

Figure S1. Defence genes expression during fungus infection or chitin treatment.

Expression of *Chitinase1* and *PBZ1* in rice plants infected with *M. oryzae* (a) and expression of *PAL1* and *PBZ1* in rice suspension cells treated with chitin (b) were quantified by qRT-PCR with three biological replicates. Error bars indicate S.E. Statistically significant differences between infected plants or treated suspension cells with mock controls are depicted with asterisks (*, $P < 0.05$; **, $P < 0.01$ and ***, $P < 0.001$) according to the two-tailed *t*-test.

(a)

1.5 0 -1.5

1 d 2 d 3 d

Cluster 1
6 genes

LOC_Os07g38630				expressed protein
LOC_Os03g55290				GASR3 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed
LOC_Os03g44450				expressed protein
LOC_Os01g04050				BBT112 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
LOC_Os03g63740				NFD2, putative, expressed

LOC_Os01g03320				beta-expansin precursor, putative, expressed
LOC_Os08g37930				phytosulfokines precursor, putative, expressed
LOC_Os07g03200				SCP-like extracellular protein, expressed
LOC_Os01g28500				WIP4 - Wound-induced protein precursor, expressed
LOC_Os11g37960				Cupin domain containing protein, expressed

LOC_Os03g58980				PME/invertase inhibitor, putative, expressed
LOC_Os04g29810				membrane associated DUF588 domain containing protein, putative, expressed
LOC_Os04g36770				expressed protein
LOC_Os11g42970				WIP5 - Wound-induced protein precursor, expressed
LOC_Os12g12090				thaumatin, putative, expressed

Cluster 2
24 genes

LOC_Os11g37970				cupin domain containing protein, expressed
LOC_Os12g43440				LTPL11 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os10g41710				stromal cell-derived factor 2-like protein precursor, putative, expressed
LOC_Os08g13440				dirigent, putative, expressed
LOC_Os12g02310				zinc finger, C3HC4 type domain containing protein, expressed

LOC_Os08g17680				LTPL7 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os11g42550				expressed protein
LOC_Os07g48680				Cupin domain containing protein, expressed
LOC_Os02g37200				CHIT2 - Chitinase family protein precursor, expressed
LOC_Os11g02369				LTPL98 - Protease inhibitor/seed storage/LTP family protein precursor, expressed

Cluster 3
10 genes

LOC_Os10g34940				expressed protein
LOC_Os02g32980				expressed protein
LOC_Os04g41620				expressed protein
LOC_Os11g34660				expressed protein
LOC_Os11g13750				hypothetical protein

LOC_Os12g11550				expressed protein
LOC_Os11g31530				SCP-like extracellular protein, expressed
LOC_Os12g11980				glycine rich protein family protein, putative, expressed
LOC_Os07g03710				expressed protein
LOC_Os06g21270				wall-associated receptor kinase-like 5 precursor, putative, expressed

Cluster 4
21 genes

LOC_Os09g10010				expressed protein
LOC_Os10g34930				secretory protein, putative, expressed
LOC_Os08g24200				expressed protein
LOC_Os03g52390				PIII1 - Proteinase inhibitor II family protein precursor, expressed
LOC_Os03g01320				LTPL116 - Protease inhibitor/seed storage/LTP family protein precursor, expressed

LOC_Os11g37950				LTPL114 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os03g01300				Cupin domain containing protein, expressed
LOC_Os08g09080				RIPER6 - Ripening-related family protein precursor, expressed
LOC_Os10g34840				expressed protein
LOC_Os06g20820				citrate-binding protein precursor, putative, expressed

Cluster 5
9 genes

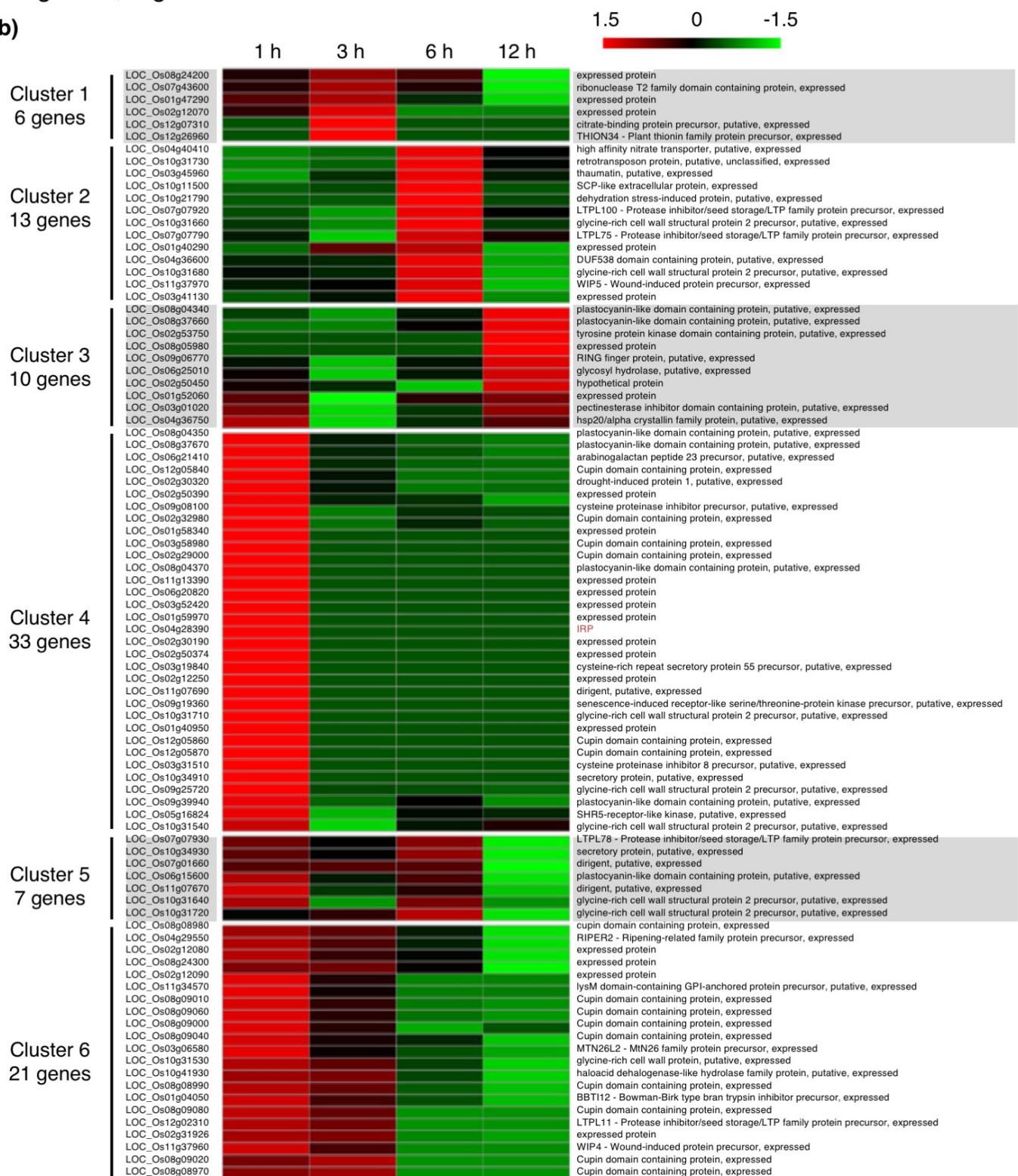
LOC_Os12g07310				thaumatin, putative, expressed
LOC_Os02g12070				Cupin domain containing protein, expressed
LOC_Os12g43390				glycine rich protein family protein, putative, expressed
LOC_Os08g09010				protease inhibitor/seed storage/LTP family, putative, expressed
LOC_Os06g21210				LTPL152 - Protease inhibitor/seed storage/LTP family protein precursor, expressed

Cluster 7
7 genes

LOC_Os05g47700				expressed protein
LOC_Os08g30510				SCP-like extracellular protein, expressed
LOC_Os01g28450				expressed protein
LOC_Os06g39110				SCP-like extracellular protein, expressed
LOC_Os07g03730				thaumatin, putative, expressed

LOC_Os04g29550				DUF538 domain containing protein, putative, expressed
LOC_Os04g36600				lysine-rich arabinogalactan protein 19 precursor, putative, expressed
LOC_Os03g56944				meiosis 5, putative, expressed
LOC_Os07g44250				pectinesterase inhibitor domain containing protein, putative, expressed
LOC_Os02g12150				canopy homolog 2 precursor, putative, expressed

(b)

**Figure S2. Clustering analysis of the expression profiles of up-regulated SSP genes**

The *k*-means algorithm was used to cluster up-regulated SSP genes in plants (a) and suspension cells (b) using the Pearson correlation coefficient as the distance metric. The colour scale indicates the relative expression levels of SSP genes: red indicates higher expression, while green indicates lower expression.

