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Original Paper

Transcription profiling identifies candidate genes for secondary cell wall formation and hydroxycinnamoyl-arabinoxylan biosynthesis in the rice internode

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Abstract Microarray analysis was used to identify candidate genes that are involved in the formation of secondary cell walls and hydroxycinnamoyl-arabinoxylan (AX) in rice. In order to identify genes involved in secondary cell wall formation, gene expression was compared between wild-type whole internodes that contain cells with thickened secondary cell walls, such as vascular and cortical fiber cells, and wild-type internode parenchyma cells without secondary cell walls. In addition, gene expression was compared between the internode parenchyma of Fukei71 (F71), a rice dwarf mutant that accumulates large amounts of hydroxycinnamoyl-AX in pith parenchyma cells, and wild-type pith parenchyma cells to identify hydroxycinnamoyl-AX-related genes. Significant expression of candidate genes, gene lists were prepared for the phenylpropanoid pathway, major carbon metabolism, and cell wall biosynthesis, which is a useful platform to analyze cell wall formation in rice. The data indicated that a number of rice genes are potentially associated with secondary cell wall formation, such as the up-regulation of genes encoding cellulose synthase subunit A and ferulate 5-hydroxylase in wild-type whole internodes. Similarly, for hydroxycinnamoyl-AX synthesis, the expression of several genes changed, such as the down-regulation of genes encoding cinnamoyl-CoA reductase and the up-regulation of the phospho*enol*pyruvate carboxykinase gene in F71 pith parenchyma.

Key words: Hydroxycinnamoyl-arabinoxylan, lignin, microarray, rice, secondary cell wall.

Since ancient times, grass crops have contributed to many human activities where they serve as food, feed, and fuel. However, in recent years, the demand for grass crops as a biofuel has rapidly increased. Bioethanol is a typical biofuel that is produced mainly from carbohydrates, such as sucrose from sugarcane and starch from corn. However, using these carbohydrates in biofuel production competes with their availability as a food source. Sugar and starch are now expected to be replaced cellulosic carbohydrates (cellulose and hemicellulose) in biofuel production. Lignocellulose (cellulose, hemicellulose, and lignin) is estimated to account for approximately 50% of the world's biomass, which is approximately 10–50 billion tons according to Claasen et al. (1999). This natural, potentially inexpensive, and abundant polymer is found in agricultural waste (straw, corn stalks, soybean residues, and sugarcane bagasse), industrial waste (waste paper

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Abbreviations: 4CL, 4-coumarate-CoA ligase; AX, arabinoxylan; BAHD, benzylalcohol *O*-acetyltransferase (BEAT), anthocyanin *O*-hydroxycinnamoyltransferase (AHCT), anthranilate *N*-hydroxycinnamoyl/benzoyltransferase (HCBT), deacetylvindoline 4-*O*-acetyltransferase (DAT); C3H, coumaroyl-quinate/shikimate 3-hydroxylase; C4H, cinnamate 4-hydroxylase; CAD, cinnamyl alcohol dehydrogenase; CCR, cinnamoyl-CoA reductase; CesA, cellulose synthase subunit A; CCoAOMT, caffeoyl CoA *O*-methyltransferase; COMT, caffeic acid *O*-methyltransferase; Csl, cellulose synthase like; E4P, erythrose-4-phosphate; F5H, ferulate 5-hydroxylase; F71, Fukei71; fer-AX, feruloyl arabinoxylan; FDR, false discovery rate; Fruc, fructose; GalA, galactonic acid; Glc, glucose; GlucA, glucuronic acid; GH, glycoside hydrolases; GT, glycosyl transferase; HCT, *p*-hydroxycinnamoyl CoA quinate/shikimate *p*-hydroxycinnamoyl transferase; INT, whole internode; -P, phosphate; PAL, phenylalanine ammonia-lyase; *p*C-AX, *p*-coumaroyl arabinoxylan; PEP, phospho*enol*pyruvate; PEP-CK, phospho*enol*pyruvate carboxykinase; PEP-Cx, phospho*enol*pyruvate carboxylase; PK, pyruvate kinase; PR, pathogenesis related; RT-PCR, reverse transcription-polymerase chain reaction; SPS, sucrose phosphate synthase; Suc, sucrose; SuSy, sucrose synthase; UBQ, ubiquitin.

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and other construction waste), forest residues, and other waste (Wiselogel et al. 1996). However, the fermentable sugars of lignocellulose are not readily available because lignocellulose must be pre-treated in order to break down into its intermediates and remove lignin, which prevents cellulosic carbohydrates from being hydrolyzed by enzymes. In addition, grass cell walls are rich in low-molecular-weight phenolic acid (*p*-coumaric acid and ferulic acid) esters that link to the arabinose side chains of the xylan backbone, hydroxycinnamoyl-arabinoxylan (AX) (Iiyama et al. 1994). Because these phenolic acids can form dimers and ether linkages with other aromatic constituents, they are formidable obstacles during the pre-treatment process. Thus, it is more costly to obtain fermentable sugars from lignocellulose than from sucrose and starch. Therefore, we need to engineer genetically modified plants with new configurations of lignin and hydroxycinnamoyl-AX and develop new methods of modifying the contents of plants.

Hydroxycinnamoyl-AX is a component of grass cell walls that is thought to be one of the most important structures of cell walls because it is involved in terminating wall extensibility, wall strengthening, and blocking pathogen entry (Iiyama et al. 1994). Although studies have identified key enzymes that are involved in hydroxycinnamoyl-AX synthesis, including xylosyl transferase from barley (Urahara et al. 2004), arabinosyl transferase from wheat (Porchia et al. 2002), and feruloyl transferase from parsley, *Festuca arundinacea*, and rice (Meyer et al. 1991; Myton and Fry 1994; Yoshida-Shimokawa et al. 2001), the genes encoding these enzymes are still unknown. Using public EST databases for cereals and dicots, Mitchell et al. (2007) proposed candidate genes for xylan synthase, arabinosyl transferase, feruloyl transferase, and acyltransferase, of which several genes encoding glycosyl transferase (GT) 61 family were experimentally shown to be responsible for the activity of arabinosyl transferase and xylosyl transferase (Anders et al. 2012; Chiniquy et al. 2012).

A powerful tool for identifying candidate genes that are closely associated with various aspects of cell wall biosynthesis is an approach that combines bioinformatics and microarray analysis. Several groups have examined secondary cell wall formation using microarray techniques and identified a number of genes involved in secondary cell wall formation in Arabidopsis and other plant species, including zinnia, poplar, and eucalyptus (reviewed in Demura and Fukuda 2007). However, microarray analyses have been still limited on grass crops to comprehensively identify genes involved in secondary cell wall formation.

In this study, the expression of genes involved in secondary cell wall formation and hydroxycinnamoyl-AX in the rice internode was profiled using the GeneChip® rice genome array (Affymetrix). Candidate genes related to secondary cell wall formation were examined in wild-type rice by comparing pith parenchyma cells without secondary cell walls and whole internodes containing cells with secondary cell walls. The rice dwarf mutant Fukei71 (F71) was previously isolated by gamma-ray irradiation, which has non-uniform internode pith parenchyma cells with abnormally thickened cell walls that contain large amounts of hydroxycinnamoyl-AX (Kitano and Futsuhara 1981, 1982; Nishikubo et al. 2000). Recently, the F71 causal gene, *D50*, was found to encode an inositol polyphosphate 5-phosphatase and to possibly function in formation of intercalary meristem, including the direction of cell division, deposition of cell wall pectins and control of actin organization (Sato-Izawa et al. 2012). Even though it remains unclear why F71 accumulates large amounts of hydroxycinnamoyl-AX as a consequence of mutation in *D50* gene, it is worth using for identifying candidate genes that are closely associated with hydroxycinnamoyl-AX. Therefore, we compared pith parenchyma cells from F71 with those from wild-type to identify candidate genes involved in hydroxycinnamoyl-AX synthesis.

Materials and methods

Plant materials

A single recessive rice dwarf mutant with irregularly shaped parenchyma cells in the internodes, termed F71, and its parent cultivar Fujiminori (*Oryza sativa* L.; wild-type) were grown in soil in an environment-controlled greenhouse under a 12 h light (30°C), 12 h dark (23°C) photoperiod. Histochemical analyses using the phloroglucin-HCl and Mäule reactions were performed to show the deposition of phenolic compounds in the cell wall. Elongating third internode segments of both F71 and wild-type were collected at the rapid culm elongation stage (70–80 days after sowing; Counce et al. 2002), and their pith parenchyma regions were excised with a razor blade. To minimize vascular cell contamination in the pith parenchyma samples, several inner layers of pith parenchyma cells were sliced from the internodes. Microscopic observations were randomly performed to confirm that the parenchyma regions did not contain vascular bundles (Figures 1I to L). Three biologically independent samples were collected from 8 to 10 plants for microarray analysis. The collected samples were stored at −80°C until RNA extraction was performed.

Histochemical analysis

For the phloroglucin-HCl reaction, 80–100 μm sections were prepared with a microslicer (ZERO 1; DSK) and incubated in a mixture of 1% phloroglucinol in 20% calcium chloride and 12 N hydrochloric acid (25 : 4, v/v) for 5 min. For the Mäule reaction, the sections were immersed in 1% potassium permanganate at room temperature for 5 min, rinsed in distilled water, decolorized with 1 N hydrochloric acid for 5 min, washed thoroughly in water, and treated with a few drops of

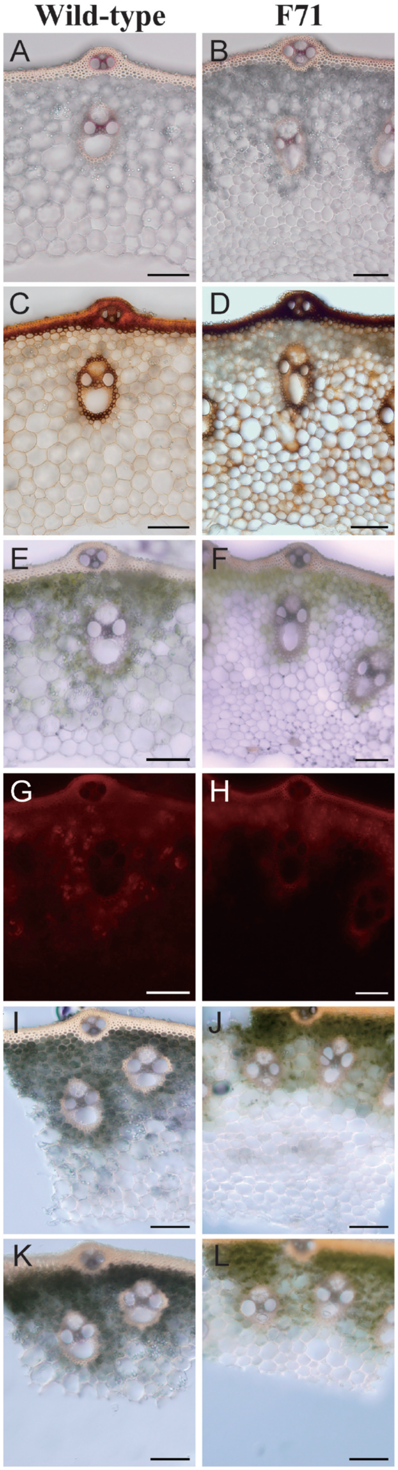


Figure 1. Cross sections of the third internodes from wild-type and F71. (A, B) Lignin in the cell wall is stained bright red by phloroglucin-HCl reagent. (C, D) The Mäule reaction results in brownish-red and brownish-yellow staining of the syringyl and guaiacyl moieties in the cell walls, respectively. The pith parenchyma cell walls are more strongly stained in the F71 internode (D) than in the wild-type whole internode (C). (E–L) Hand sections. Chloroplasts were observed under bright field illumination (E, F), and UV irradiation (G, H). Pith parenchyma cells from F71 (F, H) contained fewer chloroplasts than wild-type (E, G). To prepare the pith parenchyma samples, several inner layers of pith parenchyma cells were sliced off with a razor blade; (I, J) before slicing, (K, L) after slicing. Scale bars=100 μm.

concentrated ammonia solution. The stained samples were observed under a microscope (BX51, Olympus) using a digital camera (DP70, Olympus). Chloroplast autofluorescence was observed with a WIG filter cube under UV-irradiation.

Microarray analysis

For microarray analysis, RNA was extracted using the RNeasy Plant Mini Kit (Qiagen) and purified and concentrated using a Montage PCR filter unit (Millipore). The microarray analysis was performed using a GeneChip® rice genome array (Affymetrix), which contains probes to query 51,279 transcripts representing two rice cultivars, with 48,564 *japonica* transcripts and 1,269 transcripts representing the *indica* cultivar. Each RNA was amplified (100 ng), and double-stranded cDNA was prepared using two-cycle target labeling and control reagents (Affymetrix). Next, hybridization, washing, staining, and scanning were performed according to the manufacturer's protocol. All manipulations were carried out independently for each RNA sample. The data analysis was performed using GeneChip® Operating Software (GCOS using MAS5 algorithm, Affymetrix) and GeneSpring GX 7.3 software (Agilent Technologies). Each chip was normalized to the 50th percentile of the measurements taken from that chip (per chip normalization). Per gene normalization was performed using the measurements of the wild-type parenchyma samples as controls. Array elements showing a present or marginal call in at least one of the nine chip experiments (33,340 probes) were selected for further classification. The probes were extracted using a one-way analysis of variance (ANOVA) applying the Benjamini and Hochberg multiple testing correction (Benjamini and Hochberg 1995) with a false discovery rate (FDR) and Tukey's *post hoc* test. As a result, 589 probes ($FDR<0.001$), 3,104 probes ($FDR<0.005$), and 4,954 probes ($FDR<0.01$) were selected that exhibited significant differences among wild-type pith parenchyma cells, F71 pith parenchyma cells, and wild-type whole internode cells. Microarray data sets were deposited in the ArrayExpress public database, series accession number E-MEXP-2311.

Assigning probe sets to genes

Probe sets were assigned to annotated genes using the rice multiplatform table that was downloaded from the National Science Foundation's Rice Oligonucleotide Array Project website (http://www.ricearray.org/index.shtml) and verified by the NetAffx Analysis Center (http://www.affymetrix.com/analysis/index.affx). Annotations are based on TIGR pseudomolecule release 5 of 2007 (http://www.tigr.org/tdb/e2k1/osa1/).

Semi-quantitative reverse transcription-polymerase chain reaction (RT-PCR)

Total RNA was purified using the RNeasy Plant Mini Kit (Qiagen) and DNA-free (Life Technologies). First-strand cDNA synthesis was performed using SuperScript III RT (Life Technologies) with oligo $(dT)_{12\text{–}18}$ primers and 500 ng of RNA

Table 1. The top 15 probe sets with increased or decreased expression in the wild-type whole internode.

Systematic name	TIGR loci	Description	Fold change[a]	Raw signal[b]	
				WT Pa	WT INT
Increased					
Os.56337.1.S1_at	LOC_Os11g19210	Beta-D-xylosidase	276.86	2	440
OsAffx.13655.1.S1_at	LOC_Os04g04060	Dynamin GTPase effector	177.87	3	459
Os.53254.1.S1_at	LOC_Os06g12210	DNA binding protein	168.90	3	509
Os.11563.1.S1_at	LOC_Os11g43980	Peroxidase	157.20	9	1256
Os.49289.1.S1_x_at	LOC_Os06g21270	Glycine-rich cell wall structural protein	154.04	5	694
Os.8638.1.S1_at	LOC_Os10g05950	Proline-rich protein	138.08	34	4747
Os.55437.1.S1_at	LOC_Os03g43770	F-box domain containing protein	130.56	3	369
Os.6417.1.S1_at	LOC_Os07g37850	Expressed protein	119.78	43	4930
Os.16018.1.S1_at	LOC_Os01g63010	Universal stress protein family	113.03	31	3527
OsAffx.21591.1.S1_at	LOC_Os01g56660	Expressed protein	111.22	3	286
Os.12387.1.S1_at	LOC_Os04g39150	Major latex protein	109.34	55	6006
Os.20313.1.S1_s_at	LOC_Os01g72290	Germin-like protein subfamily	100.39	41	3911
Os.37913.1.S1_at	LOC_Os04g31870	Expressed protein	88.19	3	294
Os.11398.1.S1_at	LOC_Os10g05980	Proline-rich protein	85.04	111	9416
Os.4380.1.S1_at	LOC_Os11g02350, LOC_Os12g02300	Nonspecific lipid-transfer protein	81.11	29	2379
Decreased					
Os.54944.1.S1_at	LOC_Os02g52670	Ethylene-responsive element binding protein	0.013	182	2
Os.3808.4.S1_x_at	LOC_Os01g09220	Transposon protein	0.015	3058	42
Os.12240.1.S1_at	LOC_Os02g52010	Phosphate-induced protein	0.029	2278	69
Os.36651.1.S1_at	LOC_Os04g43560	NAC domain-containing protein	0.050	3757	187
Os.20420.1.S1_at	LOC_Os01g18120	Cinnamoyl-CoA reductase	0.067	8121	557
OsAffx.14373.1.S1_s_at	LOC_Os04g52090	Ethylene-responsive transcription factor	0.067	7702	528
OsAffx.27508.7.S1_s_at	LOC_Os11g44380	Expressed protein	0.087	5777	535
Os.5860.1.S1_at	LOC_Os03g04310	BHLH transcription factor	0.089	2284	207
Os.14444.1.S1_at	LOC_Os10g38700	Glutathione S-transferase	0.095	735	71
Os.50598.1.S1_at	LOC_Os12g03370	Harpin-induced protein	0.095	217	21
Os.7028.1.S1_at	LOC_Os02g45710	RING zinc finger protein-like	0.095	2586	244
Os.56294.1.S1_at	LOC_Os11g36400	Expressed protein	0.096	24	2
Os.46160.2.S1_x_at	LOC_Os10g30790	Inorganic phosphate transporter	0.097	6422	641
OsAffx.22181.1.S1_s_at	LOC_Os01g17050	VQ domain containing protein	0.102	5901	618
Os.37565.1.S1_at	AK063697[c]	Unknown protein	0.105	1178	130

[a] The fold changes were calculated by dividing the normalized values for the wild-type whole internode (WT INT) by those for the wild-type pith parenchyma (WT Pa). [b] The raw signals are the means of three experiments. [c] No TIGR Loci corresponded with this probe, so the representative cDNA clone is listed.

as a template in a reaction volume of 20 μl. A 0.25 μl aliquot of the reaction mixture was PCR amplified using ExTaq DNA polymerase (Takara Bio) in a reaction volume of 20 μl containing 6 μM of each primer (Table S1). To avoid saturating the PCR amplification, the number of cycles varied for each examined gene as follows: *pathogenesis-related* (*PR*) *protein*, 27 cycles; *benzoate carboxyl methyltransferase*, 29 cycles; *beta-D-xylosidase*, 32 cycles; *NAC*, 28 cycles; *CCR*, 29 cycles; *CesA4*, 29 cycles; *PEP-CK*, 35 cycles; and *ubiquitin* (*UBQ*), 24 cycles. The PCR products were separated on 1.5% (w/v) agarose gels and stained with ethidium bromide.

Results and discussion

Genes with significant differences in expression

The over-accumulation of hydroxycinnamoyl-AX in F71 pith parenchyma cells at the internode elongation stage (70–80 days after sowing; Counce et al. 2002) was confirmed by histochemical analysis of cross sections of the third internodes (Figure 1). The F71 pith parenchyma cells had thickened cell walls with few chloroplasts compared to wild-type pith parenchyma cells. Bright red lignin staining by the phloroglucin-HCl reaction was observed in several vascular cells in both wild-type and F71 (Figures 1A, B). Strong lignin and hydroxycinnamoyl moiety staining was observed in both wild-type and F71 vascular bundles and cortical fibers using the Mäule reaction (Figures 1C, D), but only the pith parenchyma cells in F71 samples exhibited strong staining (Figure 1D). Chloroplasts were observed under bright field illumination (Figures 1E, F) and UV irradiation (Figures 1G, H). Pith parenchyma cells from F71 (Figures 1F, H) contained few chloroplasts compared to those from wild-type (Figures 1E, G). Three samples were prepared from these internodes for microarray analysis: wild-type pith parenchyma, F71 pith parenchyma, and wild-type whole internodes containing vascular bundles, cortical fibers, and all parenchyma cells.

Genes that were differentially expressed in the wild-type pith parenchyma, F71 pith parenchyma, and

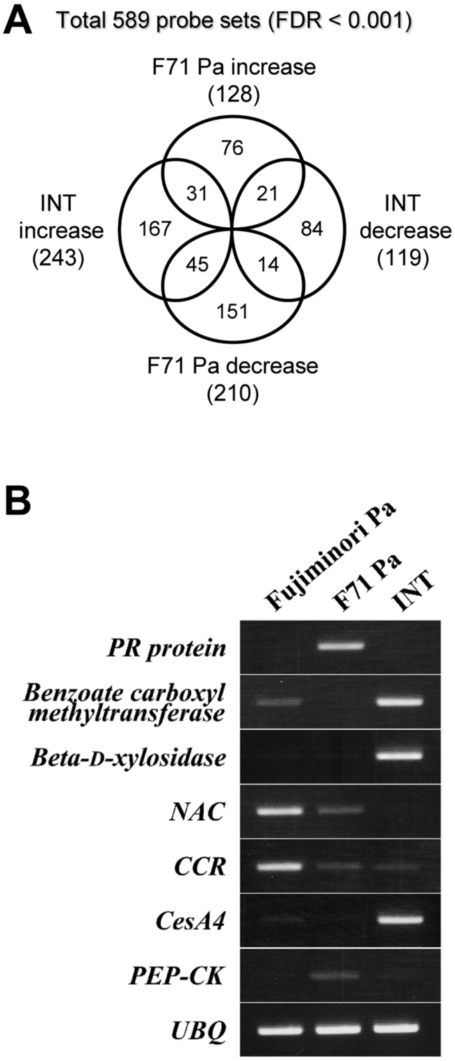


Figure 2. (A) Venn diagram showing significant differential gene expression in the wild-type whole internode (WT INT) and F71 pith parenchyma (F71 Pa) compared to wild-type pith parenchyma (FDR <0.001). The number in each area denotes the number of probes in the set. (B) Semi-quantitative RT-PCR analysis of differentially expressed genes. The same RNA samples that were used for the microarray analysis were subjected to PCR. *UBQ*, which encodes ubiquitin fusion protein (Miki et al. 2005), was used as an extraction and loading control.

wild-type whole internode were selected through a statistical analysis of triplicate microarray data using a one-way ANOVA with a stringent FDR of less than 0.001 and Tukey's *post hoc* test. Fold changes in the normalized intensities were calculated to compare the F71 pith parenchyma to wild-type pith parenchyma and wild-type whole internode to wild-type pith parenchyma. A Venn diagram was used to display the number of probe sets that had significant differential expression (Figure 2A). A total of 589 probes was significantly different (for a list of these probes, see Tables S2 and S3). The probe expression levels were as follows: F71 pith parenchyma, 128 increased and 210 decreased; wild-type whole internode, 243 increased and 119 decreased; both F71 pith parenchyma and wild-type whole internode (intersections in the Venn diagram), 111 with significantly different expression levels. In a subsequent analysis of the specific functions and metabolic pathways discussed below, we also considered differentially expressed genes with a lower significance level (FDR<0.01 and <0.005). In addition to significance, we carefully noted the expression levels, including the expression levels of other genes in the same family, in order to avoid over-evaluating genes with lower expression levels.

RT-PCR confirmation of microarray results

To confirm the microarray results, semi-quantitative RT-PCR was performed for four arbitrarily selected probe sets that were highly differentially expressed in the F71 pith parenchyma and wild-type whole internode (Tables 1 and 2; FDR<0.001): the gene encoding the PR protein (LOC_Os12g36830) increased specifically in the F71 pith parenchyma; the gene encoding benzoate carboxyl methyltransferase (LOC_Os05g01140) decreased in the F71 pith parenchyma but increased in the wild-type whole internode; the gene encoding β-D-xylosidase (LOC_Os11g19210) increased specifically in the wild-type whole internode; and the gene encoding the NAC domain-containing transcription factor (LOC_Os04g43560) decreased specifically in the wild-type whole internode. For all four probe sets, RT-PCR amplification exactly matched the increased or decreased patterns in the array data (Figure 2B).

Genes differentially expressed in the wild-type whole internode

We hypothesized that the transcripts of genes related to secondary cell wall synthesis would be more abundant in the whole internode than the internode pith parenchyma. Therefore, the first step was to evaluate genes that were differentially expressed at significantly higher levels in the whole internode compared to the wild-type pith parenchyma (FDR<0.001; Table S2). The top 15 probe sets that were up- or down-regulated in the wild-type whole internode based on fold changes in the normalized intensities are listed in Table 1. The up-regulated genes included those encoding proteins that are associated with cell walls, such as peroxidase, glycine-rich protein, and proline-rich protein. The probe that increased the most in the whole internode was annotated as one of the β-D-xylosidases (LOC_Os11g19210), which are classified into the glycoside hydrolase (GH) 3 family according to the CAZy database (http://www.cazy.org/). The 16 putative genes are members of the GH3 family in rice. Among these 16 genes, only LOC_Os11g19210 was significantly increased in the whole internode, whereas expression of this gene was only minimally detected in the pith parenchyma (flags are called "absent; A"). A putative

Table 2. The top 15 probe sets with increased or decreased expression in the F71 pith parenchyma.

Systematic name	TIGR loci	Description	Fold change[a]	Raw signal[b]	
				WT Pa	F71 Pa
Increased					
Os.5031.1.S1_at	LOC_Os12g36830	PR10 (RSOsPR10)	848.82	6	5311
Os.32890.1.S1_at	LOC_Os11g47600	Class 3 chitinase	557.33	3	1382
Os.165.1.S1_at	LOC_Os12g36880	PR10 (PR10a)	430.50	32	15228
Os.20230.1.S1_at	LOC_Os11g37950	PR4	168.24	58	10651
OsAffx.3144.1.S1_x_at	LOC_Os03g06010	Alpha-expansin (OsEXPA25)	157.72	6	1148
Os.47743.1.S1_at	Os07g0167700[c]	Unknown protein	134.36	28	4105
Os.11290.1.S1_at	LOC_Os06g44170	Leucoanthocyanidin reductase	124.47	1	146
OsAffx.24234.2.S1_s_at	LOC_Os02g13780	Leucine Rich Repeat family protein	107.29	1	148
Os.23635.1.S1_at	Os01g0847100[c]	Unknown protein	103.65	55	5907
Os.51172.1.S1_x_at	LOC_Os06g51050	Basic endochitinase (CHIT7)	89.11	57	5576
OsAffx.28152.2.S1_at	LOC_Os06g47470	Protein kinase domain containing protein	86.54	2	184
Os.8838.2.S1_at	LOC_Os08g04250	Protein kinase	62.77	2	145
Os.6763.1.S1_at	LOC_Os01g48710	Metal ion binding protein	44.50	4	174
Os.316.1.S1_at	LOC_Os07g01560	Sugar transport protein	42.98	187	8268
Os.33131.1.A1_at	LOC_Os03g20550	OsWRKY family protein	35.81	5	186
Decreased					
Os.14938.1.S1_at	LOC_Os05g01140	Benzoate carboxyl methyltransferase	0.010	481	2
Os.8482.1.S1_s_at	LOC_Os04g55159	Expressed protein	0.012	428	4
Os.6812.1.S1_at	LOC_Os10g21670	Dehydration stress-induced protein	0.013	1443	16
Os.17563.1.S1_at	LOC_Os02g17920	Lactoylglutathione lyase	0.020	80	2
Os.53724.1.S1_at	LOC_Os11g26340	Expressed protein	0.029	4423	134
Os.28218.1.S1_at	LOC_Os12g19394	Ribulose bisphosphate carboxylase small chain C	0.035	7669	290
Os.28218.1.S1_x_at	LOC_Os12g19394	Ribulose bisphosphate carboxylase small chain C	0.043	8946	417
Os.49129.1.S1_at	LOC_Os04g33630	Ferredoxin-3	0.044	2280	115
Os.46487.1.S1_at	LOC_Os10g30719	Myb-like DNA-binding domain containing protein	0.050	199	11
OsAffx.12382.1.S1_at	LOC_Os02g37060[d]	Expressed protein	0.053	8393	508
Os.46924.1.S1_at	LOC_Os07g40690	Leucoanthocyanidin reductase	0.061	1548	102
Os.48879.1.S1_at	LOC_Os09g31502	Dihydroflavonol-4-reductase	0.061	3167	218
Os.49874.2.S1_x_at	LOC_Os02g54060	Chaperonin	0.061	1597	109
Os.9814.1.S1_at	LOC_Os01g55570	Thylakoid membrane phosphoprotein	0.062	1168	78
Os.7218.1.S1_at	LOC_Os02g01150	Hydroxypyruvate reductase	0.062	705	49

[a] The fold changes were calculated by dividing the normalized values for the F71 pith parenchyma (F71 Pa) by those for the wild-type pith parenchyma (WT Pa). [b] The raw signals are the means of three experiments. [c] No TIGR Loci corresponded with this probe, so the representative RAP-DB Locus is listed up. [d] This probe is designed for CT835332, which is the cDNA for the *indica* cultivar-group, and LOC_Os02g37060 is the corresponding gene for the *japonica* cultivar-group.

β-D-xylosidase gene (*AtBXL1*) has been reported to be involved in secondary cell wall xylan synthesis (Goujon et al. 2003). Although LOC_Os11g19210 does not have higher sequence similarity to AtBXL1, it is possible that LOC_Os11g19210 is involved in secondary cell wall synthesis in rice because this gene is highly expressed in the whole internode.

Various types of genes were down-regulated, including four genes that encode the putative transcription factors, ethylene-responsive element binding protein, NAC domain-containing protein, ethylene-responsive transcription factor, and BHLH transcription factor. The gene expression profile of the NAC domain-containing protein was confirmed by RT-PCR (Figure 2B). These down-regulated genes may be expressed mainly in the pith parenchyma.

Genes differentially expressed in the F71 parenchyma

When F71 is grown at a high temperature (25–30°C), it exhibits a dwarf phenotype and over-accumulates hydroxycinnamoyl-AX in irregularly shaped internode pith parenchyma cells (Kitano and Futsuhara 1981, 1982; Nishikubo et al. 2000). All probe sets are listed in Table S3, and the top 15 probe sets are listed in Table 2 according to the fold changes in the normalized intensities. Contrary to expectations, genes that potentially encode hydroxycinnamoyl-AX, glycosyl transferases, and phenylpropanoid synthesis-related enzymes were not included in the list. Instead, a number of genes encoding putative elicitor- or pathogen-induced and defense-related proteins were up-regulated. LOC_Os12g36830 encodes RSOsPR10, a member of the PR 10 protein family; *RSOsPR10* was previously shown to be induced by salt, drought, jasmonic acid treatment, and blast fungus infection (Hashimoto et al. 2004). Chitin-elicitor treatment induced the up-regulation of LOC_Os11g47600, which encodes a class III chitinase (Chujo et al. 2008). Chitinases are thought to play a role in host defense because their substrate chitin is the main component of many fungal walls, and pathogens induce the expression of many chitinase genes. LOC_Os12g36880 also encodes a PR10 protein, PR10a. The expression of *PR10a* is strongly induced by salicylic acid, jasmonic acid, and blast fungus infection, and *PR10a* transcripts are localized at the sites of fungal infections (Agrawal et al. 2001; McGee et al. 2001). Moreover, in parsley, cell wall-bound *p*-coumaric acid and ferulic acid esters were detected as early components of the defense response to pathogens (Hahlbrock and Scheel 1989). Therefore, elicitor- or pathogen-induced and defense-related gene up-regulation may be relevant to the over-accumulation of hydroxycinnamoyl-AX in F71.

Among 210 probe sets that were down-regulated in the F71 parenchyma, 47 probe sets were related to photosynthesis, and four of these were in the top 15 probe sets (Table 2). These data are consistent with the microscopic observation results, which showed that F71 had fewer chloroplasts than wild-type pith parenchyma (Figures 1E, H).

Specific gene groups in the phenylpropanoid pathway, major carbon metabolism, and cell wall biosynthesis

To consider how gene expression integrates with the gene annotations, such as metabolic pathways and functional classifications, specific gene groups were examined for their association with the phenylpropanoid pathway, major carbon metabolism, and cell wall biosynthesis. The gene lists and corresponding probe lists were compiled as outlined below. These lists further our understanding of cell wall biosynthesis and provide a useful platform for analyzing the microarray data.

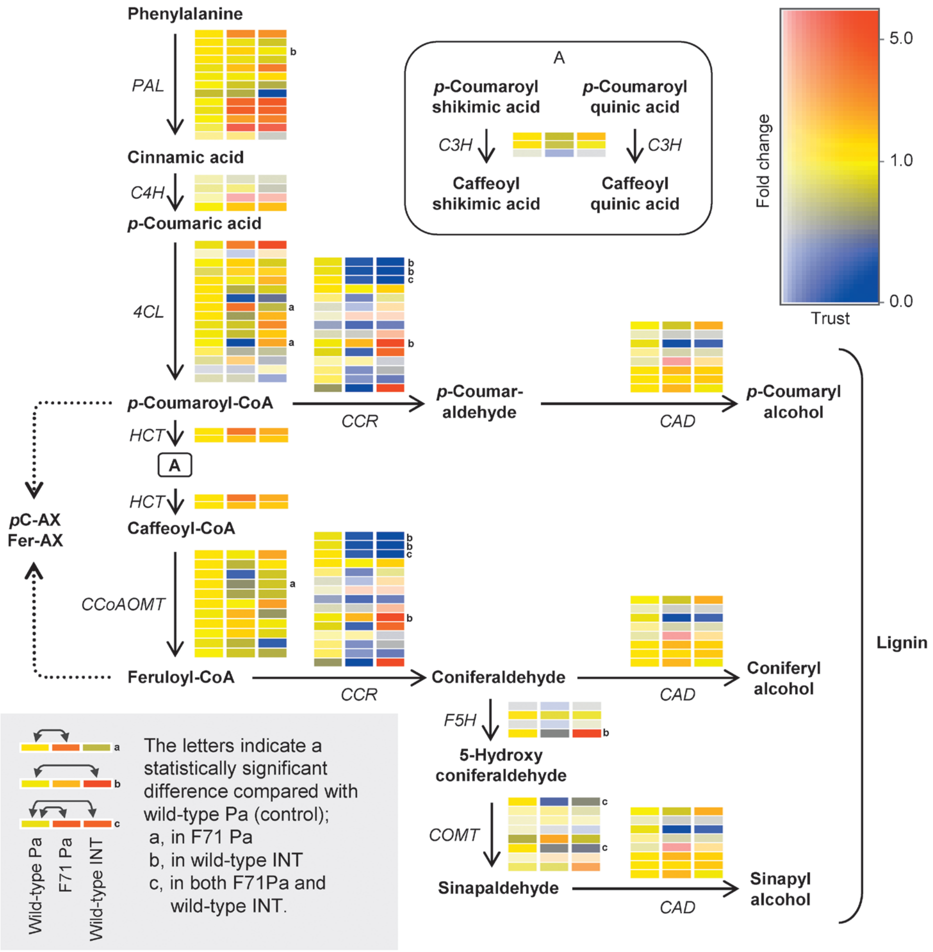
Phenylpropanoid pathway genes

Ligin is mainly composed of three monolignols (*p*-coumaryl, coniferyl, and sinapyl alcohol) derived from the phenylpropanoid pathway and is the third most abundant constituent of plant cell walls after cellulose and hemicellulose, which makes up roughly 20% of the dry weight of the secondary cell walls in crops, including rice (Vogel 2008). *p*-Coumaroyl-CoA and feruloyl-CoA, collectively called hydroxycinnamoyl-CoA, are intermediates in the phenylpropanoid pathway and serve as the donor for the hydroxycinnamoyl moieties of AX. Monolignol synthesis and hydroxycinnamoyl-CoA synthesis were expected to be up-regulated in the wild-type whole internode and F71 pith parenchyma, respectively, and the expression profiles of genes in the phenylpropanoid pathway were determined. Although many researchers have studied genes in the phenylpropanoid pathway in rice, in many cases only a subset of these genes were targeted, and not all of the genes in this pathway have been identified (Kawasaki et al. 2006; Lee et al. 2007, 2008; Ma 2007; Minami et al. 1989; Tobias and Chow 2005; Zhang et al. 2006; Zhao et al. 2004; Zhu et al. 1995). The list of phenylpropanoid pathway genes in rice and the corresponding probe sets was based on all of these studies and a report on Arabidopsis genes by Raes et al. (2003) (Table S4). The expression pattern of each probe set is shown as a heat map in the major phenylpropanoid pathway (Boerjan et al. 2003) (Figure 3).

Notably, most gene families in the phenylpropanoid pathway have at least one gene that is relatively highly expressed in the wild-type pith parenchyma, suggesting that monolignol biosynthesis is active even in the wild-type pith parenchyma, where little lignin is detected. This is an interesting possibility that will be explored in future work.

Next, changes in the expression of phenylpropanoid pathway genes in the wild-type whole internode that contains cells with thickened secondary cell walls were examined to identify genes that are closely associated with secondary cell wall formation. The expression of several genes involved in monolignol synthesis was significantly changed. Two cinnamoyl-CoA reductase (CCR) genes, LOC_Os01g18110 and LOC_Os01g18120, whose transcripts were the most abundant in the wild-type pith parenchyma, were significantly down-regulated in the wild-type whole internode. In contrast, the expression of a CCR gene, LOC_Os08g34280, was significantly up-regulated. These data suggest that CCR genes expressed during secondary cell wall biosynthesis are different from those expressed in wild-type pith parenchyma cells. It is also important to note that one of the ferulate 5-hydroxylase (F5H) genes, LOC_Os10g36848, was specifically and significantly up-regulated in the wild-type whole internode, whereas three other F5H genes were expressed at very low levels. These results suggest that there are certain sets of enzymes, including CCR and F5H, that are specialized for monolignol synthesis during secondary cell wall formation in rice.

To identify the gene sets that are relevant to hydroxycinnamoyl-AX accumulation in F71 pith parenchyma, we focused on the gene expression profiles involved in hydroxycinnamoyl-CoA synthesis. Genes encoding CCRs were markedly down-regulated, and LOC_Os01g18120 was significantly down-regulated in the F71 pith parenchyma. This expression profile was confirmed by RT-PCR (Figure 2B). In the F71 pith parenchyma, the conversion of hydroxycinnamoyl-CoA into hydroxycinnamaldehyde for monolignol synthesis may be limited by CCR down-regulation; instead, the unconverted hydroxycinnamoyl-CoA might be used for hydroxycinnamoyl-AX synthesis. The hydroxycinnamoyl-CoA that is not used in monolignol biosynthesis has been shown to be redirected for the synthesis of other phenolic compounds, such as sinapoyl



The letters indicate a statistically significant difference compared with wild-type Pa (control);
a, in F71 Pa
b, in wild-type INT
c, in both F71Pa and wild-type INT.

Figure 3. Gene expression leading to *p*-coumaroyl-CoA and feruloyl-CoA biosynthesis. The diagram illustrates the phenylpropanoid pathway according to Boerjan et al. (2003). The data are expressed as a heat map that shows the signal intensities from the microarray analysis: left, wild-type pith parenchyma; middle, F71 pith parenchyma; right, wild-type whole internode. The probes with significant differential expression were identified by one-way ANOVA (FDR <0.01) with Tukey's *post hoc* test. a, b and c indicate a significant difference compared to wild-type pith parenchyma: a, F71 pith parenchyma; b, wild-type whole internode; and c, both the F71 pith parenchyma and wild-type whole internode. The probes and corresponding genes are listed in Table S4.

malate and feruloyl malate, in an Arabidopsis *CCR1*-knockout mutant (Derikvand et al. 2008). The CCR-down-regulated tomato plant accumulates much more soluble phenolic compounds without affecting the total phenolic content (van der Rest et al. 2006). The down-regulation of CCR genes might be one of the main factors that affects hydroxycinnamoyl-AX accumulation in F71.

