

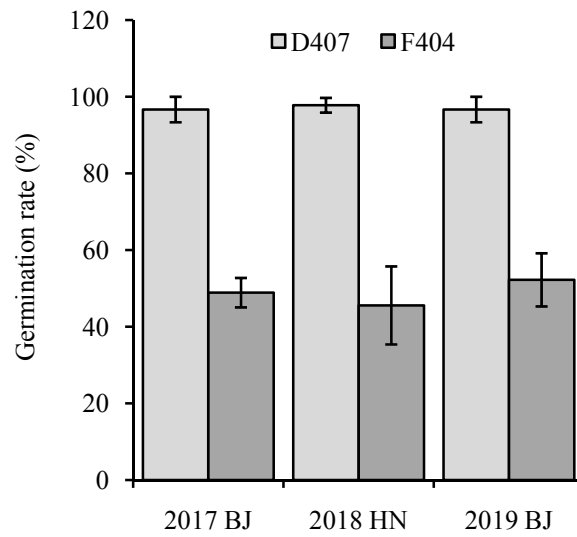


Fig. S1 Germination rate at 25°C of different inbred lines harvested in different year
D407 and F404 are two different inbred lines. 2017BJ and 2019BJ represent seeds harvested in spring of 2017 and 2019 in Beijing ,respectively. 2018HN represent seeds harvested in winter of 2018 in Hainan

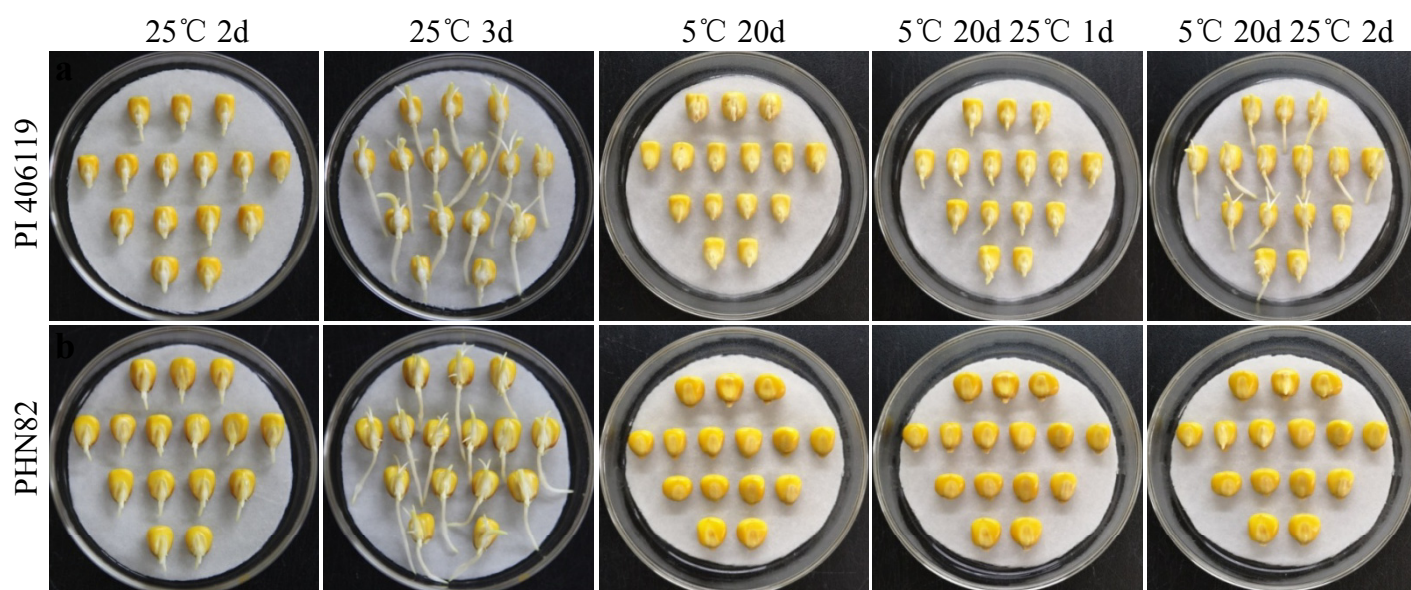


Fig. S2 Comparison of germination between PI 406119 and PHN82 under 25°C, 5°C treatment and 25°C recovery after 5°C treatment
 PI 406119 and PHN82 are two inbred lines. d represents day

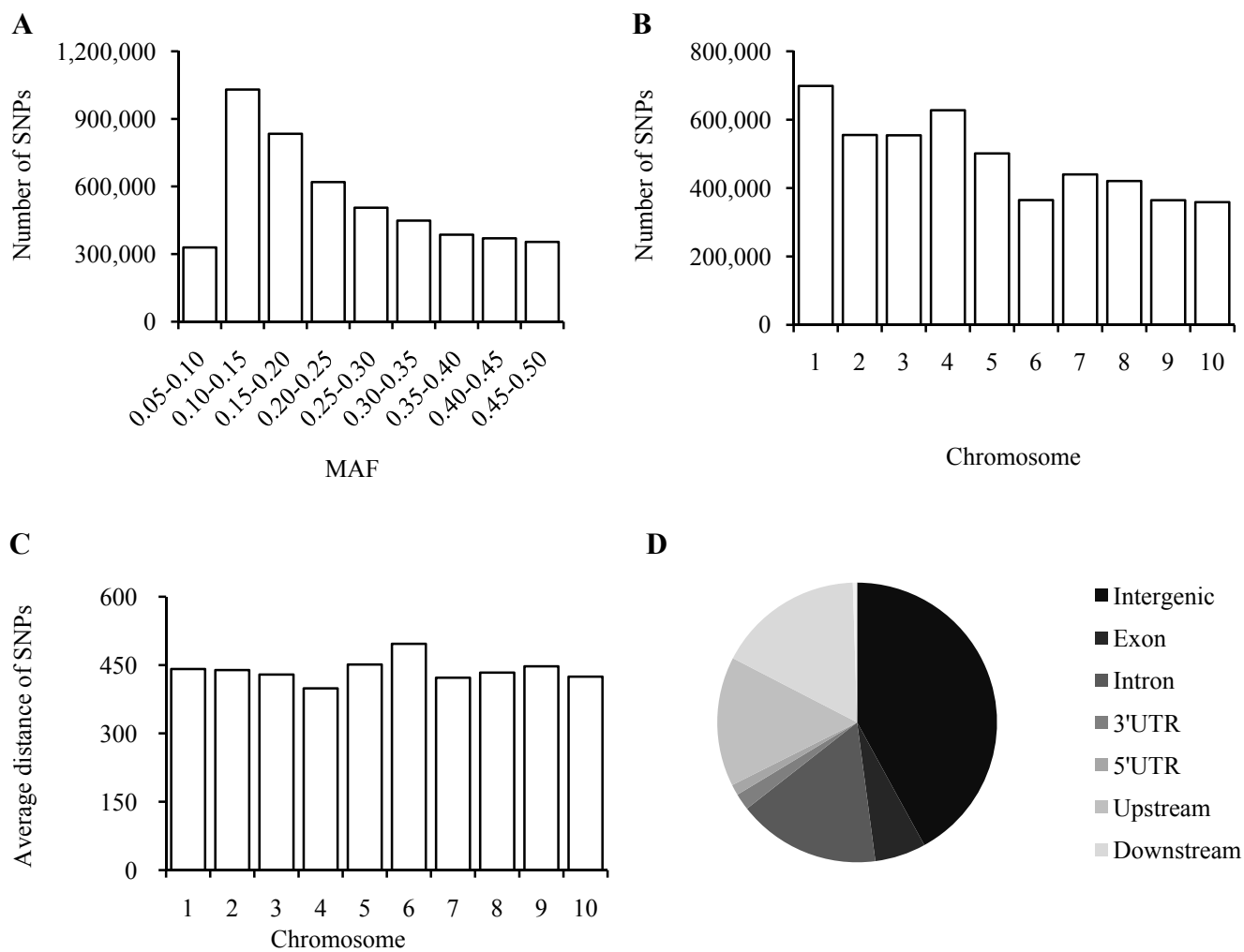


Fig. S3 Distribution pattern of high quality SNPs after filtering with miss rate > 20% and MAFs < 5%

A. Distribution of minor allele frequencies (MAFs); **B.** The number of 4,886,919 SNPs across the 10 chromosomes; **C.** Average distance between SNPs on the 10 chromosomes; **D.** Pie chart of distribution types and region containing SNPs

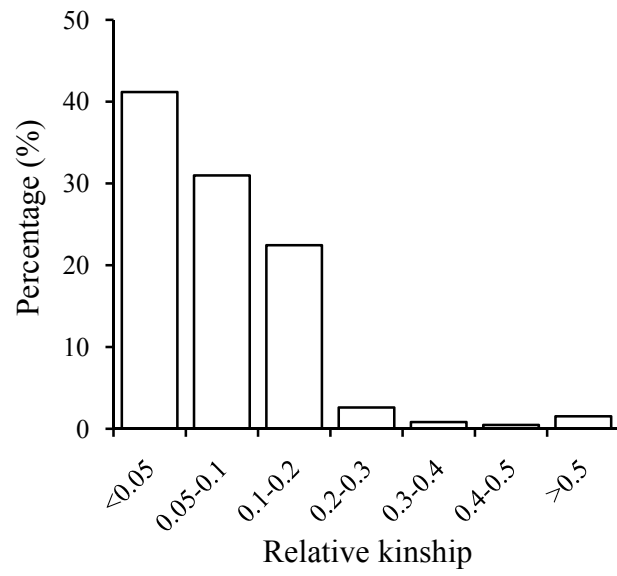


Fig. S4 The distribution pattern of pairwise relative kinship between the 190 accessions

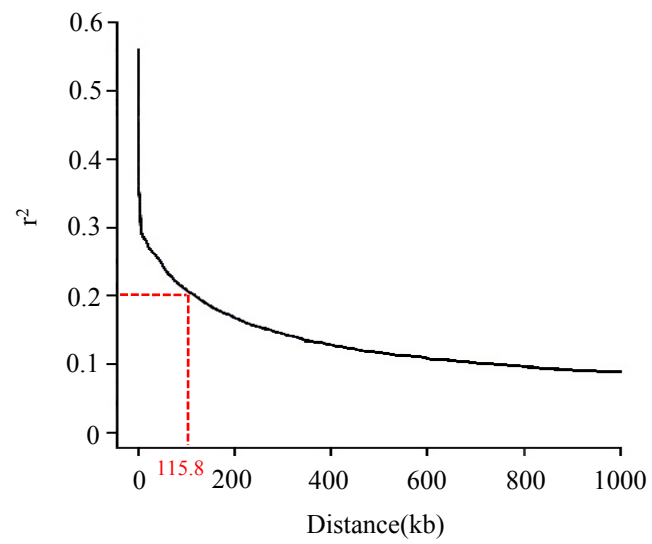


Fig. S5 Genome-wide average distance of LD decayed to $r^2 = 0.2$ for 190 diverse accessions

