

Article title

A blast resistance gene *Pi65* with LRR-RLK domain is required for resistance to *M. oryzae*

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a

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WT      GGCCTATCCCTGGTAATACAAGTTTCAGCCTCCCAGTTCT-ACGATGGTTCGCCATCAGTAAAAACAATTTCTTTGGTCAGATTCCAC
KO-C1   GGCCTATCCCTGGTAATACAAGTTTCAGCCTCCCAGTTCTAACGATGGTTCGCCATCAGTAAAAACAATTTCTTTGGTCAGATTCCAC +1
KO-C2   GGCCTATCCCTGGTAATACAAGTTTCAGCCTCCCAGTTC---CGATGGTTCGCCATCAGTAAAAACAATTTCTTTGGTCAGATTCCAC -2
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b

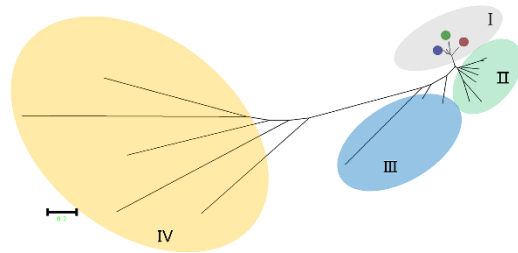


Fig. S1 Edit type of Os11g0694850 and evolutionary analysis of *Pi65* and *Pi* genes. a CRISPR/Cas9-mediated mutation of Os11g0694850 in GY129. b Phylogenetic analysis of *Pi65* and other kinase genes. The red circle represents the *Pi65* gene, the green circle represents the LOC_Os11g47210 gene, and the dark blue is the LOC_Os11g46980 gene. The trees are constructed based on the whole predicted amino acid sequences using neighborhood linkage algorithms. The bootstrap value corresponding to the number of branch order (1,000 replicates) matches is displayed on the nodes at each branch point. The unit branch length of each site corresponds to a substitution of 0.2 nucleotides. The neighbor-joining method: A new method for reconstructing phylogenetic trees

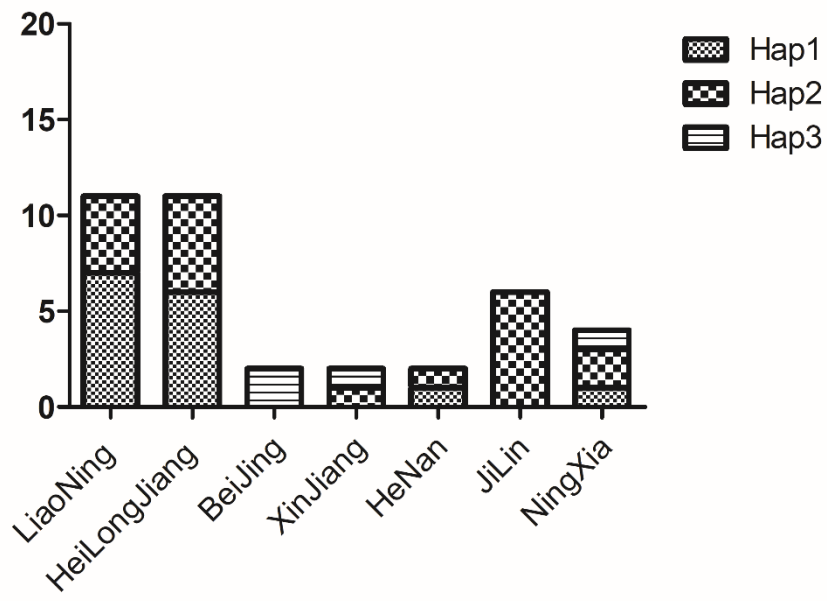


Fig. S2 Distributions of three haplotypes at the *Pi65* locus in rice varieties from different regions.

Table S1 Primer sequences

Gene	Primer	Primer sequence	Purpose
Os11t0694600	F	<u>TGTGTGCACTGCCATTGCTCTTGCT</u>	CRISPR/Cas9 sgRNA1
	R	<u>AAACAGCAAGAGCAATGGCAGTGCA</u>	
	F	<u>TGTGTGGCAAGAATGCCGAGAGGGT</u>	CRISPR/Cas9 sgRNA2
	R	<u>AAACACCCTCTCGGCATTCTTGCCA</u>	
Os11t0694850	F	<u>TGTGTGGGCCTGCAAGTTAAGGTGT</u>	CRISPR/Cas9
	R	<u>AAACACACCTTAACTTGCAGGCCCA</u>	
Os11t0694600	F	GTAAAACGACGGCCAGT	Test CRISPR/Cas9 editing sites
	R	AAACAGCAAGAGCAATGGCAGTGCA	
Os11t0694850	F	GTAAAACGACGGCCAGT	Test CRISPR/Cas9 editing sites
	R	AAACACACCTTAACTTGCAGGCCCA	
Os11g0694500	F	ATGATCAGCAGCACAACAGATAT	Sequence analysis
	R	TTAACAACTCACAACTGGGAAAG	
Os11t0694600	F	ATGATTCCTGTCTTGCCAACG	Sequence analysis
	R	CAGAAGCAGAAATGGACACAG	
Os11g0694850	F	ATGCCAATCCTCCAACACC	Sequence analysis
	R	TCACTGCTGCACAACGCTCA	
Os11g0695000	F	TGCAGCTCTTTCTCTCCAAT	Sequence analysis
	R	GGTACCGCCTCCACCTGCTG	
Os11t0694600	F	<u>caggtcgactctagag</u> ATGGCGTTTAGAATGCCAGTACGGA	Pi65 clone
	R	<u>agctcggtagccggg</u> TCATTCTTTCGTATATGCAGGCAGGGCCAC	
Actin1	F	CAACACCCCTGCTATGTACG	Rice Actin
	R	CACCAGAGTCCAACACAA	
Os11t0694600	F	TACTCCAATTATCTCACC GGAA	qRT-PCR
	R	GTTATTCGAAAGGTCTAGCACAA	
35s::GFP-Pi65	F	<u>ctcccctgctccgtagatcc</u> ATGGCGTTTAGAATGCCAGTACGGA	Intracellular localization of Pi65
	R	<u>gccttgctcaccatgtagatcc</u> TTCTTTCGTATATGCAGGCAGGGCCAC	

The underline represents the cleavage site junction

Table S2 Plasmids used in this study

	Description	Purpose
ZmUbi, OsU6, Hpt	CRISPR/CAS9 vector for <i>Pi65</i> gene	CRISPR/Cas9
pCambia1301-UbiN	full-length <i>Pi65</i> cDNA coding sequence in GY129 at the BamH1 sites of pCambia1301-UbiN	overexpression
HBT95::sGFP-NOS	Subcellular localization of Pi65	Transient expression of Pi65

Table S3 Haplotypes at the *Pi65* locus in different rice varieties and their disease reactions

Accession No.	Vartity	Origin	Reaction	Haplotype
1	Gangyu129	Liaoning	R	Hap1
2	Liaoxing1	Liaoning	S	Hap2
3	Danjing17	Liaoning	R	Hap1
4	Danjing18	Liaoning	R	Hap1
5	Danjing20	Liaoning	R	Hap1
6	Dan219	Liaoning	S	Hap1
7	Suojing18	Heilongjiang	S	Hap2
8	Suojing21	Heilongjiang	S	Hap2
9	Kendao27	Heilongjiang	R	Hap1
10	Kendao31	Heilongjiang	S	Hap1
11	Kendao32	Heilongjiang	R	Hap1
12	Kendao33	Heilongjiang	S	Hap2
13	Tiejing7	Liaoning	S	Hap1
14	Tiejing11	Liaoning	S	Hap2
15	Tiejing15	Liaoning	S	Hap2
16	Tiejing1605	Liaoning	S	Hap2
17	Jijing515	Jilin	R	Hap2
18	Jijing528	Jilin	S	Hap2
19	Jijing809	Jilin	R	Hap2
20	Tonghe99	Jilin	R	Hap2
21	Tongyu269	Jilin	R	Hap2
22	Tongyu256	Jilin	S	Hap2
23	Yunongjing11	Henan	S	Hap2
24	Yunongjing16	Henan	R	Hap1
25	Xingnongjing3	Xinjinag	R	Hap3
26	Xindao36	Xinjinag	R	Hap2
27	Jingdao2	Beijing	R	Hap3
28	Jingdao3	Beijing	R	Hap3
29	Fuyuan4	Ningxia	R	Hap2
30	2009G-19	Ningxia	S	Hap2
31	Ningjing43	Ningxia	R	Hap3
32	Ningjing48	Ningxia	R	Hap1
33	Kenjing8	Heilongjiang	S	Hap2
34	Longjing20	Heilongjiang	R	Hap1
35	Longjing39	Heilongjiang	R	Hap1
36	Longjing46	Heilongjiang	R	Hap1
37	Longjing47	Heilongjiang	S	Hap2
38	C787	Liaoning	R	Hap1

Table S4 Sequence analysis of haplotypes at the *Pi65* locus in different rice varieties

Nonsynonymous substitutions within CDS at <i>Pi65</i> locus																			
Hap	193 ^a	458	526	610	1186	1228	1240	1271	1668	1840	1956	2186	2395	2476	3264	3286	3383	No. of varieties	Reaction to QY-13
Hap1	C	A	G	C	C	C	T	T	G	T	A	G	T	G	G	A	A	15 ^b	R ^c
Hap2	T	G	A	T	A	A	C	C	C	G	C	A	C	A	G	C	C	19	R/S
Hap3	C	A	G	C	C	C	T	T	G	T	A	G	T	G	A	A	A	4	S

Hap1 is the GY129 genotype.

Hap2 is the NIP genotype.

Hap3 is the JD 2 genotype.

^aThe SNP positions were based on the GY129, LX1 and JD2 of *Pi65* genomic DNA .

^bTotal number of varieties with the corresponding haplotype.

^cR indicates resistance and S indicates susceptible evaluated seven days post-inoculation.

Table S5 GY129-specifically up expressed DEGs

Gene ID	Regulated	Annotation
LOC_Os07g39720	up	--
LOC_Os04g59160	up	Cationic peroxidase SPC4 OS=Sorghum bicolor OX=4558 GN=Sb03g046810 PE=1 SV=2
LOC_Os09g23620	up	Transcription factor MYB20 OS=Arabidopsis thaliana OX=3702 GN=MYB20 PE=2 SV=1
LOC_Os02g43790	up	Ethylene-responsive transcription factor 1 OS=Solanum lycopersicum OX=4081 GN=ERF1 PE=2 SV=1
LOC_Os06g37224	up	Ent-kaurene oxidase-like 5 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP701A9 PE=2 SV=1
LOC_Os01g10110	up	Cytokinin dehydrogenase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=CKX2 PE=2 SV=1
LOC_Os08g09080	up	Germin-like protein 8-11 OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0190100 PE=1 SV=1
LOC_Os07g26110	up	CASP-like protein 1D1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0442900 PE=2 SV=1
LOC_Os10g30390	up	Ent-cassadiene C2-hydroxylase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP71Z7 PE=1 SV=1
LOC_Os09g38830	up	Wall-associated receptor kinase 5 OS=Arabidopsis thaliana OX=3702 GN=WAK5 PE=2 SV=1
LOC_Os04g09920	up	9-beta-pimara-7,15-diene oxidase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP99A3 PE=1 SV=1
LOC_Os06g06750	up	MADS-box transcription factor 5 OS=Oryza sativa subsp. japonica OX=39947 GN=MADS5 PE=1 SV=1
LOC_Os07g47090	up	Protein NETWORKED 3A OS=Arabidopsis thaliana OX=3702 GN=NET3A PE=2 SV=1
LOC_Os01g44950	up	4-coumarate--CoA ligase-like 3 OS=Arabidopsis thaliana OX=3702 GN=4CLL3 PE=2 SV=2
LOC_Os02g39764	up	Cytochrome P450 734A4 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP734A4 PE=2 SV=1
LOC_Os11g44630	up	--
LOC_Os04g41229	up	Transcription factor bHLH128 OS=Arabidopsis thaliana OX=3702 GN=BHLH128 PE=1 SV=1
LOC_Os10g03440	up	U-box domain-containing protein 20 OS=Arabidopsis thaliana OX=3702 GN=PUB20 PE=2 SV=1
LOC_Os04g57670	up	Pentatricopeptide repeat-containing protein At3g50420 OS=Arabidopsis thaliana OX=3702 GN=PCMP-E85 PE=2 SV=1
LOC_Os09g20510	up	--
LOC_Os07g38840	up	--
LOC_Os04g38930	up	Putative pentatricopeptide repeat-containing protein At1g09680 OS=Arabidopsis thaliana OX=3702 GN=At1g09680 PE=3 SV=1
LOC_Os06g10130	up	--
LOC_Os07g03170	up	--
LOC_Os10g04490	up	Disease resistance protein RGA2 OS=Solanum bulbocastanum OX=147425 GN=RGA2 PE=1 SV=1
LOC_Os04g39010	up	--

LOC_Os08g34300	up	Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum OX=4097 PE=2 SV=1
LOC_Os04g41380	up	Disease resistance RPP13-like protein 4 OS=Arabidopsis thaliana OX=3702 GN=RPP13L4 PE=1 SV=2
LOC_Os01g02780	up	Rust resistance kinase Lr10 OS=Triticum aestivum OX=4565 GN=LrK10 PE=2 SV=1
LOC_Os04g03164	up	--
LOC_Os01g53390	up	Anthocyanidin 5,3-O-glucosyltransferase OS=Rosa hybrid cultivar OX=128735 GN=RhGT1 PE=2 SV=1
LOC_Os01g62060	up	--
LOC_Os01g36220	up	--
LOC_Os02g15270	up	Probable inactive dual specificity protein phosphatase-like At4g18593 OS=Arabidopsis thaliana OX=3702 GN=At4g18593 PE=2 SV=1
LOC_Os07g08240	up	--
LOC_Os08g03600	up	--
LOC_Os08g39850	up	Probable lipoxygenase 8, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=CM-LOX2 PE=2 SV=1
LOC_Os12g36110	up	Calmodulin-binding protein 60 B OS=Arabidopsis thaliana OX=3702 GN=CBP60B PE=2 SV=1
LOC_Os11g39450	up	Putative receptor-like protein kinase At4g00960 OS=Arabidopsis thaliana OX=3702 GN=At4g00960 PE=3 SV=2
LOC_Os02g37960	up	--
LOC_Os03g58040	up	Glutamate dehydrogenase 1, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=GDH1 PE=2 SV=1
LOC_Os12g41110	up	Calmodulin-like protein 5 OS=Oryza sativa subsp. japonica OX=39947 GN=CML5 PE=2 SV=1
LOC_Os08g39840	up	Lipoxygenase 7, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=CM-LOX1 PE=2 SV=2
LOC_Os11g11960	up	Disease resistance protein RPM1 OS=Arabidopsis thaliana OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os01g22249	up	Peroxidase 1 OS=Zea mays OX=4577 GN=PER1 PE=1 SV=1
LOC_Os01g48000	up	Putative receptor protein kinase ZmPK1 OS=Zea mays OX=4577 GN=PK1 PE=2 SV=2
LOC_Os02g56420	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os05g24660	up	Adenylate isopentenyltransferase 3, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=IPT3 PE=1 SV=1
LOC_Os11g01030	up	--
LOC_Os01g05900	up	Histone H2B.10 OS=Oryza sativa subsp. indica OX=39946 GN=H2B.10 PE=3 SV=1
LOC_Os08g01240	up	Uncharacterized protein At4g14100 OS=Arabidopsis thaliana OX=3702 GN=At4g14100 PE=2 SV=1
LOC_Os02g47160	up	Transcription initiation factor TFIID subunit 8 OS=Arabidopsis thaliana OX=3702 GN=TAF8 PE=1 SV=1
LOC_Os09g27500	up	Cytochrome P450 76M5 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP76M5 PE=1 SV=1
LOC_Os11g40850	up	--
LOC_Os09g15330	up	Sugar transport protein 14 OS=Arabidopsis thaliana OX=3702 GN=STP14 PE=2 SV=2

LOC_Os01g04550	up	Protein SUPPRESSOR OF NPR1-1 CONSTITUTIVE 4 OS=Arabidopsis thaliana OX=3702 GN=LRK10L-2.6 PE=1 SV=1
LOC_Os11g14040	up	Glutathione S-transferase zeta class OS=Euphorbia esula OX=3993 PE=2 SV=1
LOC_Os11g07690	up	Dirigent protein 21 OS=Arabidopsis thaliana OX=3702 GN=DIR21 PE=3 SV=1
LOC_Os03g39690	up	Premnaspirodiene oxygenase OS=Hyoscyamus muticus OX=35626 GN=CYP71D55 PE=1 SV=1
LOC_Os05g43390	up	Signal recognition particle 54 kDa protein 2 OS=Hordeum vulgare OX=4513 GN=SRP54-2 PE=2 SV=1
LOC_Os07g46060	up	--
LOC_Os11g41100	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os01g08760	up	Probable choline kinase 1 OS=Arabidopsis thaliana OX=3702 GN=CK1 PE=2 SV=1
LOC_Os01g40870	up	Aldehyde dehydrogenase family 2 member C4 OS=Arabidopsis thaliana OX=3702 GN=ALDH2C4 PE=1 SV=2
LOC_Os11g19850	up	--
LOC_Os06g38730	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os04g01874	up	L-type lectin-domain containing receptor kinase IV.2 OS=Arabidopsis thaliana OX=3702 GN=LECRK42 PE=2 SV=1
LOC_Os12g32190	up	--
LOC_Os04g30240	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os12g38770	up	Probable inactive purple acid phosphatase 1 OS=Arabidopsis thaliana OX=3702 GN=PAP1 PE=2 SV=1
LOC_Os04g09260	up	Acyl transferase 15 OS=Oryza sativa subsp. japonica OX=39947 GN=AT15 PE=2 SV=1
LOC_Os04g10160	up	Cytochrome P450 99A2 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP99A2 PE=2 SV=2
LOC_Os04g43550	up	--
LOC_Os01g09990	up	Putative transcription factor bHLH041 OS=Arabidopsis thaliana OX=3702 GN=BHLH41 PE=3 SV=1
LOC_Os01g07970	up	--
LOC_Os11g47560	up	Xylanase inhibitor protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=Chib3H-h PE=1 SV=1
LOC_Os12g36860	up	Major pollen allergen Bet v 1-G OS=Betula pendula OX=3505 GN=BETV1G PE=1 SV=2
LOC_Os07g03279	up	Pathogenesis-related protein 1 OS=Hordeum vulgare OX=4513 PE=2 SV=1
LOC_Os08g04370	up	Uclacyanin 1 OS=Arabidopsis thaliana OX=3702 GN=UCC1 PE=1 SV=1
LOC_Os08g24300	up	--
LOC_Os06g30400	up	--
LOC_Os06g27370	up	--
LOC_Os05g46840	up	--
LOC_Os09g26144	up	Glutamate receptor 2.8 OS=Arabidopsis thaliana OX=3702 GN=GLR2.8 PE=2 SV=2

