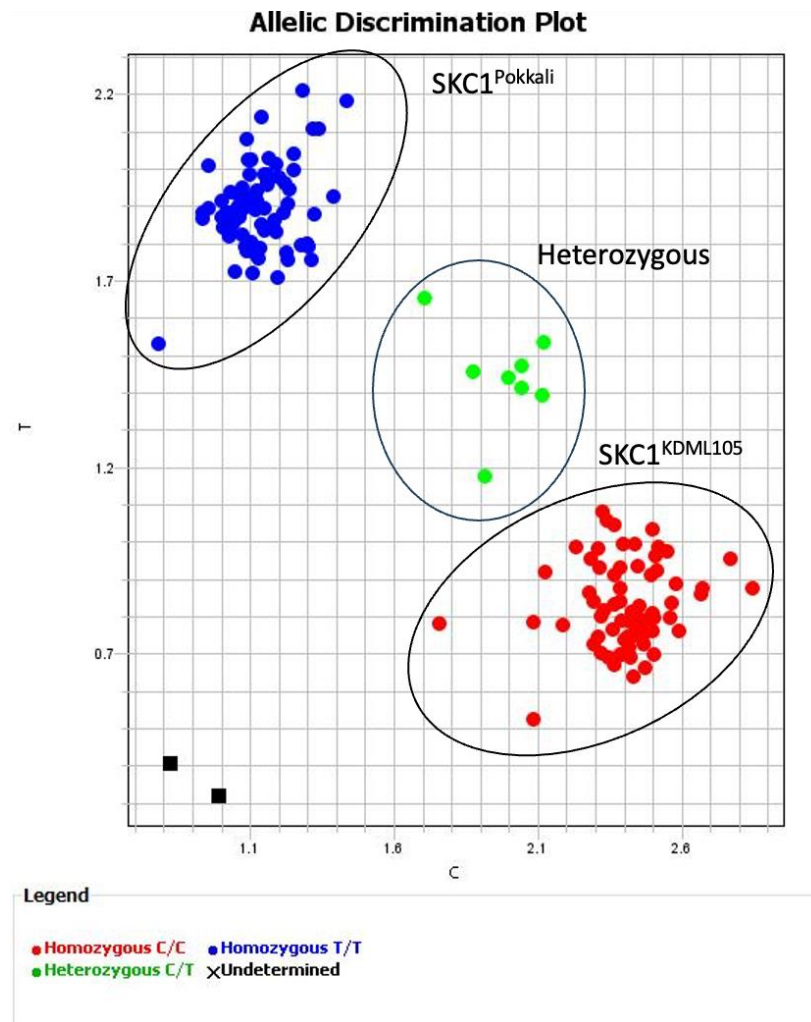


## **Supplementary Information**

### **QTL-seq Identifies Pokkali-derived QTLs and Candidate Genes for Salt Tolerance at Seedling Stage in Rice (*Oryza sativa* L.)**

Decha Songtorsesakul, Wanchana Aesomnuk, Sarinthip Pannak, Jonaliza Lanceras Siangliw, Meechai

Siangliw, Theerayut Toojinda, Samart Wanchana\*, Siwaret Arikrit\*



**Figure S1.** Allelic discrimination plots of the PCR results of the SKC1-KASP marker genotyped in the RIL population. Red dots represent the homozygous C/C genotype, blue dots represent the homozygous T/T genotype and green dots represent the heterozygous genotype.



**Figure S2.** Distribution of SNPs on the 12 rice chromosomes. Vertical rectangular blocks represent 1-Mb windows. Different frequencies of SNPs in 1-Mb windows were indicated by different color codes.

**Table S1.** Annotated genes within the detected QTLs.

QTL	Chr	Start	Stop	Locus ID	Description
<i>qST1.1</i>	1	5002454	5004321	Os01g0192900	1-aminocyclopropane-1-carboxylic acid synthase, Submergence response
	1	5016279	5020150	Os01g0193400	TNFR/CD27/30/40/95 cysteine-rich region domain containing protein
	1	5021104	5025704	Os01g0193600	Methyltransferase small domain containing protein
	1	5028275	5037189	Os01g0193900	ALWAYS EARLY/LIN-9 homologous protein
	1	5053133	5055753	Os01g0194200	IQ calmodulin-binding region domain containing protein
	1	5060605	5065209	Os01g0194300	Ankyrin-repeat protein, Herbivore-induced defense response, Blast disease resistance
	1	5085833	5086504	Os01g0194600	Thioredoxin fold domain containing protein
	1	5099555	5102080	Os01g0195000	Zinc finger and indeterminate domain (IDD) family transcription factor, Regulation of secondary cell wall formation
	1	5109949	5112457	Os01g0195200	Similar to Serine/threonine-protein kinase PBS1 (EC 2.7.1.37) (AvrPphB susceptible protein 1)
	1	5131629	5132915	Os01g0195400	Harpin-induced 1 domain containing protein
	1	5138518	5140925	Os01g0195500	Translation initiation factor SUI1 domain containing protein
	1	5196418	5197056	Os01g0196133	Similar to H0315A08.1 protein
	1	5201862	5203996	Os01g0196300	Basic helix-loop-helix (bHLH) transcription factor, Diterpenoid phytoalexin factor, Biosynthesis of diterpenoid phytoalexins, Stress response
	1	5213979	5216701	Os01g0196500	Prenylated rab acceptor PRA1 family protein
	1	5218573	5220335	Os01g0196600	Similar to 260 kDa major acidic fibroblast growth factor-stimulated phosphoprotein
	1	5236623	5244520	Os01g0197100	Cytochrome P450, Brassinosteroids biosynthesis, Regulation of plant architecture
	1	5247340	5251192	Os01g0197200	Similar to predicted protein
	1	5261189	5263102	Os01g0197450	Pentatricopeptide repeat domain containing protein
	1	5264691	5266158	Os01g0197500	Similar to predicted protein
	1	5270449	5275585	Os01g0197700	Cytokinin oxidase/dehydrogenase, Regulation of grain production
	1	5288136	5302247	Os01g0197900	$\gamma$ -clade RNA-dependent RNA polymerase 3, Rice growth and development, Regulation of the expression of repeat-rich regions in the genome, Polymerase activity on both RNA and DNA templates
	1	5307415	5324478	Os01g0198000	$\gamma$ -clade RNA-dependent RNA polymerase 4, Rice growth and development
	1	5329063	5335518	Os01g0198200	Similar to Casein kinase-like protein
	1	5373630	5374681	Os01g0198900	Polyketide cyclase/dehydrase domain containing protein
	1	5384196	5385088	Os01g0199300	Similar to lachrymatory factor synthase
	1	5389837	5394412	Os01g0199400	Alpha/beta hydrolase family protein
	1	5398321	5402018	Os01g0199700	Protein of unknown function DUF1677
	1	5406050	5412737	Os01g0199900	Similar to Phosphoribosylaminoimidazole carboxylase catalytic subunit (EC 4.1.1.21) (AIR carboxylase)
	1	5413595	5416778	Os01g0200000	Similar to autophagocytosis protein AUT1-like
	1	5424059	5424581	Os01g0200200	Protein of unknown function DUF1677
	1	5426582	5429390	Os01g0200300	Similar to Homeobox-leucine zipper protein HOX29
	1	5435443	5442646	Os01g0200400	Thioredoxin domain 2 containing protein
	1	5442866	5446246	Os01g0200500	MPPN family protein
	1	5454772	5455667	Os01g0200600	Similar to Avr9/Cf-9 rapidly elicited protein 111A
	1	5478545	5479749	Os01g0200700	Metallothionein-like protein, Tolerance to salinity and heavy metal stresses, Abiotic stress response
	1	5498215	5499226	Os01g0201000	Similar to protein kinase family protein
<i>qST1.2</i>	1	41002584	41003731	Os01g0934700	Alpha/beta hydrolase fold-1 domain containing protein
	1	41004305	41005945	Os01g0934800	Alpha/beta hydrolase fold-1 domain containing protein
	1	41007465	41008440	Os01g0934900	Probable esterase PIR7A
	1	41011330	41015063	Os01g0935000	Zinc finger, C2H2-type domain containing protein
	1	41021478	41021912	Os01g0935100	Nuclear factor Y (NF-Y) transcription factor B5, CCAAT box binding factor, Heme-associated protein 3J