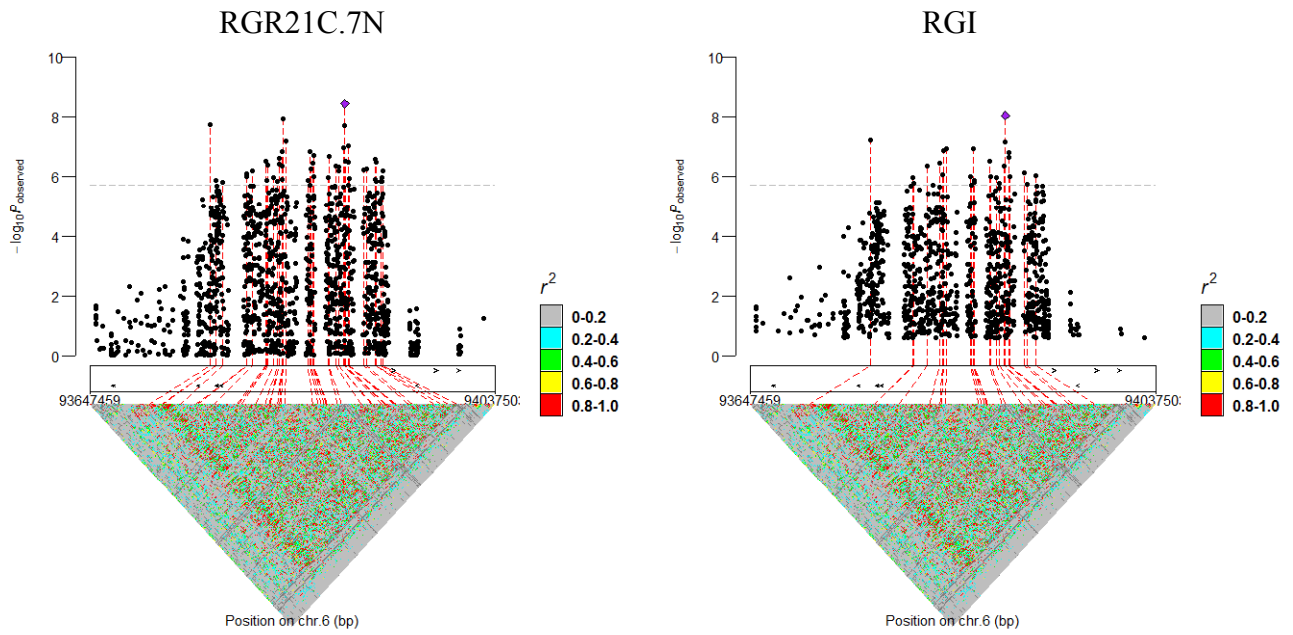


Fig. S6 Regional association plot of the major QTL including the top SNP as well as SNPs within LD decay distance.

The 115.8Kb genomic region on either side of significant SNPs are shown. The top SNP is represented as a diamond. The inverted triangle show the matrix of each pairwise LD. All r^2 values are colored according to the color scale. The vertical axis is the observed $-\log_{10}P$. The gray dotted line indicates the threshold ($-\log_{10}P = 5.72$)

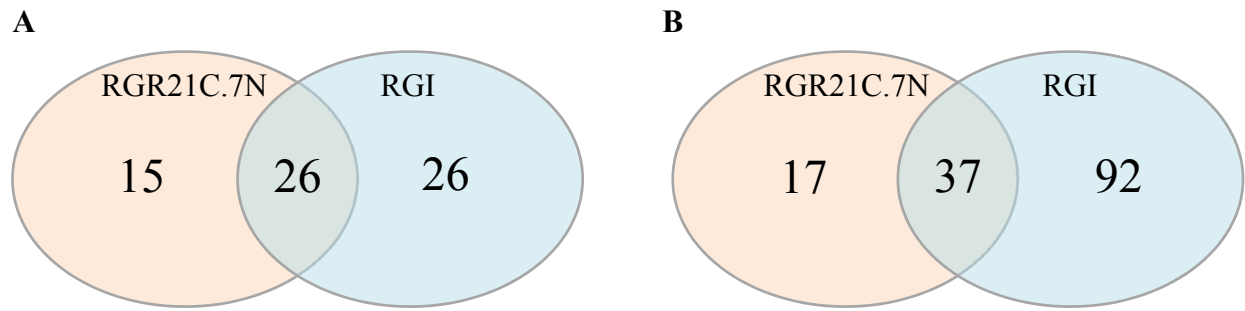


Fig. S7 Venn diagrams.

Number distribution patterns of significant SNPs (A) and associated candidate genes (B) in RGR21C.7N and RGI

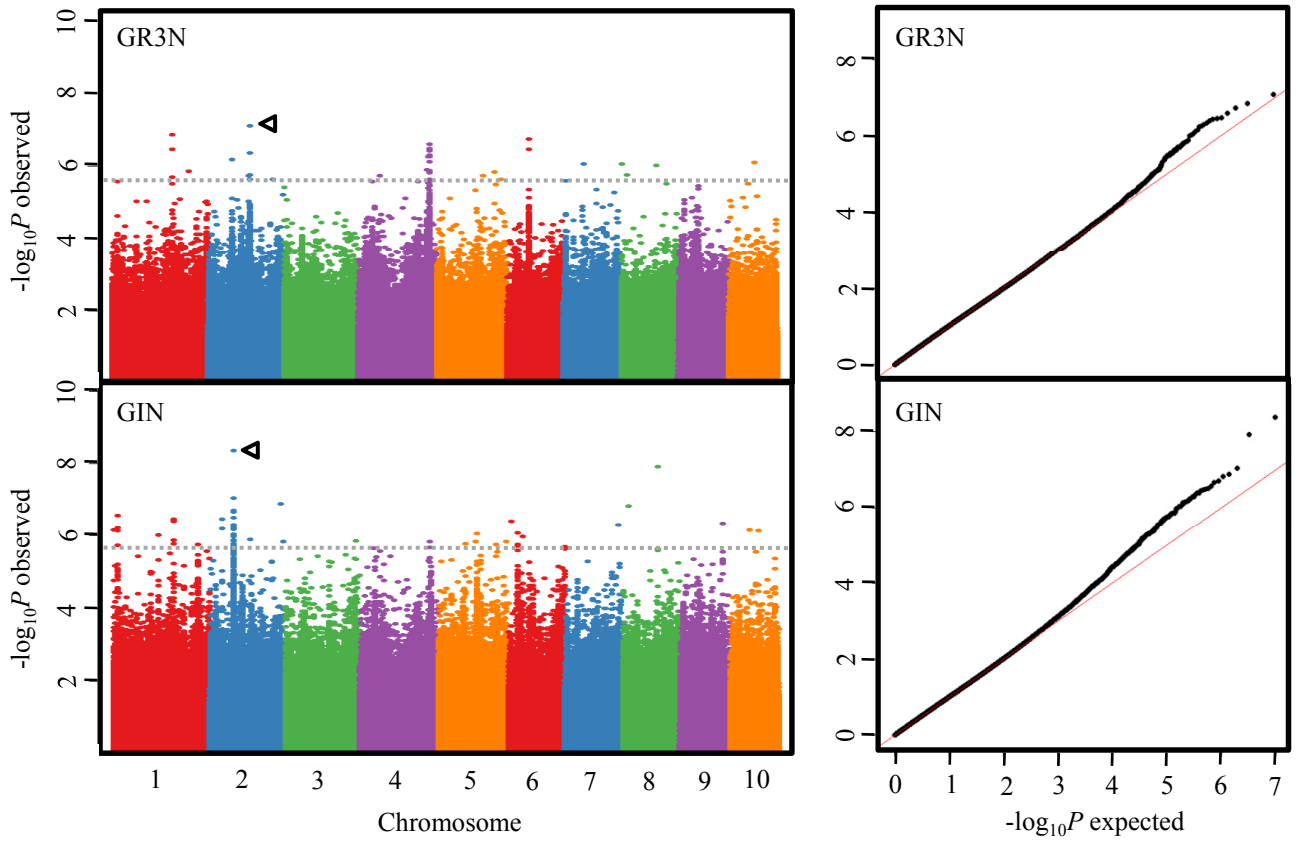


Fig. S8 Manhattan and Q-Q plots of GWAS results for two indices related to germination under normal condition

GWAS was performed on the GR3N and GIN which are two indices related to germination at 25°C. The left panels show the signals of associations across 10 chromosomes for GR3N (upper panel) and GIN (lower panel). The horizontal axis shows the 10 chromosomes. The right panels show the overlaps and exceeded associations between the observed signals (black dots) and the expected signals (red lines) for GR3N (upper) and GIN (lower). The horizontal axis is the expected $-\log_{10}P$. The vertical axes in the Manhattan and Q-Q plots are the observed $-\log_{10}P$. The black triangles in the Manhattan shows the top SNPs in GR3N and GIN. The gray dotted lines in the Manhattan indicates the threshold ($-\log_{10}P = 5.72$)

Table S1 Pedigree and Q matrix of the 190 diverse accessions

Name	Pedigree	Proportion for each cluster (k = 3)			Subpopulation
		SS	NSS	TST	
P12	Selected from American hybrid	0.199199	0.416222	0.384579	Mixed
Huang85B		0.149143	0.311945	0.538912	Mixed
Ji856	Huangzaosi×Zi330F2	0.024519	0.679506	0.295975	NSS
Jing4380		0.370809	0.173139	0.456052	Mixed
Liao613	Liao68×Dan340	0.185614	0.381362	0.433024	Mixed
Tai113-1	(Mexico02× Temperate	0.215551	0.368389	0.416061	Mixed
Zao709		0.145657	0.309154	0.545189	Mixed
Qi410		0.375407	0.068642	0.555951	Mixed
Qi406		0.225197	0.098055	0.676748	TST
236		0.102758	0.380176	0.517066	Mixed
H18	Synthetic	0.518982	0.132979	0.348039	Mixed
CL1451	American hybrid dicyclic line	0.293847	0.123069	0.583084	Mixed
Ames 10261		0.18688	0.24087	0.57225	Mixed
PI539921	ND246×Early Mo17 Composite	0.171441	0.372046	0.456513	Mixed
PB80	1067-1×B73 × B73Ht.1 BC6	0.999979	0.00001	0.000011	SS
PHG83	PH814×PH207	0.047709	0.952281	0.00001	NSS
792	235×B73	0.93429	0.0657	0.00001	SS
PHT55	A33GB4×A34CB4	0.809746	0.190244	0.00001	SS
LH132	(H93×B73)×B73	0.99998	0.00001	0.00001	SS
PHT77	PH814×PH995	0.078038	0.760536	0.161426	NSS
LH39	Oh43×L120	0.003097	0.996893	0.00001	NSS
LH1	(B37×Holden line 644)×B37	0.406552	0.554387	0.039061	Mixed
LH150	Certificate	0.204871	0.317685	0.477444	Mixed
ML606	Certificate	0.067961	0.789104	0.142935	NSS
LH38	L120×A619	0.000254	0.999736	0.00001	NSS
PHG47	PH041×MKSDTE	0.111676	0.667266	0.221058	NSS
Q381	Pioneer Hyb 3369	0.00001	0.99998	0.00001	NSS
DJ7	B73×BS16 Synthetic	0.99998	0.00001	0.00001	SS
LH74	A632×B73	0.99998	0.00001	0.00001	SS
PHW65	PH861×PH595	0.122342	0.648744	0.228913	NSS
Zhong106	Derived from Yemen tropical germplasm	0.082752	0.380129	0.537119	Mixed
Fu80	Lv9×Youfu	0.14911	0.391869	0.459021	Mixed
Zhi100		0.139265	0.202917	0.657818	TST
Zhi25		0.120138	0.306254	0.573607	Mixed
D9046	Shen5003×Tie7922	0.598071	0.118871	0.283058	Mixed
Su80-1	Jinhuang55×	0.049306	0.183422	0.767272	TST