(a)

OsRALFL6|LOC_Os01g25540
 OsRALFL7|LOC_Os01g25560
 OsRALFL8|LOC_Os02g44940
 AtRALF23|AT3G16570

1 --MAKSLLAASALLAL-LLAVA-G-GA-----AAAGEVPL-AW-----ELGVGGGG 41
 1 MARPAI-VAAPALLLAL-LIALATGGAD-----AAPGEVPL-SW-----ELGVV--- 42
 1 MARAATVAAASSALLAL-LLALAWG-AA-----AGAGEVPL-GW-----ELGVGVGG 45
 1 MRGLSRNSGAAAIFAILLILAVHNWSVAVSSQSTEFAGDFPPFETECRGTTIAECSVSAAL 60

OsRALFL6|LOC_Os01g25540
 OsRALFL7|LOC_Os01g25560
 OsRALFL8|LOC_Os02g44940
 AtRALF23|AT3G16570

42 GGGEEEDSF--GFSSEDAADGAAVVRRVLQQCYISYGALRRDTTPCSVRGASYYNCRPG 99
 43 --GADDAF--GFPGEAADSATAVVRRVLQQGSYISYGALRRDTTPCSVRGASYYNCQPG 98
 46 GSGDDDGFF-GFSG--AAADGAAVVRRVLQQGYISYGALRRDTTPCSVRGASYYNCRPG 101
 61 GDGGDLFYGGGEMGE-EFEMDSEINRRILATRFYISYGALRRNTTPCSRGRGASYYNCRRG 119

OsRALFL6|LOC_Os01g25540
 OsRALFL7|LOC_Os01g25560
 OsRALFL8|LOC_Os02g44940
 AtRALF23|AT3G16570

100 QQANPYSRGCSAITRCRG- 117
 99 AEANPYSRGCSAITQCRG- 116
 102 QQANPYSRGCSAITRCRG- 119
 120 AQANPYSRGCSAITRCRRS 138

(b)

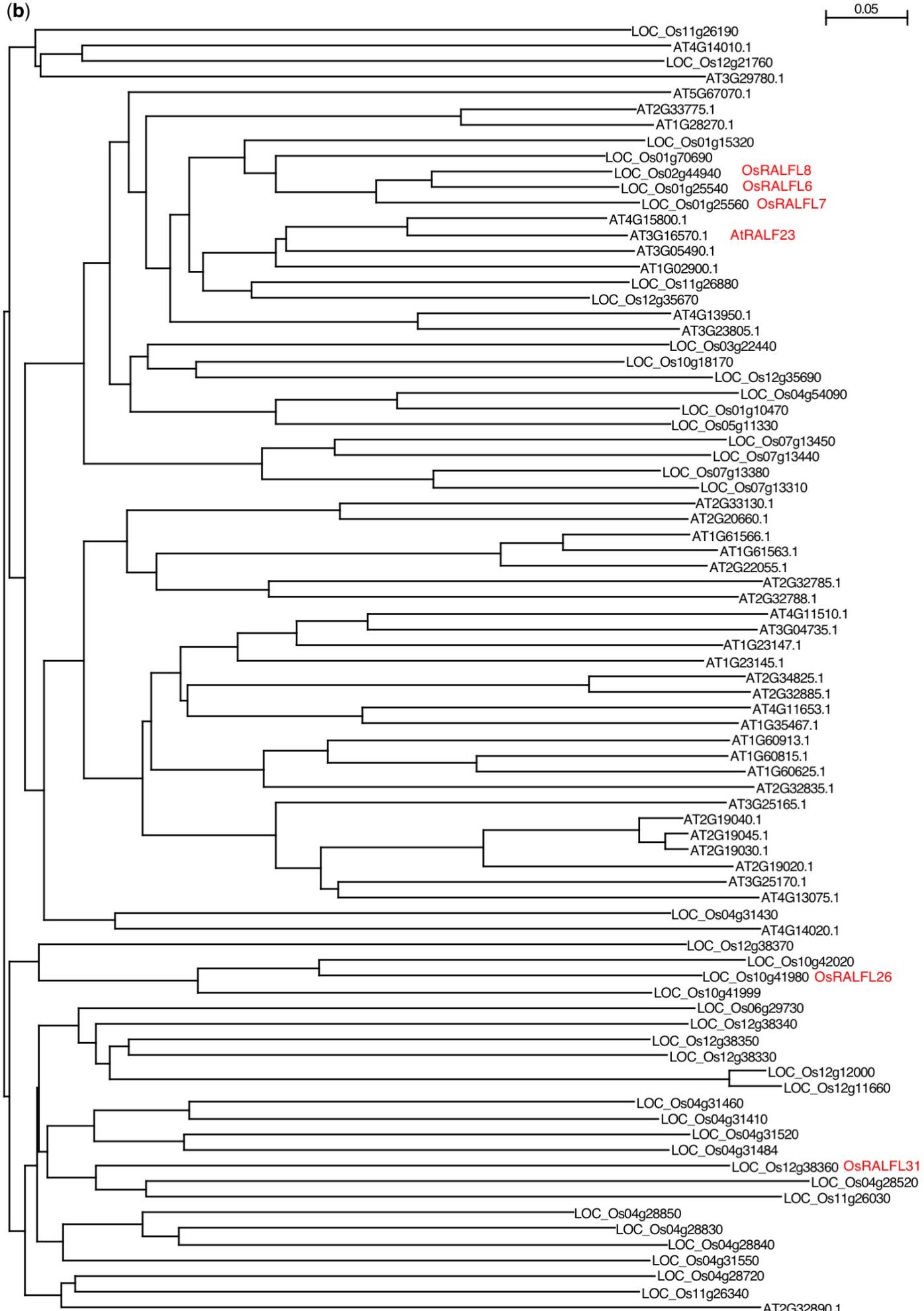
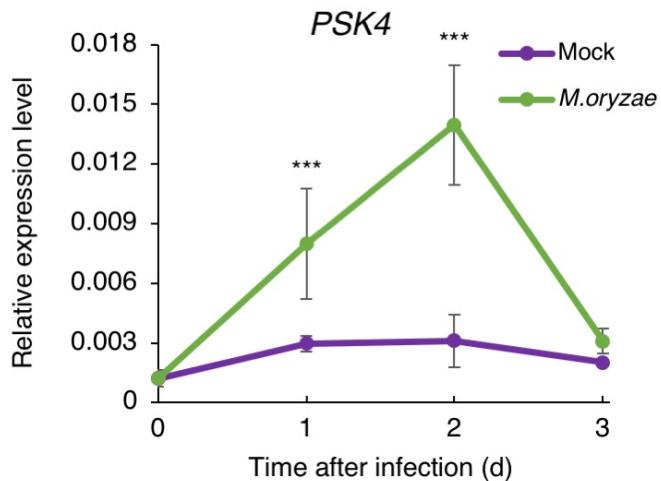


Figure S3. Phylogenetic analysis of RALFs in rice and *Arabidopsis*.