LOC_Os12g10260	up	Zinc finger BED domain-containing protein DAYSLEEPER OS=Arabidopsis thaliana OX=3702 GN=HAT PE=1 SV=1
LOC_Os01g34880	up	Callose synthase 7 OS=Arabidopsis thaliana OX=3702 GN=CALS7 PE=3 SV=3
LOC_Os02g50460	up	U-box domain-containing protein 20 OS=Arabidopsis thaliana OX=3702 GN=PUB20 PE=2 SV=1
LOC_Os02g32980	up	Germin-like protein 2-4 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0532500 PE=2 SV=1
LOC_Os01g02730	up	Rust resistance kinase Lr10 OS=Triticum aestivum OX=4565 GN=LRK10 PE=2 SV=1
LOC_Os06g45960	up	Ent-isokaurene C2-hydroxylase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP71Z6 PE=1 SV=1
LOC_Os08g09020	up	Germin-like protein 8-8 OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0189700 PE=2 SV=1
LOC_Os01g60020	up	NAC domain-containing protein 68 OS=Oryza sativa subsp. japonica OX=39947 GN=NAC068 PE=2 SV=1
LOC_Os10g42750	up	Cellulose synthase-like protein D1 OS=Oryza sativa subsp. japonica OX=39947 GN=CSLD1 PE=2 SV=1
LOC_Os02g01510	up	L-lactate dehydrogenase A OS=Hordeum vulgare OX=4513 PE=1 SV=1
LOC_Os03g37090	up	Protein FATTY ACID EXPORT 5 OS=Arabidopsis thaliana OX=3702 GN=FAX5 PE=3 SV=1
LOC_Os07g35810	up	Cysteine-rich receptor-like protein kinase 10 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK10 PE=2 SV=1
LOC_Os07g35390	up	Cysteine-rich receptor-like protein kinase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK6 PE=1 SV=1
LOC_Os08g10310	up	Probable LRR receptor-like serine/threonine-protein kinase At1g56130 OS=Arabidopsis thaliana OX=3702 GN=At1g56130 PE=2 SV=2
LOC_Os11g18670	up	Polyubiquitin 9 OS=Arabidopsis thaliana OX=3702 GN=UBQ9 PE=3 SV=1
LOC_Os07g32060	up	UDP-glycosyltransferase 43 OS=Pueraria montana var. lobata OX=3893 GN=UGT43 PE=1 SV=2
LOC_Os01g52790	up	Cytochrome P450 72A14 OS=Arabidopsis thaliana OX=3702 GN=CYP72A14 PE=2 SV=1
LOC_Os04g29950	up	Wall-associated receptor kinase 1 OS=Arabidopsis thaliana OX=3702 GN=WAK1 PE=1 SV=2
LOC_Os02g04170	up	L-aspartate oxidase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0134400 PE=3 SV=1
LOC_Os01g61510	up	Ammonium transporter 2 member 3 OS=Oryza sativa subsp. japonica OX=39947 GN=AMT2-3 PE=2 SV=1
LOC_Os01g14440	up	WRKY transcription factor 6 OS=Arabidopsis thaliana OX=3702 GN=WRKY6 PE=1 SV=1
LOC_Os04g10750	up	Probable inorganic phosphate transporter 1-4 OS=Oryza sativa subsp. japonica OX=39947 GN=PHT1-4 PE=2 SV=1
LOC_Os01g71830	up	Glucan endo-1,3-beta-glucosidase GV OS=Hordeum vulgare OX=4513 PE=2 SV=2
LOC_Os12g24490	up	E3 ubiquitin-protein ligase ATL9 OS=Arabidopsis thaliana OX=3702 GN=ATL9 PE=1 SV=1
LOC_Os01g50100	up	ABC transporter B family member 10 OS=Arabidopsis thaliana OX=3702 GN=ABCB10 PE=1 SV=2
LOC_Os04g57660	up	Phytosulfokine receptor 1 OS=Daucus carota OX=4039 GN=PSKR PE=1 SV=1
LOC_Os02g11070	up	3-ketoacyl-CoA synthase 11 OS=Arabidopsis thaliana OX=3702 GN=KCS11 PE=1 SV=1
LOC_Os07g38260	up	Insulin-degrading enzyme-like 1, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=PXM16 PE=2 SV=1
LOC_Os06g35560	up	Berberine bridge enzyme-like 13 OS=Arabidopsis thaliana OX=3702 GN=At1g30760 PE=1 SV=1

LOC_Os03g21710	up	Probable WRKY transcription factor 70 OS=Arabidopsis thaliana OX=3702 GN=WRKY70 PE=2 SV=1
LOC_Os09g29600	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os07g03580	up	Pathogenesis-related protein PRB1-2 OS=Hordeum vulgare OX=4513 PE=2 SV=1
LOC_Os09g39620	up	U-box domain-containing protein 70 OS=Oryza sativa subsp. japonica OX=39947 GN=PUB70 PE=1 SV=1
LOC_Os10g17960	up	Cysteine-rich receptor-like protein kinase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK6 PE=1 SV=1
LOC_Os01g25970	up	Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum OX=4097 PE=2 SV=1
LOC_Os01g40499	up	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 OS=Arabidopsis thaliana OX=3702 GN=At2g19130 PE=2 SV=1
LOC_Os04g52190	up	Vacuolar-sorting receptor 7 OS=Arabidopsis thaliana OX=3702 GN=VSR7 PE=2 SV=2
LOC_Os01g43890	up	Serine carboxypeptidase-like 50 OS=Arabidopsis thaliana OX=3702 GN=SCPL50 PE=2 SV=1
LOC_Os01g23580	up	Pyrophosphate-energized vacuolar membrane proton pump OS=Hordeum vulgare OX=4513 PE=2 SV=2
LOC_Os01g48030	up	--
LOC_Os08g37760	up	E3 ubiquitin-protein ligase ATL6 OS=Arabidopsis thaliana OX=3702 GN=ATL6 PE=1 SV=2
LOC_Os03g56500	up	--
LOC_Os04g34120	up	Protein DMP3 OS=Arabidopsis thaliana OX=3702 GN=DMP3 PE=2 SV=1
LOC_Os03g24930	up	Probable serine/threonine-protein kinase PBL15 OS=Arabidopsis thaliana OX=3702 GN=PBL15 PE=1 SV=1
LOC_Os03g19670	up	GDSL esterase/lipase At4g16230 OS=Arabidopsis thaliana OX=3702 GN=At4g16230 PE=3 SV=2
LOC_Os02g16060	up	Disease resistance protein RGA2 OS=Solanum bulbocastanum OX=147425 GN=RGA2 PE=1 SV=1
LOC_Os10g39300	up	Aspartic proteinase nepenthesin-1 OS=Nepenthes gracilis OX=150966 GN=nep1 PE=1 SV=1
LOC_Os12g37770	up	Disease resistance protein RPM1 OS=Arabidopsis thaliana OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os01g29330	up	Protein DMP10 OS=Arabidopsis thaliana OX=3702 GN=DMP10 PE=2 SV=1
LOC_Os05g49100	up	Probable WRKY transcription factor 71 OS=Arabidopsis thaliana OX=3702 GN=WRKY71 PE=2 SV=1
LOC_Os03g18130	up	Asparagine synthetase [glutamine-hydrolyzing] 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0291500 PE=2 SV=1
LOC_Os02g13780	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os01g41240	up	Strigolactone esterase D14 OS=Oryza sativa subsp. japonica OX=39947 GN=D14 PE=1 SV=1
LOC_Os04g24510	up	Wall-associated receptor kinase-like 4 OS=Arabidopsis thaliana OX=3702 GN=WAKL4 PE=2 SV=2
LOC_Os01g40260	up	Probable WRKY transcription factor 50 OS=Arabidopsis thaliana OX=3702 GN=WRKY50 PE=2 SV=1
LOC_Os10g05250	up	Wall-associated receptor kinase-like 4 OS=Arabidopsis thaliana OX=3702 GN=WAKL4 PE=2 SV=2
LOC_Os01g04450	up	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2 OS=Arabidopsis thaliana OX=3702 GN=LRK10
LOC_Os05g19910	up	Acyl transferase 5 OS=Oryza sativa subsp. japonica OX=39947 GN=AT5 PE=2 SV=1

LOC_Os08g30100	up	DIBOA-glucoside dioxygenase BX6 OS= <i>Zea mays</i> OX=4577 GN=BX6 PE=1 SV=1
LOC_Os11g05800	up	HVA22-like protein j OS= <i>Arabidopsis thaliana</i> OX=3702 GN=HVA22J PE=2 SV=2
LOC_Os11g37700	up	ABC transporter G family member 48 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ABCG48 PE=3 SV=1
LOC_Os02g34650	up	--
LOC_Os10g33210	up	Protein NRT1/ PTR FAMILY 5.2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=NPF5.2 PE=2 SV=1
LOC_Os03g18740	up	Sex determination protein tasselseed-2 OS= <i>Zea mays</i> OX=4577 GN=TS2 PE=2 SV=1
LOC_Os06g17050	up	--
<i>Oryza sativa</i> _newGene_2082	up	--
LOC_Os04g43650	up	Probable low-specificity L-threonine aldolase 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=THA1 PE=1 SV=1
LOC_Os05g25390	up	Wall-associated receptor kinase-like 20 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=WAKL20 PE=2 SV=1
LOC_Os06g12030	up	--
LOC_Os07g23980	up	--
LOC_Os06g19260	up	--
LOC_Os10g18260	up	Cysteine-rich receptor-like protein kinase 10 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CRK10 PE=1 SV=3
LOC_Os01g68730	up	--
LOC_Os11g47150	up	Wall-associated receptor kinase 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os11g38160	up	Hexose carrier protein HEX6 OS= <i>Ricinus communis</i> OX=3988 GN=HEX6 PE=2 SV=1
LOC_Os12g36840	up	Major pollen allergen Cor a 1 isoforms 5, 6, 11 and 16 OS= <i>Corylus avellana</i> OX=13451 PE=1 SV=3
LOC_Os02g42160	up	Wall-associated receptor kinase-like 8 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=WAKL8 PE=2 SV=1
LOC_Os06g43384	up	Cytochrome P450 71D7 OS= <i>Solanum chacoense</i> OX=4108 GN=CYP71D7 PE=3 SV=1
LOC_Os02g17090	up	Subtilisin-like protease SBT3.9 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SBT3.9 PE=3 SV=1
LOC_Os06g19070	up	Cytochrome P450 76C2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CYP76C2 PE=2 SV=1
LOC_Os09g19290	up	RNA-directed DNA polymerase homolog OS= <i>Oenothera berteriana</i> OX=3950 PE=4 SV=1
LOC_Os11g31540	up	Leucine-rich repeat protein 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=LRR2 PE=2 SV=1
LOC_Os05g40700	up	--
LOC_Os04g59200	up	Cationic peroxidase SPC4 OS= <i>Sorghum bicolor</i> OX=4558 GN=Sb03g046810 PE=1 SV=2
LOC_Os09g23595	up	--
LOC_Os12g07310	up	Citrate-binding protein OS= <i>Hevea brasiliensis</i> OX=3981 GN=CBP PE=1 SV=1
LOC_Os02g36210	up	Ent-copalyl diphosphate synthase 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CPS2 PE=2 SV=1

LOC_Os02g33590	up	E3 ubiquitin-protein ligase PUB23 OS=Arabidopsis thaliana OX=3702 GN=PUB23 PE=1 SV=1
LOC_Os08g24310	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os07g34280	up	2-hydroxyisoflavanone dehydratase OS=Glycyrrhiza echinata OX=46348 GN=HIDM PE=1 SV=1
Oryza_sativa_newGene_4431	up	--
LOC_Os12g01490	up	Putative Myb family transcription factor At1g14600 OS=Arabidopsis thaliana OX=3702 GN=At1g14600 PE=2 SV=2
LOC_Os10g25030	up	Red chlorophyll catabolite reductase (Fragment) OS=Hordeum vulgare OX=4513 GN=rccR PE=1 SV=1
LOC_Os07g39030	up	--
LOC_Os04g32920	up	Potassium transporter 1 OS=Oryza sativa subsp. japonica OX=39947 GN=HAK1 PE=1 SV=2
LOC_Os10g38740	up	Probable glutathione S-transferase GSTU6 OS=Oryza sativa subsp. japonica OX=39947 GN=GSTU6 PE=2 SV=2
LOC_Os05g37140	up	Ferredoxin-6, chloroplastic OS=Zea mays OX=4577 GN=FDX6 PE=2 SV=1
LOC_Os02g30190	up	RPM1-interacting protein 4 OS=Arabidopsis thaliana OX=3702 GN=RIN4 PE=1 SV=1
Oryza_sativa_newGene_2970	up	Auxin-responsive protein SAUR36 OS=Oryza sativa subsp. japonica OX=39947 GN=SAUR39 PE=2 SV=1
Oryza_sativa_newGene_562	up	--
LOC_Os04g43400	up	Putative beta-glucosidase 17 OS=Oryza sativa subsp. japonica OX=39947 GN=BGLU17 PE=5 SV=3
LOC_Os04g49194	up	Flavanone 3-dioxygenase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=F3H-2 PE=1 SV=1
LOC_Os02g36000	up	--
LOC_Os06g14260	up	L-type lectin-domain containing receptor kinase IV.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK41 PE=2 SV=1
LOC_Os10g09990	up	UDP-glycosyltransferase 73C5 OS=Arabidopsis thaliana OX=3702 GN=UGT73C5 PE=2 SV=1
LOC_Os12g29950	up	--
LOC_Os07g31190	up	Putative wall-associated receptor kinase-like 16 OS=Arabidopsis thaliana OX=3702 GN=WAKL16 PE=3 SV=1
LOC_Os11g02520	up	Probable WRKY transcription factor 46 OS=Arabidopsis thaliana OX=3702 GN=WRKY46 PE=2 SV=1
LOC_Os04g56470	up	Amino acid permease 2 OS=Arabidopsis thaliana OX=3702 GN=AAP2 PE=1 SV=1
LOC_Os04g29680	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os12g43640	up	Receptor-like protein kinase HAIKU2 OS=Arabidopsis thaliana OX=3702 GN=IKU2 PE=1 SV=1
LOC_Os05g45070	up	--
LOC_Os11g01480	up	Putative Myb family transcription factor At1g14600 OS=Arabidopsis thaliana OX=3702 GN=At1g14600 PE=2 SV=2
LOC_Os01g47070	up	Acidic endochitinase OS=Cicer arietinum OX=3827 PE=2 SV=1
LOC_Os07g29960	up	Cytochrome P450 87A3 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP87A3 PE=2 SV=3
LOC_Os11g44430	up	Putative serine/threonine-protein kinase-like protein CCR3 OS=Arabidopsis thaliana OX=3702 GN=CCR3 PE=2 SV=1

LOC_Os07g03790	up	L-type lectin-domain containing receptor kinase IV.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK41 PE=2 SV=1
LOC_Os01g29280	up	Protein DMP5 OS=Arabidopsis thaliana OX=3702 GN=DMP5 PE=2 SV=1
LOC_Os10g28299	up	--
LOC_Os10g40360	up	Proline dehydrogenase 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=POX2 PE=2 SV=1
LOC_Os07g26550	up	--
LOC_Os01g69140	up	Uncharacterized protein At4g15970 OS=Arabidopsis thaliana OX=3702 GN=At4g15970 PE=2 SV=1
LOC_Os04g01470	up	Caffeate O-methyltransferase-like protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=COMTL2 PE=2 SV=2
LOC_Os01g68720	up	--
LOC_Os07g35160	up	--
LOC_Os01g64310	up	NAC domain-containing protein 90 OS=Arabidopsis thaliana OX=3702 GN=NAC090 PE=1 SV=1
LOC_Os07g35350	up	Glucan endo-1,3-beta-glucosidase 13 OS=Arabidopsis thaliana OX=3702 GN=At5g56590 PE=1 SV=1
LOC_Os11g44860	up	G-type lectin S-receptor-like serine/threonine-protein kinase At1g67520 OS=Arabidopsis thaliana OX=3702 GN=At1g67520 PE=2 SV=3
LOC_Os11g29210	up	--
LOC_Os01g02360	up	Rust resistance kinase Lr10 OS=Triticum aestivum OX=4565 GN=LRK10 PE=2 SV=1
LOC_Os01g42330	up	Disease resistance protein RGA2 OS=Solanum bulbocastanum OX=147425 GN=RGA2 PE=1 SV=1
LOC_Os05g34854	up	Gibberellin 20 oxidase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=20ox2 PE=1 SV=1
LOC_Os09g32100	up	--
LOC_Os10g33130	up	Probable leucine-rich repeat receptor-like protein kinase At1g35710 OS=Arabidopsis thaliana OX=3702 GN=At1g35710 PE=2 SV=1
LOC_Os04g43680	up	Transcription factor MYB4 OS=Oryza sativa subsp. japonica OX=39947 GN=MYB4 PE=2 SV=2
LOC_Os06g48520	up	Disease resistance protein RPM1 OS=Arabidopsis thaliana OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os06g33100	up	Peroxidase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=PRX112 PE=2 SV=1
LOC_Os12g36620	up	Pentatricopeptide repeat-containing protein At4g13650 OS=Arabidopsis thaliana OX=3702 GN=PCMP-H42 PE=2 SV=2
LOC_Os01g09150	up	--
LOC_Os08g29570	up	ABC transporter G family member 44 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG44 PE=2 SV=2
LOC_Os11g29290	up	Cytochrome P450 94B3 OS=Arabidopsis thaliana OX=3702 GN=CYP94B3 PE=1 SV=1
LOC_Os02g15520	up	Zinc finger BED domain-containing protein RICESLEEPER 4 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0518400 PE=2 SV=3
LOC_Os11g41034	up	--
LOC_Os06g08610	up	Putrescine hydroxycinnamoyltransferase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=PHT2 PE=2 SV=1
LOC_Os06g38580	up	--