	1	41028860	41030025	Os01g0935200	Nuclear factor Y (NF-Y) transcription factor B6, CCAAT box binding factor, Heme-associated protein 3G
	1	41052368	41056409	Os01g0935300	Similar to cullin-1
	1	41057220	41058809	Os01g0935400	2OG-Fe(II) oxygenase domain containing protein
	1	41061106	41067020	Os01g0935500	Similar to Potassium transporter 7 (OsHAK7)
	1	41066946	41070506	Os01g0935600	Immunoglobulin/major histocompatibility complex
	1	41074431	41079262	Os01g0935700	Similar to Cytochrome c1, heme protein
	1	41079487	41080890	Os01g0935800	Similar to BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1
	1	41085902	41088168	Os01g0935900	Similar to Succinate dehydrogenase subunit 4
	1	41087786	41090680	Os01g0936000	Putative glutaredoxin-C2
	1	41095911	41100367	Os01g0936100	Receptor-like cytoplasmic kinase 55
	1	41100496	41105054	Os01g0936200	Lipase, class 3 family protein
	1	41117216	41122215	Os01g0936800	PapD-like domain containing protein
	1	41126538	41127824	Os01g0936900	Peptidase A1 domain containing protein
	1	41133500	41134904	Os01g0937000	Peptidase aspartic, catalytic domain containing protein
	1	41139355	41140629	Os01g0937050	Homolog of xylanase inhibitor, Chitinase-like protein, Defense response against pathogens, Growth regulation through calcium signaling
	1	41142013	41143416	Os01g0937100	Similar to Xylanase inhibitor precursor (Xylanase inhibitor TAXI-I)
	1	41145301	41146727	Os01g0937200	Peptidase aspartic, catalytic domain containing protein
	1	41149956	41154666	Os01g0937300	NB-ARC domain containing protein
	1	41155827	41163821	Os01g0937400	NB-ARC domain containing protein
	1	41166235	41167902	Os01g0937500	Peptidase aspartic, catalytic domain containing protein
	1	41169527	41171002	Os01g0937600	Peptidase aspartic, catalytic domain containing protein
	1	41187052	41188691	Os01g0938100	Photosystem II protein Psb28, class 1 domain containing protein
	1	41193350	41198903	Os01g0938200	Similar to RNA-binding protein BRUNOL5 (Fragment)
	1	41214311	41217063	Os01g0938900	Similar to Nascent polypeptide-associated complex alpha subunit-like protein 3 (NAC-alpha-like protein 3)
	1	41220037	41227329	Os01g0939100	Similar to Calmodulin-stimulated calcium-ATPase
	1	41230854	41235586	Os01g0939300	BRCT domain containing protein
	1	41242467	41243777	Os01g0939500	Similar to Eukaryotic peptide chain release factor subunit 1-2 (eRF1-2)
	1	41245588	41249894	Os01g0939600	Similar to Glycerol-3-phosphate dehydrogenase-like protein
	1	41251235	41272093	Os01g0939700	Similar to Esterase D (EC 3.1.1.1)
	1	41300203	41302983	Os01g0940000	Cytokinin oxidase/dehydrogenase, Crown root formation
	1	41305317	41314346	Os01g0940100	Hexokinase 3, Positive regulation of grain size
	1	41346647	41348373	Os01g0940700	Similar to Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39)
	1	41349731	41351118	Os01g0940800	Beta-1,3-glucanase 6, Defense response against <i>M. oryzae</i>
	1	41365160	41366543	Os01g0941200	Similar to Glucan endo-1,3-beta-glucosidase GII precursor (EC 3.2.1.39)
	1	41375254	41376297	Os01g0941500	Similar to Beta-1,3-glucanase
	1	41384339	41386372	Os01g0941800	Metallophosphoesterase domain containing protein
	1	41394739	41396203	Os01g0942200	Cyclin-like F-box domain containing protein
	1	41398051	41399089	Os01g0942300	Endo-(1,3;1,4)- $\beta$ -glucanase
	1	41439358	41447125	Os01g0942900	Similar to cDNA clone:J023028M23
	1	41470283	41478321	Os01g0943800	Similar to cDNA, clone: J100054L12
<i>qST2</i>	2	27262061	27263495	Os02g0671200	Protein of unknown function DUF295 domain containing protein
	2	27266202	27269207	Os02g0671300	Basic helix-loop-helix dimerisation region bHLH domain containing protein
	2	27297098	27300008	Os02g0671800	Integrase, catalytic core domain containing protein
	2	27316157	27325651	Os02g0672100	C2H2-type zinc finger transcription factor, Promotion of flowering
	2	27330175	27341732	Os02g0672200	Argonaute 1a protein, Target gene of osa-miR168a-5p, Salt tolerance
	2	27352171	27357013	Os02g0672400	Sugar transporter, conserved site domain containing protein.
	2	27357591	27359660	Os02g0672500	Similar to Mitochondrial import inner membrane translocase subunit tim23
	2	27360447	27365739	Os02g0672600	Subunit of RNA N6-methyladenosine methyltransferase, Regulation of embryo development

