The localisation of *Pseudomonas*-induced acquired resistance in barley

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Abstract

Systemic Acquired Resistance (SAR) provides systemic protection against a broad-spectrum of previously virulent pathogens. While SAR is well characterised in a range of dicot species including *Arabidopsis*, there is limited evidence for the biological induction of SAR in any cereal species. In order to test the localisation of biologically-induced acquired resistance in barley, a robust bioassay was developed, using the SAR-inducing pathogen *Pseudomonas syringae*. Infiltration of barley cultivar Golden Promise with non-host isolate *Pseudomonas syringae pv. tomato avrRpm1* (*PstavrRpm1*) resulted in an active, local defence response that appeared to be triggered by the type III secretion system. Furthermore, infiltration of barley with *PstavrRpm1* resulted in the induction of broad-spectrum acquired resistance, at a distance from the local lesion. This adjacent acquired resistance was effective against compatible isolates of *Pseudomonas syringae* pv. *syringae* and *Magnaporthe oryzae*. Global transcriptional profiling of the adjacent acquired resistance response revealed the induction of transcripts with similarity to pathogenesis related (PR) genes previously associated with *Arabidopsis* SAR, as well as transcripts previously associated with chemically-induced acquired resistance and basal defence in barley. In order to gain further insight into biologically-induced acquired resistance in cereals, the conservation in cereals of SAR-specific *Arabidopsis* gene *DIR1* was also investigated. The results presented suggest that rice homologues of *DIR1* may complement the *Arabidopsis dir1-1* mutant. However, heterologous expression of rice *DIR1* homologues in barley appeared to affect local defence gene expression and symptom development, rather than the translocation of acquired resistance. This suggests that mechanisms of induction of acquired resistance differ between *Arabidopsis* and cereal species. Taken together, the research presented in this thesis provides important insights into acquired resistance in cereals, and a strong basis for further investigation of the signalling and mechanisms involved.

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Contents

Abbreviations

AR	acquired resistance
avr	avirulence
BCI	barley chemically induced gene
Bgh	*Blumeria graminis* f. sp. *hordei*
Bgt	*Blumeria graminis* f. sp. *tritici*
BLAST	Basic Local Alignment Search Tool
bp	base pair(s)
BTH	benzo(1,2,3)thiadiazole-7-carbothiocic acid S-methyl ester
cDNA	complementary DNA
CDS	coding sequence
CFU	colony forming units
C_t	threshold cycle
DIR1	Defective in Induced Resistance 1
DNA	deoxyribonucleic acid
dpi	days post inoculation
EST	expressed sequence tag
ET	ethylene
ETI	effector triggered immunity
f. sp.	formae specialis
HR	hypersensitive response
hpi	hours post inoculation
INA	2, 6-dichloroisonicotinic acid
ISR	induced systemic resistance
JA	jasmonic acid
L	litre
LAR	localised acquired resistance
Log	logarithm
LRR	leucine rich repeat
LTP	lipid transfer protein
LUX	luciferase
MeSA	methyl salicylate
Mol	molar
mRNA	messenger RNA
nahG	bacterial salicylate hydrolase
NCBI	National Centre for Biotechnology Information
OD	optical density
PAL	phenylalanine ammonia-lyase
PAMP	pathogen associated molecular pattern
PCR	polymerase chain reaction
PR	pathogenesis related

PRR	pattern recognition receptor
Pst	*Pseudomonas syringae* pv. *tomato*
Pss	*Pseudomonas syringae* pv. *syringae*
PTI	PAMP triggered immunity
pv	pathovar
qRT-PCR	quantitative reverse transcription PCR
R-gene	resistance gene
RNA	ribonucleic acid
SA	salicylic acid
SAR	systemic acquired resistance
SD	standard deviation
SE	standard error
TMV	*Tobacco Mosaic Virus*
WCI	wheat chemically induced gene

Chapter 1: General introduction

1.1 Induced resistance

Plants employ both constitutive and inducible defences to protect themselves against pathogens. Constitutive defences include the presence of physical barriers, or toxic compounds within the leaf, and are effective against most non-adapted pathogens (pathogens which have not closely coevolved with the plant, and which fail to colonise plant tissue) (Heath, 2000). Resistance to infection by both non-adapted and adapted pathogens is also mediated by a complex network of inducible mechanisms (Jones & Dangl, 2006). Plant Pattern Recognition Receptors (PRRs) detect conserved pathogen-associated-molecular-patterns (PAMPs), such as a highly conserved domain of bacterial flagellin (Zipfel *et al.*, 2004), triggering defence responses sufficient to limit the growth of non-adapted pathogens (PAMP-triggered Immunity (PTI)). Pathogens that are closely adapted to their host plants also trigger PTI, but suppress the response via the secretion of effector molecules into the plant cell. In resistant hosts, specific recognition of pathogen effectors by host resistance (R) proteins leads to the induction of the hypersensitive response (HR), in which rapid, programmed cell death of invaded cells helps to restrict pathogen growth (effector-triggered immunity (ETI)) (Jones & Dangl, 2006). As such, non-host resistance, PTI and ETI can all involve inducible resistance mechanisms. However, 'induced resistance' is a separate phenomenon, induced alongside defences triggered by primary infection, but expressed only upon secondary challenge (van Loon, 1997). The response was defined by van Loon (1997) as "the additional capacity for defensive activities resulting from the primary infection, and dependent on the concomitant triggering of resistance responses". Put simply, induced resistance occurs when inducible-defence mechanisms restrict a subsequent pathogen challenge. Here, the term 'acquired resistance', commonly used synonymously with induced resistance (van Loon, 1997), will be used in order to emphasise the distinction between inducible responses to primary inoculation, and induced resistance to secondary challenge.

1.2 Systemic Acquired Resistance (SAR)

The first systematic characterisation of acquired resistance (AR) was reported by Ross (1961a, b). Infiltration of *Tobacco Mosaic Virus* (*TMV*) into leaves of *Nicotiana tabacum* (Samsun NN) resulted in an HR lesion. A subsequent, secondary challenge of these leaves with *TMV* revealed a 1-2 mm zone of near-immunity surrounding the original lesion (termed 'localised acquired resistance' (LAR)) (Ross, 1961a). Furthermore, the number and size of challenger lesions was reduced throughout the leaf, and in secondary leaves, compared to plants which did not receive the primary, ‘inducing’ inoculation (Ross, 1961b). This systemic response was termed ‘systemic acquired resistance’ (SAR). Both the localised and systemic AR were broad-spectrum (ie effective against pathogens other than that involved in the primary inoculation) (Ross 1961a, b). SAR has subsequently been reported in a wide range of species and pathosystems (Sticher *et al.*, 1997), and has been well characterised in tobacco (Ward *et al.*, 1991), cucumber (Kuc, 1982), and *Arabidopsis thaliana* (*Arabidopsis*) (Cameron *et al.*, 1994). Although there are species-specific differences (Kessmann *et al.*, 1994), SAR is characterised by its spectrum of effectiveness, distinctive profile of pathogenesis related (PR) gene induction, and dependence on the plant phytohormone salicylic acid (SA) (Ryals *et al.*, 1996). The response is one of a number of forms of systemic immunity, each associated with a particular inducing interaction, and hormonal signalling pathway (Ton *et al.*, 2002). Induced systemic resistance (ISR) is induced by an interaction between plant roots and growth promoting rhizobacteria, is mediated by jasmonic acid (JA) and ethylene (ET) and is not associated with transcriptional activation pre-challenge (Pieterse *et al.*, 1996, Pieterse *et al.*, 1998), whilst herbivore-induced wounding also induces JA/ET-mediated systemic resistance (Creelman & Mullet, 1997, Green & Ryan, 1972). The distinguishing characteristics, mode of action, and genetic and hormonal control of SAR are described below. The relationship between localised and systemic acquired resistance is discussed further in Section 4.2.

1.3 SAR induction and genetic control

Plants in which SAR has been induced are protected against subsequent challenge by a broad-spectrum of previously virulent pathogens (Ryals *et al.*, 1996). The AR is quantitative, in contrast to the specific and qualitative defence mediated by ETI (Sticher et al., 1997), and in *Arabidopsis* SAR shares transcriptional similarities with local PTI (Truman *et al.*, 2007). Long associated with a local necrotising interaction, recent work has demonstrated that neither HR nor necrosis is required for SAR to be induced (Liu *et al.*, 2010, Mishina & Zeier, 2007a). R-gene mediated resistance in the absence of HR (Liu *et al.*, 2010), PTI to virulent pathogens, the application of PAMPs, and non-host interactions (Mishina & Zeier, 2007a) all induce SAR in *Arabidopsis*. In tobacco, cucumber and *Arabidopsis*, the level of protection provided by SAR depends on the nature of the inducing interaction (Mishina & Zeier, 2007a, Ross, 1961b, Smith *et al.*, 1991). The efficiency of SAR induction in *Arabidopsis* depends on an active local defence response, with a low dose of virulent *Pseudomonas syringae* inducing SAR more efficiently than an avirulent isolate (Mishina & Zeier, 2007a). This appears to be consistent with reports in tobacco that SAR develops most rapidly during the period of most active replication of the ‘inducer’ pathogen (Ross, 1961b).

The time-scale for SAR induction also varies between inducing interactions and between species (Cameron *et al.*, 1994, Ross, 1961b, Smith *et al.*, 1991); systemic responses in *Arabidopsis* are seen by 4 hours post local inoculation (Truman *et al.*, 2007), whilst 7-10 days are needed in tobacco for maximal protection to be established (Ross, 1961b).

SAR is thought to be induced by one or several mobile signal(s), transmitted through the plant vasculature, and possibly by volatiles, from the leaf receiving the primary inoculation (Dean & Kuc, 1986, Guedes *et al.*, 1980, Heil & Ton, 2008, Vlot *et al.*, 2008a). Although SAR signalling and the genetic components involved in the response have been studied intensively for around 20 years, major advances in our understanding are still being made. SAR induction is dependent on a functional salicylic acid (SA) signalling pathway, but SA itself is not a mobile SAR signal (Vernooij *et al.*, 1994). Tobacco plants expressing the bacterial salicylate hydroxylase (*nahG*) are unable to accumulate SA and fail to develop SAR, because the accumulation of SA in systemic leaves is essential for SAR to develop (Vernooij *et al.*, 1994). Furthermore, *Arabidopsis* mutants deficient in local, SA-mediated basal defence (*enhanced disease susceptibility 1* (*eds1*)/ *phytoalexin deficient 4* (*pad4*) (Feys *et al.*, 2001, Parker *et al.*, 1996) and SA biosynthesis (*salicylic acid induction deficient 2* (*sid2*) (Wildermuth *et al.*, 2001)) (Mishina & Zeier, 2007a), or mediation of antagonistic SA/ jasmonic acid (JA) signalling (MAP kinase 4 (Brodersen *et al.*, 2006)) all fail to induce SAR. Local SA-mediated defence responses lead to the induction of SAR (Ton *et al.*, 2002), and SAR signal generation appears to be a general feature of such interactions (Vlot *et al.*, 2008a). Recent work in *Nicotiana tabacum* suggests that methyl salicylate (MeSA) is a mobile SAR signal (Park *et al.*, 2007). SA methyl transferase in primary inoculated tobacco leaves converts SA to MeSA, which is translocated systemically. Once in secondary leaves, MeSA is believed to be converted back to SA by Salicylic acid-Binding Protein 2 (SABP2). A complex feedback loop involving SA mediated inhibition of SABP2 in primary inoculated leaves ensures sufficient MeSA is produced for SAR to be established (Park *et al.*, 2007). However, despite proposals that MeSA is a conserved SAR signal (Vlot *et al.*, 2008b), results from *Arabidopsis* seem to preclude this (Attaran *et al.*, 2009). Although MeSA accumulates upon inoculation with *Pseudomonas syringae pv. maculicola* (*Psm*), the profile of MeSA accumulation is not affected in a range of SAR-deficient *Arabidopsis* mutants (Attaran *et al.*, 2009). Furthermore, SAR is not affected in an *Arabidopsis* mutant which fails to accumulate MeSA (*bsmt1,* Attaran *et al.*, 2009)). Whether the mobile SAR signal is SA-derived or not, the critical role of SA in SAR is also demonstrated by characterisation in *Arabidopsis* of the key SAR regulator Non-Expressor of PR genes 1 (NPR1) (Cao *et al.*, 1994, Delaney *et al.*, 1995). *npr1* mutants fail to induce SAR and are also deficient in local SA-mediated defence (Cao *et al.*, 1994, Delaney *et al.*, 1995). Molecular characterisation of NPR1 suggests that a rapid oxidative burst triggered by SA accumulation is followed by a rebound to reducing conditions (Mou *et al.*, 2003). Under these conditions, NPR1 is converted from an oligomeric to a monomeric form, which allows transport into the nucleus (Mou *et al.*, 2003). This nuclear localisation is essential for NPR1 function (Kinkema *et al.*, 2000). Here, interaction with the TGA family of bZIP (basic leucine zipper) transcription factors regulates the expression of PR genes such as *PR1*, a key marker of the SAR response (Zhou *et al.*, 2000). The WRKY family of transcription factors have also been implicated in NPR1-dependent SAR gene induction (Maleck *et al.*, 2000, Wang *et al.*, 2006). The early systemic induction of genes such as *Glutathione-S-Transferase* (*GST*) (Alvarez *et al.*, 1998), involved in the response to oxidative stress, during the establishment of SAR may therefore contribute to the conditions needed for NPR1-mediated SAR gene induction (Dong, 2004). *GST* appears to be activated via an SA-dependent but NPR1-independent mechanism (Uquillas *et al.*, 2004). Consistent with this key role of SA, SAR can also be induced by the chemical analogues of SA, 2,6-dichloroisonicotinic acid (INA) (Ward *et al.*, 1991, Uknes *et al.*, 1992), and benzo(1,2,3)thiadiazole-7-carbothiocic acid S-methyl ester (BTH) (Friedrich *et al.*, 1996, Lawton *et al.*, 1996). Like application of SA itself, these chemicals induce the nuclear localisation of NPR1 (Kinkema *et al.*, 2000) and the same set of PR genes as the biological induction of SAR (Ryals *et al.*, 1996). The chemicals are however translocated throughout the plant (Oostendorp *et al.*, 2001), and as such chemical induction does not completely reflect the situation during biological induction of the response (where *de novo* SA synthesis in distal leaves leads to NPR1 activation).

Along with MeSA (Park et al., 2007), recent studies implicate a number of long-distance signals in the establishment of SAR, including the plant hormone jasmonic acid (JA). SAR has been reported to be compromised in *Arabidopsis* lines deficient in JA biosynthesis (*opr3* (Stintzi & Browse, 2000)) and responsiveness (*jin1* (Lorenzo *et al.*, 2004)) (Truman *et al.*, 2007), and JA accumulates in systemic leaves during SAR establishment (until 11 hours post local inoculation) (Truman *et al.*, 2007). It has been hypothesised that JA signalling acts in an early initiation phase of SAR signals, acting in tandem with later, SA-mediated SAR establishment (Truman *et al.*, 2007). In tomato, JA induced the expression of genes encoding SA methyl transferases (Ament *et al.*, 2004), supporting the idea that these two signals work in tandem (Vlot *et al.*, 2008a). However, separate studies indicate that both these and other JA-related mutants are SAR competent (Attaran et al., 2009, Mishina & Zeier, 2007a), which calls into question the role of JA. It has been suggested that these discrepancies could be related to the dosage of the inducing pathogen, via an effect on HR-induction or the ability of the pathogen to overcome basal resistance (Shah, 2009).

Several lines of evidence support the role of a lipid factor in SAR signalling, although this may not be JA (Chaturvedi *et al.*, 2008). *Arabidopsis Defective in Induced Resistance 1* (*DIR1*) encodes a lipid transfer protein (LTP) which is essential for the production or transmission of a mobile SAR signal from an inoculated leaf (Maldonado *et al.*, 2002). Several *Arabidopsis* mutants specifically deficient in SAR due to defects in plastid-derived lipid metabolism (*sfd1, sfd2* and *fad7* (Chaturvedi *et al.*, 2008) have also been identified. Furthermore, a second LTP-like gene was also recently implicated in the production, transmission or translocation of a mobile SAR signal ((Jung *et al.*, 2009). As with *dir1-1* mutants, petiole exudate from ‘induced’ *azelaic acid induced 1* (*azi1*) seedlings fails to induce SAR when applied to naïve plants, in contrast to petiole exudate from induced wild-type seedlings (Jung *et al.*, 2009). In both cases, the defect is SAR specific, and seedlings retain the capacity to perceive and develop SAR when wild-type exudate from induced wild-type seedlings is applied (Jung *et al.*, 2009, Maldonado *et al.*, 2002). *AZI1* was identified by its transcriptional response to the metabolite azelaic acid, which also appears to be a translocated SAR signal (Jung *et al.*, 2009). Peptide signalling (Xia *et al.*, 2004), nitric oxide (Rusterucci *et al.*, 2007), and the auxin signalling pathway (Wang *et al.*, 2007) have also all recently been linked to SAR signalling, but their precise roles currently remain unclear. Reports that ectopic expression of *Mitogen Activated Protein (MAP) Kinase Kinase 7* in *Arabidopsis* leaves is sufficient to induce SAR in distal leaves also suggests a key role in production of a systemic signal (Zhang *et al.*, 2007), but as discussed above, the nature of the signal is still being debated.