Alignment of RALF proteins. Predicted N-terminal signal sequences are in a blue box, the RR motifs are in an orange box, and the YISY motifs are in a green box. Blue and grey arrowheads indicate the cleavage sites and the conserved cysteine residues, respectively. (b) Phylogenetic tree of RALFs in rice and *Arabidopsis*. Multiple sequence alignment and phylogenetic tree analysis were performed by Clustal Omega (<http://www.ebi.ac.uk/Tools/msa/clustalo/>), and the tree was drawn using NJplot (Mac: Ver. 2.3) using the neighbour-joining method.

(a)



(b)

OsPSK1	1 MVNPGRTA---RALCLLCALLLGGQDTHS-----RKLLLQEKGHSHGVG-----	41
OsPSK2	1 MSTTRGVSSSSAAALALLLFALCFFSFH---FAAAARAPRDEHQENGKVAVAIAAA	57
OsPSK3	1 MRPTGRRSSPPVAAALALLLVLFFFSHC---ASAARPLPASAAAELVLQ-----	48
OsPSK4	1 -MAARTVA---VAAALAVLLIFAAASSATVA---MAGRPTPTTSL-----	37
OsPSK5	1 --MSPKVI---AICLVALLLPISISHCGRI---GPIEPSKASSKVVERGN-----	42
OsPSK6	1 MASSKLS---ALFLTAILLCLICTRSQAA---RPEPGSSGHKSQGV-----	41
OsPSK7	1 -MAPPRCT---ALLLASLFFLCISATHEARTASGQPQIQQEQEQEIQHGV-----	48
AtPSK1	1 MMKTKEV---LIFFFFTLVLLLSMASSVILREDGFAPPKPSPTTHEKASTKG-----	49
AtPSK4	1 ---MGKFT---TIFIMALLLCSTLTYAARL---TPTTTTALSRENSVKEI-----	41
OsPSK1	42 -----NGTTTTQEPEPSRENGG-----STGSNNNNQLQFD SAK WEEFH TD	79
OsPSK2	58 DQLVLQLEGDTGNGDEVSELMAAEEEEAAA-----CEEGKN-NDECVCRR_LSDAHL D	109
OsPSK3	49 -----DGATGNGDEVSELMAAEEEEAAAGL-----CEEG---NEECVERR_MLRDAHL D	92
OsPSK4	38 -----DEAAQAQAQSEIGGG-----CKEGEG-EEECLARR_TLT-AH TD	74
OsPSK5	43 -----YDGRVEG-----CE-----EDDCCLVER_LV-AH TD	66
OsPSK6	42 -----VASSIAHQKSVGSSIGVEMHQGEPDQAVECKGGEA-EEECLMRRTLV-AH TD	92
OsPSK7	49 -----EEFTMAASFAAVEEQ-----CGGEGEEECLMRRTLV-AH TD	85
AtPSK1	50 -----DRDGVE-----CKNSDS-EEECLVKKTVVA-AH TD	76
AtPSK4	42 -----EGDKVEEES-----CNGIG--EEECLIRRSLV-LH TD	70
OsPSK1	80 YIYTQDVK-KP	89
OsPSK2	110 YIYTQHKN-KP	119
OsPSK3	93 YIYTQKRN-RP	102
OsPSK4	75 YIYTQQ-H-HN	83
OsPSK5	67 YIYTQG-K-HN	75
OsPSK6	93 YIYTQG-N-HN	101
OsPSK7	86 YIYTQG-N-HN	94
AtPSK1	77 YIYTQDLNLSP	87
AtPSK4	71 YIYTQN-H-KP	79

(c)

OsPSK1 LOC_Os06g42680.2	0.42331
AtPSK3 At3g44735	0.36594
OsPSK2 LOC_Os11g05190.1	0.19209
OsPSK3 LOC_Os12g05260.1	0.14454
OsPSK5 Os03g0675600 LOC_Os03g47230.1	0.30189
OsPSK7 LOC_Os11g35310.1	0.28477
AtPSK1 At1g13590	0.35457
OsPSK4 LOC_Os07g03200.1	0.27364
AtPSK2 At2g22860	0.20002
AtPSK6 At4g37720	0.22351
AtPSK4 At3g49780	0.18706
AtPSK5 At5g65870	0.15078
OsPSK6 LOC_Os03g12990.1	0.27981

Figure S4. Expression analysis of OsPSK4 and phylogenetic analysis of PSKs in rice and *Arabidopsis*.

(a) The OsPSK4 expression in rice plants infected with *M. oryzae* was quantified by qRT-PCR. Error bars indicate S.E. Statistically significant differences between infected plants and mock control are depicted with asterisks (***, $P < 0.001$) according to the two-tailed *t*-test. (b) Protein alignment of PSKs. Predicted N-terminal signal sequences are in a blue box, the RR motifs are in an orange box, and the YIYTQ motifs are in a green box. A blue arrowhead indicates the putative cleavage site. (c) Phylogenetic trees of PSKs in rice and *Arabidopsis*. Multiple sequence alignments and phylogenetic construction using the neighbour-joining method without distance corrections were made by Clustal Omega.

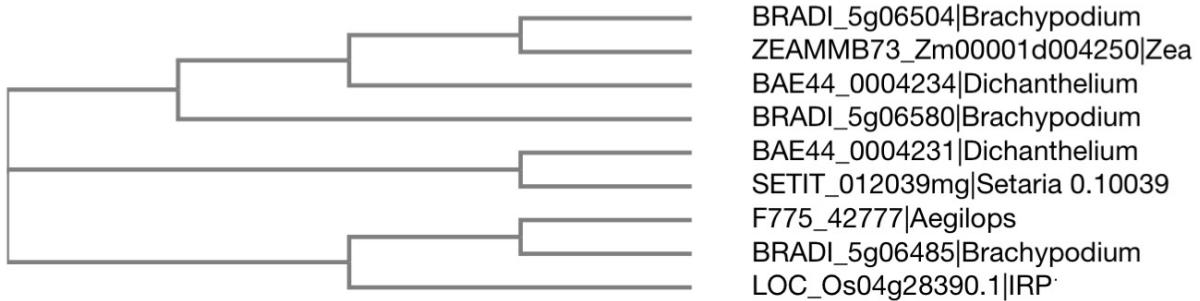


Figure S5. Phylogenetic tree of IRP.

Multiple sequence alignments and phylogenetic construction using the neighbour-joining method without distance corrections were made by Clustal Omega.