	2	27369142	27371727	Os02g0672700	DNA-directed RNA polymerase, M/15 kDa subunit domain containing protein
	2	27372060	27376761	Os02g0672800	Similar to Protein kinase
	2	27386926	27388940	Os02g0673000	Uncharacterised protein family UPF0005 domain containing protein
	2	27390847	27394188	Os02g0673100	Aluminum-activated malate transporter, Maintenance of panicle size and grain yield
	2	27416559	27421828	Os02g0673500	Basic helix-loop-helix (bHLH) DNA-binding protein, Regulation of metaxylem vessel number and area, Repression of drought-induced metaxylem plasticity
	2	27422921	27427541	Os02g0673600	ORMDL family protein
	2	27435303	27438545	Os02g0673700	Similar to OSIGBa0103M18.3 protein
	2	27480264	27484556	Os02g0674700	Similar to protein binding protein
	2	27487866	27494913	Os02g0674800	Homeodomain leucine zipper class IV transcriptional factor , Ortholog of Arabidopsis GLABRA2, Modulation of leaf rolling
	2	27507087	27511190	Os02g0675400	Similar to OSIGBa0111L12.2 protein
	2	27531016	27534623	Os02g0675700	Protein of unknown function DUF248, methyltransferase putative family protein
	2	27548414	27551592	Os02g0675800	Cyclin-like F-box domain containing protein
	2	27559285	27567041	Os02g0676000	Membrane bound O-acyl transferase, MBOAT family protein
	2	27591163	27592963	Os02g0676400	Multi antimicrobial extrusion protein MatE family protein
	2	27602322	27606779	Os02g0676500	Similar to OSIGBa0127A14.6 protein
	2	27621222	27622912	Os02g0676800	Similar to Dehydration responsive element binding protein 1E (DREB1E protein)
	2	27652935	27654206	Os02g0677300	Typical CBF/DREB1 transcription factor, Dehydration-responsive element binding protein 1G, Cold stress tolerance, Positive regulation of heat, salt and drought tolerance
	2	27662418	27667350	Os02g0677700	Similar to Nucleic acid binding protein
	2	27667933	27671383	Os02g0677800	Similar to 40S ribosomal protein S13
	2	27696289	27702009	Os02g0678200	SPX-MFS protein, Pi homeostasis
	2	27702873	27705211	Os02g0678300	Similar to protein HOTHEAD
	2	27709385	27713141	Os02g0678400	NAD(P)-binding domain containing protein
	2	27727857	27728960	Os02g0678800	Transcriptional activator/repressor, Regulation of KNOX gene, Oskn2 (regulator of meristem function), Floral organogenesis
	2	27737378	27738930	Os02g0679200	Pentatricopeptide repeat domain containing protein
	2	27744016	27747252	Os02g0679500	Similar to Rac GTPase activating protein 1
<i>qST3</i>	3	31718262	31721710	Os03g0765800	Pyridoxal phosphate-dependent transferase
	3	31725194	31725857	Os03g0765900	PetM of cytochrome b6/f complex subunit 7 domain containing protein
	3	31726005	31732261	Os03g0766000	Similar to seven transmembrane domain protein
	3	31729638	31730211	Os03g0766100	10 kDa prolamin precursor
	3	31732515	31733057	Os03g0766200	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein
	3	31735442	31736253	Os03g0766350	Bifunctional inhibitor/plant lipid transfer protein/seed storage domain containing protein
	3	31749469	31755280	Os03g0766500	Similar to Two-component response regulator ARR1
	3	31759195	31767544	Os03g0766900	Allene oxide synthase
	3	31764991	31766985	Os03g0767000	Allene oxide synthase (CYP74A1), Biosynthesis of jasmonic acid (JA)
	3	31778339	31781372	Os03g0767500	Thioredoxin domain 2 containing protein
	3	31785151	31788078	Os03g0767600	BTB domain containing protein
	3	31790621	31793202	Os03g0767800	Cold acclimation protein WCOR413-like protein
	3	31802310	31804146	Os03g0767900	Uncharacterised protein family UPF0497, trans-membrane plant domain containing protein
	3	31825518	31829665	Os03g0769000	Similar to ternary complex factor MIP1
	3	31840737	31844402	Os03g0769050	Similar to EMB2756
	3	31845464	31847238	Os03g0769100	Chloroplast ribosomal protein S9, Early chloroplast development
	3	31853946	31857784	Os03g0769400	BTB/POZ fold domain containing protein
	3	31858526	31859454	Os03g0769500	EF-Hand type domain containing protein
	3	31860523	31863362	Os03g0769600	ResB-like family protein