1.4 Resistance to challenge

Early systemic events in the perception of the mobile SAR signal(s) and establishment of the SAR state have not been fully elucidated. As noted above, in *Arabidopsis*, rapid systemic induction of *GST* preceded systemic, localised oxidative bursts and the development of micro-HRs, necessary for the establishment of SAR (Alvarez *et al.*, 1998). Transcriptional changes occur in systemic leaves as early as 4 hours post inoculation (hpi), and include the induction of a subset of local responses with similarity to local basal defence (Truman *et al.*, 2007).

The establishment phase of the SAR response (24-48 hours post local inoculation in *Arabidopsis*) has been more extensively characterised, and is associated with the induction of a set of PR genes, encoding defence related proteins (PR proteins) (Maleck *et al.*, 2000). The subset of PR genes induced systemically during SAR establishment have been termed ‘SAR genes’(Ward *et al.*, 1991). Many of these genes encode extracellular proteins, and are known to have antimicrobial properties thought to act in an additive, or even synergistic manner to produce a toxic effect on challenger pathogens as they attempt to colonise the apoplast (van Loon *et al.*, 2006). For example, β-1-3-glucanase (PR2) and chitinase (PR3) are likely to act directly against fungi, (Kim & Hwang, 1997, Schlumbaum *et al.*, 1986) and also release oligomers from fungal cell walls that elicit further plant defence responses (Shetty *et al.*, 2009, Takeuchi *et al.*, 1990). Defensins (PR12), thionins (PR13) and some lipid transfer proteins (PR14) have also shown antibacterial and antifungal activity (Broekaert *et al.*, 1997, van Loon *et al.*, 2006).

Alongside these responses, the strengthening of plant structural defences is also thought to contribute to SAR (Sticher *et al.*, 1997). Biologically-induced SAR against fungal challengers has been associated with enhanced lignification, both prior to challenge, and at sites of attemptedpenetration or hyphal growth (Dean & Kuc, 1987, Hammerschmidt & Kuc, 1982, Mauch-Mani & Slusarenko, 1996, Stein *et al.*, 1993). The induction of peroxidase, encoded by the *PR9* gene family, is correlated with SAR and implicated in both the cross-linking of several compounds to strengthen cell walls, and in lignin biosynthesis (Passardi *et al.*, 2004, Smith *et al.*, 1991) (although direct evidence for this role in SAR is lacking (Hammerschmidt, 1999)). The systemic induction of hydroxyproline-rich glycoproteins (extensins) is also consistent with cell wall strengthening (Showalter *et al.*, 1985), while lignin precursors, such as coniferyl alcohol, may also have direct toxic effects on pathogens (Hammerschmidt & Kuc, 1982, Sticher *et al.*, 1997). Furthermore, the frequency of papilla formation upon fungal challenge is enhanced in potato, cucumber and barley showing induced resistance (local resistance in the case of barley) (Jarosch *et al.*, 2003, Kováts *et al.*, 1991, Strömberg & Brishammar, 1993, Stumm & Gessler, 1986). Although, as noted, direct evidence for a role of these components in SAR is often limited (Hammerschmidt, 1999), several studies have shown a causal link between ectopic/ over-expression of PR proteins and enhanced disease resistance (Alexander *et al.*, 1993, Brogue *et al.*, 1991, Epple *et al.*, 1997, Oldach *et al.*, 2001, Zhu *et al.*, 1994). The resistance conferred is not complete, which further supports that each of the components mentioned above contributes quantitatively to SAR.

In addition to events pre-challenge, plants induced for SAR are also primed to respond more rapidly to pathogen challenge. The lignification seen in SAR-induced cucumber plants challenged with *Colletotrichum lagenarium* occurs more rapidly than in controls (Dean & Kuc, 1987). This is consistent with the more rapid induction of phenylalanine ammonia lyase (*PAL*) seen post-challenge in SAR-induced *Arabidopsis* (Conrath *et al.*, 2001). Transcript levels of *PR1*, *PR2* and *PR5* increase more rapidly post-challenge in *Arabidopsis* seedlings primed for SAR (Cameron *et al.*, 1999); as does *PR1* in tobacco (Mur *et al.*, 1996). Furthermore, parsley (*Petroselinum crispum*) cells primed for SAR show enhanced oxidative burst (Kauss & Jeblick, 1995), phytoalexin production (Katz *et al.*, 1998), and incorporation of phenolics and lignin into cell walls (Kauss *et al.*, 1993) upon treatment with a *Phytophthora sojae* elicitor, suggesting that these responses could also be involved in SAR post-challenge.

While SAR is a broad-spectrum form of resistance, the resistance is not effective against all challengers. SA-mediated induced defences are known to be effective against those pathogens that also induce SA-mediated basal defence (Ton *et al.*, 2002), including biotrophic pathogens and viruses. In *Arabidopsis*, basal resistance to the necrotroph *Alternaria brassicicola* is mediated by JA and ET signalling pathways, and SAR was not effective against this pathogen (Ton *et al.*, 2002). Conversely, ISR, which is JA/ ET-dependent (Pieterse *et al.*, 1996, Pieterse *et al.*, 1998), is effective against nectrophs such as *Alternaria*, but ineffective against biotrophic oomycete *Peronospora parasitica* and *Turnip Crinkle Virus* (Ton *et al.*, 2002). Both ISR and SAR were effective against *Xanthomonas campestris* pv. *armoraciae*, which induces both SA- and JA-mediated basal defence responses (Ton *et al.* 2002) (as does *Pseudomonas syringae* (Glazebrook, 2005)).

1.5 Systemic acquired resistance in monocots

SAR has been reported in a wide range of plant species (Sticher *et al.*, 1997), however these species are almost exclusively dicotyledonous (dicots). In monocotyledonous plants (monocots), biologically induced SAR has been reported in rice (Smith & Metraux, 1991) and barley (Hwang & Heitefuss, 1982). In rice, SAR effective against *Pyricula oryzae* (anamorphic stage of *Magnaporthe oryzae*) was reportedly induced in second leaves of rice seedlings, 2, 4 and 6 days post inoculation of first leaves with *Pseudomonas syringae* pv. *syringae* (Smith & Metraux, 1991). However, in subsequent tests this could not be repeated (Reimmann *et al.*, 1995). In barley, SAR has been reported after induction with powdery mildew (*Blumeria graminis*) (Hwang & Heitefuss, 1982). In that test, inoculation of first and second leaves of seedlings with virulent or avirulent *Blumeria graminis f. sp. hordei* (*Bgh*) led to reduced colony formation and hyphal development of a virulentchallenger, applied to the third leaf 6 days post induction (Hwang & Heitefuss, 1982). Again, subsequent research groups could not repeat this systemic protection (Martinelli, 1990). As noted by Martinelli (1990), treatment controls for the use of Fluorinert Electronic Liquid (FC43) in spore suspensions are not reported by Hwang & Heitefuss (1982). A range of other factors could also have affected results, including the use of different varieties, isolates, inoculum densities and environmental conditions (Martinelli, 1990). These conflicting reports mean it is currently unclear whether a biologically inducible SAR response is present in monocot species (Kogel & Langen, 2005).

Despite the conflicting evidence for SAR, local AR has been reported and characterised in several cereal species. This includes: AR to yellow rust (*Puccina striiformis*) (Johnson & Allen, 1975) and stem rust (*Puccinia graminis*) in wheat (Cheung & Barber, 1975) induced by avirulent isolates of the same pathogen species; AR to *Bgh* (Ouchi *et al.*, 1974) and *Magnaporthe oryzae* (Jarosch *et al.*, 2003) in barley induced by an avirulent *Bgh*; AR to *Puccinia coronata avenae* and *Puccinia graminis avenae* in oat previously inoculated with *Puccinia graminis tritici* or *Puccinia recondita tritici* (Kochman & Brown, 1975); and AR to compatible *Xanthomonas oryzae* by pre-inoculation with a strain that did not cause disease, in rice (Horino, 1976). In several of these pathosystems, the extent of localisation of the response has been studied. AR induced in oat and wheat by rust fungi appears to be strictly localised (Cheung & Barber, 1975, Johnson, 1978, Kochman & Brown, 1975). Application of an avirulent isolate of *Puccinia striiformis* to the upper (adaxial) leaf surface of wheat reportedly induced resistance to a virulent isolate subsequently applied to the lower (abaxial) leaf surface (Johnson & Allen, 1975), however this effect could not be seen in barley with *Bgh* (Martinelli, 1990). Localisation has been best characterised with the barley-powdery mildew pathosysem. In 1974, Ouchi *et al*. reported that barley epidermal cells in which penetration by an avirulent *Bgh* or non-host *Blumeria graminis* f. sp. *tritici* (*Bgt*) isolate had failed, became more resistant to a subsequently applied, previously virulent isolate of *Bgh* (Ouchi *et al.*, 1974). The resistance was not seen in regions of the leaf 5 mm proximal or distal to the primary inoculation (Ouchi *et al.*, 1976). In addition to this induced resistance, Ouchi *et al*. (1974) reported 'induced susceptibility', whereby a cell successfully penetrated by a virulent *Bgh* isolate was significantly more susceptible to subsequent infection by a previously avirulent isolate. Induced susceptibility was also localised, with the effect reducing in strength up to 4 transversely adjacent cells away (Ouchi et al., 1976). Subsequent detailed characterisation of this response by Kunoh *et al.* led to the use of the terms 'induced inaccessibility' and 'induced accessibility' to describe this effect at the cellular level (Kunoh *et al.*, 1988). In tests using a single epidermal cell layer of a barley coleoptile inoculated with individual germlings of *Bgh* (virulent) and *Erysiphe pisi* (*E. pisi*) (non-host), penetration efficiency of *Bgh* was reduced from 70-80 % to 29 % on average where cells had suffered attempted penetration by *E. pisi* more than 1 hr previously (Kunoh *et al.*, 1985). The entire cell was conditioned towards the inaccessible state by 2 hours after the formation of cytoplasmic aggregates associated with penetration resistance to *E. pisi* (Kunoh et al., 1988). Adjacent cells (longitudinally (distal and proximal), and laterally adjacent) showed induced inaccessibility over 23 hours after induction, with the adjacent protection reduced in comparison to directly challenged cells (Kunoh *et al.*, 1988). In a double inoculation test using intact barley seedlings, failed penetration attempts by a virulent*Bgh* isolate also led to induced inaccessibility, but this enhanced resistance was not transferred to adjacent cells (Lyngkjaer & Carver, 1999). This strict localisation of induced inaccessibility is also supported by other reports (Cho & Smedegard-Peterson, 1986, Martinelli, 1990, Woolacott & Archer, 1984). Induced accessibility enhanced *E. pisi* penetration efficiency from 0 % to 40 % on average, and was induced across the entire cell by 14 hours after haustoria formation by *Bgh*. The response transferred to adjacent cells after 18 hours (Kunoh *et al.*, 1986), but was not seen in more distant cells in further tests (Lyngkjaer & Carver, 1999). Based on the differences in timing of induced inaccessibility and accessibility, Kunoh *et al.* (1988) conclude that the two responses are independent of one another. This is line with our current understanding, which suggests that induced susceptibility is caused by suppression of defence by the pathogen (Lyngkjaer & Carver, 1999). As for induced inaccessibility, the strict localisation and timing suggests the response is not related to SAR (Kunoh, 2002).

In contrast to results from the barley-powdery mildew pathosystem, there is evidence from other cereal pathosystems that suggest AR responses may be translocated. In rice, Horino (1976) reports that symptom development after infiltration with a compatible *Xanthomonas oryzae* isolate was reduced by prior infiltration with an incompatible strain of the same pathogen; this inhibition was present 5 cm from the site of pre-inoculation, but its effectiveness reduced with distance (2, 3 or 5 cm) (Horino, 1976). In wheat spikelets, localised inoculation with *Fusarium graminearum* led to the induction of PR genes (*PR1* to *5*, peroxidase) in both directly inoculated and uninoculated spikes (Pritsch *et al.*, 2001). This data adds to the current confusion over whether AR responses are translocated within and between organs in cereals, and monocot species more generally. Detailed spatial and temporal characterisation of the AR response in dicot plants further emphasises the contrast between described dicot and monocot responses, and this is described further in Section 4.2. Importantly, the chemical analogues of SA, BTH and INA, known to induce AR in *Arabidopsis* and tobacco (Uknes et al., 1992, Ward et al., 1991) have also been shown to induce AR in cereals (Besser *et al.*, 2000, Gorlach *et al.*, 1996, Schweizer *et al.*, 1999). The significance of this is discussed further in Sections 4.2 and 5.2.

1.6 Conservation of defence responses in monocots

The apparent differences- outlined above, between the translocation of AR in dicot and monocot plants raise questions about the general comparability of monocot and dicot responses to pathogen attack. Specific Resistance (R) genes have been identified and cloned from both clades, and the defence mechanisms triggered by R-gene mediated recognition also appear to be similar (Ayliffe & Lagudah, 2004, Piffanelli *et al.*, 1999). Most R-genes encode Nucleotide-Binding Site (NBS) Leucine Rich Repeat (LRR) proteins (Meyers *et al.*, 2003), which may either have an N-terminal Coiled Coil (CC) domain, or an N-terminal domain with homology to the *Drosophila*-Toll protein and mammalian Interleukin-1 receptor (TIR domain). Whilst both NBS-LRR subgroups are found in dicots, only CC-NBS-LRR genes have been identified in monocots, the TIR class appear to have been lost from monocot species (Bai *et al.*, 2002, Pan *et al.*, 2000, Tarr & Alexander, 2009). On the surface, differences such as this could suggest that disease resistance in cereals is induced via fewer and simpler pathways (Bai *et al.*, 2002). However, several lines of evidence suggest that this is not the case. For example, orthologues of *Arabidopsis* EDS1, which is required in *Arabidopsis* for TIR-NBS-LRR mediated R-gene function, are expressed in monocot species (Wiermer *et al.*, 2005). Furthermore, despite their similar sequence and structure, barley Mla1 and Mla6 differ in their requirements for additional defence-related proteins (Azevedo *et al.*, 2002, Bai et al., 2002, Halterman *et al.*, 2001, Zhou *et al.*, 2001). As such, it seems likely that the use of different signalling pathways depends on factors other than structural domains (Bai *et al.*, 2002). Additionally, a range of genes contributing to race non-specific or non-host resistance have been identified in cereals (eg *Lr34* (Krattinger *et al.*, 2009), *Rpg1* (Brueggeman *et al.*, 2002), *mlo* (Büschges *et al.*, 1997)) and *Arabidopsis* (*Pen* (Collins *et al.*, 2003, Lipka *et al.*, 2005)). For the *mlo* gene family, homologues are present in both monocots and dicots (Devoto *et al.*, 2003). PTI is less well studied in cereals, but the characterisation of rice *Xa21* as a PRR indicates this type of response is also present (Lee *et al.*, 2009). Together, this evidence suggests that major classes of plant defence responses are present in both cereals and dicots.

Importantly, key molecular components of the SAR response have been shown to be functionally conserved in cereal species (described in Section 5.2). Expression of *Arabidopsis NPR1* in rice and wheat leads to enhanced resistance to *Xanthomonas oryzae* pv. *oryzae* (*Xoo*), and Fusarium head blight, respectively (Chern *et al.*, 2001, Makandar *et al.*, 2006). Furthermore, over-expression of *OsNPR1* (also described as *OsNPR1 Homologue 1 (NHI)*) in rice also leads to enhanced resistance to *Xoo*, while RNAi lines that fail to accumulate *OsNPR1* transcripts display enhanced susceptibility to *Xoo*, and *OsNPR1* can complement the *Arabidopsis npr1-1* mutant (Yuan *et al.*, 2007). As described above for *Arabidopsis* NPR1, redox change triggers nuclear localisation of *Os*NPR1 in rice, and this localisation is required for functionality (Yuan *et al.*, 2007). The interaction of *Os*NPR1 with TGA transcription factors that bind to SA-responsive elements in rice PR genes has also been demonstrated in yeast-2-hybrid tests (Chern *et al.*, 2001). However, there do appear to be some differences in regulation of *NPR1* between *Arabidopsis* and rice. Over-expression of *AtNPR1* in *Arabidopsis* leads to enhanced pathogen resistance, enhanced sensitivity to SA and BTH, and enhanced PR gene induction after pathogen challenge (Cao *et al.*, 1998, Friedrich *et al.*, 2001). In contrast, rice lines over-expressing *Os* or *At NPR1* constitutively express PR genes (Chern *et al.*, 2005). Furthermore, while *Arabidopsis* seedlings over-expressing *AtNPR1* show no detrimental phenotype, rice over-expressing *AtNPR1* or *OsNPR1* develop a lesion mimic or cell death (LMD) phenotype after transfer from a greenhouse to a growth chamber (with reduced light) (Chern *et al.*, 2005, Fitzgerald *et al.*, 2004, Quilis *et al.*, 2008). Over-expression of *OsNPR1* in rice is also associated with dwarfing when grown under reduced light conditions, indicating altered sensitivity to light (Chern *et al.*, 2005). Additionally, both *OsNPR1* and *AtNPR1* over-expressing rice lines show altered SA accumulation relative to wild-type plants under growth chamber and glasshouse conditions, suggesting that, in rice, NPR1 could be involved in the regulation of SA in response to environmental stimuli (Chern *et al.*, 2005, Fitzgerald *et al.*, 2004). The differential defence gene activation induced by NPR1 in rice and *Arabidopsis* has led to suggestions that in rice*,* NPR1 activates defence genes more readily than *Arabidopsis*, and that this could be related to permanent activation of the cereal NPR1 pathway by high endogenous SA levels in cereals (Kogel & Langen, 2005). Raskin *et al.* (1990) report endogenous SA in rice at 37.19 µg g^{-1} fresh weight, compared to <0.01 µg g^{-1} fresh weight for tobacco. The level in barley was 2.13 µg g^{-1} fresh weight, and wheat was 0.09 µg g^{-1} fresh weight (Raskin *et al.*, 1990). As wheat over-expressing *AtNPR1* shows enhanced resistance without the detrimental side-effects seen in rice, these side-effects are not common to all cereals (Makandar *et al.*, 2006). A high basal level of SA does not preclude the development of SAR, as potato has high endogenous SA (141 ng g^{-1} fresh weight free SA, and 5040 ng g^{-1} conjugated SA), and yet still develops SAR against *Phytophthora infestans* (Yu *et al.*, 1997). The development of SAR in potato is not associated with increased SA levels in untreated leaves, but SA is required for SAR to develop (Yu *et al.*, 1997). This suggests that SAR induction in potato is regulated at the level of SA perception or transduction, rather than SA biosynthesis (Yu *et al.*, 1997). Chern *et al.* (2001) speculate that an SA receptor in rice may be further controlled by another signal, or that SA in rice might be localised in a different cellular compartment than in *Arabidopsis*. It seems likely that the regulation of NPR1-mediated resistance in rice differs from that in *Arabidopsis* (Chern *et al.*, 2001), although this may not be the case for all cereals. The conservation of functional NPR1 in rice, in addition to a range of other elements described in full in Section 5.2, strongly suggests there is some conservation of the SAR induction pathway in cereals. Recent evidence from rice showing the induction of a classical ISR response by the non-pathogenic, root colonising bacteria *Pseudomonas fluorescens* again supports that induced resistance responses in cereal species are comparable to those characterised in dicots (De Vleesschauwer *et al.*, 2008). However, for SAR, our understanding of the pathways involved is limited by the absence of a reliable model system for the biological induction of the response.

