
154	Younghojinmi	18.89	5.48	T	G	ATTCG	78
155	Sinjinbaek	19.72	6.65	T	G	ATTCG	78
156	Mipum	19.03	5.61	T	G	ATTCG	79
157	Chindeul	17.91	5.30	T	G	ATTCG	79
158	Manbaek	17.50	6.21	T	G	ATTCG	79
159	Saeshin	19.89	6.76	T	G	ATTCG	79

160	Dacheong	18.83	5.17	T	G	ATTCG	80	
161	Dodamssal[a]	39.09	7.93	G	A	G	-	excluded from the analysis
162	Goami	27.09	7.60	G	G	G	-	
163	Saegoami	27.10	6.46	G	G	G	-	
164	Goami2[a]	32.00	6.93	T	A	G	-	

Note:

[a], Dodamssal and Goami2 had *sbe3* mutant allele at position -19358818 on chromosome 2

[b], *GBSS1* :*granule-bound starch synthase I* , G nucleotide (Wx^{a}); T nucleotide (Wx^{b})

[c], *PDIL1-1* :*protein disulfide isomerase 1-1*

Table S4. List of markers used in this study.

Code	Marker Name	Gene Name	Chr.	Physical Position (bp)	SNP/InDel	Forward Sequence (5'→3')	Reverse sequence (5'→3')	Restriction enzyme	Remarks	References
1	CS02_001	*SBE3*	2	-19358818	T/C	ATGTGCTGGATTTGGTCATA	GTGTAGACTGCAGAAAGCCTA	*SpeI*		Adeva *et al.* 2020
2	CS06_001	*GBSS1*	6	1765761	G/T	GCTTCACTTCTCTGCTTGTG	TTTCCAGCCCAACACCTTAC	*AccI*		
3	PDIL1-1_ex5	*PDIL1-1*	11	-4973180	G/A	CTGCTTTGGAGAAGTTCATTGA	GAATGGAGCTTTTCAGAGAGC	*PvuII*		in this study
4	PDIL1-1_InDel1			-4974161	ATTCG/G	GTGTCTAATTGGATAAACCCTATTC	AAGGTTGGTTGCGTCTTCTGGT	-	Dominant marker	
	PDIL1-1_InDel2					GCTTGTGCATCGTGCTATTG	CATACCTCTGGAGCGAGCTT	-	Co-dominant marker	