	3	31867214	31867887	Os03g0769700	Uncharacterised conserved protein UCP031279 domain containing protein
	3	31869151	31871497	Os03g0769800	Similar to Homeodomain-leucine zipper protein interfascicular fiberless 1 (Revoluta)
	3	31874977	31876331	Os03g0769900	Similar to CF9
	3	31885024	31885617	Os03g0770000	bZIP transcription factor
	3	31930835	31934477	Os03g0770800	CSLC9
	3	31952891	31954550	Os03g0771100	MYELOBLASTOSIS (MYB) transcription factor 36c, Regulation of Casparian strip formation at the root endodermis
	3	31964738	31970261	Os03g0771500	Similar to Isoform 2 of Homeobox protein knotted-1-like 8
	3	31986608	31991587	Os03g0772100	Similar to Homeobox protein knotted-1-like 8
	3	32008474	32010598	Os03g0772600	Similar to Lectin-like receptor kinase 7;2
	3	32013259	32015229	Os03g0772700	Similar to lectin-like receptor kinase 7
	3	32017648	32019527	Os03g0772800	Cytochrome c oxidase, subunit VIa family protein
	3	32028145	32029878	Os03g0773000	Protein of unknown function DUF1005 family protein
	3	32035018	32040880	Os03g0773100	Similar to Myb/SANT domain protein
	3	32041607	32043400	Os03g0773150	40S ribosomal protein S29
	3	32043966	32048393	Os03g0773300	Protein kinase, core domain containing protein
	3	32064251	32071104	Os03g0773600	Kinesin, motor region domain containing protein. (Os03t0773600-01);Hypothetical conserved gene. (Os03t0773600-02)
	3	32079178	32082438	Os03g0773700	Similar to Receptor-like protein kinase 2
	3	32086041	32089677	Os03g0773800	Similar to Malate dehydrogenase, glyoxysomal precursor (EC 1.1.1.37) (mbNAD-MDH)
	3	32092409	32095619	Os03g0774200	Similar to NADH-ubiquinone oxidoreductase subunit 8 (EC 1.6.5.3)
	3	32096850	32103996	Os03g0774300	HAD superfamily (subfamily IG) hydrolase, 5'-Nucleotidase protein
	3	32107062	32109944	Os03g0774400	Similar to predicted protein
	3	32136863	32139508	Os03g0775000	Leucine carboxyl methyltransferase domain containing protein
	3	32142168	32146666	Os03g0775200	Protein of unknown function DUF248, methyltransferase putative family protein
	3	32147180	32150669	Os03g0775300	Flavodoxin/nitric oxide synthase domain containing protein
	3	32150822	32153382	Os03g0775400	Tetratricopeptide-like helical domain containing protein
	3	32153925	32157349	Os03g0775500	Protein of unknown function DUF59 domain containing protein
	3	32160235	32163775	Os03g0775600	Similar to predicted protein
	3	32175291	32182089	Os03g0776000	Glucose-6-phosphate isomerase, cytosolic A (EC 5.3.1.9) (GPI-A)
	3	32208931	32210830	Os03g0776900	Similar to mitochondrial import inner membrane translocase subunit TIM14
	3	32234319	32236419	Os03g0777000	NAC transcription factor, Positive regulation of resistance to blast and bacterial blight
	3	32244456	32246820	Os03g0777500	Protein of unknown function DUF1068 family protein
<i>qST6</i>	6	3507359	3509141	Os06g0169900	Similar to GOS9 protein
	6	3515130	3518031	Os06g0170100	Similar to WAK80 - OsWAK receptor-like protein kinase
	6	3536683	3540219	Os06g0170500	Similar to RNA-binding protein-like
	6	3558158	3559922	Os06g0170800	Similar to H0124B04.16 protein
	6	3559947	3561401	Os06g0170866	F-box domain, cyclin-like domain containing protein
	6	3588217	3595865	Os06g0171600	Membrane insertion protein, OxaA/YidC domain containing protein
	6	3596001	3598291	Os06g0171700	Cdk-activating kinase assembly factor (MAT1) family protein
	6	3598466	3605188	Os06g0171800	VRR-NUC domain containing protein
	6	3632670	3639453	Os06g0171900	WD40 subfamily protein, Salt stress (Os06t0171900-01)
	6	3640786	3643222	Os06g0172000	Pentatricopeptide repeat domain containing protein
	6	3649517	3650686	Os06g0172200	EF-Hand type domain containing protein
	6	3656494	3657055	Os06g0172600	Similar to predicted protein
	6	3675795	3679085	Os06g0172800	Similar to alkaline alpha galactosidase 2
	6	3682377	3688555	Os06g0173000	Armadillo-type fold domain containing protein
	6	3689676	3694342	Os06g0173100	26S proteasome 19S regulatory particle triple-A ATPase subunit 5b
	6	3723342	3725225	Os06g0173800	SANT domain, DNA binding domain containing protein
	6	3759843	3762120	Os06g0174300	Similar to predicted protein
	6	3773690	3776480	Os06g0174400	Similar to Vesicle-associated membrane protein 712 (AtVAMP712)
	6	3801240	3807766	Os06g0175500	Epsin-like, N-terminal domain containing protein

	6	3823021	3827326	Os06g0175800	Similar to Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL)
	6	3828103	3830152	Os06g0175900	Similar to Cytochrome b-c1 complex subunit 8
	6	3832018	3833094	Os06g0176000	Proteasome subunit alpha type 4 (EC 3.4.25.1)
	6	3834088	3836629	Os06g0176100	Similar to H0201G08.5 protein
	6	3837428	3839409	Os06g0176150	Similar to Ribosomal protein S15 containing protein
	6	3840732	3844710	Os06g0176200	Glycosyl transferase, family 31 protein
	6	3846106	3848325	Os06g0176300	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 5
	6	3851122	3854303	Os06g0176500	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 4
	6	3855568	3857390	Os06g0176700	HIS1-like protein, Fe(II)/2-oxoglutarate-dependent oxygenase
	6	3858434	3860468	Os06g0176850	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 6
	6	3861480	3865179	Os06g0176900	Similar to Cystathionine gamma-synthase
	6	3866159	3868208	Os06g0177000	Similar to Cytochrome b-c1 complex subunit 8
	6	3870074	3871150	Os06g0177100	Proteasome subunit alpha type 4 (EC 3.4.25.1)
	6	3872144	3874685	Os06g0177200	Similar to H0201G08.5 protein
	6	3875484	3877465	Os06g0177250	Similar to Ribosomal protein S15 containing protein
	6	3878788	3882766	Os06g0177300	Glycosyl transferase, family 31 protein
	6	3884162	3886381	Os06g0177600	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 5
	6	3889178	3892359	Os06g0177700	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 4
	6	3893624	3895446	Os06g0178500	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 1
	6	3896490	3898524	Os06g0178650	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 6
	6	3900488	3903056	Os06g0178700	Putative Fe(II)/2-oxoglutarate-dependent oxygenase, HIS1-like protein 2
	6	3919532	3924302	Os06g0178900	Vacuolar H <sup>+</sup> -pyrophosphatase
	6	3924758	3927818	Os06g0179000	Glycoside hydrolase family 79, N-terminal protein
	6	3932020	3933032	Os06g0179100	Similar to H0306F03.13 protein
	6	3934027	3937229	Os06g0179200	Similar to Nodulin-like protein
	6	3941687	3943447	Os06g0179500	Protein of unknown function DUF247
	6	3947927	3952217	Os06g0179700	Similar to DNA-binding protein phosphatase 2C
	6	3956913	3961586	Os06g0179800	Leucine-rich repeat, N-terminal domain containing protein
	6	3961923	3964854	Os06g0179900	Major facilitator superfamily protein
	6	3966107	3969423	Os06g0180000	Similar to Root determined nodulation 1
	6	3992690	3993053	Os06g0180533	Similar to predicted protein
<i>qST8</i>	8	26501167	26506198	Os08g0531600	Transcription factor, Positive regulator of cell proliferation, Control of grain size, shape and quality
	8	26507926	26512261	Os08g0531700	MADS-box transcription factor, Regulation of floral identity, Regulation of amylose content at high temperature
	8	26518976	26529016	Os08g0531900	Similar to MADS box transcription factor-like protein (MADS-box protein AGL72)
	8	26531415	26534074	Os08g0532200	Glutamate 1-semialdehyde 2,1-aminomutase, Tetrapyrrole biosynthesis
	8	26535221	26537302	Os08g0532300	Similar to Nuclear transport factor 2 (NTF-2)
	8	26537672	26542835	Os08g0532400	Similar to AT.I.24-7 protein
	8	26546039	26549956	Os08g0532600	Similar to Peroxidase
	8	26546988	26549806	Os08g0532700	Similar to Peroxidase 55 precursor (EC 1.11.1.7) (Atperox P55) (ATP20a)
	8	26554159	26557021	Os08g0532800	Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor domain containing protein. (Os08t0532800-02);Similar to Lipid transfer protein. (Os08t0532800-03)
	8	26558909	26562152	Os08g0532900	emp24/gp25L/p24 family protein
	8	26572162	26574946	Os08g0533300	Similar to ACR5. (Os08t0533300-01)
	8	26601165	26605539	Os08g0533600	Similar to ACR4. (Os08t0533600-01)