1.7 Research aims

A major focus of current crop research is the identification and understanding of durable, broad-spectrum disease resistance. AR represents a form of broad-spectrum resistance that is inducible in the field, and that has been shown to contribute to pathogen control under field conditions (Vallad & Goodman, 2004). In order to contribute to our fundamental understanding of disease resistance signalling in cereals, and as a potential source of broad-spectrum resistance for crops, it is important that we further elucidate the pathways and mechanisms involved in AR in cereals.

The overarching aim of the work presented in the following chapters is to provide insight into whether a functional SAR pathway is present in cereal species, with the primary focus on barley. As outlined above, it is currently unclear whether AR responses in barley and other cereals are translocated within, or between, organs of the plant. There is a clear need for a systematic approach to developing a model pathosystem for testing the translocation of AR in a cereal species. The induction of SAR in *Arabidopsis* by the bacterial pathogen *Pseudomonas syringae* is well characterised. The research presented in Chapter 3 aims to establish whether *Pseudomonas syringae* can be used as an inducer of AR in barley. Markers such as symptom development, restriction of bacterial growth and defence gene induction are used to identify isolates, inoculation densities and time-points associated with the induction of an active, local defence response. . The localisation of resistance induced by *Pseudomonas syringae* in barley is addressed in Chapter 4, with the aim of determining whether the local interaction results in the development of AR at a distance from the local lesion. In order to characterise the nature of the translocated AR response, global transcriptional profiling is performed and the gene expression changes identified are compared with previously described AR responses in cereal and dicot systems (Chapter 4). A further aim is to investigate the conservation in cereals of molecular components shown in *Arabidopsis* to function specifically in SAR. As described above, *Arabidopsis DIR1* encodes a lipid transfer protein which functions specifically in the production or transmission of a mobile SAR signal. As outlined in Section 5.2, the position of DIR1 in the *Arabidopsis* SAR signalling pathway makes it an interesting target for characterisation in cereals. In order to determine whether functional homologues of *Arabidopsis DIR1* are present in cereal species, bioinformatic and phylogenetic analyses are performed in rice and barley to identify candidate homologues. With the aim of testing functionality in *Arabidopsis*, rice homologues are heterologously expressed in the *Arabidopsis dir1-1* mutant, and complementation tests performed. For further characterisation, rice homologues of *Arabidopsis DIR1* are expressed in barley cultivar Golden Promise, via *Agrobacterium*-mediated transformation. Tests of local induced defence responses, as well as the translocation of the defence response in these lines, aim to provide insights into mechanisms of AR in cereals (Chapter 5).

Chapter 2: Materials and Methods

2.1 Materials

2.1.1 Plants

Barley (*Hordeum vulgare*) cultivar Golden Promise and landraces were from the John Innes Centre germplasm collection. *Arabidopsis* Ws and *dir1-1* seeds were provided by Dr Gary Creissen, John Innes Centre, Norwich, UK.

2.1.2 Bacterial strains

Escherichia coli (*E. coli*) strain DH5α, derived from DH1 (Hannahan, 1983), was used for for general cloning. *E. coli* strain DB3.1 (Invitrogen, Carlsbad, CA, USA) was used for Gateway cloning.

Agrobacterium tumefaciens (*Agrobacterium*) strain GV3101::mp90 was used for *Arabidopsis* transformation. *Agrobacterium* strain AGL1 was used for barley transformation.

Pseudomonas syringae pv. *tomato* (*Pst*) strains: DC3000; DC3000 *hrcC*- mutant (rifampicin resistance on the chromosome); *PstavrRpm1* (rifampicin resistance on the chromosome and kanamycin resistance on plasmid pVSP61 (with avirulence gene *avrRpm1*)); and DC3000 chromosomally tagged with *luxCDABE* (rifampicin resistance on the chromosome and kanamycin resistance on plasmid) (Fan *et al.*, 2008) were provided by Dr Jun Fan, John Innes Centre.

Pseudomonas syringae pv. *syringae* and *japonica* isolates were obtained from Dr Kee Sohn, The Sainsbury Laboratory, Norwich, UK. Isolates are originally described by Hwang *et al*. (2005).

2.1.3 *Magnaporthe oryzae*

Magnaporthe oryzae strain Guy11 was provided by Dr Ane Sesma, John Innes Centre.

2.1.4 Plasmids

Vector construction for *Arabidopsis* and barley transformation used the Gateway system (Invitrogen) which enables efficient, directional cloning. The entry vector used was pENTR^{TM}1A (Invitrogen; provided by Dr Nicola Leyland, John Innes Centre), designed for cloning DNA sequences using restriction endonucleases and DNA ligase. The resulting entry vector is ready for recombination with a destination vector to create an expression vector for plant transformation.

For *Arabidopsis* transformation destination vector pMDC32 (Curtis & Grossniklaus, 2003) was used (provided by Dr Kate Thodey, John Innes Centre). Destination vector pBract 214 was used for barley transformation (provided by Dr Wendy Harwood, John Innes Centre, http://www.bract.org/bract.html). pBract 204 was also used as a transformation control. pBract vectors are based on pGreen and as such were co-transformed into *Agrobacterium* with helper plasmid pSoup (Hellens *et al.*, 2000). pMDC32 is based on pCambia (http://www.cambia.org/). Vector maps and cloning details are given in Section 2.2.7.4.

Entry vectors containing the coding sequence of *Arabidopsis Defective in Induced Resistance 1* (*DIR1*); '*RICE A*' (full-length cDNA AK105204); or '*RICE B*' (full-length cDNA AK062503) were created. The coding sequence of *DIR1* was obtained by restriction digest of plasmid pGEM®-T-Easy (Promega, Madison, WI, USA) containing the *DIR1* CDS (plasmid 'A76', provided by Dr Nathalie Buhot, John Innes Centre). Full-length cDNA clones of *RICE A* and *RICE B* were obtained from the Rice Genome Resource Centre, National Institute of Agrobiological Sciences, Japan. Clones were provided inserted into DraIII sites at 808 and 1191 bp of plasmid pME18SFL3 (AB009864).

2.1.5 Enzymes, chemicals and antibiotics

Restriction enzymes and incubation buffers were from Roche (Basel, Switzerland) or New England Biolabs (Ipswich, MA, USA). Primers were ordered from Sigma Genosys. Chemicals were from Sigma-Aldrich (St. Louis, MO, USA), unless otherwise stated. Antibiotics were as follows: ampicillin (Sigma-Aldrich), chloramphenicol (Sigma-Aldrich), hygromycin (Duchefa, Haarlem, The Netherlands), kanamycin (Sigma-Aldrich), rifampicin (Duchefa); carbenicillin (Formedium, Hunstanton, U.K.); streptomycin (Fischer Scientific, Leicestershire, UK); or as stated in text.

2.1.6 Bacterial culture media

LB – G broth and LB – G agar (LB: Luria-Bertani, Maniatis *et al*. 1982)

Formula per 1 litre of de-ionised water
10.0 g Tryptone
5.0 g Yeast Extract
10.0 g NaCl
pH 7.0
For solid medium add per litre
10.0 g Lab M No.1 agar

KB (Kings B Medium, King *et al*. 1954))

Formula per 1 litre de-ionised water:

20 g Proteose Peptone

1.6 g Glycerol

pH 7.2

For solid 15 g Lab M agar

MG/L broth (Garfinkel & Nester, 1980)

5.0 g / L Tryptone

5.0 g / L Mannitol

2.5 g / L Yeast extract

1.0 g / L glutamic acid

250 mg / L KH2PO4

100 mg / L NaCl

100 mg / L MgSO4.7H2O

10 µl Biotin (0.1 mg / mL stock)

pH 7.0

2.1.7 *Magnaporthe oryzae* culture media

Complete Media Agar (Talbot *et al*. 1993)

<u>1 litre</u>
$NaNO_3$ 6 g
KCl 0.52 g
$MgSO_4 \times 7H_2O$ 0.52 g
KH_2PO_4 1.52 g

Trace elements (1 mL of stock; see below) 0.1 %
D-Glucose 10 g
Peptone 2 g
Yeast extract 1 g
Casamino acids 1 g
Vitamin solution (see below) 1 mL

pH 6.5 with NaOH. For solid media add 15 g agar / L.

Vitamin solution 100 mL

Biotin 0.01 g

Pyridoxin (vit. B_6) 0.01 g

Thiamine (vit. B_1) 0.01 g

Riboflavin (vit. B_2) 0.01 g

PABA (p-aminobenzoic acid) 0.01 g

Nicotinic acid 0.01 g

2.1.8 Plant detached leaf test media

Leaf bleaching assay (as Wang & Waterhouse, 1997)

Formula per 1 litre of de-ionised water.

8 g agarose

4.4 g Murashige and Skoog plant salt base (including vitamins)

pH 5.7

75 mg Hygromycin

0.5 mg BAP (6-benzylaminopurine)

2.1.9 Plant growth media

Arabidopsis

MS 0.8 % **(Weigel & Glazebrook, 2002)**

Formula per 1 litre of de-ionised water.

4.41 g Murashige and Skoog plant salt base (including vitamins)

30.0 g Sucrose

pH 5.8

Barley (Bartlett *et al*. 2008)

Barley callus induction (BCI)

4.3 g / L Murashige & Skoog plant salt base (M0221)

30 g / L Maltose

1.0 g / L Casein hydrolysate

350 mg / L Myo-inositol

690 mg / L Proline
1.0 mg / L Thiamine HCl
2.5 mg / L Dicamba
1.25 mg / L CuSO4.5H2O
pH 5.8
3.5 g / L Phytagel

Barley transition media

2.7 g / L Murashige & Skoog modified plant salt base (without NH_4NO_3)
20 g / L Maltose
165 mg / L NH4NO3
1.25 mg / L CuSO4.5H2O
750 mg / L Glutamine
100 mg / L Myo-inositol
0.4 mg / L Thiamine HCl
2.5 mg / L 2,4D (2,4-Dichlorophenoxyacetic acid)
0.1 mg / L BAP
pH 5.8
3.5 g / L Phytagel

Barley regeneration media

2.7 g / L Murashige & Skoog modified plant salt base (without NH_4NO_3)
20 g / L Maltose
165 mg / L NH_4NO_3
750 mg / L Glutamine
100 mg / L Myo-inositol
0.4 mg / L Thiamine HCl
pH 5.8
3.5 g / L Phytagel

2.1.10 Plant growth mixes

Peat and Sand

870 L fine grade peat
200 L 4 mm grit

2.7 kg Osmocote Plus® (Scotts Professional, Ipswich, UK)
1.8 kg Garden Lime
1.8 kg Dolodust
64 L water

Barley mix

375 L Levington M3 compost (Scotts Professional)
100 L Perlite medium
200 L 4 mm grit
1.6 kg Osmocote Plus™

Arabidopsis mix

Levington F2 compost
Nemasys™ (Becker Underwood, West Sussex, UK) as manufacturer's instructions

2.2 Methods

2.2.1 Plant growth

Barley plant growth

For disease tests:

Seeds were sown directly into peat and sand in plantpak (p)24 cells, or into barley mix in p15 cells, and transferred to a Snidjers cabinet (18 °C / 16 h light period; 12 °C / 8 h dark period. Humidity 75 – 85 %. Irradiance approximately 100 µmol m^{-2} s^{-1}). Watering was as required. Seedlings grown in peat and sand were watered with 2g L^{-1} potassium sulphate.

On occasion, to facilitate selection of viable seed, seeds were pre-germinated on damp filter paper (dark, 20 °C, 2-3 days).

For seed bulking:

Seedlings were transferred to 2 L pots containing barley mix and grown under glasshouse conditions. Mature seeds were collected from dessicated plants.

Transgenics:

Donor plants, and post-tissue culture T_0 seedlings, were grown in a Controlled Environment Room (CER) with a 16 hr light period (500 µmol m^{-2} s^{-1} at mature canopy level provided by metal halide lamps (HQI) supplemented with tungsten bulbs) and 80 % humidity. For disease tests transgenic barley lines were grown as Golden Promise.

***Arabidopsis* seed surface sterilisation and plant growth**

Arabidopsis seeds to be plated on MS 0.8 % media were sterilised by washing approximately 50 µL of seeds 3 to 7 times in 1 mL of 70 % ethanol. Seeds were resuspended in 0.1 % agarose and placed in the dark at 4 °C for 3 days prior to sowing, in order to break dormancy. *Arabidopsis* seeds for sowing on *Arabidopsis* mix were suspended in water and placed in the dark at 4 °C for 3 days prior to sowing, for stratification.

Arabidopsis seedlings growing on selective media were placed in a controlled environment cabinet (Sanyo, Leicestershire, UK) (23 °C, 9 h photoperiod). Seedlings pricked out from media, and those sown directly onto F2 compost, were grown in a controlled environment room under short day conditions (23 °C, 9 h photoperiod, approximately 100 µmol m^{-2} s^{-1}). Seedlings were sown / pricked out into p 24 (disease tests), 40, or 60 trays. After sowing, trays were covered with a clear propagator lid until after germination. After pricking out from media, seedlings were watered in and covered with a clear propagator lid for 48 hours. Watering was as required.

Seedlings to be transformed by floral dipping were transferred to glasshouse conditions soon after bolting and returned to containment glasshouse conditions to set seed after transformation (as described in Section 2.2.1).

For seed collection, plants were transferred to containment glasshouse conditions soon after bolting. Drying bolts were covered with a paper bag and sealed at the base until siliques shattered.

2.2.2 Plant pathology

Pseudomonas syringae

Plant inoculation and bacterial growth determination was performed in accordance with Whalen *et al*. (1991).

Maintenance of *Pseudomonas syringae* isolates

Isolates of *Pseudomonas syringae* were maintained as glycerol stocks (15 % glycerol). Isolates were retrieved by streaking onto KB agar plates (containing rifampicin (50 µg mL^{-1}) and kanamycin (50 µg mL^{-1}) where necessary). Cultures were incubated overnight at 28 °C and stored at 4 °C for 2-4 weeks.

Preparation of inoculum

Approximately 16 hrs prior to inoculation, a loop was taken from a fresh culture (plate) and resuspended in 100 µL sterile water. *PstavrRpm1* suspensions were diluted to OD_{600} 1, to aid uniform growth between independent experiments. This suspension was spread onto a KB agar plate with the appropriate antibiotics for selection and incubated overnight at 28 °C. Immediately before inoculation, a loop from the overnight plate was resuspended in 100 µL sterile water and the OD_{600} determined using a spectrophotometer. The dilution was calculated and the appropriate volume of suspension added to 10 mls sterile water to result in desired OD_{600} for inoculation.

Infiltration of leaves (barley and *Arabidopsis*)

Barley seedlings were placed in the laboratory for one hour prior to infiltration as leaves were more easily infiltrated after a period of adaptation (likely due to high humidity in the growth cabinet). Bacterial suspension was hand infiltrated into the abaxial surface of leaves using a 1 mL needleless syringe. Leaves were infiltrated via small punctures created by piercing the epidermis using a 200 µL pipette tip.

Determination of bacterial counts in leaves

Barley

The number of Colony forming units (CFU) recovered from barley leaves was determined as follows. Leaf disks (0.5 mm diameter) from the leaf position described were placed into KB broth in a 1.5 mL eppendorf. Disks were ground using a micropestle attached to a hand drill. Leaf disk suspension was diluted serially in KB broth and 100 µL plated on KB agar with appropriate selection. Plates were incubated at 28 °C overnight and colony number counted on plates with 100 – 1000 colonies.

Arabidopsis

Lux-tagged *Pst* DC3000 is chromosomally tagged with the bioluminescent *luxCDABE* operon from *Photorhabdus luminescens*, which confers luminescence without the need for an exogenous substrate. Photon count is measured in an FB12 luminometer (Berthold Detection Systems, Pforzheim, Germany), over a pre-determined time. This results in a reading of which has been shown to reliably report bacterial growth (Fan *et al.*, 2008). As such, in tests of bacterial growth in *Arabidopsis*, photon counts from leaf discs (0.5 mm diameter) sampled from inoculated leaves were used to estimate bacterial growth.