LOC_Os06g45110	up	--
LOC_Os02g40200	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os04g30260	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os03g61310	up	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK3 OS=Oryza sativa subsp. japonica OX=39947 GN=LECRK3 PE=3 SV=2
LOC_Os03g29190	up	Probable nucleoredoxin 1-1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0405500 PE=2 SV=1
LOC_Os01g51690	up	Probable WRKY transcription factor 51 OS=Arabidopsis thaliana OX=3702 GN=WRKY51 PE=1 SV=1
LOC_Os11g06780	up	Leucine-rich repeat receptor protein kinase MSP1 OS=Oryza sativa subsp. japonica OX=39947 GN=MSP1 PE=1 SV=1
LOC_Os04g32480	up	Protein TIFY 9 OS=Oryza sativa subsp. japonica OX=39947 GN=TIFY9 PE=1 SV=1
LOC_Os02g12820	up	Putative transcription factor bHLH041 OS=Arabidopsis thaliana OX=3702 GN=BHLH41 PE=3 SV=1
LOC_Os01g68740	up	--
LOC_Os11g42970	up	CASP-like protein 1U2 OS=Oryza sativa subsp. japonica OX=39947 GN=Os11g0649700 PE=2 SV=1
LOC_Os04g59190	up	Cationic peroxidase SPC4 OS=Sorghum bicolor OX=4558 GN=Sb03g046810 PE=1 SV=2
LOC_Os10g39100	up	--
LOC_Os03g58890	up	Probable prolyl 4-hydroxylase 7 OS=Arabidopsis thaliana OX=3702 GN=P4H7 PE=2 SV=1
LOC_Os04g25800	up	UDP-glycosyltransferase 85A3 OS=Arabidopsis thaliana OX=3702 GN=UGT85A3 PE=2 SV=2
LOC_Os03g15050	up	Phosphoenolpyruvate carboxykinase (ATP) OS=Zea mays OX=4577 PE=2 SV=1
LOC_Os09g38850	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os06g44160	up	Chaperone protein dnaJ 8, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ATJ8 PE=2 SV=1
LOC_Os03g13740	up	U-box domain-containing protein 20 OS=Arabidopsis thaliana OX=3702 GN=PUB20 PE=2 SV=1
LOC_Os06g45970	up	Auxin-responsive protein SAUR71 OS=Arabidopsis thaliana OX=3702 GN=SAUR71 PE=2 SV=1
LOC_Os09g34214	up	UDP-glycosyltransferase 79 OS=Oryza sativa subsp. japonica OX=39947 GN=UGT79 PE=1 SV=2
LOC_Os06g03810	up	--
LOC_Os01g39330	up	Putative transcription factor bHLH041 OS=Arabidopsis thaliana OX=3702 GN=BHLH41 PE=3 SV=1
LOC_Os09g04430	up	--
LOC_Os04g33870	up	Transcription repressor OFP13 OS=Arabidopsis thaliana OX=3702 GN=OFP13 PE=1 SV=1
LOC_Os01g58310	up	--
LOC_Os10g39140	up	Flavanone 3-dioxygenase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=F3H-2 PE=1 SV=1
LOC_Os06g50180	up	Probable magnesium transporter NIPA6 OS=Arabidopsis thaliana OX=3702 GN=At2g21120 PE=2 SV=1
LOC_Os03g19700	up	UPF0481 protein At3g47200 OS=Arabidopsis thaliana OX=3702 GN=At3g47200 PE=2 SV=1

LOC_Os09g38350	up	Butyrate--CoA ligase AAE11, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=AAE11 PE=1 SV=1
LOC_Os09g27450	up	Homeobox-leucine zipper protein HOX11 OS=Oryza sativa subsp. japonica OX=39947 GN=HOX11 PE=2 SV=1
LOC_Os11g35450	up	Receptor-like protein EIX2 OS=Solanum lycopersicum OX=4081 GN=EIX2 PE=1 SV=2
LOC_Os03g32100	up	U-box domain-containing protein 4 OS=Arabidopsis thaliana OX=3702 GN=PUB4 PE=1 SV=3
LOC_Os11g02510	up	--
LOC_Os12g31540	up	Cell number regulator 13 OS=Zea mays OX=4577 GN=CNR13 PE=2 SV=1
LOC_Os06g11520	up	--
LOC_Os01g47900	up	Putative receptor protein kinase ZmPK1 OS=Zea mays OX=4577 GN=PK1 PE=2 SV=2
LOC_Os01g65992	up	Protein DMP1 OS=Arabidopsis thaliana OX=3702 GN=DMP1 PE=2 SV=1
LOC_Os09g28650	up	Tuliposide A-converting enzyme b1, amyloplastic OS=Tulipa gesneriana OX=13306 GN=TCEA-B1 PE=1 SV=1
LOC_Os02g18080	up	Putative disease resistance protein RGA4 OS=Solanum bulbocastanum OX=147425 GN=RGA4 PE=2 SV=1
LOC_Os08g07630	up	--
LOC_Os06g11450	up	E3 ubiquitin-protein ligase ATL31 OS=Arabidopsis thaliana OX=3702 GN=ATL31 PE=1 SV=2
LOC_Os02g50450	up	--
ChrSy.fgenes.h.gene.86	up	Probable pterin-4-alpha-carbinolamine dehydratase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ATP1 PE=1 SV=1
LOC_Os04g30330	up	Wall-associated receptor kinase-like 2 OS=Arabidopsis thaliana OX=3702 GN=WAKL2 PE=2 SV=1
LOC_Os04g59210	up	Peroxidase 12 OS=Arabidopsis thaliana OX=3702 GN=PER12 PE=1 SV=1
LOC_Os10g26940	up	BURP domain-containing protein 16 OS=Oryza sativa subsp. japonica OX=39947 GN=BURP16 PE=2 SV=1
LOC_Os08g31250	up	Probable nucleoredoxin 1-1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0405500 PE=2 SV=1
LOC_Os01g04530	up	--
LOC_Os06g37410	up	Putative transcription factor bHLH041 OS=Arabidopsis thaliana OX=3702 GN=BHLH41 PE=3 SV=1
LOC_Os06g34960	up	G-type lectin S-receptor-like serine/threonine-protein kinase At1g67520 OS=Arabidopsis thaliana OX=3702 GN=At1g67520 PE=2 SV=3
LOC_Os04g57850	up	Probable acyl-activating enzyme 5, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=AAE5 PE=1 SV=1
LOC_Os02g36070	up	Oryzalexin D synthase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP76M8 PE=1 SV=1
LOC_Os06g05910	up	Ubiquinone biosynthesis O-methyltransferase, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=COQ3 PE=1 SV=2
LOC_Os12g01400	up	Probable calcium-binding protein CML25/26 OS=Oryza sativa subsp. japonica OX=39947 GN=CML25 PE=3 SV=1
LOC_Os04g50950	up	Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana OX=3702 GN=NPF8.3 PE=1 SV=1
LOC_Os08g10290	up	Probable LRR receptor-like serine/threonine-protein kinase At1g56130 OS=Arabidopsis thaliana OX=3702 GN=At1g56130 PE=2 SV=2
LOC_Os05g16930	up	Probable LRR receptor-like serine/threonine-protein kinase At1g56130 OS=Arabidopsis thaliana OX=3702 GN=At1g56130 PE=2 SV=2

LOC_Os04g56900	up	Agmatine coumaroyltransferase-2 OS=Hordeum vulgare OX=4513 GN=ACT-2 PE=1 SV=1
Oryza_sativa_newGene_3826	up	--
LOC_Os05g39580	up	Abscisic acid receptor PYL4 OS=Arabidopsis thaliana OX=3702 GN=PYL4 PE=1 SV=1
LOC_Os03g20290	up	Aspartic proteinase nepenthesin-1 OS=Nepenthes gracilis OX=150966 GN=nep1 PE=1 SV=1
LOC_Os06g50650	up	Basic blue protein OS=Cucumis sativus OX=3659 PE=1 SV=1
LOC_Os03g04560	up	Protein unc-13 homolog OS=Arabidopsis thaliana OX=3702 GN=PATROL1 PE=2 SV=1
LOC_Os07g35380	up	Cysteine-rich receptor-like protein kinase 10 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK10 PE=2 SV=1
LOC_Os11g40810	up	Receptor kinase-like protein Xa21 OS=Oryza sativa subsp. indica OX=39946 GN=XA21 PE=1 SV=1
LOC_Os10g37570	up	--
LOC_Os01g56690	up	Transcription factor BHLH148 OS=Oryza sativa subsp. japonica OX=39947 GN=BHLH148 PE=1 SV=1
LOC_Os01g64450	up	NDR1/HIN1-like protein 3 OS=Arabidopsis thaliana OX=3702 GN=NHL3 PE=1 SV=1
LOC_Os04g55980	up	--
LOC_Os01g03549	up	Multicopper oxidase LPR1 homolog 2 OS=Oryza sativa subsp. japonica OX=39947 GN=LPR2 PE=2 SV=1
LOC_Os07g11870	up	Ent-cassadiene C2-hydroxylase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP71Z7 PE=1 SV=1
LOC_Os06g17020	up	UDP-glycosyltransferase 89B1 OS=Arabidopsis thaliana OX=3702 GN=UGT89B1 PE=2 SV=2
LOC_Os04g46210	up	--
Oryza_sativa_newGene_5075	up	U-box domain-containing protein 4 OS=Arabidopsis thaliana OX=3702 GN=PUB4 PE=1 SV=3
LOC_Os08g38110	up	UDP-glycosyltransferase 89B2 OS=Stevia rebaudiana OX=55670 GN=UGT89B2 PE=2 SV=1
LOC_Os03g59180	up	--
LOC_Os04g41050	up	NEP1-interacting protein 1 OS=Arabidopsis thaliana OX=3702 GN=NIP1 PE=1 SV=2
LOC_Os07g01560	up	Sugar transport protein MST3 OS=Oryza sativa subsp. japonica OX=39947 GN=MST3 PE=2 SV=1
LOC_Os08g04540	up	Aromatic-L-amino-acid decarboxylase OS=Catharanthus roseus OX=4058 GN=TDC PE=2 SV=1
LOC_Os02g36280	up	Oryzaalexin E synthase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP76M6 PE=1 SV=1
LOC_Os08g36310	up	Cytochrome P450 76M5 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP76M5 PE=1 SV=1
LOC_Os01g04570	up	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1 OS=Arabidopsis thaliana OX=3702 GN=LRK10
LOC_Os11g39000	up	Transcription factor ILI2 OS=Oryza sativa subsp. japonica OX=39947 GN=ILI2 PE=3 SV=1
LOC_Os09g23650	up	TPR repeat-containing thioredoxin TDX OS=Oryza sativa subsp. japonica OX=39947 GN=Os09g0401200 PE=2 SV=1
LOC_Os12g44070	up	--
Oryza_sativa_newGene_245	up	--

LOC_Os04g27340	up	Alpha-humulene synthase OS=Zingiber zerumbet OX=311405 GN=ZSS1 PE=1 SV=1
LOC_Os02g17534	up	Galactoside 2-alpha-L-fucosyltransferase OS=Pisum sativum OX=3888 GN=FT1 PE=2 SV=1
LOC_Os08g03240	up	L-type lectin-domain containing receptor kinase IX.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK91 PE=1 SV=1
LOC_Os07g35370	up	Cysteine-rich receptor-like protein kinase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK6 PE=1 SV=1
LOC_Os09g09560	up	--
LOC_Os02g42640	up	CBS domain-containing protein CBSX5 OS=Arabidopsis thaliana OX=3702 GN=CBSX5 PE=2 SV=2
LOC_Os02g15290	up	--
LOC_Os01g52320	up	Putative disease resistance protein RGA3 OS=Solanum bulbocastanum OX=147425 GN=RGA3 PE=2 SV=2
LOC_Os07g30369	up	7-deoxyloganetic acid glucosyltransferase OS=Catharanthus roseus OX=4058 GN=UGT709C2 PE=1 SV=1
LOC_Os04g30250	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os11g11970	up	--
LOC_Os07g14820	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os04g56030	up	--
LOC_Os07g09630	up	Probable prolyl 4-hydroxylase 7 OS=Arabidopsis thaliana OX=3702 GN=P4H7 PE=2 SV=1
LOC_Os09g04320	up	--
LOC_Os07g03368	up	Pathogenesis-related protein 1 OS=Hordeum vulgare OX=4513 PE=2 SV=1
LOC_Os11g45740	up	Transcription factor JAMYB OS=Oryza sativa subsp. japonica OX=39947 GN=JAMYB PE=2 SV=1
LOC_Os06g09620	up	--
LOC_Os02g58100	up	--
LOC_Os11g02530	up	Probable WRKY transcription factor 70 OS=Arabidopsis thaliana OX=3702 GN=WRKY70 PE=2 SV=1
LOC_Os11g34660	up	--
LOC_Os01g27480	up	Probable glutathione S-transferase GSTF1 OS=Oryza sativa subsp. japonica OX=39947 GN=GSTF1 PE=1 SV=2
LOC_Os07g03870	up	L-type lectin-domain containing receptor kinase IV.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK41 PE=2 SV=1
LOC_Os02g42150	up	Wall-associated receptor kinase 5 OS=Arabidopsis thaliana OX=3702 GN=WAK5 PE=2 SV=1
LOC_Os06g04140	up	--
LOC_Os04g39290	up	Heavy metal-associated isoprenylated plant protein 47 OS=Arabidopsis thaliana OX=3702 GN=HIP47 PE=3 SV=1
LOC_Os12g06410	up	E3 ubiquitin-protein ligase PUB23 OS=Arabidopsis thaliana OX=3702 GN=PUB23 PE=1 SV=1
LOC_Os09g19300	up	--
LOC_Os02g11960	up	ABC transporter A family member 8 OS=Arabidopsis thaliana OX=3702 GN=ABCA8 PE=2 SV=3

LOC_Os04g41370	up	Putative disease resistance protein RGA1 OS=Solanum bulbocastanum OX=147425 GN=RGA1 PE=2 SV=2
LOC_Os02g32520	up	Chaperone protein ClpD1, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=CLPD1 PE=2 SV=1
LOC_Os02g02780	up	Serine/threonine-protein kinase STY17 OS=Arabidopsis thaliana OX=3702 GN=STY17 PE=1 SV=1
LOC_Os09g13440	up	--
LOC_Os02g42620	up	Cold-responsive protein kinase 1 OS=Arabidopsis thaliana OX=3702 GN=CRPK1 PE=1 SV=1
LOC_Os04g58920	up	E3 ubiquitin-protein ligase PUB23 OS=Arabidopsis thaliana OX=3702 GN=PUB23 PE=1 SV=1
LOC_Os06g44170	up	Putative anthocyanidin reductase OS=Ginkgo biloba OX=3311 PE=2 SV=1
LOC_Os07g34850	up	Aspartic proteinase nepenthesin-1 OS=Nepenthes gracilis OX=150966 GN=nep1 PE=1 SV=1
LOC_Os04g29580	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os12g09250	up	Basic leucine zipper 61 OS=Arabidopsis thaliana OX=3702 GN=BZIP61 PE=1 SV=1
LOC_Os08g07380	up	Disease resistance protein RPP13 OS=Arabidopsis thaliana OX=3702 GN=RPP13 PE=2 SV=2
LOC_Os01g41770	up	Receptor-like protein EIX2 OS=Solanum lycopersicum OX=4081 GN=EIX2 PE=1 SV=2
LOC_Os01g26174	up	Wall-associated receptor kinase 5 OS=Arabidopsis thaliana OX=3702 GN=WAK5 PE=2 SV=1
LOC_Os01g06882	up	--
LOC_Os08g42840	up	Receptor-like protein EIX2 OS=Solanum lycopersicum OX=4081 GN=EIX2 PE=1 SV=2
LOC_Os06g37280	up	--
LOC_Os07g36570	up	G-type lectin S-receptor-like serine/threonine-protein kinase B120 OS=Arabidopsis thaliana OX=3702 GN=B120 PE=2 SV=1
LOC_Os02g50710	up	--
LOC_Os03g55010	up	UDP-glycosyltransferase 83A1 OS=Arabidopsis thaliana OX=3702 GN=UGT83A1 PE=2 SV=1
LOC_Os09g39290	up	RNA-directed DNA polymerase homolog OS=Oenothera berteroaana OX=3950 PE=4 SV=1
LOC_Os08g40990	up	Probable LRR receptor-like serine/threonine-protein kinase At4g31250 OS=Arabidopsis thaliana OX=3702 GN=At4g31250 PE=2 SV=1
LOC_Os05g49630	up	--
LOC_Os03g06080	up	Heavy metal-associated isoprenylated plant protein 27 OS=Arabidopsis thaliana OX=3702 GN=HIP27 PE=1 SV=1
LOC_Os05g47750	up	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 2.1 OS=Arabidopsis thaliana OX=3702 GN=LRK10
LOC_Os02g56630	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os06g34970	up	Cell number regulator 13 OS=Zea mays OX=4577 GN=CNR13 PE=2 SV=1
LOC_Os02g36190	up	Ent-cassadiene C2-hydroxylase OS=Oryza sativa subsp. japonica OX=39947 GN=CYP71Z7 PE=1 SV=1
LOC_Os09g29510	up	Wall-associated receptor kinase 3 OS=Arabidopsis thaliana OX=3702 GN=WAK3 PE=2 SV=2
LOC_Os01g04800	up	AP2/ERF and B3 domain-containing protein Os01g0141000 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0141000 PE=2 SV=1