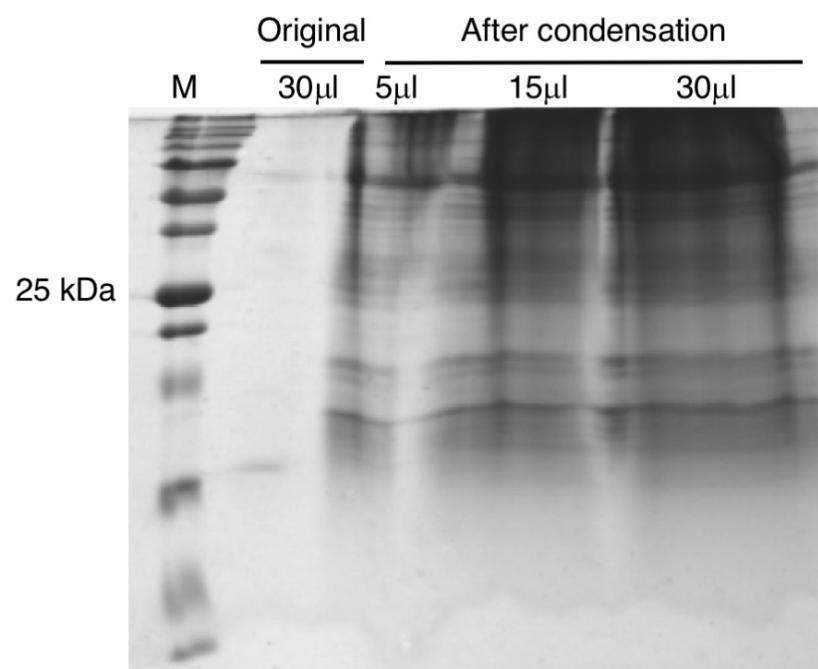
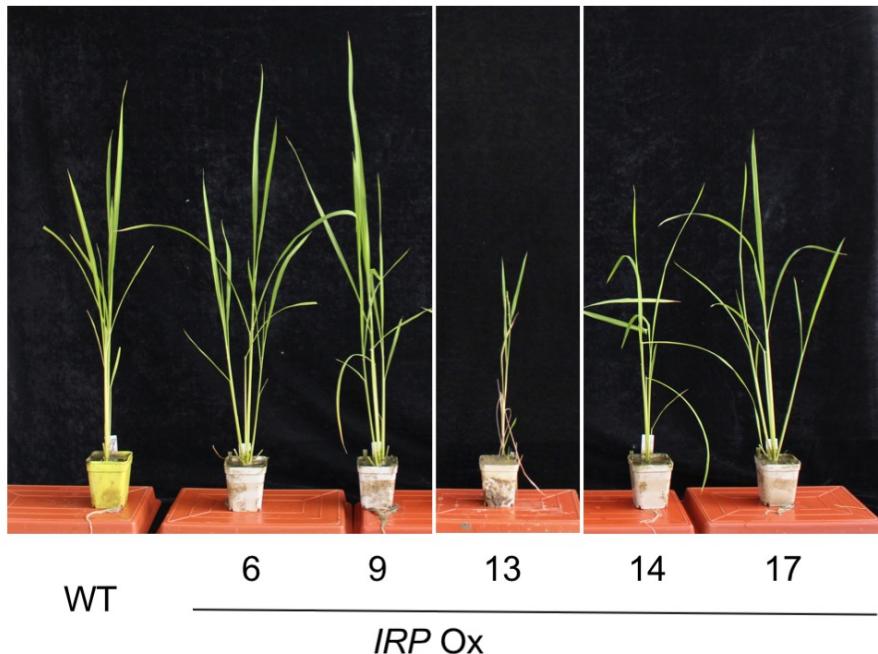


Figure S6. SDS-PAGE analysis of protein in medium sample after anion-exchange chromatography and acetone precipitation

(a)



(b)

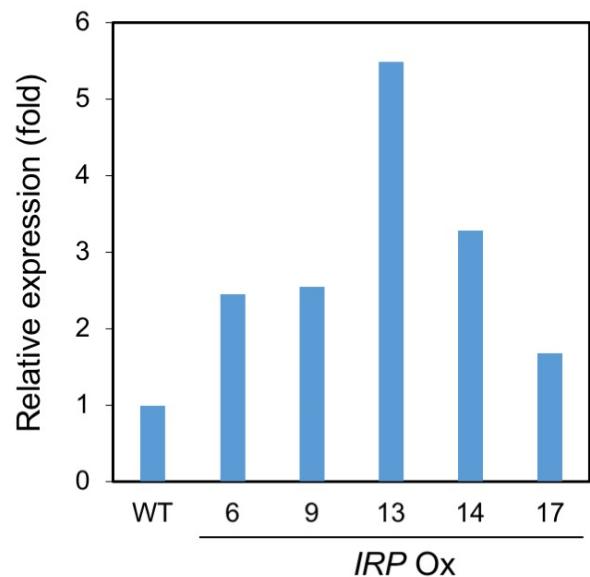


Figure S7. Phenotype of plants overexpressing *IRP*

Phenotype of plants overexpressing *IRP*. (b) Expression level of *IRP* was quantified by qRT-PCR.

Table S1. GO terms of upregulated genes overlapping in plants and suspension cells**P:** Biological process, **F:** molecular function, **C:** cellular component.The significant GOs (*p*-value < 0.01) were chosen.

BP	GO.ID	Term	Annotated	Significant	Expected	<i>p</i> -value
MF	1 GO:0006468	protein phosphorylation	1546	50	10	6E-21
	2 GO:0009607	response to biotic stimulus	18	6	0.12	0.00000079
	3 GO:0008152	metabolic process	9641	126	62.35	0.0000032
	4 GO:0006032	chitin catabolic process	25	4	0.16	0.000019
	5 GO:0016998	cell wall macromolecule catabolic process	43	4	0.28	0.00017
	6 GO:0050832	defense response to fungus	5	2	0.03	0.00041
	7 GO:0042742	defense response to bacterium	6	2	0.04	0.00061
	8 GO:0006559	L-phenylalanine catabolic process	8	2	0.05	0.00114
	9 GO:0016567	protein ubiquitination	71	4	0.46	0.00118
	10 GO:0006952	defense response	435	10	2.81	0.00693
CC	GO.ID	Term	Annotated	Significant	Expected	<i>pva_wei</i>
CC	1 GO:0004713	protein tyrosine kinase activity	1400	50	9.03	7.3E-23
	2 GO:0004674	protein serine/threonine kinase activity	1395	48	9	5.3E-20
	3 GO:0005524	ATP binding	2973	67	19.18	1.3E-19
	4 GO:0045735	nutrient reservoir activity	78	7	0.5	0.00000077
	5 GO:0005509	calcium ion binding	384	13	2.48	0.0000016
	6 GO:0003824	catalytic activity	8998	134	58.04	0.0000025
	7 GO:0004568	chitinase activity	25	4	0.16	0.000019
	8 GO:0020037	heme binding	605	14	3.9	0.000046
	9 GO:0030145	manganese ion binding	53	4	0.34	0.00039
	10 GO:0005488	binding	11431	149	73.73	0.00108
	11 GO:0016841	ammonia-lyase activity	8	2	0.05	0.00113
	12 GO:0004497	monooxygenase activity	413	9	2.66	0.00157
	13 GO:0004842	ubiquitin-protein transferase activity	82	4	0.53	0.002
	14 GO:0043169	cation binding	3127	36	20.17	0.0022
	15 GO:0016211	ammonia ligase activity	12	2	0.08	0.00262
	16 GO:0016887	ATPase activity	402	6	2.59	0.00292
	17 GO:0004707	MAP kinase activity	16	2	0.1	0.00469
BP	GO.ID	Term	Annotated	Significant	Expected	<i>pva_wei</i>
BP	1 GO:0048046	apoplast	71	4	0.46	0.0012
	2 GO:0000151	ubiquitin ligase complex	87	4	0.56	0.0025

Table S2. SSPs identified in our study.

P,Plant; SC, suspension cell; M, Medium.