Magnaporthe oryzae

Growth and inoculation of barley with *Magnaporthe oryzae* was performed in accordance with Tufan *et al*. (2009).

Maintenance of isolate

All manipulations of *Magnaporthe oryzae* isolate Guy11 took place in a class II biological safety cabinet. Isolate was stored as dried mycelia on pieces of cellulose filter paper (-20 °C).

Preparation of inoculum

Fungus was retrieved by cutting a small piece of filter paper (approx 1x2 mm) and placing on solid Complete Media Agar (CMA) containing carbenicillin (100 µg mL^{-1}) and streptomycin 60 µg Ml^{-1}. Plates were then incubated at 25 °C, 16 hr light/ 8 h dark, for 10 days. On day of inoculation, conidia were harvested from fungal mycelium by applying 5 mLs of 0.25 % weight/ volume (w/ v) gelatine with 0.2 % Tween 20 to plate, before scraping plate surface with a sterile glass spreader. The spore suspension (from multiple plates) was filtered through double sterile miracloth into a falcon tube, and conidia density measured using a haemocytometer. Conidia concentration was adjusted to 1×10^5 conidia mL with 0.25 % w/ v gelatine solution, plus 0.2 % Tween 20.

Plant inoculation

Seedlings were mist inoculated with 2-4 mls of conidia suspension. Plants were sealed in plastic propagators to maintain relative humidity at c. 100 % and kept at 25 °C in the dark for 24 hrs post inoculation. At this point, propagator lids were removed and plants were placed in a Sanyo Fitotron growth cabinet (Sanyo Gallenkamp PLC, Loughborough, UK) with 16 h light/ 8 h dark, 23 °C.

Disease scoring

Symptoms were photographed 5 days post inoculation and lesion area measured using ImageJ (Abramoff, 2004).

2.2.3 Microscopy

Leaf sections were cleared by heating to 70 °C in a 3:1 ethanol: water solution. For microscopy, leaf sections were immersed for 14 hours in trypan blue (0.1 % in lactoglycerol), destained for approximately 5 hours in chloralhydrate storage solution (2.5 g mL^{-1} chloralhydrate) and then mounted on a glass microscope slide.

2.2.4 Tests of local and adjacent responses induced by *Pseudomonas syringae* (barley)

Barley seedlings inoculated with *Pseudomonas syringae* were between the 1 and 2 leaf stage (15-21 days old; within experiments seedlings were same age except where stated). Seedlings were grown, inoculum prepared, and leaves infiltrated as described above. For tests of local response described in Chapter 3, the central third of the first true leaf was infiltrated via 3 pairs of small punctures, with one of each pair either side of the mid-rib. Where local and adjacent leaf regions were tested (Section 3.3.5, Chapter 4 and Chapter 5), positions of 'local' and 'adjacent' leaf regions are described for individual experiments**.** All control / mock-inoculated samples were infiltrated with sterile water only. For tests described in Chapters 4 and 5, leaves were infiltrated with *PstavrRpm1* in the local region with a bacterial suspension adjusted to OD_{600} 0.2 (2×10^8 CFU mL^{-1}), via a single puncture towards the distal end of the mid-rib of the first (true) leaf. Controls were infiltrated with sterile water. After inoculation, seedlings were returned to a Snijders climate-controlled cabinet (Snijders Scientific) at 23 °C (as described above), to provide optimal conditions for bacterial growth.

Samples were taken for RNA extraction at the time-points described for each experiment. The infiltrated, local leaf section was sampled 0.5 cm above the boundary of infiltration to ensure sample represented flooded leaf tissue. Three biological replicates were taken, each consisting of leaf samples from 3 pooled individuals, except where stated. Samples were immediately placed in liquid nitrogen and transferred to -80 °C for storage. Several seedlings remained in the cabinet for monitoring of symptom development.

For tests of adjacent AR to PS86, challenge infiltrations were made (24 hours post local *PstavrRpm1* infiltration) with a bacterial suspension adjusted to OD_{600} 0.02, via 2 punctures, one each side of the mid-rib, in the adjacent region of the same leaf. As leaves flooded, the limit of infiltration was observed by a water soaked appearance, and the boundary marked with a marker pen. A single leaf disc was taken from the challenged adjacent region of each of four replicate samples per treatment (unless otherwise stated) after the indicated time interval, and CFU assayed as described above (Section 2.2.2).

For tests of adjacent AR to *Magnaporthe oryzae* isolate Guy11, seedlings were infiltrated with *PstavrRpm1* or water (control) as described above. 24 hrs later, seedlings were mist-inoculated with *Magnaporthe oryzae*, as described above. Between 5 and 15 replicate seedlings (per treatment) were tested, in 3 independent experiments.

2.2.5 Testing secondary leaf responses after local inoculation with *PstavrRpm1* (barley)

For tests of AR responses in secondary leaves, seedlings received a primary 'inducer' inoculation with *PstavrRpm1* in the first true leaf at 18 or 19 days old. *PstavrRpm1* or water (control) infiltrations were carried out as described above, except that the distal 2 thirds of the first (true) leaves of seedlings were infiltrated. For gene expression tests, the flooded area of the first leaf was sampled, and the entire secondary leaf was sampled. To test for AR, one secondary leaf per seedling (detail as described for individual experiments) was challenged with PS86 at the time-point described for each experiment, by infiltration of the central third of the leaf via 2 punctures, one each side of the mid-rib. 4 replicate seedlings (per treatment) were tested at each time-point. CFU were then recovered and counted as described in Section 2.2.2.

2.2.6 Testing systemic acquired resistance in *Arabidopsis*

SAR was monitored by comparing growth of virulent *Pst* in plants induced for SAR to growth in uninduced plants. SAR was induced by inoculation of one leaf with avirulent *PstavrRpm1* (OD_{600} 0.002, (10^6 CFU mL^{-1})). Uninduced seedlings were mock-inoculated with water. Two days later, three uninoculated leaves per seedling were challenged by inoculation with the isogenic virulent lux-tagged *Pst* DC3000 strain (Fan *et al.*, 2008) (OD_{600} 0.002, 10^6 CFU mL^{-1}). Two days later, a leaf disk (0.5 mm diameter) was sampled from each challenge-infiltrated leaf, and photon count measured as described in Section 2.2.2.

2.2.7 Molecular biology methods

2.2.7.1 Isolation of nucleic acids

Isolation of plant genomic DNA

DNA was extracted from a maximum of 100 mg leaf tissue using the DNeasy Plant Mini Kit (Qiagen, West Sussex, UK) according to manufacturer's instructions.

Isolation of plant RNA

Leaf tissue was flash frozen in liquid nitrogen immediately after harvesting, ground under liquid nitrogen and stored at -80 °C prior to RNA extraction. RNA was extracted from a maximum of 100 mg leaf tissue using the RNeasy Plant Mini Kit (Qiagen) according to manufacturer's instructions (with the exception that β-mercaptoethanol was not used).

Plasmid isolation from *E. coli*

Plasmids were isolated from *E. coli* using the QIAprep Spin Miniprep kit (Qiagen), according to manufacturer's instructions.

Quantification of nucleic acids

DNA was quantified by measurement of OD_{260} in water using a spectrophotometer. For qRT-PCR, RNA was quantified using a NanoDrop® ND-1000 (Thermo Scientific, Wilmington, DE, USA) or Picodrop (Picodrop Ltd, Cambridge, UK). Contamination and quality of nucleic acids was estimated by the OD_{260}/OD_{280} ratio, with 1.8 considered ideal for DNA and 2.0 considered ideal for RNA.

Visualisation of nucleic acids

6 x loading buffer (0.1 M EDTA, 0.1 % bromophenol blue, 0.1 % xylene cyanol, 30 % glycerol) was added to nucleic acid before loading onto an agarose gel containing ethidium bromide.

DNA sequencing

Plasmid inserts were sequenced using the BigDye® Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster City, CA, USA) according to the manufacturer's instructions. Gene or plasmid specific primers were used. Sequencing analysis was performed by the Genome Laboratory (John Innes Centre).

2.2.7.2 Amplification of nucleic acids

Primers

Sequences of all primers used in Chapters 3, 4 and 5 can be found in Tables 2.1 to 2.5.

Polymerase Chain Reaction (PCR)

Gene	Primer direction	Primer sequence	Primer Reference
α-tubulin (AK252410.1)	Forward	AGTGTCCTGTCCACCCACTC	Burton *et al*. (2004)
	Reverse	AGCATGAAGTGGATCCTTGG	
Ubiquitin 1 (AK2050942.1)	Forward	GCCGCACCCTCGCCGACTAC	Rostocks *et al*. (2003)
	Reverse	CGGCGTTGGGGCACTCCTTC	
Cyclophilin (AK253120.1)	Forward	CCTGTCGTGTCGTCGGTCTAAA	Burton *et al*. (2004)
	Reverse	ACGCAGATCCAGCAGCCTAAAG	
Ubiquitin conjugating enzyme (AK251127.1)	Forward	GGTTCTGCTTTCAATCTGCTCGCTG	Gjetting *et al*. (2004)
	Reverse	GGGAGACACACGCAACCGACAAGTA	
PR5 (AJ276225)	Forward	AACTGCGGCTCCACAATATG	Bryngelsson & Gréen (1989)
	Reverse	CCGGAGAGAGAGCATGAGAG	
PR9 (L36093.1)	Forward	GGCATGGAACAAAACGCTAT	Scott-Craig *et al*. (1994) *unpubl.*
	Reverse	GTCCGTGTTTGCCTCATTCT	
PRb-1 (Z21494)	Forward	TTGCAGTCGTTGATCCTCTG	Muradov *et al*. (1993)
	Reverse	CCAAGCTAGCCATCTTGCTC	
prx8 (AJ276227.1)	Forward	GGCTAACATCGACACCACCT	Boyd *et al*. (1994)
	Reverse	TCGTTGTTGAAGAGCACCTG	
PAL (Z49146.1)	Forward	GTTGACGGAAAGAAGGTGGA	Kervinen *et al*. (1997)
	Reverse	CAGGACCTCGGAGAGAACAG	

Table 2.1 Primers used in qRT-PCR: amplification of barley reference genes and PR genes. For reference genes (*α-tubulin* to *Ubiquitin conjugating enzyme*) Primer Reference cites first use of the described primers. For target genes (*PR5* to *PAL*) Primer Reference cites the relevant gene.

Annotation	Primer direction	Primer sequence	Affymetrix Gene Identifier
WCI-5 (Wheat Chemically Induced-5)	Forward	GCAAGCTCAAGGATGGCTAC	Contig538_at
	Reverse	CGCTCCAGTCAATACAGCAA	
Methyl-jasmonate inducible lipoxygenase (lipox)[1]	Forward	GTCGGACGAGGAGTACATGG	Contig2305_at
	Reverse	TTAGCGTCCATGGGATTACC	
Expansin	Forward	AACTGGCAGAGCAACACCTT	Contig3674_at
	Reverse	GGAGATGGAGATGGAGTGGGA	
Wheat Induced Resistance 1 (WIR1A)	Forward	CCCCAACAATGGAGTAATCG	Contig939_s_at
	Reverse	GATGGGAACACCGTTCATCT	
Glutathione-S-Transferase (GST)	Forward	GAGGAGGAGGAGGAGCTGAC	Contig9632_at
	Reverse	ACTGCACGATGAGCTGTGAC	
Nodulin-like family protein	Forward	ATGGGTCGCAAGTGCTACTC	Contig14067_at
	Reverse	CTAACCCAGTCCACCCAGAA	

Table 2.2 Primers used in qRT-PCR: amplification of contigs differentially expressed in microarray analysis (Section 4.3.5). 1. Voros *et al*. (1998), other transcripts have not previously been published.

Gene	Primer direction	Primer sequence
PR1 (At2g14610)[1]	Forward Reverse	AGTGTCCTGTCCACCCACTC AGCATGAAGTGGATCCTTGG
Glutathione-S-transferase (AK319075.1)	Forward Reverse	CCAGCCTTTGAAGATGGAGA TCCCAAACAAGCTTTGAACC
Actin (NM_179953.2)	Forward Reverse	CTCTGTCTGGATTGGAGGGT GTGAACAATCGATGGACCTG

Table 2.3 Primers used in qRT-PCR: Chapter 5 (*Arabidopsis*). 1. Uknes *et al*. (1992).

(a)

Target	Primer name	Primer direction	Primer sequence
DIR1 CDS	LTP50	Forward	TCAGTCGAGATGGCGAGCAGCAAGAA
	LTP52	Reverse	GGGTCTAGTTTAACAAGTTGGGG
*RICE A**[a]	Rice A Vergne F	Forward	GGCTAGAACTGCTACAGGGATAG
	Rice A Vergne R	Reverse	ATGACAACACTCTCACAGACAAAC
RICE B [a]	Rice B Vergne F	Forward	GGCAAGGGGAGATGAATAAA
	Rice B Vergne R	Reverse	GAATAGGTTGGGTGTTTAACCAA

(b)

Target	Primer name	Primer direction	Primer sequence
pME18SFL3 insert	pME18SFL3_F	Forward	GGTGCAAATCAAAGAACTGC
	pME18SFL3_R2	Reverse	TTATTTGTAACCATTATAAGCTGC
pENTR™1A insert	pENTR1A 5'	Forward	GCCAGGCATCAAACTAAGCAG
pBract214 Ubi prom	pAHUBI prmD	Forward	GCATATGCAGCAGCTATATGTG
pBract214 nos term	nosterm 3'	Reverse	GATATCAGCTTGCATGCCGGTC
35S promoter	G0261	Forward	CTTCGCAAGACCCTTCCTCT
nos terminator	G0115	Reverse	TCGCGTATTAAATGTATAATTGCGG
pMDC32 RB	pMDC32 RB fwd	Forward	AATGCGTCCTCACGGAAG
pMDC32 nos term	pMDC32 nos term fwd	Forward	TCGTTCAAACATTTGGCAAT
RICE A	AK105204 5' REV	Reverse	GGAGAGGTGAGGAGCTGGAT
RICE B	AK062503 5' REV	Reverse	CTGTTTGGCCATGGATATGA

Table 2.4 Primers used in Chapter 5. (a) Primers used in PCR and qRT-PCR of *DIR1, RICE A* and *RICE B.* *indicates primers were published in Vergne *et al*. (2007). [a] indicates PCR was performed using the alternative cycling conditions described in Section 2.2.7.2 **(b) Primers used in sequencing and PCR of transformation vectors.**

Target	Type	Sequence
p35SF	Primer	CGTCTTCAAAGCAAGTGGATTG
p35SR	Primer	TCTTGCGAAGGATAGTGGGATT
p35S	Probe	6FAM-TCTCCACTGACGTAAGGGATGACGCA-TAMRA
HvCon2F1	Primer	TGCTAACCGTGTGGCATCAC
HvCon2-R1	Primer	GGTACATAGTGCTGCTGCATCTG
HvCon2P	Probe	VIC-CATGAGCGTGTGCGTGTCTGCG-TAMRA

Table 2.5 Primers and TaqMan^{TM} probe sequences used in qPCR analysis of copy number and zygosity of barley transformants (Chapter 5).

Standard PCR was performed using Taq DNA polymerase (Qiagen). Reactions were prepared to a final volume of 20 µL; with approximately 25 ng DNA template, 1.25 units polymerase, 0.2 x polymerase buffer, 0.2 mM dNTPs, 0.5 µM forward and reverse primer and sterile water. Cycling conditions were: initial denaturation at 94 °C for 2 mins (4 minutes when amplifying direct from bacterial cells); 35 cycles of 94 °C for 15 s, 50 – 60 °C for 15 s, 72 °C for 1 minute per KB of DNA; final elongation at 72 °C for 10 minutes.

RICE A and *RICE B* sequences are GC rich, and as such Phusion^{TM} High-Fidelity DNA polymerase and GC buffer (Finnzymes, Espoo, Finland) were used for PCR where the CDS was amplified.

Reactions were prepared to a final volume of 20 µL; with 4 µL 5x GC buffer; 0.4 µL 2mM dNTPs; 1 µL 10 µM primers; 1 µL DNA (approximately 25 ng DNA); 0.1 µL Phusion Taq Polymerase (0.2 units) and sterile water. Cycling conditions were: denaturation at 98 °C for 30s; 35 cycles of 98 °C for 10 s, 70 °C for 15 s, 72 °C for 5 s; final elongation at 72 °C for 10 minutes.

Reverse Transcription-PCR (RT-PCR)

DNase I digest

Prior to first stand cDNA synthesis RNA was treated with Turbo DNA-free^{TM} DNase I treatment (Ambion, Austin, TX, USA) according to manufacturer’s instructions (rigorous protocol). A control PCR reaction was performed on the same dilution of RNA used for cDNA synthesis to reveal any genomic DNA remaining after DNase I treatment. Any contaminated samples were excluded.

First strand cDNA synthesis

cDNA was synthesised from 500 ng-1 µg of RNA using the Superscript^{TM} III first strand synthesis kit (Invitrogen, primed with random hexamers), with the exception of experiments shown in Figures 3.6, 4.5 (c) and 4.6, in which 500 ng- 1 µg of RNA was reverse transcribed as follows; 1 µL random hexamers (250 ng µl^{-1}) and 1 µL 10 mM dNTPs were added to RNA (<13 µL); Incubation at 65 °C for 5 minutes; mixture placed on ice for at least 1 minute; addition of 4 µL 10X RT Buffer, 1 µL 0.1 M DTT and 1 µL Superscript II Reverse Transcriptase (50 units µl^{-1}) were added (all Invitrogen); incubation at room temperature for 10 minutes; 42 °C for 50 minutes, 70 °C for 10 minutes. Where material was to be tested for the presence of *RICE A* or *RICE B* transcript, cDNA synthesis was carried out according to the “First-strand cDNA Synthesis of Transcripts with High-GC Content” protocol (Superscript^{TM} III first strand synthesis kit (Invitrogen)).