B09	Y82	0.520148	0.435814	0.044038	Mixed
LH146HT	(B73×CM105)×	0.938828	0.061162	0.00001	SS
LH93	BS11(FR)C3	0.119643	0.438601	0.441756	Mixed
HPHR47		0.432804	0.424623	0.142573	Mixed
OQ603	PH3713	0.126693	0.873297	0.00001	NSS
11430	A	0.00001	0.99998	0.00001	NSS
PHW52	composite(including (B73×G39)×	0.99998	0.00001	0.00001	SS
MBPM	400M(A broad base composite)	0.171203	0.456785	0.372012	Mixed
MBST	LH38×4726-1	0.00001	0.89508	0.10491	NSS
S8324	(CH593-9×B73)S2 × B73	0.99998	0.00001	0.00001	SS
PHT60	PHW94 × PHV80 specifically PHW94× PHV80)2111	0.006959	0.708308	0.284733	NSS
PHW79	(PHT90×PH595)× 211XX	0.346911	0.52065	0.132439	Mixed
PHN47	(207×PHB60)×	0.164646	0.64135	0.194004	NSS
787	VA17×VA29	0.280598	0.409457	0.309945	Mixed
6M502	MAWU.4913	0.145047	0.491752	0.363202	Mixed
IBB14	Pioneer 3901 hybrid× H99	0.251737	0.748253	0.00001	NSS
L139	Pioneer 3901 hybrid× Pioneer 3780 hybrid	0.00001	0.99998	0.00001	NSS
PHK29	(B47×AC54)× NX711233X	0.456971	0.543019	0.00001	Mixed
PHN29	(G69×G40)×A6211	0.106071	0.774733	0.119196	NSS
W8555	B73Ht×B84	0.112527	0.605457	0.282016	NSS
D047	Landrace	0.00001	0.00001	0.99998	TST
BNP44	The former Soviet	0.180725	0.363703	0.455572	Mixed
Zhong71		0.279634	0.570106	0.15026	Mixed
RS710		0.393509	0.320934	0.285557	Mixed
PHP02	PHG44/PHG29)× 1211X	0.00001	0.99998	0.00001	NSS
LH123HT	Pioneer Hyb3535	0.132512	0.763061	0.104427	NSS
PHG39	PHA33GB4× PHA34CB4	0.888992	0.110998	0.00001	SS
KW4M029		0.99998	0.00001	0.00001	SS
Ye478	U8112×Shen5003	0.612234	0.092846	0.29492	SS
PI 406119		0.095478	0.280541	0.623981	TST
SK516		0.776833	0.00001	0.223157	SS
SK1098		0.025793	0.746784	0.227423	NSS
Jing27	(Lancaster×JN15)	0.084003	0.861712	0.054285	NSS
KWS49		0.147061	0.203341	0.649598	TST
Lv28	LvDaHongGu	0.147066	0.353287	0.499647	Mixed

764		0.99998	0.00001	0.00001	SS
KW5G321	German variety, bulletin no. M9123	0.00001	0.99998	0.00001	NSS
6F576		0.302915	0.524265	0.17282	Mixed
JG06		0.117086	0.882904	0.00001	NSS
Gan41		0.189934	0.359485	0.450581	Mixed
Ai68		0.134875	0.236318	0.628808	TST
Baihuanghun	Baijiushu(Suburban Beijing farm variety)	0.124369	0.387584	0.488047	Mixed
Yeduobai		0.329253	0.122521	0.548226	Mixed
Tongxi85-2		0.02581	0.00001	0.97418	TST
Hengte		0.00001	0.00001	0.99998	TST
Ji58		0.163943	0.331943	0.504115	Mixed
PHK76	PHAD18×PHB02	0.111867	0.608567	0.279566	NSS
NS501	Certificate	0.555841	0.317766	0.126394	Mixed
BA	Bijianba×A240	0.719524	0.056445	0.224031	SS
Zhi29		0.301408	0.359164	0.339428	Mixed
F101M		0.442714	0.091896	0.46539	Mixed
PHG72	PH369×PH207	0.154823	0.845167	0.00001	NSS
2369	(2702H×B73)×B73	0.99998	0.00001	0.00001	SS
4N506	B73×Iowa Stiff Stalk Synthetic	0.958731	0.041259	0.00001	SS
L135	P3901×W117	0.00001	0.99998	0.00001	NSS
PHW43	(995×G35)×33311X	0.091111	0.864943	0.043945	NSS
W182BN	(WD×W22) Outcross	0.295418	0.330784	0.373798	Mixed
H130024		0.128183	0.871807	0.00001	NSS
F399		0.516936	0.278713	0.204351	Mixed
F518		0.34452	0.390403	0.265077	Mixed
PHN82	(PHG29×HD38)× 5333X	0.00001	0.99998	0.00001	NSS
449	Tuxpenol P. B.	0.052709	0.009326	0.937965	TST
PHG29	PH207×(PH207× PH806)	0.328391	0.533608	0.138001	Mixed
K14	Shen5005×6917	0.247898	0.180853	0.571248	Mixed
740	Mo17×Mexican Deep Kernel	0.31278	0.467509	0.219711	Mixed
P9-10		0.160701	0.279639	0.55966	Mixed
G433		0.165363	0.277021	0.557616	Mixed
Zhong128	2118×Zhongzi7490	0.103976	0.18904	0.706984	TST
PH4CV	PH7V0×PHBE2	0.00001	0.877837	0.122153	NSS
B73	BSSS	0.99998	0.00001	0.00001	SS
M5972	((Dan598×Chang7-2) ×Chang7-2)8	0.056627	0.310945	0.632427	TST
Shuang741	(Aijin525×Weier44) ×(Huangzao4×	0.00001	0.273514	0.726476	TST
Jing02	Synthetic	0.00001	0.397508	0.602482	TST

Jing404	(Huangzao4× Tuxepeno-2)×	0.00001	0.00001	0.99998	TST
Q126	Huangzaosi4×	0.146282	0.212201	0.641516	TST
Huangzaosi	Derived from Tangsipingtou	0.00001	0.00001	0.99998	TST
P178	American Hybrid P78599	0.177883	0.327136	0.494981	Mixed
Ben7884-7	78-6×H84 ^{HT} /78-6	0.271126	0.227137	0.501736	Mixed
Ye52106	(Ye1075×Ye106)× AiJin525	0.242074	0.261362	0.496564	Mixed
Zhong134		0.276379	0.238529	0.485092	Mixed
A801	Dan9042×(Dan9046 ×Mohuang9)	0.559518	0.05262	0.387862	Mixed
U8112	American Hybrid	0.874841	0.00001	0.125149	SS
Duo25		0.099531	0.168837	0.731632	TST
Ji35	Huangzao4×	0.202727	0.089797	0.707476	TST
428	414×330	0.102404	0.25471	0.642886	TST
9902	Waxy maize	0.00001	0.084447	0.915543	TST
Jing594	Huangzao4×P78599	0.00001	0.102182	0.897808	TST
Zhe391		0.00001	0.269602	0.730388	TST
9503	Zao9503	0.00001	0.392634	0.607356	TST
Zhong85		0.065957	0.098851	0.835192	TST
C50change		0.134812	0.366167	0.49902	Mixed
PHG42	Synthetic	0.00001	0.99998	0.00001	NSS
CIMBL117	(OBATANPA- SRc1F3(balbulk1)- #bal/[BETASYN]BC 1-65-2-1-BB)-B (P84c3Bc×Line recycle LL TpreAsia ×MIRT F59-2-1-1-1- (P84c3Bc× LLTtardAsia× MIRTF41-2-1-2-2- (TZI18-BBBB)-B (ZM305/[BETASYN]BC1-29-1-1-B)-B ((CML161xCML413)-B×(CML172 × CML451)-B-B-25-1- 1-3-2-B)-B (DTPYC9-F65-2-3- 1-1-BBBBB)-B (Florida A plus Syn- FS2-2-1-BB)-B	0.045979	0.00001	0.954011	TST
CIMBL124		0.00001	0.00001	0.99998	TST
CIMBL125		0.131345	0.00001	0.868645	TST
CIMBL154		0.00001	0.298084	0.701906	TST
CIMBL155		0.055029	0.116911	0.82806	TST
CIMBL20		0.00001	0.00001	0.99998	TST
CIMBL93		0.023135	0.106938	0.869927	TST
CIMBL95		0.055452	0.273269	0.671279	TST

CIMBL97	(KUI carotenoid syn- FS17-3-1-BBB)-B	0.00001	0.00001	0.99998	TST
CML114	P45C2F-B-88-###1- 1-2-BB	0.093326	0.104292	0.802382	TST
CML122	(MP704/MP78:518)- 8-3-4-B1-4-2-3-B1- B1#B1	0.00001	0.00001	0.99998	TST
CML130	P33C1F118-5-1-4-5- 4-B1-B1#B1	0.067033	0.050757	0.88221	TST
CML134	P45C2F151-1-2-5-3- 1-2-4-B1-B1#B1	0.031901	0.161462	0.806637	TST
CML172	G25QS4B-H35-2-B- 1-1-2-B-4-BBBB	0.00001	0.00001	0.99998	TST
CML226	EV88SUWAN1SR(BC5)-78-1-1-BB	0.00001	0.00001	0.99998	TST
CML282	(G22F128/G22F25)- 2-2-3-1-BB-F	0.017302	0.00001	0.982688	TST
CML287	(P24F26/27F1)-4-1- B-1-1-BB-F	0.000019	0.00001	0.999971	TST
CML29	P27F71-3-1-B-#×5-B	0.007668	0.00001	0.992322	TST
CML290	(P28/TSR)-33-3-7-3- 1-BB-F	0.006674	0.00001	0.993316	TST
CML307	SINTAMTSR-61-3- 2-8-2-BB-F	0.001625	0.00001	0.998365	TST
CML31	P27F117-1-4-B-####	0.024407	0.00001	0.975583	TST
CML40	P36C5F144-2-2-B-	0.047609	0.00001	0.952381	TST
CML430	AMATLCOHS169-1- 1-1-1-2-2-1-B×3	0.00001	0.036398	0.963592	TST
CML451	[NPH28- 1/G25)/NPH28]-1-2- 1-1-3-1-B×6	0.037459	0.00001	0.962531	TST
CIMBL102	(LAMA2002-53-5- B)-B	0.133838	0.00001	0.866152	TST
PHW03		0.303762	0.331793	0.364445	Mixed
E220		0.362127	0.470585	0.167288	Mixed
P167		0.106368	0.399252	0.49438	Mixed
H620		0.119203	0.322047	0.55875	Mixed
CIMBL119	(P390Am/CMLc4F2 53-B-2-2-4-1-BB)-B	0.00001	0.00001	0.99998	TST
CML121	(PI218191/PI209135/ /PI226685/P1317328 /3/P47/MPSWCB4) 6-3-1-5-1-B1- B1#B1(MP704/MP7 8:518)-8-3-4-B1-4-2- 3-B1-B1-#B1	0.00001	0.00001	0.99998	TST