Gene ID	Strategy	Sample	Annotation
LOC_Os06g21410	RNA-seq	SC	arabinogalactan peptide 23 precursor, putative, expressed
LOC_Os01g03310	MS	P	BBT11 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
LOC_Os01g04050	RNA-seq	SC/P	BBT12 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
LOC_Os01g03320	RNA-seq	P	BBT12 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
LOC_Os01g03390	MS	SC	BBT17 - Bowman-Birk type bran trypsin inhibitor precursor, expressed
LOC_Os08g37930	RNA-seq	P	beta-expansin precursor, putative, expressed
LOC_Os01g17250	MS	M	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed
LOC_Os01g59440	MS	M	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed
LOC_Os03g32580	MS	M	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed
LOC_Os11g31530	RNA-seq	P	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed
LOC_Os02g02524	RNA-seq	P	canopy homolog 2 precursor, putative, expressed
LOC_Os10g41710	RNA-seq/MS	SC/P	chaperonin, putative, expressed
LOC_Os04g41620	RNA-seq/MS	M/P	CHIT2 - Chitinase family protein precursor, expressed
LOC_Os12g07310	RNA-seq	SC/P	citrate-binding protein precursor, putative, expressed
LOC_Os06g13100	MS	SC/P	CREG1 precursor, putative, expressed
LOC_Os05g19670	MS	SC/P	Cupin domain containing protein, expressed
LOC_Os03g48760	MS	M/P	Cupin domain containing protein, expressed
LOC_Os01g14670	MS	M/P	Cupin domain containing protein, expressed
LOC_Os03g48770	MS	M/P	Cupin domain containing protein, expressed
LOC_Os01g72300	MS	SC/M	Cupin domain containing protein, expressed
LOC_Os03g44880	MS	M	Cupin domain containing protein, expressed
LOC_Os08g09080	RNA-seq	SC/P	Cupin domain containing protein, expressed
LOC_Os08g09060	RNA-seq	SC/P	Cupin domain containing protein, expressed
LOC_Os03g58980	RNA-seq	SC/P	Cupin domain containing protein, expressed
LOC_Os08g08980	RNA-seq	SC	cupin domain containing protein, expressed
LOC_Os08g08970	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os08g09020	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os08g09000	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os08g08990	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os08g09040	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os02g29000	RNA-seq	SC	Cupin domain containing protein, expressed
LOC_Os02g32980	RNA-seq/MS	SC/P	Cupin domain containing protein, expressed
LOC_Os08g09010	RNA-seq/MS	P/SC/M	Cupin domain containing protein, expressed
LOC_Os12g05860	RNA-seq/MS	SC/M	Cupin domain containing protein, expressed
LOC_Os12g05870	RNA-seq/MS	SC/M	Cupin domain containing protein, expressed
LOC_Os12g05840	RNA-seq/MS	SC/M	Cupin domain containing protein, expressed
LOC_Os08g13440	RNA-seq/MS	P	cupin domain containing protein, expressed
LOC_Os03g31510	RNA-seq/MS	SC/P	cysteine proteinase inhibitor 8 precursor, putative, expressed
LOC_Os01g58890	MS	P	cysteine proteinase inhibitor precursor protein, putative, expressed
LOC_Os04g28250	MS	SC/M	cysteine proteinase inhibitor precursor, putative, expressed
LOC_Os09g08100	RNA-seq	SC	cysteine proteinase inhibitor precursor, putative, expressed
LOC_Os03g19840	RNA-seq	SC	cysteine-rich repeat secretory protein 55 precursor, putative, expressed
LOC_Os07g14150	MS	M	cytidine deaminase, putative, expressed
LOC_Os08g29669	MS	SC	cytochrome b5-like Heme/Steroid binding domain containing protein, expressed
LOC_Os10g21790	RNA-seq	SC	dehydration stress-induced protein, putative, expressed
LOC_Os11g10870	MS	P	dirigent, putative, expressed
LOC_Os11g07690	RNA-seq	SC	dirigent, putative, expressed
LOC_Os07g44250	RNA-seq	P	dirigent, putative, expressed
LOC_Os11g07670	RNA-seq/MS	SC/M	dirigent, putative, expressed
LOC_Os07g01660	RNA-seq/MS	SC/M	dirigent, putative, expressed
LOC_Os11g42550	RNA-seq/MS	P	dirigent, putative, expressed
LOC_Os02g30320	RNA-seq	SC	drought-induced protein 1, putative, expressed
LOC_Os04g36600	RNA-seq	SC/P	DUF538 domain containing protein, putative, expressed
LOC_Os01g14410	RNA-seq	P	early light-induced protein, chloroplast precursor, putative, expressed
LOC_Os07g08150	RNA-seq	P	early light-induced protein, chloroplast precursor, putative, expressed
LOC_Os07g08160	RNA-seq	P	early light-induced protein, chloroplast precursor, putative, expressed
LOC_Os01g07780	MS	P	embryo-specific 3, putative, expressed
LOC_Os06g10760	MS	SC	emp24/gp25L/p24 family protein, putative, expressed
LOC_Os03g13750	MS	SC	erwinia induced protein 2, putative, expressed
LOC_Os05g39990	MS	SC	expansin precursor, putative, expressed
LOC_Os12g09620	MS	M/P	expressed protein
LOC_Os02g54680	MS	SC	expressed protein
LOC_Os07g29300	MS	M	expressed protein
LOC_Os06g09840	MS	SC	expressed protein
LOC_Os05g44160	MS	SC	expressed protein
LOC_Os05g07640	MS	SC	expressed protein
LOC_Os07g36410	MS	SC	expressed protein
LOC_Os03g07660	MS	M	expressed protein
LOC_Os11g25770	MS	M	expressed protein
LOC_Os07g09150	MS	M	expressed protein
LOC_Os03g48626	MS	P	expressed protein
LOC_Os03g39830	MS	P	expressed protein
LOC_Os03g48710	MS	P	expressed protein
LOC_Os02g12080	RNA-seq	SC/P	expressed protein
LOC_Os08g24200	RNA-seq	SC/P	expressed protein
LOC_Os02g12070	RNA-seq	SC/P	expressed protein

LOC_Os06g20820	RNA-seq	SC/P	expressed protein
LOC_Os03g41130	RNA-seq	SC	expressed protein
LOC_Os01g40290	RNA-seq	SC	expressed protein
LOC_Os02g31926	RNA-seq	SC	expressed protein
LOC_Os01g59970	RNA-seq	SC	expressed protein
LOC_Os04g28390	RNA-seq	SC	expressed protein
LOC_Os03g52420	RNA-seq	SC	expressed protein
LOC_Os08g05980	RNA-seq	SC	expressed protein
LOC_Os02g30190	RNA-seq	SC	expressed protein
LOC_Os11g13390	RNA-seq	SC	expressed protein
LOC_Os02g50390	RNA-seq	SC	expressed protein
LOC_Os02g12090	RNA-seq	SC	expressed protein
LOC_Os01g52060	RNA-seq	SC	expressed protein
LOC_Os08g24300	RNA-seq	SC	expressed protein
LOC_Os01g58340	RNA-seq	SC	expressed protein
LOC_Os01g40950	RNA-seq	SC	expressed protein
LOC_Os01g47290	RNA-seq	SC	expressed protein
LOC_Os02g12250	RNA-seq	SC	expressed protein
LOC_Os02g50374	RNA-seq	SC	expressed protein
LOC_Os12g12090	RNA-seq	P	expressed protein
LOC_Os02g12150	RNA-seq	P	expressed protein
LOC_Os06g39110	RNA-seq	P	expressed protein
LOC_Os09g10010	RNA-seq	P	expressed protein
LOC_Os03g40000	RNA-seq	P	expressed protein
LOC_Os07g38630	RNA-seq	P	expressed protein
LOC_Os04g29810	RNA-seq	P	expressed protein
LOC_Os03g44450	RNA-seq	P	expressed protein
LOC_Os01g10640	RNA-seq	P	expressed protein
LOC_Os10g07450	RNA-seq	P	expressed protein
LOC_Os10g34940	RNA-seq	P	expressed protein
LOC_Os12g11980	RNA-seq	P	expressed protein
LOC_Os08g30510	RNA-seq	P	expressed protein
LOC_Os11g13750	RNA-seq/MS	M/P	expressed protein
LOC_Os08g16130	RNA-seq	P	fiber protein Fb34, putative, expressed
LOC_Os03g55290	RNA-seq/MS	SC/P	GASR3 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed
LOC_Os06g15620	MS	SC/M	GASR7 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed
LOC_Os03g47270	MS	SC	GCRP4 - Glycine and cysteine rich family protein precursor, expressed
LOC_Os05g43690	MS	M	glucan endo-1,3-beta-glucosidase-like protein 3 precursor, putative, expressed
LOC_Os11g18170	MS	SC	glutathione peroxidase, putative, expressed
LOC_Os06g21270	RNA-seq	P	glycine rich protein family protein, putative, expressed
LOC_Os06g21210	RNA-seq	P	glycine rich protein family protein, putative, expressed
LOC_Os10g31530	RNA-seq	SC	glycine-rich cell wall protein, putative, expressed
LOC_Os10g31680	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os09g25720	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os10g31540	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os10g31660	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os10g31720	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os10g31710	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os10g31640	RNA-seq	SC	glycine-rich cell wall structural protein 2 precursor, putative, expressed
LOC_Os06g25010	RNA-seq	SC	glycosyl hydrolase, putative, expressed
LOC_Os02g48980	MS	SC/M	GPI-anchored protein, putative, expressed
LOC_Os05g09740	MS	P	HAD superfamily phosphatase, putative, expressed
LOC_Os10g41930	RNA-seq	SC	haloacid dehalogenase-like hydrolase family protein, putative, expressed
LOC_Os03g27040	MS	P	heavy metal-associated domain containing protein, expressed
LOC_Os04g40410	RNA-seq	SC	high affinity nitrate transporter, putative, expressed
LOC_Os04g36750	RNA-seq	SC	hsp20/alpha crystallin family protein, putative, expressed
LOC_Os02g37200	RNA-seq	P	hydrophobin, putative, expressed
LOC_Os02g50450	RNA-seq	SC	hypothetical protein
LOC_Os12g11550	RNA-seq	P	hypothetical protein
LOC_Os12g18560	MS	M	invertase/pectin methylesterase inhibitor family protein, putative, expressed
LOC_Os05g08920	MS	M	late embryogenesis abundant protein, putative, expressed
LOC_Os07g07920	RNA-seq	SC	LTPL100 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os12g02310	RNA-seq/MS	SC/P	LTPL11 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os03g01300	RNA-seq/MS	P	LTPL114 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os03g01320	RNA-seq	P	LTPL116 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os04g46820	MS	P	LTPL121 - Protease inhibitor/seed storage/LTP family protein precursor, putative, expressed
LOC_Os04g46830	MS	P	LTPL122 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os04g52260	MS	P	LTPL124 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os05g47700	RNA-seq	P	LTPL152 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os01g60740	MS	M	LTPL16 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os05g40010	MS	P	LTPL17 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os03g20760	RNA-seq	P	LTPL66 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os11g02369	RNA-seq/MS	P	LTPL7 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os07g07790	RNA-seq	SC	LTPL75 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os07g07930	RNA-seq/MS	SC/M	LTPL78 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os11g02400	MS	P/SC/M	LTPL8 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os06g49770	MS	M/P	LTPL86 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os11g02424	MS	P	LTPL9 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os11g34660	RNA-seq	P	LTPL98 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os03g56944	RNA-seq	P	lysine-rich arabinogalactan protein 19 precursor, putative, expressed

