

S5 Table. Summary of candidate genes co-located with SNPs identified in this study as associated with cold tolerance at the germination and reproductive stages. These candidate genes were verified as part of cold tolerance studies in other plant species.

QTL	Population group /Trait ¹⁾	Gene	Chr.	Position (Mb)	Distance from targeted region (bp)	Description
Germination						
<i>qCTGERM1-1</i>	<i>ALL</i>	LOC_Os01g02750	1	0.954-0.956	0	protein kinase domain containing protein, expressed
<i>qCTGERM1-2</i>	<i>JAPONICA</i>	LOC_Os01g07980	1	3.855-3.856	883	ankyrin, putative, expressed
<i>qCTGERM1-3</i>	<i>ALL</i>	LOC_Os01g14630	1	8.191-8.192	549	polyprenyl synthetase, putative, expressed
<i>qCTGERM1-8</i>	<i>ALL</i>	LOC_Os01g71830	1	41.603-41.604	0	glycosyl hydrolases family 17, putative, expressed
<i>qCTGERM1-9</i>	<i>JAPONICA</i>	LOC_Os01g74470	1	43.125-43.134	0	ABC transporter, ATP-binding protein, putative, expressed
<i>qCTGERM2-2</i>	<i>ALL</i>	LOC_Os02g12540	2	6.556-6.558	0	cytochrome P450, putative, expressed
	<i>INDICA</i>	LOC_Os02g12540	2	6.556-6.558	0	cytochrome P450, putative, expressed
	<i>ALL</i>	LOC_Os02g36150	2	21.788-21.791	0	cytochrome P450, putative, expressed
	<i>INDICA</i>	LOC_Os02g36140	2	21.765-21.773	65,266	terpene synthase, putative, expressed
	<i>JAPONICA</i>	LOC_Os02g36150	2	21.788-21.791	6,740	cytochrome P450, putative, expressed
	<i>temperate japonica</i>	LOC_Os02g36150	2	21.788-21.791	0	cytochrome P450, putative, expressed
<i>qCTGERM2-4</i>	<i>INDICA</i>	LOC_Os02g36210	2	21.841-21.847	2,375	ent-kaurene synthase, chloroplast precursor, putative, expressed
	<i>temperate japonica</i>	LOC_Os04g02410	4	0.8681-0.8687	1,767	expressed protein
	<i>JAPONICA</i>	LOC_Os04g02450	4	0.8884-0.8907	22,058	rust-resistance protein Lr21, putative, expressed
	<i>ALL</i>	LOC_Os04g02850	4	1.110-1.113	3,391	pentatricopeptide, putative, expressed
	<i>INDICA</i>	LOC_Os04g45950	4	27.217-27.214	0	amino acid permease family protein, putative, expressed
	<i>JAPONICA</i>	LOC_Os04g52800	4	31.434-31.435	508	expressed protein
<i>qCTGERM4-4</i>	<i>temperate japonica</i>	LOC_Os04g52920	4	31.524-31.527	443	remorin family protein, putative, expressed
	<i>tropical japonica</i>	LOC_Os05g36240	5	21.482-21.485	0	expressed protein
<i>qCTGERM5-1</i>	<i>tropical japonica</i>	LOC_Os05g36240	5	21.482-21.485	0	expressed protein
<i>qCTGERM6-1</i>	<i>JAPONICA</i>	LOC_Os06g11410	6	6.019-6.021	4,656	cyclin, putative, expressed
<i>qCTGERM6-2</i>	<i>ALL</i>	LOC_Os06g11650	6	6.177-6.179	166	phosphate-induced protein 1 conserved region domain containing protein, expressed
<i>qCTGERM7-4</i>	<i>ALL</i>	LOC_Os07g33690	7	20.129-20.135	0	NBS-LRR type disease resistance protein Hom-F, putative, expressed
	<i>JAPONICA</i>	LOC_Os07g33480	7	20.012-20.015	11,932	cytochrome P450 domain containing protein, expressed
	<i>JAPONICA</i>	LOC_Os07g33600	7	20.067-20.068	1,234	hydroxylase, putative, expressed