LOC_Os08g30780	up	ABC transporter A family member 8 OS=Arabidopsis thaliana OX=3702 GN=ABCA8 PE=2 SV=3
LOC_Os02g56300	up	Long chain base biosynthesis protein 1b OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0806900 PE=2 SV=1
LOC_Os04g29930	up	Wall-associated receptor kinase-like 2 OS=Arabidopsis thaliana OX=3702 GN=WAKL2 PE=2 SV=1
LOC_Os07g46030	up	--
LOC_Os03g20330	up	--
LOC_Os02g36030	up	Cytochrome P450 76M5 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP76M5 PE=1 SV=1
LOC_Os03g20600	up	--
LOC_Os01g25560	up	Protein RALF-like 33 OS=Arabidopsis thaliana OX=3702 GN=RALFL33 PE=2 SV=1
LOC_Os04g03830	up	Wall-associated receptor kinase 5 OS=Arabidopsis thaliana OX=3702 GN=WAK5 PE=2 SV=1
LOC_Os01g64440	up	--
LOC_Os08g34910	up	Probable pectinesterase/pectinesterase inhibitor 13 OS=Arabidopsis thaliana OX=3702 GN=PME13 PE=2 SV=2
LOC_Os04g12600	up	G-type lectin S-receptor-like serine/threonine-protein kinase LECRK4 OS=Oryza sativa subsp. japonica OX=39947 GN=LECRK4 PE=3 SV=1
LOC_Os08g34790	up	Probable 4-coumarate--CoA ligase 5 OS=Oryza sativa subsp. japonica OX=39947 GN=4CL5 PE=2 SV=1
LOC_Os02g06160	up	Probable L-type lectin-domain containing receptor kinase S.5 OS=Arabidopsis thaliana OX=3702 GN=LECRKS5 PE=2 SV=1
LOC_Os11g12340	up	Disease resistance protein RPM1 OS=Arabidopsis thaliana OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os09g30412	up	Heat shock protein 81-2 OS=Oryza sativa subsp. japonica OX=39947 GN=HSP81-2 PE=2 SV=1
LOC_Os06g39650	up	Pentatricopeptide repeat-containing protein At1g31430 OS=Arabidopsis thaliana OX=3702 GN=PCMP-E55 PE=2 SV=1
LOC_Os12g42540	up	RING-H2 finger protein ATL70 OS=Arabidopsis thaliana OX=3702 GN=ATL70 PE=2 SV=1
LOC_Os11g29870	up	Probable WRKY transcription factor 75 OS=Arabidopsis thaliana OX=3702 GN=WRKY75 PE=2 SV=1
LOC_Os12g28590	up	AAA-ATPase ASD, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=AATP1 PE=1 SV=1
LOC_Os09g20090	up	L-ascorbate oxidase OS=Cucumis sativus OX=3659 PE=1 SV=1
LOC_Os09g28680	up	Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum OX=4097 PE=2 SV=1
LOC_Os03g20440	up	--
LOC_Os11g33970	up	UPF0481 protein At3g47200 OS=Arabidopsis thaliana OX=3702 GN=At3g47200 PE=2 SV=1
LOC_Os10g33190	up	--
Oryza_sativa_newGene_5074	up	Probable esterase D14L OS=Oryza sativa subsp. japonica OX=39947 GN=D14L PE=1 SV=1
LOC_Os12g10180	up	Putative disease resistance protein RGA4 OS=Solanum bulbocastanum OX=147425 GN=RGA4 PE=2 SV=1
LOC_Os10g11200	up	Long chain base biosynthesis protein 1c OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0189600 PE=2 SV=2
LOC_Os04g10530	up	Probable amidase At4g34880 OS=Arabidopsis thaliana OX=3702 GN=At4g34880 PE=2 SV=1

LOC_Os07g48830	up	Galactinol synthase 2 OS=Solanum lycopersicum OX=4081 GN=GOLS2 PE=2 SV=1
LOC_Os07g26870	up	Cytochrome P450 89A9 OS=Arabidopsis thaliana OX=3702 GN=CYP89A9 PE=2 SV=1
LOC_Os08g40850	up	Probable mitochondrial adenine nucleotide transporter BTL1 OS=Arabidopsis thaliana OX=3702 GN=At3g20240 PE=2 SV=1
LOC_Os07g37320	up	Sugar transport protein MST6 OS=Oryza sativa subsp. japonica OX=39947 GN=MST6 PE=1 SV=1
LOC_Os06g05070	up	Probable receptor-like protein kinase At5g20050 OS=Arabidopsis thaliana OX=3702 GN=At5g20050 PE=2 SV=1
LOC_Os08g02110	up	Peroxidase 47 OS=Arabidopsis thaliana OX=3702 GN=PER47 PE=2 SV=2
LOC_Os09g19280	up	Disease resistance protein RPM1 OS=Arabidopsis thaliana OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os04g03796	up	Subtilisin-like protease SBT3.8 OS=Arabidopsis thaliana OX=3702 GN=SBT3.8 PE=3 SV=1
LOC_Os08g16050	up	Tetraspanin-7 OS=Arabidopsis thaliana OX=3702 GN=TET7 PE=2 SV=1
LOC_Os05g25920	up	--
LOC_Os01g66530	up	--
LOC_Os02g03710	up	--
LOC_Os07g23410	up	Fatty acid desaturase DES2 OS=Sorghum bicolor OX=4558 GN=DES2 PE=2 SV=1
LOC_Os06g38710	up	--
LOC_Os04g56000	up	--
LOC_Os06g41980	up	Protein LYK5 OS=Arabidopsis thaliana OX=3702 GN=LYK5 PE=2 SV=1
LOC_Os04g28470	up	Retrovirus-related Pol polyprotein from transposon RE2 OS=Arabidopsis thaliana OX=3702 GN=RE2 PE=4 SV=1
LOC_Os02g22160	up	--
LOC_Os12g43790	up	--
LOC_Os05g45410	up	Heat stress transcription factor A-4d OS=Oryza sativa subsp. japonica OX=39947 GN=HSFA4D PE=1 SV=1
LOC_Os09g37880	up	G-type lectin S-receptor-like serine/threonine-protein kinase At1g11330 OS=Arabidopsis thaliana OX=3702 GN=At1g11330 PE=1 SV=3
LOC_Os07g35180	up	--
LOC_Os05g50090	up	Probable 2-oxoglutarate-dependent dioxygenase AOP1.2 OS=Arabidopsis thaliana OX=3702 GN=AOP1.2 PE=2 SV=1
LOC_Os09g09550	up	Putative UPF0481 protein At3g02645 OS=Arabidopsis thaliana OX=3702 GN=At3g02645 PE=3 SV=1
LOC_Os01g35330	up	--
LOC_Os08g44640	up	Serine carboxypeptidase-like 51 OS=Arabidopsis thaliana OX=3702 GN=SCPL51 PE=2 SV=2
LOC_Os09g09830	up	--
LOC_Os09g19229	up	Probable LRR receptor-like serine/threonine-protein kinase At1g51810 OS=Arabidopsis thaliana OX=3702 GN=At1g51810 PE=2 SV=1
LOC_Os03g15080	up	--

LOC_Os02g16940	up	Subtilisin-like protease SBT3.9 OS=Arabidopsis thaliana OX=3702 GN=SBT3.9 PE=3 SV=1
LOC_Os07g30469	up	7-deoxyloganetic acid glucosyltransferase OS=Catharanthus roseus OX=4058 GN=UGT709C2 PE=1 SV=1
LOC_Os04g10010	up	Momilactone A synthase OS=Oryza sativa subsp. japonica OX=39947 GN=Os04g0179200 PE=2 SV=1
LOC_Os05g30760	up	Esterase PIR7B OS=Oryza sativa subsp. japonica OX=39947 GN=PIR7B PE=2 SV=2
LOC_Os06g43780	up	--
LOC_Os12g38170	up	Osmotin-like protein OS=Solanum lycopersicum OX=4081 PE=1 SV=1
LOC_Os08g09060	up	Germin-like protein 8-10 OS=Oryza sativa subsp. japonica OX=39947 GN=GLP2 PE=2 SV=1
LOC_Os08g43630	up	--
LOC_Os02g14630	up	Hydroquinone glucosyltransferase OS=Rauvolfia serpentina OX=4060 GN=AS PE=1 SV=1
LOC_Os12g36830	up	Major allergen Mal d 1 OS=Malus domestica OX=3750 PE=1 SV=3
LOC_Os02g48690	up	--
LOC_Os02g08440	up	WRKY transcription factor WRKY71 OS=Oryza sativa subsp. indica OX=39946 GN=WRKY71 PE=1 SV=1
LOC_Os03g16950	up	Cysteine-rich repeat secretory protein 55 OS=Arabidopsis thaliana OX=3702 GN=CRRSP55 PE=2 SV=1
LOC_Os02g01090	up	Transcriptional regulator SUPERMAN OS=Arabidopsis thaliana OX=3702 GN=SUP PE=1 SV=1
LOC_Os03g47280	up	--
LOC_Os01g54380	up	Pentatricopeptide repeat-containing protein At2g27800, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At2g27800 PE=3 SV=2
LOC_Os08g07660	up	--
LOC_Os07g48450	up	NAC transcription factor 29 OS=Arabidopsis thaliana OX=3702 GN=NAC029 PE=2 SV=1
LOC_Os07g03200	up	Phytosulfokines 4 OS=Oryza sativa subsp. japonica OX=39947 GN=PSK4 PE=1 SV=1
LOC_Os02g48200	up	Probable L-type lectin-domain containing receptor kinase S.5 OS=Arabidopsis thaliana OX=3702 GN=LECRKS5 PE=2 SV=1
LOC_Os06g23760	up	Acyl-coenzyme A oxidase 4, peroxisomal OS=Arabidopsis thaliana OX=3702 GN=ACX4 PE=1 SV=1
LOC_Os04g28780	up	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 OS=Arabidopsis thaliana OX=3702 GN=At2g19130 PE=2 SV=1
LOC_Os12g42730	up	COP9 signalosome complex subunit 6b OS=Arabidopsis thaliana OX=3702 GN=CSN6B PE=1 SV=2
LOC_Os06g47530	up	Cysteine-rich receptor-like protein kinase 10 OS=Arabidopsis thaliana OX=3702 GN=CRK10 PE=1 SV=3
LOC_Os10g39260	up	Aspartic proteinase nepenthesin-1 OS=Nepenthes gracilis OX=150966 GN=nep1 PE=1 SV=1
LOC_Os02g17000	up	Subtilisin-like protease SBT3.10 OS=Arabidopsis thaliana OX=3702 GN=SBT3.10 PE=3 SV=2
LOC_Os07g03458	up	Pathogenesis-related protein 1 OS=Hordeum vulgare OX=4513 PE=2 SV=1
LOC_Os06g13940	up	--
LOC_Os06g06350	up	Long chain acyl-CoA synthetase 4 OS=Arabidopsis thaliana OX=3702 GN=LACS4 PE=2 SV=1

LOC_Os04g09570	up	--
LOC_Os04g59150	up	Peroxidase 12 OS=Arabidopsis thaliana OX=3702 GN=PER12 PE=1 SV=1
LOC_Os09g29560	up	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
LOC_Os05g47770	up	LEAF RUST 10 DISEASE-RESISTANCE LOCUS RECEPTOR-LIKE PROTEIN KINASE-like 1.2 OS=Arabidopsis thaliana OX=3702 GN=LRK10
LOC_Os09g19360	up	Probable LRR receptor-like serine/threonine-protein kinase At1g51810 OS=Arabidopsis thaliana OX=3702 GN=At1g51810 PE=2 SV=1
LOC_Os01g05870	up	Probable LRR receptor-like serine/threonine-protein kinase At3g47570 OS=Arabidopsis thaliana OX=3702 GN=At3g47570 PE=2 SV=1
LOC_Os04g43070	up	Ammonium transporter 1 member 1 OS=Oryza sativa subsp. japonica OX=39947 GN=AMT1-1 PE=2 SV=1
LOC_Os02g18070	up	Disease resistance protein RGA2 OS=Solanum bulbocastanum OX=147425 GN=RGA2 PE=1 SV=1
LOC_Os01g42410	up	ABC transporter G family member 37 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG37 PE=2 SV=1
LOC_Os03g14090	up	--
LOC_Os02g27310	up	Cysteine-rich receptor-like protein kinase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CRK6 PE=1 SV=1
LOC_Os09g09540	up	--
LOC_Os01g71860	up	Glucan endo-1,3-beta-glucosidase GV OS=Hordeum vulgare OX=4513 PE=2 SV=2
LOC_Os03g20970	up	Phospholipid-transporting ATPase 1 OS=Arabidopsis thaliana OX=3702 GN=ALA1 PE=2 SV=1
LOC_Os11g42290	up	Tryptamine benzoyltransferase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=TBT1 PE=1 SV=1
LOC_Os10g34840	up	Ripening-related protein 3 OS=Oryza sativa subsp. japonica OX=39947 GN=Os10g0490100 PE=2 SV=1
LOC_Os08g44220	up	ACD11 homolog protein OS=Arabidopsis thaliana OX=3702 GN=At4g39670 PE=2 SV=1
LOC_Os03g08999	up	Alcohol dehydrogenase-like 1 OS=Arabidopsis thaliana OX=3702 GN=At1g22430 PE=2 SV=1
LOC_Os03g12500	up	Allene oxide synthase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=CYP74A2 PE=2 SV=2
LOC_Os07g33780	up	ABC transporter G family member 43 OS=Oryza sativa subsp. japonica OX=39947 GN=ABCG43 PE=2 SV=2
LOC_Os03g45450	up	Probable WRKY transcription factor 57 OS=Arabidopsis thaliana OX=3702 GN=WRKY57 PE=2 SV=1
LOC_Os05g48680	up	--
LOC_Os02g03400	up	65-kDa microtubule-associated protein 3 OS=Arabidopsis thaliana OX=3702 GN=MAP65-3 PE=1 SV=1
LOC_Os02g35490	up	MLO-like protein 1 OS=Arabidopsis thaliana OX=3702 GN=MLO1 PE=1 SV=1
LOC_Os07g09190	up	Probable 1-deoxy-D-xylulose-5-phosphate synthase 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0190000 PE=2 SV=1
LOC_Os11g16940	up	--
LOC_Os04g22120	up	L-type lectin-domain containing receptor kinase IX.1 OS=Arabidopsis thaliana OX=3702 GN=LECRK91 PE=1 SV=1
LOC_Os12g03350	up	--

Table S6 GY129-specifically down expressed DEGs

Gene ID	Regulated	Annotation
LOC_Os05g33900	down	WAT1-related protein At5g07050 OS=Arabidopsis thaliana OX=3702 GN=At5g07050 PE=2 SV=1
LOC_Os01g42280	down	Pentatricopeptide repeat-containing protein At5g55740, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CRR21 PE=2 SV=1
LOC_Os02g05000	down	--
LOC_Os07g01540	down	--
LOC_Os04g54930	down	ABC transporter B family member 19 OS=Arabidopsis thaliana OX=3702 GN=ABCB19 PE=1 SV=1
LOC_Os02g39080	down	--
LOC_Os06g21020	down	Anthranilate O-methyltransferase 3 OS=Zea mays OX=4577 GN=AAMT3 PE=1 SV=1
LOC_Os03g21450	down	--
LOC_Os01g50980	down	Cullin-1 OS=Arabidopsis thaliana OX=3702 GN=CUL1 PE=1 SV=1
LOC_Os07g43390	down	4-alpha-glucanotransferase DPE1, chloroplastic/amyloplastic OS=Oryza sativa subsp. japonica OX=39947 GN=DPE1 PE=2 SV=2
LOC_Os10g07200	down	--
Oryza_sativa_newGene_2277	down	--
LOC_Os02g43710	down	Probable enoyl-CoA hydratase 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=At4g16800 PE=2 SV=1
LOC_Os01g67360	down	Probable methyltransferase PMT17 OS=Arabidopsis thaliana OX=3702 GN=At4g10440 PE=3 SV=1
LOC_Os03g63480	down	Ankyrin repeat domain-containing protein 2A OS=Arabidopsis thaliana OX=3702 GN=AKR2A PE=1 SV=2
LOC_Os07g48980	down	Nicotianamine synthase 3 OS=Oryza sativa subsp. japonica OX=39947 GN=NAS3 PE=2 SV=1
LOC_Os01g43500	down	--
LOC_Os06g43900	down	50S ribosomal protein L35, chloroplastic OS=Spinacia oleracea OX=3562 GN=RPL35 PE=1 SV=1
LOC_Os07g24992	down	Uncharacterized protein ycf68 OS=Oryza sativa subsp. japonica OX=39947 GN=ycf68-1 PE=3 SV=1
LOC_Os01g66379	down	Peptide chain release factor PrfB2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PRFB2 PE=3 SV=1
LOC_Os02g05744	down	Endoglucanase 5 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0151300 PE=2 SV=1
LOC_Os02g53130	down	Nitrate reductase [NAD(P)H] OS=Hordeum vulgare OX=4513 GN=NAR-7 PE=2 SV=1
LOC_Os03g19350	down	Lon protease homolog, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0689300 PE=2 SV=1
LOC_Os08g30719	down	--
LOC_Os04g58504	down	Choline transporter protein 1 OS=Arabidopsis thaliana OX=3702 GN=CHER1 PE=1 SV=1
LOC_Os05g01350	down	Formin-like protein 14 OS=Oryza sativa subsp. japonica OX=39947 GN=FH14 PE=2 SV=1