LOC_Os11g34570	RNA-seq	SC	lysM domain-containing GPI-anchored protein precursor, putative, expressed
LOC_Os02g13660	RNA-seq	P	meiosis 5, putative, expressed
LOC_Os11g42970	RNA-seq	P	membrane associated DUF588 domain containing protein, putative, expressed
LOC_Os03g57420	MS	SC/M	ML domain protein, putative, expressed
LOC_Os03g06580	RNA-seq	SC	MTN26L2 - MtN26 family protein precursor, expressed
LOC_Os03g63740	RNA-seq/MS	P	NFD2, putative, expressed
LOC_Os06g44910	MS	SC	OsGrx_C4 - glutaredoxin subgroup I, expressed
LOC_Os03g17860	MS	SC	OsPDIL5-1 protein disulfide isomerase PDIL5-1, expressed
LOC_Os03g01020	RNA-seq	SC/P	pectinesterase inhibitor domain containing protein, putative, expressed
LOC_Os09g32526	MS	SC	peptidyl-prolyl cis-trans isomerase, FKBP-type, putative, expressed
LOC_Os06g49470	MS	P/SC/M	peptidyl-prolyl cis-trans isomerase, putative, expressed
LOC_Os07g03200	RNA-seq	P	phytosulfokines precursor, putative, expressed
LOC_Os03g52390	RNA-seq	P	PIII1 - Proteinase inhibitor II family protein precursor, expressed
LOC_Os07g02200	MS	M/P	plastocyanin-like domain containing protein, putative, expressed
LOC_Os03g57740	MS	M	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g17160	MS	M	plastocyanin-like domain containing protein, putative, expressed
LOC_Os04g46130	MS	P	plastocyanin-like domain containing protein, putative, expressed
LOC_Os06g15600	RNA-seq	SC	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g04340	RNA-seq	SC	plastocyanin-like domain containing protein, putative, expressed
LOC_Os09g39940	RNA-seq	SC	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g04370	RNA-seq	SC	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g37670	RNA-seq/MS	SC/M	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g04350	RNA-seq/MS	SC/M	plastocyanin-like domain containing protein, putative, expressed
LOC_Os08g37660	RNA-seq/MS	SC	plastocyanin-like domain containing protein, putative, expressed
LOC_Os04g36770	RNA-seq	P	PME/invertase inhibitor, putative, expressed
LOC_Os05g45480	MS	SC	POE145 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os07g47750	MS	P	POE149 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os05g45460	MS	SC/M	POE152 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os02g21650	MS	SC	prefoldin, putative, expressed
LOC_Os11g02389	RNA-seq/MS	P/SC/M	protease inhibitor/seed storage/LTP family, putative, expressed
LOC_Os01g47420	MS	SC/P	pterin-4-alpha-carbinolamine dehydratase, putative, expressed
LOC_Os10g41980	RNA-seq	P	RALFL26 - Rapid ALkalinization Factor RALF family protein precursor, expressed
LOC_Os12g38360	RNA-seq	P	RALFL31 - Rapid ALkalinization Factor RALF family protein precursor, expressed
LOC_Os01g25540	MS	SC	RALFL6 - Rapid ALkalinization Factor RALF family protein precursor, expressed
LOC_Os01g25560	MS	M	RALFL7 - Rapid ALkalinization Factor RALF family protein precursor, expressed
LOC_Os02g44940	MS	M	RALFL8 - Rapid ALkalinization Factor RALF family protein precursor, expressed
LOC_Os04g39440	MS	SC/P	ras-related protein, putative, expressed
LOC_Os09g18310	RNA-seq	P	retrotransposon protein, putative, unclassified
LOC_Os10g31730	RNA-seq	SC	retrotransposon protein, putative, unclassified, expressed
LOC_Os08g33710	MS	M/P	ribonuclease T2 family domain containing protein, expressed
LOC_Os07g43600	RNA-seq	SC	ribonuclease T2 family domain containing protein, expressed
LOC_Os01g47330	MS	P	ribosomal protein L7/L12 C-terminal domain containing protein, expressed
LOC_Os09g06770	RNA-seq	SC	RING finger protein, putative, expressed
LOC_Os04g29550	RNA-seq	SC/P	RIPER2 - Ripening-related family protein precursor, expressed
LOC_Os10g34840	RNA-seq/MS	M/P	RIPER6 - Ripening-related family protein precursor, expressed
LOC_Os11g02150	MS	SC/M	saposin-like type B, region 1 family protein, putative, expressed
LOC_Os10g11500	RNA-seq	SC	SCP-like extracellular protein, expressed
LOC_Os07g03730	RNA-seq	P	SCP-like extracellular protein, expressed
LOC_Os07g03710	RNA-seq	P	SCP-like extracellular protein, expressed
LOC_Os01g28500	RNA-seq	P	SCP-like extracellular protein, expressed
LOC_Os01g28450	RNA-seq/MS	P	SCP-like extracellular protein, expressed
LOC_Os06g43650	MS	SC	secreted salivary protein, putative, expressed
LOC_Os10g34910	RNA-seq	SC	secretory protein, putative, expressed
LOC_Os10g34930	RNA-seq/MS	M/P	secretory protein, putative, expressed
LOC_Os01g66960	MS	SC	selenoprotein precursor, putative, expressed
LOC_Os09g19360	RNA-seq	SC	senescence-induced receptor-like serine/threonine-protein kinase precursor, putative, expressed
LOC_Os05g16824	RNA-seq	SC	SHR5-receptor-like kinase, putative, expressed
LOC_Os01g11230	MS	P	SOUL heme-binding protein, putative, expressed
LOC_Os08g17680	RNA-seq	P	stromal cell-derived factor 2-like protein precursor, putative, expressed
LOC_Os05g25850	MS	M/P	superoxide dismutase, mitochondrial precursor, putative, expressed
LOC_Os12g38120	MS	P/SC/M	thaumatin family domain containing protein, expressed
LOC_Os01g62260	MS	M	thaumatin, putative, expressed
LOC_Os12g43380	MS	P	thaumatin, putative, expressed
LOC_Os12g43440	RNA-seq	P	thaumatin, putative, expressed
LOC_Os12g43390	RNA-seq	P	thaumatin, putative, expressed
LOC_Os03g45960	RNA-seq/MS	SC/M	thaumatin, putative, expressed
LOC_Os03g46070	RNA-seq/MS	P	thaumatin, putative, expressed
LOC_Os03g08710	MS	SC	THION26 - Plant thionin family protein precursor, expressed
LOC_Os12g26960	RNA-seq	SC	THION34 - Plant thionin family protein precursor, expressed
LOC_Os06g45510	MS	M/P	thioredoxin, putative, expressed
LOC_Os05g01262	MS	SC	translocon-associated protein beta domain containing protein, expressed
LOC_Os01g01307	MS	P	translocon-associated protein beta domain containing protein, expressed
LOC_Os02g53750	RNA-seq	SC	tyrosine protein kinase domain containing protein, putative, expressed
LOC_Os04g30250	RNA-seq	P	wall-associated receptor kinase-like 5 precursor, putative, expressed
LOC_Os11g37940	MS	M	WIP2 - Wound-induced protein precursor, expressed
LOC_Os11g37950	RNA-seq	P	WIP3 - Wound-induced protein precursor, expressed
LOC_Os11g37960	RNA-seq/MS	P/SC/M	WIP4 - Wound-induced protein precursor, expressed
LOC_Os11g37970	RNA-seq	SC/P	WIP5 - Wound-induced protein precursor, expressed
LOC_Os02g51710	MS	SC/P	wound/stress protein, putative, expressed
LOC_Os07g48680	RNA-seq	P	zinc finger, C3HC4 type domain containing protein, expressed