Major carbon metabolism genes

All polysaccharides that make up the plant cell wall are derived from UDP-D-glucose (UDP-D-Glc) that is provided by starch and sucrose metabolism. Phenylalanine that is used for protein synthesis and secondary metabolites, such as lignin and flavonoids, is provided by the shikimate pathway, which requires two substrates, phospho*enol*pyruvate (PEP) supplied by pyruvate metabolism and erythrose-4-phosphate (E4P) supplied by the pentose phosphate and triose phosphate pools. To determine whether the expression of genes involved in these carbon metabolism pathways is related to the biosynthesis of secondary cell walls and hydroxycinnamoyl-AX, the TIGR database, referred to in the KEGG PATHWAY database (http://www.genome.jp/kegg/pathway.html), was searched for genes that are associated with these pathways. Subsequently, the identified genes were manually verified and are listed with the corresponding probe sets in Table S5. The expression patterns of each probe are shown as a heat map that is referred to in the KEGG PATHWAY database (http://www.genome.jp/kegg/).

First, the gene expression patterns in the whole internode were evaluated to identify genes related to secondary cell wall biosynthesis. Several genes were significantly up-regulated, including the cellulose synthase subunit A (CesA) gene families, UDP-D-Glc 6-dehydrogenase converting UDP-D-Glc to UDP-D-glucuronic acid (UDP-D-GlcA), PEP-CK converting oxaloacetate into PEP, and transketolase converting D-

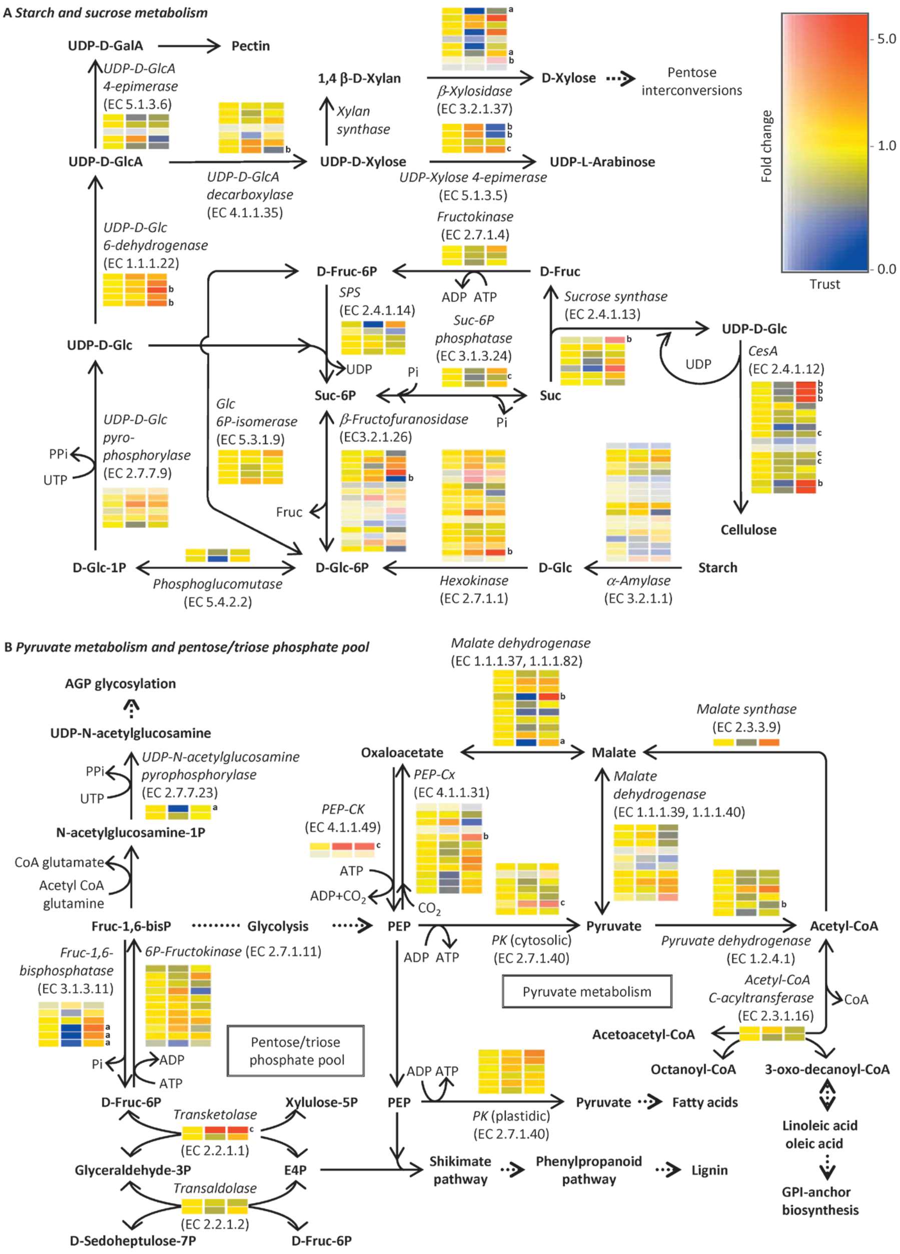


Figure 4. Gene expression in the major carbon flux. (A) Starch and sucrose metabolism; (B) pyruvate metabolism and the pentose/triose phosphate pool. The pathways are described in detail on the KEGG encyclopedia website (http://www.genome.jp/kegg/kegg2.html). The data are expressed as a heat map that shows the signal intensities determined by the microarray analysis: left, wild-type pith parenchyma; middle, F71 pith-parenchyma; right, wild-type whole internode. The probes with significant differential expression were identified by one-way ANOVA (FDR <0.01) with Tukey's *post hoc* test. a, b and c indicate statistically significant differences compared to wild-type pith parenchyma: a, F71 pith parenchyma; b, wild-type whole internode; and c, both the F71 pith parenchyma and wild-type whole internode. The probes and corresponding genes are listed in Table S5.

fructose-6-phosphate (D-Fruc-6P) and glyceraldehyde-3P into xylulose-5P and E4P.

The rice CesA genes were classified into two groups based on previous reports (Richmond and Somerville 2000; Tanaka et al. 2003). In the wild-type whole internode, the putative genes for primary cell wall-specific CesA (*OsCesA1*, LOC_Os05g08370; *OsCesA6*, LOC_Os07g14850; *OsCesA8*, LOC_Os07g10770) were slightly down-regulated, whereas those for secondary cell wall-specific CesA (*OsCesA4*, LOC_Os01g54620; *OsCesA9*, LOC_Os09g25490) were significantly up-regulated. The expression of *OsCesA4* was confirmed by RT-PCR (Figure 2B). These data are consistent with a previous report describing rice *Tos17* mutants lacking OsCesA4 and OsCesA9, which showed a brittle culm phenotype caused by reduced cellulose content and secondary cell wall thickening in the cortical fiber cells (Tanaka et al. 2003).

Because the conversion of UDP-D-Glc to UDP-D-GlcA is essential for hemicellulose synthesis, the significant up-regulation of UDP-D-Glc 6-dehydrogenase genes in the whole internode might contribute to hemicellulose biosynthesis during secondary cell wall formation. The expression of PEP-CK by LOC_Os03g15050 and transketolase by LOC_Os04g19740 was significantly up-regulated in the wild-type whole internode, suggesting that concomitant activation of PEP and E4P synthesis may activate lignification during secondary cell wall formation.

Next, genes that were differentially expressed in the F71 pith parenchyma were evaluated. Most CesA genes were significantly down-regulated, which is consistent with a previous report that the cell walls of F71 pith parenchyma have a 25% reduction in glucose that is presumably derived from cellulose (Nishikubo et al. 2000). Furthermore, β-xylosidase was down-regulated, leading to the accumulation of 1,4-β-D-xylan, and UDP-xylose 4-epimerase was up-regulated, leading to an increase in UDP-L-arabinose in the F71 pith parenchyma, which might be closely associated with the activation of AX synthesis in the F71 pith parenchyma. In addition, LOC_Os03g15050 PEP-CK and LOC_Os04g19740 transketolase expression was significantly up-regulated in the F71 pith parenchyma, which indicates activation of the shikimate pathway and potentially subsequent activation of hydroxycinnamoyl-CoA synthesis.

Genes encoding fructose-1,6-bisphosphatase were down-regulated in the F71 pith parenchyma. These genes were all chloroplast-type, which may reflect the development of fewer chloroplasts in F71 pith parenchyma compared to wild-type pith parenchyma (Figure 1).

Other cell wall-related genes

Several carbohydrate-active enzymes (CAZymes), such as GHs, GTs, polysaccharide lyases, and carbohydrate esterases, as well as some cell wall-related proteins have been shown to be closely involved in secondary cell wall biosynthesis (Andersson-Gunnerås et al. 2006; Demura et al. 2002; Penning et al. 2009; Vogel 2008). The CAZyme genes were examined using the CAZy database (http://www.cazy.org/), which describes families of structurally related catalytic and carbohydrate-binding modules (or functional domains) of enzymes that degrade, modify, or create glycosidic bonds. The EXPANSIN home page (http://www.bio.psu.edu/expansins/) was searched for genes encoding expansins, and the TIGR database was examined for genes encoding other proteins, such as extensins and arabinogalactan proteins. All identified genes were verified manually and are listed with their corresponding probes in Table S6. Of these genes, those with significant differential expression are listed in Table 3.

In addition to three CesA genes in the GT2 family, *CslF* (LOC_Os07g36690) expression was significantly up-regulated only in the wild-type whole internode. Cellulose synthase-like (Csl) genes are divided into eight families, *CslA* to *CslH*; the *CslF* and *CslH* families are unique to grasses, whereas the *CslB* and *CslG* families are unique to dicots (Hazen et al. 2002; Richmond and Somerville 2000). A recent advance in our understanding of the unique biology of grass cell walls was the finding that grass-specific CslF genes are involved in the synthesis of grass cell wall-specific (1,3;1,4)-β-glucan in the primary cell walls of barley, wheat, and rice (Burton et al. 2006, 2008; Nemeth et al. 2010). Therefore, it is interesting and important to elucidate the function of *CslF* (LOC_Os07g36690) in secondary cell wall formation.

AX is the major hemicellulose in both the primary and secondary cell walls of grasses. Although recent studies using Arabidopsis mutants with a defective xylan structure showed that several GT43s and GT47s are specifically involved in the synthesis of the xylan backbone (Brown et al. 2007; Lee et al. 2010; Oikawa et al. 2010; Wu et al. 2010; York and O'Neill 2008). Bioinformatics approaches and mutant analyses suggested that several genes in the GT43, 47, and 61 families are potentially involved in AX synthesis (Anders et al. 2012; Chiniquy et al. 2012, 2013; Mitchell et al. 2007). Mitchell et al. (2007) also suggested that the members of the PF02458 family, which is one of the subclades of benzylalcohol *O*-acetyltransferase (BEAT), anthocyanin *O*-hydroxycinnamoyltransferase (AHCT), anthranilate *N*-hydroxycinnamoyl/benzoyltransferase (HCBT), deacetylvindoline 4-*O*-acetyltransferase (DAT) (BAHD) acyltransferase family, might act as AX hydroxycinnamoyl transferases. In addition, a recent study demonstrated that a BAHD acyltransferase, LOC_Os06g39390, might be a *p*-coumaric acid transferase (Bartley et al. 2013). Although our microarray results showed only a few significant changes in the expression of these gene families in wild-type whole internode and F71 parenchyma compared to wild-type pith parenchyma (Table 3 and Table S6), the expression of LOC_Os02g22480 in the GT61 and LOC_Os06g39390 in a BAHD family was slightly but significantly up-regulated in the F71 pith parenchyma and the wild-type whole internode, respectively (Table S6), suggesting the involvement of these genes in hydroxycinnamoyl-AX biosynthesis in rice internode. However, because a number of other genes in these GT families and BAHD family are expressed at a certain level (Table S6), it is hard to deny the possibility that these genes without any significant expression changes function in the synthesis of secondary cell walls and hydroxycinnamoyl-AX in rice internode.

Genes in the GH17 family encode glucan endo-(1,3)-β-glucosidases or lichenases (Levy et al. 2007;

Table 3. Other cell wall-related genes with significant differential expression (FDR <0.01, more than 4-fold change).

Systematic name	TIGR loci	Annotation	Fold change[a]	
			F71 Pa/ WT Pa	WT INT/ WT Pa
Os.18724.1.S1_a_at	LOC_Os01g54620	GT2 (OsCESA4)	—	7.99
Os.18724.1.S1_at	LOC_Os01g54620	GT2 (OsCESA4)	—	5.17
Os.18724.2.S1_x_at	LOC_Os01g54620	GT2 (OsCESA4)	—	6.96
Os.10206.1.S1_at	LOC_Os09g25490	GT2 (OsCESA9)	—	11.53
Os.52482.1.S1_at	LOC_Os07g36630	GT2 (OsCSLF8)	0.11	0.24
Os.15704.1.S1_at	LOC_Os07g36690	GT2 (OsCSLF2)	—	188.89
Os.48353.1.S1_at	LOC_Os02g51130	GT8	—	5.64
Os.50009.1.S1_at	LOC_Os03g08600	GT8	0.23	—
Os.11323.1.S1_at	LOC_Os03g20120	GT8	—	23.00
Os.11691.1.S1_at	LOC_Os05g35200	GT8	0.17	—
Os.45991.1.S1_x_at	LOC_Os01g10440	GT14	20.48	—
Os.6437.1.S1_at	LOC_Os01g65590	GT31	—	12.01
Os.5255.1.S1_at	LOC_Os05g47880	GT31	—	0.17
Os.51638.1.S1_s_at	LOC_Os09g26310	GT31	—	0.20
Os.6350.1.S1_at	LOC_Os03g05110	GT47	—	0.23
Os.7246.1.S1_s_at	LOC_Os06g27560	GT61	—	0.21
Os.28032.1.A1_at	LOC_Os01g21070	GH9	9.47	—
Os.18421.1.S1_a_at	LOC_Os03g01800	GH16	0.02	—
Os.46631.1.S1_x_at	LOC_Os10g39840	GH16	5.07	—
Os.11465.1.S1_at	LOC_Os11g33270	GH16	5.27	7.70
Os.4159.1.S1_at	LOC_Os01g51570	GH17	230.95	—
Os.53440.1.S1_at	LOC_Os02g33000	GH17	0.20	—
Os.14978.1.S1_a_at	LOC_Os07g35510	GH17	4.67	0.26
Os.7086.1.S1_at	LOC_Os07g35520	GH17	—	142.95
Os.7086.1.S1_s_at	LOC_Os07g35520	GH17	—	217.04
OsAffx.16567.1.S1_at	LOC_Os07g35520	GH17	—	5.90
Os.54847.1.S1_at	LOC_Os08g12800	GH17	—	7.92
OsAffx.31336.1.S1_at	LOC_Os11g36940	GH17	—	61.95
OsAffx.31336.1.S1_x_at	LOC_Os11g36940	GH17	—	10.59
Os.11894.1.S1_at	LOC_Os02g39330	GH19	71.86	—
Os.1191.1.S1_at	LOC_Os03g04060	GH19	271.32	—
Os.47564.1.S1_at	LOC_Os05g33140	GH19	89.56	—
Os.2692.1.S1_x_at	LOC_Os06g51050	GH19	49.80	—
Os.51172.1.S1_x_at	LOC_Os06g51050	GH19	89.11	—
Os.22000.1.S1_at	LOC_Os06g51060	GH19	20.02	—
Os.3415.1.S1_at	LOC_Os10g39680	GH19	48.37	—
Os.54804.1.S1_at	LOC_Os02g03750	GH28	—	39.38
Os.14358.1.S1_at	LOC_Os02g12730	GH35	—	9.17
Os.11983.1.S1_at	LOC_Os03g04110	Receptor-like GPI-anchored protein	—	0.22
Os.37902.1.S1_at	LOC_Os03g30250	BRITTLE CULM 1	—	5.21
Os.49999.1.S1_x_at	LOC_Os03g18910	COBRA-like protein	—	0.09
Os.17961.1.S1_a_at	LOC_Os02g20560	Fasciclin-like arabinogalactan protein	0.04	—
Os.53492.1.S1_at	LOC_Os02g49420	Fasciclin-like arabinogalactan protein	—	23.81
OsAffx.30093.1.S1_at	LOC_Os09g30010	Fasciclin-like arabinogalactan protein	—	10.25
Os.46008.1.S1_at	LOC_Os01g13320	Pectinesterase	—	6.94
Os.37598.1.S1_at	LOC_Os01g20980	Pectinesterase	12.65	—
Os.47330.1.S1_at	LOC_Os02g54190	Pectinesterase	0.16	7.09
Os.51088.1.S1_at	LOC_Os04g05050	Pectate lyase	4.89	8.70
OsAffx.3726.1.S1_at	LOC_Os04g05050	Pectate lyase	4.49	8.44
Os.28773.1.S1_at	LOC_Os01g14650	Alpha-expansin	112.84	—
OsAffx.3144.1.S1_at	LOC_Os03g06010	Alpha-expansin	213.54	—
OsAffx.3144.1.S1_x_at	LOC_Os03g06010	Alpha-expansin	157.72	—
Os.410.1.S1_at	LOC_Os05g19570	Alpha-expansin	—	0.08
Os.54103.1.S1_at	LOC_Os06g41700	Alpha-expansin	0.20	—
Os.2403.1.S1_at	LOC_Os04g46650	Beta-expansin	45.34	—
Os.12234.1.S1_s_at	LOC_Os10g40730	Beta-expansin	13.78	6.83
Os.27244.1.A1_s_at	LOC_Os04g32850	Extensin	—	6.24
Os.54602.1.S1_s_at	LOC_Os04g32850	Extensin	—	9.34
OsAffx.14103.1.S1_x_at	LOC_Os04g32850	Extensin	—	4.85
Os.25734.2.S1_a_at	LOC_Os04g34170	Extensin	689.30	—
OsAffx.28006.1.S1_at	LOC_Os06g39390	PF02458/BAHD	—	19.33

[a] The fold changes were calculated by dividing normalized values for the F71 internode parenchyma (F71 Pa) and those for the wild-type whole internode (WT INT) by those for the wild-type internode parenchyma (WT Pa). Genes that do not meet the criteria are marked as —.

Minic 2008), and two (LOC_Os01g51570 and LOC_Os07g35510) and three (LOC_Os07g35520, LOC_Os08g12800, and LOC_Os11g36940) genes in this family were significantly up-regulated in F71 pith parenchyma and wild-type whole internode, respectively, compared to wild-type pith parenchyma. Many genes in the GH19 family, which putatively encodes chitinase, were up-regulated in the F71 pith parenchyma. Moreover, several genes encoding cell wall-related proteins, such as fasciclin-like arabinogalactan proteins, pectate lyases, expansins, and extensins, were significantly up-regulated in the F71 pith parenchyma and wild-type whole internode. A functional analysis of these genes for GHs and cell wall proteins will provide invaluable information on the fine mechanisms underlying secondary cell wall and hydroxycinnamoyl-AX synthesis.

Conclusion

We identified genes that are potentially powerful candidates that can be used to modify the contents and configurations of lignin and hydroxycinnamoyl-AX in the rice cell wall. Microarray analysis is one of the most powerful tools to comprehensively understand the expression of genes that are associated with certain biological processes, such as cell wall biosynthesis. Because there are only a few reports describing microarray data to comprehensively identify rice genes involved in the formation of the secondary cell wall and hydroxycinnamoyl-AX (Oikawa et al. 2010), the data presented in this paper will help our understanding on cell wall formation in rice. We showed that the up-regulation of a set of genes encoding CesAs (*OsCesA4*, LOC_Os01g54620; *OsCesA9*, LOC_Os09g25490), a CCR (LOC_Os08g34280), an F5H (LOC_Os10g36848), and some CAZymes (*CslF*, LOC_Os07g36690; *GH17*, LOC_Os07g35520, LOC_Os08g12800, and LOC_Os11g36940) is a key event for secondary cell wall formation and that the down-regulation of specific CCR genes is potentially involved in the accumulation of hydroxycinnamoyl-AX in F71 pith parenchyma cells. Further functional analyses on the identified genes will provide insight into the fundamental modifications of cell wall biosynthesis in grass crops.

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Supplementary Table S1. (Nakano et al.)

RT-PCR primers

Description	Loci	Forward primer	Reverse primer	Cycle No.
PR protein	LOC_Os12g36830	5'- ACTGTCACCACCATGAAGCTCAAC -3'	5'- TAATTATCAGGAAGCAGCAATACGG -3'	27
Benzoate carboxyl methyltransferase	LOC_Os05g01140	5'- ATTTGACTTCATTCATCCCATCCTT -3'	5'- GACATTTGTCAAGAGAAAGCCACTC -3'	29
Beta-D-xylosidase	LOC_Os11g19210	5'- ACAACAACATCAGAAGGTGATGAGA -3'	5'- TATGCACCACCTGTAATTCCTTCC -3'	32
NAC	LOC_Os04g43560	5'- GAGGCAGAACGAGATACTCGACAG -3'	5'- GGACGAAATAACTGTATCAATGGAA -3'	28
CCR	LOC_Os01g18120	5'- ATCACCTCCAGATGTAAGGACAACA -3'	5'- CTCCATTCCTTTTCACAATGCATAC -3'	29
CesA4	LOC_Os01g54620	5'- GTGGAGGAGGAAGTGGAAGAGAG -3'	5'- ATCTGTTCTTCAACAGGTGGAGCTT -3'	29
PEP-CK	LOC_Os03g15050	5'- GGAAGGTATCTGCTACTGTCCACTG -3'	5'- TGTATAGCAGAAATGGCATGAACTG -3'	35
UBQ	LOC_Os03g13170	5'- CCAGGACAAGATGATCTGCC -3'	5'- AAGAAGCTGAAGCATCCAGC -3'	24

Supplementary Table S2 (Nakano Y et al.)
Probes with significantly differentially expression in wild type whole internode (FDR < 0.001).

Systematic Name	**TIGR Loci**	**Description**	**WT Pa normalized**	**WT INT normalized**	**Fold Change WT INT/ WT**	**WT Pa raw**	**WT Pa flags**	**WT INT raw**	**WT INT flags**
Os.56337.1.S1_at	LOC_Os11g19210	beta-D-xylosidase	0.93	257.20	276.86	2	A	440	P
OsAffx.13655.1.S1_at	LOC_Os04g04060	Dynamin GTPase effector	0.99	176.80	177.87	3	A	459	P
Os.53254.1.S1_at	LOC_Os06g12210	DNA-binding protein	0.99	166.70	168.90	3	A	509	P
Os.11563.1.S1_at	LOC_Os11g43980	peroxidase	0.81	127.80	157.20	9	A	1256	P
Os.49289.1.S1_x_at	LOC_Os06g21270	glycine-rich cell wall structural protein	0.93	143.10	154.04	5	A	694	P,M
Os.8638.1.S1_at	LOC_Os10g05950	proline-rich protein	0.99	136.70	138.08	34	P,A	4747	P
Os.55437.1.S1_at	LOC_Os03g43770	F-box domain-containing protein	0.88	114.50	130.56	3	A	369	P
Os.6417.1.S1_at	LOC_Os07g37850	expressed protein	0.92	110.20	119.78	43	A	4930	P
Os.16018.1.S1_at	LOC_Os01g63010	universal stress protein family	0.98	111.00	113.03	31	A	3527	P
OsAffx.21591.1.S1_at	LOC_Os01g56660	expressed protein	1.00	111.00	111.22	3	A	286	P
Os.12387.1.S1_at	LOC_Os04g39150	major latex protein	0.95	104.20	109.34	55	M,A	6006	P
Os.20313.1.S1_s_at	LOC_Os01g72290	germin-like protein subfamily	0.86	86.54	100.39	41	P,A	3911	P
Os.37913.1.S1_at	LOC_Os04g31870	expressed protein	0.95	83.34	88.19	3	A	294	P
Os.11398.1.S1_at	LOC_Os10g05980	proline-rich protein	0.98	83.08	85.04	111	P	9416	P
Os.4380.1.S1_at	LOC_Os11g02350, LOC_Os12g02300	nonspecific lipid transfer protein	0.99	79.89	81.11	29	P,A	2379	P
Os.4404.1.S1_s_at	LOC_Os06g01966	nodulin protein	0.96	74.86	78.22	26	P,A	2041	P
Os.4764.1.S1_at	LOC_Os03g08360	3-ketoacyl-CoA synthase	0.91	68.62	75.41	32	P,A	2246	P
Os.30696.1.S1_at	LOC_Os01g10180	unknown protein	0.98	73.71	74.98	29	P,A	2234	P
Os.50672.1.S2_at	LOC_Os02g02140	receptor protein kinase	1.00	64.32	64.51	5	A	312	P
Os.7187.1.S1_at	LOC_Os05g09740	stem 28 kDa glycoprotein precursor	0.99	62.31	63.13	98	P	6341	P
Os.21524.1.S1_at	LOC_Os10g05820	proline-rich protein	0.84	51.86	62.11	228	P	12181	P
OsAffx.27633.1.S1_at	LOC_Os06g14280	secretory protein-like	0.89	53.05	59.81	21	P,A	1148	P
Os.50973.1.S1_at	LOC_Os02g20040	expressed protein	0.91	49.78	54.46	102	P,A	5173	P
OsAffx.31976.1.S1_at	LOC_Os12g32290	expressed protein	0.95	51.25	54.12	2	A	105	P
Os.11510.1.S1_s_at	LOC_Os09g31430	non-cyanogenic beta-glucosidase precursor	0.99	51.41	51.88	49	P,A	2605	P
Os.8061.1.S1_at	LOC_Os01g53240	dehydration-induced protein RD22-like protein 2	0.94	48.03	51.26	38	A	1886	P
Os.56026.1.A1_at	LOC_Os02g50200	secretory protein-like	0.97	49.55	50.87	34	P,M,A	1710	P
Os.12201.1.S1_at	LOC_Os09g27750	1-aminocyclopropane-1-carboxylate oxidase 1	0.97	47.64	49.27	107	P	5407	P
Os.6039.1.S1_at	LOC_Os02g45250	homeobox protein FWA	0.92	45.37	49.21	19	A	876	P
Os.31907.1.S1_x_at	LOC_Os02g46680	multidrug resistance protein 2	0.92	45.24	49.17	6	A	279	P
Os.18511.1.S1_s_at	LOC_Os10g07210	small heat shock protein	0.85	41.37	48.44	130	P	5625	P
Os.11341.1.S1_a_at	LOC_Os10g01134	serine carboxypeptidase 1 precursor	0.97	46.92	48.22	5	A	255	M,A
Os.41164.1.S1_at	LOC_Os01g44390	DNA-binding protein	0.99	45.81	46.18	4	A	186	P
Os.51299.1.S1_at	LOC_Os05g38880	expressed protein	0.96	43.75	45.72	59	P,A	2684	P
Os.6763.1.S1_at	LOC_Os01g48710	metal ion-binding protein	0.99	44.59	45.09	4	A	165	P
Os.10063.1.S1_at	LOC_Os05g14010	expressed protein	0.96	42.84	44.81	54	P	2410	P
Os.27379.1.S1_at	LOC_Os08g44360	male sterility protein 2	0.98	43.94	44.79	38	P,A	1724	P
Os.57314.1.S1_at	Os03g0803200	expressed protein	1.00	43.93	44.06	2	A	109	P
Os.10534.1.S1_at	LOC_Os05g09704	stem 28 kDa glycoprotein precursor	0.98	43.05	43.93	38	A	1668	P
Os.45893.1.S1_at	LOC_Os01g57880	early nodulin-like protein 3 precursor	0.99	42.24	42.84	2	A	96	P
Os.24865.1.A1_at	LOC_Os05g09724	stem 28 kDa glycoprotein precursor	0.96	39.67	41.41	73	P	3117	P
Os.6256.2.S1_at	AK241797	expressed protein	0.99	38.55	39.14	137	P,A	5432	P
Os.12279.2.S1_a_at	LOC_Os01g72009	expressed protein	0.95	35.92	37.89	69	P	2572	P
Os.8437.1.S1_at	LOC_Os06g44610	membrane protein	0.98	36.83	37.43	42	P	1617	P
Os.6845.1.S1_at	LOC_Os10g36160	nonspecific lipid-transfer protein precursor	0.91	33.13	36.57	5	A	169	P,A
OsAffx.27905.1.S1_at	LOC_Os06g32730	eukaryotic initiation factor MIF4G domain	0.95	34.50	36.51	77	P,A	2726	P
Os.54285.1.S1_at	LOC_Os11g43140	expressed protein	0.96	33.89	35.34	52	M,A	1820	P
Os.54857.1.S1_at	LOC_Os02g56750	phloem-specific lectin-like	0.97	30.45	31.52	41	P	1260	P
Os.16014.1.S1_at	LOC_Os04g47860	translation initiation factor IF-2	0.94	29.29	31.13	5	A	155	P
Os.4659.1.S1_at	Os06g0143100	Conserved hypothetical protein	0.99	29.43	29.61	79	P	2437	P
Os.7131.1.S1_at	LOC_Os03g56782	expressed protein	1.00	28.78	28.92	62	P,A	1849	P
Os.37630.1.S1_x_at	LOC_Os04g21320	salicylic acid-induced fragment 1 protein	0.95	27.03	28.60	66	P,A	1858	P
Os.24050.1.S1_at	LOC_Os12g27440	expressed protein	0.97	27.66	28.49	22	P	646	P
Os.4404.1.S1_at	LOC_Os06g01966	nodulin protein	0.95	23.87	25.21	22	P,M	546	P
OsAffx.13702.1.S1_at	LOC_Os04g07050	hypothetical protein	0.95	23.53	24.85	2	A	42	P,A
Os.7609.2.S1_a_at	AK065501	expressed protein	0.95	23.04	24.23	145	P	3517	P
Os.11443.1.S1_a_at	LOC_Os01g65630	expressed protein	0.99	23.73	24.07	10	A	236	P
Os.52419.1.S1_at	LOC_Os06g02000	uridylate kinase	0.94	21.86	23.26	84	P	1910	P
OsAffx.2542.1.S1_at	LOC_Os02g07730	catalytic/hydrolase/phosphoglycolate phosphatase	0.98	22.61	23.12	4	A	96	P
Os.11323.1.S1_at	LOC_Os03g20120	galactinol synthase 3	0.98	22.63	23.00	34	A	811	P
Os.49270.1.S1_at	LOC_Os06g40960	zinc finger protein	0.99	22.53	22.87	21	P,A	493	P
Os.13246.1.S1_at	LOC_Os01g59870	lipid transfer protein	0.92	21.06	22.82	33	P,A	724	P
Os.14520.1.S1_at	LOC_Os03g48030	HPP hypothetical protein	0.96	21.58	22.53	15	P,A	341	P
Os.8862.1.S1_at	LOC_Os09g28510	EF-hand family protein	0.96	20.84	21.78	251	P	5396	P
Os.47560.1.S1_at	LOC_Os12g06660	actin-7	0.97	20.59	21.34	108	P,M,A	2314	P
Os.9277.1.S1_at	LOC_Os11g07680	dirigent-like protein pDIR7	0.96	20.30	21.19	32	P,M	681	P
OsAffx.30108.1.S1_at	LOC_Os09g31370	expressed protein	0.98	20.57	20.95	4	A	90	P
Os.47938.1.S1_at	LOC_Os04g43290	ARPC2B	0.98	20.05	20.50	149	P	3079	P
Os.8482.1.S1_s_at	LOC_Os04g55159	expressed protein	0.86	17.51	20.41	428	P,A	7752	P
Os.6354.1.S1_at	LOC_Os12g02370	chalcone--flavonone isomerase	0.96	19.48	20.29	254	P	5100	P
Os.54952.1.S1_at	LOC_Os09g07290	anther-specific proline-rich protein APG precursor	0.98	19.53	19.95	31	P	614	P
OsAffx.4953.1.S1_at	LOC_Os06g28630	expressed protein	0.96	18.85	19.57	29	P,M	573	P
Os.46584.1.S1_x_at	LOC_Os06g05120	expressed protein	0.99	18.37	18.56	159	P	3101	P
Os.11290.1.S1_at	LOC_Os06g44170	leucoanthocyanidin reductase	1.00	18.21	18.26	1	A	20	P,A
Os.11988.1.S1_at	LOC_Os08g08820	homeobox protein GLABRA2	0.99	18.04	18.15	40	P	747	P
Os.18298.1.S1_at	CT836138	*Oryza sativa* (*indica* cultivar-group) cDNA clone	0.92	16.34	17.68	52	P	881	P
Os.56029.1.S1_at	AK109146	hypothetical protein	0.98	17.28	17.60	40	P	722	P
Os.20378.1.S1_at	LOC_Os05g28830	expressed protein	0.98	17.29	17.59	149	P	2655	P
Os.54734.1.S1_at	LOC_Os06g09220	cytochrome P450 72A1	0.97	16.82	17.34	2	A	42	M,A
Os.41637.1.S1_at	LOC_Os01g50080	multidrug resistance protein 4	0.94	16.27	17.25	175	P	2933	P
Os.13972.1.S1_at	LOC_Os07g44430	peroxiredoxin	0.98	16.69	17.07	49	P,M	839	P
OsAffx.5170.1.S1_at	LOC_Os07g01110	L-ascorbate oxidase precursor	0.98	16.74	17.01	5	A	94	M,A
Os.52978.1.S1_at	LOC_Os08g43654	transparent testa 12 protein	0.98	16.56	16.85	24	A	414	P
Os.46842.1.S1_at	Os10g0466800	expressed protein	0.97	15.77	16.29	74	P	1200	P
Os.24830.1.S1_at	LOC_Os04g08390	Leucine rich repeat family protein	0.98	15.93	16.27	72	P,A	1186	P
Os.50062.1.S1_at	LOC_Os03g21730	receptor-like protein kinase precursor	0.95	14.65	15.36	41	P,A	622	P
Os.57449.1.S1_x_at	LOC_Os11g32650	chalcone synthase	0.96	14.32	14.90	164	P	2407	P
Os.47743.1.S1_at	Os07g0167700	unknown	0.98	14.41	14.73	28	A	426	P
Os.50548.1.S1_at	LOC_Os09g17610	protein-binding protein	0.98	13.83	14.07	55	P	798	P
Os.49192.1.S1_at	LOC_Os12g17530	expressed protein	0.98	13.22	13.55	37	P	506	P
Os.51629.1.S1_at	LOC_Os02g09850	expressed protein	0.99	13.20	13.33	102	P,A	1395	P
Os.12364.1.S1_at	LOC_Os09g28600	expressed protein	0.97	12.56	12.92	310	P	4033	P
Os.38043.1.S1_x_at	Os01g0150900	expressed protein	0.97	12.43	12.88	48	P	622	P
Os.4931.1.S1_s_at	LOC_Os03g18710	expressed protein	0.99	12.58	12.69	31	A	397	P
Os.46457.1.S1_at	LOC_Os10g11980	transferase family protein	0.98	12.42	12.65	29	P,A	375	P
Os.57036.1.S1_at	LOC_Os08g38580	harpin-induced protein	0.96	11.91	12.42	83	P,A	1020	P
Os.50867.1.S1_at	LOC_Os01g52480	senescence-associated protein 12	0.99	12.15	12.34	43	A	541	P
Os.6814.2.S1_s_at	LOC_Os11g01790	catalytic/protein phosphatase type 2C	0.97	11.95	12.27	49	P	611	P
Os.18381.1.S1_at	LOC_Os04g19740	transketolase, chloroplast precursor	0.99	12.15	12.22	75	P	939	P
Os.8507.1.S1_at	LOC_Os09g35800	UDP-glucose 4-epimerase	0.98	11.83	12.12	3	A	32	A
Os.23119.1.S1_at	LOC_Os03g04250	glutathione S-transferase 6	0.99	11.62	11.80	174	P	2137	P
Os.15440.1.S1_at	LOC_Os01g37050	endoribonuclease Dcr-1	0.97	11.08	11.42	33	P,A	373	P
OsAffx.11879.1.S1_at	LOC_Os02g03570	18.3 kDa class I heat shock protein	0.98	11.03	11.30	60	M,A	693	P
Os.46749.1.S1_x_at	LOC_Os09g27990	fiber annexin	0.98	11.03	11.21	30	P,A	346	P
Os.55104.1.S1_at	LOC_Os06g25950	expressed protein	1.00	10.84	10.84	28	P	316	P