Quantitative RT-PCR (qRT-PCR)

cDNA was diluted 1:10 or 1:20 in sterile water. cDNA was amplified using SYBR® Green JumpStart^{TM} Taq ReadyMix (Sigma-Aldrich, as manufacturer's instructions), with a DNA engine Opticon2 Continuous Fluorescence Detector (MJ Research Inc., Alameda, CA, USA). Cycling conditions were as follows: 95 °C 4 mins; 40 cycles of 94 °C 30 s, 59-66 °C (anneal temp) 30 s, 72 °C 30 s (plate read); followed by extension at 72 °C for 10 mins. Primer pairs used to amplify *RICE A* and *RICE B* (designated '^{a}' in Table 2.4) were amplified using the following protocol: 95 °C 10 minutes; 40 cycles of 95 °C 15 s, 62 °C 1 minute, 72 °C 30 s (plate read); followed by extension at 72 °C for 10 mins.

Melt curve analysis (65-95 °C) was performed for each reaction to distinguish PCR products from amplification artifacts (Nolan *et al.*, 2006). Product size was verified by running PCR products on an agarose gel against a DNA ladder. PCR products were sequenced to verify specificity, by ligation into pGEM®-T-Easy (Promega, as manufacturer's instructions) and subsequent sequencing using M13 or sequence specific primers. Data were analysed using Opticon Monitor analysis software v2.02 (MJ Research Inc.). Each reaction was run in duplicate or triplicate, and the average Ct (threshold cycle) value for each reaction calculated.

Assay optimisation

Gene specific primer pairs were designed using primer3 v4.0 (Rozen & Skaletsky, 2000), or taken from the literature. Primer specificity was checked against the NCBI *Hordeum vulgare* non-redundant database using BLASTn. PCR efficiency was optimised by selecting the most efficient temperature from a gradient, and estimated using a classical calibration dilution curve and slope calculation (www.gene-quantification.info/).

Reference gene selection

For most experiments, the stability of between 3 and 5 reference genes in all samples was tested using genorm v3.5 (http://medgen.ugent.be/~jvdesomp/genorm/; (Vandesompele *et al.*, 2002)). RNA transcript levels were normalised to the geometric mean of the two most stable reference genes, or to a single gene whose expression had been shown to be stable under the relevant experimental conditions.

Data analysis

Relative expression was calculated from normalised expression ratios, according to Pfaffl *et al.* (2001).

2.2.7.3 Microarray processing and analysis

Global transcriptional profiling was performed using the Affymetrix Barley1 GeneChip (Affymetrix, Santa Clara, CA, USA). Samples were collected, and RNA was extracted and prepared as described above. RNA quality assessment, cRNA preparation and Affymetrix GeneChip hybridisations were carried out by Cogenics (NC, USA). The standard Affymetrix GeneChip protocol (Expression S2 manual available at http://media.affymetrix.com) was used to prepare biotinylated cRNA. Briefly, RNA quantity was determined by spectrophotometry and size distribution was assessed using an Agilent 2100 Bioanalyzer RNA LabChip (Agilent, Santa Clara, CA, USA). The two-cycle target labelling method was used. 50 ng of total RNA from each sample (with poly A spikes for labelling control) was converted to double-stranded cDNA. This double-stranded cDNA was used as a template to transcribe unlabelled RNA using T7 RNA polymerase and Megascript kit (Ambion). The GeneChip Sample Cleanup Module (Affymetrix) was used to purify the transcribed cRNA produced; the cRNA was then used as a template for a second round of amplification. Round 2 first-strand cDNA was synthesised using random primers; and subsequently annealed to Oligo dT-T7 primer to generate round 2 second-strand cDNA.

After second-strand synthesis, the cDNA was purified with the GeneChip Sample Cleanup Module (Affymetrix), and was then used to generate multiple copies of biotinylated cRNA by *in vitro* transcription (using the GeneChip 3'-Amplification Reagent Kit for IVT Labeling (Affymetrix)). The 260/280 ratio and yield of each of the cRNAs were in accordance with Affymetrix guidelines. For each sample, ten µg of biotinylated cRNA (spiked with standard hybridisation controls bioB, bioC, bioD and cre) was hybridized to an Affymetrix Barley1 GeneChip (16 hours at 45 ˚C). Subsequently, all arrays were washed and stained in an Affymetrix GeneChip Fluidics Station. Scanning of the stained arrays was performed with the Affymetrix GeneChip Scanner 3000. Quality check and data analysis were carried out using Affymetrix GeneChip Operating Software (GCOS) and Expression Console. All 12 arrays passed Affymetrix and Cogenics internal quality control metrics.

Data analysis

GeneChip data analysis was performed by Dr Rene Dreos, John Innes Centre. Quality assessment of array data was made using Affymetrix QA metrics, and by exploratory examination during data pre-processing. Data were normalised using Bioconductor software's Robust Multiarray Average measure (RMA) (Irizarry *et al.*, 2003). Subsequent analysis was performed using the Limma package. Mean signal intensity was calculated from the three biological replicates per treatment, and compared to the equivalent value from the relevant control samples. Differentially expressed probe sets were identified using a moderated t-statistic with a multiple testing correction applied (false discovery rate; Benjamini & Hochberg, 1995). Probe sets with a fold change of >2 relative to the control and a (moderated t-statistic of) $p < 0.05$ were considered differentially expressed.

2.2.7.4 Vector construction and plasmid manipulation

Expression vectors for plant transformation were created using the Gateway system (Invitrogen). Full length cDNA's (*RICE A* and *RICE B*) and the *DIR1* CDS were cloned into pENTR^{TM}1A by restriction digest and ligation. pME18S-FL3 containing FL-cDNA AK105204 or AK062503 (*RICE A* and *RICE B* respectively) was digested with Xho1 producing a fragment that was extracted from an agarose gel (Qiagen Gel Extraction kit), and ligated into pENTR^{TM}1A between the Sal1 and Xho1 sites. A restriction digest of plasmid 'A76' containing the *DIR1* CDS was performed with enzymes Xho1 and Spe1 and the resulting fragment extracted from a gel and ligated into the Sal1 and Xba1 restriction sites of pENTR^{TM}1A. The LR reaction in which entry vectors and destination vectors are recombined in a site-specific reaction was performed according to manufacturer's instructions with destination vectors pBract 214 (barley constructs, http://www.bract.org/bract.html) and pMDC32 (*Arabidopsis* constructs, Curtis & Grossniklaus (2003)). Entry, destination and expression vectors are shown in Figure 2.1. Plasmids were subsequently transformed independently into DH5α. Insert orientation was subsequently checked by restriction digest or PCR, and insert DNA sequence was verified by sequencing in both entry and expression vectors. Primer sequences used are given in Table 2.4 (b).

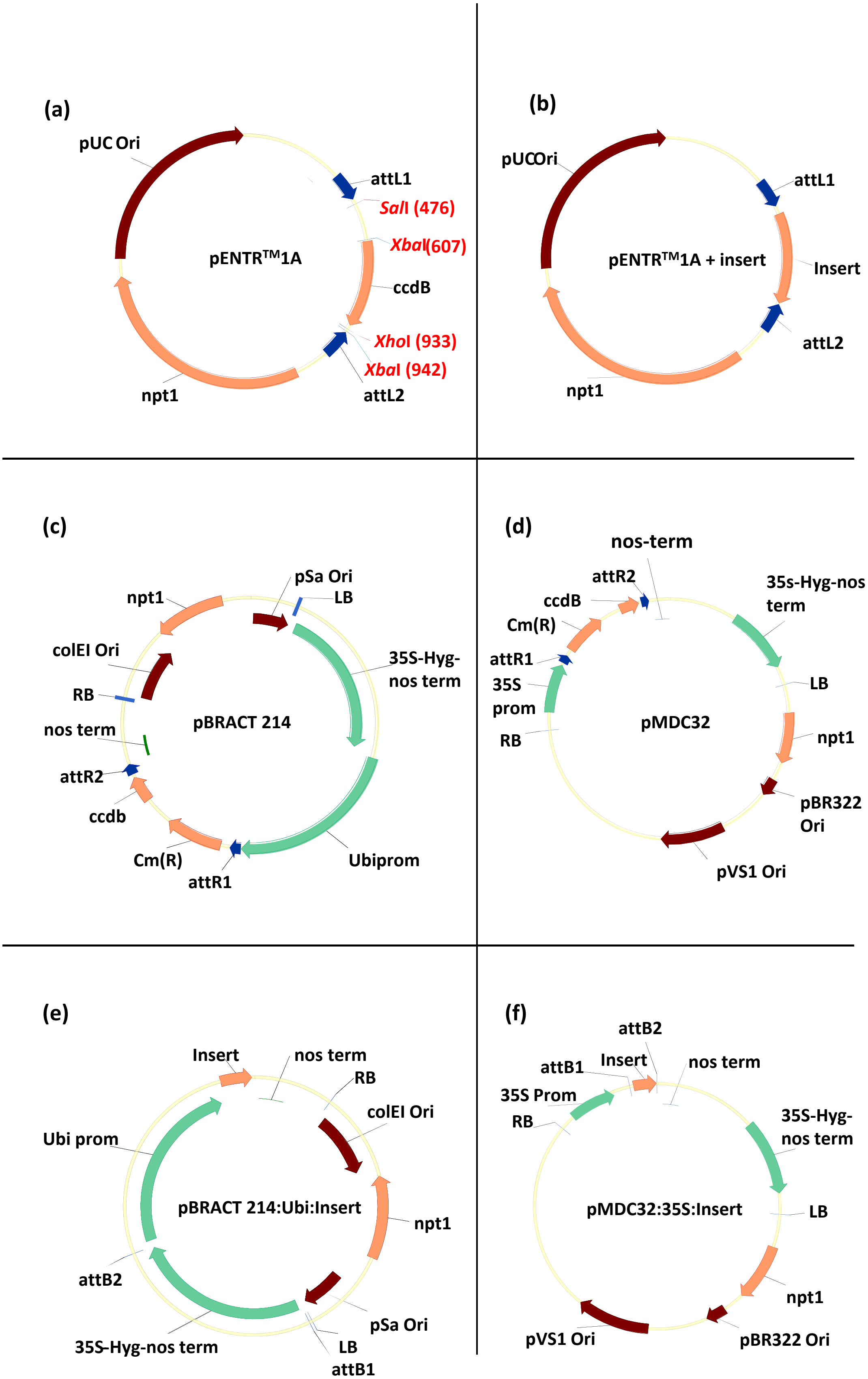
Restriction Digests

DNA restriction digests were prepared in a 20 µL reaction, with enzyme and buffer concentrations as manufacturer's instructions. Reactions were performed at 37 °C or room temperature as manufacturer's instructions.

Gel extraction

Products were run on a 1 % agarose gel, seperated alongside DNA ladder and visualised by Ethidium bromide staining under UV. The desired bands were cut from the gel using a razor blade,

Figure 2.1 Construction of expression vectors. (a) Entry vector pENTR^{TM}1A (b) Entry vector pENTR^{TM}1A with insert (*DIR1* CDS / *RICE A*/ *RICE B*) (c) Destination vector pBract 214 (d) Destination vector pMDC32 (e) Expression vector pBract 214 with insert (f) Expression vector pMDC32 with insert. The pBract backbone is based on pGreen and carries a kanamycin selectable marker ('npt1') (Hellens *et al.* (2000)). The T-DNA contains a hygromycin selectable marker ('Hyg', *hpt* gene) under the control of a CaMV double 35S promoter and a nopaline synthase transcriptional terminator (nos term), and a maize Ubiquitin promoter ('Ubi promoter'). A chloramphenicol gene ('Cm(R)', selectable marker) and the ccdB gene (cytotoxic in DH5α) are found in the Gateway cassette between the recombination sites attR1 and attR2. During site-specific recombination with pENTR^{TM}1A (the LR reaction), these sites recombine with attL1 and attL2 to produce attB sites in the Expression vector. For full details of pBract vectors see http://www.bract.org/bract.html. pMDC32 is based on pCambia. The T-DNA contains the same elements as pBract 214, except expression of the Gateway cassette / insert is under the control of the CaMV double 35S promoter. For full details of pMCD32 see Curtis & Grossniklaus (2003). Ribosomal RNA operon T1 terminator regions (rrnBT1/2) and several origins of replication ('Ori') are also indicated on vector maps. Vector maps produced using VectorNTI (Invitrogen).


(a)
pUC Ori
attL1
SalI (476)
XbaI(607)
pENTR™1A
ccdB
XhoI (933)
XbaI (942)
npt1
attL2
(b)
pUCOri
attL1
pENTR™1A + insert
Insert
attL2
npt1
(c)
pSa Ori
LB
npt1
colEI Ori
35S-Hyg-
nos term
RB
pBRACT 214
nos term
attR2
ccdb
Cm(R)
attR1
Ubiprom
(d)
nos-term
attR2
35s-Hyg-nos
term
ccdB
Cm(R)
attR1
LB
35S
prom
pMDC32
RB
npt1
pBR322
Ori
pVS1 Ori
(e)
Insert
nos term
RB
colEI Ori
Ubi prom
pBRACT 214:Ubi:Insert
npt1
attB2
pSa Ori
35S-Hyg-nos term
LB
attB1
(f)
attB2
attB1
Insert
nos term
35S Prom
RB
35S-Hyg-
nos term
pMDC32:35S:Insert
LB
npt1
pVS1 Ori
pBR322 Ori

DNA was then extracted using a QIAquick Gel Extraction kit (Qiagen) according to the manufacturer's instructions.

Ligation of DNA fragments

Ligations were performed in a 3:1 insert: vector molar ratio in a 10 µL reaction. T4 DNA ligase (Roche) was used according to manufacturer's instructions.

2.2.7.5 Transformation of bacterial cells

Heat shock transformation of *E. coli*

Competent DH5α cells (50 µL) were thawed on ice and 10 ng of plasmid added. Cells and plasmid were incubated on ice for 20 minutes. Cells were then placed at 42 °C for 45 seconds to induce uptake of DNA, before immediately being placed back on ice. 500 µL SOC was added and cells were incubated at 37 °C with shaking for 1 hr. 10 – 100 µL of bacterial suspension was then spread onto LB-G agar plates containing the appropriate selection (kanamycin at 50 µg mL^{-1}; chloramphenicol at 30 µg mL^{-1}; ampicillin at 50 µg mL^{-1}). Plates were incubated overnight at 37 °C.

Electroporation of *E. coli*

DNA (2-10 ng) was added to 50 µL electrocompetent cells thawed on ice. Mixture was then transferred into a 2 mm electroporation cuvette pre-chilled on ice. Cuvette was placed into an electroporator (BioRad Gene Pulser (BioRad, Hertfordshire, UK)) and cells pulsed at 2.5 kV (400 ohms, 25 µFd). Cells were then added to 0.5 mL of SOC and shaken at 37 °C for 2 hours. Suspension (100 µL) was then spread onto LB-G agar plates containing the appropriate selection, and plates were incubated overnight at 37 °C.

Transformation of *Agrobacterium tumefaciens*

Transformation of *Agrobacterium* was performed as for electroporation of *E. coli*, with the exception that cells were transferred to 2 mL L broth and shaken at room temperature for 2-3 hrs after pulsing. 10-100 µL of this suspension was then spread on L agar (with rifampicin for *Agrobacterium* selection (50 µg mL^{-1}) and appropriate selection for plasmid). Plates were incubated for 1-2 days at 28 °C.

2.2.8 Plant transformation methods

2.2.8.1 *Arabidopsis* floral dip method

Arabidopsis was transformed according to Clough & Bent (1998). Plants to be transformed were transferred from a short day CER to glasshouse conditions shortly after bolting. First bolts were clipped to encourage multiple bolts. Plants were transformed at the immature flower cluster stage. 10 mL L broth (50 µg mL^{-1} rifampicin, 50 µg mL^{-1} kanamcyin) was inoculated with *Agrobacterium* containing the plasmid of interest and grown overnight with shaking at 28 °C. L broth (500 mL, 50 µg mL^{-1} rifampicin, 50 µg mL^{-1} kanamcyin) was inoculated with 3 mL of the overnight culture and grown overnight with shaking at 28 °C. Cultures were centrifuged at 7000 rpm for 20 mins to pellet *Agrobacterium* cells. Cells were resuspended in 5 % sucrose solution containing 0.05 % Silwet L-77 as surfactant. Plants were inverted and flower heads submerged for 10 seconds with agitation. Plants were then placed into clear plastic bags away from direct light in the lab for 24 hrs, before being returned to glasshouse conditions to set seed.

Selection of transformants

Seeds collected from floral-dipped plants were sterilised as described in Section 2.2.1 and sown onto the surface of MS 0.8 % plates containing Timentin (Ticarcillin/ Clavulanic Acid (Duchefa) (250 µg mL^{-1}) and hygromycin (25 µg mL^{-1}). Hygromycin resistant seedlings could be identified after approximately 2 weeks as those that had developed beyond the cotyledon leaf stage, susceptible seedlings appeared yellow and stunted. Hygromycin resistant seedlings were transferred onto soil and grown as described in Section 2.2.1.

