

Table 1 Descriptive statistics for germination-related traits at 25°C and 5°C

Trait	Number	Mean	Median	SD	Range
GR3N	190	96.23	97.78	4.84	77.78~100.00
GR7N	190	97.67	100.00	3.51	82.22~100.00
GR11C	190	26.35	12.22	29.70	0~97.78
GR21C	190	52.42	50.00	32.78	0~100.00
GIN	190	45.95	46.56	2.30	31.67~47.62
GIC	190	20.15	13.54	19.05	0~80.08
RGI	190	0.44	0.29	0.41	0~1.68
RGR11C.3N	190	0.27	0.13	0.30	0~0.98
RGR21C.7N	190	0.54	0.53	0.33	0~1.08

Table 2 Position, MAF and *P* values of 26 significant SNPs associated with both RGR21C.7N and RGI

No.	SNPs	Chromosome	Position	MAF	<i>P</i> value in	
					RGR21C.7N	RGI
1	chr4_181394117	4	181394117	0.116	1.41E-06	1.11E-06
2	chr6_93763259	6	93763259	0.073	1.73E-08	5.94E-08
3	chr6_93804119	6	93804119	0.175	6.15E-07	1.03E-06
4	chr6_93817680	6	93817680	0.189	1.26E-06	4.25E-07
5	chr6_93829267	6	93829267	0.192	2.37E-07	3.47E-07
6	chr6_93832400	6	93832400	0.178	4.41E-07	8.43E-07
7	chr6_93833496	6	93833496	0.186	1.10E-08	1.32E-07
8	chr6_93859258	6	93859258	0.164	1.37E-07	9.69E-07
9	chr6_93859868	6	93859868	0.192	5.26E-07	1.82E-06
10	chr6_93861491	6	93861491	0.122	3.29E-07	1.08E-07
11	chr6_93862794	6	93862794	0.172	1.94E-07	1.31E-06
12	chr6_93862996	6	93862996	0.181	9.59E-07	1.48E-06
13	chr6_93877558	6	93877558	0.192	2.00E-07	2.88E-07
14	chr6_93883692	6	93883692	0.192	4.23E-07	1.01E-06
15	chr6_93887057	6	93887057	0.178	6.31E-07	1.65E-06
16	chr6_93891301	6	93891301	0.178	1.04E-07	4.11E-07
17	chr6_93892729	6	93892729	0.161	3.50E-09	8.71E-09
18	chr6_93892736	6	93892736	0.133	1.87E-08	6.61E-08
19	chr6_93896199	6	93896199	0.164	9.13E-08	2.26E-07
20	chr6_93896425	6	93896425	0.200	3.16E-07	1.52E-07
21	chr6_93896703	6	93896703	0.172	1.08E-06	9.60E-07
22	chr6_93910576	6	93910576	0.164	5.87E-07	7.22E-07
23	chr6_93913471	6	93913471	0.181	5.43E-07	1.80E-06
24	chr6_93921703	6	93921703	0.178	2.55E-07	8.89E-07
25	chr8_166223522	8	166223522	0.144	1.23E-06	3.57E-07
26	chr9_106376520	9	106376520	0.242	3.07E-07	1.16E-06

The red SNP is the top SNP shared by RGR21C.7N and RGI

Table 3 Candidate genes were identified within LD decay regions of 26 significant SNPs associated with both RGR21C.7N and RGI

No.	Significant SNPs	Associated Gene	Annotation	Orthologs		Orthologs annotation	Homologs function		
				Arabidopsis	Rice		Related to cold stress	Related to	Related to other
1	chr4__1 81394117	Zm00001e b192980	Chaperone protein DnaJ	AT3G 14200		Chaperone DnaJ-Similar to Heat	[42]	[3]	[1] [39] [42]
2	chr4__1 81394117	Zm00001e b192990	None	AT2G 26670	Os02g 07823	Encodes a plastid Heme-oxygenase			[34] [35] [45]
3	chr4__1	Zm00001e	None						
4	chr4__1	Zm00001e	None						
5	chr6__9 3763259	Zm00001e b272340	None	AT1G 78060	Os07g 06428	Glycosyl hydrolase Similar to	[27]		
6	chr6__9 3763259 、 chr6__9 chr6__9	Zm00001e b272350	Uncharacterized LOC100275040	AT4G 17670	Os06g 07148	Senescence-Protein of P-loop		[33]	[28]
7	3804119 、 chr6__9 chr6__9	Zm00001e b272360	Uncharacterized LOC100273669	AT4G 27680	Os06g 07145	contains ATPase family RNA	[8] [10]	[2] [31]	[8] [34]
8	3832400 、 chr6__9	Zm00001e b272370	None	AT2G 35920	Os10g 04713	helicase Similar to	[8] [20]	[20]	[20]
9	chr6__9 3859868	Zm00001e b272380	None						
10	chr6__9 3877558 、 chr6__9 chr6__9	Zm00001e b272390	None	AT2G 24530	Os04g 06581	Member of Histone-fold SAUR-like		[7] [22]	
11	3887057 、 chr6__9	Zm00001e b272400	Uncharacterized LOC100279159	AT2G 46690	Os06g 07143	Auxin responsive		[31]	[13] [25]
12	chr8__1 66223522	Zm00001e b363570	Protein LURP-one-related	AT3G 14260	Os01g 09316	LURP-one-like Tubby, C-			