Os.35576.1.S1_at	LOC_Os04g58800	ubiquitin-conjugating enzyme spm2	0.98	10.36	10.63	981	P	10494	P
Os.4612.1.S1_at	LOC_Os03g07100	lipid transfer protein	0.97	10.27	10.55	28	A	298	P
Os.50356.1.A1_at	LOC_Os04g38910	atypical receptor-like kinase MARK	0.99	10.42	10.55	195	P	2105	P
Os.21454.1.S1_at	LOC_Os02g04810	auxin response factor 2	0.97	10.20	10.50	126	P	1332	P
Os.47971.1.A1_at	LOC_Os05g49350	expressed protein	0.96	10.00	10.37	197	M,A	2035	P
Os.16582.1.S1_at	LOC_Os07g42910	cytochrome c oxidase subunit	0.97	9.86	10.22	2	A	21	P,A
Os.15900.1.A1_at	LOC_Os06g03220	expressed protein	0.99	9.90	10.01	33	A	340	P
Os.31338.1.S1_at	LOC_Os07g12100	expressed protein	0.98	9.78	9.97	38	M,A	384	P
Os.9784.1.S1_at	LOC_Os01g01520	anthranilate N-benzoyltransferase protein 1	1.00	9.77	9.79	173	P	1745	P
Os.49497.1.S1_at	LOC_Os09g10840	transcription factor HBP-1b	1.00	9.30	9.35	38	P,A	361	P
Os.36919.1.S1_at	LOC_Os01g62010	monoglyceride lipase	0.98	9.15	9.32	94	P	890	P
Os.47982.2.S1_x_at	LOC_Os01g08260	ATPase, coupled to transmembrane movement of substan	1.00	9.24	9.28	83	P	808	P
Os.51071.1.A1_x_at	LOC_Os12g44100	peptide transporter PTR2	0.99	9.17	9.27	23	P,A	215	P
Os.24759.1.A1_at	LOC_Os11g29350	ELMO domain-containing 2	0.98	8.84	9.03	224	P	2060	P
Os.49920.2.S1_at	LOC_Os03g61780	expressed protein	0.96	8.63	8.98	127	P	1141	P
Os.15898.1.S1_at	LOC_Os09g28580	expressed protein	0.99	8.80	8.94	72	P	656	P
Os.20276.1.S1_at	LOC_Os01g07570	carboxyl-terminal proteinase	0.98	8.77	8.92	89	P	811	P
Os.33131.1.A1_at	LOC_Os03g20550	OsWRKY55	1.00	8.86	8.90	5	A	42	A
Os.54942.1.S1_at	LOC_Os09g30411	UBX domain-containing protein	1.00	8.81	8.82	60	P	537	P
Os.8575.1.S1_at	LOC_Os12g08200	expressed protein	0.99	8.73	8.82	137	P	1226	P
Os.20580.1.S1_at	LOC_Os02g55870	heparanase-like protein 3 precursor	0.96	8.37	8.72	152	P	1315	P
Os.9727.1.S1_at	LOC_Os10g36848	cytochrome P450 84A1	1.00	8.50	8.55	163	A	1440	P
Os.25325.1.A1_at	LOC_Os06g49200	CUE domain-containing protein	1.00	8.24	8.28	211	P	1786	P
Os.41468.1.S1_at	LOC_Os01g47050	F-box domain-containing protein	0.97	7.90	8.11	28	A	225	P
Os.16030.1.S1_at	AK107816	expressed protein	0.99	8.01	8.06	87	P	715	P
Os.9420.1.S1_at	LOC_Os07g15370	metal transporter Nramp6	0.99	7.98	8.06	295	P	2471	P
Os.49545.1.S1_at	LOC_Os11g32030	sex determination protein tasselseed-2	0.99	7.99	8.05	320	P	2648	P
Os.46743.3.S1_a_at	LOC_Os03g53660	putative unconventional myosin	0.99	7.90	7.99	83	P	680	P
Os.27509.1.S1_at	LOC_Os01g53790	expressed protein	0.98	7.63	7.79	92	P,M	728	P
Os.52854.1.S1_at	LOC_Os07g28480	glutathione S-transferase	0.98	7.56	7.74	36	P,M	282	P
Os.46589.1.S1_at	LOC_Os10g17790	remorin, C-terminal region family protein	0.98	7.51	7.68	34	P,M,A	267	P
OsAffx.14250.1.S1_at	LOC_Os04g43060	enzyme of the cupin superfamily	0.99	7.38	7.44	78	P,A	589	P
OsAffx.23844.1.S1_s_at	LOC_Os01g58760	DNA-binding protein	0.99	7.28	7.35	21	A	156	P
Os.27615.1.S1_at	LOC_Os03g11734	antiporter/drug transporter	0.98	7.18	7.34	369	P	2727	P
Os.53950.1.S1_at	LOC_Os05g48850	NAC domain containing protein	0.99	7.23	7.28	448	P	3399	P
OsAffx.31975.1.S1_at	LOC_Os12g32260	expressed protein	0.97	7.02	7.23	99	P	722	P
Os.23482.1.S1_at	LOC_Os08g19420	O-methyltransferase ZRP4	0.99	7.07	7.12	383	P	2772	P
Os.47330.1.S1_at	LOC_Os02g54190	pectinesterase-2 precursor	0.97	6.86	7.09	256	P	1838	P
Os.5091.1.S1_at	LOC_Os08g44750	nodulin-like protein 5NG4	0.98	6.87	6.99	658	P	4667	P
OsAffx.24785.1.S1_at	LOC_Os02g48570	peptide transporter PTR2	0.99	6.91	6.95	97	P,M	697	P
Os.46008.1.S1_at	LOC_Os01g13320	pectinesterase-2 precursor	1.00	6.94	6.94	32	P,A	225	P
Os.12234.1.S1_s_at	LOC_Os10g40730	beta-expansin 1a precursor	0.97	6.65	6.83	817	P	5622	P
Os.6539.1.S1_at	LOC_Os04g44670	AP2 domain-containing protein	1.00	6.34	6.36	32	P,A	206	P
Os.27536.1.A1_at	LOC_Os03g07920	expressed protein	1.00	6.32	6.35	347	P	2269	P
OsAffx.29776.1.S1_x_at	LOC_Os09g09370	protein-binding protein	1.00	6.21	6.22	61	P,M,A	387	P
Os.17522.1.S1_s_at	LOC_Os10g37290	expressed protein	0.98	5.91	6.05	336	P	2053	P
Os.52552.1.S1_at	LOC_Os06g22390	expressed protein	0.99	5.95	5.99	39	P,M,A	241	P
Os.46541.2.S1_s_at	LOC_Os10g28030	acylamino-acid-releasing enzyme	0.97	5.60	5.76	161	P	934	P
Os.55701.1.S1_at	LOC_Os12g09220	expressed protein	1.00	5.55	5.56	85	P	483	P
OsAffx.2268.1.S1_at	LOC_Os01g47820	S-locus-like receptor protein kinase	0.99	5.47	5.50	42	P	238	P
OsAffx.13195.1.S1_at	LOC_Os03g36080	expressed protein	1.00	5.47	5.49	616	P	3504	P
Os.48704.1.S1_at	LOC_Os05g51190	ATP-binding protein	0.94	5.14	5.48	318	P	1708	P
Os.48975.1.S1_at	LOC_Os05g40200	ATP-binding protein	1.00	5.33	5.35	177	P	984	P
Os.49098.1.S1_x_at	LOC_Os02g21090	expressed protein	1.00	5.23	5.25	81	A	437	P
Os.14938.1.S1_at	LOC_Os05g01140	benzoate carboxyl methyltransferase	0.99	5.14	5.21	481	P	2581	P
Os.55572.1.S1_at	LOC_Os11g19490	protein kinase domain-containing protein	0.97	4.98	5.13	103	P	530	P
Os.36919.1.S1_x_at	LOC_Os01g62010	monoglyceride lipase	1.00	5.11	5.11	103	P	542	P
Os.55094.1.S1_at	AK107479	expressed protein	1.00	5.07	5.07	155	P	819	P
Os.31545.1.S1_at	LOC_Os07g46560	ubiquitin ligase SINAT5	1.00	4.96	4.98	42	P,A	216	P
Os.1307.1.S1_a_at	LOC_Os11g05190	phytosulfokines 2 precursor	0.99	4.91	4.95	100	P,A	508	P
Os.27183.1.S1_at	LOC_Os06g07100	RING-H2 finger protein ATL5I	1.00	4.94	4.94	107	P	543	P
Os.16113.1.S1_s_at	LOC_Os03g21870	plant-specific domain TIGR01568 family protein	0.99	4.80	4.87	97	P	477	P
Os.27178.1.S1_s_at	LOC_Os04g54474	transcription factor TGA4	1.00	4.71	4.73	1767	P	8537	P
Os.56287.1.S1_at	LOC_Os04g46470	dioxygenase	0.98	4.63	4.72	86	P,A	411	P
Os.4863.1.S1_at	LOC_Os01g44050	siroheme synthase	0.99	4.63	4.67	345	P	1646	P
Os.17560.1.A1_at	LOC_Os07g36800	expressed protein	0.99	4.60	4.66	32	A	152	P
Os.55256.1.S1_at	Os10g0467000	expressed protein	1.00	4.43	4.45	81	A	369	P
Os.12520.1.S1_a_at	LOC_Os02g32814	heavy metal-associated domain-containing protein	0.98	4.17	4.25	597	P	2568	P
Os.35335.1.A1_s_at	LOC_Os04g54800	shikimate kinase, chloroplast precursor	1.00	4.23	4.24	2153	P	9368	P
Os.34312.1.S1_at	LOC_Os07g12470	expressed protein	1.00	4.10	4.11	217	P	914	P
Os.26349.1.S1_at	LOC_Os04g44590	expressed protein	1.00	4.03	4.04	254	P	1053	P
Os.18714.1.S1_a_at	LOC_Os10g14920	nodulin-like protein	0.99	3.98	4.01	199	P	814	P
Os.18057.1.A1_at	LOC_Os02g50640	microtubule-associated protein	0.99	3.94	3.99	1010	P	4074	P
Os.27274.1.S1_at	LOC_Os03g53050	WRKY	0.99	3.89	3.92	712	P	2851	P
Os.10107.1.S1_at	LOC_Os04g58700	ATP-binding protein	0.99	3.84	3.88	230	P	913	P
Os.52488.1.S1_at	LOC_Os06g18990	cadmium tolerance factor	0.99	3.85	3.88	52	P,A	206	P
Os.27817.1.A1_at	LOC_Os05g11510	salt tolerance-like protein	0.99	3.83	3.87	123	P	482	P
Os.49428.1.S1_at	LOC_Os01g67770	two-component response regulator ARR11	0.99	3.73	3.78	500	P	1919	P
Os.6367.2.S1_x_at	LOC_Os01g48060	auxin response factor 3	0.99	3.72	3.76	252	P	966	P
Os.19187.1.S1_at	LOC_Os02g10470	calcium ion-binding protein	0.99	3.61	3.63	147	P	545	P
Os.10760.1.S1_at	LOC_Os01g62110	expressed protein	1.00	3.62	3.62	18	A	68	P
Os.21823.1.S1_at	LOC_Os03g27960	vacuolar cation/proton exchanger 2	1.00	3.56	3.57	143	P	520	P
Os.54142.1.S1_at	LOC_Os12g41350	HORMA domain-containing protein	1.00	3.52	3.53	22	P,A	81	P
Os.38638.2.S1_at	LOC_Os06g04950	early nodulin 93	1.00	3.47	3.47	92	A	327	P
Os.20614.1.S1_at	LOC_Os10g41838	F-box protein interaction domain-containing protein	1.00	3.44	3.46	381	P	1348	P
Os.50118.1.S1_a_at	LOC_Os03g03860	expressed protein	1.00	3.42	3.42	52	P,A	184	P
Os.53419.1.S1_at	LOC_Os02g43840	EREBP-4-like protein	1.00	3.33	3.34	72	P	248	P
Os.20521.1.S1_at	LOC_Os03g54040	50S ribosomal protein L6	0.99	3.25	3.27	170	P	566	P
OsAffx.3061.1.S1_x_at	LOC_Os02g54030	endo-polygalacturonase precursor	1.00	3.27	3.27	431	P	1464	P
Os.46866.2.S1_at	Os10g0540200	expressed protein	1.00	3.24	3.26	98	P	330	P
Os.50271.1.S1_at	LOC_Os06g05359	NBS-LRR disease resistance protein	0.98	3.19	3.25	389	P	1279	P
Os.24816.1.A1_at	LOC_Os04g33660	carbonic anhydrase precursor	0.99	3.19	3.23	83	P	274	P
Os.56229.1.S1_at	LOC_Os11g04330	kelch motif family protein	1.00	3.17	3.18	266	P	869	P
OsAffx.15772.1.S1_at	LOC_Os06g36310	receptor-like protein kinase 5 precursor	1.00	3.16	3.17	86	A	279	P
Os.27224.2.A1_at	Os08g0460600	expressed protein	1.00	3.14	3.15	219	P	708	P
Os.54269.1.S1_s_at	LOC_Os05g48060	phosphatidylserine synthase 2	1.00	3.12	3.12	221	P	709	P
Os.8586.1.S1_at	LOC_Os03g57780	ATP-binding protein	1.00	3.06	3.06	147	P,M,A	462	P
Os.4698.1.S1_at	LOC_Os01g70770	glutathione S-transferase III	1.00	2.91	2.92	187	P	560	P
Os.7707.1.S1_at	LOC_Os04g54320	expressed protein	0.99	2.76	2.80	659	P	1878	P
Os.6367.1.S1_at	LOC_Os01g48060	auxin response factor 3	0.99	2.74	2.77	1571	P	4435	P
Os.8469.1.S1_at	LOC_Os09g34140	expressed protein	0.99	2.72	2.76	967	P	2713	P
OsAffx.23903.2.S1_s_at	LOC_Os01g63490, LOC_Os02g04860	hypothetical protein	1.00	2.72	2.73	77	P	216	P
Os.5012.1.S1_at	LOC_Os01g40860	retinal dehydrogenase 1	0.98	2.62	2.68	100	P	267	P
Os.7948.1.S1_a_at	LOC_Os01g17150	50S ribosomal protein L40, chloroplast precursor	0.99	2.64	2.67	330	P	902	P
Os.25444.1.S1_at	LOC_Os02g54030	endo-polygalacturonase precursor	1.00	2.62	2.63	797	P	2160	P
OsAffx.27525.1.S1_at	LOC_Os06g09340	pectinesterase U1 precursor	1.00	2.59	2.59	160	P,A	430	P
OsAffx.12287.1.S1_s_at	LOC_Os02g01130, LOC_Os02g30330	expressed protein	0.99	2.57	2.58	276	P	729	P
Os.17148.1.A1_at	LOC_Os03g64320	expressed protein	1.00	2.58	2.58	2803	P	7431	P

Os.8604.1.S1_a_at	LOC_Os11g47730	expressed protein	1.00	2.54	2.55	394	P	1030	P
Os.32447.1.S1_at	LOC_Os01g59080	expressed protein	1.00	2.46	2.47	613	P	1546	P
Os.37097.1.S1_at	LOC_Os07g46570	electron transporter	1.00	2.40	2.41	2002	P	4953	P
OsAffx.27459.2.S1_s_at	LOC_Os06g05000	early nodulin 93	0.99	2.31	2.33	407	P	968	P
Os.20144.1.S1_a_at	LOC_Os01g70400	expressed protein	1.00	2.30	2.30	308	P	731	P
Os.18494.1.S1_at	LOC_Os07g05110	nutrient reservoir	1.00	2.29	2.30	78	P	182	P
Os.47590.1.A1_s_at	LOC_Os05g39080	ATP-binding protein	0.99	2.12	2.14	1276	P	2777	P
Os.5753.1.S1_x_at	LOC_Os04g56060	BRASSINOSTEROID INSENSITIVE 1-associated receptor	0.99	2.12	2.13	530	P	1150	P
Os.51848.1.S1_x_at	LOC_Os10g31330	glycine-rich cell wall structural protein 2 precursor	0.99	2.11	2.12	3429	P	7451	P
Os.165.1.S1_at	LOC_Os12g36880	pathogenesis-related protein 10	1.00	2.12	2.12	32	A	70	P,M
Os.20642.1.S1_at	LOC_Os02g08540	expressed protein	1.00	1.99	1.99	177	P	362	P
Os.27914.1.S1_at	LOC_Os08g02390	ribonucleoprotein, chloroplast precursor	1.00	1.99	1.99	216	P	441	P
Os.5261.1.S1_a_at	LOC_Os03g20100	30S ribosomal protein S1, chloroplast precursor	1.00	1.97	1.97	883	P	1788	P
Os.2230.1.S1_at	LOC_Os02g50960	auxin efflux carrier component 1	1.00	1.92	1.93	1295	P	2546	P
Os.24548.1.A1_at	LOC_Os02g07480	transglycosylase SLT domain-containing protein	1.00	1.83	1.83	580	P	1092	P
Os.50976.1.S1_at	LOC_Os03g48040	ferredoxin-6, chloroplast precursor	1.00	1.82	1.83	1237	P	2305	P
Os.36566.2.S1_at	LOC_Os01g13660	expressed protein	0.99	1.80	1.81	1076	P	1994	P
Os.2152.1.S1_at	LOC_Os01g54550	heat shock factor	1.00	1.81	1.81	408	P	759	P
OsAffx.23954.1.S1_at	LOC_Os01g67300	hypothetical protein	1.00	1.75	1.75	56	P	102	P
Os.15711.1.S1_at	LOC_Os09g28310	bZIP transcription factor	1.00	1.65	1.65	1650	P	2793	P
Os.15764.1.S1_at	LOC_Os03g26450	F-actin capping protein beta subunit	1.00	1.63	1.63	1172	P	1966	P
Os.14529.1.S1_x_at	LOC_Os02g58790	expressed protein	1.00	1.63	1.63	295	P	494	P
Os.7689.1.S1_a_at	LOC_Os01g73230	syntaxin-6	1.00	1.61	1.62	1041	P	1726	P
Os.24768.1.S1_x_at	LOC_Os04g54640	expressed protein	1.00	1.61	1.61	756	P	1247	P
Os.27489.1.A1_at	LOC_Os01g11120	CID11	1.00	1.59	1.59	1070	P	1752	P
Os.17692.1.S1_at	LOC_Os10g35140	permeases of the drug/metabolite transporter	1.00	1.57	1.57	853	P	1380	P
Os.53778.1.A1_s_at	LOC_Os12g29990	O-sialoglycoprotein endopeptidase	1.00	1.44	1.44	1502	P	2217	P
Os.534.2.S1_x_at	LOC_Os01g05800	inner membrane protein ALBINO3, chloroplast precursor	1.00	1.43	1.43	4296	P	6296	P
Os.49239.1.S1_at	LOC_Os05g32390	dynamin family protein	1.00	1.41	1.41	519	P	751	P
Os.23161.2.S1_x_at	LOC_Os08g33380	threonine endopeptidase	1.00	1.31	1.31	2106	P	2840	P
Os.7300.1.S1_at	LOC_Os03g57100	serologically defined breast cancer antigen NY-BR-84	1.00	0.86	0.86	8390	P	7403	P
Os.6828.1.S1_at	LOC_Os03g59220	ubiquinol-cytochrome c reductase complex 14 kDa protein	1.00	0.73	0.73	5123	P	3848	P
Os.7237.1.S1_a_at	LOC_Os03g54200	expressed protein	1.00	0.72	0.72	2424	P	1803	P
Os.48055.1.S1_at	LOC_Os03g08450	eukaryotic translation initiation factor 3 subunit 12	1.00	0.70	0.70	5425	P	3877	P
Os.25587.1.S1_s_at	LOC_Os04g57320	IMMUTANTS protein	1.00	0.69	0.69	800	P	565	P
Os.5282.1.S1_at	LOC_Os03g10340	40S ribosomal protein S3a	1.00	0.63	0.63	2928	P	1885	P
Os.3905.1.S1_at	LOC_Os03g52750	cyclin-H	1.00	0.63	0.63	1325	P	853	P
Os.9707.1.S1_at	LOC_Os04g01250	glutamyl-tRNA	1.00	0.62	0.62	4690	P	2968	P
Os.15792.1.S1_at	LOC_Os06g08470	expressed protein	1.00	0.61	0.61	2629	P	1640	P
Os.12818.1.S1_at	LOC_Os03g27460	heat shock protein-binding protein	1.00	0.59	0.59	5082	P	3094	P
Os.7.1.S1_a_at	LOC_Os06g04290	40S ribosomal protein S20	1.00	0.59	0.59	4217	P	2537	P
Os.53565.1.A1_x_at	LOC_Os03g22400	sentrin-specific protease 2	1.00	0.58	0.58	2277	P	1358	P
Os.35186.1.S1_x_at	LOC_Os03g22400	sentrin-specific protease 2	1.00	0.58	0.58	2398	P	1423	P
Os.7152.1.S1_at	LOC_Os06g44910	OsGrx_C4 - glutaredoxin subgroup I	1.00	0.56	0.56	4583	P	2654	P
Os.18524.2.S1_at	AK066383	expressed protein	1.00	0.56	0.56	2987	P	1719	P
Os.33229.1.S1_at	LOC_Os06g06450	heat shock protein STI	1.00	0.53	0.53	33	P,A	18	A
Os.4654.1.S1_at	LOC_Os01g16510	expressed protein	1.00	0.53	0.53	3969	P	2152	P
Os.16051.1.S1_at	LOC_Os11g10780	ulp1 protease family protein	1.00	0.53	0.53	703	P	381	P
Os.50556.1.S1_at	LOC_Os12g07280	TRANSPARENT TESTA 1 protein	1.00	0.52	0.52	3972	P	2132	P
Os.10985.1.S1_at	LOC_Os11g09280	*Oryza sativa* protein disulfide isomerase	1.00	0.52	0.52	5508	P	2951	P
Os.20026.1.S1_at	LOC_Os09g06740	protein-binding protein	1.00	0.51	0.51	184	P	96	P
Os.51695.1.S1_at	LOC_Os06g04360	expressed protein	1.00	0.51	0.51	303	P	159	P
Os.17528.2.A1_a_at	LOC_Os03g10500	adenylyl-sulfate kinase, chloroplast precursor	1.00	0.50	0.50	6795	P	3482	P
Os.50956.1.S1_at	LOC_Os03g27040	copper-transporting ATPase PAA1	1.00	0.49	0.49	422	P	213	P
Os.54097.1.A1_at	LOC_Os02g15270	tyrosine-protein phosphatase YVH1	1.00	0.49	0.49	271	P	136	P
Os.53765.1.S1_at	LOC_Os03g46610	ATP-dependent RNA helicase DDX47	1.00	0.49	0.49	1279	P	643	P
Os.47947.1.A1_at	LOC_Os08g37390	cyclin delta-2	1.00	0.47	0.47	244	P	119	P
Os.52020.1.S1_at	LOC_Os11g12010	expressed protein	0.99	0.45	0.46	468	P	218	P
Os.26858.1.S1_at	LOC_Os02g38840	glucose-6-phosphate 1-dehydrogenase, cytoplasmic isofor	1.00	0.45	0.45	552	P	254	P
AFFX-Os_Cyph_3_at	None		1.00	0.44	0.44	908	P	408	P
Os.8125.1.S1_x_at	LOC_Os03g11590	expressed protein	1.00	0.44	0.44	7243	P	3234	P
Os.15831.3.S1_x_at	LOC_Os08g40560	expressed protein	1.00	0.43	0.43	971	P	433	P
Os.18198.1.S1_at	LOC_Os03g18410	DNA-directed RNA polymerase I 40 kDa polypeptide	1.00	0.43	0.43	469	P	209	P
OsAffx.18556.1.S1_at	LOC_Os10g37490	mating-type switching protein swi10	1.00	0.43	0.43	335	P	148	P
Os.17568.1.S1_at	LOC_Os02g45054	INDETERMINATE-related protein 9	1.00	0.43	0.43	598	P	264	P
Os.54810.1.A1_at	Os08g0368000	expressed protein	1.00	0.43	0.43	650	P	286	P
Os.4918.1.S1_at	LOC_Os07g05700	expressed protein	0.99	0.42	0.42	2376	P	1014	P
Os.16142.1.S1_at	LOC_Os03g31510	cystatin	0.99	0.41	0.41	3580	P	1501	P
Os.4636.1.S2_at	LOC_Os01g64170	glucan endo-1,3-beta-glucosidase 7 precursor	1.00	0.39	0.39	13158	P	5321	P
Os.51616.1.S1_at	Os03g0272900	expressed protein	1.00	0.38	0.38	3201	P	1234	P
Os.50428.1.S1_at	LOC_Os04g11820	ABC transporter-like protein	1.00	0.37	0.37	343	P	131	P
OsAffx.13522.1.S1_at	LOC_Os03g57320	expressed protein	1.00	0.37	0.37	1550	P	583	P
Os.7607.1.S1_at	LOC_Os07g47480	copper chaperone	1.00	0.36	0.36	6994	P	2601	P
Os.14143.1.S1_at	LOC_Os11g07500	helicase C6F12.16c	1.00	0.36	0.36	1117	P	413	P
Os.18948.1.S1_at	LOC_Os02g04840	GHMP kinase-like protein	1.00	0.36	0.36	987	P	365	P
OsAffx.6495.1.S1_s_at	LOC_Os09g36830	SKP1-like protein 1B	1.00	0.35	0.35	1231	P	449	P
Os.49812.1.S1_at	LOC_Os01g33110	receptor-like protein kinase 5 precursor	1.00	0.34	0.34	191	P	68	P
Os.27603.1.S1_at	LOC_Os01g25386	multidrug resistance-associated protein 4	0.99	0.34	0.34	648	P	224	P
Os.26767.1.A1_at	LOC_Os11g28104	protein kinase	0.99	0.34	0.34	7162	P	2468	P
OsAffx.3994.1.S1_at	LOC_Os04g34250	serine/threonine-protein kinase receptor precursor	1.00	0.33	0.33	10350	P	3553	P
Os.9454.1.S1_at	LOC_Os11g32780	expressed protein	0.98	0.33	0.33	2662	P	898	P
Os.46662.2.S1_s_at	LOC_Os10g34220, LOC_Os11g28104	expressed protein	1.00	0.33	0.33	1839	P	624	P
Os.20079.1.S1_s_at	LOC_Os11g25160	short chain alcohol dehydrogenase	1.00	0.33	0.33	5507	P	1861	P
Os.6360.2.S1_x_at	LOC_Os08g02996	lectin-like receptor kinase 1	0.99	0.33	0.33	2152	P	725	P
Os.36023.1.S1_at	LOC_Os07g02360	expressed protein	0.99	0.33	0.33	475	P	160	P
Os.6411.1.S1_a_at	LOC_Os07g42260	proteasome subunit alpha type 6	0.99	0.32	0.33	434	P	144	P
Os.22967.1.S1_s_at	LOC_Os03g02070	metal ion-binding protein	1.00	0.32	0.32	4470	P	1482	P
Os.18692.1.S1_at	LOC_Os02g43290	protein kinase APK1A, chloroplast precursor	1.00	0.31	0.31	4094	P	1292	P
Os.15175.1.S1_at	LOC_Os04g31030	nitrate-induced NOI protein	1.00	0.31	0.31	1371	P	432	P
Os.19978.1.S1_at	LOC_Os07g35580	putative serine/threonine kinase protein	1.00	0.30	0.30	1271	P	386	P
OsAffx.30966.4.S1_x_at	LOC_Os07g46060	expressed protein	1.00	0.29	0.29	348	P	106	P
Os.20364.1.S1_at	LOC_Os05g39240	ammonium transporter 2	1.00	0.29	0.29	383	P	116	P
OsAffx.30680.1.S1_at	CT835750	expressed protein	0.99	0.28	0.28	1305	P	377	P
Os.9778.1.S1_at	LOC_Os07g45570	expressed protein	0.99	0.28	0.28	110	P	32	P,A
Os.15904.1.S1_at	LOC_Os01g56880	purple acid phosphatase precursor	1.00	0.28	0.28	2968	P	849	P
Os.51343.1.S1_at	LOC_Os03g10740	expressed protein	0.98	0.27	0.27	936	P	257	P
Os.9778.1.S2_at	LOC_Os07g45570	expressed protein	1.00	0.27	0.27	3095	P	855	P
OsAffx.7301.1.S1_at	LOC_Os11g35410	expressed protein	1.00	0.26	0.26	345	P	92	P
Os.14530.2.S1_x_at	LOC_Os09g36880	anther-specific proline-rich protein APG precursor	1.00	0.25	0.25	3180	P	829	P
Os.5429.1.S1_at	LOC_Os11g40970	Leucine rich repeat family protein	0.97	0.24	0.25	320	P	80	A
OsAffx.23914.1.S1_at	LOC_Os01g64410	plant-specific domain TIGR01568 family protein	1.00	0.24	0.24	2819	P	704	P
Os.20614.2.S1_at	LOC_Os04g49757	purine transporter	0.99	0.24	0.24	426	P	107	P
Os.7322.1.S1_at	LOC_Os10g22730	expressed protein	1.00	0.24	0.24	3393	P	839	P
Os.3388.2.S1_a_at	LOC_Os04g43680	myb-related protein Myb4	0.99	0.23	0.24	3358	P	806	P
Os.52259.1.S1_at	LOC_Os11g01590	major facilitator superfamily protein	0.99	0.23	0.24	586	P	141	P
Os.53275.1.S1_at	LOC_Os05g08420	expressed protein	1.00	0.23	0.23	5543	P	1326	P
Os.11983.1.S1_at	LOC_Os03g04110	receptor-like GPI-anchored protein 2	0.98	0.22	0.22	2217	P	502	P
Os.7246.1.S1_s_at	LOC_Os06g27560	HGA4	0.99	0.21	0.21	4931	P	1043	P
Os.49803.1.S1_at	LOC_Os07g35690	putative serine/threonine kinase protein	1.00	0.20	0.20	555	P	118	P

Os.50390.1.S1_at	LOC_Os05g30280	cyanogenic beta-glucosidase precursor	1.00	0.20	0.20	1111	P	223	P
Os.15708.1.S1_a_at	LOC_Os04g38720	NAC domain containing protein	0.99	0.19	0.19	1948	P	387	P
Os.27388.1.S1_s_at	LOC_Os10g01470	homeobox-leucine zipper protein HAT22	0.99	0.19	0.19	5999	P	1156	P
OsAffx.32171.3.S1_at	LOC_Os12g43490	alpha-amylase/trypsin inhibitor	0.98	0.19	0.19	482	P	92	P
Os.20292.1.S1_at	LOC_Os04g49748	purine transporter	1.00	0.19	0.19	2629	P	513	P
Os.20278.1.S1_at	LOC_Os06g46330	serine/threonine-protein kinase receptor precursor	1.00	0.18	0.18	1861	P	352	P
Os.20717.1.S1_at	LOC_Os01g61460	expressed protein	1.00	0.18	0.18	752	P	140	P
OsAffx.3365.1.S1_s_at	LOC_Os03g29740	small nuclear ribonucleoprotein G	0.98	0.17	0.18	4063	P	730	P
Os.51029.1.S1_at	LOC_Os09g02770	PE-PGRS family protein	0.98	0.17	0.18	550	P	99	P
Os.28433.4.A1_at	LOC_Os01g58290	cucumisin precursor	0.97	0.17	0.17	552	P	96	P
Os.9556.1.S1_at	LOC_Os12g44060	nitrate and chloride transporter	0.99	0.17	0.17	622	P	109	P
Os.35827.1.S1_at	LOC_Os01g14510	receptor-like protein kinase	0.99	0.17	0.17	1814	P	317	P
OsAffx.3180.1.S1_at	LOC_Os03g09940	low affinity sulphate transporter 3	1.00	0.17	0.17	3098	P	537	P
Os.9416.1.S1_at	LOC_Os02g33110	beta-fructofuranosidase	1.00	0.16	0.16	1608	P	257	P
Os.54708.1.S1_at	LOC_Os05g05180	indole-3-acetic acid-amido synthetase GH3.6	0.99	0.15	0.15	342	P,A	54	A
OsAffx.9749.1.S1_at	LOC_Os01g72760	cytochrome P450 71D10	1.00	0.15	0.15	8468	P	1348	P
Os.8940.1.S1_at	LOC_Os06g12030	electron transporter	1.00	0.14	0.14	710	P	104	P
Os.7268.1.S1_at	AK111542	Protein kinase domain-containing protein	0.99	0.13	0.13	569	P	77	P
Os.12654.1.S1_at	LOC_Os09g39930	serine/threonine-protein kinase NAK	1.00	0.13	0.13	851	P	119	P
Os.15426.1.S1_at	LOC_Os07g35370	Serine/threonine-specific protein kinase	1.00	0.13	0.13	2022	P	275	P
Os.49577.1.S1_at	LOC_Os02g50340	MAC/Perforin domain-containing protein	0.98	0.12	0.13	615	P	79	A
Os.55488.1.S1_at	LOC_Os08g28790	Disease resistance response protein-like	0.99	0.12	0.12	4399	P	555	P
Os.23103.1.S1_at	LOC_Os05g41780	ethylene-responsive transcription factor 4	0.99	0.11	0.12	6468	P	762	P
Os.27915.1.S1_at	LOC_Os02g04130	expressed protein	0.98	0.11	0.11	839	P	97	P
OsAffx.7733.1.S1_at	LOC_Os12g29330	NAC domain-containing protein	0.99	0.11	0.11	1132	P	126	P
Os.37565.1.S1_at	AK063697	unknown protein	1.00	0.11	0.105	1178	P	130	P
OsAffx.22181.1.S1_s_at	LOC_Os01g17050	VQ domain-containing protein	0.99	0.10	0.102	5901	P	618	P
Os.46160.2.S1_x_at	LOC_Os10g30790	inorganic phosphate transporter 1-4	0.99	0.10	0.097	6422	P	641	P
Os.56294.1.S1_at	LOC_Os11g36400	expressed protein	0.97	0.09	0.096	24	A	2	A
Os.7028.1.S1_at	LOC_Os02g45710	RING zinc finger protein-like	0.96	0.09	0.095	2586	P	244	P
Os.50598.1.S1_at	LOC_Os12g03370	harpin-induced protein	0.98	0.09	0.095	217	P	21	P,A
Os.14444.1.S1_at	LOC_Os10g38700	glutathione S-transferase	0.99	0.09	0.095	735	P	71	P
Os.5860.1.S1_at	LOC_Os03g04310	BHLH transcription factor	0.99	0.09	0.089	2284	P	207	P,A
OsAffx.27508.7.S1_s_at	LOC_Os11g44380	expressed protein	1.00	0.09	0.087	5777	P	535	P
OsAffx.14373.1.S1_s_at	LOC_Os04g52090	ethylene-responsive transcription factor	0.99	0.07	0.067	7702	P	528	P
Os.20420.1.S1_at	LOC_Os01g18120	cinnamoyl-CoA reductase	0.99	0.07	0.067	8121	P	557	P
Os.36651.1.S1_at	LOC_Os04g43560	NAC domain-containing protein	0.97	0.05	0.050	3757	P	187	P
Os.12240.1.S1_at	LOC_Os02g52010	phosphate-induced protein	0.99	0.03	0.029	2278	P	69	P
Os.3808.4.S1_x_at	LOC_Os01g09220	transposon protein	0.97	0.01	0.015	3058	P	42	A
Os.54944.1.S1_at	LOC_Os02g52670	ethylene-responsive element-binding protein	0.96	0.01	0.013	182	P,A	2	A

Supplementary Table S3 (Nakano Y et al.)
Probes with significantly differentially expression in the F71 pith parenchyma (FDR < 0.001).

Systematic Name	TIGR Loci	Description	WT Pa normalized	F71 Pa normalized	Fold Change F71Pa/ WT Pa	WT Pa raw	WT Pa flags	F71 Pa raw	F71 Pa flags
Os.5031.1.S1_at	LOC_Os12g36830	pathogenesis-related protein 10 (RSOsPR10)	0.97	825.90	848.82	6	A	5,311	P
Os.32890.1.S1_at	LOC_Os11g47600	class 3 chitinase	0.90	501.60	557.33	3	A	1,382	P
Os.165.1.S1_at	LOC_Os12g36880	pathogenesis-related protein 10 (PR10a)	1.00	430.50	430.50	32	A	15,228	P
Os.20230.1.S1_at	LOC_Os11g37950	pathogenesis-related protein 4	0.97	163.70	168.24	58	A	10,651	P
OsAffx.3144.1.S1_x_at	LOC_Os03g06010	alpha-expansin (OsEXPA25)	1.00	157.40	157.72	6	A	1,148	P
Os.47743.1.S1_at	Os07g0167700	unknown protein	0.98	131.40	134.36	28	A	4,105	P
Os.11290.1.S1_at	LOC_Os06g44170	Leucoanthocyanidin reductase	1.00	124.10	124.47	1	A	146	P
OsAffx.24234.2.S1_s_at	LOC_Os02g13780	Leucine-rich repeat family protein	0.99	105.90	107.29	1	A	148	P
Os.23635.1.S1_at	Os01g0847100	unknown protein	0.92	95.05	103.65	55	P,A	5,907	P
Os.51172.1.S1_x_at	LOC_Os06g51050	Basic endochitinase (CHIT7)	0.98	87.24	89.11	57	P,A	5,576	P
OsAffx.28152.2.S1_at	LOC_Os06g47470	Protein kinase domain-containing protein	0.91	78.32	86.54	2	A	184	P
Os.8838.2.S1_at	LOC_Os08g04250	Protein kinase	0.93	58.63	62.77	2	A	145	P,M,A
Os.6763.1.S1_at	LOC_Os01g48710	metal ion-binding protein	0.99	44.01	44.50	4	A	174	P
Os.316.1.S1_at	LOC_Os07g01560	sugar transport protein	0.93	39.93	42.98	187	P	8,268	P
Os.33131.1.A1_at	LOC_Os03g20550	OsWRKY family protein	1.00	35.67	35.81	5	A	186	P
Os.17273.1.S1_at	LOC_Os05g27010	peptide transporter POT family	0.96	34.29	35.79	97	P	3,715	P
OsAffx.32171.3.S1_at	LOC_Os12g43490	alpha-amylase/trypsin inhibitor, PR protein	0.98	34.00	34.73	482	P	17,984	P
Os.54734.1.S1_at	LOC_Os06g09220	cytochrome P450 72A1	0.97	28.88	29.77	2	A	75	P
Os.15440.1.S1_at	LOC_Os01g37050	endoribonuclease Dcr-1	0.97	26.73	27.56	33	P,A	967	P
Os.40045.1.S1_at	LOC_Os12g43640	receptor-like protein kinase 5 precursor	0.96	26.42	27.46	90	P	2,662	P
Os.18255.1.S1_at	LOC_Os01g48900	dynamin-related protein 1A	0.99	26.33	26.62	4	A	129	P
Os.11962.1.S1_at	LOC_Os09g29200	glutathione S-transferase	0.99	25.13	25.49	60	A	1,717	P
Os.8507.1.S1_at	LOC_Os09g35800	UDP-glucose 4-epimerase	0.98	24.66	25.27	3	A	71	P,A
Os.12761.1.S1_at	LOC_Os03g46060	pathogenesis-related protein 5	0.95	23.06	24.25	473	P	12,113	P
OsAffx.13260.2.S1_at	LOC_Os03g40194	disease resistance RPP13-like protein 1	0.99	22.19	22.41	54	P	1,339	P
Os.32889.1.S1_at	LOC_Os07g03040	expressed protein	0.99	21.42	21.61	44	A	1,051	P
Os.52285.1.S1_at	LOC_Os11g10120	expressed protein	0.98	19.59	20.03	24	P,A	533	P
Os.22000.1.S1_at	LOC_Os06g51060	class 1 chitinase	0.98	19.70	20.02	716	P	15,625	P
Os.6256.2.S1_at	AK241797	expressed protein	0.99	19.35	19.64	137	P,A	3,009	P
Os.30512.1.S1_at	LOC_Os01g43650	OsWRKY family protein	1.00	17.16	17.19	21	A	406	P
Os.6125.1.S1_at	LOC_Os03g29190	PDI-like protein	0.95	15.13	15.96	405	P	6,765	P
Os.4856.1.S1_at	LOC_Os01g71090	xylanase inhibitor	0.99	15.72	15.85	28	P,A	505	P
OsAffx.13195.1.S1_at	LOC_Os03g36080	expressed protein	1.00	15.22	15.28	616	P	10,477	P
Os.6148.1.S1_at	LOC_Os11g31700	expressed protein	0.97	13.87	14.27	173	P	2,686	P
Os.16014.1.S1_at	LOC_Os04g47860	translation initiation factor IF-2	0.94	13.38	14.22	5	A	76	P,M
Os.12234.1.S1_s_at	LOC_Os10g40730	beta-expansin	0.97	13.41	13.78	817	P	12,307	P
Os.27647.2.S1_x_at	LOC_Os07g07300	expressed protein	0.98	13.37	13.66	46	P,A	686	P
Os.54521.1.S1_at	LOC_Os05g39190	expressed protein	0.99	13.45	13.56	52	P,A	785	P
Os.5562.1.S1_at	LOC_Os04g51150	transposon protein	0.98	13.12	13.39	29	P,A	422	P
OsAffx.28152.1.S1_s_at	LOC_Os06g47530	serine/threonine-protein kinase receptor precursor	0.99	13.20	13.29	48	A	694	P
Os.46431.1.S1_at	LOC_Os01g35330	unknown protein	0.97	12.35	12.76	281	P	3,930	P
Os.31431.1.S1_at	LOC_Os01g40580	hypersensitive-induced response protein	1.00	11.94	11.96	79	P,M,A	1,090	P
Os.7207.1.S1_at	LOC_Os03g42464	expressed protein	0.98	11.38	11.60	104	P	1,301	P
Os.26706.1.S1_at	LOC_Os07g48229	vacuolar sorting receptor 1 precursor	0.97	11.11	11.43	202	P	2,481	P
Os.55701.1.S1_at	LOC_Os12g09220	expressed protein	1.00	11.40	11.42	85	P	1,075	P
Os.27422.2.S1_at	LOC_Os02g27000	ATP-binding protein	0.99	10.50	10.64	140	P	1,643	P
Os.6039.1.S1_at	LOC_Os02g45250	homeobox protein FWA	0.92	9.48	10.28	19	A	196	P
Os.34438.2.A1_x_at	LOC_Os07g39740	esterase precursor	1.00	9.90	9.90	330	P	3,616	P
OsAffx.19473.1.S1_s_at	LOC_Os12g03740	F-box family protein-like	0.96	9.11	9.51	284	P	2,838	P
Os.5429.1.S1_at	LOC_Os11g40970	Leucine-rich repeat family protein	0.97	8.88	9.14	320	P	3,089	P
Os.18381.1.S1_at	LOC_Os04g19740	transketolase, chloroplast precursor	0.99	8.52	8.57	75	P	727	P
Os.4659.1.S1_at	Os06g0143100	Conserved hypothetical protein	0.99	8.18	8.23	79	P	718	P
Os.49329.1.S1_at	LOC_Os02g35490	MLO-like protein 1	0.98	7.39	7.53	21	P	175	P
Os.17560.1.A1_at	LOC_Os07g36800	expressed protein	0.99	7.00	7.08	32	A	243	P
Os.22662.2.S1_at	AK068160	expressed protein	0.99	6.89	6.93	25	P,A	189	P
Os.17177.1.S1_at	LOC_Os02g36940	expressed protein	0.99	6.84	6.90	121	P	916	P
OsAffx.2268.1.S1_at	LOC_Os01g47820	S-locus-like receptor protein kinase	0.99	6.75	6.79	42	P	313	P
Os.54722.1.S1_at	LOC_Os07g33710	expressed protein	0.99	6.65	6.71	54	P	400	P
Os.15825.1.S2_at	LOC_Os04g53720	ATP-binding protein	0.99	6.59	6.68	169	P	1,222	P
OsAffx.19473.1.S1_at	LOC_Os12g03740	F-box family protein-like	0.99	6.10	6.19	140	P	935	P
Os.20614.2.S1_at	LOC_Os04g49757	purine transporter	0.99	5.78	5.85	426	P	2,719	P
Os.15573.1.A1_s_at	LOC_Os04g58734	expressed protein	0.99	5.74	5.81	672	P	4,251	P
Os.37128.1.S1_at	LOC_Os07g35004	receptor-like protein kinase	0.98	5.28	5.39	38	P,A	223	P
Os.12279.2.S1_a_at	LOC_Os01g72009	expressed protein	0.95	5.03	5.30	69	P	386	P
Os.15696.1.S1_a_at	LOC_Os02g43010	vacuolar processing enzyme, beta-isozyme precursor	1.00	5.26	5.29	235	P	1,368	P
Os.6534.1.A1_at	(AK071082)		1.00	5.15	5.16	31	P,M,A	173	P
Os.56294.1.S1_at	LOC_Os11g36400	expressed protein	0.97	4.80	4.95	24	A	127	P
Os.54142.1.S1_at	LOC_Os12g41350	HORMA domain-containing	1.00	4.90	4.91	22	P,A	121	P
Os.26856.1.S1_at	LOC_Os07g16970	putative GDP dissociation inhibitor	1.00	4.65	4.67	158	P	816	P
Os.53419.1.S1_at	LOC_Os02g43840	EREBP-4-like protein	1.00	4.52	4.53	72	P	359	P
OsAffx.5133.1.S1_at	LOC_Os06g47130	calcium lipid-binding protein-like	1.00	4.26	4.26	101	P	471	P
Os.17111.2.S1_x_at	LOC_Os04g48460	cytochrome P450 86A1	0.99	4.17	4.21	267	P	1,224	P
Os.51848.1.S1_x_at	LOC_Os10g31330	glycine-rich cell wall structural protein 2 precursor	0.99	4.11	4.13	3429	P	15,524	P
Os.55638.1.S1_at	LOC_Os09g36750	L-ascorbate peroxidase 4	1.00	3.88	3.90	249	P	1,075	P
OsAffx.14250.1.S1_at	LOC_Os04g43060	cupin superfamily	0.99	3.72	3.75	78	P,A	319	P
Os.52978.1.S1_at	LOC_Os08g43654	transparent testa 12 protein	0.98	3.61	3.67	24	A	95	P
Os.49812.1.S1_at	LOC_Os01g33110	receptor-like protein kinase 5 precursor	1.00	3.63	3.64	191	P	765	P
Os.52520.1.S1_at	LOC_Os12g08180	receptor-like protein kinase precursor	0.99	3.60	3.63	1105	P	4,409	P
Os.34438.1.S1_x_at	LOC_Os07g39740	esterase precursor	1.00	3.55	3.56	566	P	2,236	P
Os.20364.1.S1_at	LOC_Os05g39240	ammonium transporter 2	1.00	3.45	3.46	383	P	1,455	P
Os.20717.1.S1_at	LOC_Os01g61460	expressed protein	1.00	3.43	3.44	752	P	2,869	P
Os.18101.1.S1_at	(AK103159)		1.00	3.33	3.33	309	P	1,132	P
OsAffx.13491.1.S1_at	LOC_Os03g55180	expressed protein	1.00	3.28	3.29	80	P	288	P
Os.46584.1.S1_x_at	LOC_Os06g05120	expressed protein	0.99	3.22	3.25	159	P	564	P
Os.5525.1.S1_at	LOC_Os06g05480	expressed protein	1.00	3.11	3.13	4168	P	14,290	P
Os.33229.1.S1_at	LOC_Os06g06450	heat shock protein STI	1.00	3.08	3.09	33	P,A	111	P
Os.11895.1.S2_at	LOC_Os02g05430	expressed protein	1.00	3.03	3.04	250	P	835	P
OsAffx.30966.4.S1_x_at	LOC_Os07g46060	expressed protein	1.00	3.03	3.04	348	P	1,159	P
Os.49898.2.S1_at	LOC_Os06g20310	expressed protein	0.99	3.02	3.04	126	P	418	P
Os.54774.1.S1_x_at	AK106732	expressed protein	1.00	3.03	3.03	100	P	333	P
Os.48497.1.S1_at	LOC_Os06g48880	expressed protein	1.00	3.01	3.02	65	P	215	P
Os.56259.1.S1_at	LOC_Os02g18640	F-box domain-containing protein	1.00	2.94	2.94	384	P	1,247	P
Os.10784.1.S1_at	LOC_Os02g26700	cation transport protein chaC	1.00	2.91	2.92	2190	P	7,049	P
Os.45887.2.S1_x_at	LOC_Os01g12750	cytochrome P450 71A4	0.99	2.88	2.90	1044	P	3,315	P
Os.16142.1.S1_at	LOC_Os03g31510	cystatin	0.99	2.83	2.84	3580	P	11,136	P
Os.9778.1.S2_at	LOC_Os07g45570	expressed protein	1.00	2.73	2.74	3095	P	9,330	P
OsAffx.7301.1.S1_at	LOC_Os11g35410	expressed protein	1.00	2.68	2.68	345	P	1,029	P
OsAffx.30680.1.S1_at	CT835750	expressed protein	0.99	2.59	2.62	1305	P	3,700	P
OsAffx.30157.1.S1_s_at	LOC_Os09g36750	L-ascorbate peroxidase 4	1.00	2.60	2.61	167	P	475	P
Os.49497.1.S1_at	LOC_Os09g10840	transcription factor HBP-1b	1.00	2.60	2.61	38	P,A	107	P
Os.1316.1.S1_a_at	LOC_Os01g58890	cystatin-1 precursor	0.99	2.58	2.60	4178	P	11,824	P
OsAffx.3763.1.S1_s_at	LOC_Os04g10420	CW7	1.00	2.57	2.57	221	P	624	P
Os.46831.1.S1_at	LOC_Os10g34602	unknown protein	1.00	2.50	2.50	708	P	1,941	P
Os.8102.1.S1_at	LOC_Os03g57330	calmodulin-binding protein	1.00	2.39	2.39	261	P	686	P