CML170	G26QC22H9-3-1-5-1-BB	0.00001	0.00001	0.99998	TST
CML28	P27F35-8-3-B-####-	0.00001	0.00001	0.99998	TST
CML285	P24C5F34-2-3-B-F-2#-BBB-F	0.00001	0.00001	0.99998	TST
CML304	SINTAMTSR-76-1-2-3-2-BB-F	0.00001	0.00001	0.99998	TST
CML360	SA4C2F(21/26)-1-2-2-2-B	0.00001	0.00001	0.99998	TST
CML470	P31C4S5B-39-##-1-BB	0.032522	0.05653	0.910948	TST
BD132891	Selected from American hybrid	0.103103	0.357258	0.53964	Mixed
BD132626	696F×JN15	0.00001	0.99998	0.00001	NSS
H5	Selection from Minnesota 22-35	0.761902	0.00001	0.238088	SS
D1798Z		0.757241	0.00001	0.242749	SS
CML171	G25QS4B-H13-5-B-1-1-2-B-1-BBB	0.000014	0.00001	0.999976	TST
CML118	SIYFS3#B1-7-B1-B1#B1	0.00001	0.138301	0.861689	TST
CML361	SA4C2F(21/26)-4-2-7-3-B	0.032281	0.00001	0.967709	TST
CML480	SINTAMTSRC2-88-2-2-B×8	0.00001	0.00001	0.99998	TST
H102	Mb 19-3(selection of PI 209135)/C123	0.099061	0.271493	0.629446	TST
F254		0.221585	0.135454	0.642961	TST
BD132675	696F×JN15	0.00001	0.99998	0.00001	NSS
LH88		0.180445	0.430923	0.388632	Mixed
Qianjin		0.428763	0.191355	0.379882	Mixed
Mei801		0.568118	0.385609	0.046273	Mixed
H130050		0.00001	0.99998	0.00001	NSS
CIMBL12	(((CML150×CML451)-B-33-3-1-BB×(CML176×CL-G2501)-B-43-1)-B-38-1-2-2-1-B)-B	0.020254	0.00001	0.979736	TST
B47	(A392×R61) -1-9 -1-1 -1-1[NURSERYROW138 5IN1956]	0.546802	0.316602	0.136595	Mixed
LH82-1change		0.144898	0.660978	0.194124	NSS
LP5	(Yugoslavian GLAMOS×B73Ht)×	0.502577	0.497413	0.00001	Mixed
MC0303	(9042×Jing89)×9046	0.561663	0.055202	0.383135	Mixed

PH3901		0.00001	0.99998	0.00001	NSS
Ji818	(VT157×Ji63)×Ji63 BC4	0.353685	0.26027	0.386045	Mixed
CIMBL17	((CML 326/B104)-B- 9-BBBB)-B	0.259281	0.159229	0.581491	Mixed
Cheng18	Dingshangyumi× (Gong70×60-22)	0.189801	0.353893	0.456306	Mixed
Tian77	(HuangXiao162× Mei1865)×(187-2× Nan55)	0.080179	0.101981	0.81784	TST

Table S2 Position, MAF and *P* values of significant SNPs in either RGR21C.7N or RGI

No.	SNPs	Chromosome	Position	MAF	<i>P</i> value in	
					RGR21C.7N	RGI
1	chr6__8888470	6	8888470	0.154	1.35E-06	
2	chr6__8888597	6	8888597	0.169	9.87E-07	
3	chr6__8888809	6	8888809	0.157	1.18E-06	
4	chr6__8889059	6	8889059	0.151	6.67E-07	
5	chr9__106322769	9	106322769	0.253	1.06E-06	
6	chr9__106324774	9	106324774	0.235	1.19E-06	
7	chr9__106329326	9	106329326	0.224	6.24E-07	
8	chr9__106330804	9	106330804	0.221	1.15E-06	
9	chr9__106330935	9	106330935	0.201	5.83E-07	
10	chr9__106330948	9	106330948	0.206	1.54E-07	
11	chr9__106332803	9	106332803	0.189	1.60E-06	
12	chr9__106344188	9	106344188	0.235	2.80E-07	
13	chr9__106346584	9	106346584	0.198	1.18E-06	
14	chr9__106371229	9	106371229	0.215	1.76E-06	
15	chr9__144509417	9	144509417	0.166	2.63E-07	
16	chr1__68972106	1	68972106	0.281		1.80E-06
17	chr1__211878734	1	211878734	0.281		6.75E-07
18	chr1__211878742	1	211878742	0.278		1.30E-06
19	chr1__266090186	1	266090186	0.164		9.29E-07
20	chr2__221293214	2	221293214	0.258		4.41E-07
21	chr3__4001194	3	4001194	0.131		1.62E-06
22	chr3__176092112	3	176092112	0.311		1.60E-06
23	chr3__176092127	3	176092127	0.308		8.03E-07
24	chr3__176093045	3	176093045	0.300		4.77E-07
25	chr3__176095024	3	176095024	0.317		1.90E-06
26	chr3__176126864	3	176126864	0.186		1.15E-06
27	chr3__218788587	3	218788587	0.122		1.88E-06
28	chr4__195995305	4	195995305	0.289		1.71E-07
29	chr4__195995340	4	195995340	0.269		1.08E-06
30	chr4__195998946	4	195998946	0.267		1.37E-06
31	chr4__196018776	4	196018776	0.311		1.40E-06
32	chr4__196021971	4	196021971	0.314		7.13E-07
33	chr4__196049310	4	196049310	0.289		4.57E-07
34	chr5__129881563	5	129881563	0.103		8.40E-08
35	chr6__12389446	6	12389446	0.147		3.57E-07
36	chr6__44464136	6	44464136	0.147		2.46E-07
37	chr6__76002567	6	76002567	0.081		1.03E-06
38	chr6__169747642	6	169747642	0.350		3.62E-07
39	chr9__22300499	9	22300499	0.408		1.17E-06
40	chr9__27134483	9	27134483	0.175		1.42E-07

41	chr9__109951672	9	109951672	0.100	1.59E-06
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Table S3 Candidate genes were identified within LD decay regions of 41 significant SNPs associated with RGR21C.7N or RGI

No.	Trait	Significant SNPs	Associated Gene	Annotation	Orthologs		Orthologs annotation	Homologs function		
					Arabis dopsis	Rice		Related to cold stress	Related to germination	Related to other stress
1	RG	chr6__8	Zm00001eb260710	Fructokinase 2	AT4G10260		Encodes a member			
	R21 C.7 N	888470 chr6__8				Os08g0113	Fructokinase,			
2	RG	chr6__8	Zm00001eb260720	EMBRYO DEFECTIVE	AT4G24270		A locus involved			
	R21 C.7 N	888470 chr6__8				Os08g0113	RNA-processing			
3	RG	chr6__8	Zm00001eb260730	Uncharacterized LOC10	AT3G07370		Encodes AtCHIP, a	[12] [41]		
	R21 C.7 N	888470 chr6__8				Os08g0113	Similar to STIP1	[74]	[12]	[11] [74]
4	RG	chr6__8	Zm00001eb260740	None	AT3G05390		S-adenosyl-			
	R21 C.7 N	888470 chr6__8				Os08g0113	Methyltransferase			
5	RG	chr6__8	Zm00001eb260750	Cytochrome P450 89A9	AT3G03470		P450 monooxygenase			
	R21 C.7 N	888470 chr6__8				Os10g0515	Cytochrome P450	[16]		[16]
6	RG	chr6__8	Zm00001eb260760	Probable acyl-activating	AT1G20560		Acyl activating			
	R21 C.7 N	888470 chr6__8				Os01g0342	Similar to Adenosine			
7	RG	chr9__1	Zm00001eb3882	Uncharacterized		Os04g0624	Polyphenol oxidase,	[87]	[49]	[75]
	R21 C.7 N	0632276 chr9__1								
8	RG	chr9__1	Zm00001eb388260	Uncharacterized LOC10	AT3G57880		Required for			
	R21 C.7 N	0632276 chr9__1				Os05g0370	A member of the			
9	RG	chr9__1	Zm00001eb388270	Uncharacterized	AT5G06839		BZIP transcript			
	R21 C.7 N	0632276 chr9__1				Os06g0614	A member of the	[39]	[23]	[23] [39]
10	RG	chr9__1	Zm00001eb3971	Putative RNA-						
	R21 C.7 N	4450941 chr9__1								
11	RG	chr9__1	Zm00001eb3971	Organic anion	AT3G11320		Nucleotide-sugar			
	R21 C.7 N	4450941 chr9__1								