	8	26606691	26609530	Os08g0533700	Similar to cation cation antiporter
	8	26652114	26655784	Os08g0534200	Similar to HEAT repeat family protein
	8	26656152	26656650	Os08g0534300	Similar to calmodulin binding protein
	8	26658525	26667717	Os08g0534350	Similar to cation cation antiporter
	8	26662244	26664175	Os08g0534400	EKC/KEOPS complex, subunit Pcc1 domain containing protein
	8	26687987	26694103	Os08g0534900	Armadillo-type fold domain containing protein
	8	26694471	26694969	Os08g0534950	Similar to calmodulin binding protein
	8	26696844	26699288	Os08g0535000	Similar to cation cation antiporter
	8	26725952	26728794	Os08g0535200	Sugar transporter, A member of the MtN3 gene family, Host disease-susceptibility gene for bacterial blight
	8	26744957	26748439	Os08g0535400	Zinc finger, DHHC-type domain containing protein
	8	26749784	26751095	Os08g0535600	Zinc finger, Tim10/DDP-type family protein
	8	26751395	26754247	Os08g0535700	Similar to glycerophosphodiester phosphodiesterase
	8	26766816	26770335	Os08g0535800	No apical meristem (NAM) protein domain containing protein
	8	26777982	26783294	Os08g0536000	Similar to Pyruvate dehydrogenase E1 beta subunit isoform 1 (EC 1.2.4.1)
	8	26791868	26792452	Os08g0536200	Uncharacterised protein family UPF0497, trans-membrane plant subgroup domain containing protein
	8	26792942	26797114	Os08g0536300	CONSTANS-like transcription factor, Rice ortholog of AtCOL15, Floral regulator, Suppression of flowering
	8	26841064	26843300	Os08g0536800	Similar to TA1 protein
	8	26871277	26879986	Os08g0537600	Arf GTPase activating protein family protein
	8	26883126	26887362	Os08g0537800	Otubain-like protease with deubiquitination activity, Determination of grain size and shape
	8	26887813	26895496	Os08g0537900	ERF-X-type transcription factor, Negative regulation of shoot growth and tolerance to salinity stress
	8	26900384	26904520	Os08g0538000	Glycyl-tRNA synthetase 3, Heading date
	8	26905017	26906620	Os08g0538200	Protein of unknown function DUF247, plant family protein
	8	26909127	26913494	Os08g0538300	LysM receptor-like kinase, Chitin elicitor signaling
	8	26918197	26921534	Os08g0538600	Stress up-regulated Nod 19 family protein
	8	26922222	26928300	Os08g0538700	Retinoblastoma-related protein, Control of inner floral organ formation, Establishment and maintenance of floral meristem function
	8	26932311	26935259	Os08g0538800	Pentatricopeptide repeat domain containing protein
	8	26938833	26942097	Os08g0539100	Zinc finger, DHHC-type domain containing protein
	8	26948601	26953317	Os08g0539300	C3HC4-type zinc finger protein, Target of miR528, Regulation of flowering under LD conditions
	8	26968546	26978236	Os08g0539400	Similar to Resistance protein T1orga2-1A
	8	26982655	26986692	Os08g0539600	Similar to Ankyrin repeat domain-containing protein 2
	8	26989664	26997637	Os08g0539700	Rice blast resistance protein Pib homologue
<i>qST10</i>	10	17755806	17763648	Os10g0476600	Similar to Protein phosphatase 2A 62 kDa B
	10	17766864	17772031	Os10g0476700	Esterase, SGNH hydrolase-type
	10	17773251	17776920	Os10g0476900	Pentatricopeptide repeat domain containing protein
	10	17778502	17793323	Os10g0477000	Armadillo-like helical domain containing protein
	10	17794333	17799688	Os10g0477100	Pectin methyltransferase, Maintenance of the cell wall properties in pistil transmitting tissues, Pectin modification
	10	17800146	17803220	Os10g0477200	Pentatricopeptide repeat domain containing protein
	10	17849091	17851345	Os10g0477600	Similar to NAM / CUC2-like protein
	10	17857988	17872546	Os10g0477800	Similar to Nuclear transportin. (Os10t0477800-01)
	10	17873385	17876746	Os10g0477900	Similar to NAD dependent epimerase/dehydratase family protein, expressed
	10	17888297	17889724	Os10g0478000	Transcriptional regulator, Regulator of meristem activity, Regulation of inflorescence development
	10	17905870	17910800	Os10g0478100	Heat shock protein DnaJ, N-terminal domain containing protein
	10	17913831	17917765	Os10g0478200	NAD-dependent cytosolic malate dehydrogenase (CMDH), Starch synthesis, Seed development
	10	17923596	17926286	Os10g0478300	SG2-type MYB transcription factor, Resistance to fungal and bacterial pathogens
	10	17945273	17946549	Os10g0478450	MATH domain containing protein