LOC_Os03g47016	down	Homeobox protein knotted-1-like 4 OS=Oryza sativa subsp. japonica OX=39947 GN=OSH10 PE=2 SV=1
LOC_Os02g33450	down	2-Cys peroxiredoxin BAS1, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=BAS1 PE=1 SV=1
LOC_Os01g63190	down	Laccase-7 OS=Oryza sativa subsp. japonica OX=39947 GN=LAC7 PE=2 SV=1
LOC_Os01g59120	down	Cyclin-B1-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCB1-1 PE=2 SV=2
LOC_Os01g08140	down	BTB/POZ domain-containing protein NPY5 OS=Arabidopsis thaliana OX=3702 GN=NPY5 PE=2 SV=2
LOC_Os11g05552	down	Signal recognition particle 54 kDa protein, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=FFC PE=1 SV=1
LOC_Os03g03020	down	50S ribosomal protein L11, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=RPL11 PE=2 SV=1
LOC_Os05g35930	down	--
LOC_Os12g37610	down	--
LOC_Os12g38850	down	Protein ENHANCED DISEASE RESISTANCE 2 OS=Arabidopsis thaliana OX=3702 GN=EDR2 PE=2 SV=1
LOC_Os04g44610	down	ABC transporter G family member 11 OS=Arabidopsis thaliana OX=3702 GN=ABCG11 PE=1 SV=1
LOC_Os04g54759	down	--
LOC_Os02g41500	down	Wall-associated receptor kinase 2 OS=Arabidopsis thaliana OX=3702 GN=WAK2 PE=1 SV=1
Oryza_sativa_newGene_4536	down	--
LOC_Os04g02580	down	--
LOC_Os01g72300	down	Germin-like protein 1-4 OS=Oryza sativa subsp. japonica OX=39947 GN=Os01g0952100 PE=1 SV=1
LOC_Os01g06580	down	Fasciclin-like arabinogalactan protein 11 OS=Arabidopsis thaliana OX=3702 GN=FLA11 PE=2 SV=2
LOC_Os03g19120	down	Myb-related protein P OS=Zea mays OX=4577 GN=P PE=2 SV=1
LOC_Os07g38150	down	--
LOC_Os05g38170	down	Uracil phosphoribosyltransferase OS=Nicotiana tabacum OX=4097 GN=UPP PE=2 SV=1
LOC_Os01g37470	down	--
Oryza_sativa_newGene_3711	down	Endoglucanase 18 OS=Oryza sativa subsp. japonica OX=39947 GN=Os06g0715300 PE=2 SV=1
LOC_Os07g26690	down	Probable aquaporin PIP2-1 OS=Oryza sativa subsp. japonica OX=39947 GN=PIP2-1 PE=2 SV=1
LOC_Os07g25800	down	F-box protein At2g05970 OS=Arabidopsis thaliana OX=3702 GN=At2g05970 PE=2 SV=1
LOC_Os12g29500	down	Protein LAX PANICLE 2 OS=Oryza sativa subsp. japonica OX=39947 GN=LAX2 PE=1 SV=1
LOC_Os03g14040	down	Protein SPA, chloroplastic OS=Solanum lycopersicum OX=4081 GN=SPA PE=2 SV=1
LOC_Os02g04500	down	--
LOC_Os10g02690	down	--
LOC_Os10g41860	down	--

LOC_Os05g33520	down	--
LOC_Os07g47130	down	Homeobox-leucine zipper protein ROC8 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ROC8 PE=2 SV=2
LOC_Os02g42810	down	Salutaridine reductase OS= <i>Papaver bracteatum</i> OX=215227 GN=SALR PE=1 SV=1
LOC_Os03g42240	down	B3 domain-containing protein Os03g0619800 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os03g0619800 PE=3 SV=1
LOC_Os10g35644	down	Protein NEOXANTHIN-DEFICIENT 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=NDX1 PE=3 SV=2
LOC_Os01g55350	down	Phosphoenolpyruvate carboxylase, housekeeping isozyme OS= <i>Saccharum hybrid</i> OX=15819 PE=3 SV=1
LOC_Os11g04150	down	Protein ZINC INDUCED FACILITATOR-LIKE 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ZIFL1 PE=2 SV=1
LOC_Os07g43940	down	Glucan endo-1,3-beta-glucosidase 4 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g13560 PE=1 SV=1
Oryza_sativa_newGene_1725	down	Pullulanase 1, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PU1 PE=1 SV=2
LOC_Os07g46930	down	Secoisolariciresinol dehydrogenase (Fragment) OS= <i>Forsythia intermedia</i> OX=55183 PE=1 SV=1
LOC_Os07g42994	down	--
LOC_Os01g09450	down	Auxin-responsive protein IAA2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=IAA2 PE=2 SV=1
LOC_Os06g02810	down	--
LOC_Os09g30462	down	--
LOC_Os12g32970	down	CASP-like protein 2B1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os12g0514300 PE=2 SV=2
LOC_Os11g42240	down	--
LOC_Os10g36530	down	DNA mismatch repair protein MSH3 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=MSH3 PE=1 SV=2
LOC_Os04g20400	down	UDP-glycosyltransferase 92A1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=UGT92A1 PE=2 SV=1
LOC_Os04g55230	down	Protein TSS OS= <i>Arabidopsis thaliana</i> OX=3702 GN=TSS PE=1 SV=1
LOC_Os12g42090	down	2-methyl-6-phytyl-1,4-hydroquinone methyltransferase 2, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os12g0615400 PE=2 SV=2
LOC_Os07g42860	down	Cyclin-D2-2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CYCD2-2 PE=2 SV=1
LOC_Os10g21266	down	ATP synthase subunit beta, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=atpB PE=1 SV=2
LOC_Os03g13860	down	Small GTPase LIP1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=LIP1 PE=1 SV=1
LOC_Os04g35210	down	--
LOC_Os04g51340	down	Pectin acetylerase 7 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PAE7 PE=2 SV=1
LOC_Os03g37780	down	--
LOC_Os03g16290	down	--
LOC_Os09g02300	down	--
LOC_Os05g12640	down	BURP domain-containing protein 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=BURP2 PE=2 SV=1

LOC_Os11g32620	down	Bisdemethoxycurcumin synthase OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os07g0271500 PE=1 SV=2
Oryza_sativa_newGene_2150	down	--
LOC_Os06g46930	down	50S ribosomal protein L24, chloroplastic OS= <i>Nicotiana tabacum</i> OX=4097 GN=RPL24 PE=1 SV=1
LOC_Os01g25270	down	Pentatricopeptide repeat-containing protein At3g57430, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PCMP-H81 PE=2 SV=2
LOC_Os01g08370	down	Putative disease resistance RPP13-like protein 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=RPPL1 PE=3 SV=1
LOC_Os02g44380	down	BEACH domain-containing protein C2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=BCHC2 PE=1 SV=1
LOC_Os02g54830	down	Putative RING-H2 finger protein ATL49 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ATL49 PE=3 SV=1
LOC_Os01g36390	down	DNA replication licensing factor MCM4 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=MCM4 PE=3 SV=2
LOC_Os04g39864	down	Beta-glucosidase 11 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=BGLU11 PE=3 SV=2
LOC_Os03g62950	down	--
LOC_Os02g21550	down	Protein SRG1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SRG1 PE=2 SV=1
LOC_Os03g18890	down	Probable galacturonosyltransferase-like 7 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GATL7 PE=2 SV=1
LOC_Os10g21130	down	--
LOC_Os02g43594	down	Vesicle-associated protein 2-1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PVA21 PE=1 SV=1
LOC_Os04g44620	down	--
LOC_Os01g35590	down	--
LOC_Os03g47140	down	Growth-regulating factor 9 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=GRF9 PE=2 SV=1
LOC_Os03g59030	down	Putative UDP-rhamnose:rhamnosyltransferase 1 OS= <i>Fragaria ananassa</i> OX=3747 GN=GT4 PE=2 SV=1
LOC_Os06g19740	down	--
LOC_Os08g06550	down	Acyl-CoA-binding domain-containing protein 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ACBP1 PE=1 SV=1
LOC_Os09g35600	down	Protein DETOXIFICATION 51 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=DTX51 PE=2 SV=1
LOC_Os05g37730	down	Transcription factor DIVARICATA OS= <i>Antirrhinum majus</i> OX=4151 GN=DIVARICATA PE=2 SV=1
LOC_Os01g01090	down	--
LOC_Os05g14270	down	--
LOC_Os06g21360	down	Sodium/hydrogen exchanger 4 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=NHX4 PE=2 SV=2
LOC_Os07g24030	down	--
LOC_Os07g03150	down	BTB/POZ domain-containing protein At3g50780 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g50780 PE=2 SV=1
LOC_Os02g50320	down	Microtubule-associated protein 70-2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=MAP70.2 PE=2 SV=1
LOC_Os12g10640	down	Uncharacterized protein ycf45 OS= <i>Porphyra purpurea</i> OX=2787 GN=ycf45 PE=3 SV=1

LOC_Os02g43110	down	Magnesium/proton exchanger 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=MHX2 PE=3 SV=2
LOC_Os12g19285	down	--
LOC_Os05g19670	down	Germin-like protein 5-1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os05g0277500 PE=2 SV=1
LOC_Os03g21960	down	Alanine--glyoxylate aminotransferase 2 homolog 3, mitochondrial OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g08860 PE=2 SV=1
LOC_Os04g36820	down	--
LOC_Os02g09359	down	PTI1-like tyrosine-protein kinase At3g15890 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g15890 PE=2 SV=1
LOC_Os01g04250	down	--
LOC_Os01g69060	down	Probable 1-acylglycerol-3-phosphate O-acyltransferase OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os09g0520200 PE=3 SV=3
LOC_Os07g36460	down	Transcription factor UDT1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=UDT1 PE=2 SV=2
LOC_Os01g70340	down	Protein LAX PANICLE 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=LAX2 PE=1 SV=1
LOC_Os05g36970	down	Transcription repressor OFP8 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=OFP8 PE=1 SV=1
LOC_Os01g10800	down	Pentatricopeptide repeat-containing protein DOT4, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=DOT4 PE=2 SV=1
LOC_Os08g28670	down	--
LOC_Os02g50630	down	E2F transcription factor-like E2FE OS= <i>Arabidopsis thaliana</i> OX=3702 GN=E2FE PE=1 SV=1
LOC_Os03g04310	down	Transcription factor bHLH93 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=BHLH93 PE=1 SV=1
LOC_Os05g43140	down	--
LOC_Os03g49480	down	Elongation of fatty acids protein 3-like OS= <i>Arabidopsis thaliana</i> OX=3702 GN=HOS3 PE=2 SV=1
Oryza_sativa_newGene_1207	down	--
LOC_Os07g47520	down	--
LOC_Os05g06320	down	Probable ethylene response sensor 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ERS2 PE=2 SV=1
LOC_Os01g64230	down	--
LOC_Os01g25600	down	Protein LOW PSII ACCUMULATION 1, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=LPA1 PE=1 SV=1
LOC_Os04g47220	down	Probable aquaporin PIP1-2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=PIP1-2 PE=2 SV=3
LOC_Os08g20130	down	Cytosolic sulfotransferase 5 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SOT5 PE=1 SV=1
LOC_Os10g21236	down	ATP synthase subunit a, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=atpI PE=3 SV=1
LOC_Os05g25974	down	--
LOC_Os04g05580	down	L-type lectin-domain containing receptor kinase IX.1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=LECRK91 PE=1 SV=1
LOC_Os05g01270	down	Photosynthetic NDH subunit of lumenal location 5, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PNSL5 PE=1 SV=1
LOC_Os01g16030	down	ADP-ribosylation factor 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ARF PE=2 SV=2

Oryza_sativa_newGene_854	down	--
LOC_Os04g42784	down	DNA mismatch repair protein MSH1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=MSH1 PE=1 SV=1
Oryza_sativa_newGene_4794	down	--
LOC_Os05g16054	down	--
LOC_Os02g53000	down	LysM domain-containing GPI-anchored protein LYP6 OS=Oryza sativa subsp. japonica OX=39947 GN=LYP6 PE=1 SV=1
LOC_Os07g44370	down	Dirigent protein 5 OS=Arabidopsis thaliana OX=3702 GN=DIR5 PE=2 SV=1
LOC_Os03g03724	down	--
LOC_Os02g34520	down	Protein FAR1-RELATED SEQUENCE 12 OS=Arabidopsis thaliana OX=3702 GN=FRS12 PE=2 SV=1
LOC_Os02g18612	down	--
LOC_Os01g44210	down	50S ribosomal protein L31, chloroplastic OS=Spinacia oleracea OX=3562 GN=RPL31 PE=1 SV=2
LOC_Os03g13030	down	Lecithin-cholesterol acyltransferase-like 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0232800 PE=2 SV=1
LOC_Os05g36010	down	Subtilisin-like protease SBT1.7 OS=Arabidopsis thaliana OX=3702 GN=SBT1.7 PE=1 SV=1
LOC_Os11g05690	down	Cationic amino acid transporter 7, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CAT7 PE=3 SV=1
LOC_Os04g52320	down	Polygalacturonase QRT3 OS=Arabidopsis thaliana OX=3702 GN=QRT3 PE=2 SV=1
Oryza_sativa_newGene_1036	down	--
LOC_Os08g35750	down	Germin-like protein 8-13 OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0459700 PE=3 SV=1
LOC_Os06g27860	down	Protein POOR HOMOLOGOUS SYNAPSIS 1 OS=Zea mays OX=4577 GN=PHS1 PE=1 SV=1
Oryza_sativa_newGene_2677	down	--
LOC_Os06g07941	down	Protein SRG1 OS=Arabidopsis thaliana OX=3702 GN=SRG1 PE=2 SV=1
LOC_Os08g37040	down	Probable carboxylesterase 2 OS=Arabidopsis thaliana OX=3702 GN=CXE2 PE=2 SV=1
LOC_Os09g10600	down	Enoyl-[acyl-carrier-protein] reductase [NADH] 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os09g0277800 PE=2 SV=1
LOC_Os01g11620	down	GDSL esterase/lipase At5g45910 OS=Arabidopsis thaliana OX=3702 GN=At5g45910 PE=2 SV=1
LOC_Os03g60480	down	Protein SODIUM POTASSIUM ROOT DEFECTIVE 2 OS=Arabidopsis thaliana OX=3702 GN=NAKR2 PE=2 SV=1
LOC_Os09g37710	down	Protein NLP1 OS=Oryza sativa subsp. japonica OX=39947 GN=NLP1 PE=2 SV=1
LOC_Os03g53900	down	Universal stress protein A-like protein OS=Arabidopsis thaliana OX=3702 GN=At3g01520 PE=1 SV=2
LOC_Os03g59100	down	Protochlorophyllide-dependent translocon component 52, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PTC52 PE=2 SV=1
LOC_Os10g31240	down	UPF0481 protein At3g47200 OS=Arabidopsis thaliana OX=3702 GN=At3g47200 PE=2 SV=1
LOC_Os04g49900	down	ABC transporter C family member 9 OS=Arabidopsis thaliana OX=3702 GN=ABCC9 PE=2 SV=2
LOC_Os11g38920	down	HVA22-like protein a OS=Arabidopsis thaliana OX=3702 GN=HVA22A PE=2 SV=1

LOC_Os02g19970	down	Nicotianamine aminotransferase A OS=Hordeum vulgare OX=4513 GN=naat-A PE=1 SV=2
LOC_Os01g15170	down	--
LOC_Os05g40960	down	Myb-related protein 1 OS=Arabidopsis thaliana OX=3702 GN=MYR1 PE=1 SV=1
LOC_Os06g49240	down	Protein NRT1/ PTR FAMILY 8.5 OS=Arabidopsis thaliana OX=3702 GN=NPF8.5 PE=2 SV=1
LOC_Os03g45340	down	Inactive protein RESTRICTED TEV MOVEMENT 2 OS=Arabidopsis thaliana OX=3702 GN=RTM2 PE=3 SV=1
LOC_Os03g19080	down	--
LOC_Os05g22614	down	Protein plastid transcriptionally active 16, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PTAC16 PE=1 SV=1
LOC_Os11g02840	down	Probable serine/threonine-protein kinase PBL8 OS=Arabidopsis thaliana OX=3702 GN=PBL8 PE=1 SV=1
LOC_Os01g29104	down	--
LOC_Os06g01210	down	Plastocyanin, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=PETE PE=1 SV=1
LOC_Os12g34108	down	ATP synthase subunit 9, mitochondrial OS=Petunia sp. OX=4104 GN=ATP9 PE=3 SV=1
LOC_Os07g47750	down	Phylloplanin OS=Nicotiana tabacum OX=4097 PE=1 SV=1
LOC_Os10g35580	down	Microtubule-associated protein RP/EB family member 1C OS=Arabidopsis thaliana OX=3702 GN=EB1C PE=1 SV=1
LOC_Os02g22260	down	Fruit protein pKIWI502 OS=Actinidia deliciosa OX=3627 GN=pKIWI502 PE=2 SV=1
Oryza_sativa_newGene_3077	down	--
LOC_Os02g50560	down	DExH-box ATP-dependent RNA helicase DExH15 chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ISE2 PE=1 SV=2
LOC_Os03g39110	down	--
LOC_Os06g02730	down	Aspartyl protease family protein At5g10770 OS=Arabidopsis thaliana OX=3702 GN=At5g10770 PE=2 SV=1
LOC_Os01g54020	down	Tryptophan--tRNA ligase, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=OVA4 PE=1 SV=1
LOC_Os01g72205	down	--
LOC_Os10g13850	down	--
LOC_Os02g43900	down	--
Oryza_sativa_newGene_3625	down	F-box/LRR-repeat protein At4g14096 OS=Arabidopsis thaliana OX=3702 GN=At4g14096 PE=2 SV=1
LOC_Os02g51480	down	Pentatricopeptide repeat-containing protein PPR5 homolog, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0750400 PE=3 SV=1
LOC_Os02g20540	down	Fasciclin-like arabinogalactan protein 6 OS=Arabidopsis thaliana OX=3702 GN=FLA6 PE=2 SV=2
LOC_Os05g45770	down	--
LOC_Os01g14550	down	Pathogen-related protein OS=Hordeum vulgare OX=4513 PE=2 SV=2
LOC_Os08g37940	down	Haloacid dehalogenase-like hydrolase domain-containing protein At4g39970 OS=Arabidopsis thaliana OX=3702 GN=At4g39970 PE=2 SV=1
LOC_Os04g02640	down	3-ketoacyl-CoA synthase 6 OS=Arabidopsis thaliana OX=3702 GN=CUT1 PE=1 SV=1