Os.21823.1.S1_at	LOC_Os03g27960	vacuolar cation/proton exchanger 2	1.00	2.37	2.37	143	P	371	P
Os.51616.1.S1_at	Os03g0272900	expressed protein	1.00	2.35	2.35	3201	P	8,351	P
Os.10483.1.S1_at	LOC_Os07g39620	C2 domain-containing protein	1.00	2.28	2.29	1115	P	2,802	P
Os.19187.1.S1_at	LOC_Os02g10470	calcium ion binding-protein	0.99	2.27	2.28	147	P	366	P
Os.7322.1.S1_at	LOC_Os10g22730	expressed protein	1.00	2.24	2.25	3393	P	8,403	P
Os.24417.3.S1_at	LOC_Os08g30634	DC1 domain-containing protein	1.00	2.20	2.21	141	P	339	P
Os.4698.1.S1_at	LOC_Os01g70770	glutathione S-transferase III	1.00	2.13	2.14	187	P	438	P
Os.47918.1.S1_at	LOC_Os11g05160	DNA-binding protein	1.00	2.09	2.09	109	P	251	P
Os.35335.1.A1_s_at	LOC_Os04g54800	shikimate kinase, chloroplast precursor	1.00	2.02	2.03	2153	P	4,793	P
Os.23533.1.S1_at	LOC_Os03g17550	serine/threonine-protein kinase NAK	1.00	1.92	1.92	253	P	533	P
Os.26858.1.S1_at	LOC_Os02g38840	glucose-6-phosphate 1-dehydrogenase, cytoplasmic	1.00	1.88	1.88	552	P	1,148	P
Os.50390.1.S1_at	LOC_Os05g30280	cyanogenic beta-glucosidase precursor	1.00	1.86	1.86	1111	P	2,271	P
Os.7982.1.S1_at	LOC_Os03g32580	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor	1.00	1.83	1.84	1951	P	3,924	P
Os.22967.1.S1_s_at	LOC_Os03g02070	metal ion-binding protein	1.00	1.83	1.84	4470	P	8,996	P
OsAffx.30773.1.S1_x_at	LOC_Os12g01916	bcpLH protein	1.00	1.83	1.83	546	P	1,097	P
Os.17516.1.S1_at	LOC_Os04g40840	histone acetyltransferase ELP3	1.00	1.79	1.80	1827	P	3,598	P
Os.10850.1.S1_at	LOC_Os05g25210	expressed protein	1.00	1.78	1.78	685	P	1,343	P
Os.54566.1.S1_at	LOC_Os02g35940	gibberellin receptor GID1L2	1.00	1.76	1.76	691	P	1,334	P
AFFX-OS-25SrRNA_s_a	LOC_Os09g00998	expressed protein	1.00	1.73	1.73	2022	P	3,842	P
Os.18152.1.S1_at	LOC_Os03g58720	RNA-binding protein 28	1.00	1.52	1.52	380	P	633	P
Os.20026.1.S1_at	LOC_Os09g06740	protein-binding protein	1.00	1.46	1.46	184	P	295	P
Os.50556.1.S1_at	LOC_Os12g07280	TRANSPARENT TESTA 1 protein	1.00	1.42	1.42	3972	P	6,183	P
Os.25587.1.S1_s_at	LOC_Os04g57320	IMMUTANS protein	1.00	1.31	1.31	800	P	1,146	P
Os.15711.1.S1_at	LOC_Os09g28310	bZIP transcription factor	1.00	1.28	1.28	1650	P	2,315	P
Os.7300.1.S1_at	LOC_Os03g57100	serologically defined breast cancer antigen NY-BR-84	1.00	0.92	0.92	8390	P	8,493	P
Os.48055.1.S1_at	LOC_Os03g08450	eukaryotic translation initiation factor 3 subunit 12	1.00	0.88	0.88	5425	P	5,205	P
Os.9707.1.S1_at	LOC_Os04g01250	glutamyl-tRNA	1.00	0.77	0.77	4690	P	3,966	P
Os.16458.1.S1_at	LOC_Os05g24020	emp24/gp25L/p24 family protein	1.00	0.74	0.74	2329	P	1,893	P
Os.15764.1.S1_at	LOC_Os03g26450	F-actin capping protein beta subunit	1.00	0.70	0.70	1172	P	903	P
OsAffx.23995.1.S1_at	LOC_Os01g71106	NBS-LRR disease resistance protein	1.00	0.68	0.68	749	P	556	P
Os.50956.1.S1_at	LOC_Os03g27040	copper-transporting ATPase PAA1	1.00	0.68	0.68	422	P	312	P
Os.27489.1.A1_at	LOC_Os01g11120	CID11	1.00	0.67	0.67	1070	P	788	P
OsAffx.6495.1.S1_s_at	LOC_Os09g36830	SKP1-like protein 1B	1.00	0.65	0.65	1231	P	881	P
Os.22996.1.S1_a_at	LOC_Os03g39010	decarboxylase family protein	1.00	0.64	0.64	884	P	625	P
Os.17692.1.S1_at	LOC_Os10g35140	permeases of the drug/metabolite transporter	1.00	0.64	0.64	853	P	601	P
Os.49239.1.S1_at	LOC_Os05g32390	dynamin family protein	1.00	0.64	0.64	519	P	364	P
Os.38638.2.S1_at	LOC_Os06g04950	early nodulin 93	1.00	0.63	0.63	92	A	64	A
Os.8351.1.S1_at	LOC_Os08g04790	xylosyltransferase 2	1.00	0.63	0.63	1674	P	1,151	P
Os.534.2.S1_x_at	LOC_Os01g05800	inner membrane protein ALBINO3, chloroplast precursor	1.00	0.62	0.62	4296	P	2,900	P
Os.11564.1.S1_at	LOC_Os09g38420	cysteinyl-tRNA synthetase	1.00	0.61	0.61	700	P	472	P
Os.23161.2.S1_x_at	LOC_Os08g33380	threonine endopeptidase	1.00	0.59	0.59	2106	P	1,364	P
Os.31563.1.S1_at	LOC_Os03g08730	uroporphyrinogen III synthase	1.00	0.59	0.59	922	P	595	P
Os.9698.1.S1_at	LOC_Os04g02780	ATAMI1	1.00	0.57	0.57	1179	P	732	P
Os.36566.2.S1_at	LOC_Os01g13660	expressed protein	0.99	0.56	0.57	1076	P	665	P
Os.2976.1.S1_at	LOC_Os10g42840	NADH-ubiquinone oxidoreductase subunit B17.2	1.00	0.54	0.54	4724	P	2,817	P
Os.38100.1.S1_at	LOC_Os01g67240	AFH1	1.00	0.54	0.54	1908	P	1,129	P
OsAffx.29776.1.S1_x_at	LOC_Os09g09370	protein-binding protein	1.00	0.53	0.53	61	P,M,A	35	A
OsAffx.17026.1.S1_at	LOC_Os08g16570	expressed protein	1.00	0.52	0.52	350	P	201	P
Os.19784.1.S1_at	LOC_Os01g62230	histone H2B.4	1.00	0.52	0.52	3956	P	2,261	P
Os.25529.1.S1_at	LOC_Os05g44330	4-methyl-5-thiazole monophosphate biosynthesis protein	1.00	0.50	0.50	541	P	298	P
Os.4948.1.S1_x_at	LOC_Os02g42290	ATP-dependent Clp protease proteolytic subunit	1.00	0.50	0.50	13843	P	7,598	P
Os.6828.1.S1_at	LOC_Os03g59220	ubiquinol-cytochrome c reductase complex 14 kDa protein	1.00	0.50	0.50	5123	P	2,819	P
OsAffx.13616.1.S1_x_at	LOC_Os04g01780	uncharacterized ACR, COG1399 family protein	1.00	0.50	0.50	923	P	504	P
Os.27914.1.S1_at	LOC_Os08g02390	ribonucleoprotein, chloroplast precursor	1.00	0.49	0.49	216	P	117	P
Os.17148.1.A1_at	LOC_Os03g64320	expressed protein	1.00	0.48	0.48	2803	P	1,500	P
OsAffx.27459.2.S1_s_at	LOC_Os06g05000	early nodulin 93	0.99	0.47	0.47	407	P	210	P
Os.54269.1.S1_s_at	LOC_Os05g48060	phosphatidylserine synthase 2	1.00	0.46	0.46	221	P	113	P
Os.20473.1.S1_s_at	LOC_Os05g33620	expressed protein	1.00	0.44	0.44	1724	P	843	P
Os.47590.1.A1_s_at	LOC_Os05g39080	ATP-binding protein	0.99	0.43	0.44	1276	P	604	P
Os.23434.1.S1_at	LOC_Os06g51460	ATPase, coupled to transmembrane movement of	1.00	0.44	0.44	147	P	71	P
Os.2230.1.S1_at	LOC_Os02g50960	auxin efflux carrier component 1	1.00	0.42	0.42	1295	P	598	P
Os.8604.1.S1_a_at	LOC_Os11g47730	expressed protein	1.00	0.42	0.42	394	P	183	P
OsAffx.3061.1.S1_x_at	LOC_Os02g54030	endo-polygalacturonase precursor	1.00	0.40	0.40	431	P	192	P
Os.5860.1.S1_at	LOC_Os03g04310	DNA-binding protein	0.99	0.40	0.40	2284	P	995	P
OsAffx.14935.1.S1_at	LOC_Os05g33290	expressed protein	1.00	0.40	0.40	2047	P	896	P
Os.5753.1.S1_x_at	LOC_Os04g56060	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor	0.99	0.39	0.39	530	P	227	P
Os.8765.1.S1_a_at	LOC_Os01g47690	hydroxyacylglutathione hydrolase 3, mitochondrial precursor	1.00	0.39	0.39	3877	P	1,668	P
Os.49423.1.S1_at	LOC_Os11g05556	signal recognition particle 54 kDa protein, chloroplast	1.00	0.39	0.39	701	P	301	P
Os.37097.1.S1_at	LOC_Os07g46570	electron transporter	1.00	0.38	0.38	2002	P	856	P
OsAffx.17904.1.S1_s_at	LOC_Os09g26190	CBS domain-containing protein	1.00	0.38	0.38	1054	P	436	P
OsAffx.27525.1.S1_at	LOC_Os06g09340	pectinesterase U1 precursor	1.00	0.37	0.38	160	P,A	66	A
Os.37093.1.S1_at	LOC_Os01g11340	CYP710A1	1.00	0.37	0.37	1768	P	715	P
OsAffx.27508.22.S1_s_a	LOC_Os04g52230	ent-kaurene synthase B, chloroplast precursor	0.99	0.37	0.37	1893	P	762	P
Os.5012.1.S1_at	LOC_Os01g40860	retinal dehydrogenase 1	0.98	0.36	0.37	100	P	39	M,A
OsAffx.23914.1.S1_at	LOC_Os01g64410	plant-specific domain TIGR01568 family protein	1.00	0.37	0.37	2819	P	1,136	P
Os.52411.1.S1_at	LOC_Os03g02640	expressed protein	1.00	0.36	0.36	929	P	369	P
Os.55256.1.S1_at	Os10g0467000	expressed protein	1.00	0.36	0.36	81	A	33	A
Os.8597.1.S1_at	LOC_Os03g02040	remorin	1.00	0.36	0.36	8531	P	3,360	P
Os.7021.1.S1_at	LOC_Os08g02630	photosystem II core complex proteins psbY, chloroplast	1.00	0.35	0.35	36	P,M,A	14	A
Os.14245.1.S1_s_at	LOC_Os03g05320	expressed protein	1.00	0.35	0.35	1559	P	597	P
Os.14194.1.S1_at	LOC_Os03g59640	magnesium-chelatase subunit chlD, chloroplast precursor	1.00	0.35	0.35	1639	P	627	P
Os.52259.1.S1_at	LOC_Os11g01590	major facilitator superfamily protein	0.99	0.35	0.35	586	P	222	P
Os.16692.1.S1_x_at	LOC_Os10g35810	uncharacterized low-complexity proteins	1.00	0.34	0.34	1708	P	633	P
Os.5261.1.S1_a_at	LOC_Os03g20100	30S ribosomal protein S1, chloroplast precursor	1.00	0.34	0.34	883	P	328	P
Os.6830.1.S1_at	LOC_Os02g09590	ribosome-like protein	1.00	0.33	0.33	1787	P	649	P
Os.15065.1.S1_at	LOC_Os06g45370	fructose-1,6-bisphosphatase, chloroplast precursor	1.00	0.33	0.33	1319	P	482	P
OsAffx.9749.1.S1_at	LOC_Os01g72760	cytochrome P450 71D10	1.00	0.33	0.33	8468	P	3,053	P
Os.46685.1.S1_x_at	LOC_Os10g25570	expressed protein	1.00	0.33	0.33	1876	P	678	P
Os.20420.1.S1_at	LOC_Os01g18120	CCR	0.99	0.32	0.33	8121	P	2,891	P
Os.26499.1.S1_at	LOC_Os03g45710	ferredoxin, chloroplast precursor	0.99	0.32	0.32	1088	P	381	P,M,A
Os.15792.1.S1_at	LOC_Os06g08470	expressed protein	1.00	0.32	0.32	2629	P	925	P
Os.19594.1.A1_at	LOC_Os02g02520	expressed protein	0.99	0.32	0.32	1101	P	385	P
Os.9093.1.S1_at	LOC_Os06g05930	expressed protein	1.00	0.32	0.32	8477	P	2,918	P
Os.5136.1.S1_at	LOC_Os02g52744	DCL protein, chloroplast precursor	1.00	0.31	0.31	4212	P	1,450	P
Os.27301.1.S1_at	LOC_Os06g05980	solute carrier family 35 member C2	1.00	0.31	0.31	1580	P	551	P
Os.53291.1.S1_at	LOC_Os03g64280	1-aminocyclopropane-1-carboxylate oxidase	1.00	0.31	0.31	133	P	46	A
Os.11671.1.S1_at	LOC_Os02g02390	RNA binding protein	1.00	0.31	0.31	2152	P	739	P
Os.10635.1.S1_s_at	LOC_Os04g51880	galactokinase	1.00	0.31	0.31	15103	P	5,142	P
Os.12520.1.S1_a_at	LOC_Os02g32814	heavy metal-associated domain-containing protein	0.98	0.30	0.30	597	P	198	P
Os.27686.1.S1_at	LOC_Os02g42570	ferredoxin-thioredoxin reductase, variable chain	0.99	0.30	0.30	672	P	223	P
Os.54578.1.S1_at	LOC_Os07g35600	expressed protein	1.00	0.30	0.30	1046	P	344	P
OsAffx.6386.1.S1_at	LOC_Os09g24530	ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase	0.98	0.29	0.30	256	P	83	P
Os.55458.1.S1_at	LOC_Os03g20760	lipid binding protein	1.00	0.29	0.29	2934	P	953	P
Os.47381.2.S1_at	LOC_Os04g36800	3-oxoacyl-synthase I, chloroplast precursor	1.00	0.29	0.29	2602	P	832	P
Os.46632.1.S1_at	AK241004	expressed protein	0.98	0.28	0.29	385	P	120	P,A
Os.24794.1.S1_x_at	LOC_Os03g24860	solute carrier family 2, facilitated glucose transporter	1.00	0.29	0.29	1216	P	384	P
Os.27717.1.S1_a_at	LOC_Os01g58470	expressed protein	1.00	0.29	0.29	1563	P	490	P

Os.20614.1.S1_at	LOC_Os10g41838	F-box protein interaction-domain containing protein	1.00	0.28	0.29	381	P	123	P
Os.20603.1.S1_s_at	LOC_Os06g28970	transcription regulator	0.99	0.28	0.29	2424	P	751	P
Os.16906.1.S1_at	LOC_Os04g50110	plastid-specific 30S ribosomal protein 2, chloroplast	1.00	0.28	0.28	600	P	187	P
Os.27598.1.S1_at	LOC_Os03g16470	expressed protein	1.00	0.28	0.28	5496	P	1,712	P
Os.53685.1.S1_at	LOC_Os05g36960	ATP-binding protein	1.00	0.28	0.28	423	P	129	P
Os.19611.3.S1_at	LOC_Os10g32300	TPR domain-containing protein	1.00	0.27	0.27	1001	P	303	P
Os.26818.1.S1_a_at	LOC_Os03g19650	PPR2	1.00	0.27	0.27	1015	P	303	P
Os.17091.1.S1_at	LOC_Os08g41040	expressed protein	0.99	0.26	0.27	688	P	200	P
Os.14745.1.S1_at	LOC_Os11g42500	disease resistance response protein 206	0.99	0.26	0.26	13508	P	3,872	P
Os.17528.2.A1_a_at	LOC_Os03g10500	adenylyl-sulfate kinase, chloroplast precursor	1.00	0.26	0.26	6795	P	1,964	P
Os.15725.1.S1_at	LOC_Os03g64050	receptor protein kinase-like protein	1.00	0.26	0.26	250	P	72	P
Os.50271.1.S1_at	LOC_Os06g05359	NBS-LRR disease resistance protein	0.98	0.26	0.26	389	P	111	P
Os.4251.1.S1_at	LOC_Os02g09940	peroxiredoxin-5, mitochondrial precursor	1.00	0.26	0.26	179	P	52	A
Os.50867.1.S1_at	LOC_Os01g52480	senescence-associated protein 12	0.99	0.26	0.26	43	A	12	A
Os.20144.1.S1_a_at	LOC_Os01g70400	expressed protein	1.00	0.26	0.26	308	P	88	P
Os.18494.1.S1_at	LOC_Os07g05110	nutrient reservoir	1.00	0.26	0.26	78	P	22	P,A
Os.18428.1.S1_at	LOC_Os07g06880	gibberellin receptor GID1L2	1.00	0.25	0.25	3256	P	913	P
Os.5753.1.S1_at	LOC_Os04g56060	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor	0.99	0.25	0.25	918	P	253	P
Os.11152.1.S1_at	LOC_Os01g54540	50S ribosomal protein L13, chloroplast precursor	1.00	0.25	0.25	3500	P	969	P
Os.14530.2.S1_x_at	LOC_Os09g36880	anther-specific proline-rich protein APG precursor	1.00	0.25	0.25	3180	P	872	P
Os.20702.1.S1_at	LOC_Os04g53230	aminomethyltransferase, mitochondrial precursor	0.99	0.25	0.25	4295	P	1,156	P
Os.27694.1.S1_at	LOC_Os02g46750	expressed protein	0.99	0.25	0.25	768	P	208	P
Os.4997.1.S1_s_at	LOC_Os01g69950	50S ribosomal protein L27, chloroplast precursor	1.00	0.25	0.25	1523	P	415	P
Os.20284.1.S1_x_at	LOC_Os12g34524	peroxidase 24 precursor	1.00	0.24	0.24	499	P	134	P,A
Os.55236.1.S1_at	LOC_Os02g37970	expressed protein	0.98	0.24	0.24	699	P	183	P,A
Os.8520.1.S1_at	LOC_Os06g22690	bundle sheath defective protein 2	1.00	0.24	0.24	5607	P	1,482	P
Os.37602.1.S1_at	LOC_Os07g38000	cytochrome c6	1.00	0.24	0.24	264	P	69	P,M
Os.11469.1.S1_at	LOC_Os04g26870	auxin-induced protein PCNT115	1.00	0.23	0.23	6707	P	1,712	P
Os.5439.1.S1_a_at	LOC_Os01g18320	protoporphyrinogen oxidase, chloroplast precursor	1.00	0.23	0.23	1379	P	350	P
Os.46403.1.S1_at	LOC_Os01g69950	50S ribosomal protein L27, chloroplast precursor	0.99	0.23	0.23	1746	P	444	P
Os.6011.1.S1_at	LOC_Os10g16974	flavonoid 3'-monooxygenase	1.00	0.23	0.23	6152	P	1,561	P
Os.50009.1.S1_at	LOC_Os03g08600	transferase, transferring glycosyl groups	1.00	0.23	0.23	2374	P	598	P
OsAffx.3129.1.S1_x_at	LOC_Os03g04470	expressed protein	0.98	0.22	0.22	710	P	169	P
OsAffx.26384.8.S1_x_at	LOC_Os05g09400	PSRP4	0.99	0.22	0.22	1678	P	406	P
Os.14529.1.S1_x_at	LOC_Os02g58790	expressed protein	1.00	0.22	0.22	295	P	70	P
Os.15183.1.S1_at	LOC_Os01g40710	OHP2	0.99	0.21	0.21	2585	P	604	P
Os.26040.1.S1_at	LOC_Os03g62630	structural constituent of ribosome	1.00	0.21	0.21	1308	P	303	P
Os.27375.1.A1_at	LOC_Os02g04460	50S ribosomal protein L3, chloroplast precursor	1.00	0.21	0.21	3646	P	847	P
Os.11588.1.S1_at	LOC_Os08g44810	malate dehydrogenase 1, chloroplast precursor	1.00	0.20	0.21	5832	P	1,321	P
Os.27509.1.S1_at	LOC_Os01g53790	expressed protein	0.98	0.20	0.20	92	P,M	20	A
Os.53663.1.S1_at	LOC_Os03g03724	expressed protein	1.00	0.19	0.19	137	P	29	P,A
Os.39363.1.A1_x_at	(CF298180)		1.00	0.19	0.19	245	P	52	P
Os.12024.1.S1_at	LOC_Os06g43900	50S ribosomal protein L35, chloroplast precursor	1.00	0.19	0.19	2921	P	615	P
Os.9773.1.S1_at	LOC_Os01g59060	50S ribosomal protein L34, chloroplast precursor	1.00	0.19	0.19	2145	P	439	P
Os.24759.1.A1_at	LOC_Os11g29350	ELMO domain-containing 2	0.98	0.18	0.19	224	P	46	A
Os.35677.1.S1_at	LOC_Os03g09060	1,4-dihydroxy-2-naphthoate octaprenyltransferase	1.00	0.18	0.18	704	P	143	P
Os.38257.1.S1_x_at	LOC_Os12g08730	thioredoxin M-type, chloroplast precursor	1.00	0.18	0.18	1248	P	254	P
Os.24768.1.S1_x_at	LOC_Os04g54640	expressed protein	1.00	0.18	0.18	756	P	151	P,M
Os.48704.1.S1_at	LOC_Os05g51190	ATP-binding protein	0.94	0.17	0.18	318	P	60	M,A
Os.7826.2.A1_at	LOC_Os05g10730	multidrug resistance-associated protein 6 precursor	0.95	0.17	0.18	495	P	94	P,M,A
Os.4612.1.S1_at	LOC_Os03g07100	lipid transfer protein	0.97	0.17	0.17	28	A	5	A
Os.53326.1.S1_at	LOC_Os01g24090	TPR repeat	1.00	0.17	0.17	348	P	66	P
Os.27652.1.S1_at	LOC_Os02g39740	tab2 protein	0.97	0.16	0.17	587	P	106	P
Os.8143.1.S2_at	LOC_Os07g32020	anthocyanidin 3-O-glucosyltransferase	0.99	0.17	0.17	1646	P	300	P
Os.5432.1.A1_at	LOC_Os02g57030	expressed protein	1.00	0.17	0.17	1604	P	300	P
Os.5229.1.S1_at	LOC_Os05g33280	beta-propeller domains of methanol dehydrogenase type	1.00	0.17	0.17	349	P	64	P,A
Os.5188.2.S1_x_at	LOC_Os08g23410	rubredoxin	1.00	0.17	0.17	411	P,M	75	A
Os.7707.1.S1_at	LOC_Os04g54320	expressed protein	0.99	0.16	0.16	659	P	117	P,A
Os.9074.1.S1_s_at	LOC_Os03g02960	nascent polypeptide-associated complex alpha subunit-like	0.99	0.16	0.16	2489	P	450	P
Os.47330.1.S1_at	LOC_Os02g54190	pectinesterase-2 precursor	0.97	0.16	0.16	256	P	47	A
Os.17487.1.S1_at	LOC_Os03g50310	CCT motif family protein	0.97	0.15	0.16	1728	P	295	P
Os.51517.1.A1_s_at	LOC_Os02g51470	ATP synthase delta chain, chloroplast precursor	0.99	0.16	0.16	1887	P	326	P
Os.8553.1.S1_at	LOC_Os03g52130	expressed protein	0.97	0.15	0.16	331	P	56	P,M
Os.15071.2.S1_s_at	LOC_Os02g51470	ATP synthase delta chain, chloroplast precursor	0.99	0.15	0.16	590	P	99	P
Os.15249.1.S1_at	LOC_Os03g63930	acyl carrier protein 3, chloroplast precursor	0.98	0.15	0.15	1186	P	198	P
Os.14368.1.S1_at	LOC_Os08g29370	peptidyl-prolyl cis-trans isomerase, chloroplast precursor	0.99	0.15	0.15	1306	P	216	P
Os.32447.1.S1_at	LOC_Os01g59080	expressed protein	1.00	0.15	0.15	613	P	102	P
Os.7948.1.S1_a_at	LOC_Os01g17150	50S ribosomal protein L40, chloroplast precursor	0.99	0.15	0.15	330	P	54	P
Os.7137.2.S1_x_at	LOC_Os01g66980	expressed protein	0.99	0.15	0.15	244	P	41	P,A
Os.49624.1.S1_at	LOC_Os05g33520	expressed protein	0.99	0.15	0.15	1699	P	278	P
Os.11756.1.S1_s_at	LOC_Os03g16050	fructose-1,6-bisphosphatase, chloroplast precursor	0.98	0.14	0.15	444	P	71	P,A
Os.7140.1.S1_at	LOC_Os11g16550	expressed protein	0.99	0.14	0.14	787	P	124	M,A
Os.2248.1.S1_at	LOC_Os07g37030	cytochrome b6-f complex iron-sulfur subunit, chloroplast	1.00	0.14	0.14	6980	P	1,107	P
Os.2467.1.S1_at	LOC_Os04g31040	violaxanthin de-epoxidase	0.98	0.14	0.14	220	P	34	P
Os.5401.1.S1_at	LOC_Os02g57670	50S ribosomal protein L9, chloroplast precursor	1.00	0.14	0.14	2961	P	457	P
Os.33308.1.S1_at	LOC_Os04g53490	OsCHL - *Oryza sativa* Chloroplastic lipocalin	1.00	0.14	0.14	944	P	145	P
Os.11610.1.S1_at	AK105924	hypothetical protein	0.97	0.13	0.14	1831	P	271	P
Os.32506.1.S1_at	LOC_Os06g47940	NFU3	0.97	0.13	0.14	1312	P	190	P
Os.17549.1.S1_at	LOC_Os04g44340	expressed protein	1.00	0.14	0.14	434	P	65	P
Os.51132.1.S1_at	LOC_Os08g07060	expressed protein	0.97	0.13	0.13	777	P	110	P
Os.7589.1.S1_at	LOC_Os06g46930	50S ribosomal protein L24, chloroplast precursor	0.98	0.13	0.13	2944	P	420	P
Os.8469.1.S1_at	LOC_Os09g34140	expressed protein	0.99	0.13	0.13	967	P	138	P
Os.405.1.S1_a_at	LOC_Os12g37260	lipoxygenase 2.1, chloroplast precursor	0.99	0.13	0.13	539	P	76	P,M,A
Os.9420.1.S1_at	LOC_Os07g15370	metal transporter Nramp6	0.99	0.13	0.13	295	P	42	A
Os.20378.1.S1_at	LOC_Os05g28830	expressed protein	0.98	0.12	0.12	149	P	20	A
Os.5660.1.S1_at	LOC_Os05g04170	ACS-like protein	1.00	0.12	0.12	12708	P	1,621	P
Os.50976.1.S1_at	LOC_Os03g48040	ferredoxin-6, chloroplast precursor	1.00	0.12	0.12	1237	P	156	P
Os.7137.1.S1_at	LOC_Os01g66980	expressed protein	0.98	0.11	0.11	566	P	71	P,M
Os.26537.2.S1_x_at	LOC_Os01g70520	beta-glucosidase homolog precursor	0.99	0.11	0.11	1888	P	228	P
Os.46187.1.S1_at	LOC_Os07g40940	glucan endo-1,3-beta-glucosidase 3 precursor	1.00	0.11	0.11	3774	P	462	P
Os.6767.1.S1_at	LOC_Os08g16830	retrotransposon protein, putative, SINE subclass	1.00	0.10	0.10	3588	P	425	P
Os.11674.1.S1_at	LOC_Os07g05000	aldo-keto reductase yakc	0.96	0.10	0.10	483	P	52	P,A
Os.7754.1.S1_at	LOC_Os08g44640	retinoid-inducible serine carboxypeptidase precursor	0.98	0.10	0.10	576	P	64	P,A
Os.7850.1.S1_at	LOC_Os11g42550	disease resistance response protein 206	1.00	0.10	0.10	11553	P	1,228	P
Os.7931.1.S1_a_at	LOC_Os06g51290	phytoene synthase, chloroplast precursor	0.99	0.09	0.094	533	P	55	P
Os.24901.1.A1_at	LOC_Os01g39960	lycopene epsilon cyclase, chloroplast precursor	1.00	0.09	0.094	698	P	72	P,A
Os.33788.1.S1_at	LOC_Os01g73540	YGGT family protein	1.00	0.09	0.093	966	P	98	M,A
Os.7931.1.S1_s_at	LOC_Os06g51290	phytoene synthase, chloroplast precursor	0.99	0.09	0.091	1262	P	125	P
Os.11404.1.S1_s_at	LOC_Os08g17390	expressed protein	0.97	0.08	0.087	507	P	48	A
OsAffx.2768.1.S1_x_at	LOC_Os02g27620	inositol 1,4,5-trisphosphate 5-phosphatase	1.00	0.08	0.085	412	P	39	A
Os.57176.1.S1_at	LOC_Os01g07620	expressed protein	1.00	0.08	0.082	1112	P	101	P
Os.51220.1.S1_at	LOC_Os09g31502	dihydroflavonol-4-reductase	1.00	0.08	0.082	2814	P	263	P
Os.10696.1.S1_at	LOC_Os06g01850	ferredoxin--NADP reductase, leaf isozyme, chloroplast	0.96	0.07	0.078	1696	P	141	P
Os.17906.1.S1_at	LOC_Os10g01044	NAD-dependent epimerase/dehydratase family	0.99	0.08	0.077	458	P	39	P
Os.8479.1.S1_s_at	LOC_Os04g34460	structural molecule	0.95	0.07	0.076	1290	P	103	P
Os.51220.1.S1_x_at	LOC_Os09g31502	dihydroflavonol-4-reductase	0.98	0.07	0.076	1574	P	132	P
Os.12837.1.S1_at	LOC_Os03g55720	plastoquinol-plastocyanin reductase	0.99	0.07	0.075	3552	P	289	P
Os.15243.2.S1_x_at	LOC_Os02g01340	ferredoxin--NADP reductase, leaf isozyme, chloroplast	1.00	0.07	0.072	379	P	32	A
Os.48879.1.S1_x_at	LOC_Os09g31502	dihydroflavonol-4-reductase	0.99	0.07	0.072	1727	P	140	P

Os.7680.1.S1_at	LOC_Os07g04020	expressed protein	0.98	0.07	0.072	1234	P	96	P
Os.27695.1.S1_at	LOC_Os12g37510	transferase, transferring glycosyl groups	0.99	0.07	0.071	2323	P	183	P
Os.27944.1.S1_at	LOC_Os03g08080	YGGT family protein	1.00	0.07	0.066	2942	P	220	P
Os.7218.1.S1_at	LOC_Os02g01150	hydroxypyruvate reductase	0.99	0.06	0.062	705	P	49	A
Os.9814.1.S1_at	LOC_Os01g55570	thylakoid membrane phosphoprotein 14 kDa	0.97	0.06	0.062	1168	P	78	P
Os.49874.2.S1_x_at	LOC_Os02g54060	chaperonin, chloroplast precursor	1.00	0.06	0.061	1597	P	109	P
Os.48879.1.S1_at	LOC_Os09g31502	dihydroflavonol-4-reductase	0.99	0.06	0.061	3167	P	218	P
Os.46924.1.S1_at	LOC_Os07g40690	leucoanthocyanidin reductase	0.98	0.06	0.061	1548	P	102	P
OsAffx.12382.1.S1_at	LOC_Os02g37060 (CT835332 indica cultivar-group)	expressed protein	0.99	0.05	0.053	8393	P	508	P
Os.46487.1.S1_at	LOC_Os10g30719	myb-like DNA-binding domain-containing protein	0.99	0.05	0.050	199	P	11	P,A
Os.49129.1.S1_at	LOC_Os04g33630	ferredoxin-3, chloroplast precursor	0.99	0.04	0.044	2280	P	115	P
Os.28218.1.S1_x_at	LOC_Os12g19394	ribulose bisphosphate carboxylase small chain C, chloroplast precursor	0.97	0.04	0.043	8946	P	417	P
Os.28218.1.S1_at	LOC_Os12g19394	ribulose bisphosphate carboxylase small chain C, chloroplast precursor	0.97	0.03	0.035	7669	P	290	P
Os.53724.1.S1_at	LOC_Os11g26340	expressed protein	0.97	0.03	0.029	4423	P	134	P
Os.17563.1.S1_at	LOC_Os02g17920	lactoylglutathione lyase	0.99	0.02	0.020	80	P	2	A
Os.6812.1.S1_at	LOC_Os10g21670	dehydration stress-induced protein	0.91	0.01	0.013	1443	P	16	A
Os.8482.1.S1_s_at	LOC_Os04g55159	expressed protein	0.86	0.01	0.012	428	P,A	4	A
Os.14938.1.S1_at	LOC_Os05g01140	benzoate carboxyl methyltransferase	0.99	0.01	0.010	481	P	2	A

Supplementary Table S4 (Nakano Y et al.)
Gene and probe sets for phenylpropanoid pathways. The probes with significant differential expression were identified by one-way ANOVA (FDR; *** < 0.001; ** < 0.005; * < 0.01) with Tu