	10	17949628	17952014	Os10g0478500	MATH domain containing protein
	10	17967690	17971234	Os10g0478900	Multi-organelle localized protein, Control of leaf senescence, Disease resistance, Salt tolerance
	10	18000856	18005796	Os10g0479500	Similar to carboxy-lyase
	10	18006974	18009702	Os10g0479600	Protein Transporter, Pam16 family protein
	10	18011909	18018928	Os10g0479700	Protein of unknown function DUF250 domain containing protein
	10	18038745	18040810	Os10g0479800	Protein of unknown function DUF1336 domain containing protein
	10	18051857	18056890	Os10g0479900	Transcriptional factor B3 family protein
	10	18085539	18092497	Os10g0480200	Similar to Rolled leaf1. (Os10t0480200-01);Similar to Rolled leaf1. (Os10t0480200-02);Similar to Homeobox-leucine zipper protein HOX9. (Os10t0480200-03)
	10	18102674	18108764	Os10g0480500	Double-stranded RNA-binding protein 2, Modulation of leaf rolling by regulating accumulation of microRNAs related to leaf development (Os10t0480500-01)
	10	18120546	18121067	Os10g0480900	Similar to H0515C11
	10	18141088	18142764	Os10g0481100	Similar to Aquaporin
	10	18145792	18149595	Os10g0481300	Similar to Glutathione S-transferase, N-terminal domain containing protein
	10	18150730	18152862	Os10g0481400	Similar to Zinc finger, C3HC4 type family protein, expressed
	10	18153642	18156878	Os10g0481450	Similar to Zinc finger, C3HC4 type family protein, expressed
	10	18169120	18172321	Os10g0481500	Similar to Flotillin-like protein 1
	10	18203248	18205758	Os10g0482200	Cold tolerance at the booting stage
	10	18214554	18217773	Os10g0482450	Similar to Flotillin-like protein 3
	10	18225297	18227300	Os10g0482700	Similar to Flotillin-like protein 2
	10	18231655	18236510	Os10g0482900	Thioredoxin fold domain containing protein
	10	18240660	18243388	Os10g0483000	Basal transcription factor 3-like protein, Vegetative growth and reproductive development
<i>qST11</i>	11	5755644	5758642	Os11g0210600	Similar to Alcohol dehydrogenase
	11	5773790	5777594	Os11g0211200	Similar to Tubulin-specific chaperon-like protein
	11	5777015	5787839	Os11g0211300	Similar to NBS-LRR disease resistance protein homologue
	11	5798254	5799120	Os11g0211600	Similar to Leucine Rich Repeat family protein
	11	5799558	5802020	Os11g0211650	Similar to Leucine Rich Repeat family protein
	11	5808714	5809427	Os11g0211800	Cysteine-rich peptide, Short-chain peptide, ABA-dependent drought tolerance
	11	5820879	5826729	Os11g0212000	Similar to Leucine Rich Repeat family protein, expressed
	11	5828346	5828666	Os11g0212100	Similar to NBS-LRR disease resistance protein family-4
	11	5839249	5840796	Os11g0212300	Similar to Protein kinase domain containing protein, expressed
	11	5859750	5868313	Os11g0212900	Serine/threonine protein kinase-related domain containing protein
	11	5873537	5881813	Os11g0213000	Similar to Protein kinase domain containing protein, expressed
	11	5895364	5897167	Os11g0213500	Pentatricopeptide repeat protein, Mitochondrial nad7 transcript editing, Seed development
	11	5898818	5902693	Os11g0213600	Peptidase S10, serine carboxypeptidase family protein
	11	5908294	5911943	Os11g0213700	Leucine-rich repeat, typical subtype containing protein
	11	5916975	5919022	Os11g0213800	Similar to NBS-LRR disease resistance protein homologue
	11	5936538	5938449	Os11g0214100	Plant disease resistance response protein domain containing protein
	11	5947363	5948231	Os11g0214400	Plant disease resistance response protein family protein
	11	5962686	5974624	Os11g0214700	Plant disease resistance response protein domain containing protein
	11	5978273	5978986	Os11g0214900	Plant disease resistance response protein family protein
	11	5996508	5997392	Os11g0215100	Plant disease resistance response protein family protein.
	11	6020972	6024097	Os11g0215400	Peptidase aspartic, catalytic domain containing protein
	11	6059390	6065434	Os11g0216000	Pyruvate kinase, Regulation of seed germination, Glycolytic metabolism and GA/ABA balance
	11	6065311	6066797	Os11g0216100	Similar to Heat shock protein binding protein
	11	6068242	6073759	Os11g0216300	ABC-1 domain containing protein
	11	6088031	6091472	Os11g0216400	Peptidase S8, subtilisin-related domain containing protein
	11	6102863	6106487	Os11g0216900	Similar to IDI2
	11	6109578	6113725	Os11g0217300	Mevalonate and galactokinase family protein
	11	6114798	6127569	Os11g0217500	Similar to mRNA capping enzyme, C-terminal domain containing protein, expressed

	11	6143031	6146613	Os11g0218000	bZIP transcription factor, bZIP-1 domain containing protein
	11	6146834	6148416	Os11g0218100	Similar to RNAPol24
	11	6155842	6156093	Os11g0218200	Similar to RNAPol24
	11	6187696	6188042	Os11g0218560	Similar to Protein kinase domain containing protein, expressed
	11	6188378	6188807	Os11g0218619	Similar to Protein kinase domain containing protein, expressed
	11	6189723	6190015	Os11g0218678	Similar to Protein kinase domain containing protein, expressed
	11	6192714	6193229	Os11g0218737	Similar to Protein kinase domain containing protein, expressed
	11	6201172	6204657	Os11g0219000	Peptidase S16, lon N-terminal domain containing protein
	11	6218498	6226650	Os11g0219400	Ankyrin repeat containing protein
<i>qST12</i>	12	26506314	26507238	Os12g0621400	Conserved hypothetical protein
	12	26507440	26513551	Os12g0621500	Similar to IRE
	12	26543468	26544296	Os12g0621832	Similar to H0315A08.1 protein
	12	26548466	26555878	Os12g0621900	Similar to Mov34/MPN/PAD-1 family protein, expressed
	12	26578011	26580981	Os12g0622500	Homologue of the archaeal topoisomerase VIA, Mediation of double-strand DNA cleavage, Required for meiosis
	12	26599762	26604728	Os12g0622900	Mov34/MPN/PAD-1 family protein
	12	26621211	26626093	Os12g0623500	Similar to Cationic amino acid transporter-like protein
	12	26629926	26632504	Os12g0623600	Protein of unknown function DUF1637 family protein
	12	26635697	26637314	Os12g0623800	Similar to GLA1
	12	26645025	26651101	Os12g0623900	Similar to Ethylene-responsive methionine synthase
	12	26657277	26662924	Os12g0624000	Similar to Methionine synthase protein
	12	26663164	26664821	Os12g0624100	Similar to Small heat shock-like protein
	12	26669155	26670534	Os12g0624200	Similar to K-exchanger-like protein
	12	26684734	26685828	Os12g0624700	Protein of unknown function DUF1677
	12	26693520	26696511	Os12g0624900	Similar to GATA transcription factor 2
	12	26698650	26703087	Os12g0625000	O-acetylserine(thiol) lyase, Cysteine synthase
	12	26759757	26762339	Os12g0626100	Similar to HEAT-like
	12	26768220	26768893	Os12g0626200	Auxin responsive SAUR protein family protein
	12	26770732	26779064	Os12g0626300	Similar to MRNA, complete cds, clone
	12	26780492	26783584	Os12g0626400	Similar to Phytoene synthase 1, chloroplast precursor (EC 2.5.1.-) (Fruit ripening specific protein pTOM5)
	12	26793127	26793851	Os12g0626500	Similar to late embryogenesis abundant protein D-34
	12	26888810	26890166	Os12g0628100	Similar to Actin-depolymerizing factor 6 (ADF-6) (AtADF6)
	12	26902158	26905922	Os12g0628400	Fatty acid 2-hydroxylase, Resistance to rice blast fungus infection
	12	26906313	26910025	Os12g0628500	Similar to Methionine aminopeptidase
	12	26913087	26913851	Os12g0628600	Similar to Thaumatin-like pathogenesis-related protein 3 precursor
	12	26922175	26922699	Os12g0629300	Similar to Thaumatin-like protein
	12	26932273	26933292	Os12g0629600	Thaumatin-like protein
	12	26946904	26947698	Os12g0629700	Similar to Thaumatin-like protein precursor
	12	26956203	26956894	Os12g0630100	Thaumatin protein, Tolerance to nitrogen deficiency
	12	26960487	26961383	Os12g0630200	Thaumatin, pathogenesis-related family protein
	12	26980121	26981082	Os12g0630500	Similar to Thaumatin-like protein
	12	26985401	26986264	Os12g0630600	Carbohydrate/puine kinase, PfkB, conserved site containing protein