Table S3. SSPs with post translational modifications identified by MS.

Gene ID	Annotation	Peptide sequences with post translational modifications identified by MS
LOC_Os01g59440	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor, putative, expressed	arabinosyl Hyp (P)-LTGPIPR
LOC_Os10g41710	chaperonin, putative, expressed	SVGGVLLPKSAVK arabinosyl Hyp (P)
LOC_Os04g41620	CHIT2 - Chitinase family protein precursor, expressed	QWPCQPGKK arabinosyl Hyp (P)
LOC_Os03g44880	Cupin domain containing protein, expressed	DYAPWGSLSPPHTHR Oxidation (P)
		DYAPWGSLSPPHTHR Oxidation (P); Sulfo (STY)
		ILATFAVVFLALAATSLAGDP Oxidation (P); Sulfo (STY)
		DTLFGAAPPLPS Oxidation (P)
		GPLRLNGIPCK Oxidation (P)
		DYAPWGSLSPPHTHR Oxidation (P); Sulfo arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
		NSGNTSALAAAFNSQLPGTQSIACTLFGAAPPLPS arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
LOC_Os03g48760	Cupin domain containing protein, expressed	VTVNGHACKPASAAG Oxidation (P)
LOC_Os01g14670	Cupin domain containing protein, expressed	TVNGHACKPASAAG Oxidation (P)
LOC_Os03g48770	Cupin domain containing protein, expressed	DFAPGGTNPPHVHPRATEVGIVLR Oxidation (P)
LOC_Os01g72300	Cupin domain containing protein, expressed	VPGLNLTGLVSLAR Oxidation (P)
LOC_Os05g19670	Cupin domain containing protein, expressed	DYAPGGLNPPPHTHR Oxidation (P); Sulfo (STY)
LOC_Os02g32980	Cupin domain containing protein, expressed	DKPAAVVSAFNSQLPGTQSIAATLFAASPAVP arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
LOC_Os08g09010	Cupin domain containing protein, expressed	GELLVGIIGTLDTGNR Sulfo (STY)
LOC_Os12g05870	Cupin domain containing protein, expressed	DVAEWPGVNTLGVSMNRV Oxidation (M)
LOC_Os12g05840	Cupin domain containing protein, expressed	IPGLNLTGLVSMAR Oxidation (M)
LOC_Os08g13440	cupin domain containing protein, expressed	SVGEKPAVAISAFDSQLPGTQAADALFGSSSPAVPTDVLAR Oxidation (P)
LOC_Os01g58890	cysteine proteinase inhibitor precursor protein, putative, expressed	DVFVFPRLPGLNLTGLVSMSR Oxidation (M)
LOC_Os04g28250	cysteine proteinase inhibitor precursor, putative, expressed	ARPSLPCAVVAVLLLALLPTPSTAGDP Oxidation (P); Sulfo (STY)
LOC_Os08g29669	cytochrome b5-like Heme/Steroid binding domain containing protein, expressed	ARPSLPCAVVAVLLLALLPTPSTAGDP arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
LOC_Os11g10870	dirigent, putative, expressed	LPGLNLTGLVSMAR Oxidation (P)
LOC_Os01g07780	embryo-specific 3, putative, expressed	IPATVFGSGIREAVLER arabinosyl Hyp (P)
LOC_Os06g10760	emp24/gp25L/p24 family protein, putative, expressed	AAMLDTPR Oxidation (P)
LOC_Os05g39990	expansin precursor, putative, expressed	VGSNVTLINVMQIPGLNLTGSIARIIDYAPLGENPPHTHPR arabinosyl Hyp (P); Oxidation (M); Sulfo (STY)
LOC_Os07g29300	expressed protein	MASSNNFLIPLIALVTTQAMASDPSPLQDLCVADKNSPVR Oxidation (M); Oxidation (P); Sulfo (STY)
LOC_Os11g25770	expressed protein	LTGLNLTGISMARI Oxidation (M)
LOC_Os07g09150	expressed protein	GQNPPHTHPR/LAGLNLTISIMAR Oxidation (M)
		ENKLFTK Sulfo (STY)
		AGSNVTLINVMK Oxidation (M); Sulfo (STY)
		FDMPR Oxidation (M); Oxidation (P)
		VWEKPWMDFK arabinosyl Hyp (P); Oxidation (M)
		VWEKPWMDFK Oxidation (M)
		QVSGVAYYLKVAASAR Sulfo (STY)
		VAASARDPR Oxidation (P)
		AAEASIVNRGHDIMVR Oxidation (M)
		MGSTRLLVLAASLLATAVPAAR Oxidation (P); Sulfo (STY)
		GVAAAALPGDAVNR arabinosyl Hyp (P)
		RRPPPQR arabinosyl Hyp (P)
		MAAAVAMVVVALLGGGAVEAVWLDPPTGK arabinosyl Hyp (P); Sulfo (STY)
		AGIVPVFSR Oxidation (P)
		DGAPGQAATGREK arabinosyl Hyp (P)
		SISLPLSPLFPLHPLLSLLSQAAK Oxidation (P); Sulfo (STY)
		QLPISLPLVATPSPLAAGSRPSFRHPSCRPR Oxidation (P); Sulfo (STY)
		GTPMSFSPLIR Oxidation (M); Oxidation (P)
		DDLGGTPLPASVTAITSSIHR arabinosyl Hyp (P)
		QLPISLPLVATPSPLAAGSRPSFR arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
		RSSHHPKR Oxidation (P)
		MARPLHR Oxidation (M); Oxidation (P)
		MARPLHRLWR arabinosyl Hyp (P); Oxidation (M)
		DPPPPPSPTPWPER Oxidation (P)
		MPPPPPPLLLAAVLASAAAALA Oxidation (P); Sulfo (STY)
		DWPGRG Oxidation (P)
		MPPPPPPLLLAAVLASAAAALADPPPPSPTPWPER arabinosyl Hyp (P); Oxidation (M); Sulfo (STY)

LOC_Os03g48626 expressed protein
LOC_Os03g48710 expressed protein

LOC_Os02g54680 expressed protein

LOC_Os06g09840 expressed protein
LOC_Os05g07640 expressed protein

LOC_Os06g15620 GASR7 - Gibberellin-regulated GASA/GAST/Snakin family protein precursor, expressed