TIGR loci	Systematic Name	WT Pa normalized	F71 Pa normalized	F71 Pa FDR	INT normalized	INT FDR	WT Pa raw	WT Pa flags	F71 Pa raw	F71 Pa flags	INT raw	INT flags
Phenylalanine ammonia-lyase (PAL)												
LOC_Os02g41630	Os.9330.1.S1_x_at	0.97	1.78		1.65		3,757	P	7,338	P	6,410	P
LOC_Os02g41630	Os.9330.1.S2_x_at	0.99	0.88		0.81		16,432	P	16,038	P	13,666	P
LOC_Os02g41630	Os.9330.2.S1_a_at	1.00	1.05		0.91	**	15,641	P	18,084	P	14,584	P
LOC_Os02g41630	Os.9330.4.S1_x_at	0.99	0.88		0.82		16,678	P	16,274	P	14,048	P
LOC_Os02g41650	Os.28397.1.S1_at	0.88	1.14		2.22		1,861	P	2,317	P	4,194	P
LOC_Os02g41650	Os.28397.1.S2_x_at	0.94	0.92		1.03		3,231	P	3,252	P	3,379	P
LOC_Os02g41650	Os.28397.1.S3_at	0.97	0.80		0.70		14,714	P	12,907	P	10,538	P
LOC_Os02g41670	Os.10930.1.S1_at	0.78	0.69		0.13		129	P,A	100	P	18	A
LOC_Os02g41680	Os.25687.1.S1_at	0.95	2.98		3.44		246	P	806	P	867	P
LOC_Os02g41680	Os.25687.1.S1_x_at	0.90	3.37		3.22		280	P	1,041	P	930	P
LOC_Os04g43760	Os.37893.1.S1_at	0.96	1.47		2.11		1,618	P	2,629	P	3,487	P
LOC_Os04g43800	Os.52536.1.S1_at	0.92	10.59		5.60		47	P	676	P	272	P
LOC_Os12g33610	Os.27728.1.S1_at	1.00	1.06		0.53		19	P,A	22	P,A	13	P,A
LOC_Os05g35290	None											
LOC_Os11g48110	None											
Cinnamate 4-hydroxylase (C4H)												
LOC_Os01g60450	OsAffx.2373.1.S1_at	0.87	0.68		0.63		14	A	12	A	10	A
LOC_Os01g60450	OsAffx.2373.1.S1_x_at	0.87	0.91		0.56		22	A	32	A	15	A
LOC_Os02g26810	Os.11417.1.S1_at	0.92	8.48		4.38		15	A	148	P	76	P,A
LOC_Os05g25640	Os.53884.1.S1_at	0.96	1.11		1.18		337	P	412	P	409	P
LOC_Os02g26770	None											
4-Coumarate: CoA ligase (4CL)												
class 1												
LOC_Os02g08100	Os.10669.1.S1_at	0.90	2.20		5.14		1,489	P	3,565	P	7,822	P
LOC_Os02g46970	Os.4377.1.S1_at	0.91	0.24		1.36		5	A	1	A	8	A
LOC_Os03g05780	Os.11459.1.S1_at	0.96	1.07		0.81		3,943	P	4,591	P	3,270	P
LOC_Os04g24530	OsAffx.13955.1.S1_at	0.83	1.09		1.10		52	A	61	P,A	58	M,A
LOC_Os04g24530	OsAffx.13955.1.S1_x_at	1.00	0.91		1.26		68	P,A	68	P,A	88	P
LOC_Os06g44620	Os.8020.1.S1_at	1.00	0.69		0.82		4,926	P	3,740	P	4,155	P
LOC_Os08g14760	Os.52921.1.S1_at	0.99	0.25		0.46		1,385	P	404	P	661	P
LOC_Os08g34790	Os.19375.1.S1_at	1.00	2.62	**	0.73		84	P	244	P	64	P
class 2												
LOC_Os01g67530	Os.5174.1.S1_at	1.00	0.62		1.19		406	P	282	P	497	P
LOC_Os01g67540	OsAffx.21790.1.S1_at	0.90	0.80		1.82		109	P,A	112	P,M	205	P
LOC_Os03g04000	Os.18327.1.S1_at	0.91	0.77		1.12		897	P	757	P	1,022	P
LOC_Os07g17970	Os.15398.1.S1_at	0.94	0.17	**	1.38		125	P	23	A	180	P
LOC_Os07g44560	OsAffx.5636.1.S1_at	1.00	0.57		0.64		34	P	23	P,A	23	P,A
4CL-like												
LOC_Os08g04770	OsAffx.29036.1.S1_at	0.76	1.42		0.49		25	A	41	A	15	A
LOC_Os10g42800	OsAffx.30755.1.S1_x_at	0.43	0.45		0.99		12	A	9	A	13	P,A
LOC_Os10g42800	OsAffx.30755.2.S1_at	0.70	0.63		0.20		17	A	13	A	4	A
***p* -Coumarate 3-hydroxylase (C3H)**												
LOC_Os05g41440	Os.5391.1.S1_at	0.99	0.76		1.15		6,584	P	5,592	P	7,750	P
LOC_Os10g12050	Os.49279.1.S1_at	0.99	0.75		0.92		68	M,A	58	A	65	M,A
LOC_Os10g12080	Os.17812.1.S1_at	0.63	0.14		0.50		13	A	2	A	7	A
***p* -Hydroxycinnamoyl-CoA: quinate shikimate hydroxycinnamoyltransferase (HCT)**												
LOC_Os02g39850	Os.7870.1.S1_at	0.97	2.30		1.25		1,703	P	4,308	P	2,184	P
LOC_Os04g42250	Os.12225.1.S1_at	0.98	1.16		1.09		6,398	P	8,107	P	7,139	P
Caffeoyl-CoA *O* -methyltransferase (CCoAOMT)												
class 1												
LOC_Os06g06980	Os.4198.1.S1_at	0.99	0.92		1.39		2,135	P	2,166	P	3,053	P
LOC_Os06g06980	Os.4198.1.S1_x_at	0.99	0.74		0.99		1,588	P	1,293	P	1,613	P
LOC_Os08g05790	Os.24052.1.S1_at	1.00	0.36		0.79		150	P	68	P	124	P
LOC_Os08g05790	Os.24052.1.S1_x_at	1.00	0.56	*	0.78		365	P	225	P	295	P
LOC_Os08g05790	OsAffx.5720.1.S1_at	1.00	0.66		0.77		1,015	P	738	P	806	P
LOC_Os08g38900	Os.4244.1.S1_at	0.98	0.97		1.47		8,396	P	8,865	P	12,603	P
LOC_Os09g30360	Os.4830.1.S1_at	0.93	1.21		0.61		307	P	415	P	193	P
LOC_Os09g30360	Os.4830.1.S1_x_at	1.00	1.07		0.93		267	P,A	322	P,M,A	256	A
class 2												
LOC_Os08g38910	Os.7348.1.S1_a_at	0.97	1.07		0.86		9,406	P	11,491	P	8,592	P
LOC_Os08g38910	Os.7348.1.S1_at	0.90	0.73		0.31		5,074	P	4,063	P	1,617	P
LOC_Os08g38910	Os.7348.2.S1_x_at	0.96	0.81		0.68		2,414	P	2,125	P	1,689	P
LOC_Os08g38920	None											
Cinnamoyl-CoA reductase (CCR)												
LOC_Os01g18110	Os.45894.1.S1_at	0.89	0.29		0.08	*	1,188	P	373	P	94	P
LOC_Os01g18110	Os.45894.1.S1_x_at	0.90	0.26		0.07	**	3,563	P	1,019	P	259	P
LOC_Os01g18120	Os.20420.1.S1_at	0.99	0.32	***	0.07	***	8,121	P	2,891	P	557	P
LOC_Os02g08420	Os.12948.1.S1_at	1.00	0.95		1.07		341	P	357	P	375	P
LOC_Os02g56460	Os.6757.1.S1_at	0.99	0.17		0.82		26	A	8	A	22	P,A
LOC_Os02g56690	OsAffx.24898.2.S1_at	0.63	0.27		1.46		14	A	5	A	22	M,A
LOC_Os02g56700	Os.20154.1.S1_at	0.80	3.06		2.76		2	A	8	A	7	A
LOC_Os02g56720	Os.55206.1.A1_at	0.42	0.04		0.15		33	A	2	A	6	A
LOC_Os08g17500	Os.54671.1.S1_at	0.67	0.53		3.03		17	A	12	A	53	P
LOC_Os08g34280	Os.8544.1.S1_at	0.93	1.23		5.16	*	448	P	605	P	2,358	P
LOC_Os09g04050	Os.53814.1.S1_at	0.85	0.34		2.94		426	P	158	P	1,291	P
LOC_Os09g08720	OsAffx.29770.1.S1_at	0.95	1.01		0.47		14	A	17	A	7	A
LOC_Os09g09230	OsAffx.17611.1.S1_at	0.99	0.22		0.52		27	A	8	A	16	A
LOC_Os09g09270	OsAffx.29775.1.S1_at	1.00	0.31		0.14		32	A	13	A	5	A
LOC_Os09g25150	Os.9685.1.S1_a_at	0.61	0.19		6.79		800	P	175	P	5,541	P
LOC_Os02g56680	None											
Ferulate 5-hydroxylase (F5H)												
LOC_Os03g02180	Os.16138.1.S1_s_at	0.52	0.27		0.54		8	A	3	A	6	A
LOC_Os03g02180	OsAffx.12708.1.S1_x_at	0.99	0.87		0.88		60	M,A	58	A	55	M,A
LOC_Os06g24180	OsAffx.4924.1.S1_at	0.55	0.34		0.73		9	A	4	A	12	A
LOC_Os10g36848	Os.9727.1.S1_at	1.00	0.52		8.50	***	163	A	96	A	1,440	P
Caffeic acid O-methyltransferase (COMT)												
COMT												
LOC_Os02g57760	Os.54406.1.S1_at	0.99	0.38	*	0.55	*	672	P	283	P	381	P
LOC_Os12g10170	OsAffx.19584.1.S1_at	1.00	0.97		0.72		17	A	18	A	16	A
LOC_Os12g13800	OsAffx.7586.1.S1_at	0.85	0.99		0.91		12	A	18	A	12	A
COMT-Like												
LOC_Os04g01470	Os.23187.1.S1_at	0.85	0.50		0.33		8	A	4	A	3	A
LOC_Os04g09604	Os.26569.1.S1_at	0.70	1.33		0.77		190	P,A	307	P	154	P
LOC_Os04g09654	Os.10277.1.S1_at	1.00	0.51	*	0.48	*	5,440	P	3,088	P	2,701	P
LOC_Os12g10140	OsAffx.31676.1.S1_at	0.92	1.61		1.70		6	A	13	A	16	A
LOC_Os12g13810	OsAffx.19658.1.S1_at	0.90	0.83		2.08		40	A	39	A	84	A
LOC_Os04g09670	None											
LOC_Os04g09680	None											
Cinnamyl alcohol dehydrogenase (CAD)												
LOC_Os02g09490	Os.8684.1.S1_a_at	0.96	0.79		1.28		7,729	P	6,789	P	10,083	P
LOC_Os03g12270	Os.45954.1.S1_at	0.79	0.54		0.54		16	A	15	A	12	A
LOC_Os04g15920	Os.6089.1.S1_at	0.88	0.21		0.35		2,247	P	563	P	795	P
LOC_Os04g52280	Os.32904.1.S1_at	0.99	0.66		0.70		20	P,A	15	A	15	A
LOC_Os09g23530	Os.5983.1.S1_at	0.79	19.06		1.26		17	A	374	P	24	A
LOC_Os09g23550	Os.6862.2.A1_at	0.97	1.19		1.06		3,003	P	3,943	P	3,288	P
LOC_Os10g11810	Os.7543.1.S1_at	0.98	1.00		1.10		3,477	P	3,853	P	3,921	P
LOC_Os10g29470	Os.7496.1.S1_a_at	0.97	1.18		0.93		744	P	1,062	P	703	P
LOC_Os08g16910	None											
LOC_Os09g23540	None											
LOC_Os09g23560	None											
LOC_Os11g40690	None											

Supplementary Table S5 (Nakano Y et al.)

Gene and probe sets for major carbon metabolism genes. The probes with significant differential expression were identified by one-way ANOVA (FDR; *** < 0.001; ** < 0.005; * < 0.01) with Tukey's post hoc test, which are indicated

TIGR Loci	Systematic Name	WT Pa normalized	F71 Pa normalized	F71 Pa FDR	WT INT normalized	WT INT FDR	WT Pa raw	WT Pa flags	F71 Pa raw	F71 Pa flags	WT INT raw	WT INT flags	Description
(A)													
Alpha-amylase (Starch→D-Glc) EC 3.2.1.1													
LOC_Os01g25510	Os.12293.2.S1_at	0.51	0.21		0.26		8	A	2	A	2	A	alpha-amylase isozyme C
LOC_Os01g51754	Os.24868.1.S1_at	0.99	0.92		1.09		2,070	P	2,105	P	2,330	P	alpha-amylase isozyme C2 precursor
LOC_Os01g51754	Os.24868.2.S1_x_at	1.00	1.05		1.34		635	P	736	P	876	P	alpha-amylase isozyme C2 precursor
LOC_Os01g51754	Os.49305.2.S1_x_at	1.00	0.69		0.81		30	P	24	P,A	25	P,A	alpha-amylase isozyme C2 precursor
LOC_Os02g52700	Os.57437.1.S1_at	1.00	0.75		0.62		51	P	43	P	35	P,A	alpha-amylase precursor
LOC_Os02g52700	Os.57437.1.S1_x_at	0.62	0.14		0.21		11	A	2	A	3	A	alpha-amylase precursor
LOC_Os02g52700	Os.57438.1.A1_at	0.94	0.65		0.48		5	A	4	A	3	A	alpha-amylase precursor
LOC_Os02g52700	Os.57438.1.S1_at	0.97	0.65		0.54		1	A	1	A	1	A	alpha-amylase precursor
LOC_Os02g52710	Os.49249.1.S1_at	0.90	0.68		0.61		1	A	1	A	0	A	alpha-amylase precursor
LOC_Os04g33040	Os.7294.1.S1_at	1.00	1.13		1.16		2,010	P	2,494	P	2,380	P	alpha-amylase type B isozyme precursor
LOC_Os06g49970	Os.50953.1.S1_at	0.82	1.08		0.44		430	P	505	P	191	P	alpha-amylase isozyme C2 precursor
LOC_Os08g36900	Os.12593.1.S1_s_at	0.92	0.80		1.93		2	A	2	A	7	A	alpha-amylase isozyme 3E precursor (RAmy3E)
LOC_Os08g36910	Os.10908.1.S1_a_at	0.95	0.89		0.95		2	A	3	A	4	A	alpha-amylase isozyme 3D precursor (RAmy3D)
LOC_Os08g36910	Os.10908.4.S1_at	0.93	1.32		1.10		23	A	34	A	27	A	alpha-amylase isozyme 3D precursor (RAmy3D)
LOC_Os08g36910	Os.12452.1.S1_s_at	0.11	0.52		1.32		18	P,A	16	P,A	26	P	alpha-amylase isozyme 3D precursor (RAmy3D)
LOC_Os09g28400	Os.51838.1.S1_at	0.99	0.46		0.46		18	A	12	A	14	P,A	alpha-amylase isozyme 3A precursor (RAMy3A)
LOC_Os09g28420	Os.39991.1.A1_at	0.97	0.40		0.33		17	A	9	P,A	7	A	alpha-amylase isozyme 3B precursor (RAmy3B)
LOC_Os09g28430	Os.33211.1.S1_at	0.84	3.09		2.31		2	A	8	A	5	A	alpha-amylase isozyme 3C precursor (RAmy3C)
Beta-fructofuranosidase (Suc-6P→D-Glc-6P+Fruc) EC 3.2.1.26													
cytosol													
LOC_Os01g22900	Os.17741.1.S1_at	0.93	0.93		0.51		828	P	863	P	438	P	beta-fructofuranosidase
LOC_Os03g20020	Os.32659.1.S1_at	0.98	1.26		1.56		549	P	753	P	878	P	beta-fructofuranosidase
cell wall													
LOC_Os01g73580	Os.11387.1.S1_a_at	0.97	0.53		2.10		58	P	36	P	125	P	beta-fructofuranosidase, insoluble isoenzyme 4 precurs
LOC_Os02g01590	Os.47792.1.S1_at	0.89	1.14		4.73		254	P,A	366	P,A	1,255	P	beta-fructofuranosidase 1 precursor
LOC_Os02g33110	Os.9416.1.S1_at	1.00	1.38		0.16	***	1,608	P	2,439	P	257	P	beta-fructofuranosidase, insoluble isoenzyme 1 precurs
LOC_Os03g52560	OsAffx.13470.1.S1_at	0.61	0.49		0.64		18	A	15	A	15	A	beta-fructofuranosidase, insoluble isoenzyme 3 precurs
LOC_Os04g33720	Os.50337.1.S1_at	1.00	0.97		1.41		23	A	25	P,A	33	P,A	beta-fructofuranosidase, insoluble isoenzyme 3 precurs
LOC_Os04g33740	Os.50640.1.S1_at	0.62	4.52		1.84		18	A	124	P,A	34	A	beta-fructofuranosidase, insoluble isoenzyme 2 precurs
LOC_Os04g45290	Os.19361.1.S1_at	0.93	0.67		1.14		2	A	2	A	3	A	beta-fructofuranosidase 1 precursor
LOC_Os04g45290	Os.19361.1.S2_at	0.94	1.23		37.17		2	A	3	A	59	A	beta-fructofuranosidase 1 precursor
LOC_Os04g56920	OsAffx.14447.1.S1_at	0.94	0.82		0.28		4	A	5	A	1	A	beta-fructofuranosidase, insoluble isoenzyme 6 precurs
LOC_Os04g56930	OsAffx.14448.1.S1_at	0.76	0.09		0.16		12	A	1	A	2	A	beta-fructofuranosidase, insoluble isoenzyme 5
LOC_Os09g08072	Os.2296.1.S1_at	0.96	0.91		0.55		4,642	P	4,686	P	2,637	P	beta-fructofuranosidase, insoluble isoenzyme 7 precurs
LOC_Os09g08072	Os.55782.1.S1_at	0.91	0.34		1.38		5	A	2	A	10	A	beta-fructofuranosidase, insoluble isoenzyme 7 precurs
LOC_Os09g08120	OsAffx.29757.2.S1_at	0.82	2.30		2.17		22	A	57	A	51	A	beta-fructofuranosidase, insoluble isoenzyme 7 precurs
LOC_Os09g08120	OsAffx.29757.2.S1_x_at	0.99	0.94		0.44		173	P	179	P	79	P,A	beta-fructofuranosidase, insoluble isoenzyme 7 precurs
Beta-xylosidase (1,4 beta-D-Xylan→D-Xylose) EC 3.2.1.37													
LOC_Os01g19220	Os.2075.1.S1_at	1.00	0.11	**	0.56		1,544	P	196	P	895	P	beta-D-xylosidase
LOC_Os02g51620	Os.38849.1.S1_at	0.90	1.27		3.92		449	P	800	P	1,823	P	beta-D-xylosidase
LOC_Os04g44840	Os.16394.1.S1_at	0.99	1.26		0.82		474	P	666	P	400	P	beta-D-xylosidase
LOC_Os04g54810	Os.48101.1.S1_at	0.99	0.26		2.58		2,353	P	851	P	6,257	P	beta-D-xylosidase
LOC_Os11g18690	OsAffx.31043.1.S1_at	0.55	0.17		0.71		20	A	4	A	22	A	beta-xylosidase
LOC_Os11g18730	Os.27453.1.S1_at	0.97	0.13		0.80		65	P,A	10	A	53	A	beta-D-xylosidase
LOC_Os11g19160	Os.52968.1.S1_at	0.99	0.54	*	1.14		71	P	43	A	84	P	beta-D-xylosidase
LOC_Os11g19210	Os.56337.1.S1_at	0.93	0.76		257.20	***	2	A	2	A	440	P	beta-D-xylosidase
LOC_Os11g47350	OsAffx.7440.1.S1_at	0.57	0.59		0.48		8	A	7	A	5	A	beta-D-xylosidase
LOC_Os11g44950	None												
CesA													
LOC_Os01g54620	Os.18724.1.S1_a_at	0.91	0.55		7.30	**	923	P	570	P	6,986	P	CESA4 - cellulose synthase, expressed AtCESA8
LOC_Os01g54620	Os.18724.1.S1_at	0.95	0.50		4.91	*	2,477	P	1519	P	12,576	P	CESA4 - cellulose synthase, expressed AtCESA8
LOC_Os01g54620	Os.18724.2.S1_x_at	0.95	0.62		6.60	**	790	P	555	P	5,433	P	CESA4 - cellulose synthase, expressed AtCESA8
LOC_Os03g59340	Os.14979.1.S1_at	1.00	0.73		0.97		152	P	125	P	152	P	CESA2 - cellulose synthase, expressed AtCESA3
LOC_Os03g59340	Os.14979.1.S2_at	0.98	1.04		0.55		131	P	150	P	75	P,A	CESA2 - cellulose synthase, expressed AtCESA3
LOC_Os03g62090	Os.4857.1.S1_at	1.00	0.73		0.82		10,603	P	8578	P	8,897	P	CESA5 - cellulose synthase, expressed AtCESA6
LOC_Os05g08370	Os.10183.1.S1_at	0.97	0.36		0.49		388	P	164	P	193	P	CESA1 - cellulose synthase, expressed AtCESA1
LOC_Os05g08370	Os.10183.1.S2_at	1.00	0.68	*	0.69	*	16,298	P	12060	P	11,490	P	CESA1 - cellulose synthase, expressed AtCESA1
LOC_Os06g39970	OsAffx.15853.1.S1_at	0.59	0.15		0.34		18	A	3	A	7	A	CESA11 - cellulose synthase AtCESA10
LOC_Os06g39970	OsAffx.15853.1.S1_x_at	0.80	0.54		0.71		8	A	4	A	6	A	CESA11 - cellulose synthase AtCESA10
LOC_Os07g10770	Os.10176.1.S1_at	1.00	0.74	**	0.75	**	14,544	P	11846	P	11,159	P	CESA8 - cellulose synthase, expressed AtCESA3
LOC_Os07g14850	Os.10926.1.S1_at	1.00	0.69	**	0.64	**	14,347	P	10778	P	9,404	P	CESA6 - cellulose synthase, expressed AtCESA6
LOC_Os07g24190	Os.10178.1.S1_a_at	1.00	0.73		0.95		1,790	P	1434	P	1,773	P	CESA3 - cellulose synthase, expressed AtCESA6
LOC_Os07g24190	Os.10178.2.S1_a_at	1.00	0.80		0.80		20,578	P	18013	P	16,916	P	CESA3 - cellulose synthase, expressed AtCESA6
LOC_Os09g25490	Os.10206.1.S1_at	0.85	0.41		9.76	*	533	P	287	P	5,437	P	CESA9 - cellulose synthase, expressed AtCESA7
LOC_Os10g32980	Os.3206.1.S1_at	0.93	0.57		5.06		2,186	P	1535	P	11,429	P	CESA7 - cellulose synthase, expressed AtCESA4
LOC_Os12g29300	None												CESA10 - cellulose synthase, expressed AtCSLD3
Fructokinase (D-Fruc→D-Fruc-6P) EC 2.7.1.4													
LOC_Os01g66940	Os.8324.1.S1_a_at	0.96	0.76		1.30		393	P	324	P	539	P	fructokinase-1
LOC_Os06g12600	Os.27745.1.A1_at	1.00	0.74		0.75		5,237	P	4,277	P	4,021	P	fructokinase-2
LOC_Os08g02120	Os.12780.1.S1_at	0.96	0.63		0.91		3,036	P	2,094	P	2,828	P	fructokinase-2
Glc 6P-isomerase (D-Glc-6P=D-Fruc-6P) EC 5.3.1.9													
cytosol													
LOC_Os03g56460	Os.154.1.S1_at	0.99	0.93		0.90		5,836	P	6,066	P	5,395	P	glucose-6-phosphate isomerase, cytosolic A
LOC_Os03g56460	Os.57457.1.S1_x_at	1.00	1.04		1.38		1,113	P	1,271	P	1,576	P	glucose-6-phosphate isomerase, cytosolic A
LOC_Os06g14510	Os.4697.1.S1_at	1.00	0.75		0.98		2,854	P	2,366	P	2,873	P	glucose-6-phosphate isomerase, cytosolic B
chroloplastic													
LOC_Os08g37380	Os.23365.1.S1_at	0.99	0.76		0.86		775	P	644	P	686	P	glucose-6-phosphate isomerase
LOC_Os09g29070	Os.26384.1.S1_at	0.99	1.30		1.09		2,928	P	4,182	P	3,286	P	glucose-6-phosphate isomerase
Hexokinase (D-Glc→D-Glc-6P) EC 2.7.1.1													
LOC_Os01g09460	Os.33758.1.S1_s_at	0.97	1.16		1.07		368	P	492	P	412	P	hexokinase-1
LOC_Os01g09460	Os.33758.2.S1_s_at	0.99	1.34		0.74		47	P,A	70	P	36	P	hexokinase-1
LOC_Os01g09460	Os.33758.2.S1_x_at	0.99	1.64		1.05		45	P	82	P	50	P	hexokinase-1
LOC_Os01g52450	Os.41826.1.S1_x_at	0.60	6.74		4.11		13	P,A	101	P	57	P	hexokinase-2
LOC_Os01g53930	Os.11775.1.S2_at	0.81	14.75		1.28		16	A	287	P	42	P,A	hexokinase-1
LOC_Os01g53930	Os.5547.1.S1_s_at	0.99	0.59		0.71		7,456	P	4,868	P	5,451	P	hexokinase-1
LOC_Os01g53930	OsAffx.11594.1.S1_at	1.00	1.13		0.45		64	P,A	81	P,A	30	A	hexokinase-1
LOC_Os01g71320	Os.52037.1.S1_at	1.00	1.03		0.75		38	P	44	P	30	P	hexokinase-1
LOC_Os01g71320	OsAffx.23999.1.S1_x_at	1.00	1.12		1.25		44	P	55	P,M	57	P	hexokinase-1
LOC_Os05g09500	Os.6114.1.S1_at	0.99	2.69		1.41		299	P	913	P	433	P	hexokinase-1
LOC_Os05g31110	OsAffx.4483.1.S1_at	0.99	1.33		0.97		1	A	2	A	1	A	hexokinase-1
LOC_Os05g44760	Os.20973.1.S1_s_at	0.99	0.75		0.85		2,344	P	1,940	P	2,054	P	hexokinase-2
LOC_Os05g44760	Os.3293.1.S1_at	0.99	0.82		0.87		1,145	P	1,027	P	1,024	P	hexokinase-2
LOC_Os05g45590	Os.17535.1.S1_at	0.99	1.23		1.24		155	P	211	P	197	P	hexokinase-2
LOC_Os05g45590	OsAffx.27327.1.S1_at	0.99	1.44		1.28		32	P	51	P	43	P	hexokinase-2
LOC_Os07g09890	Os.3294.1.S1_at	0.99	1.62		5.37	**	395	P,M	715	P	2,224	P	hexokinase-1
LOC_Os07g26540	OsAffx.22372.1.S1_at	0.94	0.60		0.92		8	A	5	A	8	A	hexokinase-1
Phosphoglucomutase (D-Glc-6P=D-Glc-1P) EC 5.4.2.2													
LOC_Os03g50480	Os.5894.1.S1_at	0.99	0.63		0.86		11,280	P	7,806	P	9,916	P	phosphoglucomutase, cytoplasmic 2
LOC_Os10g11140	Os.5319.1.S1_at	0.89	0.30		1.03		8,441	P	3,122	P	8,766	P	phosphoglucomutase, chloroplast precursor
SPS (UDP-D-Glc+D-Fruc-6P→Suc-6P+UDP) EC 2.4.1.14													
LOC_Os01g69030	Os.3454.1.S1_at	0.87	0.18		1.50		373	P	83	P,A	569	P	sucrose-phosphate synthase
LOC_Os02g09170	Os.22727.1.S1_at	1.00	0.64		0.35		32	P,M	23	P,A	15	A	sucrose-phosphate synthase 1
LOC_Os06g43630	Os.27130.1.S1_at	0.99	0.90		0.76		4,493	P	4,435	P	3,535	P	sucrose-phosphate synthase 1
LOC_Os06g43630	OsAffx.15911.1.S1_x_at	1.00	1.04		0.76		1,218	P	1,385	P	958	P	sucrose-phosphate synthase 1
LOC_Os08g20660	Os.27359.1.S1_at	0.99	0.79		0.89		2,953	P	2,563	P	2,691	P	sucrose-phosphate synthase 1
LOC_Os11g12810	None												
Sucrose synthase (SUC→UDP-D-Glc+D-Fruc) EC 2.4.1.13													
LOC_Os02g58480	Os.52194.1.S1_at	0.81	0.77		17.60	**	25	P,A	21	A	456	P	sucrose synthase
LOC_Os03g22120	Os.17890.1.S1_at	0.97	1.07		0.95		1,826	P	2,178	P	1,801	P	sucrose synthase
LOC_Os03g28330	Os.25677.1.S1_at	0.99	0.66		0.81		16,150	P	11,774	P	13,460	P	sucrose synthase 2
LOC_Os03g28330	Os.57465.1.S1_x_at	0.93	0.51		1.26		7,111	P	3,963	P	9,100	P	sucrose synthase 2
LOC_Os04g24430	Os.48521.1.S1_at	0.56	0.13		12.68		40	P,A	7	A	534	P	sucrose synthase
LOC_Os06g09450	Os.9127.1.S1_a_at	0.98	0.88		1.14		12,020	P	11,836	P	14,191	P	sucrose synthase 1
LOC_Os07g42490	Os.9860.1.S1_at	0.96	0.93		0.66		76	A	79	A	60	M,A	sucrose synthase 3
LOC_Os04g17650	None												sucrose synthase

Sucrose-6P phosphatase (Suc-6P→SUC) EC 3.1.3.24													
LOC_Os01g27880	Os.13071.1.S1_at	0.98	0.64		1.31		854	P	594	P	1,139	P	Sucrose phosphatase
LOC_Os02g05030	Os.49155.1.S1_at	1.00	0.50	**	0.71	**	6,351	P	3,514	P	4,639	P	Sucrose phosphatase
LOC_Os05g05270	Os.49091.1.S1_at	0.96	0.67		1.11		280	P	208	P	324	P	Sucrose phosphatase
UDP-D-Glc 6-dehydrogenase (UDP-Glc→UDP-GlcA) EC 1.1.1.22													
LOC_Os03g55070	Os.5016.1.S1_at	1.00	1.37		1.21		959	P	1,438	P	1,199	P	UDP-glucose 6-dehydrogenase
LOC_Os12g25690	Os.10473.1.S1_at	0.96	1.05		2.10		5,090	P	5,889	P	10,969	P	UDP-glucose 6-dehydrogenase
LOC_Os12g25700	Os.20425.1.S1_at	0.97	1.15		4.00	**	234	P	295	P	966	P	UDP-glucose 6-dehydrogenase
LOC_Os12g25700	Os.20425.2.S1_at	1.00	1.00		1.70		1,339	P	1,469	P	2,355	P	UDP-glucose 6-dehydrogenase
LOC_Os12g25700	Os.20425.2.S1_x_at	0.99	1.14		2.33	**	2,377	P	2,977	P	5,708	P	UDP-glucose 6-dehydrogenase
LOC_Os03g31210	None												UDP-glucose 6-dehydrogenase
LOC_Os03g40720	None												UDP-glucose 6-dehydrogenase
UDP-glc pyro phosphorylase (D-Glc-1P→UDP-D-Glc) EC 2.7.7.9													
LOC_Os01g15910	OsAffx.11069.1.S1_x_at	0.76	1.32		0.91		23	P,A	39	P,A	22	P,A	UTP--glucose-1-phosphate uridylyltransferase family p
LOC_Os01g15910	OsAffx.11069.3.S1_at	0.95	2.38		1.59		47	A	122	M,A	79	A	UTP--glucose-1-phosphate uridylyltransferase family p
LOC_Os01g15910	OsAffx.11069.3.S1_x_at	0.96	1.34		1.43		32	A	49	A	48	A	UTP--glucose-1-phosphate uridylyltransferase family p
LOC_Os01g15910	OsAffx.11069.4.S1_at	0.79	1.12		1.36		8	A	10	A	11	A	UTP--glucose-1-phosphate uridylyltransferase family p
LOC_Os02g02560	Os.2370.1.S1_at	0.98	0.96		1.26		36	P,A	39	P	49	P	UTP--glucose-1-phosphate uridylyltransferase
LOC_Os09g38030	Os.10118.1.S1_at	0.95	0.57		0.85		10,741	P	6,627	P	9,300	P	UTP--glucose-1-phosphate uridylyltransferase
UDP-D-glcA 4-epimerase (UDP-GlcA→UDP-GalA) EC 5.1.3.6													
LOC_Os02g54890	Os.8158.1.S1_at	0.91	0.52		0.62		1,163	P	702	P	756	P	expressed protein
LOC_Os03g14540	Os.39979.1.A1_at	1.00	0.76		0.75		2,677	P	2,242	P	2,053	P	expressed protein
LOC_Os06g08810	Os.54870.1.S1_at	0.60	0.45		0.79		7	A	4	A	11	A	expressed protein
LOC_Os08g41440	Os.53946.1.S1_at	0.97	1.59		0.43		1,703	P	3,096	P	747	P	NAD-dependent epimerase/dehydratase family protein
LOC_Os09g32670	Os.18486.1.S1_at	0.93	0.57		0.50		3,502	P	2,434	P	1,829	P	protein capl
UDP-glcA acid decarboxylase (UDP-GlcA → UDP-Xly) EC 4.1.1.35													
LOC_Os01g21320	Os.5892.1.S1_s_at	1.00	0.89		0.85		3,466	P	3,372	P	3,057	P	UDP-glucuronic acid decarboxylase 1 (OsUXS2)
LOC_Os01g62020	Os.9835.1.S1_a_at	0.99	0.68		0.97		4,379	P	3,333	P	4,345	P	UDP-glucuronic acid decarboxylase 1 (OsUXS4)
LOC_Os03g16980	Os.12349.1.S1_at	0.99	0.84		1.14		13,959	P	12,799	P	16,311	P	UDP-glucuronic acid decarboxylase 1 (OsUXS3)
LOC_Os03g17230	Os.49763.1.S1_s_at	0.73	1.00		0.66		11	A	14	A	12	M,A	UDP-glucuronic acid decarboxylase 1 (OsUXS1)
LOC_Os03g17230	Os.49763.2.S1_at	0.95	0.31		1.01		28	P,A	16	P,A	30	P	UDP-glucuronic acid decarboxylase 1 (OsUXS1)
LOC_Os05g29990	Os.46115.1.S1_at	1.00	1.54		1.30		1,619	P	2,730	P	2,164	P	UDP-glucuronic acid decarboxylase 1 (OsUXS5)
LOC_Os07g47700	Os.7085.2.S1_x_at	1.00	1.51		0.49	**	7,682	P	12,720	P	3,922	P	UDP-glucuronic acid decarboxylase 1 (OsUXS6)
UDP-xylose 4-epimerase (UDP-Xly = UDP-Ara) EC 5.1.3.5													
LOC_Os04g52730	Os.20272.1.S1_a_at	0.98	1.67		0.34	*	1,156	P	2,174	P	408	P	UDP-arabinose 4-epimerase 2
LOC_Os04g52730	OsAffx.4159.1.S1_x_at	0.99	1.54		0.34	**	1,264	P	2,156	P	447	P	UDP-arabinose 4-epimerase 2
LOC_Os07g04690	Os.11609.1.S1_at	1.00	0.81		0.84		10,895	P	9,641	P	9,403	P	UDP-arabinose 4-epimerase 1
LOC_Os08g03570	Os.5729.1.S1_at	1.00	1.36	*	1.73	*	1,293	P	1,928	P	2,304	P	UDP-arabinose 4-epimerase 3
(B)													
6P-fructokinase (D-Fruc-6P→Fruc-1,6-bisP) EC 2.7.1.11													
LOC_Os01g09570	Os.12230.1.S1_a_at	0.73	0.65		0.93		805	P	566	P	757	P	6-phosphofructokinase 2
LOC_Os01g53680	Os.1991.1.S1_at	0.99	0.72		1.53		2,064	P	1,637	P	3,237	P	6-phosphofructokinase
LOC_Os04g39420	Os.4760.1.S1_at	0.99	0.81		0.66		1,541	P	1,378	P	1,050	P	6-phosphofructokinase 2
LOC_Os05g10650	Os.9848.1.S1_at	0.87	1.80		0.32		69	P	140	P	22	P,A	6-phosphofructokinase 2
LOC_Os05g44922	Os.12014.1.S1_s_at	0.98	1.08		0.87		1,908	P	2,257	P	1,689	P	6-phosphofructokinase
LOC_Os05g44922	OsAffx.27312.1.S1_at	0.98	1.02		0.74		1,596	P	1,828	P	1,209	P	6-phosphofructokinase
LOC_Os06g05860	Os.26885.1.A1_at	1.00	1.22		1.00		5,679	P	7,637	P	5,863	P	6-phosphofructokinase
LOC_Os06g05860	OsAffx.15279.1.S1_x_at	0.99	1.26		1.30		1,695	P	2,341	P	2,254	P	6-phosphofructokinase
LOC_Os08g34050	OsAffx.29501.1.S1_at	0.94	1.45		0.65		47	P	78	P	32	P,M	6-phosphofructokinase 2
LOC_Os09g24910	Os.5137.1.S1_at	0.98	0.98		1.07		572	P	617	P	633	P	6-phosphofructokinase 2
LOC_Os09g30240	Os.56193.1.S1_at	0.61	0.19		0.71		29	A	6	A	23	A	6-phosphofructokinase
LOC_Os10g26570	Os.17997.1.S1_at	0.99	1.14		0.77		776	P	1011	P	615	P	pyrophosphate--fructose 6-phosphate 1-phosphotransferase, putative, expressed
LOC_Os10g26570	Os.17997.2.S1_x_at	0.97	1.16		0.96		506	P	652	P	499	P	pyrophosphate--fructose 6-phosphate 1-phosphotransferase, putative, expressed
Acetyl-CoA C-acyltransferase EC 2.3.1.16													
LOC_Os02g57260	Os.8733.1.S1_at	0.99	1.06		0.74		6,065	P	7,123	P	4,591	P	3-ketoacyl-CoA thiolase 2, peroxisomal precursor
LOC_Os10g31950	Os.12690.1.S1_at	0.99	0.67		0.75		9,787	P	7,118	P	7,481	P	3-ketoacyl-CoA thiolase 2, peroxisomal precursor
Fructose-1,6-bisphosphatase (Fruc-1,6-bisP→D-Fruc-6P) EC 3.1.3.11													
cytosolic													
LOC_Os01g64660	Os.3408.1.A1_x_at	0.75	1.13		0.70		20	A	26	A	16	A	fructose-1,6-bisphosphatase, cytosolic
LOC_Os01g64660	Os.3408.1.A2_a_at	0.99	0.44		1.07		35	P,M,A	22	A	41	P,A	fructose-1,6-bisphosphatase, cytosolic
LOC_Os05g36270	Os.25619.1.S1_at	1.00	0.89		1.49		2,372	P	2,338	P	3,651	P	fructose-1,6-bisphosphatase, cytosolic
plastidic													
LOC_Os03g16050	Os.11756.1.S1_at	0.94	0.02	**	2.38		186	P	7	A	454	P	fructose-1,6-bisphosphatase, chloroplast precursor
LOC_Os03g16050	Os.11756.1.S1_s_at	0.98	0.14	***	1.62		444	P	71	P,A	736	P	fructose-1,6-bisphosphatase, chloroplast precursor
LOC_Os06g45370	Os.15065.1.S1_at	1.00	0.33	***	1.10		1,319	P	482	P	1,495	P	fructose-1,6-bisphosphatase, chloroplast precursor
Malate dehydrogenase (Malate=Oxaloacetate)													
EC 1.1.1.37 NAD dependent													
LOC_Os01g46070	Os.12729.1.S1_at	0.99	0.75		0.83		8,103	P	6,602	P	6,862	P	malate dehydrogenase, mitochondrial precursor
LOC_Os01g61380	Os.5740.1.S1_at	0.99	1.34		1.34		2,449	P	3,595	P	3,358	P	malate dehydrogenase, mitochondrial precursor
LOC_Os03g56280	Os.26206.1.S1_at	1.00	1.09		1.16		3,744	P	4,510	P	4,454	P	malate dehydrogenase, glyoxysomal precursor
LOC_Os04g46560	Os.23248.1.A1_at	0.78	0.20		8.80	**	92	P,A	21	A	850	P	malate dehydrogenase, cytoplasmic
LOC_Os05g49880	Os.11139.1.S1_at	0.98	0.60		0.94		8,734	P	5,766	P	8,401	P	malate dehydrogenase, mitochondrial precursor
LOC_Os07g43700	Os.17814.2.S1_x_at	0.98	0.41		0.46		784	P	364	P	365	P	malate dehydrogenase, glyoxysomal precursor
LOC_Os08g33720	Os.13993.1.S1_at	0.97	0.84		0.92		2,199	P	2,116	P	2,071	P	malate dehydrogenase, mitochondrial precursor
LOC_Os10g33800	Os.12171.1.S1_at	0.98	0.58		0.73		15,423	P	9,874	P	11,425	P	malate dehydrogenase, cytoplasmic
LOC_Os12g43630	Os.4155.1.S1_at	0.99	1.23		0.88		1,564	P	2,122	P	1,413	P	malate dehydrogenase, glyoxysomal precursor
EC 1.1.1.82 NADP dependent													
LOC_Os08g44810	Os.11588.1.S1_at	1.00	0.20	***	1.32		5,832	P	1,321	P	7,901	P	malate dehydrogenase 1, chloroplast precursor
Malate dehydrogenase (Malate=Pyruvate)													
EC 1.1.1.39 NAD depandent													
LOC_Os10g35960	Os.9251.1.S1_at	1.00	0.99		0.65		6,460	P	7,082	P	4,287	P	NAD-dependent malic enzyme 59 kDa isoform, mitoch
EC1.1.1.40 NADP dependent													
LOC_Os01g09320	Os.12492.1.S1_at	0.95	1.10		0.54		4,936	P	5,935	P	2,703	P	NADP-dependent malic enzyme, chloroplast precursor
LOC_Os01g52500	Os.421.1.S1_a_at	0.99	0.98		0.63		15,346	P	16,507	P	9,908	P	NADP-dependent malic enzyme
LOC_Os01g54030	Os.20712.2.A1_at	0.60	1.80		0.64		3	A	5	A	2	A	NADP-dependent malic enzyme
LOC_Os01g54030	Os.47303.1.S1_at	0.98	0.54		0.33		25	P	15	P,M,A	8	A	NADP-dependent malic enzyme
LOC_Os01g54030	Os.47303.1.S1_s_at	0.79	0.38		0.63		20	A	9	A	14	A	NADP-dependent malic enzyme
LOC_Os02g44550	Os.52949.1.S1_s_at	1.00	0.95		1.05		512	P	544	P	553	P	NADP-dependent malic enzyme
LOC_Os02g44550	Os.8062.1.S1_at	0.97	1.26		1.41		472	P	660	P	689	P	NADP-dependent malic enzyme
LOC_Os02g44550	Os.8062.2.S1_x_at	1.00	0.88		1.34		201	P	200	P	278	P	NADP-dependent malic enzyme
LOC_Os05g09440	Os.9145.1.S1_at	0.97	0.80		3.79		27	P,A	25	P,M	108	P	NADP-dependent malic enzyme, chloroplast precursor
Malate synthase (Acetyl-CoA→Malate) EC 2.3.3.9													
LOC_Os04g40990	Os.26687.1.S1_at	1.00	0.56		2.24		104	P	65	P,A	242	P	malate synthase, glyoxysomal
PEP-CK (ATP+Oxaloacetate→PEP+ADP+CO2) EC 4.1.1.49													
LOC_Os03g15050	Os.12699.1.S1_at	0.99	31.15	**	5.67	**	41	A	1,480	P	244	P	phosphoenolpyruvate carboxykinase
LOC_Os10g13700	Os.8805.1.S1_at	0.78	1.01		1.21		6	A	11	A	10	A	phosphoenolpyruvate carboxykinase
PEP-Cx (PEP+CO2→Oxaloacetate) EC 4.1.1.31													
LOC_Os01g02050	Os.33406.1.A1_x_at	0.93	0.99		0.48		5	A	6	A	3	A	phosphoenolpyruvate carboxylase 4
LOC_Os01g02050	Os.49998.1.S1_at	0.97	0.95		0.66		399	P	420	P	285	P	phosphoenolpyruvate carboxylase 4
LOC_Os01g11054	Os.27513.1.A1_a_at	1.00	1.73		0.26		58	M,A	114	P	21	A	phosphoenolpyruvate carboxylase 1
LOC_Os01g11054	Os.27513.2.S1_at	0.96	0.54		0.69		3	A	2	A	2	A	phosphoenolpyruvate carboxylase 1
LOC_Os01g55350	Os.22285.1.S1_a_at	0.98	1.05		3.75	*	40	A	48	A	156	P	phosphoenolpyruvate carboxylase, housekeeping isoz
LOC_Os02g14770	Os.2450.1.S1_a_at	1.00	0.69		0.82		4,337	P	3,279	P	3,648	P	phosphoenolpyruvate carboxylase 1
LOC_Os02g14770	Os.2450.3.S1_x_at	0.99	0.62		1.27		230	P	159	P	304	P	phosphoenolpyruvate carboxylase 1
LOC_Os08g27840	Os.10454.1.S1_a_at	0.98	0.84		1.88		143	P	133	P	279	P	phosphoenolpyruvate carboxylase 2
LOC_Os08g27840	Os.6248.1.S1_s_at	0.98	1.00		1.52		3,875	P	4,415	P	6,129	P	phosphoenolpyruvate carboxylase 2
LOC_Os09g14670	Os.5177.1.S1_s_at	0.89	0.45		0.91		351	P	172	P	325	P	phosphoenolpyruvate carboxylase 2
LOC_Os09g14670	OsAffx.29848.1.S1_at	0.93	0.48		1.13		564	P	300	P	648	P	phosphoenolpyruvate carboxylase 2
LOC_Os09g14670	OsAffx.29848.1.S1_x_at	0.93	0.50		1.13		703	P	384	P	808	P	phosphoenolpyruvate carboxylase 2
PK (PEP→Pyruvate) EC 2.7.1.40													
cytosol													
LOC_Os01g16960	Os.213.1.S1_at	0.99	0.88		1.04		775	P	750	P	829	P	pyruvate kinase, cytosolic isozyme
LOC_Os03g20880	OsAffx.12959.1.S1_at	0.83	0.66		1.43		16	A	13	A	24	P,A	pyruvate kinase, cytosolic isozyme
LOC_Os04g58110	Os.57474.1.S1_x_at	0.92	0.64		0.94		648	P	450	P	616	P	pyruvate kinase, cytosolic isozyme