11	C.7 N	4450941 7	1eb3971 50	transpo rter		Os03 g0286	Similar to Phosphate				
12	RG R21	chr9__1 4450941	Zm0000 1eb3971	None		Os05 g0121	Hypotheti cal gene				
13	RG R21 C.7 N	chr9__1 4450941 7	Zm0000 1eb3971 70	Unchar acterize d LOC10	AT3G 07630	Os03 g0286	Encodes a plastid- Similar to Prephenat	[22]			
14	RG R21 C.7 N	chr9__1 4450941 7	Zm0000 1eb3971 80	L- ascorba te peroxid	AT1G 07890	Os03 g0285	Encodes a cytosolic Cytosolic ascorbate	[84]	[48]	[30] [40] [48][84]	
15	RG R21 C.7 N	chr9__1 4450941 7	Zm0000 1eb3971 90	Unchar acterize d LOC10	AT3G 45640	Os03 g0285	Encodes a mitogen- MAP Kinase	[66] [69]	[7] [10]	[62] [67] [69]	
16	RG R21 C.7 N	chr9__1 4450941 7	Zm0000 1eb3972 00	Pentatri copepti de repeat-	AT5G 02830	Os03 g0284	Tetratrico peptide Annexin repeat,			[53]	
17	RG R21 C.7 N	chr9__1 4450941 7	Zm0000 1eb3972 20	None	AT3G 45740	Os03 g0284	Hydrolase family HAD- superfamil				
18	RGI	chr1__6 8972106	Zm0000 1eb0192 00	None	AT1G 74040	Os11 g0142	Encodes an active Isopropyl malate	[21]			
19	RGI	chr1__6 8972106	Zm0000 1eb0192 10	Acetyl- CoA acetyltr ansfera	AT5G 48230	Os09 g0252	Encodes an Similar to Acetyl-			[57]	
20	RGI	chr1__6 8972106	Zm0000 1eb0192 20	P-loop containi ng nucleos	AT2G 15730	Os03 g0394	P-loop containing Similar to nodulation	[17] [19]	[8] [59]	[17]	
21	RGI	chr1__6 8972106	Zm0000 1eb0192 30	60S riboso mal protein	AT3G 16080	Os02 g0111	Zinc- binding Similar to 60S	[5]		[47]	
22	RGI	chr1__6 8972106	Zm0000 1eb0192 40	Putativ e protein phosph	AT1G 47380	Os03 g0395	Protein phosphata Protein phosphata	[29]			

23	RGI	chr1__6 8972106	Zm0000 1eb0192 50	Unchar acterize d LOC10	AT2G 26570	Encodes a coiled-coil Protein of unknown			
					Os03 g0395				
24	RGI	chr1__2 1187873 4、 chr1__2	Zm0000 1eb0401 40	Unchar acterize d LOC10	AT2G 17880	Chaperon e DnaJ- Similar to chaperone			[6] [77]
					Os08 g0548				
25	RGI	chr1__2 1187873 4、 chr1__2	Zm0000 1eb0401 50	ER lumen protein- retainin	AT4G 38790	ER lumen protein- Similar to ER lumen			
					Os08 g0548				
26	RGI	chr1__2 1187873 4、 chr1__2	Zm0000 1eb0401 60	Unchar acterize d LOC10	AT4G 22680	Encodes a transcripti Myb	[1]	[54]	[50]
					Os09 g0532				
27	RGI	chr1__2 1187873 4、 chr1__2	Zm0000 1eb0401 80	Geranio l 8- hydrox ylase-	AT4G 12320	CYP706A 6, Similar to Flavonoid			
					Os01 g0700		[16]		[16]
28	RGI	chr1__2 1187873 4、 chr1__2	Zm0000 1eb0401 90	Putativ e carboxy lesteras	AT2G 45600	Alpha/bet a- Alpha/bet a			
					Os08 g0547				
29	RGI	chr1__2 6609018 6	Zm0000 1eb0528 40	None	AT1G 11090	Alpha/bet a- Alpha/bet a			
					Os07 g0565				
30	RGI	chr1__2 6609018 6	Zm0000 1eb0528 50	Unchar acterize d LOC10	AT1G 28760	Encodes an orthlog Domain of unknown			
					Os03 g0654				
31	RGI	chr1__2 6609018 6	Zm0000 1eb0528 60	Cationi c amino acid transpo	AT1G 58030	Encodes a member Similar to Cationic			
					Os03 g0654				
32	RGI	chr2__2 2129321 4	Zm0000 1eb1105 60	Unchar acterize d LOC10	AT1G 10390	DRA2 is a homolog Hypotheti cal			
					Os12 g0165				
33	RGI	chr2__2 2129321	Zm0000 1eb1105	None					
34	RGI	chr2__2 2129321	Zm0000 1eb1105	Unchar acterize	AT3G 07950	Rhomboid protein-			

34	RGI	chr2__2	Zm00000	BTB/P	AT5G	Os07	Protein of			
		4	1eb1105	LOC10		g0655	unknown			
				OZ and	19000		Encodes a			
35	RGI	chr2__2	Zm00000	MATH		Os07	Kelch			[4] [56]
		4	1eb1105	domain		g0655	related			
				Unchar	AT5G		Member			
36	RGI	chr2__2	Zm00000	acterize	58740		of the			
		4	1eb1106	d		Os01	CS			
				LOC10		g0668	domain			
				Unchar	AT5G		Plasma-			
37	RGI	chr2__2	Zm00000	acterize	13760		membrane			
		4	1eb1106	d		Os07	Similar to			
				LOC10		g0656	predicted			
38	RGI	chr3__4	Zm00000	Unchar						
		001194	1eb1201	acterize						
					AT4G		Encodes			
39	RGI	chr3__4	Zm00000	None	18270		protein			
		001194	1eb1201			Os01	Conserved			
			80			g0210	hypothetic			
				Potassi	AT5G		Encodes a			
40	RGI	chr3__4	Zm00000	um	46240		potassium			
		001194	1eb1201	channel		Os01	Inward	[83]	[65]	[83]
			90	4		g0210	rectifying			
				Unchar	AT1G		Encodes a			
41	RGI	chr3__4	Zm00000	acterize	17100		cytosolic			
		001194	1eb1202	d		Os01	Similar to			
			00	LOC10		g0210	SOUL-			
				Transm	AT5G		Encodes a			
42	RGI	chr3__4	Zm00000	embran	46220		protein			
		001194	1eb1202	e		Os01	Ortholog			
			20	protein		g0210	of			
				Unchar		Os01	Conserved			
43	RGI	chr3__4	Zm00000	acterize		g0210	hypothetic			
		001194	1eb1202							
				Cationi	AT2G		Encodes a			
44	RGI	chr3__4	Zm00000	c amino	34960		member			
		001194	1eb1202	acid		Os01	Similar to			
			40	transpo		g0209	Cationic			
				Gibbere	AT1G		Encodes a			
45	RGI	chr3__4	Zm00000	llin 2-	78440		gibberelli			
		001194	1eb1202	beta-		Os01	Similar to	[34]		[43]
			50	dioxyge		g0209	GA 2-			
					AT5G		Hypotheti			
46	RGI	chr3__1	Zm00000	Filaggri	35090		cal protein			
		7609211	1eb11456							

46	RGI	2、 chr3__1	1eb1450 50	n-2		Os10	Hypotheti g0331 cal			
47	RGI	2、 chr3__1	Zm0000 1eb1456 60	MADS 16	AT5G 20240		Floral homeotic Rice PISTILLA	[15]	[15]	[35]
48	RGI	2、 chr3__1	Zm0000 1eb1456 70	Amino acid permea se 2	AT1G 77380		Amino acid Amino acid			
49	RGI	2、 chr3__1	Zm0000 1eb1456 80	Unchar acterize d	AT5G 58260		Encodes subunit Similar to NADH			
50	RGI	2、 chr3__1	Zm0000 1eb1456 90	Unchar acterize d	AT1G 71900		Magnesi um			
51	RGI	chr3__1	Zm0000 1eb1457	None		Os01	Protein of g0882 unknown			
52	RGI	2、 chr3__1	Zm0000 1eb1457 10	None	AT2G 02220		Leucine- rich repeat	[76]	[51]	[85]
53	RGI	chr3__2	Zm0000 1878858 7	Zinc finger CCCH domain	AT5G 53440		Encodes a protein Leucine- rich repeat LOW protein: Conserved hypothetic	[76]	[51]	[85]
54	RGI	chr3__2	Zm0000 1878858 7	None	AT4G 27910		Encodes a SET TRITHOR AX-like	[76]	[51]	[85]
55	RGI	chr3__2	Zm0000 1878858 7	Seed maturat ion protein	AT1G 65930		Encodes a NADP+- Similar to NADP-	[18] [73]	[14]	[14] [18] [73]
56	RGI	chr3__2	Zm0000 1878858 1eb1580	None		Os01	g0655	[33]		[52]
57	RGI	chr4__1	Zm0000 9599534 1eb1973 70	Unchar acterize d	AT2G 36080		Encodes a plant- Similar to AP2	[72]	[81]	[36] [81]
58	RGI	chr4__1	Zm0000 9599530 1eb1973	Lysoso mal	AT2G 24280		Alpha/bet a-			

58	RGI	5, chr4__1	1eb1973 80	Pro-X carboxy		Os11	Peptidase g0156 S28			
		chr4__1	Zm0000		AT1G		RING/U- box			
59	RGI	9599534 0, chr4__1	1eb1973 90	None	55530	Os01	Similar to g0844 protein			
		chr4__1	Zm0000	Unchar	AT5G		One of			
60	RGI	9601877 6, chr4__1	1eb1974 00	acterize d	06270	Os12	Hypotheti cal			
		chr5__1	Zm0000	LOC10		Os03	Similar to			
61	RGI	2988156	1eb2367	None		g0608	10A19I15			
		chr6__4	Zm0000	Glutath	AT5G		Encodes			
62	RGI	4464136	1eb2666 70	ione S- transfer ase T1	41210	Os11	Similar to g0588 Glutathion			[9]
63	RGI	chr6__4 4464136	Zm0000 1eb2666	None						
		chr6__4	Zm0000	Protein	AT5G		Receptor- like			
64	RGI	4464136	1eb2666 90	kinase	48540	Os05	Protein of g0112 unknown			
		chr6__7	Zm0000	Phosdu	AT5G		Thioredox in			
65	RGI	6002567	1eb2698 70	cin-like protein 3	14240	Os01	Thioredox g0184 in fold	[45]	[2]	[26]
		chr6__7	Zm0000	Unchar	AT4G		Transmem brane			
66	RGI	6002567	1eb2698 80	acterize d	16180	Os03	CAP, g0310 conserved	[60]		
		chr6__1	Zm0000	LOC10						
67	RGI	2389446	1eb2613	None						
		chr6__1	Zm0000	Serine- rich	AT1G		Plant/prot ein			
68	RGI	2389446	1eb2614 00	adhesin for	03610	Os04	Similar to g0675 H0103C0			
		chr6__1	Zm0000	Transcr	AT1G		Encodes a member			
69	RGI	2389446	1eb2614 20	iption factor bHLH9	49770	Os04	Helix- g0429 loop-helix	[88]		[88]
		chr6__1	Zm0000	Cytosol	AT3G		Encodes			
70	RGI	2389446	1eb2614 30	ic glycerol dehyde-	04120	Os08	cytosolic Similar to g0126 Glycerald	[44]		[20] [44]