2.2.8.2 Barley transformation

Barley transformation was performed as described by Bartlett *et al.* (2008). Briefly, immature embryos were isolated from immature Golden Promise spikes, placed on Barley Callus Induction (BCI) media and inoculated with *Agrobacterium* suspension. Excess suspension was removed before embryos were transferred to a fresh BCI plate. Embryos and *Agrobacterium* were co-cultivated in the dark for 3 days at 23- 24 °C. Hygromycin-resistant transformants were then selected by transferring embryos to BCI plates with 50 mg L^{-1} hygromycin and 160 mg L^{-1} Timentin (Duchefa). During this time, embryos were transferred to fresh plates every 2 weeks. After 4- 6 weeks, embryos were transferred to transition media, and kept in low light conditions. Two weeks later, embryo derived callus was transferred to regeneration media (with selection as BCI), with full light. Regenerated shoots were transferred to glass culture tubes containing BCI media (with selection as above, without Dicamba or growth regulators). Once a root system had developed, seedlings were transferred to soil as described in Section 2.2.1. Fifty embryos per construct were inoculated with *Agrobacterium*, in three independent transformation experiments.

Estimation of copy number in T_0 seedlings was performed by iDNA Genetics (Norwich, UK), by quantitative PCR (qPCR) of the 35S promoter sequence. Primers and a TaqMan^{TM} probe were designed to the 35S promoter (p35S) of the transformation construct, using Applied Biosystems software Primer Express, with the TaqMan probe and Primer design module. The *Constans-2* (*CO2*) gene (AF490469) was used as an internal positive control against which the 35S amplification signal was normalised. Primer and probe sequences for p35S and *CO2* are given in Table 2.5. The p35S and *CO2* gene were assayed in multiplex, in duplicate, using ABGene AbSolute 2 x qPCR Rox Mix in an Applied Biosystems ABI7900. 5 µL of 5 ng µL^{-1} DNA was used per sample, in a 20 µL reaction (plus 3 µL water; 10 µL 2 x qPCR mix; and 2 µL 10 x primer and probe mix). The detectors used were FAM-TAMRA and VIC-TAMRA with Rox internal passive reference. No 9600 emulation was used. The PCR cycling conditions were: 50 °C 2 mins, 95 °C 10 minutes, 40 cycles of 95 °C 15 s, 60 °C 60 s. PCR efficiencies were calculated from a dilution series of a positive control line (known to contain the 35S promoter). Efficiencies of p35S and *CO2* were determined to be equivalent and close to 100 %. As such, it was appropriate for the delta Ct (Ct p35S minus Ct IPC) to be used to determine copy number/ zygosity.

Hygromycin leaf bleaching assay, and T_1 zygosity determination.

As a first step towards determining the zygosity of T_1 seedlings, a leaf bleaching assay was performed by Ruth Maccormack. The assay was based on the method of Wang & Waterhouse (1997), and qualitatively identifies seedlings sensitive to hygromycin, which bleach white in the presence of the antibiotic. Transgenic lines tested were those identified as single (or low) copy by qPCR, and 20 T_1 individuals from each independent T_0 line were tested. Briefly, leaf tips were cut from T_1 seedlings germinated on damp filter paper for 7 days. The exposed surface of cut leaf tips were embedded into solid media, made up of 4.4 mg mL^{-1} Murashige & Skoog salts (adjusted to pH 5.7), 0.5 µg µL^{-1} BAP and 8 gL^{-1} agarose, plus hygromycin at 75 µg mL^{-1}. Plates were kept in a CER (conditions as described for barley transgenics, Section 2.2.1). Leaf bleaching was assessed by eye 14 days later, with bleached leaves presumed to be null segregants sensitive to hygromycin. Seedlings from which leaf tips were cut were transferred to soil (glasshouse conditions) and genomic DNA was prepared from all positive (non-bleached, hygromycin resistant) and 2 negative (bleached, null-segregant) individuals per line. qPCR was then performed as described above for T_1 copy number determination, in order to confirm zygosity (also see Figure 5.7).

2.2.9 Bioinformatics methods

DNA sequences were aligned using ContigExpress, from Vector NTI Suite 10 (Invitrogen). Tools and databases used are as described in text, or in Table 2.6.

2.2.10 Statistical analysis

Data were analysed using Excel (Microsoft Office 2007), or Genstat^{TM} v10 (VSN International, UK).

Tool / Database	Website	Reference
BLAST		Altschul *et al*. (1990)
NCBI (sequence database)	http://blast.ncbi.nlm.nih.gov/Blast.cgi	
MUSCLE sequence alignment	http://www.ebi.ac.uk/Tools/webservices/services/muscle	Edgar *et al*. (2004)
GeneDoc	http://www.nrbsc.org/gfx/genedoc/	Nicolas *et al*. (1997)
GreenPhyl Orthologs Search Tool	http://greenphyl.cirad.fr/cgi-bin/greenphyl.cgi	Conte *et al*. (2008)
Genevestigator 3.0	https://www.genevestigator.com/gv/index.jsp	Hruz *et al*. (2008)
Needle	http://www.ebi.ac.uk/emboss/align/	
The Institute for Genomic Research (TIGR) Rice database	http://rice.plantbiology.msu.edu/	
Pfam	http://www.sanger.ac.uk/Software/Pfam/	Finn *et al*. (2008)
SignalP (3.0)	http://www.cbs.dtu.dk/services/SignalP/	Bendsten *et al*. (2004)
ExPasy pI/MW prediction	http://www.expasy.ch/tools/pi_tool.html	Gasteiger *et al*. (2005)
Phobius	http://phobius.sbc.su.se/	Kall *et al*. (2007)

Table 2.6 Bioinformatics tools and databases used.

Chapter 3: Assay development: inducing acquired resistance in barley

3.1 Aim

The research presented in this chapter was undertaken with the aim of developing a *Pseudomonas*-based assay designed to induce acquired resistance (AR) in barley. The focus was on developing a tractable assay, comparable to the previously-characterised *Arabidopsis-Pseudomonas syringae* SAR induction pathosystem.

3.2 Introduction

The characterisation of SAR has primarily focussed on defence responses in secondary leaves (Hammerschmidt, 1999, Maleck *et al.*, 2000, Truman *et al.*, 2007, Uknes *et al.*, 1992, Ward *et al.*, 1991), molecular components ((Dong, 2004, Maldonado *et al.*, 2002, Mishina & Zeier, 2006, Nandi *et al.*, 2004, Shimono *et al.*, 2007, Wiermer *et al.*, 2005)), and the nature of the systemic signals ((Chaturvedi *et al.*, 2008, Park *et al.*, 2007, Truman *et al.*, 2007, Vlot *et al.*, 2008a, Vernooij *et al.*, 1994). Less attention has been paid to understanding which elements of the local interaction are important in triggering the systemic response. In the best characterised SAR system, *Arabidopsis* - *Pseudomonas syringae*, SAR is typically induced by infiltrating one leaf of *Arabidopsis* seedlings with an avirulent *Pseudomonas syringae* isolate (usually pathovar *tomato* or *maculicola*). Two days later, challenge inoculation of secondary leaves with a virulent isolate results in symptoms and bacterial growth resembling that of an avirulent interaction (Cameron *et al.*, 1994). Classically, SAR was thought to be induced by a necrotising interaction, either avirulent or compatible ((Cameron *et al.*, 1994, Durrant & Dong, 2004, Sticher *et al.*, 1997)). However, recent work has demonstrated that SAR can be induced by a virulent, avirulent, or non-host interaction, or by PAMPs, even in the absence of macro-, or microscopic cell death (Liu *et al.*, 2010, Mishina & Zeier, 2007a, Mishina & Zeier, 2007b). SAR is induced more efficiently by a virulent isolate growing rapidly in *Arabidopsis* leaf tissue than by an avirulent isolate where defence responses are curtailed by an HR (Mishina & Zeier, 2007a). Furthermore, the strength of SAR induction is determined by the strength of local, active plant defence responses, which are maximal after infiltration with a low dose of virulent bacteria (Mishina & Zeier, 2007a). Inoculum density is critical in this, as different isolates induce varying strength of local defence at different inoculation densities. SAR induced by non-adapted strains, PTI, and R-gene mediated interactions utilise the same SA-dependent signalling pathway (Mishina & Zeier, 2007a, Liu et al., 2010). In contrast to the situation for SAR, HR in the infiltrated region (‘zone 1’) of tobacco leaves is needed for the development of LAR in 'zone 2' (a 5 mm zone surrounding the lesion). This suggests the near-immunity to challenge described in this region could be mediated by signalling distinct from that inducing SAR (Costet *et al.*, 1999).

As described in Section 1.5, studies of the localisation of acquired resistance responses, or of 'local interference', in barley have mainly utilised the barley-powdery mildew (*Blumeria graminis*) pathosystem. Experimentally, this usually involves applying spores of an 'inducer' isolate to a leaf, removing any resulting superficial fungal structures, then applying 'challenger' isolate spores. Removal of the inducer isolate (by rubbing with wet cotton balls (Cho & Smedegard-Peterson, 1986, Ouchi *et al.*, 1976, Thordal-Christensen & Smedegard-Peterson, 1988), micromanipulator ((Kunoh *et al.*, 1989), or cellulose actetate strips (Lyngkjaer & Carver, 1999)) allows differentiation between inducer and challenger, and precludes direct interference between isolates. Leaves are also usually secured horizontally on a surface and held in place by rubber bands or weights to facilitate spore attachment, while leaf areas to remain uninoculated are covered with paper (Cho & Smedegard-Peterson, 1986, Hwang & Heitefuss, 1982, Martinelli *et al.*, 1993, Thordal-Christensen & Smedegard-Peterson, 1988, Woolacott & Archer, 1984). Infection efficiency of the challenger is then scored, relative to the position of 'inducer' haustoria or papillae (Kunoh et al., 1988, Lyngkjaer & Carver, 1999, Ouchi *et al.*, 1976, Thordal-Christensen & Smedegard-Peterson, 1988, Woolacott & Archer, 1984). These tests led to the identification of 'induced accessibility', where an epidermal cell successfully penetrated by *Bgh* becomes more accessible to subsequent challenge during a second inoculation. Thus, the rate of penetration success increases from 67 % on first inoculation, to >90 % on second inoculation. 'Induced inaccessibility' has also been described, in which an unsuccessful penetration attempt protects attacked cells from subsequent challenges (Lyngkjaer & Carver, 1999). As discussed earlier (Section 1.5), these responses are strictly localised, or transferred only to adjacent cells (Lyngkjaer & Carver, 1999, Ouchi *et al.*, 1976) approximately 25 hours after 'inducer' penetration attempts (Kunoh *et al.*, 1988). As such, there are key differences in localisation and timing between induced inaccessibility in barley and the development of acquired resistance responses in *Arabidopsis*, where the response develops in secondary leaves by 24-48 hours after exposure to the inducing pathogen (Cameron *et al.*, 1994).

The uncertainty surrounding the ability of powdery mildew to induce any kind of systemic AR response in barley (Collinge *et al.*, 2002, Kogel & Langen, 2005, Kunoh, 2002) or other species, as well as the relatively intractable experimental systems needed for these tests, call into question the suitability of this pathosystem for investigating LAR and SAR in barley. Other aspects of the interaction are also at odds with characterised SAR induction systems. Vallelian-Bindschedler *et* *al.* (1998) measured local accumulation of SA and SA conjugates in barley after inoculation with a virulent or non-host powdery mildew, or after infiltration with an isolate of *Pseudomonas syringae* pv. *syringae* (*Pss*).. Only *Pss* led to the local accumulation of SA and SA conjugates, although patterns of PR protein accumulation were remarkably similar (Vallelian-Bindschedler *et al.*, 1998). The absence of SA accumulation during the local barley-powdery mildew interaction was also noted by Hucklehoven *et al*. (1999). In tobacco, SA accumulates locally and systemically during SAR development, but accumulation of SA itself is essential only in secondary leaves for SAR to develop (Gaffney *et al.*, 1993, Vernooij *et al.*, 1994). In tobacco, it appears that local conversion of SA to mobile MeSA is needed for SAR to develop (Park *et al.*, 2007). The role of SA in induced resistance in cereals is poorly understood (Kogel & Langen, 2005), and the mechanisms by which SA induces SAR in different species may differ (Durrant & Dong, 2004). However, given the hormone's central role in SAR development, this lack of accumulation following powdery mildew inoculation could be significant. Together, these factors led me to consider the development of an alternative, more experimentally tractable assay for barley that would facilitate comparison with a previously characterised SAR system.

As noted, the best characterised SAR assay system is *Arabidopsis-Pseudomonas syringae*. The interaction of *Pseudomonas* (or any bacterial pathogen) with barley is not well characterised, and of course, the factors leading to the biological induction of SAR in barley may be entirely different to those leading to SAR in *Arabidopsis*, or tobacco. Nevertheless, there is strong case supporting the use of *Pseudomonas* as an 'inducer' of LAR and SAR in barley. *Pseudomonas syringae* induces SAR in *Arabidopsis*, tobacco and cucumber (Cameron *et al.*, 1994, Mur *et al.*, 1996, Smith *et al.*, 1991), showing it to be effective as an inducer across different species. In rice, *Pss* has been reported to induce systemic resistance to *Pyricularia oryzae* (anamorphic stage of *Magnaporthe oryzae*), although this has not been repeatable (Reimmann *et al.*, 1995). As described above, the work of Vallelian-Bindschedler *et al.* (1998) also strongly suggests *Pss* induces defence responses in barley cultivar Golden Promise. As such, the use of *Pseudomonas syringae* as an 'inducer' was investigated further in this chapter. A range of *Pseudomonas syringae* isolates were obtained from a collection held in The Sainsbury Laboratory (Personal Communication, Kee Sohn). These isolates were described by Hwang *et al.* (2005). In *Arabidopsis*, SAR is likely to be efficiently induced at a time-point where local defence responses are strong (Mishina & Zeier, 2007a). The interaction between barley cultivar Golden Promise and a range of these *Pseudomonas syringae* isolates was therefore characterised, in order to identify the isolate / inoculation density / time-point where local defence responses were strongest.

Environmental and developmental factors also affect the development of SAR and were taken into account in developing this assay. For example, SAR in *Arabidopsis* is light-dependent (Griebel & Zeier, 2008, Zeier *et al.*, 2004). SA-associated systemic defences require phytochrome photoperception, and thus, when primary inoculation takes place in the absence of light, SAR does not develop (Griebel & Zeier, 2008). Furthermore, the length of the light period during the early plant-pathogen interaction affects local HR, SA accumulation, *PR1* expression and disease resistance to *Pseudomonas* (Griebel & Zeier 2008), and as such the efficiency of SAR development (Mishina & Zeier, 2007a). Here, barley seedlings were inoculated in the light, and consistently returned to a lit growth cabinet for 5-6 hrs before the start of the dark period. In terms of development, both old and young leaves of *Arabidopsis* (and tobacco) can induce, and develop, SAR (Kiefer & Slusarenko, 2003, Zeier, 2005, Ross, 1961b). However, SAR is most efficiently induced, and established in young leaves (Zeier, 2005). Therefore, first leaves of barley seedlings were used here.

3.3 Results

3.3.1 *Pseudomonas syringae* isolates induce symptoms in Golden Promise

As noted above, it appears that HR or a necrotising interaction are not necessary for the induction of SAR, but that the efficiency of SAR induction correlates with the induction of local defence responses (Mishina & Zeier, 2007a). As such, the aim here was to identify an isolate inducing strong, active, local defence responses, rather than to precisely define the nature of the interaction. As a preliminary screen, isolates of *Pseudomonas syringae* pv *syringae* (*Pss*)*, japonica* (*Psj*) or *tomato* (*Pst*) were infiltrated into first leaves of Golden Promise seedlings, and macroscopic symptoms recorded (Figure 3.1). In *Arabidopsis*, virulent interactions are usually characterised by the development of a grey-brown lesion, with marginal or spreading chlorosis appearing by 48-72 hpi. Avirulent (R-gene mediated) interactions either do not develop macroscopic symptoms, or develop mild chlorosis or necrosis (Whalen *et al.*, 1991). Non-host isolates usually fail to induce any symptoms (Katagiri, 2002, Mishina & Zeier, 2007a, Whalen *et al*., 1991). Symptom development is however dependent on dose, above an inoculation density of 5 x 10^7 CFU mL^{-1}, avirulent bacteria often cause necrosis and chlorosis. Here, macroscopic symptoms could be seen on all leaves infiltrated with bacteria by 72 hpi, either a mild chlorosis, or a combination of necrosis and chlorosis (Figure 3.1). Isolates representing a range of symptoms were selected for further investigation. These were: PS86, a *Pss* isolate from wheat; PS13, a *Psj*

Collection Identifier	Pathovar	Strain Identifier	Host	Response
PS44	syringae	B728A	Snap bean	Chlorosis (1)
PS57	syringae	NCPPB 281	Lilac	Chlorosis (1)
PS66	syringae	FTRS W6601	Japanese apricot	Chlorosis (1)
PS88	syringae	PSC1B	Corn	Chlorosis (1)
PS89	syringae	B76	Tomato	Chlorosis (1)
PS104	syringae	A2	Ornamental pear	Chlorosis (1)
PS109	syringae	1212R	Pea	Chlorosis (1)
PS4	syringae	LOB2-1	Lilac	Chlorosis (2)
PS65	syringae	L 177	Lilac	Chlorosis (2)
PS67	syringae	FTRS W7835	Japanese apricot	Chlorosis (2)
PS86	syringae	B64	Wheat	Necrosis & chlorosis
PS13*	japonica	M301072	Barley	Necrosis & chlorosis
PstavrRpm1	tomato		Tomato	Chlorosis (2)

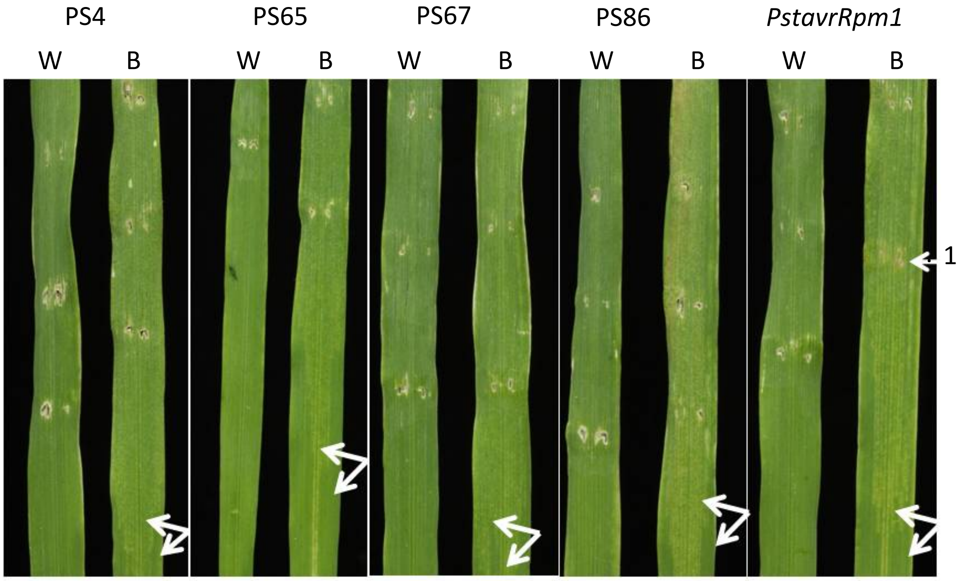


Figure 3.1 Screen of *Pseudomonas syringae* isolates on Golden Promise. First leaves of 14 day old Golden Promise seedlings were infiltrated with one isolate (OD_{600} 0.002), and macroscopic symptoms recorded 72 hours later. Experiment performed under glasshouse conditions. **(a) Macroscopic symptoms of all isolates tested**. 'Collection Identifier' indicates identifier used in The Sainsbury Laboratory collection. 'Strain Identifier' indicates identifier used by Hwang *et al.* (2005). Chlorosis (1) indicates mild chlorosis, (2) indicates more defined chlorosis. PS13* was tested separately. *PstavrRpm1* was also tested, but is not part of the Hwang *et al.* (2005) collection. **(b) Macroscopic symptoms from selected isolates, 10 dpi**. 'W' indicates water-infiltrated control, 'B' indicates leaf infiltrated with bacterial isolate at OD_{600} 0.002. Arrows highlight the symptoms at the limit of infiltrated leaf area.