LOC_Os01g19200	down	--
LOC_Os04g51290	down	Multiple organellar RNA editing factor 2, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MORF2 PE=1 SV=1
Oryza_sativa_newGene_4194	down	--
LOC_Os08g23430	down	Ribonuclease E/G-like protein, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=RNE PE=1 SV=1
LOC_Os03g51980	down	--
LOC_Os08g43654	down	Protein DETOXIFICATION 33 OS=Arabidopsis thaliana OX=3702 GN=DTX33 PE=2 SV=1
LOC_Os02g37654	down	Lecithin-cholesterol acyltransferase-like 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0232800 PE=2 SV=1
Oryza_sativa_newGene_551	down	--
LOC_Os02g52650	down	Photosystem I chlorophyll a/b-binding protein 5, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=LHCA5 PE=1 SV=1
LOC_Os03g50900	down	Protein FAR1-RELATED SEQUENCE 5 OS=Arabidopsis thaliana OX=3702 GN=FRS5 PE=1 SV=1
LOC_Os11g06720	down	--
LOC_Os02g49680	down	Calcium sensing receptor, chloroplastic OS=Zea mays OX=4577 PE=1 SV=1
LOC_Os04g37880	down	--
LOC_Os01g65780	down	UDP-glucuronate:xylan alpha-glucuronosyltransferase 1 OS=Arabidopsis thaliana OX=3702 GN=GUX1 PE=2 SV=1
LOC_Os12g05900	down	Rho GTPase-activating protein 1 OS=Arabidopsis thaliana OX=3702 GN=ROPGAP1 PE=2 SV=1
LOC_Os06g37610	down	(S)-coclaurine N-methyltransferase OS=Thalictrum flavum subsp. glaucum OX=150095 PE=1 SV=1
LOC_Os11g06880	down	Long chain acyl-CoA synthetase 9, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=LACS9 PE=1 SV=1
LOC_Os03g05210	down	Zinc finger CCCH domain-containing protein 48 OS=Arabidopsis thaliana OX=3702 GN=ZFWD1 PE=2 SV=1
LOC_Os08g37400	down	Zinc-finger homeodomain protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=ZHD2 PE=2 SV=1
LOC_Os12g16650	down	3-hydroxy-16-methoxy-2,3-dihydrotabersonine N-methyltransferase OS=Catharanthus roseus OX=4058 GN=NMT PE=1 SV=1
LOC_Os08g29110	down	Thioredoxin-like protein CITRX, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os08g0378900 PE=2 SV=1
LOC_Os07g36000	down	Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum OX=4097 PE=2 SV=1
LOC_Os10g33790	down	--
LOC_Os09g21460	down	Protein PLASTID REDOX INSENSITIVE 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=PRIN2 PE=2 SV=1
LOC_Os06g36480	down	NAC domain-containing protein 75 OS=Arabidopsis thaliana OX=3702 GN=NAC075 PE=2 SV=1
LOC_Os10g07010	down	3-ketoacyl-CoA synthase 1 OS=Arabidopsis thaliana OX=3702 GN=KCS1 PE=1 SV=1
LOC_Os06g11400	down	Protein CURVATURE THYLAKOID 1D, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CURT1D PE=1 SV=1
LOC_Os03g14334	down	--
LOC_Os08g37250	down	Patatin-like protein 2 OS=Oryza sativa subsp. japonica OX=39947 GN=PLP2 PE=3 SV=1

LOC_Os05g12150	down	Endoglucanase 15 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os05g0212300 PE=2 SV=1
LOC_Os04g39060	down	CRM-domain containing factor CFM2, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CFM2 PE=1 SV=1
LOC_Os02g37800	down	Lecithin-cholesterol acyltransferase-like 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os03g0232800 PE=2 SV=1
LOC_Os04g38026	down	Sugar transport protein MST1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=MST1 PE=2 SV=1
LOC_Os02g11680	down	High-affinity nitrate transporter 2.2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=NRT2.2 PE=1 SV=1
LOC_Os11g29050	down	Disease resistance protein RPM1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=RPM1 PE=1 SV=1
LOC_Os01g50470	down	PH, RCC1 and FYVE domains-containing protein 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PRAF1 PE=1 SV=1
LOC_Os04g38750	down	30S ribosomal protein 3, chloroplastic OS= <i>Hordeum vulgare</i> OX=4513 GN=PSRP3 PE=2 SV=1
LOC_Os02g51970	down	Protein EXORDIUM OS= <i>Arabidopsis thaliana</i> OX=3702 GN=EXO PE=2 SV=1
LOC_Os07g49110	down	--
LOC_Os02g52450	down	Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At5g16450 PE=1 SV=1
LOC_Os12g18770	down	Oxysterol-binding protein-related protein 1D OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ORPID PE=2 SV=1
LOC_Os01g69080	down	Stearoyl-[acyl-carrier-protein] 9-desaturase 2, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=SSI2 PE=2 SV=1
LOC_Os10g30080	down	Beta-glucuronosyltransferase GlcAT14B OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GLCAT14B PE=2 SV=1
LOC_Os02g44155	down	--
LOC_Os06g49070	down	--
LOC_Os05g42190	down	NAD(P)H dehydrogenase (quinone) FQR1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FQR1 PE=1 SV=1
LOC_Os03g50100	down	Myosin-binding protein 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=MYOB2 PE=1 SV=1
LOC_Os05g43660	down	CLAVATA3/ESR (CLE)-related protein 10 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CLE10 PE=1 SV=1
LOC_Os11g04330	down	F-box/kelch-repeat protein At5g26960 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At5g26960 PE=2 SV=1
LOC_Os11g34210	down	Glutamyl-tRNA(Gln) amidotransferase subunit B, chloroplastic/mitochondrial OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=GATB PE=2 SV=1
LOC_Os01g53990	down	Probable pectinesterase 53 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PME53 PE=2 SV=1
LOC_Os09g33850	down	Protein FLOWERING LOCUS T OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FT PE=1 SV=2
LOC_Os02g49830	down	Pentatricopeptide repeat-containing protein At5g66520 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PCMP-H61 PE=2 SV=1
LOC_Os03g14010	down	--
LOC_Os02g17620	down	Probable inactive nicotinamidase At3g16190 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g16190 PE=2 SV=1
LOC_Os01g37510	down	Peptide deformylase 1A, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=PDF1A PE=2 SV=1
LOC_Os05g31280	down	Protein GAST1 OS= <i>Solanum lycopersicum</i> OX=4081 GN=GAST1 PE=2 SV=1
LOC_Os10g20890	down	pEARLI1-like lipid transfer protein 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At4g12490 PE=2 SV=1

LOC_Os03g02670	down	UDP-galactose/UDP-glucose transporter 2 OS=Arabidopsis thaliana OX=3702 GN=UTR2 PE=2 SV=1
LOC_Os01g06310	down	--
LOC_Os07g36690	down	Mixed-linked glucan synthase 2 OS=Oryza sativa subsp. japonica OX=39947 GN=CSLF2 PE=2 SV=1
LOC_Os06g13280	down	Acetylserotonin O-methyltransferase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=ASMT1 PE=1 SV=1
LOC_Os01g57960	down	--
Oryza_sativa_newGene_3002	down	--
LOC_Os03g59430	down	Probable galactinol--sucrose galactosyltransferase 2 OS=Arabidopsis thaliana OX=3702 GN=RFS2 PE=2 SV=2
LOC_Os04g58840	down	Aspartic proteinase nepenthesin-2 OS=Nepenthes gracilis OX=150966 GN=nep2 PE=1 SV=1
Oryza_sativa_newGene_2057	down	--
LOC_Os04g53370	down	1-acyl-sn-glycerol-3-phosphate acyltransferase OS=Cocos nucifera OX=13894 PE=1 SV=1
LOC_Os03g27370	down	Phospholipase D alpha 1 OS=Oryza sativa subsp. japonica OX=39947 GN=PLD1 PE=1 SV=2
LOC_Os01g56940	down	Exonuclease 1 OS=Oryza sativa subsp. japonica OX=39947 GN=EXO1 PE=2 SV=1
LOC_Os11g04960	down	NAC transcription factor 29 OS=Arabidopsis thaliana OX=3702 GN=NAC029 PE=2 SV=1
LOC_Os09g30340	down	Photosystem I reaction center subunit V, chloroplastic OS=Hordeum vulgare OX=4513 GN=PSAG PE=1 SV=1
LOC_Os05g18790	down	Phosphoribosylglycinamide formyltransferase, chloroplastic OS=Vigna unguiculata OX=3917 GN=PUR3 PE=2 SV=2
LOC_Os05g47850	down	CRM-domain containing factor CFM3, chloroplastic/mitochondrial OS=Zea mays OX=4577 GN=CFM3 PE=1 SV=1
LOC_Os08g40170	down	Cyclin-dependent kinase B2-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CDKB2-1 PE=1 SV=1
LOC_Os07g14540	down	Vesicle-associated membrane protein 724 OS=Arabidopsis thaliana OX=3702 GN=VAMP724 PE=2 SV=2
LOC_Os07g09370	down	Pentatricopeptide repeat-containing protein At1g59720, chloroplastic/mitochondrial OS=Arabidopsis thaliana OX=3702 GN=PCMP-H51 PE=1 SV=1
LOC_Os04g56420	down	--
LOC_Os08g44000	down	Uncharacterized protein ycf39 OS=Cyanophora paradoxa OX=2762 GN=ycf39 PE=3 SV=1
LOC_Os03g02460	down	Short-chain dehydrogenase TIC 32, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=TIC32 PE=2 SV=1
LOC_Os01g01302	down	Probable inactive shikimate kinase like 1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=SKL1 PE=2 SV=1
LOC_Os12g32260	down	--
LOC_Os08g24390	down	--
LOC_Os10g40120	down	U-box domain-containing protein 36 OS=Arabidopsis thaliana OX=3702 GN=PUB36 PE=2 SV=2
LOC_Os06g05020	down	Early nodulin-93 OS=Glycine max OX=3847 PE=2 SV=1
LOC_Os12g01410	down	--
LOC_Os03g11734	down	Protein DETOXIFICATION 42 OS=Arabidopsis thaliana OX=3702 GN=DTX42 PE=2 SV=2

LOC_Os12g03070	down	--
LOC_Os02g49870	down	Protein CURVATURE THYLAKOID 1A, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CURT1A PE=1 SV=1
LOC_Os09g04220	down	--
LOC_Os01g74510	down	Protein NETWORKED 2D OS=Arabidopsis thaliana OX=3702 GN=NET2D PE=3 SV=1
LOC_Os03g47230	down	Phytosulfokines 3 OS=Oryza sativa subsp. japonica OX=39947 GN=PSK3 PE=1 SV=1
LOC_Os07g32600	down	Glucan endo-1,3-beta-glucosidase 1 OS=Arabidopsis thaliana OX=3702 GN=At1g11820 PE=1 SV=3
Oryza_sativa_newGene_2720	down	--
LOC_Os07g47550	down	Beta-D-glucosyl crocetin beta-1,6-glucosyltransferase OS=Gardenia jasminoides OX=114476 GN=UGT94E5 PE=1 SV=1
LOC_Os04g53180	down	--
LOC_Os04g40510	down	--
LOC_Os04g25560	down	Serine carboxypeptidase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=CBP1 PE=2 SV=1
LOC_Os12g38810	down	--
LOC_Os10g30690	down	Single myb histone 3 OS=Zea mays OX=4577 GN=SMH3 PE=2 SV=1
LOC_Os03g06670	down	Probable histone H2A variant 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0162200 PE=2 SV=1
LOC_Os08g39460	down	Serine/threonine-protein kinase UCN OS=Arabidopsis thaliana OX=3702 GN=UNC PE=1 SV=1
LOC_Os02g50000	down	GDSL esterase/lipase At5g37690 OS=Arabidopsis thaliana OX=3702 GN=At5g37690 PE=2 SV=1
Oryza_sativa_newGene_621	down	--
LOC_Os03g63240	down	Putative disease resistance protein RGA4 OS=Solanum bulbocastanum OX=147425 GN=RGA4 PE=2 SV=1
LOC_Os03g07440	down	--
Oryza_sativa_newGene_4850	down	Kinesin-like protein KIN-14G OS=Oryza sativa subsp. japonica OX=39947 GN=KIN14G PE=2 SV=2
LOC_Os03g19090	down	--
LOC_Os04g01130	down	Protein MRG1 OS=Arabidopsis thaliana OX=3702 GN=MRG1 PE=1 SV=1
LOC_Os04g07890	down	--
LOC_Os03g56840	down	Obg-like ATPase 1 OS=Arabidopsis thaliana OX=3702 GN=YchF1 PE=1 SV=1
LOC_Os01g63540	down	Cytochrome P450 86A1 OS=Arabidopsis thaliana OX=3702 GN=CYP86A1 PE=1 SV=2
LOC_Os04g35760	down	--
LOC_Os01g64270	down	--
LOC_Os04g47020	down	5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PYRP2 PE=1 SV=1
LOC_Os05g47730	down	Non-specific lipid-transfer protein 2 OS=Oryza sativa subsp. indica OX=39946 GN=LTP-2 PE=3 SV=2

LOC_Os03g20100	down	30S ribosomal protein S1, chloroplastic OS=Spinacia oleracea OX=3562 GN=RPS1 PE=1 SV=1
LOC_Os01g05820	down	Glutathione hydrolase 3 OS=Arabidopsis thaliana OX=3702 GN=GGT3 PE=2 SV=1
LOC_Os03g12236	down	Chaperone protein dnaJ A6, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=DJA6 PE=2 SV=2
LOC_Os06g46910	down	--
LOC_Os08g34240	down	CBL-interacting protein kinase 6 OS=Oryza sativa subsp. japonica OX=39947 GN=CIPK6 PE=2 SV=1
LOC_Os01g67520	down	GDP-L-galactose phosphorylase 2 OS=Arabidopsis thaliana OX=3702 GN=VTC5 PE=1 SV=1
LOC_Os12g34018	down	Putative ATP synthase protein YMF19 OS=Triticum aestivum OX=4565 GN=YMF19 PE=2 SV=1
LOC_Os12g02340	down	Probable non-specific lipid-transfer protein 3 OS=Triticum aestivum OX=4565 GN=LTP3 PE=2 SV=1
LOC_Os06g50950	down	GDSL esterase/lipase At5g55050 OS=Arabidopsis thaliana OX=3702 GN=At5g55050 PE=2 SV=1
LOC_Os01g43950	down	Transcription factor IBH1 OS=Oryza sativa subsp. japonica OX=39947 GN=IBH1 PE=1 SV=2
LOC_Os04g48840	down	Protein FATTY ACID EXPORT 4, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=FAX4 PE=2 SV=1
LOC_Os03g38470	down	GDSL esterase/lipase At5g55050 OS=Arabidopsis thaliana OX=3702 GN=At5g55050 PE=2 SV=1
LOC_Os10g05780	down	Protein NRT1/ PTR FAMILY 5.11 OS=Arabidopsis thaliana OX=3702 GN=NPF5.11 PE=2 SV=1
LOC_Os07g04160	down	Peptidyl-prolyl cis-trans isomerase FKBP19, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=FKBP19 PE=1 SV=1
Oryza_sativa_newGene_2431	down	--
LOC_Os03g03470	down	--
LOC_Os11g35930	down	Chalcone synthase 3 OS=Sinapis alba OX=3728 GN=CHS3 PE=2 SV=1
LOC_Os02g35970	down	Coleoptile phototropism protein 1 OS=Oryza sativa subsp. japonica OX=39947 GN=CPT1 PE=2 SV=1
LOC_Os02g42970	down	NAC domain-containing protein 7 OS=Arabidopsis thaliana OX=3702 GN=NAC007 PE=1 SV=2
LOC_Os03g11250	down	--
LOC_Os06g43600	down	36.4 kDa proline-rich protein OS=Solanum lycopersicum OX=4081 GN=TPRP-F1 PE=2 SV=1
LOC_Os06g49300	down	--
LOC_Os01g58100	down	Polyphenol oxidase, chloroplastic OS=Malus domestica OX=3750 PE=2 SV=1
LOC_Os08g43230	down	--
LOC_Os02g01340	down	Ferredoxin--NADP reductase, leaf isozyme 2, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=LFNR2 PE=1 SV=1
LOC_Os10g38196	down	Uncharacterized protein ycf68 OS=Oryza sativa subsp. japonica OX=39947 GN=ycf68-1 PE=3 SV=1
LOC_Os01g42200	down	--
LOC_Os08g44290	down	31 kDa ribonucleoprotein, chloroplastic OS=Nicotiana sylvestris OX=4096 PE=1 SV=1
LOC_Os02g03240	down	--

LOC_Os12g36890	down	Cellulose synthase-like protein D4 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CSLD4 PE=2 SV=1
LOC_Os07g37690	down	UDP-glycosyltransferase 71K2 OS= <i>Pyrus communis</i> OX=23211 GN=UGT71K2 PE=1 SV=1
LOC_Os03g29810	down	ATP-dependent Clp protease proteolytic subunit 6, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CLPP6 PE=1 SV=1
LOC_Os01g71460	down	--
LOC_Os04g16734	down	Maturase K OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=matK PE=3 SV=2
LOC_Os06g49810	down	Polygalacturonate 4-alpha-galacturonosyltransferase OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GAUT1 PE=1 SV=1
LOC_Os03g17580	down	50S ribosomal protein L10, chloroplastic OS= <i>Nicotiana tabacum</i> OX=4097 GN=RPL10 PE=2 SV=1
LOC_Os04g53860	down	Anthocyanidin reductase ((2S)-flavan-3-ol-forming) OS= <i>Vitis vinifera</i> OX=29760 GN=ANR PE=3 SV=1
LOC_Os02g13520	down	Auxin-responsive protein IAA7 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=IAA7 PE=2 SV=1
LOC_Os04g43290	down	Actin-related protein 2/3 complex subunit 2B OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ARPC2B PE=2 SV=1
LOC_Os05g07680	down	Protein NETWORKED 4B OS= <i>Arabidopsis thaliana</i> OX=3702 GN=NET4B PE=2 SV=1
LOC_Os03g55930	down	30S ribosomal protein S9, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=RPS9 PE=2 SV=1
LOC_Os05g10370	down	Acid phosphatase 1 OS= <i>Solanum lycopersicum</i> OX=4081 GN=APS1 PE=2 SV=1
LOC_Os02g52260	down	Protein CURVATURE THYLAKOID 1D, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CURT1D PE=1 SV=1
LOC_Os10g11980	down	Acyl transferase 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=AT1 PE=2 SV=1
LOC_Os03g14920	down	Probable polyol transporter 6 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PLT6 PE=2 SV=2
LOC_Os12g33946	down	Cytochrome c oxidase subunit 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=COX1 PE=3 SV=2
LOC_Os04g51300	down	Thylakoid lumenal 29 kDa protein, chloroplastic OS= <i>Solanum lycopersicum</i> OX=4081 GN=CLEB3J9 PE=3 SV=1
LOC_Os06g10670	down	Aspartic proteinase nepenthesin-1 OS= <i>Nepenthes gracilis</i> OX=150966 GN=nep1 PE=1 SV=1
LOC_Os02g02500	down	--
LOC_Os09g09270	down	Cinnamoyl-CoA reductase 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CCR1 PE=1 SV=1
LOC_Os11g40600	down	Stress enhanced protein 1, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SEP1 PE=2 SV=1
LOC_Os11g30560	down	11-beta-hydroxysteroid dehydrogenase 1B OS= <i>Arabidopsis thaliana</i> OX=3702 GN=HSD1 PE=1 SV=1
LOC_Os05g28200	down	Chlorophyll synthase, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CHLG PE=2 SV=1
LOC_Os09g32984	down	Auxin-responsive protein SAUR71 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SAUR71 PE=2 SV=1
LOC_Os12g21760	down	--
LOC_Os06g03740	down	--
LOC_Os10g10110	down	--
LOC_Os10g21310	down	Photosystem II CP47 reaction center protein OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=psbB PE=3 SV=1