13	chr8__1 6622352 2	Zm00001e b363580	Tafazzin homolog	AT3G 05510	Phospho lipid/gly Tafazzin family	[19]		
14	chr8__1 6622352 2	Zm00001e b363590	ARM repeat superfam ily	AT4G 15830	ARM repeat Armadill o-type	[29]	[4]	[29]
15	chr8__1 6622352 2	Zm00001e b363610	Uncharac terized LOC100 193372	AT5G 27730	Heparan- alpha- Protein of			
16	chr8__1 6622352 2	Zm00001e b363620	None	AT5G 06060	NAD(P)- binding Similar to	[12]	[38]	[6]
17	chr8__1 6622352 2	Zm00001e b363630	None	AT5G 05800	Myb/SA NT-like Hypothes ical			
18	chr8__1 6622352 2	Zm00001e b363640	Putative aldehyde oxidase- like	AT2G 27150	Encodes the Aldehyd e	[9] [30]	[18] [30] [41]	
19	chr8__1 6622352 2	Zm00001e b363650	Cytochro me P450 89A2- like	AT1G 64940	Member of Similar to P450	[5]		[5]
20	chr8__1 6622352	Zm00001e b363660	Cytochro me P450					
21	chr8__1 6622352	Zm00001e b363670	Uncharac terized		Os02g 08294	Conserv ed		
22	chr8__1 6622352 2	Zm00001e b363680	ATP sulfuryla se 1, chloropla	AT3G 22890	Encodes ATP Similar to ATP	[21]	[21]	
23	chr8__1 6622352	Zm00001e b363690	Uncharac terized					
24	chr8__1 6622352	Zm00001e b363700	Uncharac terized		Os01g 09302	Conserv ed		
25	chr8__1 6622352	Zm00001e b363710	Uncharac terized		Os01g 09296	Similar to		
26	chr8__1 6622352 2	Zm00001e b363720	Aminope ptidase	AT3G 19340	Aminop eptidase Similar to	[15]		

27	chr8__1 6622352 2	Zm00001e b363730	Long chain base biosynthe	AT5G 23670	Os01g 09288	Encodes the Similar to Serine RING finger Regulati on of				[43]
28	chr8__1 6622352 2	Zm00001e b363740	None	AT5G 13250	Os04g 03965		[16]	[16]	[16]	[40]
29	chr8__1 6622352 2	Zm00001e b363750	Prefoldin chaperon e subunit family	AT1G 03760	Os01g 09283	Prefoldi n				
30	chr8__1 6622352	Zm00001e b363760	None		Os08g 05181	Hypothet ical				
31	chr8__1 6622352 2	Zm00001e b363770	Ribosom al protein eS6 pseudoge	AT5G 10360	Os03g 03900	RPS6A and Similar to			[26]	
32	chr8__1 6622352 2	Zm00001e b363780	None	AT1G 55546	Os11g 01277	2-C- methyl- Conserv ed				
33	chr8__1 6622352 2	Zm00001e b363790	None	AT3G 19540,	Os07g 05911	Glutamy l-tRNA Protein of				
34	chr8__1 6622352 2	Zm00001e b363800	tRNA (adenine(58)- N(1))-	AT2G 45730	Os04g 01123	Part of complex Eukaryot ic	[24]			[24]
35	chr8__1 6622352 2	Zm00001e b363810	Uncharac terized LOC100 273501	AT5G 62000	Os01g 09276	Encodes an auxin Auxin response	[13]	[37]		[13]
36	Chr9__1 0637652 0	Zm00001e b388280	Two- compone nt response	AT2G 25180	Os06g 06472	Encodes an B-type response	[14] [17] [44]	[11]		[17] [23]
37	Chr9__1 0637652 0	Zm00001e b388290	Cytochro me P450 93A3	AT5G 06900	Os06g 06136	Member of Cytochro me P450	[5]			[5]

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