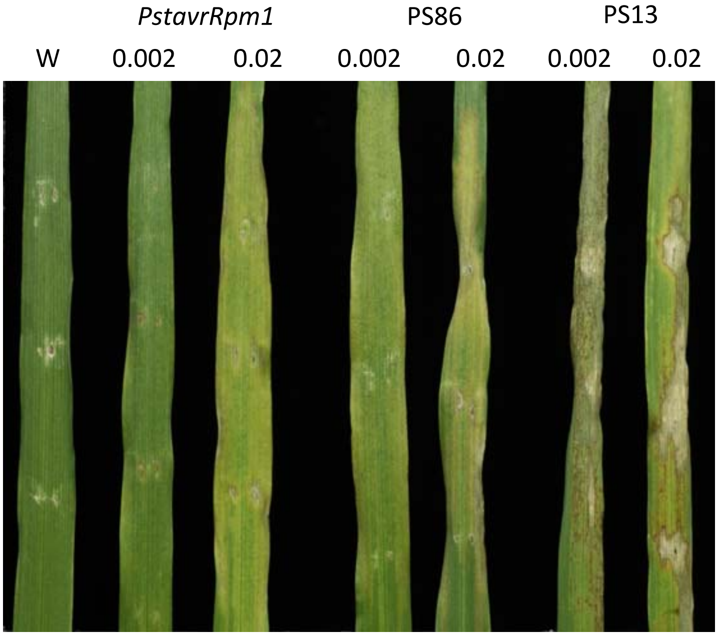
isolate from barley (both Hwang *et al*. (2005)); and *PstavrRpm1*, a *Pst* isolate (DC3000) expressing avirulence gene *avrRpm1* (on plasmid pVSP61). The latter is commonly used to induce SAR in *Arabidopsis*. Further tests of these isolates took place under growth chamber conditions. Seedlings were grown in a CE growth chamber at optimal conditions for barley growth, until post-infiltration when seedlings were placed at 23 ˚C (light regime unchanged). This provided optimal conditions for bacterial growth. Under these conditions, macroscopic symptoms were also seen (Figure 3.2 (a)-(b)). PS13 and PS86 induced virulent-type symptoms, whilst symptoms induced by *PstavrRpm1* were milder, but still macroscopically visible, especially at higher inoculation densities (Figure 3.2 (a)-(b)). As noted, *PstavrRpm1* is isogenic to *Pst* DC3000, but expresses the avrRpm1 avirulence protein. Symptoms following *Pst* DC3000 infiltration appeared to differ from those induced by *PstavrRpm1*, with more tissue collapse at 48 hpi, and more extensive, dry necrosis developing by 96 hpi. Furthermore, *Pst* DC3000 *hrcC*- (deficient in the type III secretion system) infiltration resulted in no macroscopic symptoms (Figure 3.2 (b)). As such, the interaction between *PstavrRpm1* and Golden Promise does appear to be mediated by one or more secreted factors, and may be mediated by avrRpm1.

3.3.2 Bacterial growth in Golden Promise

To further investigate the compatibility of these isolates with Golden Promise, their growth *in planta* was studied (Figure 3.2 (c)-(e)). During a virulent interaction with *Arabidopsis*, *Pst* DC3000 typically multiplies 10^3 fold within 24 hrs (after infiltration at OD_{600} 0.0002) (Dong *et al.*, 1991). Here, first leaves of Golden Promise seedlings were infiltrated at OD_{600} 0.002, 0.02 and 0.2, which are closer to the concentration previously shown to induce defence in barley (1 x 10^9 CFU mL^{-1} (equivalent to OD_{600} 2), Vallelian Bindschedler *et al*. (1998)). PS86 and PS13 grow rapidly in the leaf tissue at all inoculation densities tested. In contrast to the situation for PS13 and PS86, *PstavrRpm1* does not grow *in planta*. At all three inoculation densities tested, *PstavrRpm1* numbers drop significantly at 48 dpi. In this test, after infiltration at OD_{600} 0.02 (Figure 3.2 (d)), no *PstavrRpm1* colonies were recovered after 24 hpi. This indicates that bacterial number had fallen below that recoverable using this assay. After inoculation at OD_{600} 0.002 and 0.2, *PstavrRpm1* growth appears to recover between 48 and 72 hpi. This coincides with tissue collapse, and could indicate a shift from biotrophy to necrotrophy, as *Pseudomonas syringae* is considered a hemibiotroph (Glazebrook, 2005). In *Arabidopsis*, an avirulent interaction with *Pseudomonas* typically results in reduced bacterial growth compared to a virulent isolate, but bacterial number does still increase over time (Mishina & Zeier, 2007b). The rapid decline in initial *PstavrRpm1* numbers seen here is more consistent with a non-host interaction in *Arabidopsis* (Mishina & Zeier,

Figure 3.2 Symptoms and *in planta* growth of isolates after infiltration of Golden Promise with selected *Pseudomonas syringae* isolates. (a)-(b) Representative symptoms resulting from infiltration at the indicated inoculation density. Leaves were photographed at the time-point indicated for each photograph. **(c)-(e) Growth of isolates *in planta*.** Leaf discs were sampled from first leaves of 17 day old seedlings infiltrated with PS13, PS86, *Pst* DC3000 *hrcC*- or *PstavrRpm1* at OD_{600} 0.002 (c), 0.02 (d) and 0.2 (e), and CFU assayed. In (e), PS86 was infiltrated at OD_{600} 0.02 as a positive control. Each data point represents the mean of 3-4 leaf discs, each from a separate leaf (±SE). Where *PstavrRpm1* line is discontinued in (d), no further CFU were recovered at the subsequent time-points. Experiments performed under growth cabinet conditions. Each graph indicates an independent experiment. It should be noted that symptoms resulting from the infiltrations in (c) (data not shown) were slightly weaker than those seen in (b).

Figure 3.2 (a) 72 hpi



(b) 48 hpi, 96 hpi, OD_{600} 0.2 (PS86-0.02)

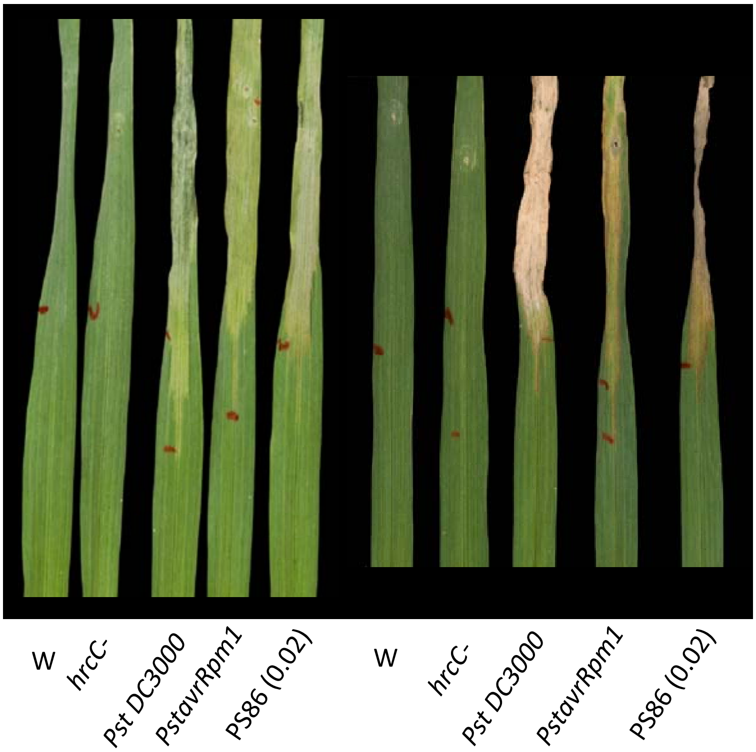
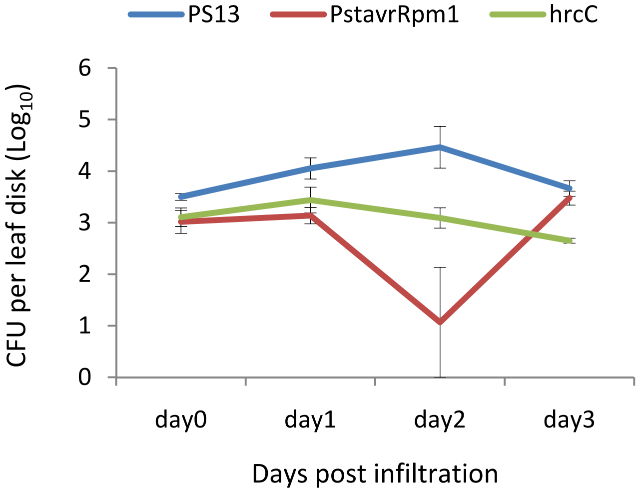
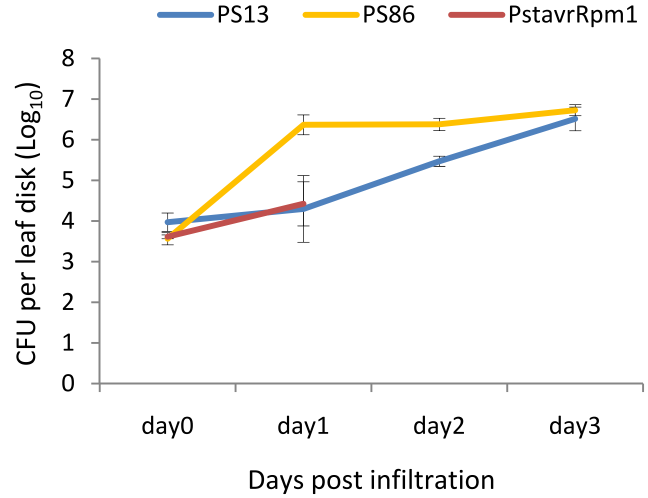


Figure 3.2 continued

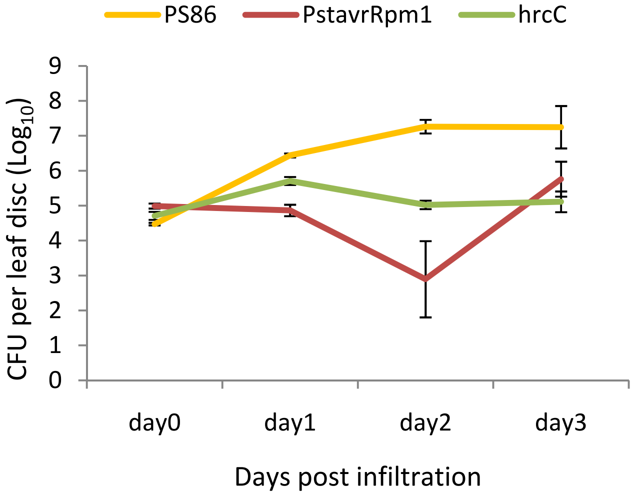
(c) OD$_{600}$ 0.002



(d) OD$_{600}$ 0.02



(e) OD$_{600}$ 0.2
(PS86-0.02)



2007b). However, the response of *Pst* DC3000 *hrcC-*, which grows slightly before dropping to its original level (Figure 3.2 (a) and (c)) does indicate the response to *PstavrRpm1* is effector-mediated. The reduction in *Pst* DC3000 *hrcC-* between 24 and 48 hpi is likely to be due to PTI.

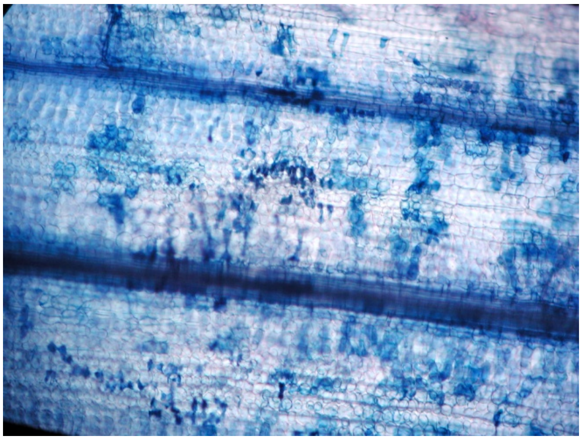
3.3.3 Microscopic cell death

The nature of the cell death resulting from the Golden Promise- *PstavrRpm1*, and PS13 interactions was investigated further at the microscopic level by staining with trypan blue (specifically retained by dead cells (Keogh *et al.*, 1980). In interactions between *Arabidopsis* and avirulent *Pseudomonas syringae* isolates, rapid (6- 24 hpi) mesophyll cell collapse can be seen at the microscopic level (Bent, 1996, Soylu, 2006). In a virulent interaction, cells at this time-point do not show defence responses but later develop disease symptoms (Bent, 1996). Non-host strains of *Pseudomonas* appear to induce minimal (pv. *glycinea* (Mishina & Zeier, 2007a)), or no (*pv. phaseolicola* (Mishina & Zeier, 2007a)) microscopic HR-lesions. Here, at 72 hpi, *PstavrRpm1*-infiltrated tissue appeared to show cell death, while PS13 infiltrated tissue did not appear to develop these microscopic lesions (Figure 3.3). Although this test was not repeated, this does again suggest the interaction between *PstavrRpm1* and Golden Promise does involve hypersensitive cell death, whilst the necrosis seen after infiltration with PS13 appears to be disease-related.

3.3.4 Defence gene induction in Golden Promise varies with isolate, inoculation density, and time post-infiltration

As noted, it has been demonstrated in *Arabidopsis* that SAR develops most efficiently when local inoculation results in the strongest local defence response (Mishina & Zeier, 2007a). As such, the induction of local defence (as measured by PR gene induction) was compared between isolates, at a range of inoculation densities and over several time-points, with the aim of optimising local defence gene induction and identifying the most appropriate conditions for testing for translocated AR responses in barley. The choice of genes, inoculation densities and time-points was informed by the work of Vallelian-Bindschedler *et al*. (1998), as well as genes and conditions associated with defence against *Pseudomonas syringae* and SAR induction in *Arabidopsis* (Cameron et al., 1999, Dong et al., 1991, Mishina & Zeier, 2007a). Biomarker analysis using microarray database and meta-analysis program Genevestigator (Zimmermann *et al.*, 2008) indicated that *prx8* (AJ276227.1, encoding a peroxidase with similarity to *PR9*) and *PAL* are consistently highly induced in barley in response to pathogen attack (data not shown), and as

(a) *PstavrRpm1*



(b) PS13

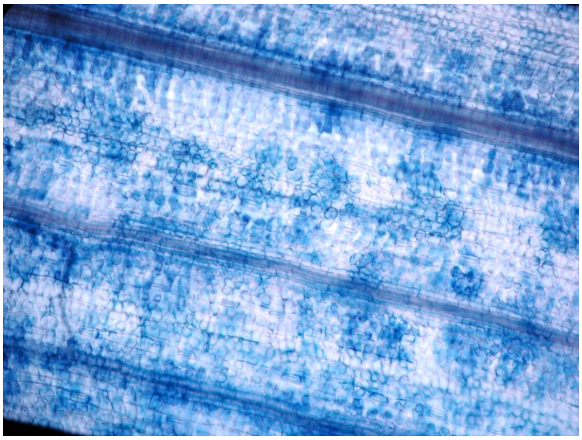


Figure 3.3. Light micrograph (x10 magnification) of cleared barley leaves stained with trypan blue**. (a)-(b)** 72 hpi with *PstAvrRpm1* and PS13 respectively, OD_{600} 0.02.

such these were also included. Firstly, the expression of *PR5* (thaumatin-like protein) (Bryngelsson & Gréen, 1989) and *PR9 (Prx8* (Gregersen *et al.*, 1997, Kerby & Somerville, 1989, Thordal-Christensen *et al.*, 1992) in Golden Promise was compared after infiltration with *PstavrRpm1*, PS13 or PS86 (Figure 3.4). Two inoculation densities (OD_{600} 0.02 and 0.2) were compared, and samples were taken 12 and 36 hrs post infiltration. Induction of *PR5* and *PR9* appeared to peak 12 hpi with *PstavrRpm1*. At the 36 hpi time-point, PS13 (OD_{600} 0.02) was associated with the strongest induction.