71	RGI	chr6__1 2389446	Zm0000 1eb2614 40	Unchar acterize d LOC10	AT5G 40780	Encodes LHT1 Os08 Amino g0127 acid			
72	RGI	chr6__1 6974764 2	Zm0000 1eb2925 30	Serine/t hreonin e- protein	AT4G 14350	AGC (cAMP- Similar to g0511 Protein			
73	RGI	chr6__1 6974764 2	Zm0000 1eb2925 40	Unchar acterize d LOC10	AT2G 32170	S- adenosyl- N2227- g0511 like			
74	RGI	chr6__1 6974764	Zm0000 1eb2925	None					
75	RGI	chr6__1 6974764 2	Zm0000 1eb2925 60	None	AT5G 09580	Heat shock Os11 Similar to g0167 predicted	[80]	[13]	[80]
76	RGI	chr6__1 6974764 2	Zm0000 1eb2925 80	None	AT3G 46450	SEC14 cytosolic Os03 Cellular g0820 retinaldeh			
77	RGI	chr6__1 6974764 2	Zm0000 1eb2925 90	Probabl e xyloglu can	AT4G 07960	Encodes a XyG Os05 Similar to g0510 Cellulose			
78	RGI	chr6__1 6974764	Zm0000 1eb2926	None		Os03 Hypotheti g0770 cal protein			
79	RGI	chr6__1 6974764 2	Zm0000 1eb2926 20	None	AT3G 01060	Lysine- tRNA Os05 Similar to g0512 T4P1326			
80	RGI	chr6__1 6974764 2	Zm0000 1eb2926 30	None	AT2G 13440	Glucose- inhibited Os01 Similar to g0960 Glucose-			
81	RGI	chr6__1 6974764	Zm0000 1eb2926	None					
82	RGI	chr6__1 6974764 2	Zm0000 1eb2926 50	None	AT1G 69320	Member of a large Os05 Similar to g0512 CLE	[42]		[42]
83	RGI	chr6__1 6974764	Zm0000 1eb2926	Unchar acterize	AT1G 26470	Chromatin modificati			

83	RGI	chr6__1	Zm00000	LOC10	Os05 CT20 g0512 family			
84	RGI	chr6__1	Zm00000	None				
85	RGI	chr6__1	Zm00000	GPI-anchore d protein	AT1G 18650 Os05 X8 g0512 domain			
86	RGI	chr6__1	Zm00000	Unchar acterize d	AT5G 60970 Os05 Similar to g0513 PLCYC4	[32]	[38]	[32]
87	RGI	chr9__2	Zm00000	Sulfate transpo				
88	RGI	chr9__2	Zm00000	Coatomer subunit beta'-1	AT1G 52360 Os06 Similar to g0143 Coatomer			
89	RGI	chr9__2	Zm00000	Unchar acterize d	AT1G 80420 Os06 Rice g0144 homologue			
90	RGI	chr9__2	Zm00000	Unchar acterize d	AT5G 37370 Os05 PRP38 g0178 family			
91	RGI	chr9__2	Zm00000	Unchar acterize d	AT5G 11380 Os06 Deoxyxyl g0142 ulose 5-	[70]		
92	RGI	chr9__2	Zm00000	None	AT5G 23310 Os06 Iron- g0143 superoxid			[68]
93	RGI	chr9__2	Zm00000	None				
94	RGI	chr9__2	Zm00000	LOC10 363907 7-like pseudo	AT3G 11490 Os11 Similar to g0153 Rac		[86]	
95	RGI	chr9__2	Zm00000	Unchar acterize d	AT1G 76940 Os06 Hypotheti g0127 cal			

96	RGI	chr9__2 7134483	Zm0000 1eb3786	None					
97	RGI	chr9__2 7134483	Zm0000 1eb3786	None					
98	RGI	chr9__2 7134483	Zm0000 1eb3786 30	Unchar acterize d LOC10	AT1G 58390	Disease resistance [24] [78] Os10 NB-ARC [79] g0183 domain			
99	RGI	chr9__2 7134483	Zm0000 1eb3786 40	Protein binding protein	AT5G 07220	A member of [64] [3] [3] Os06 Ubiquitin g0126 domain			
100	RGI	chr9__2 7134483	Zm0000 1eb3786	Unchar acterize		Os06 Conserved g0126 hypothetical			
101	RGI	chr9__2 7134483	Zm0000 1eb3786	Probabl e		Os06 ABC g0126 transporte	[63] [27] [46]		
102	RGI	chr9__2 7134483	Zm0000 1eb3786 80	Probabl e recepto r-like	AT2G 21480	BUSP2 plays a [71] [82] [82] Os06 Receptor- g0126 like			
103	RGI	chr9__2 7134483	Zm0000 1eb3786 90	Unchar acterize d LOC10	AT5G 62090	Encodes a protein [31] [55] Os06 Hypotheti g0126 cal			
104	RGI	chr9__2 7134483	Zm0000 1eb3787 00	Unchar acterize d LOC10	AT3G 63530	Encodes a novel E3 [12] [74] [12] [12] [74] Os06 RING g0125 finger			
105	RGI	chr9__2 7134483	Zm0000 1eb3787 10	Pentatri copepti de repeat-	AT5G 08510	Pentatrico peptide [25] [37] [25] [25] Os06 Hypotheti g0125 cal			
106	RGI	chr9__2 7134483	Zm0000 1eb3787 20	Oligope ptide transpo rter 9	AT4G 10770	Oligopepti de [58] Os06 Similar to g0125 Oligopepti			
107	RGI	chr9__2 7134483	Zm0000 1eb3787	None		Os03 Hypotheti g0751 cal protein			
108	RGI	chr9__1 0995167 2	Zm0000 1eb3888 20	Unchar acterize d LOC10	AT1G 07840	Sas10/Utp 3/C1D Os01 Sas10/Utp g0911 3/C1D			
109	RGI	chr9__1 0995167	Zm0000 1eb3888	Unchar acterize		Os01 Hypotheti g0909 cal			

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Table S4 KEGG analysis of maize candidate genes related to chilling-tolerant germination

No.	Gene	Annotation	KO	Description	Pathwa	Pathway name
1	Zm00001eb019210	Acetyl-CoA acetyltransferase, cytosolic 1	K00626	Acetyl-CoA C-acetyltransferase	01100 、 01110 、	Metabolic pathways、 Biosynthesis of secondary metabolites、 Microbial metabolism in
2	Zm00001eb019230	60S ribosomal protein L37-like	K02922	Large subunit ribosomal protein L37e	03010	Ribosome
3	Zm00001eb110560	Uncharacterized	K14297	Nuclear pore complex protein Nup98-Nup96	03013	Nucleocytoplasmic transport
4	Zm00001eb110590	BTB/POZ and MATH domain-containing	K10523	Speckle-type POZ protein	04340 、 04341	Hedgehog signaling pathway、 Hedgehog signaling pathway - fly
5	Zm00001eb120180	None	K01000	Phospho-N-acetylmuramoylpentapeptide-transferase	01100 、 00550	Metabolic pathways、 Peptidoglycan biosynthesis
6	Zm00001eb120250	Gibberellin 2-beta-dioxygenase 3	K04125	Gibberellin 2beta-dioxygenase	01110 、 00904	Biosynthesis of secondary metabolites、 Diterpenoid biosynthesis
7	Zm00001eb158070	Seed maturation protein PM41	K00031	Isocitrate dehydrogenase	01100 、 01110 、	Metabolic pathways、 Biosynthesis of secondary metabolites、 Microbial metabolism in
8	Zm00001eb197380	Lysosomal Pro-X carboxypeptidase	K01285	Lysosomal Pro-X carboxypeptidase	04614 、 04974	Renin-angiotensin system、 Protein digestion and absorption
9	Zm00001eb260710	Fructokinase 2	K00847	Fructokinase	01100 、 01110 、	Metabolic pathways、 Biosynthesis of secondary metabolites、 Biosynthesis of
10	Zm00001eb260730	Uncharacterized LOC100273449	K09561	STIP1 homology and U-box containing protein 1	04141 、 04120	Protein processing in endoplasmic reticulum 、 Ubiquitin mediated proteolysis

11	Zm00001eb2 61430	Cytosolic glyceroldehyd e-3-phosphate dehydrogenase Uncharacteriz	K00134	Glyceraldehyde 3- phosphate dehydrogenase (phosphorylating)	01100 、 01110 、	Metabolic pathways、 Biosynthesis of secondary metabolites、 Microbial metabolism in
12	Zm00001eb2 72400	ed LOC10027915 9 Uncharacteriz	K14488	SAUR family protein	04075	Plant hormone signal transduction
13	Zm00001eb2 92540	ed LOC10038155 1	K19787	Carnosine N- methyltransferase	01100 、 00340	Metabolic pathways、 Histidine metabolism
14	Zm00001eb3 63580	Tafazzin homolog	K13511	Monolysocardioli pin acyltransferase	01100 、 01110	Metabolic pathways、 Biosynthesis of secondary metabolites、
			K00655	1-acyl-sn- glycerol-3- phosphate acyltransferase	、 00564 、 00564	Glycerophospholipid metabolism、 Glycerophospholipid metabolism
15	Zm00001eb3 63610	Uncharacteriz ed LOC10019337 2	K10532	Heparan-alpha- glucosaminide N- acetyltransferase	01100 、 00531 、 01100	Metabolic pathways、 Glycosaminoglycan degradation、 Lysosome
16	Zm00001eb3 63620	None	K08081	Tropinone reductase I	、 01100 、 01100	Metabolic pathways、 Biosynthesis of secondary metabolites、 Tropane, piperidine and
17	Zm00001eb3 63730	Long chain base biosynthesis protein 2d	K00654	Serine palmitoyltransfera se	01100 、 00600 、 03010	Metabolic pathways、 Sphingolipid metabolism、 Sphingolipid signaling
18	Zm00001eb3 63770	Ribosomal protein eS6 pseudogene	K02991	Small subunit ribosomal protein S6e	、 04371 、	Ribosome、 Apelin signaling pathway、 HIF-1 signaling pathway 、 PI3K-Akt signaling
19	Zm00001eb3 63810	Uncharacteriz ed LOC10027350 1	K14486	Auxin response factor	04075	Plant hormone signal transduction
20	Zm00001eb3 77290	Uncharacteriz ed LOC10019119 8	K12850	pre-mRNA- splicing factor 38B	03040	Spliceosome

21	Zm00001eb3 77300	Uncharacterized LOC100384006	K01662	1-deoxy-D-xylulose-5-phosphate synthase	01100 、 01110 、 04013	Metabolic pathways、 Biosynthesis of secondary metabolites、 Thiamine metabolism、 MAPK signaling
22	Zm00001eb3 77310	None	K04564	Superoxide dismutase, Fe-Mn family	、 04068 、 01100	pathway - fly、 FoxO signaling pathway、 Peroxisome、 Longevity
23	Zm00001eb3 88240	Uncharacterized LOC100281477	K00422	Polyphenol oxidase	、 01110 、	Metabolic pathways、 Biosynthesis of secondary metabolites、 Tyrosine metabolism、
24	Zm00001eb3 88270	Uncharacterized LOC100279873	K14431	Transcription factor TGA	04075	Plant hormone signal transduction
25	Zm00001eb3 88280	Two-component response regulator	K14491	Two-component response regulator ARR-B family	04075	Plant hormone signal transduction
26	Zm00001eb3 97170	Uncharacterized LOC100273905	K05359	Arogenate/prephenate dehydratase	01100 、 01110 、 01100	Metabolic pathways、 Biosynthesis of secondary metabolites、 Biosynthesis of amino
27	Zm00001eb3 97180	L-ascorbate peroxidase 1, cytosolic	K00434	L-ascorbate peroxidase	、 00053 、	Metabolic pathways、 Ascorbate and aldarate metabolism、 Glutathione metabolism
28	Zm00001eb3 97190	Mitogen-activated	K20536	Mitogen-activated protein kinase 3	04016 、 04626	MAPK signaling pathway - plant、 Plant-pathogen interaction