LOC_Os04g58110	Os.7908.1.S1_a_at	1.00	0.77		0.73		11,511	P	9,731	P	8,586	P	pyruvate kinase, cytosolic isozyme
LOC_Os11g05110	Os.11606.1.S1_at	0.98	0.93		0.66		11,148	P	11,338	P	7,505	P	pyruvate kinase, cytosolic isozyme
LOC_Os11g10980	Os.9996.2.S1_at	0.97	3.07	*	4.80	*	32	A	111	P	159	P	pyruvate kinase, cytosolic isozyme
LOC_Os12g05110	Os.28109.1.S1_at	0.99	0.97		0.89		2,264	P	2,405	P	2,072	P	pyruvate kinase, cytosolic isozyme
plastidic													
LOC_Os01g47080	Os.41467.1.S1_at	0.94	1.12		1.96		148	P	182	P	296	P	pyruvate kinase isozyme G, chloroplast precursor
LOC_Os01g47080	Os.6058.1.S1_at	0.97	1.21		1.59		1,317	P	1,758	P	2,153	P	pyruvate kinase isozyme G, chloroplast precursor
LOC_Os03g46910	Os.25127.1.S1_at	0.95	1.16		0.86		316	P	411	P	281	P	pyruvate kinase isozyme A, chloroplast precursor
LOC_Os07g08340	Os.9225.1.S1_at	0.98	0.85		1.06		2,437	P	2,292	P	2,661	P	pyruvate kinase isozyme A, chloroplast precursor
LOC_Os10g42100	Os.12158.1.S1_at	0.99	1.25		1.08		2,566	P	3,519	P	2,857	P	pyruvate kinase isozyme G, chloroplast precursor
LOC_Os10g42100	Os.12158.1.S2_at	0.98	0.79		1.01		142	P	124	P	149	P	pyruvate kinase isozyme G, chloroplast precursor
other													
LOC_Os09g22410	Os.18503.1.S1_at	0.56	1.03		0.56		17	P,A	20	P,A	11	A	pyruvate kinase-like
LOC_Os09g22410	Os.18503.1.S1_s_at	0.68	0.43		0.91		5	A	3	A	6	A	pyruvate kinase-like
Pyruvate dehydrogenase (Pyruvate→Acetyl-CoA) EC 1.2.4.1													
LOC_Os02g50620	Os.10143.1.S1_at	0.97	0.66		0.74		7,688	P	5,501	P	5,814	P	pyruvate dehydrogenase E1 component alpha subunit,
LOC_Os04g02900	Os.15076.1.S1_at	0.99	0.63		0.77		5,008	P	3,453	P	3,972	P	pyruvate dehydrogenase E1 component alpha subunit
LOC_Os06g13720	Os.54410.1.S1_at	0.94	1.29		2.18		184	P	267	P	410	P	pyruvate dehydrogenase E1 component alpha subunit,
LOC_Os08g42410	Os.18710.1.S1_at	1.00	0.68		0.99		1,450	P	1,089	P	1,482	P	pyruvate dehydrogenase E1 component subunit beta, r
LOC_Os09g33500	Os.9587.1.S1_a_at	1.00	0.90		0.62	**	8,849	P	8,762	P	5,611	P	pyruvate dehydrogenase E1 component subunit beta, r
LOC_Os12g42230	Os.15571.1.S1_at	0.99	0.51		0.84		2,471	P	1,400	P	2,121	P	pyruvate dehydrogenase E1 component subunit beta
LOC_Os09g33540	None												pyruvate dehydrogenase E1 component subunit beta, r
Transaldorase (Glyceraldehyde-3P + D-sedoheptulose = E4P + D-Fruc-6P) EC 2.2.1.2													
LOC_Os01g70170	Os.8049.1.S1_a_at	1.00	0.83		0.75		17,410	P	15,872	P	13,535	P	transaldolase
LOC_Os08g05830	Os.40427.1.A1_s_at	1.00	0.69		1.04		1,995	P	1,520	P	2,164	P	transaldolase
Transketolase (D-Fruc-6P + glyceraldehyde-3P = Xylulose-5P + E4P) EC2.2.1.1													
LOC_Os04g19740	Os.18381.1.S1_at	0.99	8.52	***	12.15	***	75	P	727	P	939	P	transketolase, chloroplast precursor
LOC_Os06g04270	Os.609.1.S2_a_at	0.99	0.74		1.21		7,308	P	5,862	P	9,058	P	transketolase, chloroplast precursor
UDP-N-acetylglucosamine pyrophosphorylase EC 2.7.7.23													
LOC_Os04g52370	Os.6313.1.S1_at	0.99	0.23	**	0.92		5,893	P	1,498	P	5,569	P	UDP-N-acetylglucosamine pyrophosphorylase
LOC_Os08g10600	Os.8341.1.S1_at	1.00	0.72		0.96		5,735	P	4,485	P	5,638	P	UDP-N-acetylglucosamine pyrophosphorylase

Supplementary Table S6

Gene and probe sets for cell wall related genes. The probes with significantly differentially expression were identified by one-way ANOVA (FDR ; *** < 0.001; ** < 0.005; * < 0.01) with Tukey's post hoc test, whic

TIGR loci	Systematic Name	WT normalized	F71 Pa normalized	FDR	INT normalize	FDR	WT raw	flags	F71 Pa raw	flags	INT raw	flags	Description
Glycosyl Transferase													
GT2													
Cellulose synthase													
LOC_Os01g54620	Os.18724.1.S1_a_at	0.91	0.55		7.30	**	923	P	570	P	6,986	P	OsCESA4 - cellulose synthase
LOC_Os01g54620	Os.18724.1.S1_at	0.95	0.50		4.91	*	2477	P	1519	P	12,576	P	OsCESA4 - cellulose synthase
LOC_Os01g54620	Os.18724.2.S1_x_at	0.95	0.62		6.60	**	790	P	555	P	5,433	P	OsCESA4 - cellulose synthase
LOC_Os03g59340	Os.14979.1.S1_at	1.00	0.73		0.97		152	P	125	P	152	P	OsCESA2 - cellulose synthase
LOC_Os03g59340	Os.14979.1.S2_at	0.98	1.04		0.55		131	P	150	P	75	P,A	OsCESA2 - cellulose synthase
LOC_Os03g62090	Os.4857.1.S1_at	1.00	0.73		0.82		10603	P	8578	P	8,897	P	OsCESA5 - cellulose synthase
LOC_Os05g08370	Os.10183.1.S1_at	0.97	0.36		0.49		388	P	164	P	193	P	OsCESA1 - cellulose synthase
LOC_Os05g08370	Os.10183.1.S2_at	1.00	0.68	*	0.69	*	16298	P	12060	P	11,490	P	OsCESA1 - cellulose synthase
LOC_Os06g39970	OsAffx.15853.1.S1_at	0.59	0.15		0.34		18	A	3	A	7	A	OsCESA11 - cellulose synthase
LOC_Os06g39970	OsAffx.15853.1.S1_x_at	0.80	0.54		0.71		8	A	4	A	6	A	OsCESA11 - cellulose synthase
LOC_Os07g10770	Os.10176.1.S1_at	1.00	0.74	**	0.75	**	14544	P	11846	P	11,159	P	OsCESA8 - cellulose synthase
LOC_Os07g14850	Os.10926.1.S1_at	1.00	0.69	**	0.64	**	14347	P	10778	P	9,404	P	OsCESA6 - cellulose synthase
LOC_Os07g24190	Os.10178.1.S1_a_at	1.00	0.73		0.95		1790	P	1434	P	1,773	P	OsCESA3 - cellulose synthase
LOC_Os07g24190	Os.10178.2.S1_a_at	1.00	0.80		0.80		20578	P	18013	P	16,916	P	OsCESA3 - cellulose synthase
LOC_Os09g25490	Os.10206.1.S1_at	0.85	0.41		9.76	*	533	P	287	P	5,437	P	OsCESA9 - cellulose synthase
LOC_Os10g32980	Os.3206.1.S1_at	0.93	0.57		5.06		2186	P	1535	P	11,429	P	OsCESA7 - cellulose synthase
LOC_Os12g29300	None												OsCESA10 - cellulose synthase
CSLA													
LOC_Os02g09930	Os.24972.1.S1_at	0.82	8.70		1.14		446	P	4,623	P	547	P	OsCSLA1 - cellulose synthase-like family A; mannan sy
LOC_Os02g51060	Os.6170.1.S1_at	0.97	0.76		0.40		256	P	226	P	106	P	OsCSLA6 - cellulose synthase-like family A; mannan sy
LOC_Os03g07350	OsAffx.12764.2.S1_at	0.99	1.30		1.42		128	P	194	P	188	P	OsCSLA4 - cellulose synthase-like family A; mannan sy
LOC_Os03g07350	OsAffx.12764.2.S1_x_at	0.98	1.10		1.09		128	P	160	P	146	P	OsCSLA4 - cellulose synthase-like family A; mannan sy
LOC_Os03g26044	Os.23303.1.A1_at	0.87	0.45		0.94		641	P	321	P	630	P	OsCSLA5 - cellulose synthase-like family A; mannan sy
LOC_Os03g26044	Os.56873.1.S1_at	0.96	1.07		0.48		60	M,A	71	M,A	30	A	OsCSLA5 - cellulose synthase-like family A; mannan sy
LOC_Os03g26044	Os.56873.1.S1_x_at	0.67	1.48		0.20		22	A	37	A	6	A	OsCSLA5 - cellulose synthase-like family A; mannan sy
LOC_Os06g12460	OsAffx.15389.1.S1_at	0.95	0.52		2.20		32	P,A	19	A	74	P	OsCSLA3 - cellulose synthase-like family A; mannan sy
LOC_Os06g42020	Os.48268.1.S1_at	0.99	0.74		0.78		35	A	31	A	34	P,A	OsCSLA9 - cellulose synthase-like family A
LOC_Os06g42020	OsAffx.5081.1.S1_at	0.79	0.29		0.27		1	A	0	A	0	A	OsCSLA9 - cellulose synthase-like family A
LOC_Os06g42020	OsAffx.5081.1.S1_x_at	0.66	1.25		1.36		19	A	28	A	28	P,A	OsCSLA9 - cellulose synthase-like family A
LOC_Os07g43710	Os.8080.1.S1_at	0.98	0.50		0.95		674	P	379	P	662	P	OsCSLA7 - cellulose synthase-like family A; mannan sy
LOC_Os07g43710	Os.8080.2.S1_x_at	1.00	0.54		0.98		449	P	274	P	453	P	OsCSLA7 - cellulose synthase-like family A; mannan sy
LOC_Os08g33740	Os.24363.1.A1_at	0.97	1.31		2.06		261	P	376	P	559	P	OsCSLA11 - cellulose synthase-like family A
LOC_Os08g33740	OsAffx.6015.1.S1_at	0.95	1.45		2.15		125	P	204	P	277	P	OsCSLA11 - cellulose synthase-like family A
LOC_Os10g26630	Os.15231.1.S1_at	0.97	0.93		1.45		445	P	461	P	676	P	OsCSLA2 - cellulose synthase-like family A; mannan sy
CSLC													
LOC_Os01g56130	Os.29016.1.S1_at	1.00	0.68		0.75		5,210	P	3,920	P	4,034	P	OsCSLC1 - cellulose synthase-like family C
LOC_Os03g56060	Os.10855.1.S1_at	0.98	1.19		1.87		890	P	1,201	P	1,716	P	OsCSLC9 - cellulose synthase-like family C
LOC_Os05g43530	Os.15705.1.S1_x_at	0.99	0.56	**	0.40	**	3,574	P	2,218	P	1,465	P	OsCSLC7 - cellulose synthase-like family C
LOC_Os05g43530	OsAffx.20285.2.S1_at	1.00	0.52	**	0.37	**	622	P	358	P	237	P	OsCSLC7 - cellulose synthase-like family C
LOC_Os07g03260	OsAffx.28245.1.S1_at	0.95	0.17		0.44		28	A	5	A	15	A	OsCSLC10 - cellulose synthase-like family C
LOC_Os07g03260	OsAffx.30957.1.S1_s_at	0.45	0.18		0.14		8	A	4	A	3	A	OsCSLC10 - cellulose synthase-like family C
LOC_Os08g15420	Os.55417.1.S1_at	0.93	0.52		0.80		32	A	19	A	27	A	OsCSLC3 - cellulose synthase-like family C
LOC_Os08g15420	OsAffx.17009.1.S1_x_at	0.95	0.28		1.24		16	A	6	A	24	A	OsCSLC3 - cellulose synthase-like family C
LOC_Os09g25900	Os.18770.1.S1_at	0.98	0.68		0.56		1,669	P	1,267	P	973	P	OsCSLC2 - cellulose synthase-like family C
LOC_Os11g13650	OsAffx.30957.1.S1_s_at	0.45	0.18		0.14		8	A	4	A	3	A	cellulose synthase
LOC_Os11g13650	OsAffx.30957.1.S1_x_at	0.99	0.88		0.98		92	A	88	A	91	A	cellulose synthase
CSLD													
LOC_Os06g02180	Os.25614.1.S1_at	1.00	1.31		0.68		553	P	798	P	388	P	OsCSLD2 - cellulose synthase-like family D
LOC_Os06g22980	Os.53359.1.S1_at	0.76	1.30		1.16		16	A	24	A	20	P,A	OsCSLD5 - cellulose synthase-like family D
LOC_Os08g25710	OsAffx.17155.1.S1_at	0.60	0.23		0.68		13	A	4	A	14	A	OsCSLD3 - cellulose synthase-like family D
LOC_Os08g25710	OsAffx.17155.1.S1_x_at	0.97	1.03		0.48		51	A	60	A	28	A	OsCSLD3 - cellulose synthase-like family D
LOC_Os10g42750	Os.46811.1.S1_at	0.86	1.18		1.25		29	A	38	P,A	39	A	OsCSLD1 - cellulose synthase-like family D
LOC_Os12g36890	Os.57510.1.A1_at	0.80	0.50		0.53		21	A	12	A	12	A	OsCSLD4 - cellulose synthase-like family D
LOC_Os12g36890	Os.57510.1.S1_x_at	0.76	0.90		0.98		36	A	41	A	40	A	OsCSLD4 - cellulose synthase-like family D
CSLE													
LOC_Os02g49332	Os.20406.1.S1_a_at	1.00	0.67		0.88		1,952	P	1,448	P	1,773	P	OsCSLE2 - cellulose synthase-like family E
LOC_Os02g49332	Os.20406.3.S1_x_at	0.97	2.15		0.42		470	P	1,136	P	207	P	OsCSLE2 - cellulose synthase-like family E
LOC_Os09g30120	Os.6165.1.S1_a_at	1.00	2.13	*	0.93		611	P	1,443	P	587	P	OsCSLE1 - cellulose synthase-like family E
LOC_Os09g30130	Os.27376.1.S1_at	0.82	0.50		0.88		27	P,A	16	P,A	25	P	OsCSLE6 - cellulose synthase-like family E
CSLF													
LOC_Os07g36610	OsAffx.16586.1.S1_x_at	0.69	0.28		1.24		28	A	9	A	49	A	OsCSLF9 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os07g36630	Os.52482.1.S1_at	0.90	0.10	*	0.22	*	1,042	P	117	P	234	P	OsCSLF8 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os07g36690	Os.15704.1.S1_at	0.93	3.67		175.10	**	3	A	17	A	619	P	OsCSLF2 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os07g36750	OsAffx.5550.1.S1_at	0.89	0.92		0.96		23	A	23	A	24	P,A	OsCSLF3 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os08g06380	Os.51604.1.S1_at	0.99	0.56		0.53		1653	P	1034	P	894	P	OsCSLF6 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os08g06380	Os.56304.1.S1_at	0.90	0.54		0.42		29	A	25	A	15	A	OsCSLF6 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os08g06380	Os.9709.1.A1_at	0.72	0.96		1.38		15	A	17	A	21	A	OsCSLF6 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os08g06380	Os.9709.2.S1_at	1.00	0.48	**	0.49	**	4,466	P	2,346	P	2,238	P	OsCSLF6 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os10g20260	Os.46814.1.S1_at	0.63	1.57		0.27		10	A	18	A	6	A	OsCSLF7 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os07g36700	None												OsCSLF1 - cellulose synthase-like family F; beta1,3;1,4
LOC_Os07g36740	None												OsCSLF4 - cellulose synthase-like family F; beta1,3;1,4
CSLH													
LOC_Os04g35020	Os.45970.1.S1_at	0.80	0.50		0.31		38	A	30	A	12	A	OsCSLH2 - cellulose synthase-like family H
LOC_Os04g35030	Os.26822.1.S1_at	0.65	1.43		1.06		46	A	72	M,A	50	A	OsCSLH3 - cellulose synthase-like family H
LOC_Os10g20090	Os.11623.1.S1_a_at	0.97	1.03		0.95		2,234	P	2,519	P	2,184	P	OsCSLH1 - cellulose synthase-like family H
GT8													
LOC_Os01g52710	Os.32160.1.S1_a_at	0.99	0.54		0.65		111	P	72	P	75	P	glycosyl transferase 8 domain containing protein
LOC_Os01g52710	Os.32160.1.S1_at	0.99	0.93		0.60		77	P	79	P	48	P	glycosyl transferase 8 domain containing protein
LOC_Os01g52710	Os.32160.2.S1_x_at	0.99	0.75		0.81		20	P,A	18	P,A	19	P,A	glycosyl transferase 8 domain containing protein
LOC_Os01g52710	OsAffx.9329.1.S1_at	0.97	1.08		0.68		2	A	2	A	1	A	glycosyl transferase 8 domain containing protein
LOC_Os01g65780	Os.5334.2.S1_a_at	0.98	0.54		0.66		7179	P	4374	P	4889	P	glycosyl transferase
LOC_Os02g29530	Os.7819.1.S1_at	1.00	1.03		1.05		2616	P	2996	P	2816	P	glycosyl transferase 8 domain containing protein
LOC_Os02g35020	OsAffx.24582.1.S1_at	0.97	1.16		0.96		103	A	130	A	101	P,A	glycosyl transferase
LOC_Os02g41520	Os.50354.1.S1_at	1.00	0.91		0.76	*	1457	P	1453	P	1131	P	glycosyl transferase 8 domain containing protein
LOC_Os02g50600	Os.26079.1.S1_at	0.96	0.62		0.46		1792	P	1265	P	842	P	glycosyl transferase 8 domain containing protein
LOC_Os02g51130	Os.48353.1.S1_at	0.93	0.51		5.24	**	159	P	91	P	869	P	glycosyl transferase 8 domain containing protein
LOC_Os03g08600	Os.50009.1.S1_at	1.00	0.23	***	1.95		2374	P	598	P	4790	P	transferase, transferring glycosyl groups
LOC_Os03g11330	OsAffx.12825.1.S1_s_at	1.00	0.62		0.87		3738	P	2558	P	3341	P	glycosyl transferase 8 domain containing protein
LOC_Os03g18890	Os.27465.1.S1_at	0.97	0.35		0.85		3168	P	1234	P	2781	P	glycosyl transferase 8 domain containing protein
LOC_Os03g20120	Os.11323.1.S1_at	0.98	2.35		22.63	***	34	A	90	P,M,A	811	P	glycosyl transferase 8 domain containing protein
LOC_Os03g21250	Os.24770.1.S1_at	1.00	0.81		1.13		704	P	627	P	817	P	glycosyl transferase, family 8
LOC_Os03g24510	Os.53356.1.S1_at	0.96	0.29		3.73		65	M,A	33	P,A	264	P	glycosyl transferase 8 domain containing protein
LOC_Os03g30000	Os.53812.1.S1_at	0.97	0.61		0.78		2650	P	1794	P	2122	P	glycosyl transferase 8 domain containing protein
LOC_Os04g43700	Os.17432.1.S1_at	1.00	0.83		0.61		4791	P	4410	P	3013	P	glycosyl transferase 8 domain containing protein
LOC_Os04g44850	Os.50280.1.S1_at	1.00	0.38	**	0.97		1846	P	759	P	1850	P	glycosyl transferase 8 domain containing protein
LOC_Os04g46750	Os.17642.1.S1_a_at	1.00	0.90		0.66		3068	P	3096	P	2097	P	glycosyl transferase 8 domain containing protein
LOC_Os04g54360	Os.5910.1.S1_at	0.99	1.14		0.94		529	P	666	P	511	P	glycosyl transferase 8 domain containing protein
LOC_Os05g35200	Os.11691.1.S1_at	0.99	0.17	**	0.69		6615	P	1257	P	4740	P	glycosyl transferase
LOC_Os05g40720	OsAffx.15049.1.S1_at	1.00	1.26		1.17		84	P	116	P	101	P	glycosyl transferase, family 8
LOC_Os06g13760	OsAffx.27621.1.S1_s_at	1.00	0.60		0.62		1895	P	1269	P	1209	P	glycosyl transferase 8 domain containing protein
LOC_Os06g49810	Os.18081.1.S1_at	0.98	0.78		0.97		1278	P	1107	P	1270	P	glycosyl transferase, family 8
LOC_Os07g45260	Os.34356.1.S1_at	0.77	0.29		0.46		14	A	5	A	9	A	glycosyl transferase 8 domain containing protein
LOC_Os07g48370	Os.25298.1.S1_at	0.95	0.86		1.78		1219	P	1160	P	2229	P	glycosyl transferase, family 8
LOC_Os07g48830	Os.2677.1.S1_at	0.93	2.05		1.17		25	P,A	68	P	29	P,M	glycosyl transferase 8 domain containing protein
LOC_Os08g23780	Os.13608.1.S1_at	0.99	0.54		2.72	*	99	P	61	P	281	P	glycosyl transferase 8 domain containing protein
LOC_Os08g38740	OsAffx.6076.1.S1_at	0.96	2.97		0.93		21	P,A	70	P	20	P,A	glycosyl transferase 8 domain containing protein
LOC_Os09g30280	Os.5844.1.S1_at	0.97	1.57		0.82		149	P	272	P	127	P	glycosyl transferase 8 domain containing protein
LOC_Os09g36180	OsAffx.6491.1.S1_at	0.99	0.81		0.69		43	A	43	A	33	A	glycosyl transferase, family 8
LOC_Os09g36190	Os.7210.1.S1_at	0.99	1.17		1.19		3018	P	3903	P	3696	P	glycosyl transferase, family 8
LOC_Os10g21890	Os.28351.1.A1_a_at	1.00	0.79		0.83		589	P	514	P	506	P	glycosyl transferase, family 8
LOC_Os10g40640	Os.46627.1.S1_at	0.81	1.13		0.12		345	P	454	P	42	A	glycosyl transferase, family 8
LOC_Os11g03160	Os.24025.1.S1_at	0.99	2.16		6.80		59	P,A	148	P	419	P	glycosyl transferase, family 8
LOC_Os11g03160	Os.24025.1.S1_s_at	0.97	1.50		3.06	**	381	P	653	P	1205	P	glycosyl transferase, family 8
LOC_Os11g37980	Os.57033.1.S1_at	0.97	0.95		1.32		142	P	147	P	193	P	GAUT2/LGT2
LOC_Os12g02910	Os.24025.1.S1_s_at	0.97	1.50		3.06		381	P	653	P	1205	P	glycosyl transferase, family 8
LOC_Os12g38930	Os.8792.1.S1_at	0.99	0.76		0.78		2397	P	1999	P	1932	P	glycosyl transferase 8 domain containing protein
LOC_Os03g47530	None												glycosyl transferase 8 domain containing protein
LOC_Os06g51160	None												glycosyl transferase, family 8
LOC_Os10g31650	None												glycosyl transferase 8 domain containing protein
GT14													
LOC_Os01g10440	Os.18296.1.S1_x_at	0.63	6.29		1.36		6	A	43	P,M,A	9	A	xylosyltransferase
LOC_Os01g10440	Os.45991.1.S1_x_at	0.91	18.68	*	1.82		1	A	26	P,M,A	3	A	xylosyltransferase
LOC_Os01g56570	Os.29865.1.S1_at	0.65	1.92		0.92		57	P,A	123	P	56	P,M	xylosyltransferase
LOC_Os03g05180	Os.56558.1.S1_at	0.98	0.25		0.44		25	A	9	A	12	A	expressed protein
LOC_Os03g05180	OsAffx.12737.1.S1_at	1.00	0.65	*	1.32		579	P	410	P	785	P	expressed protein
LOC_Os03g16890	Os.8831.1.S1_at	0.99	0.95		0.97		672	P	697	P	673	P	N-acetylglucosaminyltransferase
LOC_Os03g48560	OsAffx.13408.1.S1_at	0.96	0.78		0.52		232	P	200	P	124	P	N-acetylglucosaminyltransferase
LOC_Os03g48560	OsAffx.13408.1.S1_x_at	1.00	0.86		0.62		131	P	123	P	83	P	N-acetylglucosaminyltransferase
LOC_Os04g23580	OsAffx.13941.1.S1_at	1.00	1.86	*	1.72	*	192	P	393	P	339	P	xylosyltransferase

LOC_Os06g40060	Os.14852.1.A1_at	1.00	0.66	**	1.16		2831	P	2056	P	3371	P	glycosyltransferase family protei
LOC_Os08g04790	Os.8351.1.S1_at	1.00	0.63	***	1.15	***	1674	P	1151	P	1983	P	xylosyltransferase
LOC_Os10g30080	Os.46676.1.A1_x_at	1.00	0.65		1.07		205	P	150	P,A	228	P	xylosyltransferase
LOC_Os10g30080	Os.51187.1.S1_at	0.98	0.62		0.86		10435	P	7101	P	9291	P	xylosyltransferase
LOC_Os10g30080	Os.51187.1.S1_s_at	1.00	0.79		1.38	**	293	P	254	P,A	416	P	xylosyltransferase
LOC_Os12g44240	Os.15359.1.S1_at	0.99	0.88		1.11		339	P	328	P	385	P	N-acetylglucosaminyltransferase
LOC_Os05g06050	None												N-acetylglucosaminyltransferase

GT31

LOC_Os01g22550	Os.53990.1.S1_at	0.98	0.64		0.86		1429	P	1014	P	1270	P	galactosyltransferase
LOC_Os01g65590	Os.6437.1.S1_at	0.98	1.12		11.82	**	15	P,A	19	P,A	183	P	galactosyltransferase
LOC_Os01g65590	OsAffx.11744.1.S1_x_a	0.98	0.40		1.93		43	A	23	A	89	P,A	galactosyltransferase
LOC_Os02g06840	Os.26531.1.S1_s_at	0.99	0.63		0.87		7476	P	5207	P	6683	P	galactosyltransferase
LOC_Os02g35870	OsAffx.2874.1.S1_at	0.96	0.65		1.71		399	P	289	P	702	P	galactosyltransferase
LOC_Os02g36770	OsAffx.24601.1.S1_at	0.90	0.67		0.65		43	P,M,A	34	P,A	29	A	galactosyltransferase
LOC_Os02g45700	Os.6297.2.S1_at	0.93	1.16		1.08		51	P,A	66	A	58	A	fringe-related protein
LOC_Os02g54370	Os.54364.1.S1_at	0.98	0.69		2.12		1	A	1	A	2	A	hypro1
LOC_Os02g54390	OsAffx.3068.1.S1_x_at	0.84	0.89		0.97		13	A	15	A	14	A	hypro1
LOC_Os02g54450	OsAffx.3069.1.S1_at	0.94	0.89		0.83		3	A	3	A	3	A	hypro1
LOC_Os03g03270	Os.54885.1.S1_at	1.00	0.90		0.56		56	P,A	56	P,A	33	A	fringe-related protein
LOC_Os03g03270	OsAffx.24949.1.S1_x_a	0.97	0.78		0.63		68	M,A	60	A	45	A	fringe-related protein
LOC_Os03g16290	Os.32462.1.S1_a_at	0.93	0.11		1.65		111	P	20	A	188	P	fringe-related protein
LOC_Os03g16334	Os.37699.2.S1_at	0.96	0.63		3.26		596	P	464	P	1982	P	fringe-related protein
LOC_Os03g16334	Os.37699.3.S1_x_at	0.86	0.70		2.46		40	A	37	A	105	P,A	fringe-related protein
LOC_Os03g38050	Os.50014.1.S1_at	1.00	0.90		1.72	*	488	P	487	P	866	P	galactosyltransferase
LOC_Os03g48610	OsAffx.13411.1.S1_at	0.98	0.43		2.11		74	P,A	37	P,A	162	P	galactosyltransferase
LOC_Os03g58900	OsAffx.13544.1.S1_at	0.85	0.91		1.33		61	P,A	67	P,A	85	P	galactosyltransferase
LOC_Os03g58920	Os.23190.1.A1_at	0.99	1.99		1.79		386	P	860	P	715	P	galactosyltransferase
LOC_Os04g48950	Os.52867.1.S1_at	0.99	1.22		0.97		48	P,A	64	P	48	P	fringe-related protein
LOC_Os05g11060	Os.51653.1.S1_at	0.99	0.57	*	1.14		2004	P	1240	P	2337	P	galactosyltransferase
LOC_Os05g35266	Os.12539.1.S1_at	0.98	1.22		1.28		203	P,M	277	P	266	P	galactosyltransferase
LOC_Os05g47880	Os.5255.1.S1_at	0.95	0.74		0.17	*	624	P	508	P	105	M,A	hypro1
LOC_Os06g06280	Os.11577.1.S1_a_at	0.99	0.78		0.86		342	P	294	P	305	P	galactosyltransferase
LOC_Os06g07905	Os.4754.1.S1_at	1.00	0.87		0.89		4425	P	4230	P	4041	P	galactosyltransferase
LOC_Os06g08005	Os.4754.1.S1_at	1.00	0.87		0.89		4425	P	4230	P	4041	P	galactosyltransferase
LOC_Os06g09270	Os.55786.1.S1_at	0.56	5.87		33.74		9	A	57	A	310	P	hypro1
LOC_Os06g12390	Os.49253.1.S1_at	0.99	2.52	**	1.25		634	P	1746	P	821	P	galactosyltransferase
LOC_Os06g46570	Os.51654.1.S1_at	1.00	1.03		0.77		719	P	828	P	567	P	galactosyltransferase
LOC_Os07g09690	Os.23410.1.A1_at	0.99	0.72		0.84		1108	P	880	P	961	P	galactosyltransferase
LOC_Os08g02370	Os.27951.1.S1_at	1.00	0.47		0.83		1780	P	938	P	1518	P	galactosyltransferase
LOC_Os08g03670	Os.12605.1.S1_s_at	0.98	0.90		1.03		1300	P	1310	P	1391	P	galactosyltransferase
LOC_Os08g04300	Os.50199.1.S1_at	0.99	1.01		1.91		182	P	207	P	359	P	fringe-related protein
LOC_Os08g29710	Os.21565.1.S1_at	0.96	0.78		1.26		785	P	677	P	1018	P	galactosyltransferase
LOC_Os09g26310	Os.51638.1.S1_s_at	0.99	0.93		0.20	*	2028	P	2171	P	419	P	hypro1
LOC_Os09g26310	Os.6003.1.S1_x_at	0.97	0.90		0.35		595	P	591	P	212	P	hypro1
LOC_Os09g26320	OsAffx.30036.1.S1_at	0.94	0.71		0.53		22	A	20	A	13	A	hypro1
LOC_Os09g26330	OsAffx.30037.1.S1_at	0.97	0.82		0.83		7	A	6	A	6	A	hypro1
LOC_Os09g27950	Os.23468.1.A1_at	0.78	3.11		0.42		70	P	254	P	31	P,A	galactosyltransferase
LOC_Os10g37260	Os.46642.1.S1_at	0.99	1.04		1.61		52	P	59	P	86	P	fringe-related protein
LOC_Os10g39020	Os.46486.1.S1_at	0.97	36.23		3.92		1	A	27	P,A	5	A	fringe-related protein
LOC_Os12g16480	OsAffx.7611.1.S1_at	0.99	2.02		1.71		88	P	198	P	156	P	conserved hypothetical protei
LOC_Os09g26300	None												hypro1

GT43

LOC_Os01g06450	OsAffx.10552.2.S1_x_a	0.64	0.92		0.54		3	A	4	A	2	A	glycosyltransferase family 43 protei
LOC_Os01g06450	OsAffx.10552.1.S1_x_a	0.93	1.41		0.96		29	M,A	45	A	29	A	glycosyltransferase family 43 protei
LOC_Os01g48440	Os.19374.2.S1_x_at	1.00	0.66	*	1.13		5618	P	4111	P	6521	P	glycosyltransferase family 43 protei
LOC_Os03g17850	OsAffx.3263.1.S1_at	0.98	0.69		0.86		46	M,A	46	P,A	43	A	glycosyltransferase family 43 protei
LOC_Os04g01280	Os.53113.1.A1_at	1.00	1.14		0.63	**	619	P	780	P	404	P	glycosyltransferase family 43 protei
LOC_Os04g55670	Os.329.1.S1_at	0.99	0.97		1.81		2384	P	2576	P	4471	P	glycosyltransferase family 43 protei
LOC_Os05g03174	Os.20262.1.S1_at	0.98	0.79		1.17		2713	P	2338	P	3289	P	glycosyltransferase family 43 protei
LOC_Os05g48600	Os.49512.1.S1_s_at	0.99	0.83		1.64	*	824	P	752	P	1393	P	glycosyltransferase family 43 protei
LOC_Os05g48600	Os.49512.1.S1_at	0.99	1.04		1.71		549	P	633	P	968	P	glycosyltransferase family 43 protei
LOC_Os06g47340	Os.425.1.S1_s_at	0.98	0.71		1.12		4792	P	3742	P	5531	P	glycosyltransferase family 43 protei
LOC_Os07g49370	Os.51101.1.S1_at	0.99	0.56		0.47		2354	P	1471	P	1151	P	glycosyltransferase family 43 protei
LOC_Os10g13810	Os.31415.1.S1_at	0.98	1.04		0.40	*	563	P	642	P	229	P	glycosyltransferase family 43 protei