LOC_Os03g47270 GCRP4 - Glycine and cysteine rich family protein precursor, expressed

LOC_Os05g43690 glucan endo-1,3-beta-glucosidase-like protein 3 precursor, putative, expressed
LOC_Os11g18170 glutathione peroxidase, putative, expressed
LOC_Os03g27040 heavy metal-associated domain containing protein, expressed

LOC_Os12g18560 invertase/pectin methylesterase inhibitor family protein, putative, expressed

LOC_Os04g46820 LTPL121 - Protease inhibitor/seed storage/LTP family protein precursor, putative, expressed

LOC_Os04g46830 LTPL122 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os05g40010 LTPL17 - Protease inhibitor/seed storage/LTP family protein precursor, expressed
LOC_Os07g07930 LTPL78 - Protease inhibitor/seed storage/LTP family protein precursor, expressed

LOC_Os03g63740 NFD2, putative, expressed

LOC_Os03g57740 plastocyanin-like domain containing protein, putative, expressed

LOC_Os08g04350 plastocyanin-like domain containing protein, putative, expressed

LOC_Os05g45480 POE145 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os07g47750 POE149 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os05g45460 POE152 - Pollen Ole e I allergen and extensin family protein precursor, expressed
LOC_Os01g47420 pterin-4-alpha-carbinolamine dehydratase, putative, expressed

LOC_Os11g02150 saposin-like type B, region 1 family protein, putative, expressed

LOC_Os01g28450 SCP-like extracellular protein, expressed
LOC_Os06g43650 secreted salivary protein, putative, expressed

LOC_Os05g25850 superoxide dismutase, mitochondrial precursor, putative, expressed

LOC_Os12g38120 thaumatin family domain containing protein, expressed

LOC_Os03g46070 thaumatin, putative, expressed

LOC_Os01g01307 translocon-associated protein beta domain containing protein, expressed

LOC_Os02g51710 wound/stress protein, putative, expressed

DPPPPPSPTPWPER arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
FFVVWSITTIVAHP Sulfo (STY)
PPPLLLLLLGLGAAAAAEEPPAAPSSSSPPPHK Oxidation (P)
MPPLLLLLLGLGAAAAAEEPPAAPSSSSPPPHK arabinosyl Hyp (P); Oxidation (M); Oxidation (P); Sulfo (STY)
PPPPLLLLLLGLGAAAAAEEPPAAPSSSSPPPHK arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
LGHGAPAFSR arabinosyl Hyp (P)
KGGSTMPLLTVK Oxidation (M); Oxidation (P); Sulfo (STY)
ELNVAQLGAGVRQATCDVATEWK Sulfo (STY)
MSLAATFVFLVL SALQMLDQVLDLVK Oxidation (M); Sulfo (STY)
HCPSFAVNHEVMMPIPKPTGFTGADPYK arabinosyl Hyp (P); Oxidation (M); Oxidation (P); Sulfo (STY)
HCPSFAVNHEVMMPIPKPTGFTGADPYK Oxidation (M); Oxidation (P)
RAMASAATPQPSPSPK Oxidation (M); Oxidation (P)
RAMASAATPQPSPSPK arabinosyl Hyp (P); Oxidation (M)
KQPAAGR Oxidation (P)
DLMSAAPS AKA Oxidation (M); Oxidation (P)
QLPVAPDDELPR Oxidation (P)
IPPCRLADLA PLLPK arabinosyl Hyp (P); Oxidation (P)
DCTQIMQSGACYQPSTIVAHCSYATNSYFQK arabinosyl Hyp (P)
YAPTT SPLK Oxidation (P)
MEAAA AVTR Oxidation (M)
MEAAA AVTRLSFVPLAA ARPLLAGFMRPR/Oxidation (M); Oxidation (P); Sulfo (STY)
VPPPASVPPPPPPP PAPA LVR arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
RVPPPASVPPPPPPP PAPA LVR arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
ASIALFLAVNL VVFSLGSACGGHCPTPTP STPTPTPAF GK arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
CPRDALK Oxidation (P)
CPTPPPAL P PPPPTPTPSYHN K arabinosyl Hyp (P); Oxidation (P)
MVPAARSGW PAAA VLVV VLSS PPGTSTVV VVAR arabinosyl Hyp (P); Oxidation (M); Oxidation (P); Sulfo (STY)
ATPATPVGSGVAPLR Oxidation (P)
VQT PVSNC SGAA APPAG QTPT PAGTGSK arabinosyl Hyp (P); Oxidation (P)
TRALGLPDACK Oxidation (P)
SGAA APPAG QTPPT PAGTGSK ATPATPVGSGVAPLR arabinosyl Hyp (P); 4 Oxidation (P)
VAAGTKPTAPPVVC GAL R/VGIPSIVR VAAGTKPTAPPVVC GAL R Oxidation (P); Sulfo (STY)
MGMAHVLSLLV VILVAIPSSRSH ALPSSSPF DAAL ATLQ NQIAY R Oxidation (M); Oxidation (P); Sulfo (STY)
VGIPSIVR arabinosyl Hyp (P)
ITVIAAGA PAPGASE APPPSSA AGK Oxidation (P); Sulfo (STY)
LKIVTAAGA PAPGASE APPPSSA AGK arabinosyl Hyp (P); Oxidation (P); Sulfo (STY)
VAVKVEAATGSNPTPSPLAPLPR arabinosyl Hyp (P); Oxidation (P)
TPTVMAPNAM PNP TNGR PT PSSASK PVG ASLV GLS LSA IVAGL MVF Oxidation (M); Oxidation (P); Sulfo (STY)
YYAMAAPS WPTV SKNL PLLGHGR arabinosyl Hyp (P); Oxidation (M); Oxidation (P)
IPVTLLR Oxidation (P); Sulfo (STY)
MVLQYVPLV VN GEK Oxidation (M)
EVSKLAI ALAMVAAMALPSQAQN SPQDYVR arabinosyl Hyp (P); 2 Oxidation (M); Sulfo (STY)
REPFSIMS LLK Oxidation (M)
REPFSIMS LLK Oxidation (P)
DAASAI AKGF GLPAK Oxidation (P)
EPFSIMS LLK Oxidation (M)
HHATYVANYNK/GVTTVALPDL PY arabinosyl Hyp (P)
GVTTVALPDL PY arabinosyl Hyp (P)
SPGELKVIFCPPTML TAAAAAA SDMLIR Oxidation (M); Oxidation (P); Sulfo (STY)
AAPAILR Oxidation (P)
FQGSPAVITYRVPTK Oxidation (P); Sulfo (STY)
RDLLPTR Sulfo (STY)
DAAPYKLEAIR Oxidation (P)

Table S4. Primer list

PSKF	CAACGCCCTACGACGTCTCTC
PSKR	AGATGTAATCGGTGTGCGCC
UbiF	AACCAGCTGAGGCCAAGA
UbiR	ACGATTGATTAAACCAGTCCATGA
PAL1F	TGAATAACAGTGGAGTGTGGAG
PAL1R	AACCTGCCACTCGTACCAAG
Chitinase1F	GCACTGATAACCACTGATCGG
Chitinase1R	TGTGGGCATTACTGATGATTG
Pbz1F:	CATGAAGCTTAACCCCTGCCG
Pbz1R:	CCTCGAGCACATCCGACTTT
IRPqF	AGGACGATGAAGGGGGAAG
IRPqR	TAGCAGCAGTGTGTGGAGA
RALFL8F	CAGGAATCGAACATCGAGTGAA
RALFL8R	TCACCGGGTTGTCACTAGTA
RALFL6F	GCTCAAACCGGGATTATTCA
RALFL6R	CACGGTTAAAACAGCGACAA
RALFL7F	CCACCACCAAAACTGTTGAA
RALFL7R	TTTAGATTAGCGGGCACCAA
IRPOF	CACCATATATCAATGGCGATGAC
IRPOR	GCAGCAGTGTGTGGAGAGTTG