Table S5 Relative expression level of *Zm00001eb272370*, *Zm00001eb272390* and *Zm00001eb272400* after chilling treatment for 3 and 10 hours

Germplasm name	Mean of RGR21C.7 N (%)	Type	Gene	3 hours	+	- 10 hours	+	-
LH123HT	102.77	Tolerant	<i>Zm00001eb272370</i>	1.41	0.22	0.21	0.91	0.05
PHT60	102.28	Tolerant	<i>Zm00001eb272370</i>	0.40	0.02	0.02	0.36	0.01
PI 406119	100.00	Tolerant	<i>Zm00001eb272370</i>	1.77	0.25	0.22	0.73	0.03
PHN47	100.00	Tolerant	<i>Zm00001eb272370</i>	2.08	0.48	0.39	0.89	0.05
LH39	100.00	Tolerant	<i>Zm00001eb272370</i>	0.63	0.07	0.06	0.78	0.09
MBPM	99.98	Tolerant	<i>Zm00001eb272370</i>	0.92	0.07	0.06	0.51	0.03
CML430	98.89	Tolerant	<i>Zm00001eb272370</i>	1.60	0.17	0.16	1.66	0.06
B09	97.91	Tolerant	<i>Zm00001eb272370</i>	0.94	0.22	0.18	1.37	0.10
9503	97.71	Tolerant	<i>Zm00001eb272370</i>	1.85	0.21	0.19	1.01	0.05
CML304	95.56	Tolerant	<i>Zm00001eb272370</i>	1.19	0.43	0.32	0.97	0.50
CML287	95.56	Tolerant	<i>Zm00001eb272370</i>	0.19	0.01	0.01	0.70	0.12
LH38	93.33	Tolerant	<i>Zm00001eb272370</i>	0.29	0.06	0.05	0.21	0.00
CML28	93.33	Tolerant	<i>Zm00001eb272370</i>	0.05	0.01	0.01	0.15	0.04
MC0303	93.33	Tolerant	<i>Zm00001eb272370</i>	0.82	0.07	0.06	0.40	0.04
CML470	93.33	Tolerant	<i>Zm00001eb272370</i>	1.06	0.09	0.08	0.84	0.05
Zhong85	93.16	Tolerant	<i>Zm00001eb272370</i>	0.02	0.00	0.00	0.08	0.01
Jing02	93.16	Tolerant	<i>Zm00001eb272370</i>	0.89	0.15	0.13	1.60	0.09
CML480	92.98	Tolerant	<i>Zm00001eb272370</i>	1.24	0.14	0.12	0.73	0.11
HPHR47	91.11	Tolerant	<i>Zm00001eb272370</i>	0.28	0.04	0.04	0.55	0.04
Lv28	90.69	Tolerant	<i>Zm00001eb272370</i>	0.02	0.00	0.00	0.03	0.01
PHW52	86.67	Tolerant	<i>Zm00001eb272370</i>	1.70	0.19	0.17	0.77	0.05
Ames 1020	86.67	Tolerant	<i>Zm00001eb272370</i>	2.17	0.11	0.11	1.18	0.10
CML307	86.67	Tolerant	<i>Zm00001eb272370</i>	2.80	0.19	0.15	1.37	0.28
PHT55	83.33	Tolerant	<i>Zm00001eb272370</i>	1.75	0.52	0.40	0.93	0.14
CIMBL97	82.22	Tolerant	<i>Zm00001eb272370</i>	1.21	0.08	0.07	1.18	0.06
CML172	80.00	Tolerant	<i>Zm00001eb272370</i>	0.86	0.07	0.07	0.73	0.03
CIMBL100	18.89	Sensitive	<i>Zm00001eb272370</i>	1.46	0.23	0.20	12.96	1.08
PB80	17.08	Sensitive	<i>Zm00001eb272370</i>	0.93	0.12	0.11	1.63	0.18
CIMBL95	15.56	Sensitive	<i>Zm00001eb272370</i>	1.43	0.09	0.09	3.45	0.19
Zhong128	15.56	Sensitive	<i>Zm00001eb272370</i>	10.35	0.79	0.74	18.46	1.45
Zhi25	15.56	Sensitive	<i>Zm00001eb272370</i>	0.69	0.08	0.07	0.76	0.04
CML118	14.55	Sensitive	<i>Zm00001eb272370</i>	1.02	0.08	0.08	1.16	0.08
LH74	9.09	Sensitive	<i>Zm00001eb272370</i>	76.90	7.64	6.95	105.44	15.04
Ji818	8.89	Sensitive	<i>Zm00001eb272370</i>	12.35	1.91	1.65	20.07	2.51
PH3901	8.89	Sensitive	<i>Zm00001eb272370</i>	88.42	10.28	9.21	17.83	9.77
F254	8.89	Sensitive	<i>Zm00001eb272370</i>	18.32	3.32	2.81	9.52	5.73
PHT77	6.67	Sensitive	<i>Zm00001eb272370</i>	1.85	0.14	0.13	0.94	0.07
H5	6.67	Sensitive	<i>Zm00001eb272370</i>	0.97	0.09	0.08	0.83	0.04
CML121	4.65	Sensitive	<i>Zm00001eb272370</i>	1.64	0.19	0.17	0.84	0.10
SK516	4.65	Sensitive	<i>Zm00001eb272370</i>	0.60	0.04	0.04	0.66	0.02
PHW65	4.44	Sensitive	<i>Zm00001eb272370</i>	0.48	0.05	0.05	0.56	0.03

CIMBL12	3.33	Sensitive	Zm00001eb272370	0.56	0.06	0.05	0.70	0.06	0.06
CIMBL11	0.00	Sensitive	Zm00001eb272370	0.94	0.24	0.19	0.59	0.02	0.02
CML170	0.00	Sensitive	Zm00001eb272370	0.71	0.08	0.07	2.74	0.03	0.03
236	0.00	Sensitive	Zm00001eb272370	1.29	0.22	0.19	0.88	0.07	0.06
G433	0.00	Sensitive	Zm00001eb272370	1.01	0.08	0.07	0.77	0.01	0.01
LH123HT	102.77	Tolerant	Zm00001eb272390	4.11	0.92	0.75	1.99	0.06	0.06
PHT60	102.28	Tolerant	Zm00001eb272390	0.34	0.04	0.03	0.29	0.02	0.02
PI 406119	100.00	Tolerant	Zm00001eb272390	2.41	0.35	0.31	0.93	0.04	0.04
PHN47	100.00	Tolerant	Zm00001eb272390	2.02	0.51	0.41	0.86	0.05	0.05
LH39	100.00	Tolerant	Zm00001eb272390	51.17	12.16	9.82	7.25	2.93	2.08
MBPM	99.98	Tolerant	Zm00001eb272390	0.63	0.03	0.03	0.53	0.03	0.03
CML430	98.89	Tolerant	Zm00001eb272390	2.17	0.15	0.14	1.73	0.10	0.10
B09	97.91	Tolerant	Zm00001eb272390	0.71	0.18	0.15	1.12	0.06	0.06
9503	97.71	Tolerant	Zm00001eb272390	0.62	0.21	0.15	0.36	0.05	0.04
CML304	95.56	Tolerant	Zm00001eb272390	0.19	0.03	0.03	1.31	1.22	0.63
CML287	95.56	Tolerant	Zm00001eb272390	1.60	0.08	0.08	0.90	0.19	0.16
LH38	93.33	Tolerant	Zm00001eb272390	0.07	0.01	0.01	0.22	0.04	0.03
CML28	93.33	Tolerant	Zm00001eb272390	0.09	0.02	0.01	0.86	0.15	0.13
MC0303	93.33	Tolerant	Zm00001eb272390	0.36	0.04	0.04	0.15	0.02	0.02
CML470	93.33	Tolerant	Zm00001eb272390	1.19	0.07	0.07	1.14	0.05	0.05
Zhong85	93.16	Tolerant	Zm00001eb272390	0.02	0.00	0.00	0.03	0.00	0.00
Jing02	93.16	Tolerant	Zm00001eb272390	1.55	0.12	0.11	1.71	0.18	0.16
CML480	92.98	Tolerant	Zm00001eb272390	0.61	0.05	0.04	0.29	0.04	0.03
HPHR47	91.11	Tolerant	Zm00001eb272390	0.16	0.03	0.02	0.63	0.08	0.07
Lv28	90.69	Tolerant	Zm00001eb272390	0.06	0.01	0.01	0.42	0.09	0.07
PHW52	86.67	Tolerant	Zm00001eb272390	0.61	0.07	0.06	0.25	0.01	0.01
Ames 1020	86.67	Tolerant	Zm00001eb272390	0.90	0.05	0.05	1.25	0.33	0.26
CML307	86.67	Tolerant	Zm00001eb272390	10.58	3.78	2.78	1.48	1.49	0.74
PHT55	83.33	Tolerant	Zm00001eb272390	1.44	0.37	0.29	2.00	1.02	0.68
CIMBL97	82.22	Tolerant	Zm00001eb272390	1.25	0.07	0.06	1.11	0.05	0.04
CML172	80.00	Tolerant	Zm00001eb272390	0.59	0.08	0.07	0.44	0.06	0.05
CIMBL10	18.89	Sensitive	Zm00001eb272390	2.25	0.36	0.31	3.36	0.39	0.39
PB80	17.08	Sensitive	Zm00001eb272390	0.69	0.12	0.11	0.80	0.05	0.05
CIMBL95	15.56	Sensitive	Zm00001eb272390	0.69	0.44	0.27	1.42	0.39	0.30
Zhong128	15.56	Sensitive	Zm00001eb272390	23.92	2.58	2.33	32.14	2.03	1.63
Zhi25	15.56	Sensitive	Zm00001eb272390	0.35	0.06	0.05	0.62	0.07	0.07
CML118	14.55	Sensitive	Zm00001eb272390	0.91	0.11	0.10	0.74	0.05	0.05
LH74	9.09	Sensitive	Zm00001eb272390	#####	16.64	15.15	224.32	22.75	20.66
Ji818	8.89	Sensitive	Zm00001eb272390	#####	35.29	28.84	24.06	0.97	0.92
PH3901	8.89	Sensitive	Zm00001eb272390	81.00	21.60	17.05	29.05	9.64	7.24
F254	8.89	Sensitive	Zm00001eb272390	#####	49.50	41.66	113.68	79.61	46.82
PHT77	6.67	Sensitive	Zm00001eb272390	2.01	0.32	0.28	0.52	0.07	0.06
H5	6.67	Sensitive	Zm00001eb272390	0.68	0.05	0.05	0.67	0.07	0.06
CML121	4.65	Sensitive	Zm00001eb272390	0.98	0.24	0.19	1.29	0.60	0.41
SK516	4.65	Sensitive	Zm00001eb272390	0.72	0.04	0.03	0.69	0.04	0.03
PHW65	4.44	Sensitive	Zm00001eb272390	0.54	0.04	0.04	0.40	0.02	0.02