LOC_Os11g06820	down	Putative auxin transporter-like protein 4 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os11g0169200 PE=3 SV=1
LOC_Os03g29730	down	--
LOC_Os11g05556	down	Signal recognition particle 54 kDa protein, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FFC PE=1 SV=1
LOC_Os06g50130	down	--
LOC_Os09g28620	down	Tuliposide A-converting enzyme b1, amyloplastic OS= <i>Tulipa gesneriana</i> OX=13306 GN=TCEA-B1 PE=1 SV=1
LOC_Os06g05980	down	Probable sugar phosphate/phosphate translocator At1g06470 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At1g06470 PE=2 SV=1
LOC_Os09g16458	down	ABC transporter G family member 52 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=ABCG52 PE=2 SV=2
Oryza_sativa_newGene_1374	down	Endoglucanase 5 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os02g0151300 PE=2 SV=1
LOC_Os10g32580	down	GDSL esterase/lipase At5g33370 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At5g33370 PE=2 SV=1
LOC_Os11g18366	down	Achilleol B synthase OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os11g0285000 PE=1 SV=1
LOC_Os01g04300	down	Putative Pol polyprotein from transposon element Bs1 OS= <i>Zea mays</i> OX=4577 PE=4 SV=1
LOC_Os01g41890	down	Disease resistance protein RPP13 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=RPP13 PE=2 SV=2
LOC_Os03g39870	down	--
LOC_Os04g08390	down	--
LOC_Os01g67500	down	U-box domain-containing protein 6 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PUB6 PE=2 SV=2
LOC_Os04g57980	down	--
LOC_Os05g40180	down	Serine/threonine-protein kinase STN8, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=STN8 PE=2 SV=1
LOC_Os02g37700	down	Lecithin-cholesterol acyltransferase-like 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os03g0232800 PE=2 SV=1
LOC_Os02g05890	down	--
LOC_Os01g60060	down	Probable leucine-rich repeat receptor-like protein kinase At5g49770 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At5g49770 PE=2 SV=1
LOC_Os04g54620	down	--
LOC_Os06g13140	down	Protein JINGUBANG OS= <i>Arabidopsis thaliana</i> OX=3702 GN=JGB PE=1 SV=1
LOC_Os02g17940	down	Protein SRG1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SRG1 PE=2 SV=1
LOC_Os01g35030	down	ABC transporter B family member 11 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ABCB11 PE=2 SV=1
LOC_Os07g13969	down	--
LOC_Os03g16050	down	Fructose-1,6-bisphosphatase, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os03g0267300 PE=2 SV=1
LOC_Os04g44200	down	PsbQ-like protein 3, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PQL3 PE=2 SV=1
LOC_Os06g12790	down	Rac-like GTP-binding protein 4 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=RAC4 PE=2 SV=1
LOC_Os01g10850	down	Peroxidase 4 OS= <i>Vitis vinifera</i> OX=29760 GN=GSVIVT00023967001 PE=1 SV=1

LOC_Os11g29150	down	--
LOC_Os11g23790	down	Protein PEP-RELATED DEVELOPMENT ARRESTED 1 homolog, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os11g0425300
LOC_Os04g46440	down	Ethylene-responsive transcription factor ERF034 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ERF034 PE=2 SV=2
LOC_Os09g31410	down	Beta-glucosidase 29 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=BGLU29 PE=2 SV=2
LOC_Os06g16980	down	DNA topoisomerase 3-alpha OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=TOP3A PE=3 SV=1
LOC_Os10g21250	down	Photosystem I P700 chlorophyll a apoprotein A1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=psaA PE=3 SV=1
LOC_Os01g22450	down	--
LOC_Os07g04930	down	--
LOC_Os03g60180	down	GTP-binding protein At2g22870 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=EMB2001 PE=2 SV=2
LOC_Os04g45490	down	Elongation factor G-1, chloroplastic OS= <i>Glycine max</i> OX=3847 GN=fusA1 PE=3 SV=2
LOC_Os05g44070	down	Ras-related protein RIC2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=RIC2 PE=2 SV=2
LOC_Os11g06910	down	Filament-like plant protein (Fragment) OS= <i>Solanum lycopersicum</i> OX=4081 GN=FPP PE=1 SV=1
LOC_Os05g46550	down	AP-1 complex subunit mu-2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=AP1M2 PE=1 SV=1
LOC_Os11g34390	down	Probable glycosyltransferase 6 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=GT6 PE=2 SV=1
LOC_Os06g12460	down	Probable mannan synthase 3 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CSLA3 PE=2 SV=1
Oryza_sativa_newGene_4051	down	--
LOC_Os12g41850	down	--
LOC_Os12g42210	down	Protease Do-like 5, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=DEGP5 PE=1 SV=3
LOC_Os09g24412	down	30S ribosomal protein S19, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=rps19-A PE=3 SV=3
Oryza_sativa_newGene_1508	down	--
LOC_Os01g34560	down	3-ketoacyl-CoA synthase 6 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CUT1 PE=1 SV=1
LOC_Os03g36110	down	--
LOC_Os05g41390	down	Cyclin-B1-5 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CYCB1-5 PE=3 SV=1
LOC_Os07g30950	down	Taxane 10-beta-hydroxylase OS= <i>Taxus cuspidata</i> OX=99806 GN=CYP725A1 PE=1 SV=1
LOC_Os04g50110	down	33 kDa ribonucleoprotein, chloroplastic OS= <i>Nicotiana glauca</i> OX=4096 PE=1 SV=1
LOC_Os08g06885	down	--
LOC_Os09g26190	down	Pentatricopeptide repeat-containing protein At5g10690 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CBSPPR1 PE=2 SV=1
LOC_Os12g14440	down	Salt stress-induced protein OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=SALT PE=1 SV=1
LOC_Os01g45914	down	--

LOC_Os03g55310	down	Zinc finger CCCH domain-containing protein 19 OS=Arabidopsis thaliana OX=3702 GN=NERD PE=1 SV=3
LOC_Os05g34040	down	--
Oryza_sativa_newGene_671	down	--
LOC_Os01g18310	down	--
LOC_Os03g03720	down	Glyceraldehyde-3-phosphate dehydrogenase GAPB, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=GAPB PE=1 SV=2
LOC_Os10g05490	down	Cytochrome P450 76C2 OS=Arabidopsis thaliana OX=3702 GN=CYP76C2 PE=2 SV=1
LOC_Os08g13330	down	--
LOC_Os09g23720	down	Protein XRI1 OS=Arabidopsis thaliana OX=3702 GN=XRI1 PE=1 SV=2
Oryza_sativa_newGene_2289	down	--
LOC_Os06g35940	down	Protein HEADING DATE 3A OS=Oryza sativa subsp. japonica OX=39947 GN=HD3A PE=1 SV=1
LOC_Os05g44610	down	--
LOC_Os06g02840	down	--
LOC_Os10g12050	down	Cytochrome P450 98A1 OS=Sorghum bicolor OX=4558 GN=CYP98A1 PE=2 SV=1
LOC_Os02g52460	down	--
LOC_Os01g72950	down	NAD(P)H-quinone oxidoreductase subunit O, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=ndhO PE=2 SV=1
LOC_Os04g47670	down	--
LOC_Os01g46120	down	GDSL esterase/lipase At1g28600 OS=Arabidopsis thaliana OX=3702 GN=At1g28600 PE=2 SV=1
LOC_Os11g30910	down	Cytosolic sulfotransferase 10 OS=Arabidopsis thaliana OX=3702 GN=SOT10 PE=1 SV=1
LOC_Os04g34600	down	--
LOC_Os11g30810	down	Cytosolic sulfotransferase 5 OS=Arabidopsis thaliana OX=3702 GN=SOT5 PE=1 SV=1
LOC_Os09g26210	down	Zinc finger protein 2 OS=Arabidopsis thaliana OX=3702 GN=ZFP2 PE=1 SV=1
LOC_Os04g38850	down	--
LOC_Os01g22520	down	Dihydrolipoyl dehydrogenase 1, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=LPD1 PE=1 SV=2
LOC_Os06g05350	down	Single-stranded DNA-binding protein WHY1, chloroplastic OS=Zea mays OX=4577 GN=WHY1 PE=2 SV=1
LOC_Os01g60900	down	EPIDERMAL PATTERNING FACTOR-like protein 6 OS=Arabidopsis thaliana OX=3702 GN=EPFL6 PE=1 SV=1
LOC_Os09g24402	down	50S ribosomal protein L23, chloroplastic OS=Triticum aestivum OX=4565 GN=rpl23-A PE=3 SV=1
LOC_Os05g15810	down	Retrovirus-related Pol polyprotein from transposon TNT 1-94 OS=Nicotiana tabacum OX=4097 PE=2 SV=1
LOC_Os07g07620	down	Pentatricopeptide repeat-containing protein At5g03800 OS=Arabidopsis thaliana OX=3702 GN=EMB175 PE=2 SV=1
LOC_Os11g42230	down	--

LOC_Os04g53230	down	Aminomethyltransferase, mitochondrial OS=Solanum tuberosum OX=4113 GN=GDCST PE=2 SV=1
LOC_Os02g07410	down	Glycine cleavage system H protein 2, mitochondrial OS=Arabidopsis thaliana OX=3702 GN=GDH2 PE=2 SV=1
LOC_Os03g40690	down	Pentatricopeptide repeat-containing protein At5g55840 OS=Arabidopsis thaliana OX=3702 GN=At5g55840 PE=3 SV=2
Oryza_sativa_newGene_1626	down	Probable DNA gyrase subunit A, chloroplastic/mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=GYRA PE=2 SV=2
LOC_Os06g10100	down	--
LOC_Os02g33944	down	--
LOC_Os02g38210	down	Elongation factor Tu, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=TUFA PE=1 SV=1
LOC_Os05g43940	down	O-methyltransferase ZRP4 OS=Zea mays OX=4577 GN=ZRP4 PE=2 SV=1
LOC_Os05g28690	down	--
LOC_Os04g46610	down	Probable plastid-lipid-associated protein 11, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PAP11 PE=2 SV=1
LOC_Os12g07270	down	Probable sodium/metabolite cotransporter BASS1, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=BASS1 PE=2 SV=1
LOC_Os08g02210	down	Beta-carotene isomerase D27, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=D27 PE=1 SV=1
LOC_Os09g08910	down	ATP synthase subunit alpha, mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=ATPA PE=1 SV=1
LOC_Os02g04430	down	Protein STRUBBELIG-RECEPTOR FAMILY 8 OS=Arabidopsis thaliana OX=3702 GN=SRF8 PE=2 SV=1
LOC_Os05g50340	down	Protein RADIALIS-like 6 OS=Arabidopsis thaliana OX=3702 GN=RL6 PE=2 SV=1
LOC_Os06g44690	down	--
LOC_Os02g54710	down	F-box protein SKIP8 OS=Arabidopsis thaliana OX=3702 GN=SKIP8 PE=1 SV=1
LOC_Os03g11310	down	Pentatricopeptide repeat-containing protein At3g29290 OS=Arabidopsis thaliana OX=3702 GN=EMB2076 PE=2 SV=1
LOC_Os08g41990	down	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=GSA PE=2 SV=1
LOC_Os04g31040	down	Violaxanthin de-epoxidase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=VDE1 PE=1 SV=1
LOC_Os11g32490	down	--
LOC_Os09g29100	down	Cyclin-D4-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCD4-1 PE=2 SV=2
LOC_Os07g05460	down	Flavonol 3-sulfotransferase OS=Flaveria chlorifolia OX=4228 PE=1 SV=2
LOC_Os04g43490	down	Casein kinase 1 OS=Oryza sativa subsp. japonica OX=39947 GN=CKI1 PE=1 SV=1
LOC_Os02g48450	down	Cysteine protease XCP1 OS=Arabidopsis thaliana OX=3702 GN=XCP1 PE=1 SV=1
LOC_Os08g43110	down	Retrovirus-related Pol polyprotein from transposon RE1 OS=Arabidopsis thaliana OX=3702 GN=RE1 PE=2 SV=1
LOC_Os12g17600	down	Ribulose biphosphate carboxylase small chain, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=RBCS PE=1 SV=1
LOC_Os07g46320	down	--
LOC_Os08g08960	down	Germin-like protein 8-2 OS=Oryza sativa subsp. japonica OX=39947 GN=GER3 PE=2 SV=1

LOC_Os12g04740	down	--
LOC_Os02g47790	down	Monodehydroascorbate reductase 1, peroxisomal OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=MDAR1 PE=2 SV=1
LOC_Os06g13060	down	Chaperone protein dnaJ 16 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ATJ16 PE=2 SV=1
LOC_Os06g43304	down	Premnaspirodien oxygenase OS= <i>Hyoscyamus muticus</i> OX=35626 GN=CYP71D55 PE=1 SV=1
LOC_Os01g21170	down	--
LOC_Os01g32849	down	--
LOC_Os03g12230	down	Peroxygenase OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=PXG PE=2 SV=1
LOC_Os01g72800	down	Cell division protein FtsY homolog, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CPFTSY PE=1 SV=2
LOC_Os07g09800	down	NAD(P)H-quinone oxidoreductase subunit S, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=ndhS PE=1 SV=1
LOC_Os05g32140	down	UDP-sulfoquinovose synthase, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SQD1 PE=1 SV=1
LOC_Os09g26670	down	--
Oryza_sativa_newGene_1666	down	--
LOC_Os12g34094	down	NADH-ubiquinone oxidoreductase chain 4 OS= <i>Triticum aestivum</i> OX=4565 GN=ND4 PE=2 SV=2
LOC_Os09g10204	down	--
LOC_Os04g55050	down	Glutamyl-tRNA(Gln) amidotransferase subunit A, chloroplastic/mitochondrial OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=GATA PE=3 SV=
LOC_Os03g14642	down	--
LOC_Os04g48200	down	Cytochrome P450 87A3 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CYP87A3 PE=2 SV=3
LOC_Os11g04710	down	Cytochrome P450 90A3 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CYP90A3 PE=2 SV=1
LOC_Os02g52840	down	Flavonol synthase/flavanone 3-hydroxylase OS= <i>Citrus unshiu</i> OX=55188 GN=FLS PE=1 SV=1
LOC_Os01g11700	down	GDSL esterase/lipase At2g27360 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At2g27360 PE=2 SV=1
LOC_Os10g29495	down	BTB/POZ and MATH domain-containing protein 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=BPM1 PE=1 SV=1
LOC_Os01g32730	down	Protein FLUORESCENT IN BLUE LIGHT, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FLU PE=1 SV=1
LOC_Os06g35490	down	Peroxidase 4 OS= <i>Vitis vinifera</i> OX=29760 GN=GSVIVT00023967001 PE=1 SV=1
LOC_Os02g26700	down	Gamma-glutamylcyclotransferase 2-2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GGCT2;2 PE=1 SV=1
LOC_Os01g49740	down	Protein PLASTID MOVEMENT IMPAIRED 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=PMI2 PE=1 SV=1
LOC_Os03g24910	down	--
LOC_Os05g32270	down	AP2-like ethylene-responsive transcription factor At2g41710 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At2g41710 PE=2 SV=2
LOC_Os01g43590	down	Heat stress transcription factor C-1a OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=HSFC1A PE=2 SV=2
LOC_Os04g59340	down	--