GT47

LOC_Os01g01780	Os.34815.1.S1_at	0.99	0.72		1.10		1318	P	1049	P	1509	P	exostosin family protei
LOC_Os01g01780	Os.34815.2.S1_x_at	1.00	0.81		1.48	**	346	P	308	P	529	P	exostosin family protei
LOC_Os01g45350	Os.34863.1.S1_at	0.56	0.25		0.24		12	A	4	A	3	A	exostosin family protei
LOC_Os01g59630	Os.23590.1.A1_at	0.99	0.80		0.90		657	P	583	P	612	P	exostosin family domain containing protei
LOC_Os01g69220	Os.50010.1.S1_at	0.98	0.76		0.66		3382	P	2864	P	2296	P	exostosin family domain containing protei
LOC_Os01g70180	Os.34126.1.S1_at	0.88	0.47		1.36		1811	P	952	P	2542	P	exostosin family domain containing protei
LOC_Os01g70190	Os.12406.1.S1_at	1.00	0.72	*	0.71	*	8061	P	6392	P	5850	P	exostosin family domain containing protei
LOC_Os01g70200	Os.18736.1.S1_at	0.99	1.10		2.11		4792	P	5888	P	10461	P	exostosin family domain containing protei
LOC_Os02g09430	Os.52186.1.S1_at	1.00	0.79		0.82		1839	P	1609	P	1551	P	exostosin family domain containing protei
LOC_Os02g32110	Os.8923.1.A1_at	0.98	1.40		1.37		241	P	371	P	343	P	exostosin family domain containing protei
LOC_Os02g32110	Os.8923.1.A1_s_at	0.99	1.13		1.00		3335	P	4134	P	3424	P	exostosin family domain containing protei
LOC_Os02g39960	OsAffx.24655.1.S1_at	0.80	0.82		1.25		8	A	8	A	11	A	exostosin family protei
LOC_Os03g01760	Os.14607.1.S1_at	0.97	0.93		1.17		219	P	221	P	262	P	exostosin family domain containing protei
LOC_Os03g01760	Os.14607.1.S1_x_at	0.96	0.90		1.42		298	P	292	P	431	P	exostosin family domain containing protei
LOC_Os03g05060	Os.53691.1.S1_at	0.69	1.43		1.49		6	A	13	A	11	A	exostosin family domain containing protei
LOC_Os03g05070	Os.50602.1.S1_at	0.85	1.02		0.49		12	A	17	A	12	A	exostosin family domain containing protei
LOC_Os03g05110	Os.6350.1.S1_at	0.98	0.80		0.23	**	1448	P	1291	P	340	P	xyloglucan galactosyltransferase KATAMARI
LOC_Os03g07820	Os.52560.1.S1_at	1.00	0.44	*	0.71		753	P	362	P	551	P	exostosin family protei
LOC_Os03g20850	OsAffx.26595.1.S1_s_a	0.94	1.89		1.37		32	A	69	A	45	A	exostosin family domain containing protei
LOC_Os03g20850	Os.15776.1.S1_at	0.96	0.98		1.12		78	P,M	84	P	90	P	exostosin family domain containing protei
LOC_Os04g01930	OsAffx.13617.1.S1_x_a	0.90	1.11		1.11		14	A	19	A	20	A	exostosin family protei
LOC_Os04g01930	OsAffx.13617.1.S1_at	0.90	0.29		0.60		19	A	8	A	13	A	exostosin family protei
LOC_Os04g32670	Os.280.1.S1_at	0.99	1.05		0.72		2538	P	2926	P	1860	P	exostosin family domain containing protei
LOC_Os04g32670	Os.280.1.S2_at	0.99	0.96		1.02		73	P,A	78	P,A	77	P	exostosin family domain containing protei
LOC_Os04g48480	Os.8906.1.S1_at	0.91	1.00		0.81		297	P	325	P	245	P	exostosin family domain containing protei
LOC_Os04g54100	OsAffx.26595.1.S1_s_a	0.94	1.89		1.37		32	A	69	A	45	A	exostosin family protei
LOC_Os04g57510	Os.11868.3.S1_x_at	1.00	0.98		0.96		432	P	465	P	426	P	exostosin family domain containing protei
LOC_Os04g57510	Os.11868.2.S1_at	0.99	0.80		0.18		44	P,A	39	P,M,A	11	A	exostosin family domain containing protei
LOC_Os06g07887	OsAffx.27499.3.S1_x_a	0.99	1.04		1.23		4	A	4	A	5	A	exostosin family protei
LOC_Os06g23420	Os.54057.1.S1_at	0.78	4.13		0.82		6	A	32	A	5	A	exostosin family domain containing protei
LOC_Os06g46690	Os.5303.1.S2_at	1.00	0.98		1.39		149	P	161	P	214	P	exostosin family protei
LOC_Os07g09050	Os.51833.3.S1_at	0.44	0.75		1.02		5	A	5	A	9	M,A	exostosin family protei
LOC_Os07g09050	Os.51833.1.S1_x_at	0.69	0.22		1.90		52	A	13	A	103	A	exostosin family protei
LOC_Os07g37960	OsAffx.22483.1.S1_at	0.99	0.78		0.82		183	P	158	P	155	P	exostosin family domain containing protei
LOC_Os08g34020	Os.15004.1.S1_at	0.90	0.85		6.90		9	A	12	A	66	A	exostosin family domain containing protei
LOC_Os10g10080	Os.22635.1.S1_s_at	0.97	1.18		1.65		3352	P	4418	P	5665	P	exostosin family domain containing protei
LOC_Os10g32080	OsAffx.18485.3.S1_at	0.56	0.18		0.17		7	A	1	A	1	A	xyloglucan galactosyltransferase KATAMARI
LOC_Os10g32110	OsAffx.8050.1.A1_at	0.97	0.88		0.89		3	A	3	A	3	A	exostosin family domain containing protei
LOC_Os10g32110	OsAffx.8050.1.S1_x_at	0.98	1.16		0.85		50	A	65	A	47	A	exostosin family domain containing protei
LOC_Os10g32110	OsAffx.8050.1.S1_at	0.99	1.14		0.75		59	A	75	A	49	A	exostosin family domain containing protei
LOC_Os10g32160	Os.46796.2.S1_x_at	0.93	0.29		0.17		39	A	15	A	9	A	xyloglucan galactosyltransferase KATAMARI
LOC_Os10g32160	Os.46796.2.S1_at	0.98	0.47		0.66		30	A	16	A	20	P,A	xyloglucan galactosyltransferase KATAMARI
LOC_Os10g32170	Os.46796.1.S1_at	0.78	0.19		0.95		10	A	4	A	11	A	xyloglucan galactosyltransferase KATAMARI
LOC_Os10g40559	OsAffx.30736.1.S1_x_a	0.98	1.22		0.98		270	P	363	P	271	P	exostosin family domain containing protei
LOC_Os12g03100	Os.15794.1.S1_at	1.00	0.92		0.81	*	2553	P	2568	P	2125	P	exostosin family domain containing protei
LOC_Os11g03410	None												exostosin family domain containing protei

GT61

LOC_Os01g02900	Os.1054.1.A1_at	0.98	3.31		1.06		251	P	940	P	277	P	HGA6
LOC_Os01g02910	OsAffx.10885.2.S1_x_a	0.98	0.79		1.93		134	P,M,A	118	M,A	266	P	glycosyltransferase
LOC_Os01g02920	Os.34721.1.S1_at	0.99	1.48		1.22		234	P	392	P	292	P	glycosyltransferase
LOC_Os01g02930	Os.32123.1.S1_at	0.98	0.92		0.48		458	P	465	P	230	P	glycosyltransferase
LOC_Os01g02940	Os.11246.1.S1_at	0.98	1.93		0.28	**	551	P	1182	P	158	P	glycosyltransferase
LOC_Os01g31370	Os.35024.1.S1_at	0.97	2.32		0.66		44	A	113	P,M,A	31	A	glycosyltransferase
LOC_Os01g72610	Os.18229.1.S1_at	0.64	0.54		1.41		110	P,A	76	P,A	158	P	glycosyltransferase
LOC_Os02g04250	Os.5398.2.S1_x_at	0.94	1.13		1.02		2101	P	2583	P	2182	P	glycosyltransferase
LOC_Os02g22190	Os.5035.1.S1_at	1.00	0.95		1.00		3596	P	3775	P	3706	P	HGA1
LOC_Os02g22380	Os.11058.1.S1_x_at	1.00	1.00		1.47		1781	P	1959	P	2730	P	glycosyltransferase
LOC_Os02g22380	OsAffx.12158.1.S1_at	0.96	0.41		0.39		38	P,A	20	A	20	P,A	glycosyltransferase
LOC_Os02g22480	Os.10041.1.S1_at	0.99	3.64	*	1.01		539	P	2254	P	564	P	glycosyltransferase
LOC_Os03g21260	OsAffx.25178.1.S1_at	0.69	0.17		0.11		15	A	3	A	2	A	2,3-bisphosphoglycer
LOC_Os03g37010	Os.3318.1.S1_at	0.99	0.54	*	0.55	*	7858	P	4614	P	4419	P	glycosyltransferase
LOC_Os04g12010	Os.49562.1.A1_at	0.96	1.34		0.78		962	P	1417	P	774	P	HGA1
LOC_Os05g32544	OsAffx.14921.1.S1_x_a	0.89	0.88		1.45		13	A	13	A	25	A	glycosyltransferase
LOC_Os06g20570	OsAffx.4884.1.S1_at	0.93	0.94		0.48		53	A	57	P,A	26	A	glycosyltransferase
LOC_Os06g27560	Os.7246.1.S1_s_at	0.99	1.11		0.21	***	4931	P	5959	P	1043	P	HGA4
LOC_Os06g27560	Os.7246.2.S1_s_at	0.91	1.17		0.27		238	P	303	P	65	P,A	HGA4
LOC_Os06g28124	Os.9486.1.S1_at	0.90	1.04		0.91		226	P	269	P	209	P	glycosyltransferase
LOC_Os06g49300	OsAffx.28184.2.S1_at	0.69	2.78		0.57		13	A	43	A	8	A	HGA1
LOC_Os06g49320	Os.11586.1.S1_at	0.96	0.42		1.50		1473	P	678	P	2264	P	glycosyltransferase

LOC_Os07g46380	Os.8756.2.A1_at	0.96	0.55		1.63		440	P	272	P	743	P	glycosyltransferase
LOC_Os08g39380	Os.21874.1.S1_at	0.98	0.69		0.92		519	P	394	P	487	P	beta-1,2-xylosyltransferase
LOC_Os10g35020	Os.2550.1.S1_at	0.99	1.86		1.03		627	P	1279	P	663	P	glycosyltransferase
LOC_Os12g13640	Os.18105.1.S1_at	0.97	1.83		1.70		67	P,A	143	P	119	P	HGA6
LOC_Os03g21310	None												ulp1 protease family
LOC_Os11g36700	None												glycosyltransferase

Glycoside Hydrolase

GH9

LOC_Os01g12030	Os.37822.1.A2_at	0.95	0.72		0.35		11	A	13	A	5	A	endoglucanase precursor
LOC_Os01g12070	Os.32667.1.S1_at	0.97	0.36		1.03		19	A	9	A	21	A	endoglucanase precursor
LOC_Os01g12070	Os.32667.2.S1_x_at	0.75	1.03		0.89		26	A	35	A	32	A	endoglucanase precursor
LOC_Os01g21070	Os.28032.1.A1_at	0.96	9.11	**	1.02		19	M,A	202	P	21	P,A	endoglucanase
LOC_Os02g03120	Os.54770.1.S1_at	0.57	0.40		0.42		7	A	5	A	5	A	endoglucanase
LOC_Os02g05744	OsAffx.11908.1.S1_at	0.66	0.95		0.39		15	A	21	A	7	A	endoglucanase
LOC_Os02g50040	Os.53973.1.S1_at	0.98	1.31		2.99	*	102	P	149	P	314	P	endoglucanase
LOC_Os02g50490	Os.17509.1.S1_at	0.99	0.56		1.91		800	P	497	P	1591	P	endoglucanase
LOC_Os02g53820	Os.53793.1.S1_at	0.81	0.29		1.07		11	P,A	4	A	13	A	endoglucanase
LOC_Os03g21210	Os.13910.1.S1_at	0.99	0.71		0.77		2421	P	2041	P	1920	P	endoglucanase
LOC_Os03g52630	Os.10701.1.S1_at	1.00	0.80		0.84		14971	P	13185	P	12921	P	endoglucanase
LOC_Os04g36610	OsAffx.14171.1.S1_at	0.97	0.39		0.42		3	A	1	A	1	A	endoglucanase
LOC_Os04g41970	OsAffx.26423.1.S1_at	0.94	0.65		0.65		173	P	124	P	118	P	endoglucanase
LOC_Os04g57860	Os.50125.1.S1_at	0.75	0.44		0.34		4	A	3	A	2	A	endoglucanase precursor
LOC_Os05g03840	OsAffx.4243.1.S1_at	0.92	0.99		0.91		7	A	8	A	7	A	endoglucanase
LOC_Os05g12150	Os.51700.1.S1_at	0.88	0.73		2.20		7	A	11	A	18	A	endoglucanase precursor
LOC_Os06g13830	Os.48095.1.S1_s_at	0.98	1.40		1.40		414	P	657	P	633	P	endoglucanase precursor
LOC_Os06g13830	OsAffx.15414.1.S1_s_at	0.97	1.04		1.17		147	A	171	P,M,A	177	P,M,A	endoglucanase
LOC_Os06g13830	OsAffx.15414.1.S1_x_at	0.99	1.58		1.96		100	P	176	P	204	P	endoglucanase
LOC_Os06g14540	Os.51106.1.S1_at	0.83	1.81		2.94		39	P,A	78	P	118	P	endoglucanase
LOC_Os06g50140	Os.50481.1.S1_at	0.81	2.10		0.77		8	A	19	P,A	6	A	endoglucanase
LOC_Os08g02220	Os.51266.1.S1_at	0.88	0.27		0.33		12	A	8	A	6	A	endoglucanase
LOC_Os08g29770	Os.53285.1.S1_x_at	0.61	0.35		0.49		8	A	3	A	5	A	endoglucanase
LOC_Os08g29770	OsAffx.17231.1.S1_at	0.78	1.16		0.53		19	A	30	P,A	17	A	endoglucanase
LOC_Os08g32940	OsAffx.22010.1.S1_at	0.68	1.23		0.30		51	A	70	A	20	A	endoglucanase
LOC_Os08g32940	OsAffx.22010.1.S1_x_at	0.98	1.08		2.05		82	P	97	P	175	P	endoglucanase
LOC_Os09g23084	Os.54551.1.S1_at	0.97	0.98		0.62		4941	P	5548	P	3142	P	endoglucanase
LOC_Os09g36060	Os.50334.1.S1_at	1.00	0.78		0.49		58	A	57	P,A	42	A	endoglucanase
LOC_Os09g36060	Os.54812.1.S1_at	0.93	1.26		26.93		2	A	3	A	49	A	endoglucanase
LOC_Os09g36350	Os.6247.1.S1_at	1.00	0.57	**	0.85		11956	P	7505	P	10441	P	endoglucanase
LOC_Os12g24040	OsAffx.31858.1.S1_at	0.91	1.56		1.48		4	A	8	A	7	A	glycosyl hydrolase family 9 protein
LOC_Os12g24040	OsAffx.31858.1.S1_x_at	0.98	1.25		0.96		40	P,M,A	55	P,M,A	40	P,A	glycosyl hydrolase family 9 protein

GH10

LOC_Os01g04290	Os.36438.1.S1_at	0.82	5.28		6.96		11	A	78	P,M	80	P	endo-1,4-beta-xylanase
LOC_Os01g04300	Os.6014.2.S1_at	0.89	1.30		2.77		504	P	942	P	1490	P	endo-1,4-beta-xylanase
LOC_Os01g04300	Os.6014.2.S1_x_at	0.89	1.03		1.84		410	P	503	P	797	P	endo-1,4-beta-xylanase
LOC_Os03g10469	Os.50461.1.S1_at	0.82	0.85		0.72		16	A	16	A	14	A	1,4-beta-xylanase
LOC_Os03g14010	Os.8022.1.S1_at	0.62	0.29		1.10		18	A	7	A	22	A	glycosyl hydrolase family 10 protein
LOC_Os03g47010	OsAffx.25591.1.S1_x_at	0.69	0.17		0.17		24	A	6	A	5	A	glycosyl hydrolase family 10 protein
LOC_Os05g23350	Os.55868.1.S1_at	0.90	1.04		0.65		8	A	10	A	9	A	endo-1,4-beta-xylanase
LOC_Os05g23350	OsAffx.14829.2.S1_x_at	1.00	0.56		0.41		32	A	24	A	18	A	endo-1,4-beta-xylanase
LOC_Os05g23924	Os.9795.1.S1_at	0.98	0.56		0.86		66	P	41	P,A	59	P	glycosyl hydrolase family 10 protein
LOC_Os05g23924	OsAffx.26991.1.S1_at	0.53	2.13		0.42		9	A	21	P,A	5	A	glycosyl hydrolase family 10 protein
LOC_Os05g25560	OsAffx.14829.1.S1_x_at	0.98	1.82		0.76		3	A	9	A	3	A	endo-1,4-beta-xylanase
LOC_Os07g27320	Os.7755.1.S1_at	1.00	0.92		1.09		1055	P	1065	P	1181	P	glycosyl hydrolase family 10 protein
LOC_Os10g21100	OsAffx.18323.1.S1_at	0.97	0.48		0.44		8	A	5	A	4	A	1,4-beta-xylanase
LOC_Os10g21110	Os.8140.1.S1_at	0.89	0.60		1.31		26	A	20	A	37	A	1,4-beta-xylanase

GH16

LOC_Os02g03550	Os.53507.1.S1_at	0.75	1.34		0.83		15	A	22	A	14	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os02g17880	OsAffx.24928.1.S1_at	0.85	1.07		2.17		22	A	26	A	56	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os02g17900	OsAffx.24297.1.S1_at	0.93	1.73		0.67		10	A	20	A	9	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os02g46910	Os.25564.1.S1_at	1.00	0.88		0.90		2600	P	2620	P	2411	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os02g57770	OsAffx.12683.1.S1_at	0.98	0.72		0.63		41	A	33	A	29	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os03g01800	Os.18421.1.S1_a_at	0.94	0.02	**	0.77		2004	P	43	A	1658	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os03g02610	Os.16862.1.S1_at	0.99	0.76		1.52	*	3911	P	3275	P	6114	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os03g02610	Os.16862.1.S1_s_at	0.98	0.88		1.70		209	P,A	204	P,M,A	367	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os03g13570	Os.51174.1.S1_at	0.99	3.99		11.77		107	P	748	P	1313	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os03g63760	Os.49099.1.S1_at	0.99	0.53		0.81		1435	P	852	P	1194	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os04g51450	Os.51755.1.S1_at	0.97	0.94		0.84		28	A	29	A	26	A	glycosyl hydrolases family 16 protein
LOC_Os04g51450	Os.53742.1.S1_at	0.99	0.35		1.61		45	P,A	21	A	75	P	glycosyl hydrolases family 16 protein
LOC_Os04g51460	Os.11354.1.S1_at	0.95	2.96		1.35		73	P,A	433	P	104	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os04g51510	OsAffx.29184.2.S1_at	0.99	1.48		0.73		14	A	25	A	13	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os04g51520	Os.50883.1.S1_at	0.38	0.16		0.01		304	P,M,A	55	A	4	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os04g53950	Os.7566.1.S1_at	0.73	5.05		2.86		12	P,A	91	P,M	36	P,A	glycosyl hydrolases family 16 protein
LOC_Os06g13040	OsAffx.15401.1.S1_at	0.92	0.79		0.60		3	A	3	A	2	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g22919	OsAffx.4907.1.S1_x_at	0.96	2.54		1.18		46	P,A	130	P	56	P,A	DEFL9 - Defensin and Defensin-like DEFL family
LOC_Os06g48160	Os.28030.1.S1_at	0.86	0.34		0.64		1818	P	1209	P	1188	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g48160	Os.28030.1.S1_s_at	0.95	0.46		0.71		6484	P	4312	P	4753	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g48170	OsAffx.15981.1.S1_at	0.43	0.22		0.41		11	A	3	A	7	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g48180	Os.27205.1.S1_at	0.82	0.53		0.07		7986	P	4715	P	602	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g48200	Os.22839.1.S1_at	0.96	0.83		0.25		4907	P	4804	P	1298	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os06g48200	Os.22839.1.S2_at	0.99	0.81		0.73		21723	P	19316	P	16255	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os07g29750	OsAffx.16482.1.S1_at	0.82	4.59		2.91		14	A	70	P	42	M,A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os07g29750	OsAffx.16482.1.S1_x_at	0.96	1.74		1.46		57	A	108	P	84	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os07g34580	Os.9967.1.S1_at	0.98	1.66		2.75		204	P,A	431	P	581	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os07g34580	Os.9967.2.S1_x_at	0.98	1.46		2.30		144	P	247	P	348	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os08g13920	Os.12288.1.S1_at	0.99	0.41		0.68		16277	P	7512	P	11334	P	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os08g13980	OsAffx.29184.1.S1_at	0.80	0.60		0.47		15	A	10	A	8	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os09g23220	Os.47986.2.A1_x_at	0.98	0.58		0.56		31	A	22	P,A	19	A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os10g02770	Os.10574.1.S1_at	0.95	0.94		3.04		40	A	47	A	127	P	glycosyl hydrolases family 16 protein
LOC_Os10g39840	Os.46631.1.S1_x_at	0.98	4.97	*	1.65		27	A	153	P	45	P,M,A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os10g42670	Os.13874.1.S1_x_at	0.95	2.77		24.08		3	A	15	A	75	P,M,A	xyloglucan endotransglucosylase/hydrolase protein
LOC_Os11g33270	Os.11465.1.S1_at	0.95	4.98	**	7.28	**	321	P	1775	P	2418	P	xyloglucan endotransglucosylase/hydrolase protein

GH17

LOC_Os01g51570	Os.4159.1.S1_at	0.71	164.90	**	0.42		10	A	1747	P	4	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g53750	Os.36264.1.S1_at	0.94	1.21		1.67		329	P	499	P	572	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g53750	Os.36264.1.S1_x_at	1.00	1.21		1.59		230	P	323	P	376	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g58730	Os.33745.1.S1_at	0.99	0.18		2.53		41	A	10	A	107	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g64170	Os.4636.1.S1_a_at	0.97	1.89		0.62		2044	P	4305	P	1303	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g64170	Os.4636.1.S2_at	1.00	0.84		0.39	***	13158	P	12110	P	5321	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g71340	Os.2416.1.S1_a_at	0.45	1.02		0.26		11	A	19	A	5	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71350	Os.32115.1.S1_at	0.60	0.34		0.36		11	A	6	A	4	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71380	Os.1385.2.S1_x_at	0.83	0.90		1.66		19	A	21	A	34	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71400	OsAffx.24006.1.S1_at	1.00	0.91		1.22		55	P,A	56	P,A	70	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71410	OsAffx.21887.1.S1_s_at	1.00	1.11		1.64		4	A	6	A	12	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71474	Os.7551.1.S1_at	0.85	0.82		5.20		23	A	22	A	124	P	lichenase-2 precursor
LOC_Os01g71474	OsAffx.22670.1.S1_s_at	0.98	1.13		1.24		2	A	3	A	3	A	lichenase-2 precursor
LOC_Os01g71650	OsAffx.24006.1.S1_at	1.00	0.91		1.22		55	P,A	56	P,A	70	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71670	Os.1385.1.S1_at	1.00	1.82		1.72		90	P,A	183	P	173	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g71680	OsAffx.2458.1.S1_at	0.80	0.53		0.41		13	A	10	A	9	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71690	Os.25266.1.S1_at	0.90	0.76		1.98		8	A	15	P,A	16	A	recA protein
LOC_Os01g71690	Os.42832.1.S1_at	0.97	0.89		0.60		52	P	54	P,A	34	P,M,A	recA protein
LOC_Os01g71810	Os.18664.1.S1_a_at	0.28	1.56		6.45		99	P,A	268	P	647	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g71810	Os.18664.2.S1_x_at	0.64	3.28		5.85		23	A	85	A	142	P,M,A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71820	Os.18664.1.S1_a_at	0.28	1.56		6.45		99	P,A	268	P	647	P	glucan endo-1,3-beta-glucosidase
LOC_Os01g71820	Os.18664.1.S1_x_at	0.43	1.11		1.04		99	P,A	153	P,A	105	P,M,A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71860	Os.12952.1.S1_at	0.75	1.02		0.12		17	P,A	19	P,A	2	A	glycosyl hydrolases family 17 protein
LOC_Os01g71930	Os.52384.1.A1_at	1.00	1.19		0.94		305	P	410	P	297	P	glycosyl hydrolases family 17 protein
LOC_Os02g04670	Os.5742.1.S1_a_at	0.98	0.65		1.19		2200	P	1574	P	2696	P	glucan endo-1,3-beta-glucosidase
LOC_Os02g04670	Os.5742.1.S2_at	1.00	0.60		0.50		53	P,A	35	A	28	A	glucan endo-1,3-beta-glucosidase
LOC_Os02g10660	Os.26628.1.S1_at	0.98	0.66		4.40		13	A	13	A	59	P	glucan endo-1,3-beta-glucosidase
LOC_Os02g33000	Os.53440.1.S1_at	0.95	0.19	*	0.60		520	P	109	P	328	P	glucan endo-1,3-beta-glucosidase
LOC_Os02g33000	Os.7691.1.S1_s_at	0.99	0.63	*	1.39		711	P	490	P	1016	P	glucan endo-1,3-beta-glucosidase
LOC_Os02g53200	Os.11714.1.S1_at	0.92	3.23		6.50		283	P	1090	P	1884	P	glucan endo-1,3-beta-glucosidase
LOC_Os02g53200	OsAffx.12622.1.S1_at	0.76	0.89		0.17		18	A	18	A	3	A	glucan endo-1,3-beta-glucosidase
LOC_Os03g12140	Os.49195.1.S1_at	0.95	0.68		2.36		39	P	33	P,A	94	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g12620	Os.25986.1.S2_at	0.75	0.74		1.14		56	A	46	A	67	A	glucan endo-1,3-beta-glucosidase
LOC_Os03g12620	Os.45998.1.S1_at	0.69	3.52		0.17		11	A	44	P,A	3	A	glucan endo-1,3-beta-glucosidase
LOC_Os03g12620	Os.45998.1.S1_x_at	0.75	2.31		0.49		40	P,A	102	P	21	A	glucan endo-1,3-beta-glucosidase
LOC_Os03g12620	OsAffx.25070.1.S1_at	1.00	0.83		0.57		44	P	43	P	29	P,M,A	glucan endo-1,3-beta-glucosidase
LOC_Os03g14210	Os.54833.1.S1_at	0.98	0.57		1.05		41	A	27	A	52	M,A	glucan endo-1,3-beta-glucosidase
LOC_Os03g25790	Os.49475.1.S1_at	0.98	1.04		3.50	**	354	P	408	P	1267	P	glycosyl hydrolases family 17 protein
LOC_Os03g40330	OsAffx.25450.1.S1_at	0.95	1.25		0.93		21	P,M	30	P,A	21	P,A	glucan endo-1,3-beta-glucosidase
LOC_Os03g45390	Os.49077.1.A1_at	0.91	0.94		0.76		617	P	643	P	491	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g46660	Os.21574.1.S1_a_at	0.99	1.88		2.01		2752	P	5826	P	5705	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g51240	Os.8114.1.A1_x_at	0.89	2.03		2.75		277	P,A	641	P	796	P	glucan endo-1,3-beta-glucosidase

LOC_Os03g57880	OsAffx.25749.1.S1_at	0.93	1.30		0.56		115	P	165	P	66	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g57880	OsAffx.25749.1.S1_s_a	0.97	1.21		0.41		453	P	604	P	191	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g62860	Os.29814.1.S1_at	0.64	1.50		0.52		16	A	26	A	10	A	glucan endo-1,3-beta-glucosidase
LOC_Os04g33640	Os.24051.2.S1_at	0.93	0.62		0.64		205	P	155	P	134	P	glucan endo-1,3-beta-glucosidase
LOC_Os04g33640	Os.47778.1.A1_s_at	0.81	0.75		0.90		227	P	198	P	209	P	glucan endo-1,3-beta-glucosidase
LOC_Os05g31140	Os.7947.1.S1_a_at	0.99	8.07		7.74		14	A	136	P	118	P	lichenase-2 precursor
LOC_Os05g31140	Os.7947.1.S1_x_at	0.51	5.54		4.92		31	A	198	P	159	P	lichenase-2 precursor
LOC_Os05g37130	Os.17542.1.S1_at	0.96	0.91		0.85		319	P	338	P	283	P	glucan endo-1,3-beta-glucosidase
LOC_Os05g37130	Os.53494.1.S1_x_at	0.95	0.91		0.52		486	P	502	P	269	P	glucan endo-1,3-beta-glucosidase
LOC_Os05g41610	Os.4160.1.S1_at	0.93	1.35		0.40		2547	P	3974	P	1048	P	glucan endo-1,3-beta-glucosidase
LOC_Os05g45860	Os.51679.1.S1_at	0.93	1.42		0.54		127	P	203	P	72	P	glucan endo-1,3-beta-glucosidase
LOC_Os06g04080	Os.54484.2.S1_at	0.93	0.21		15.11		19	A	7	A	300	P	glucan endo-1,3-beta-glucosidase
LOC_Os06g34020	OsAffx.15721.1.S1_at	0.81	1.64		8.61		3	A	6	A	30	M,A	glucan endo-1,3-beta-glucosidase
LOC_Os06g39060	Os.4941.1.S1_at	0.94	0.50		0.53		44	A	27	A	24	A	glucan endo-1,3-beta-glucosidase
LOC_Os06g40490	Os.50415.1.S1_at	0.99	0.81		0.69		7101	P	6334	P	5051	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g07340	Os.52598.1.S1_at	0.97	0.59		0.72		773	P	512	P	579	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g13580	Os.24085.1.S1_x_at	0.89	0.99		2.69		3	A	4	A	13	A	glucan endo-1,3-beta-glucosidase
LOC_Os07g32600	Os.49200.1.S1_at	0.99	0.41	**	1.38		1324	P	599	P	1881	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g35350	Os.25578.1.S1_at	0.63	1.23		0.26		23	A	33	P,A	6	A	glucan endo-1,3-beta-glucosidase
LOC_Os07g35350	Os.57525.1.S1_x_at	0.91	0.96		0.65		35	A	41	A	25	A	glucan endo-1,3-beta-glucosidase
LOC_Os07g35480	Os.6776.1.S1_at	0.91	0.98		0.18		122	P	138	P	23	A	glucan endo-1,3-beta-glucosidase
LOC_Os07g35510	Os.14978.1.S1_a_at	0.93	4.35	**	0.24	**	1022	P	4992	P	256	P	glycosyl hydrolases family 17 protein
LOC_Os07g35520	Os.7086.1.S1_at	0.96	0.11		136.80	**	38	P,A	8	A	5436	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g35520	Os.7086.1.S1_s_at	0.90	0.86		194.90	**	5	A	7	A	1045	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g35520	OsAffx.16567.1.S1_at	0.99	0.54		5.83	**	47	P,M	29	A	283	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g35560	Os.27755.1.S1_at	0.69	0.57		0.78		11	A	7	A	9	A	glucan endo-1,3-beta-glucosidase
LOC_Os07g38930	OsAffx.5572.1.S1_at	0.98	2.20		2.23		225	P	549	P	516	P	glucan endo-1,3-beta-glucosidase
LOC_Os07g41014	OsAffx.22670.2.S1_at	0.99	0.31		0.35		2	A	1	A	1	A	glycosyl hydrolases family 17 protein
LOC_Os08g12800	Os.54847.1.S1_at	0.82	0.56		6.46	*	14	A	8	A	90	P,M,A	glucan endo-1,3-beta-glucosidase
LOC_Os08g23720	Os.30016.1.S1_at	0.96	0.97		2.86		148	P	163	P	443	P	glucan endo-1,3-beta-glucosidase
LOC_Os08g41410	OsAffx.6103.1.S1_at	0.47	0.73		0.74		12	A	12	A	9	A	glucan endo-1,3-beta-glucosidase
LOC_Os09g09980	Os.16809.1.S1_at	0.99	0.61		0.92		3193	P	2155	P	3033	P	glucan endo-1,3-beta-glucosidase
LOC_Os09g32550	Os.27986.1.A1_at	0.97	1.51		3.10		82	P,M	139	P	261	P	glucan endo-1,3-beta-glucosidase
LOC_Os09g36280	OsAffx.18009.1.S1_s_a	0.83	0.76		0.79		59	P,A	49	P	47	P	glucan endo-1,3-beta-glucosidase
LOC_Os10g07290	Os.46472.1.S1_at	0.93	0.29		4.66		578	P	217	P	2824	P	glucan endo-1,3-beta-glucosidase
LOC_Os11g36940	OsAffx.31336.1.S1_at	0.72	1.64		44.42	*	6	A	12	A	265	P	glucan endo-1,3-beta-glucosidase
LOC_Os11g36940	OsAffx.31336.1.S1_x_a	0.97	0.33		10.31	**	18	A	7	A	192	P	glucan endo-1,3-beta-glucosidase
LOC_Os11g47820	Os.8051.1.S1_at	1.00	1.60		1.77		1043	P	1860	P	1904	P	glucan endo-1,3-beta-glucosidase
LOC_Os11g47820	Os.8051.2.S1_x_at	0.94	1.20		1.32		760	P	995	P	1018	P	glucan endo-1,3-beta-glucosidase
LOC_Os03g27980	OsAffx.25262.1.S1_at	0.66	0.87		2.21		20	A	19	A	45	A	glucan endo-1,3-beta-glucosidase
LOC_Os01g71950	OsAffx.23842.2.S1_x_a	0.72	0.37		0.30		10	A	4	A	3	A	expressed protein
LOC_Os01g71830	None												glucan endo-1,3-beta-glucosidase
LOC_Os08g14700	None												glucan endo-1,3-beta-glucosidase
GH19													
LOC_Os01g18400	Os.36593.1.S1_at	0.76	0.57		2.85		296	P,A	190	M,A	881	P	Chitinase family protein precursor-CHIT10
LOC_Os01g18400	Os.36593.2.S1_x_at	0.80	2.37		3.39		8	A	22	A	29	A	Chitinase family protein precursor-CHIT10
LOC_Os02g39330	Os.11894.1.S1_at	0.73	52.24	**	0.50		4	A	256	P	2	A	Chitinase family protein precursor-CHIT1
LOC_Os03g04060	Os.1191.1.S1_at	0.80	217.60	*	6.37		28	P,A	7197	P	245	P	Chitinase family protein precursor-CHIT16
LOC_Os04g41620	Os.7991.1.S1_at	0.93	2.06		4.86		131	P	307	P	664	P	Chitinase family protein precursor-CHIT2
LOC_Os04g41680	Os.10166.1.S1_at	0.98	2.12		5.17		87	P	215	P	468	P	Chitinase family protein precursor-CHIT3
LOC_Os05g04690	Os.54044.1.S1_at	0.57	0.37		0.50		7	A	5	A	5	A	Chitinase family protein precursor-CHIT11
LOC_Os05g33140	Os.47564.1.S1_at	0.98	87.32	**	0.17		24	A	2422	P	6	A	Chitinase family protein precursor-CHIT5
LOC_Os05g33150	Os.4976.1.S1_at	0.84	1.87		0.80		3	A	10	A	2	A	Chitinase family protein precursor-CHIT6
LOC_Os06g51050	Os.2692.1.S1_x_at	0.90	44.62	**	1.75		36	P,A	1800	P	66	P,A	Chitinase family protein precursor-CHIT7
LOC_Os06g51050	Os.51172.1.S1_x_at	0.98	87.24	***	1.04		57	P,A	5576	P	61	P	Chitinase family protein precursor-CHIT7
LOC_Os06g51060	Os.22000.1.S1_at	0.98	19.70	***	0.75		716	P	15625	P	551	P	Chitinase family protein precursor-CHIT8
LOC_Os08g41100	Os.9173.1.S1_at	1.00	0.79		0.58		7402	P	6476	P	4457	P	Chitinase family protein precursor-CHIT12
LOC_Os09g32080	Os.12399.1.S1_at	1.00	0.60	**	0.81		13700	P	9015	P	11360	P	Chitinase family protein precursor-CHIT13
LOC_Os10g39680	Os.3415.1.S1_at	0.96	46.34	**	0.36		32	A	2009	P	12	A	Chitinase family protein precursor-CHIT14
LOC_Os10g39680	Os.3415.1.S1_s_at	0.94	24.56		0.12		25	A	768	P	7	A	Chitinase family protein precursor-CHIT14
LOC_Os03g30470	None												Chitinase family protein precursor-CHIT4
LOC_Os05g33130	None												Chitinase family protein precursor-CHIT17
LOC_Os10g39700	None												Chitinase family protein precursor-CHIT15
GH28													
LOC_Os01g07790	OsAffx.23155.1.S1_at	1.00	1.46		2.45		1	A	2	A	6	A	polygalacturonase precursor
LOC_Os01g19170	Os.48024.1.A1_at	0.95	0.44		1.00		70	P,A	37	A	77	P	polygalacturonase precursor
LOC_Os01g19170	Os.48024.1.A1_x_at	0.96	0.49		0.71		110	P,A	61	A	84	P	polygalacturonase precursor
LOC_Os01g22590	Os.29464.1.S1_at	0.61	0.39		0.86		7	A	5	A	10	A	polygalacturonase
LOC_Os01g33300	Os.8128.1.S1_at	0.95	0.93		1.36		4	A	4	A	7	A	exopolygalacturonase precursor
LOC_Os01g36830	Os.50177.1.S1_at	0.98	0.74		0.86		121	P	99	P	107	P	polygalacturonase precursor
LOC_Os01g36830	OsAffx.23533.1.S1_x_a	0.98	1.87		1.06		4	A	8	A	4	A	polygalacturonase precursor
LOC_Os01g43160	Os.15014.1.S1_at	1.00	0.84		0.75		1286	P	1195	P	991	P	polygalacturonase
LOC_Os01g43490	Os.32727.1.S1_at	0.73	5.37		0.43		10	A	67	P,A	6	A	polygalacturonase precursor
LOC_Os01g44970	Os.47331.1.S1_at	0.42	0.13		0.28		127	P,A	19	P	37	P,M	polygalacturonase precursor
LOC_Os01g44970	Os.48563.1.S1_s_at	0.73	0.46		0.54		1233	P	621	P	664	P	polygalacturonase precursor
LOC_Os01g44970	Os.48563.1.S1_x_at	0.53	0.23		0.30		176	P	44	P	52	P	polygalacturonase precursor
LOC_Os01g45060	Os.48563.1.S1_x_at	0.53	0.23		0.30		176	P	44	P	52	P	polygalacturonase precursor
LOC_Os01g66710	OsAffx.11762.1.S1_at	0.80	0.92		0.53		3	A	4	A	2	A	polygalacturonase precursor
LOC_Os01g66710	OsAffx.11762.1.S1_x_a	0.87	0.69		0.69		3	A	2	A	2	A	polygalacturonase precursor
LOC_Os02g03750	Os.54804.1.S1_at	0.54	0.23		21.42	*	21	P,A	6	A	484	P	polygalacturonase precursor
LOC_Os02g10300	Os.10004.1.S1_s_at	0.95	0.59		0.37		17	A	14	A	12	A	exopolygalacturonase precursor
LOC_Os02g15690	Os.27198.1.S1_at	0.80	1.19		5.38		15	P,A	19	P,M,A	85	P	polygalacturonase
LOC_Os02g15690	Os.55692.1.S1_at	0.96	1.17		4.33		2	A	3	A	12	A	polygalacturonase
LOC_Os02g54030	Os.25444.1.S1_at	1.00	0.51		2.62	***	797	P	451	P	2160	P	endo-polygalacturonase precursor
LOC_Os02g54030	OsAffx.3061.1.S1_x_at	1.00	0.40	***	3.27	***	431	P	192	P	1464	P	endo-polygalacturonase precursor
LOC_Os03g11760	Os.54526.1.S1_at	1.00	0.92		0.96		14	A	14	A	14	A	polygalacturonase precursor
LOC_Os03g59330	Os.14979.1.S2_at	0.98	1.04		0.55		131	P	150	P	75	P,A	polygalacturonase precursor
LOC_Os03g59330	OsAffx.25765.1.S1_at	0.89	0.67		4.51		14	A	12	A	69	P,A	polygalacturonase precursor
LOC_Os03g61800	Os.48315.1.S1_at	0.99	1.03		0.94		1321	P	1516	P	1288	P	polygalacturonase
LOC_Os05g20020	OsAffx.14766.1.S1_at	0.79	0.56		0.29		33	A	20	A	12	A	polygalacturonase precursor
LOC_Os05g46510	Os.9759.1.S1_x_at	0.96	2.46		1.59		96	P	314	P	156	P	polygalacturonase precursor
LOC_Os05g46510	Os.9759.2.S1_at	0.98	3.31		1.91		160	P	606	P	317	P	polygalacturonase precursor
LOC_Os05g46520	Os.5687.1.S1_at	0.74	1.24		1.42		566	P	794	P	842	P	polygalacturonase precursor
LOC_Os05g50260	Os.8509.1.S1_at	0.86	0.52		1.74		142	P	89	P	252	P	polygalacturonase precursor
LOC_Os05g50260	OsAffx.15177.1.S1_at	0.37	0.16		3.51		10	A	2	A	36	P,A	polygalacturonase precursor
LOC_Os05g50260	OsAffx.15177.1.S1_x_a	0.37	0.15		1.20		9	A	1	A	12	A	polygalacturonase precursor
LOC_Os05g50960	OsAffx.15187.1.S1_at	0.50	0.80		17.58		7	A	7	A	133	P	polygalacturonase
LOC_Os06g16810	OsAffx.4854.1.S1_at	0.81	0.56		0.23		6	A	6	A	3	A	polygalacturonase precursor
LOC_Os06g17000	Os.51972.1.S1_at	0.83	1.26		0.55		4	A	5	A	2	A	BURP domain containing protein
LOC_Os06g28670	OsAffx.4954.1.S1_at	0.18	0.08		0.07		128	P,A	11	A	10	A	polygalacturonase precursor
LOC_Os06g28670	OsAffx.4954.1.S1_x_at	0.20	0.17		0.04		133	M,A	26	A	5	A	polygalacturonase precursor
LOC_Os06g35320	Os.7500.1.S1_at	0.79	0.72		0.23		9	A	9	A	2	A	exopolygalacturonase precursor
LOC_Os06g35370	Os.7500.1.S1_at	0.79	0.72		0.23		9	A	9	A	2	A	exopolygalacturonase precursor
LOC_Os06g40880	Os.49993.1.S1_at	0.60	0.23		0.17		11	A	5	A	3	A	polygalacturonase precursor
LOC_Os06g40890	Os.53450.1.S1_at	1.00	0.86		0.87		105	A	100	A	96	A	exopolygalacturonase precursor
LOC_Os07g10700	OsAffx.28391.1.S1_at	1.00	0.64		0.48		16	A	13	A	10	A	polygalacturonase precursor
LOC_Os07g10700	OsAffx.28391.1.S1_x_a	0.95	12.30		12.04		1	A	10	A	10	A	polygalacturonase precursor
LOC_Os07g10740	OsAffx.28393.1.S1_at	0.76	0.52		0.26		5	A	3	A	2	A	polygalacturonase precursor
LOC_Os07g14160	Os.38192.1.S1_at	0.99	0.84		0.70		927	P	871	P	674	P	polygalacturonase-like protein
LOC_Os08g01600	OsAffx.28980.1.S1_at	0.86	2.12		0.66		37	P,A	90	P,M	25	P,A	polygalacturonase
LOC_Os08g23790	Os.5670.1.S1_at	0.72	1.20		0.34		2	A	5	A	1	A	exopolygalacturonase precursor
LOC_Os08g29200	Os.54090.1.S1_at	0.95	1.36		2.88		376	P	601	P	1130	P	BURP domain containing protein
LOC_Os09g16010	OsAffx.6291.1.S1_at	1.00	0.80		0.89		44	P,A	40	P,A	40	P,M,A	BURP domain containing protein
LOC_Os09g26800	Os.27736.1.S1_at	0.99	0.92		0.77		1884	P	1915	P	1496	P	polygalacturonase
LOC_Os09g31270	OsAffx.17972.1.S1_at	1.00	0.78		1.22		315	P	276	P	397	P	polygalacturonase
LOC_Os10g26940	Os.37718.1.S1_at	0.96	0.52		0.51		6	A	3	A	3	A	BURP domain containing protein
LOC_Os11g14400	OsAffx.18846.1.S1_at	0.99	0.41		0.75		5	A	3	A	4	A	polygalacturonase precursor
LOC_Os11g14410	Os.56125.1.S1_at	0.70	0.84		0.95		16	A	18	A	16	A	polygalacturonase precursor
LOC_Os11g43750	Os.21183.1.S1_at	0.99	0.30	**	0.54	**	6141	P	2050	P	3399	P	polygalacturonase
LOC_Os12g36810	Os.9731.1.S1_at	1.00	0.83		1.34		1069	P	1026	P	1491	P	polygalacturonase
LOC_Os05g14150	None												polygalacturonase precursor
LOC_Os06g31270	None												polygalacturonase precursor
LOC_Os06g35300	None												polygalacturonase precursor
LOC_Os07g10680	None												polygalacturonase precursor
LOC_Os07g10730	None												polygalacturonase precursor
GH35													
LOC_Os01g34920	Os.41043.1.S1_at	0.66	0.71		0.62		6	A	7	A	5	A	beta-galactosidase precursor
LOC_Os01g39830	Os.18562.1.S1_at	1.00	2.95		2.39		615	P	2309	P	1522	P	beta-galactosidase precursor
LOC_Os01g65460	Os.42688.1.S1_x_at	1.00	3.12		4.43		187	P	705	P	861	P	beta-galactosidase precursor
LOC_Os01g65460	Os.9892.1.S1_a_at	0.99	2.81		3.50		260	P	843	P	953	P	beta-galactosidase precursor
LOC_Os01g65460	Os.9892.2.S1_at	1.00	1.88		1.90		90	P	238	P	179	P	beta-galactosidase precursor
LOC_Os02g12730	Os.14358.1.S1_at	0.84	0.51		7.72	*	28	P,M,A	16	A	227	P	beta-galactosidase precursor
LOC_Os02g12730	Os.14358.4.S1_x_at	0.94	0.59		3.05		103	P,A	70	M,A	328	P	beta-galactosidase precursor
LOC_Os03g06940	Os.13559.1.S1_at	0.96	2.73		5.03		242	P	929	P	1258	P	beta-galactosidase precursor
LOC_Os03g15020	Os.22360.1.S1_at	0.67	1.14		1.34		237	P	313	P	322	P	beta-galactosidase precursor