	<i>JAPONICA</i>	LOC_Os07g33670	7	20.115-20.123	300	patatin-like phospholipase family protein, expressed
<i>qCTGERM8-1</i>	<i>ALL</i>	LOC_Os08g17080	8	10.453-10.458	18,135	PPR repeat domain containing protein, putative, expressed
<i>qCTGERM8-2</i>	<i>JAPONICA</i>	LOC_Os08g20420	8	12.266-12.269	1,274	MGD2, putative, expressed
<i>qCTGERM9-1</i>	<i>INDICA</i>	LOC_Os09g17670	9	10.804-10.804	1,310	expressed protein
<i>qCTGERM10-2</i>	<i>tropical japonica</i>	LOC_Os10g20390	10	10.249-10.252	4,808	MATE efflux family protein, putative, expressed
<i>qCTGERM11-3</i>	<i>JAPONICA</i>	LOC_Os11g28270	11	16.249-16.258	1,004	zinc finger C-x8-C-x5-C-x3-H type family protein, expressed
<i>qCTGERM11-4</i>	<i>INDICA</i>	LOC_Os11g29970	11	17.411-17.417	0	NB-ARC domain containing protein, expressed
<i>qCTGERM11-5</i>	<i>JAPONICA</i>	LOC_Os11g33330	11	19.709-19.718	0	peptidase, M24 family protein, putative, expressed
	<i>temperate japonica</i>	LOC_Os11g33330	11	19.709-19.718	0	peptidase, M24 family protein, putative, expressed
<i>qCTGERM12-2</i>	<i>ALL</i>	LOC_Os12g42540	12	26.424-26.425	933	zinc finger, C3HC4 type domain containing protein, expressed
	<i>INDICA</i>	LOC_Os12g42420	12	26.363-26.365	441	DNA binding protein, putative, expressed
	<i>INDICA</i>	LOC_Os12g42550	12	26.425-26.430	0	methyl-CpG binding domain containing protein, putative, expressed
<i>qCTGERM12-3</i>	<i>INDICA</i>	LOC_Os12g43840	12	27.195-27.281	791	ankyrin repeat domain-containing protein, putative, expressed

Reproductive

<i>qSWTPNCT1-1</i>	SWPan	LOC_Os01g07310	1	3.446-3.450	1,589	transporter-related, putative, expressed
<i>qSWTCT1-1</i>	SWPlt	LOC_Os01g72190	1	41.861-41.863	87	glutathione S-transferase, putative, expressed
<i>qSWTCT1-2</i>	SWPlt	LOC_Os01g72250	1	41.892-41.896	0	uridine 5-monophosphate synthase, putative, expressed
<i>qSWTPNCT1-3</i>	SWPan	LOC_Os01g74300	1	43.046-43.047	389	metallothionein, putative, expressed
<i>qSWTPNCT2-1</i>	SWPan	LOC_Os02g31280	2	18.746-18.747	12,578	expressed protein
<i>qFERCT2</i>	Percent sterility	LOC_Os02g32700	2	19.423-19.423	2,003	autophagy-related protein, putative, expressed
<i>qSWTPNCT2-2</i>	SWPan	LOC_Os02g47744	2	29.190-29.195	2,847	MYB family transcription factor, putative, expressed
<i>qSWTPNCT5</i>	SWPan	LOC_Os05g47470	5	27.198-27.199	3,283	VIP1 protein, putative, expressed
<i>qFERCT6-3</i>	Percent sterility	LOC_Os06g25250	6	14.770-14.773	123	endoribonuclease Dicer, putative, expressed
<i>qSWTCT6</i>	SWPlt	LOC_Os06g41300	6	24.712-24.712	1,378	expressed gene
<i>qSWTPNCT6-1</i>	SWPan	LOC_Os06g10470	6	5.388-5.389	771	ZOS6-02 - C2H2 zinc finger protein, expressed
<i>qFERCT7</i>	Percent sterility	LOC_Os07g25060	7	14.303-14.303	12,472	thionin-like peptide, putative, expressed
<i>qSWTCT7</i>	SWPlt	LOC_Os07g38620	7	23.194-23.199	0	pyridoxamine 5'-phosphate oxidase family protein, putative, expressed
<i>qSWTCT8-1</i>	SWPlt	LOC_Os08g02094	8	0.686-0.693	0	GDSL-like lipase/acylhydrolase, putative, expressed
<i>qSWTPNCT8</i>	SWPan	LOC_Os08g05510	8	2.934-2.940	2,060	MYB family transcription factor, putative, expressed

<i>qSWTCT8-5</i>	SWPlt	LOC_Os08g44560	8	28.014-28.020	0	expressed gene
<i>qSWTCT8-2</i>	SWPlt	LOC_Os08g06710	8	3.763-3.764	0	OsFBDUF42 - F-box and DUF domain containing protein, expressed
<i>qSWTCT8-3</i>	SWPlt	LOC_Os08g10608	8	6.243-6.247	962	ribosomal protein S17, putative, expressed
<i>qSWTCT12</i>	SWPlt	LOC_Os12g42130	12	26.117-26.120	2,595	MATE efflux family protein, putative, expressed

¹⁾ “SWPan” is the mean seed weight per panicle and “SWPlt” is the mean seed weight per plant.