Table S2. Gene ontology (GO) terms and annotations for the differentially expressed genes.

QTL	RAP-DB id	MSU id	Putative Function	GOSlim ID	GO Name	Type
qST1.1	Os01g0199400	LOC_Os01g10250	hydrolase, alpha/beta fold family domain containing protein, expressed	GO:0008152	metabolic process	P
	Os01g0199400	LOC_Os01g10250	hydrolase, alpha/beta fold family domain containing protein, expressed	GO:0016787	hydrolase activity	F
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0007275	multicellular organismal development	P
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0008152	metabolic process	P
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0000166	nucleotide binding	F
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0003824	catalytic activity	F
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0009058	biosynthetic process	P
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
	Os01g0199900	LOC_Os01g10280	phosphoribosylaminoimidazole carboxylase, chloroplast precursor, putative, expressed	GO:0009536	plastid	C
qST1.2	Os01g0200700	LOC_Os01g10400	No Plant GOSlim ID has been assigned for LOC_Os01g10400.1			
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0016787	hydrolase activity	F
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0006950	response to stress	P
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0009607	response to biotic stimulus	P
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0008152	metabolic process	P
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0009987	cellular process	P
	Os01g0934900	LOC_Os01g70860	esterase, putative, expressed	GO:0006629	lipid metabolic process	P
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0006950	response to stress	P
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0009607	response to biotic stimulus	P
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0008152	metabolic process	P
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0003824	catalytic activity	F
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0016020	membrane	C
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0005773	vacuole	C

	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0016787	hydrolase activity	F
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0005488	binding	F
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0005618	cell wall	C
	Os01g0941200	LOC_Os01g71380	glycosyl hydrolases family 17, putative, expressed	GO:0009628	response to abiotic stimulus	P
qST2	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0005634	nucleus	C
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0009653	anatomical structure morphogenesis	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0030154	cell differentiation	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0007275	multicellular organismal development	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0009605	response to external stimulus	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0009628	response to abiotic stimulus	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0009058	biosynthetic process	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
	Os02g0674800	LOC_Os02g45250	homeobox and START domains containing protein, putative, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
qST3	Os03g0767800	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	GO:0003674	molecular_function	F
	Os03g0767800	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	GO:0016020	membrane	C
	Os03g0767800	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	GO:0005773	vacuole	C
	Os03g0767800	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	GO:0006950	response to stress	P
	Os03g0767800	LOC_Os03g55850	cold acclimation protein WCOR413, putative, expressed	GO:0005886	plasma membrane	C
	Os03g0769050	LOC_Os03g55920	hydrolase, acting on carbon-nitrogen, putative, expressed	GO:0003674	molecular_function	F
	Os03g0769050	LOC_Os03g55920	hydrolase, acting on carbon-nitrogen, putative, expressed	GO:0008150	biological_process	P
	Os03g0769700	LOC_Os03g55980	expressed protein	GO:0003674	molecular_function	F
	Os03g0769700	LOC_Os03g55980	expressed protein	GO:0008150	biological_process	P
	Os03g0769700	LOC_Os03g55980	expressed protein	GO:0005886	plasma membrane	C
	Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0003677	DNA binding	F

Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0005634	nucleus	C
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0007275	multicellular organismal development	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0009058	biosynthetic process	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0009653	anatomical structure morphogenesis	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0000003	reproduction	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0009791	post-embryonic development	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0009790	embryo development	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0009908	flower development	P
Os03g0769800	LOC_Os03g55990	homeobox domain containing protein, expressed	GO:0003700	sequence-specific DNA binding transcription factor activity	F
Os03g0773150	LOC_Os03g56241	40S ribosomal protein S29, putative, expressed	GO:0005840	ribosome	C
Os03g0773150	LOC_Os03g56241	40S ribosomal protein S29, putative, expressed	GO:0006412	translation	P
Os03g0773150	LOC_Os03g56241	40S ribosomal protein S29, putative, expressed	GO:0005829	cytosol	C
Os03g0773150	LOC_Os03g56241	40S ribosomal protein S29, putative, expressed	GO:0005198	structural molecule activity	F
Os03g0773600	LOC_Os03g56260	kinesin motor domain containing protein, putative, expressed	GO:0009987	cellular process	P
Os03g0773600	LOC_Os03g56260	kinesin motor domain containing protein, putative, expressed	GO:0008152	metabolic process	P
Os03g0773600	LOC_Os03g56260	kinesin motor domain containing protein, putative, expressed	GO:0000166	nucleotide binding	F
Os03g0773600	LOC_Os03g56260	kinesin motor domain containing protein, putative, expressed	GO:0003774	motor activity	F
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0003824	catalytic activity	F
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0008150	biological_process	P
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0006950	response to stress	P
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0009607	response to biotic stimulus	P
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0008152	metabolic process	P
Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0009058	biosynthetic process	P

	Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0005975	carbohydrate metabolic process	P
	Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0009987	cellular process	P
	Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0005829	cytosol	C
	Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0006091	generation of precursor metabolites and energy	P
	Os03g0776000	LOC_Os03g56460	glucose-6-phosphate isomerase, putative, expressed	GO:0009056	catabolic process	P
qST6	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0003723	RNA binding	F
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0005634	nucleus	C
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0000166	nucleotide binding	F
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0005488	binding	F
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0006950	response to stress	P
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0009607	response to biotic stimulus	P
	Os06g0170500	LOC_Os06g07350	RNA-binding motif protein, putative, expressed	GO:0003676	nucleic acid binding	F
	Os06g0171900	LOC_Os06g07540	WD-40 repeat family protein, putative, expressed	GO:0005622	intracellular	C
	Os06g0171900	LOC_Os06g07540	WD-40 repeat family protein, putative, expressed	GO:0005886	plasma membrane	C
	Os06g0171900	LOC_Os06g07540	WD-40 repeat family protein, putative, expressed	GO:0008150	biological_process	P
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0008152	metabolic process	P
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0005575	cellular_component	C
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0006950	response to stress	P
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0009628	response to abiotic stimulus	P
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0008150	biological_process	P
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0016787	hydrolase activity	F
	Os06g0172800	LOC_Os06g07600	uncharacterized glycosyltransferase, putative, expressed	GO:0009536	plastid	C
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0016020	membrane	C
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0006810	transport	P
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0009987	cellular process	P

	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0003824	catalytic activity	F
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0005215	transporter activity	F
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0005739	mitochondrion	C
	Os06g0177000	LOC_Os06g07969	cytochrome b-c1 complex subunit 8, putative, expressed	GO:0008152	metabolic process	P
	Os06g0179000	LOC_Os06g08090	heparanase-like protein precursor, putative, expressed	GO:0005618	cell wall	C
	Os06g0179000	LOC_Os06g08090	heparanase-like protein precursor, putative, expressed	GO:0008152	metabolic process	P
	Os06g0179000	LOC_Os06g08090	heparanase-like protein precursor, putative, expressed	GO:0008150	biological_process	P
	Os06g0179000	LOC_Os06g08090	heparanase-like protein precursor, putative, expressed	GO:0016787	hydrolase activity	F
qST8	Os08g0534350	LOC_Os08g42210	expressed protein	GO:0003674	molecular_function	F
	Os08g0534350	LOC_Os08g42210	expressed protein	GO:0008150	biological_process	P
	Os08g0535000	LOC_Os08g42290	expressed protein	GO:0003674	molecular_function	F
	Os08g0535000	LOC_Os08g42290	expressed protein	GO:0008150	biological_process	P
	Os08g0536200	LOC_Os08g42430	No Plant GOSlim ID has been assigned for LOC_Os08g42430.1			
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0019538	protein metabolic process	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0009987	cellular process	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0005634	nucleus	C
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0006810	transport	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0005737	cytoplasm	C
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0000003	reproduction	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0009791	post-embryonic development	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0006950	response to stress	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0009607	response to biotic stimulus	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0008150	biological_process	P
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0016020	membrane	C
	Os08g0539600	LOC_Os08g42690	ankyrin repeat domain containing protein, expressed	GO:0009536	plastid	C
qST10	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0003824	catalytic activity	F
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0008152	metabolic process	P
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0005575	cellular_component	C
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0005975	carbohydrate metabolic process	P
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0006091	generation of precursor	P

	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0009056	metabolites and energy catabolic process	P
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0009987	cellular process	P
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0005488	binding	F
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0005829	cytosol	C
	Os10g0478200	LOC_Os10g33800	lactate/malate dehydrogenase, putative, expressed	GO:0005886	plasma membrane	C
	Os10g0478900	LOC_Os10g33855	No Plant GOSlim ID has been assigned for LOC_Os10g33855.1			
	Os10g0481450	LOC_Os10g34030	zinc finger, C3HC4 type domain containing protein, expressed	GO:0003674	molecular_function	F
	Os10g0481450	LOC_Os10g34030	zinc finger, C3HC4 type domain containing protein, expressed	GO:0008150	biological_process	P
qST11	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0006950	response to stress	P
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0009628	response to abiotic stimulus	P
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0008152	metabolic process	P
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0003824	catalytic activity	F
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0008150	biological_process	P
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0005829	cytosol	C
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0006091	generation of precursor metabolites and energy	P
	Os11g0210600	LOC_Os11g10520	dehydrogenase, putative, expressed	GO:0005886	plasma membrane	C
	Os11g0212100	LOC_Os11g10620	NBS-LRR disease resistance protein, putative, expressed	GO:0005623	cell	C
	Os11g0212100	LOC_Os11g10620	NBS-LRR disease resistance protein, putative, expressed	GO:0000166	nucleotide binding	F
	Os11g0212100	LOC_Os11g10620	NBS-LRR disease resistance protein, putative, expressed	GO:0006950	response to stress	P
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0007165	signal transduction	P
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0008152	metabolic process	P
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0000166	nucleotide binding	F
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0005623	cell	C
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0016020	membrane	C
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0006950	response to stress	P
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0004872	receptor activity	F

	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0004871	signal transducer activity	F
	Os11g0213700	LOC_Os11g10760	NBS-LRR disease resistance protein, putative, expressed	GO:0016787	hydrolase activity	F
	Os11g0213800	LOC_Os11g10770	disease resistance protein RGA3, putative, expressed	GO:0005515	protein binding	F
	Os11g0213800	LOC_Os11g10770	disease resistance protein RGA3, putative, expressed	GO:0006950	response to stress	P
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0005623	cell	C
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0003674	molecular_function	F
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0009058	biosynthetic process	P
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0006464	protein modification process	P
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0006950	response to stress	P
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0009987	cellular process	P
	Os11g0215100	LOC_Os11g10870	dirigent, putative, expressed	GO:0019748	secondary metabolic process	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0008152	metabolic process	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0009987	cellular process	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0000166	nucleotide binding	F
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0009856	pollination	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0007275	multicellular organismal development	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0005975	carbohydrate metabolic process	P
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0016301	kinase activity	F
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0005829	cytosol	C
	Os11g0217300	LOC_Os11g11060	GHMP kinases ATP-binding protein, putative, expressed	GO:0003723	RNA binding	F
qST12	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0016020	membrane	C
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005576	extracellular region	C
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005634	nucleus	C
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0003824	catalytic activity	F
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005777	peroxisome	C
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0008150	biological_process	P
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005773	vacuole	C
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005515	protein binding	F
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0009058	biosynthetic process	P
	Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0009987	cellular process	P

Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005829	cytosol	C
Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0005886	plasma membrane	C
Os12g0625000	LOC_Os12g42980	cysteine synthase, putative, expressed	GO:0009536	plastid	C
Os12g0630200	LOC_Os12g43450	thaumatin family domain containing protein, expressed	GO:0005623	cell	C
Os12g0630200	LOC_Os12g43450	thaumatin family domain containing protein, expressed	GO:0006950	response to stress	P
Os12g0630200	LOC_Os12g43450	thaumatin family domain containing protein, expressed	GO:0009607	response to biotic stimulus	P
Os12g0630200	LOC_Os12g43450	thaumatin family domain containing protein, expressed	GO:0009628	response to abiotic stimulus	P