LOC_Os05g35360	OsAffx.4526.1.S1_at	0.97	0.28		0.59		32	A	17	A	20	A	beta-galactosidase precursor
LOC_Os05g46200	Os.14570.1.S1_at	1.00	0.59	**	0.58	**	5717	P	3714	P	3431	P	beta-galactosidase precursor
LOC_Os06g37560	Os.6322.1.S1_at	0.98	0.90		1.00		10054	P	10025	P	10298	P	beta-galactosidase precursor
LOC_Os08g43570	Os.18310.1.S1_at	0.70	1.04		0.90		33	A	40	A	32	A	beta-galactosidase precursor
LOC_Os09g36810	Os.49945.1.S1_at	0.99	0.85		0.77		447	P	419	P	357	P	beta-galactosidase precursor
LOC_Os10g18400	Os.46702.1.S1_at	0.87	3.78		0.59		2	A	8	A	1	A	beta-galactosidase precursor
LOC_Os10g19960	OsAffx.20496.1.S1_at	0.98	1.12		1.76		7	A	9	A	12	A	beta-galactosidase precursor
LOC_Os10g19960	OsAffx.20496.1.S1_s_at	0.96	0.78		4.62		5	A	4	A	28	A	beta-galactosidase precursor
LOC_Os12g24170	Os.52193.1.S1_at	0.92	0.54		0.31		2210	P	1353	P	697	P	BGAL9
LOC_Os06g42310	None												beta-galactosidase precursor
GH51													
LOC_Os03g20420	Os.10578.1.A1_at	0.98	0.70		0.25	**	4514	P	3526	P	1184	P	alpha-N-arabinofuranosidase A
LOC_Os07g48750	Os.9163.1.S1_at	0.90	0.61		0.83		195	P	133	P	171	P	alpha-N-arabinofuranosidase
LOC_Os11g03730	Os.8403.1.S1_a_at	0.96	1.61		0.54		4104	P	7399	P	2285	P	alpha-N-arabinofuranosidase A
LOC_Os11g03730	Os.8403.1.S1_s_at	0.96	1.99		0.54		2348	P	5333	P	1296	P	alpha-N-arabinofuranosidase A
LOC_Os11g03734	OsAffx.7470.1.S1_x_at	1.00	0.95		0.83		120	P	125	P	103	P	alpha-N-arabinofuranosidase A
LOC_Os11g03780	Os.5087.1.S1_at	0.90	1.07		0.66		391	P	473	P	269	P	alpha-N-arabinofuranosidase
LOC_Os12g03470	Os.8403.1.S1_a_at	0.96	1.61		0.54		4104	P	7399	P	2285	P	alpha-N-arabinofuranosidase A
LOC_Os12g03470	Os.8403.1.S1_s_at	0.96	1.99		0.54		2348	P	5333	P	1296	P	alpha-N-arabinofuranosidase A
LOC_Os12g03480	Os.54371.1.S1_x_at	0.98	0.71		0.84		147	P	117	P	127	P	alpha-N-arabinofuranosidase
LOC_Os12g03530	None												alpha-N-arabinofuranosidase
GPI-anchored													
LOC_Os01g44090	Os.36473.1.S1_at	0.81	2.09		1.79		329	P	759	P	598	P	GPI-anchored protein
LOC_Os02g33740	Os.31602.1.S1_at	0.55	0.37		0.31		13	A	7	A	6	A	GPI-anchored protein
LOC_Os02g48980	Os.12153.1.S1_at	1.00	1.06		0.87		7136	P	8326	P	6358	P	GPI-anchored protein
LOC_Os03g04110	Os.11983.1.S1_at	0.98	1.36		0.22	***	2217	P	3310	P	502	P	receptor-like GPI-anchored protein
LOC_Os04g42210	Os.20512.1.S1_at	0.95	2.13		0.33		13	A	32	A	7	A	GPI-anchored protein
LOC_Os04g42220	OsAffx.4055.1.S1_at	0.92	0.66		1.49		29	A	27	A	45	A	GPI-anchored protein
LOC_Os05g43690	Os.9551.1.S1_at	0.96	0.88		4.82		120	P,A	148	P,A	599	P	GPI-anchored protein
LOC_Os06g19990	Os.12376.1.S1_at	0.90	1.69		3.90		296	P	547	P	1180	P	GPI-anchored protein
LOC_Os09g12620	Os.52109.1.S1_at	0.63	0.61		0.26		16	A	15	A	5	A	GPI-anchored protein
COBL													
LOC_Os03g30260	Os.50763.1.S1_at	0.90	3.89		2.04		5	A	23	A	13	A	COBRA-like protein
LOC_Os05g32110	Os.7609.1.S1_at	1.00	0.71		0.73		12919	P	10021	P	9628	P	COBRA-like protein
LOC_Os05g32110	Os.7609.2.S2_a_at	0.99	0.85		2.40	*	154	P,M	146	P,A	385	P	COBRA-like protein
LOC_Os07g41310	Os.9592.1.S1_at	0.84	3.28		0.61		65	P,A	233	P	41	A	COBRA-like protein
LOC_Os10g35460	Os.15633.1.S1_at	0.72	4.04		0.10	*	28	A	123	P	3	A	COBRA-like protein
LOC_Os10g35460	Os.15633.1.S2_at	0.79	4.31		0.38		306	P	1429	P	120	P	COBRA-like protein
LOC_Os03g18910	Os.49999.1.S1_x_at	0.95	0.54		0.09	**	1073	P	675	P	98	P	COBRA-like protein
LOC_Os06g47110	OsAffx.15964.1.S1_at	0.69	0.63		0.56		20	A	14	A	16	A	COBRA-like protein
LOC_Os07g49080	Os.5154.1.S1_at	0.95	3.37		0.61		67	A	263	P	42	A	COBRA-like protein
LOC_Os07g45060	Os.9211.1.S1_at	0.98	0.30		0.76		8357	P	2853	P	6555	P	COBRA-like protein
LOC_Os03g30250	Os.37902.1.S1_at	0.97	0.99		5.04	*	707	P	792	P	3709	P	COBRA-like protein (BC1)
LOC_Os07g41320	OsAffx.28857.1.S1_at	0.68	2.21		16.55		5	A	13	A	83	P,A	COBRA-like protein (BC1-like)
LOC_Os03g54750	None												COBRA-like protein
AGPs													
LOC_Os01g06580	Os.1437.1.S1_at	0.92	0.68		2.92		3427	P	2861	P	10393	P	fasciclin-like arabinogalactan protein (OsFLA8
LOC_Os01g47780	Os.5908.1.S1_at	1.00	0.30	**	1.93		4184	P	1404	P	8409	P	fasciclin-like arabinogalactan protein (OsFLA7
LOC_Os01g62380	Os.42475.1.S1_at	0.97	1.03		0.76		1022	P	1162	P	809	P	fasciclin-like arabinogalactan protein (OsFLA12
LOC_Os01g62380	Os.42475.1.S2_at	0.94	0.86		0.83		35	P,A	34	P,A	30	P	fasciclin-like arabinogalactan protein (OsFLA12
LOC_Os02g20540	Os.14430.1.S1_at	0.92	0.74		2.19		13	A	11	A	29	A	fasciclin-like arabinogalactan protein (OsFLA19
LOC_Os02g20560	Os.17961.1.S1_a_at	0.77	0.03	*	2.25		191	P	7	A	455	P	fasciclin-like arabinogalactan protein (OsFLA15
LOC_Os02g26290	Os.6347.1.S1_at	0.63	1.04		0.42		3	A	4	A	1	A	fasciclin-like arabinogalactan protein (OsFLA22
LOC_Os02g26320	Os.55769.1.S1_at	0.84	0.59		0.49		4	A	3	A	2	A	fasciclin-like arabinogalactan protein (OsFLA20
LOC_Os02g49420	Os.53492.1.S1_at	1.00	1.37		23.74	**	10	A	17	A	248	P	fasciclin-like arabinogalactan protein (OsFLA21
LOC_Os03g03600	Os.5826.2.S1_a_at	0.94	0.62		1.23		9519	P	6702	P	12120	P	fasciclin-like arabinogalactan protein (OsFLA2
LOC_Os04g21570	OsAffx.26086.1.S1_at	0.54	0.55		0.41		16	A	10	A	8	A	fasciclin-like arabinogalactan protein (OsAGP3
LOC_Os04g39590	OsAffx.14208.1.S1_at	0.90	1.09		0.50		37	A	49	A	25	A	fasciclin-like arabinogalactan protein (OsFLA14
LOC_Os04g39600	Os.5963.1.S1_at	0.47	0.43		1.18		13	A	12	A	23	A	fasciclin-like arabinogalactan protein (OsFLA13
LOC_Os04g48490	OsAffx.14326.1.S1_s_at	0.97	1.39		3.23		103	P,A	230	P,A	345	P	fasciclin-like arabinogalactan protein (OsFLA1
LOC_Os05g07060	Os.54555.1.S1_at	0.96	0.92		4.35		2562	P	2962	P	11550	P	fasciclin-like arabinogalactan protein (OsFLA9
LOC_Os05g38500	OsAffx.27225.1.S1_at	0.98	0.31		1.37		90	A	31	A	128	A	fasciclin-like arabinogalactan protein
LOC_Os05g48890	OsAffx.15160.1.S1_at	1.00	1.06		0.35	**	3158	P	3677	P	1154	P	fasciclin-like arabinogalactan protein
LOC_Os05g48890	OsAffx.15160.1.S1_s_at	0.99	0.93		0.47	*	14548	P	14885	P	7048	P	fasciclin-like arabinogalactan protein
LOC_Os05g48900	Os.53704.1.S1_x_at	1.00	0.68	*	0.79	*	15835	P	11855	P	12793	P	fasciclin-like arabinogalactan protein (OsFLA6
LOC_Os06g17460	OsAffx.15475.1.S1_at	0.87	0.70		0.85		32	A	27	A	28	A	fasciclin-like arabinogalactan protein
LOC_Os06g44660	Os.20322.1.S1_at	0.81	0.84		1.49		18	A	20	A	30	A	fasciclin-like arabinogalactan protein
LOC_Os08g23180	Os.5500.1.S1_s_at	1.00	0.87		0.96		15045	P	14395	P	14887	P	fasciclin-like arabinogalactan protein (OsFLA3
LOC_Os08g38270	Os.55554.1.S1_at	1.00	0.81		0.39	*	6683	P	6024	P	2689	P	fasciclin-like arabinogalactan protein (OsFLA4
LOC_Os08g38270	OsAffx.6066.1.S1_s_at	0.96	0.88		0.39		700	P	686	P	285	P	fasciclin-like arabinogalactan protein (OsFLA4
LOC_Os08g39270	Os.54871.1.S1_at	0.94	0.84		2.43		307	P	288	P	790	P	fasciclin-like arabinogalactan protein (OsFLA5
LOC_Os09g07350	Os.49544.1.S1_at	1.00	0.62	*	0.71	*	6098	P	4137	P	4424	P	fasciclin-like arabinogalactan protein (OsFLA11
LOC_Os09g30010	Os.56233.1.S1_s_at	0.69	0.98		5.00		59	A	64	A	297	P,M	fasciclin-like arabinogalactan protein (OsFLA10
LOC_Os09g30010	OsAffx.30093.1.S1_at	0.93	0.77		9.48	*	230	P	218	P,A	2336	P	fasciclin-like arabinogalactan protein (OsFLA10
LOC_Os09g30486	Os.52641.1.S1_at	0.97	0.25		0.43		3409	P	961	P	1515	P	fasciclin-like arabinogalactan protein
LOC_Os03g57460	Os.22627.1.S1_at	0.99	0.40		1.02		280	P	131	P	296	P	fasciclin domain (OsFLA24)
LOC_Os03g57490	Os.25125.1.A1_at	0.99	0.83		0.56		123	P,M,A	111	P,M	71	P,A	fasciclin domain
LOC_Os07g06680	Os.27550.1.S1_at	1.00	0.53		0.94		3979	P	2342	P	3871	P	fasciclin domain (OsFLA16)
LOC_Os05g45480	OsAffx.27322.1.S1_at	0.99	0.97		0.90		3	A	4	A	3	A	arabinogalactan protein
LOC_Os05g45480	OsAffx.27322.1.S1_s_at	0.89	1.30		1.80		3	A	5	A	6	A	arabinogalactan protein
LOC_Os09g33800	Os.9057.1.S1_a_at	0.99	0.92		0.87		11398	P	11460	P	10191	P	arabinogalactan protein
LOC_Os02g28130	None												fasciclin-like arabinogalactan protein (OsAGP2
Pectin methyltransferase													
LOC_Os02g51860	Os.24364.1.A1_at	0.99	0.78		0.95		4945	P	4225	P	4840	P	dehydration response related protein
LOC_Os02g51860	Os.24364.1.A1_s_at	0.98	0.58		0.80		1572	P	1001	P	1286	P	dehydration response related protein
LOC_Os02g51860	OsAffx.12602.1.S1_at	0.99	0.84		0.94		780	P	717	P	755	P	dehydration response related protein
Pectin methylesterase													
LOC_Os01g13320	Os.46008.1.S1_at	1.00	0.71		6.94	***	32	P,A	25	P,M,A	225	P	pectinesterase
LOC_Os01g15039	OsAffx.23254.1.S1_at	0.84	0.41		4.18		26	A	12	A	113	A	pectinesterase
LOC_Os01g15039	OsAffx.23254.1.S1_x_at	1.00	1.06		1.90		94	A	110	A	184	A	pectinesterase
LOC_Os01g19440	OsAffx.11114.1.S1_at	0.97	0.50		1.40		55	A	40	A	83	A	pectinesterase
LOC_Os01g19440	OsAffx.11114.1.S1_x_at	0.98	0.43		1.19		39	A	20	A	51	A	pectinesterase
LOC_Os01g20980	Os.37598.1.S1_at	0.87	11.06	*	3.70		9	A	107	P	34	M,A	pectinesterase
LOC_Os01g21034	Os.32108.1.S1_s_at	0.90	5.11		7.23		340	P	2224	P	2558	P	pectinesterase
LOC_Os01g21034	Os.32108.2.S1_x_at	0.89	4.72		8.22		13	A	91	P,A	110	P	pectinesterase
LOC_Os01g44340	OsAffx.21322.1.S1_at	0.89	2.05		0.59		16	A	38	P,A	13	A	pectinesterase
LOC_Os01g53990	Os.29826.2.S1_at	0.87	0.14		0.11		77	A	22	A	13	A	pectinesterase
LOC_Os01g53990	Os.29826.2.S1_x_at	0.77	0.16		0.11		36	A	6	A	4	A	pectinesterase
LOC_Os01g57854	Os.27505.1.S1_at	0.93	0.25		2.65		46	P,A	15	P,A	125	P	pectinesterase
LOC_Os01g65790	Os.32182.1.S1_at	0.87	0.40		0.28		1173	P	546	P	346	P	pectinesterase
LOC_Os02g18650	Os.54891.1.S1_at	0.99	0.16		0.37		25	A	5	A	11	A	pectinesterase
LOC_Os02g46310	OsAffx.24752.1.S1_at	0.98	0.87		0.92		3	A	3	A	3	A	pectinesterase
LOC_Os02g54190	Os.47330.1.S1_at	0.97	0.16	***	6.86	***	256	P	47	A	1838	P	pectinesterase
LOC_Os03g18860	Os.53030.1.S1_at	0.99	0.50		0.76		29	A	18	A	23	A	pectinesterase
LOC_Os03g19610	Os.18212.1.S1_at	0.98	2.71		2.94		3	A	9	A	11	A	pectinesterase
LOC_Os03g28090	Os.52831.1.S1_at	1.00	1.43		0.66		48	A	75	P	33	A	pectinesterase
LOC_Os03g28090	Os.55086.1.S1_at	0.52	0.47		0.77		6	A	3	A	5	A	pectinesterase
LOC_Os04g35770	Os.52558.1.S1_at	0.98	1.10		1.05		1526	P	1847	P	1648	P	pectinesterase
LOC_Os04g35770	OsAffx.26346.1.S1_s_at	1.00	1.15		0.81		148	P	188	P	125	P	pectinesterase
LOC_Os04g38560	Os.18265.1.S1_at	0.96	1.46		0.54		2	A	3	A	1	A	pectinesterase
LOC_Os04g46740	Os.52445.1.S1_at	0.79	0.30		0.51		14	A	8	A	10	A	pectinesterase
LOC_Os04g51340	Os.8064.1.S1_at	1.00	0.41		2.27		189	P	107	P	447	P	pectinacetylesterase precursor
LOC_Os04g54850	Os.351.1.S1_at	0.64	0.66		0.59		8	A	11	A	9	A	pectinesterase
LOC_Os05g29790	Os.53938.1.S1_at	0.68	1.80		0.52		10	A	21	A	8	A	pectinesterase
LOC_Os05g44600	Os.9897.1.S1_at	0.72	0.31		0.19		138	P	52	P	27	P,A	pectinesterase
LOC_Os06g09340	OsAffx.27525.1.S1_at	1.00	0.37	***	2.59	***	160	P,A	66	A	430	P	pectinesterase
LOC_Os06g09340	OsAffx.27525.1.S1_x_at	0.97	0.45		2.07		174	P	87	A	371	P	pectinesterase
LOC_Os07g41650	Os.54802.1.S1_at	0.90	0.84		0.70		15	P,A	14	A	11	A	pectinesterase
LOC_Os07g46190	Os.50138.1.S1_at	0.95	0.19		0.45		17	A	5	A	11	A	pectinesterase
LOC_Os07g47830	Os.11456.1.S1_at	0.99	0.42		2.63		93	A	54	A	252	A	pectinesterase
LOC_Os07g49100	Os.34354.1.S1_at	0.92	2.36		0.83		12	A	31	A	11	A	pectinesterase
LOC_Os08g10604	OsAffx.29137.1.S1_at	0.60	0.44		0.42		10	A	9	A	7	A	pectinesterase
LOC_Os08g12410	Os.7593.1.S1_at	0.86	1.04		1.48		20	A	32	A	33	A	pectinesterase
LOC_Os08g34900	Os.20317.1.S1_at	0.81	3.63		9.65		11	A	49	P,A	116	P	pectinesterase
LOC_Os08g34910	Os.9647.1.S1_at	0.92	1.09		1.24		4	A	5	A	7	A	pectinesterase
LOC_Os09g26360	Os.53386.1.S1_at	0.90	2.57		0.29		3	A	10	A	1	A	pectinesterase
LOC_Os09g37360	OsAffx.18026.1.S1_at	0.45	0.25		0.12		18	A	5	A	3	A	pectinesterase
LOC_Os09g39760	Os.54835.1.S1_s_at	0.75	0.42		1.20		48	A	23	A	60	A	pectinesterase
LOC_Os09g39760	OsAffx.30215.1.S1_at	0.94	0.86		1.42		42	A	44	A	63	A	pectinesterase
LOC_Os10g10620	OsAffx.20662.1.A1_at	0.68	0.49		0.36		10	A	6	A	5	A	invertase/pectin methylesterase inhibitor family protei
LOC_Os10g10620	OsAffx.20662.1.A1_x_at	0.91	0.77		0.50		39	A	41	A	24	A	invertase/pectin methylesterase inhibitor family protei

LOC_Os10g10620	OsAffx.20662.1.S1_at	0.90	0.87			0.67		55	A	53	P,M,A	41	A	invertase/pectin methylesterase inhibitor family protei
LOC_Os10g26680	Os.11818.1.S1_at	0.99	0.76			0.66		3976	P	3285	P	2689	P	pectinesterase
LOC_Os10g40290	Os.52091.1.S1_at	0.88	0.70			1.41		625	P	524	P	925	P	pectinacetylesterase family protein
LOC_Os11g07090	OsAffx.30852.1.S1_at	0.86	0.54			0.32		108	A	63	A	35	A	pectinesterase
LOC_Os11g08750	Os.53818.1.S1_at	0.83	0.40			28.61		4	A	2	A	120	A	pectinesterase
LOC_Os11g36240	OsAffx.31322.1.S1_at	0.98	1.24			1.29		1	A	2	A	2	A	pectinesterase
LOC_Os11g43830	Os.54890.1.S1_at	0.46	0.76			0.27		9	A	9	A	3	A	pectinesterase
LOC_Os11g43850	OsAffx.7400.1.S1_at	0.99	0.64			0.96		5	A	4	A	5	A	pectinesterase
LOC_Os11g45720	Os.8099.1.S1_at	0.64	0.23			0.22		6	A	2	A	2	A	pectinesterase
LOC_Os11g45730	Os.6348.1.S1_x_at	0.99	2.73			1.52		2	A	10	A	4	A	pectinesterase
LOC_Os12g37660	Os.8076.1.S1_at	0.72	0.72			0.82		9	A	8	A	9	A	pectinesterase
LOC_Os04g43370	None													pectinesterase
LOC_Os07g02840	None													PS60
LOC_Os11g08760	None													pectinacetylesterase family protein
Pectate lyase (pectate→D-GalA)														
LOC_Os01g36620	Os.35614.1.S1_at	0.96	0.80			0.62		76	P	71	P	49	P,M	pectate lyase family protein
LOC_Os01g62000	OsAffx.11689.1.S1_s_at	0.92	0.50			0.67		6	A	3	A	4	A	pectate lyase 4 precursor
LOC_Os02g12300	Os.53956.1.S1_at	0.86	0.19			0.10		12	A	3	A	1	A	pectate lyase precursor
LOC_Os04g05050	Os.51088.1.S1_at	0.98	4.80	*		8.54	*	135	P	774	P	1192	P	pectate lyase precursor
LOC_Os04g05050	Os.8458.1.S1_s_at	0.91	2.84			4.20		1706	P	5526	P	7434	P	pectate lyase precursor
LOC_Os04g05050	OsAffx.3726.1.S1_at	0.96	4.32	*		8.12	*	102	P	522	P	860	P	pectate lyase precursor
LOC_Os05g22800	Os.53433.1.S1_at	0.97	0.56			1.44		17	A	14	A	26	A	pectate lyase precursor
LOC_Os06g05209	Os.5708.1.S1_at	0.89	1.00			1.80		8	A	12	A	14	A	pectate lyase precursor
LOC_Os06g05260	Os.53028.1.S1_at	0.90	0.34			0.40		33	A	17	A	15	A	pectate lyase precursor
LOC_Os06g05272	Os.5708.1.S1_at	0.89	1.00			1.80		8	A	12	A	14	A	pectate lyase precursor
LOC_Os06g38510	Os.18224.1.S1_at	0.82	0.34			0.42		3	A	1	A	1	A	pectate lyase precursor
LOC_Os06g38520	OsAffx.27990.1.S1_at	0.97	0.59			0.76		32	A	25	A	25	A	pectate lyase family protein
LOC_Os10g31910	OsAffx.18481.1.S1_x_at	0.93	1.21			1.94		6	A	11	A	15	A	pectate lyase precursor
Expansin														
Alpha-expansin														
LOC_Os01g14650	Os.28773.1.S1_at	0.86	96.48	**		2.02		11	P,A	1192	P	23	M,A	alpha-expansin
LOC_Os01g14660	OsAffx.22035.1.S1_x_at	0.71	0.44			0.19		184	P,A	90	A	36	A	alpha-expansin
LOC_Os01g60770	Os.4644.1.S1_at	0.81	2.07			0.65		1505	P	4438	P	1043	P	alpha-expansin (OsEXPA2)
LOC_Os02g16730	OsAffx.2643.1.S1_at	0.98	1.20			2.36		3	A	5	A	7	A	alpha-expansin (OsEXPA13)
LOC_Os02g16730	OsAffx.2643.1.S1_x_at	0.94	1.13			0.87		12	A	15	A	11	A	alpha-expansin (OsEXPA13)
LOC_Os02g16780	OsAffx.24284.4.S1_at	0.89	0.28			0.34		12	A	4	A	6	A	alpha-expansin (OsEXPA14)
LOC_Os02g16780	OsAffx.24284.4.S1_x_at	0.85	0.26			0.26		5	A	2	A	2	A	alpha-expansin (OsEXPA14)
LOC_Os02g16800	OsAffx.24284.3.S1_at	0.99	1.18			1.02		39	A	53	P,A	42	P,M,A	alpha-expansin (OsEXPA24)
LOC_Os02g16809	OsAffx.24284.5.S1_at	0.68	0.38			0.21		10	A	4	A	2	A	alpha-expansin (OsEXPA23)
LOC_Os02g16839	OsAffx.24284.5.S1_at	0.68	0.38			0.21		10	A	4	A	2	A	alpha-expansin (OsEXPA23)
LOC_Os02g16850	OsAffx.24284.2.S1_at	0.84	0.39			0.54		2	A	1	A	1	A	alpha-expansin
LOC_Os02g51040	Os.4613.1.S1_at	0.88	13.68			3.05		41	A	667	P	139	P,A	alpha-expansin (OsEXPA5)
LOC_Os03g06000	Os.20535.1.S1_at	0.71	0.50			0.46		63	P,A	40	A	32	A	alpha-expansin
LOC_Os03g06010	OsAffx.3144.1.S1_at	0.95	203.50	**		1.35		6	A	1370	P	8	A	alpha-expansin (OsEXPA25)
LOC_Os03g06010	OsAffx.3144.1.S1_x_at	1.00	157.40	***		1.11		6	A	1148	P	7	A	alpha-expansin (OsEXPA25)
LOC_Os03g06020	OsAffx.24987.1.S1_at	0.96	4.09			1.23		51	A	298	P	64	P,M,A	alpha-expansin (OsEXPA15)
LOC_Os03g06060	OsAffx.12748.2.S1_at	0.88	0.51			0.46		12	A	7	A	6	A	alpha-expansin (OsEXPA12)
LOC_Os03g21820	Os.2367.1.S1_at	0.99	0.64			0.98		664	P	509	P	688	P	alpha-expansin (OsEXPA6)
LOC_Os03g31480	Os.57306.1.S1_at	0.80	0.69			0.49		19	A	18	A	13	A	alpha-expansin
LOC_Os03g60720	Os.2368.1.S1_at	0.63	47.36			20.41		26	M,A	1485	P	558	P	alpha-expansin (OsEXPA7)
LOC_Os04g15840	Os.2696.1.S1_at	0.77	0.69			0.42		28	A	28	A	17	A	alpha-expansin (OsEXPA1)
LOC_Os04g49410	Os.2369.1.S1_a_at	0.99	0.89			1.33		2079	P	2049	P	2850	P	alpha-expansin (OsEXPA10)
LOC_Os05g19570	Os.410.1.S1_at	0.93	0.29			0.07	**	1030	P	336	P	74	P	alpha-expansin (OsEXPA3)
LOC_Os05g39990	Os.50825.1.S1_s_at	0.93	2.62			1.08		2216	P	7904	P	2517	P	alpha-expansin (OsEXPA4)
LOC_Os06g01920	OsAffx.22609.1.S1_x_at	0.99	0.97			0.96		66	P,A	74	M,A	65	P,M	alpha-expansin
LOC_Os06g41700	Os.54103.1.S1_at	0.93	0.18	**		3.29		285	P	58	A	976	P	alpha-expansin
LOC_Os06g50400	Os.22908.1.S1_at	0.94	4.03			2.58		3	A	19	A	12	A	alpha-expansin (OsEXPA29)
LOC_Os08g44790	Os.53024.1.S1_at	0.95	0.86			0.90		1	A	1	A	1	A	alpha-expansin
LOC_Os10g30340	OsAffx.8085.1.S1_at	0.93	0.99			0.39		42	A	48	A	17	A	alpha-expansin
LOC_Os10g30340	OsAffx.8085.1.S1_x_at	0.92	1.44			0.44		40	A	65	A	22	A	alpha-expansin
LOC_Os10g39110	OsAffx.18574.1.S1_x_at	0.87	1.37			1.23		53	A	81	A	67	A	alpha-expansin
LOC_Os12g36040	Os.20191.1.S1_at	0.90	2.23			1.57		9	A	26	A	16	A	alpha-expansin (OsEXPA26)
LOC_Os01g16770	None													alpha-expansin
LOC_Os03g06040	None													alpha-expansin (OsEXPA18)
LOC_Os03g06050	None													alpha-expansin (OsEXPA19)
LOC_Os03g25990	None													alpha-expansin (OsEXPA21)
LOC_Os05g19600	None													alpha-expansin
LOC_Os10g30330	None													alpha-expansin
Beta-expansin														
LOC_Os02g42650	OsAffx.12459.1.S1_at	0.72	1.12			1.52		28	A	38	A	44	P,M,A	beta-expansin
LOC_Os02g44106	OsAffx.24716.1.S1_at	0.85	0.19			0.14		18	A	4	A	3	A	beta-expansin (OsEXPB16)
LOC_Os02g44108	Os.7602.1.S1_at	0.87	1.21			0.71		2087	P	4657	P	1550	P	beta-expansin (OsEXPB11)
LOC_Os03g01610	Os.2402.1.S1_at	0.96	1.03			0.46		28	A	32	A	16	A	major pollen allergen Ory s 1 precursor (EXPB1)
LOC_Os03g01640	Os.2405.1.S1_at	0.87	1.69			1.42		2	A	8	A	4	A	major pollen allergen Ory s 1 precursor (EXPB10)
LOC_Os03g01650	Os.2402.1.S1_at	0.96	1.03			0.46		28	A	32	A	16	A	major pollen allergen Ory s 1 precursor
LOC_Os03g01260	Os.2615.1.S1_at	0.81	3.05			3.82		14	A	48	P,M,A	59	P,M	beta-expansin (OsEXPB8)
LOC_Os03g01270	Os.9312.1.S1_at	0.44	0.43			0.05		2218	P	1025	P	114	P	beta-expansin (OsEXPB7)
LOC_Os03g44290	Os.6436.1.S1_at	0.93	0.87			3.60		91	P	91	P,A	340	P	beta-expansin (OsEXPB12)
LOC_Os04g44780	Os.54957.1.S1_at	0.95	6.32			6.06		35	A	280	P,A	218	P	beta-expansin (EXPB17)
LOC_Os04g44780	OsAffx.4092.1.S1_s_at	0.91	0.85			3.04		9	A	14	A	33	A	beta-expansin (EXPB17)
LOC_Os04g46650	Os.2403.1.S1_at	0.99	45.02	**		2.00		4	A	175	P	8	A	beta-expansin (OsEXPB5)
LOC_Os05g15690	Os.54019.1.S1_at	0.99	0.59			1.14		2	A	1	A	3	A	beta-expansin
LOC_Os10g40090	Os.12697.1.S1_at	0.99	0.89			1.27		32	A	32	A	42	A	beta-expansin (OsEXPB9)
LOC_Os10g40700	Os.2404.1.S1_at	0.43	13.01			0.17		751	P	10712	P	126	P	beta-expansin (OsEXPB6)
LOC_Os10g40710	Os.2373.1.S1_at	0.14	1.65		0.01*			691	P,A	1244	P	4	A	beta-expansin (OsEXPB2)
LOC_Os10g40720	Os.6786.1.S1_a_at	0.99	1.17			0.78		10144	P	13589	P	8238	P	beta-expansin (OsEXPB3)
LOC_Os10g40730	Os.12234.1.S1_s_at	0.97	13.41	***		6.65	***	817	P	12307	P	5622	P	beta-expansin (OsEXPB4)
LOC_Os03g01630	None													major pollen allergen Ory s 1 precursor
LOC_Os04g46630	None													beta-expansin (OsEXPB15)
Expansin-like														
LOC_Os03g04020	Os.21349.1.S1_at	0.98	0.54			0.31		7760	P	4686	P	2460	P	expansin-like (OsEXLA1)
LOC_Os06g50960	Os.47341.1.A1_at	0.94	0.54			1.52		18	A	13	A	28	M,A	expansin-like (OsEXLA4)
LOC_Os07g29290	Os.5937.1.S1_at	0.93	1.26			1.38		437	P	637	P	623	P	expansin-like (OsEXLA3)
LOC_Os10g39640	Os.2938.1.S1_at	0.93	0.29			0.19		430	P	138	P	88	P	expansin-like (OsEXLA2)
LOC_Os10g39640	Os.2938.1.S1_x_at	0.89	0.28			0.20		445	P	139	P	91	P	expansin-like (OsEXLA2)
LOC_Os07g31390	OsAffx.22303.1.S1_at	0.97	5.31			1.75		12	A	70	A	22	A	expansin-related protein (OsEXLB1)
Extensin														
LOC_Os01g02160	OsAffx.350.1.S1_s_at	0.99	1.18			0.69		1064	P	1391	P	750	P	hydroxyproline-rich glycoprotein family protein
LOC_Os01g25460	Os.35957.1.S1_at	0.96	0.73			0.98		31	A	29	A	34	A	extensin-like protein
LOC_Os01g52660	Os.5920.1.S1_at	0.72	5.41			1.47		24	A	148	P,A	40	A	POEI51
LOC_Os01g67390	Os.28994.1.S1_at	0.95	0.20			0.11		44	A	12	A	10	A	POEI32
LOC_Os04g32850	Os.27244.1.A1_s_at	0.88	0.43			5.46	*	791	P	387	P	4441	P	basic proline-rich protein
LOC_Os04g32850	Os.54602.1.S1_s_at	0.91	0.49			8.51	**	375	P	208	P	3271	P	basic proline-rich protein
LOC_Os04g32850	OsAffx.14103.1.S1_x_at	0.96	0.53			4.64	**	1930	P	1127	P	9210	P	basic proline-rich protein
LOC_Os04g34170	Os.25734.2.S1_a_at	0.68	470.10	**		9.90		31	A	16765	P	334	P	extensin precursor
LOC_Os05g45460	Os.9327.1.S1_at	0.87	0.52			0.55		13	A	10	A	10	A	POEI52
LOC_Os11g41120	OsAffx.19293.1.S1_at	0.99	0.12			0.94		102	A	14	A	102	A	proline-rich protein
LOC_Os12g35710	Os.18286.1.S1_s_at	0.91	1.05			0.83		16	A	21	A	15	A	extensin-like protein
LOC_Os11g43640	None													extensin-like protein
PF02458/BAHD														
LOC_Os01g08380	OsAffx.9719.1.S1_x_at	0.97	0.58			0.53		149	P,A	95	P,A	86	P,M	10-deacetylbaccatin III 10-O-acetyltransferase
LOC_Os01g09010	Os.4905.1.S1_a_at	1.00	0.65			0.65		5697	P	4166	P	3828	P	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os01g09010	Os.4905.5.A1_at	0.86	1.22			0.99		44	A	63	A	46	A	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os01g18744	Os.3655.1.S1_at	0.84	2.10			4.31		668	P	1628	P	2964	P	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os01g42870	Os.1044.1.S1_at	0.99	1.02			0.90		4853	P	5446	P	4490	P	10-deacetylbaccatin III 10-O-acetyltransferase
LOC_Os01g42880	Os.21615.1.S1_at	1.00	0.87			0.96		6984	P	6651	P	6881	P	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os04g09590	OsAffx.25987.2.A1_at	0.93	1.07			0.47		23	P,A	29	P,A	12	A	10-deacetylbaccatin III 10-O-acetyltransferase
LOC_Os04g09590	OsAffx.25987.2.S1_at	0.96	0.98			0.56		9	A	11	A	6	A	10-deacetylbaccatin III 10-O-acetyltransferase
LOC_Os04g11810	OsAffx.25987.1.A1_at	0.94	1.30			0.74		4	A	6	A	4	A	acyltransferase
LOC_Os04g11810	OsAffx.25987.1.S1_at	0.98	0.38			0.52		39	A	17	A	21	A	acyltransferase
LOC_Os05g04584	Os.54875.1.S1_at	0.64	0.97			1.57		31	M,A	33	A	51	P,A	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os05g04584	Os.9847.1.S1_at	0.99	0.81			1.14		6307	P	5698	P	7336	P	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os05g08640	Os.17173.1.S1_at	0.99	1.96			0.63		1563	P	3404	P	1014	P	10-deacetylbaccatin III 10-O-acetyltransferase
LOC_Os05g19910	Os.48074.1.A1_at	0.90	1.57			1.25		127	P,A	220	P	164	P	taxadien-5-alpha-ol O-acetyltransferase
LOC_Os06g39390	OsAffx.28006.1.S1_at	0.93	0.76			19.33	**	10	A	8	A	213	P,A	3-N-debenzoyl-2-deoxytaxol N-benzoyltransferase
LOC_Os06g39470	Os.49692.1.S1_at	0.96	1.51			2.04		859	P	1431	P	1817	P	10-deacetylbaccatin III 10-O-acetyltransferase