CIMBL12	3.33	Sensitive	Zm00001eb272390	0.22	0.02	0.02	0.38	0.03	0.03
CIMBL11	0.00	Sensitive	Zm00001eb272390	3.53	0.95	0.75	13.59	1.13	1.11
CML170	0.00	Sensitive	Zm00001eb272390	1.72	0.21	0.18	0.54	0.07	0.06
236	0.00	Sensitive	Zm00001eb272390	1.29	0.20	0.17	2.92	0.17	0.14
G433	0.00	Sensitive	Zm00001eb272390	1.61	0.11	0.10	2.82	0.89	0.88
LH123HT	102.77	Tolerant	Zm00001eb272400	0.66	0.03	0.03	0.14	0.00	0.00
PHT60	102.28	Tolerant	Zm00001eb272400	0.43	0.02	0.02	0.61	0.03	0.03
PI 406119	100.00	Tolerant	Zm00001eb272400	1.23	0.15	0.13	0.75	0.03	0.03
PHN47	100.00	Tolerant	Zm00001eb272400	0.82	0.19	0.15	0.28	0.02	0.02
LH39	100.00	Tolerant	Zm00001eb272400	7.10	0.78	0.66	14.74	2.53	2.39
MBPM	99.98	Tolerant	Zm00001eb272400	0.92	0.07	0.06	0.54	0.06	0.06
CML430	98.89	Tolerant	Zm00001eb272400	1.46	0.14	0.13	1.08	0.15	0.13
B09	97.91	Tolerant	Zm00001eb272400	0.41	0.05	0.04	0.86	0.13	0.12
9503	97.71	Tolerant	Zm00001eb272400	3.02	0.34	0.33	8.39	1.77	1.46
CML304	95.56	Tolerant	Zm00001eb272400	14.39	2.79	2.34	12.90	1.55	1.57
CML287	95.56	Tolerant	Zm00001eb272400	5.97	0.39	0.36	5.26	0.56	0.56
LH38	93.33	Tolerant	Zm00001eb272400	0.12	0.01	0.01	0.48	0.02	0.02
CML28	93.33	Tolerant	Zm00001eb272400	2.14	0.23	0.22	1.14	0.43	0.31
MC0303	93.33	Tolerant	Zm00001eb272400	4.55	0.56	0.52	0.74	0.06	0.05
CML470	93.33	Tolerant	Zm00001eb272400	1.72	0.16	0.16	1.59	0.08	0.08
Zhong85	93.16	Tolerant	Zm00001eb272400	1.27	0.21	0.19	2.65	2.22	1.21
Jing02	93.16	Tolerant	Zm00001eb272400	1.21	0.10	0.09	0.64	0.04	0.04
CML480	92.98	Tolerant	Zm00001eb272400	17.55	6.45	6.72	5.46	0.16	0.16
HPHR47	91.11	Tolerant	Zm00001eb272400	0.38	0.09	0.07	0.45	0.03	0.03
Lv28	90.69	Tolerant	Zm00001eb272400	0.23	0.02	0.02	0.19	0.06	0.04
PHW52	86.67	Tolerant	Zm00001eb272400	3.22	0.36	0.34	0.21	0.02	0.02
Ames 1020	86.67	Tolerant	Zm00001eb272400	0.63	0.06	0.05	0.72	0.09	0.08
CML307	86.67	Tolerant	Zm00001eb272400	44.95	5.85	5.18	2.67	1.18	1.16
PHT55	83.33	Tolerant	Zm00001eb272400	13.84	1.15	1.13	7.06	1.19	1.02
CIMBL97	82.22	Tolerant	Zm00001eb272400	0.54	0.04	0.03	0.57	0.06	0.05
CML172	80.00	Tolerant	Zm00001eb272400	0.58	0.06	0.06	0.17	0.01	0.01
CIMBL10	18.89	Sensitive	Zm00001eb272400	1.44	0.23	0.20	0.94	0.12	0.11
PB80	17.08	Sensitive	Zm00001eb272400	0.66	0.13	0.11	3.06	0.21	0.19
CIMBL95	15.56	Sensitive	Zm00001eb272400	0.13	0.02	0.02	0.07	0.03	0.02
Zhong128	15.56	Sensitive	Zm00001eb272400	1.71	0.28	0.24	1.43	0.42	0.33
Zhi25	15.56	Sensitive	Zm00001eb272400	0.39	0.03	0.03	0.71	0.05	0.04
CML118	14.55	Sensitive	Zm00001eb272400	0.09	0.01	0.01	0.09	0.01	0.01
LH74	9.09	Sensitive	Zm00001eb272400	0.92	0.09	0.08	1.89	0.12	0.12
Ji818	8.89	Sensitive	Zm00001eb272400	0.25	0.00	0.00	0.17	0.01	0.01
PH3901	8.89	Sensitive	Zm00001eb272400	0.43	0.04	0.04	0.93	0.04	0.04
F254	8.89	Sensitive	Zm00001eb272400	0.42	0.02	0.02	0.40	0.04	0.03
PHT77	6.67	Sensitive	Zm00001eb272400	1.15	0.10	0.10	0.81	0.04	0.03
H5	6.67	Sensitive	Zm00001eb272400	0.59	0.05	0.04	0.35	0.02	0.02
CML121	4.65	Sensitive	Zm00001eb272400	0.23	0.02	0.01	0.24	0.02	0.02
SK516	4.65	Sensitive	Zm00001eb272400	0.76	0.05	0.05	1.13	0.01	0.01
PHW65	4.44	Sensitive	Zm00001eb272400	0.64	0.04	0.04	1.46	0.10	0.09

CIMBL12	3.33	SensitiveZm00001eb272400	0.03	0.00	0.00	0.03	0.00	0.00
CIMBL11'	0.00	SensitiveZm00001eb272400	1.06	0.26	0.21	0.90	0.22	0.17
CML170	0.00	SensitiveZm00001eb272400	1.00	0.16	0.14	1.24	0.05	0.05
236	0.00	SensitiveZm00001eb272400	0.98	0.15	0.13	1.03	0.16	0.14
G433	0.00	SensitiveZm00001eb272400	0.57	0.03	0.03	0.64	0.02	0.01

+ and - represent positive and negative error bars, respectively

Table S6 Candidate genes in our study which have been published in previous studies about cold-related traits

No.	Trait	Gene	Annotation	Published Trait (Treatment)	Corresponding to genes or makers	References
1	RGI	Zm00001eb040190	Putative carboxylesterase 8	WCS(5.5-6.5 °C)	GRMZM2G460383	[7]
2	RGI	Zm00001eb197370	abi40 - ABI3-VP1-transcription factor 40	SLA.AI(16/13 °C:27/25 °C)	GRMZM2G328742	[6]
3	RGI	Zm00001eb292530	Serine/threonine-protein kinase tricornet-like	rTL(11 °C)	GRMZM2G375904	[3]
4	RGI	Zm00001eb110610	Uncharacterized LOC100278156	Vigor(14 °C/14 h with light and 10 °C/10 h without	S_221805316	[1]
5	RGR21C.7 N、RGI	Zm00001eb193010	None	Days to silking	bnlg1189	[5]
6	RGI	Zm00001eb040140	Uncharacterized LOC100278133	ELT(4 °C)、MLT(10 °C)、LT(16 °C)	Zm00001d032030	[4]
7	RGI	Zm00001eb292590、Zm00001eb292600	Probable xyloglucan glycosyltransferase 7、None	Upregulated (5 °C for 12/12 h light/dark)	103630593	[8]
8	RGR21C.7 N、RGI	Zm00001eb363740	None		Zm00001d011944	
9	RGR21C.7 N、RGI	Zm00001eb192980	Chaperone protein DnaJ		Zm00001d052093	

10	RGR21C.7 N、RGI	Zm00001eb3 63780	None		Zm00001d011950	
11	RGR21C.7 N、RGI	Zm00001eb3 63800	tRNA (adenine(58)- N(1))- methyltransferase	Upregulated(16 °C /12 °C for 16 h light/8 h dark)	Zm00001d011952	
12	RGI	Zm00001eb0 19200	None		Zm00001d029415	
13	RGI	Zm00001eb2 61440	Uncharacterized LOC100273455		Zm00001d035157	
14	RGR21C.7 N	Zm00001eb2 60730	Uncharacterized LOC100273449		Zm00001d035066	
15	RGR21C.7 N	Zm00001eb3 97140	Putative RNA- binding protein ARP1		Zm00001d047753	
16	RGR21C.7 N、RGI	Zm00001eb3 63630	None		Zm00001d011931	[2]
17	RGR21C.7 N、RGI	Zm00001eb3 63650	Cytochrome P450 89A2-like		Zm00001d011932	
18	RGI	Zm00001eb0 40180	Geraniol 8- hydroxylase-like		Zm00001d032035	
19	RGI	Zm00001eb2 66690	Protein kinase		Zm00001d035646	
20	RGI	Zm00001eb1 45680	Uncharacterized LOC112268477	Downregulated (16 °C /12 °C for 16 h light/8 h dark)	Zm00001d042620	

21	RGI	Zm00001eb3 77310	None	Zm00001d045384
22	RGI	Zm00001eb3 77330	LOC103639077- like pseudogene	Zm00001d045386
23	RGR21C.7 N	Zm00001eb2 60750	Cytochrome P450 89A9	Zm00001d035069
24	RGR21C.7 N	Zm00001eb3 88270	Uncharacterized LOC100279873	Zm00001d046751

WCS(Water content of shoots and leaves);rTL(relative total length);SLA(Specific leaf area),AI(daptation Index = BLUEchilling: BLUEoptimal $\times$ 100);ELT(Extreme low temperature);MLT(Medium low-temperature).

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Table S7 Primers used in qRT-PCR

Name	Sequences
<i>beta tubulin 7</i> For	CTACCTCACGGCATCTGCTATGT
<i>beta tubulin 7</i> Rev	GTCACACACACTCGACTTCACG
<i>Zm00001eb272370</i> For	AGGTGCAATCCTTGTGTTCC
<i>Zm00001eb272370</i> Rev	TCACAGTTGGCATAGAACCATG
<i>Zm00001eb272390</i> For	TTATCGGAGAGGCTCAGCA
<i>Zm00001eb272390</i> Rev	CCCTGGTAGGCATTGTAGAGA
<i>Zm00001eb272400</i> For	ATCACCATCCCCTGCGGCG
<i>Zm00001eb272400</i> Rev	AGCCGGCGATGTGGAAGTGG