LOC_Os03g19540	down	--
LOC_Os06g47940	down	NifU-like protein 3, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=NIFU3 PE=2 SV=1
LOC_Os02g42740	down	Membrane steroid-binding protein 2 OS=Arabidopsis thaliana OX=3702 GN=MSBP2 PE=1 SV=1
LOC_Os09g24406	down	Uncharacterized protein ycf72 OS=Oryza sativa subsp. japonica OX=39947 GN=ycf72-1 PE=3 SV=1
LOC_Os05g49350	down	--
LOC_Os09g24408	down	--
LOC_Os11g06690	down	--
LOC_Os06g51160	down	Probable galacturonosyltransferase 3 OS=Arabidopsis thaliana OX=3702 GN=GAUT3 PE=2 SV=2
LOC_Os02g34710	down	--
LOC_Os03g63910	down	Pentatricopeptide repeat-containing protein At5g46580, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At5g46580 PE=2 SV=1
LOC_Os10g11270	down	Cytosolic sulfotransferase 5 OS=Arabidopsis thaliana OX=3702 GN=SOT5 PE=1 SV=1
LOC_Os11g34110	down	--
LOC_Os11g29230	down	Pentatricopeptide repeat-containing protein At1g11290, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PCMP-H40 PE=2 SV=1
LOC_Os04g40100	down	BTB/POZ domain-containing protein At1g67900 OS=Arabidopsis thaliana OX=3702 GN=At1g67900 PE=1 SV=1
LOC_Os06g37150	down	L-ascorbate oxidase OS=Cucurbita pepo var. melopepo OX=3665 PE=1 SV=1
LOC_Os02g41860	down	Probable aquaporin PIP2-2 OS=Oryza sativa subsp. japonica OX=39947 GN=PIP2-2 PE=2 SV=1
LOC_Os02g53690	down	Growth-regulating factor 1 OS=Oryza sativa subsp. japonica OX=39947 GN=GRF1 PE=3 SV=1
LOC_Os02g15500	down	UPF0481 protein At3g47200 OS=Arabidopsis thaliana OX=3702 GN=At3g47200 PE=2 SV=1
LOC_Os05g14750	down	Serine/threonine-protein kinase AGC1-7 OS=Arabidopsis thaliana OX=3702 GN=AGC1-7 PE=1 SV=1
LOC_Os02g52010	down	Protein EXORDIUM OS=Arabidopsis thaliana OX=3702 GN=EXO PE=2 SV=1
LOC_Os03g02640	down	Protein-ribulosamine 3-kinase, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=Os03g0117800 PE=2 SV=1
Oryza_sativa_newGene_733	down	Retrovirus-related Pol polyprotein from transposon RE2 OS=Arabidopsis thaliana OX=3702 GN=RE2 PE=4 SV=1
LOC_Os08g13920	down	Xyloglucan endotransglycosylase/hydrolase protein 8 OS=Oryza sativa subsp. japonica OX=39947 GN=XTH8 PE=1 SV=1
LOC_Os11g05060	down	--
LOC_Os02g38290	down	Cytochrome P450 86B1 OS=Arabidopsis thaliana OX=3702 GN=CYP86B1 PE=2 SV=1
LOC_Os09g21450	down	Cyclin-D2-1 OS=Oryza sativa subsp. japonica OX=39947 GN=CYCD2-1 PE=3 SV=2
LOC_Os03g60350	down	Protein trichome birefringence-like 33 OS=Arabidopsis thaliana OX=3702 GN=TBL33 PE=2 SV=1
LOC_Os05g46950	down	--
LOC_Os12g41060	down	Ethylene-responsive transcription factor 1 OS=Oryza sativa subsp. japonica OX=39947 GN=EREBP1 PE=1 SV=1

LOC_Os09g32320	down	Protein MANNAN SYNTHESIS-RELATED 2 OS=Arabidopsis thaliana OX=3702 GN=MSR2 PE=2 SV=1
LOC_Os04g28830	down	--
LOC_Os04g01150	down	--
LOC_Os05g32200	down	F-box protein At5g50450 OS=Arabidopsis thaliana OX=3702 GN=At5g50450 PE=2 SV=1
LOC_Os08g28010	down	--
LOC_Os10g15300	down	--
LOC_Os01g71190	down	Photosystem II reaction center PSB28 protein, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=PSB28 PE=2 SV=2
LOC_Os09g32988	down	Pollen-specific protein-like At4g18596 OS=Arabidopsis thaliana OX=3702 GN=At4g18596 PE=2 SV=1
LOC_Os07g02140	down	Flavin-containing monooxygenase FMO GS-OX-like 9 OS=Arabidopsis thaliana OX=3702 GN=At5g07800 PE=2 SV=1
LOC_Os07g38470	down	--
LOC_Os01g16290	down	DNA gyrase subunit B, chloroplastic/mitochondrial OS=Oryza sativa subsp. japonica OX=39947 GN=GYRB PE=2 SV=1
LOC_Os10g40700	down	Expansin-B6 OS=Oryza sativa subsp. japonica OX=39947 GN=EXPB6 PE=2 SV=1
LOC_Os01g74300	down	--
LOC_Os11g36570	down	--
Oryza_sativa_newGene_845	down	--
LOC_Os07g11630	down	17kDa alpha-amylase/trypsin inhibitor 1 OS=Oryza sativa subsp. japonica OX=39947 GN=Os07g0216600 PE=1 SV=1
LOC_Os09g39180	down	31 kDa ribonucleoprotein, chloroplastic OS=Nicotiana glauca OX=4096 PE=1 SV=1
LOC_Os03g39880	down	--
LOC_Os08g44770	down	Superoxide dismutase [Cu-Zn], chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=SODCP PE=1 SV=1
LOC_Os01g67570	down	Protein PLASTID TRANSCRIPTIONALLY ACTIVE 10 OS=Arabidopsis thaliana OX=3702 GN=PTAC10 PE=1 SV=1
LOC_Os06g46970	down	--
LOC_Os12g38650	down	Mitochondrial import receptor subunit TOM5 homolog OS=Arabidopsis thaliana OX=3702 GN=TOM5 PE=1 SV=3
LOC_Os10g11140	down	Phosphoglucomutase, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=PGMP PE=1 SV=2
LOC_Os03g25030	down	Sinapine esterase OS=Brassica napus OX=3708 PE=1 SV=1
LOC_Os11g14400	down	Polygalacturonase OS=Prunus persica OX=3760 PE=2 SV=1
LOC_Os07g23660	down	--
LOC_Os03g45400	down	--
LOC_Os01g63580	down	Glycerol-3-phosphate 2-O-acyltransferase 6 OS=Arabidopsis thaliana OX=3702 GN=GPAT6 PE=1 SV=1
LOC_Os06g08041	down	Protein SRG1 OS=Arabidopsis thaliana OX=3702 GN=SRG1 PE=2 SV=1

LOC_Os11g32650	down	Chalcone synthase 1 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CHS1 PE=2 SV=1
LOC_Os09g14240	down	--
LOC_Os06g39390	down	Acyl transferase 10 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=AT10 PE=3 SV=1
LOC_Os04g32940	down	--
LOC_Os07g31500	down	LRR receptor-like serine/threonine-protein kinase GSO1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GSO1 PE=1 SV=1
LOC_Os07g44160	down	Cytochrome P450 709B2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CYP709B2 PE=2 SV=1
LOC_Os07g32590	down	Methionine aminopeptidase 1B, chloroplastic OS= <i>Arabidopsis thaliana</i> OX=3702 GN=MAP1B PE=2 SV=2
LOC_Os01g68598	down	EPIDERMAL PATTERNING FACTOR-like protein 9 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=EPFL9 PE=1 SV=1
LOC_Os09g01650	down	Peptidyl-prolyl cis-trans isomerase FKBP53 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FKBP53 PE=1 SV=1
LOC_Os02g25449	down	--
LOC_Os04g57350	down	EH domain-containing protein 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=EHD1 PE=1 SV=1
LOC_Os11g45400	down	Probable glycerol-3-phosphate acyltransferase 3 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=GPAT3 PE=2 SV=1
LOC_Os05g02250	down	--
LOC_Os02g32814	down	S-type anion channel SLAH3 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=SLAH3 PE=1 SV=1
LOC_Os04g31240	down	--
LOC_Os03g12270	down	Probable cinnamyl alcohol dehydrogenase 9 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CAD9 PE=2 SV=1
LOC_Os04g39140	down	--
LOC_Os06g50670	down	--
LOC_Os01g58020	down	Ribulose biphosphate carboxylase large chain OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=rcbL PE=1 SV=1
LOC_Os10g40610	down	Flavin-containing monooxygenase FMO GS-OX-like 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At1g12200 PE=2 SV=1
LOC_Os02g15930	down	BAG family molecular chaperone regulator 6 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=BAG6 PE=1 SV=1
LOC_Os08g09270	down	Pentatricopeptide repeat-containing protein At3g59040 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At3g59040 PE=2 SV=2
LOC_Os08g44020	down	--
LOC_Os07g43560	down	Cysteine-rich receptor-like protein kinase 6 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CRK6 PE=1 SV=1
LOC_Os06g11610	down	26.2 kDa heat shock protein, mitochondrial OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=HSP26.2 PE=2 SV=1
LOC_Os04g37680	down	Probable carboxylesterase 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CXE2 PE=2 SV=1
LOC_Os04g39570	down	Probable WRKY transcription factor 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=WRKY2 PE=1 SV=1
LOC_Os04g34330	down	G-type lectin S-receptor-like serine/threonine-protein kinase At2g19130 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At2g19130 PE=2 SV=1
LOC_Os10g36090	down	Non-specific lipid-transfer protein 2 OS= <i>Oryza sativa</i> subsp. <i>indica</i> OX=39946 GN=LTP-2 PE=3 SV=2

LOC_Os03g21370	down	Uncharacterized protein ycf54 OS=Porphyra purpurea OX=2787 GN=ycf54 PE=3 SV=1
LOC_Os10g22560	down	Protein NRT1/ PTR FAMILY 8.3 OS=Arabidopsis thaliana OX=3702 GN=NPF8.3 PE=1 SV=1
LOC_Os06g45660	down	14 kDa zinc-binding protein OS=Zea mays OX=4577 GN=ZBP14 PE=1 SV=1
LOC_Os08g06530	down	--
LOC_Os03g25960	down	RNA-binding protein CP29B, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CP29B PE=1 SV=1
LOC_Os02g06340	down	EH domain-containing protein 2 OS=Arabidopsis thaliana OX=3702 GN=EHD2 PE=1 SV=1
LOC_Os04g18140	down	--
LOC_Os05g14590	down	DNA replication licensing factor MCM6 OS=Oryza sativa subsp. japonica OX=39947 GN=Os05g0235800 PE=3 SV=1
LOC_Os02g57290	down	Protein LUTEIN DEFICIENT 5, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=CYP97A3 PE=1 SV=1
LOC_Os05g46910	down	Putative AC transposase OS=Zea mays OX=4577 PE=2 SV=2
LOC_Os11g01210	down	Pentatricopeptide repeat-containing protein At3g09650, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=HCF152 PE=2 SV=1
LOC_Os01g71330	down	--
LOC_Os01g61320	down	Thioredoxin-like fold domain-containing protein MRL7 homolog, chloroplastic OS=Oryza sativa subsp. japonica OX=39947 GN=MRL7 PE=2 SV=1
LOC_Os11g19880	down	Flavonoid O-methyltransferase-like protein Os11g0303600 OS=Oryza sativa subsp. japonica OX=39947 GN=Os11g0303600 PE=2 SV=1
LOC_Os12g33958	down	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2 OS=Nicotiana glauca OX=4096 GN=NAD7 PE=2 SV=1
LOC_Os01g64880	down	Cadmium/zinc-transporting ATPase HMA3 OS=Oryza sativa subsp. japonica OX=39947 GN=HMA3 PE=1 SV=1
LOC_Os03g52640	down	--
Oryza_sativa_newGene_4661	down	--
LOC_Os07g42430	down	Peroxisomal (S)-2-hydroxy-acid oxidase GLO4 OS=Oryza sativa subsp. japonica OX=39947 GN=GLO4 PE=2 SV=2
LOC_Os07g05480	down	Photosystem I reaction center subunit psaK, chloroplastic OS=Hordeum vulgare OX=4513 GN=PSAK PE=1 SV=1
LOC_Os11g20060	down	--
LOC_Os12g16250	down	Isoflavone reductase homolog OS=Lupinus albus OX=3870 PE=2 SV=1
LOC_Os09g34180	down	Formin-like protein 15 OS=Oryza sativa subsp. japonica OX=39947 GN=FH15 PE=2 SV=1
LOC_Os04g08180	down	--
LOC_Os09g15644	down	--
LOC_Os05g41760	down	Ethylene-responsive transcription factor 12 OS=Arabidopsis thaliana OX=3702 GN=ERF12 PE=1 SV=1
LOC_Os05g40220	down	--
LOC_Os01g08510	down	MAR-binding filament-like protein 1-1 OS=Nicotiana glauca OX=4097 GN=MFP1-1 PE=2 SV=1
LOC_Os04g52100	down	Methionine aminopeptidase 1B, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=MAP1B PE=2 SV=2

LOC_Os11g13850	down	--
LOC_Os05g42340	down	--
Oryza_sativa_newGene_3592	down	--
LOC_Os07g18158	down	Putative aldehyde oxidase-like protein OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os07g0281700 PE=3 SV=1
LOC_Os03g03350	down	Probable polygalacturonase OS= <i>Vitis vinifera</i> OX=29760 GN=GSVIVT00026920001 PE=1 SV=1
LOC_Os07g06080	down	--
LOC_Os04g56400	down	Glutamine synthetase, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=GLN2 PE=1 SV=1
LOC_Os01g15240	down	--
LOC_Os06g10750	down	WAT1-related protein At1g21890 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At1g21890 PE=2 SV=1
LOC_Os05g48630	down	Photosystem I reaction center subunit VI, chloroplastic OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=PSAH PE=2 SV=1
LOC_Os07g38960	down	Chlorophyll a-b binding protein 7, chloroplastic OS= <i>Solanum lycopersicum</i> OX=4081 GN=CAB7 PE=3 SV=1
LOC_Os07g35940	down	Beta-amylase OS= <i>Triticum aestivum</i> OX=4565 GN=BMV1 PE=2 SV=1
LOC_Os06g04950	down	Early nodulin-93 OS= <i>Glycine max</i> OX=3847 PE=2 SV=1
LOC_Os04g25370	down	7-deoxyloganetin glucosyltransferase OS= <i>Gardenia jasminoides</i> OX=114476 GN=UGT85A24 PE=1 SV=1
LOC_Os07g36630	down	Probable mixed-linked glucan synthase 8 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CSFL8 PE=2 SV=1
LOC_Os03g52310	down	Zinc finger BED domain-containing protein RICESLEEPER 2 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=Os03g0733400 PE=2 SV=1
LOC_Os02g41780	down	UDP-xylose transporter 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=UXT1 PE=1 SV=1
LOC_Os10g29470	down	Probable cinnamyl alcohol dehydrogenase 3 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=CAD3 PE=2 SV=1
LOC_Os03g12030	down	3-ketoacyl-CoA synthase 6 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=CUT1 PE=1 SV=1
LOC_Os01g64680	down	Protein BOLA2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=BOLA2 PE=1 SV=1
LOC_Os01g20110	down	Uncharacterized protein At4g37920 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At4g37920 PE=2 SV=2
LOC_Os04g12669	down	UDP-glycosyltransferase 79 OS= <i>Oryza sativa</i> subsp. <i>japonica</i> OX=39947 GN=UGT79 PE=1 SV=2
LOC_Os01g66010	down	Amino acid permease 2 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=AAP2 PE=1 SV=1
LOC_Os08g15322	down	Cytochrome b559 subunit alpha OS= <i>Triticum aestivum</i> OX=4565 GN=psbE PE=1 SV=2
LOC_Os10g21230	down	ATP synthase subunit c, chloroplastic OS= <i>Zygnema circumcarinatum</i> OX=35869 GN=atpH PE=3 SV=1
LOC_Os05g49130	down	--
LOC_Os01g08130	down	Root phototropism protein 3 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=RPT3 PE=1 SV=2
LOC_Os04g48930	down	Probable ferric reduction oxidase 1 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=FRO1 PE=2 SV=1
LOC_Os11g10300	down	Putative F-box/LRR-repeat protein At4g13960 OS= <i>Arabidopsis thaliana</i> OX=3702 GN=At4g13960 PE=4 SV=1

LOC_Os04g54380	down	--
LOC_Os09g18230	down	Putative leucine-rich repeat receptor-like serine/threonine-protein kinase At2g19230 OS=Arabidopsis thaliana OX=3702 GN=At2g19230 PE=3 SV=
LOC_Os01g19610	down	UPF0481 protein At3g47200 OS=Arabidopsis thaliana OX=3702 GN=At3g47200 PE=2 SV=1
LOC_Os05g46110	down	Pathogenesis-related protein 5 OS=Arabidopsis thaliana OX=3702 GN=At1g75040 PE=1 SV=1
LOC_Os12g28880	down	--
LOC_Os07g12160	down	--
LOC_Os05g22840	down	--
LOC_Os04g28420	down	Peptidyl-prolyl cis-trans isomerase FKBP62 OS=Arabidopsis thaliana OX=3702 GN=FKBP62 PE=1 SV=2
LOC_Os04g51980	down	Anthranilate N-benzoyltransferase protein 3 OS=Dianthus caryophyllus OX=3570 GN=HCBT3 PE=1 SV=1
LOC_Os04g50770	down	Myb-related protein Zm1 OS=Zea mays OX=4577 PE=2 SV=1
LOC_Os12g34500	down	--
LOC_Os06g40170	down	Phospholipase D alpha 2 OS=Oryza sativa subsp. japonica OX=39947 GN=PLD2 PE=2 SV=2
LOC_Os04g48375	down	Zinc finger CCCH domain-containing protein 17 OS=Oryza sativa subsp. japonica OX=39947 GN=Os02g0677700 PE=2 SV=2
LOC_Os11g19840	down	Flavonoid O-methyltransferase-like protein Os11g0303600 OS=Oryza sativa subsp. japonica OX=39947 GN=Os11g0303600 PE=2 SV=1
LOC_Os12g18550	down	--
LOC_Os01g37870	down	Pentatricopeptide repeat-containing protein At1g10910, chloroplastic OS=Arabidopsis thaliana OX=3702 GN=At1g10910 PE=2 SV=1
LOC_Os05g51620	down	--
Oryza_sativa_newGene_4347	down	--
LOC_Os01g24070	down	GATA transcription factor 23 OS=Arabidopsis thaliana OX=3702 GN=GATA23 PE=2 SV=2
LOC_Os03g22040	down	WEB family protein At2g38370 OS=Arabidopsis thaliana OX=3702 GN=At2g38370 PE=2 SV=1
LOC_Os04g42610	down	Filament-like plant protein 7 OS=Arabidopsis thaliana OX=3702 GN=FPP7 PE=3 SV=2
LOC_Os01g64410	down	Transcription repressor OFP13 OS=Arabidopsis thaliana OX=3702 GN=OFP13 PE=1 SV=1
LOC_Os08g38850	down	Phosphatidylinositol/phosphatidylcholine transfer protein SFH6 OS=Arabidopsis thaliana OX=3702 GN=SFH6 PE=2 SV=1
LOC_Os08g14364	down	ATPase 3, plasma membrane-type OS=Arabidopsis thaliana OX=3702 GN=AHA3 PE=1 SV=2
LOC_Os06g44540	down	(R)-mandelonitrile lyase-like OS=Arabidopsis thaliana OX=3702 GN=At1g73050 PE=2 SV=1
LOC_Os06g17490	down	Probable L-type lectin-domain containing receptor kinase S.7 OS=Arabidopsis thaliana OX=3702 GN=LECRKS7 PE=2 SV=1