Given the differential symptoms after infiltration with PS13 at a lower inoculation density (Figure 3.2 (a)), the possibility that defence gene induction might differ at lower or higher inoculation densities with this isolate was investigated further (Figure 3.5). In this test, necrosis decreased in severity with 10-fold dilutions of inoculum density (Figure 3.5 (a)). Defence gene induction was tested 34 and 72 hpi; these later time-points were selected because higher bacterial titre resulting from bacterial growth within the leaf may lead to stronger defence induction at later time-points. In fact, expression of *prx8* and *PAL* peaked at the 34 hour time-point, with an inoculation density of OD_{600} 0.02 (Figure 3.5 (b)). When PS13 and *PstavrRpm1* were compared directly (Figure 3.4), defence gene expression resulting from infiltration of *PstavrRpm1* was higher. As such, responses to *PstavrRpm1* were investigated further.

Infiltration of Golden Promise leaves with *PstavrRpm1* resulted in induction of defence genes by 6 hpi (Figure 3.6). Induction of *PR1*, *prx8* and *PAL* appeared to peak at 12 hpi, and remained strong 24 hpi. Infiltration with OD_{600} 0.2 generally resulted in the strongest PR gene induction; where OD_{600} 1 resulted in greater induction it was generally more variable (Figure 3.6). At the peak of induction by *PstavrRpm1* (12 hpi, OD_{600} 0.2) *PAL* induction reached around 100-fold, in comparison to less than 20-fold at the peak of induction with *PS13* (34 hpi, OD_{600} 0.02). Based on these data, infiltration with *PstavrRpm1* at an OD_{600} of 0.2 was selected as the most appropriate inducer inoculation for testing AR responses in barley.

3.3.5 *PstavrRpm1* is localised to the area of infiltration

In order to accurately test the translocation of defence responses, it is crucial that the inducer inoculum remains strictly localised in the infiltrated leaf region. During local infiltration, the limit of the inoculum could be seen clearly. Additionally, no *PstavrRpm1* could be recovered from the adjacent leaf region 0, 6 or 24 hours post local infiltration (Figure 3.7 (a)-(b)). The sensitivity of the assay was sufficient to recover *PstavrRpm1* (15 CFU per leaf disk) in leaf tissue infiltrated at OD_{600} 0.2 x 10^{-4} (OD_{600} 0.00002) (Figure 3.7 (c)). 24 hours post infiltration at this density, no

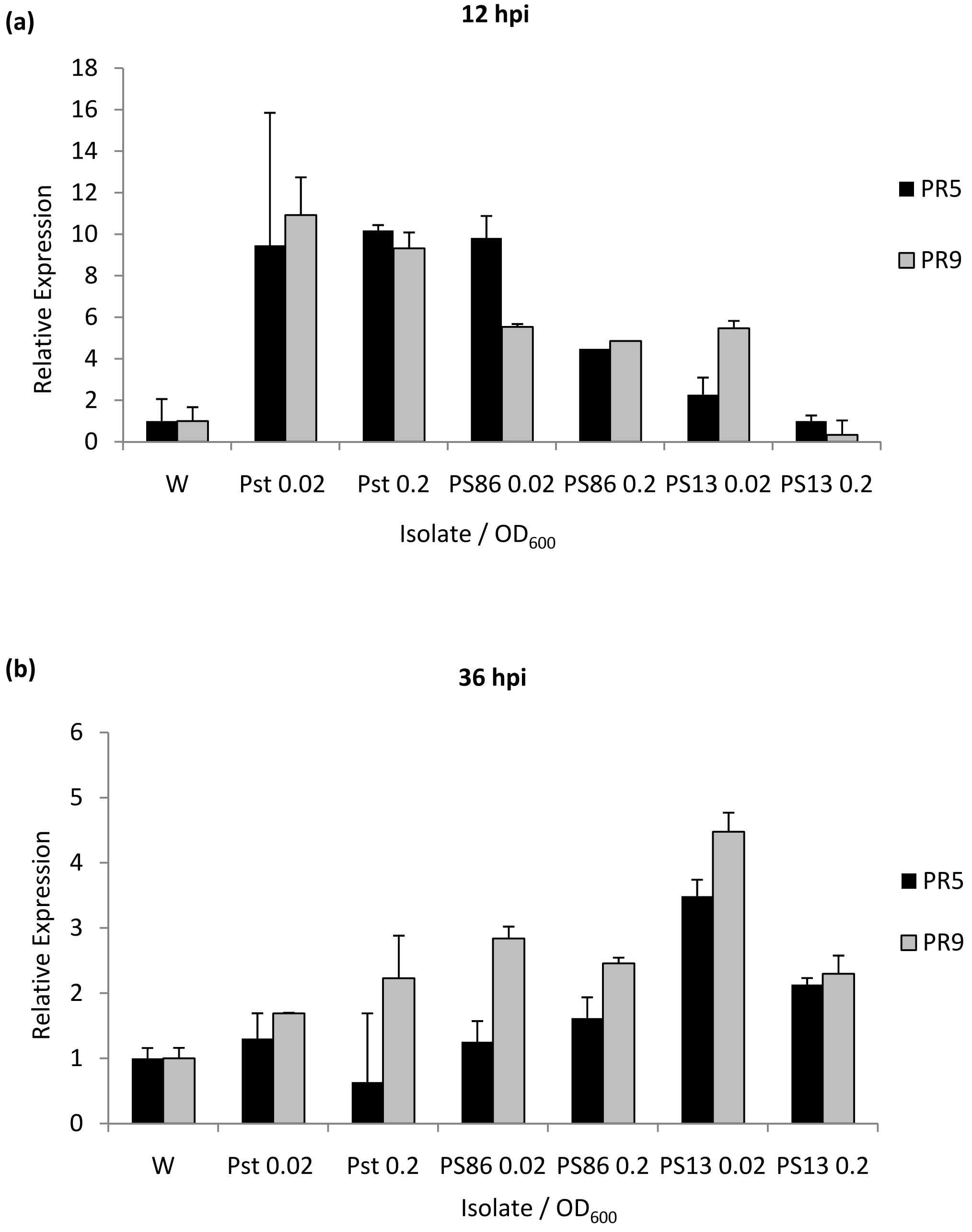
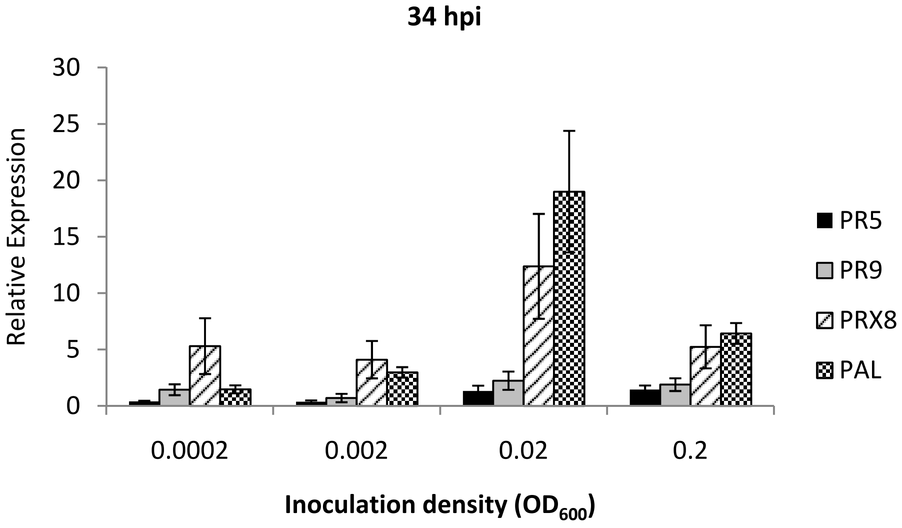


Figure 3.4 Induction of *PR5* and *PR9* 12 hours (a) and 36 hours (b) post infiltration with *PstavrRpm1* (Pst), PS86 or PS13 at OD_{600} of 0.02 or 0.2. Expression shown relative to water infiltrated control, set to 1. Bars represent mean values from 2 biological replicates ±SD, each made up of 3 pooled leaves. Expression levels normalised to *α-tubulin 2*.

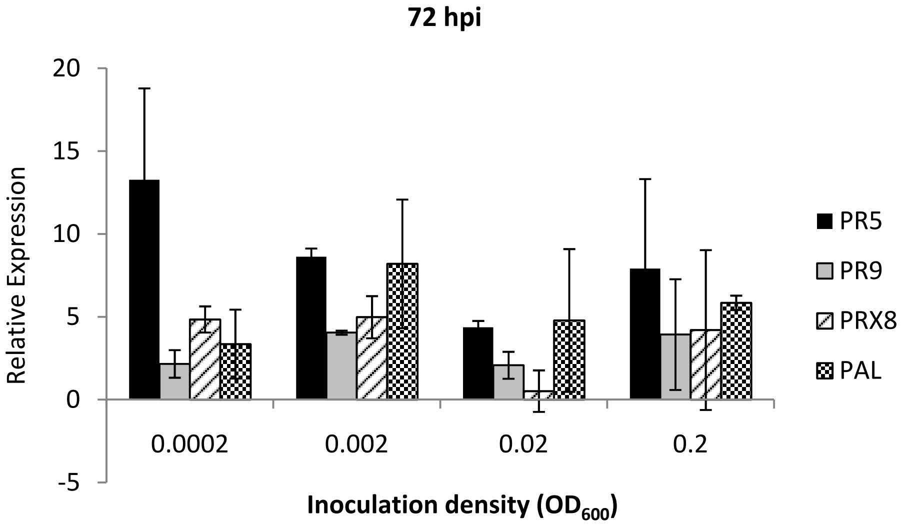
Figure 3.5 PR gene induction by PS13 at a range of inoculation densities. (a) Symptoms resulting from infiltration of first leaf of 20 day old Golden Promise seedlings with PS13 at 10-fold dilutions from OD_{600} 0.2 to 0.0002. Photographed at 72 hpi. **(b)-(c) Expression of PR and defence-related genes 34 (b) and 72 (c) hpi.** Expression shown relative to a water infiltrated control, set to 1. Values are means of 3 biological replicates, each made up of pooled samples from 3 seedlings (±SD). Transcript levels normalised using *α-tubulin 2*.

Figure 3.5 (a)

(b)


34 hpi

(c)


72 hpi

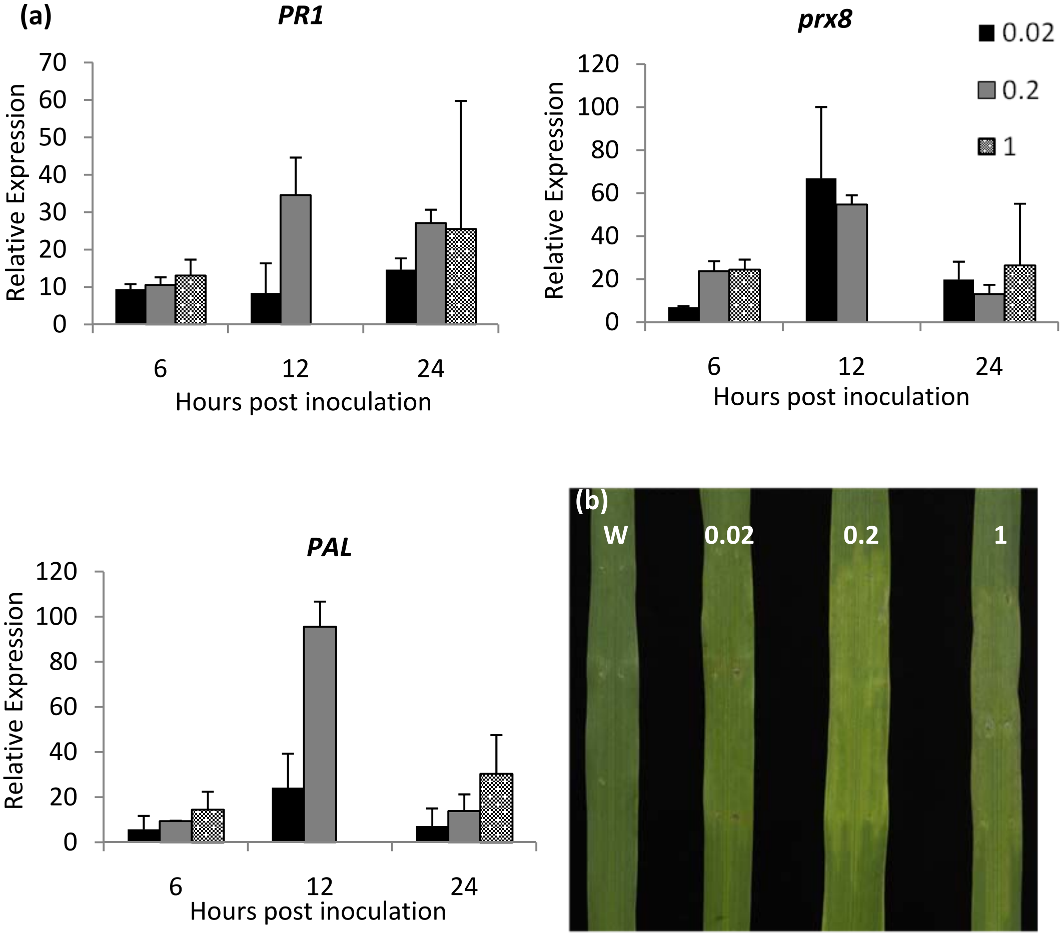


Figure 3.6 PR gene induction by *PstavrRpm1* at a range of inoculation densities. (a) Expression of *PR1*, *prx8* and *PAL*, 6, 12 and 24 hpi at 3 inoculation densities (OD_{600} 0.02, 0.2 and 1). Golden Promise seedlings 22 days old at inoculation. Expression calculated relative to a water infiltrated control, set to 1. Values are means of 3 biological replicates, each made up of pooled samples from 3 seedlings (±SD). Transcript levels normalised using *α-tubulin 2.* **(b) Representative symptoms** resulting from infiltration of first leaf of 20 day old Golden Promise seedlings with *PstavrRpm1* at indicated inoculation density (OD_{600} 0.02 to 1). Photographed 48 hpi.

(a)

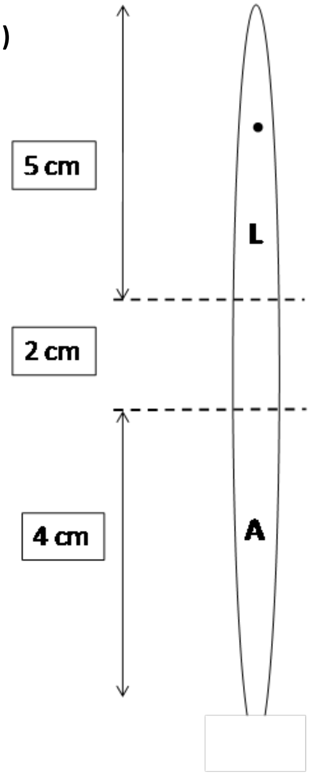


Figure 3.7 Localisation of *PstavrRpm1* to infiltrated leaf area. (a) Leaf regions L (local, *PstavrRpm1* infiltrated) and A (adjacent, uninfiltrated). Distances indicated are approximate, the L region represents the distal half of the leaf and as such varied with leaf size. **(b) *PstavrRpm1* is not recovered from the adjacent leaf region**. At 0, 6 and 24 hours post local infiltration with *PstavrRpm1* (OD_{600} 0.2), a single leaf disc was sampled from the adjacent region and CFU assayed. W indicates seedlings infiltrated with water as a control. 'lawn' indicates a confluent lawn of *PstavrRpm1* cells. **(c) Assay sensitivity is sufficient to recover on average 15 CFU per leaf disk from leaf tissue after infiltration with *PstavrRpm1* at OD_{600} 0.2 x 10^{-4}.** Up to three seedlings were infiltrated with a dilution series of *PstavrRpm1* from OD_{600} 0.2 to 0.2 x 10^{-6}. Immediately after infiltration, one leaf disc per seedling (one replicate) was sampled, and CFU assayed. Infiltration at OD_{600} 0.2 x 10^{-4} (OD_{600} 0.00002) was considered the lowest density at which bacteria could reliably be recovered. Blank cells indicate no replicate was tested.

(b)

Treatment / replicate	CFU recovered		
	0 hpi	6 hpi	24 hpi
Pst 1	0	0	0
Pst 2	0	0	0
Pst 3	0	0	0
W 1	0	0	0
W 2	0	0	0
Pst Local 1 (+ control)	lawn	lawn	lawn

(c)

Infiltration density (OD_{600})	CFU recovered		
	Rep1	Rep2	Rep3
W (- control)	0	0	0
Pst 0.2	lawn		
Pst 0.2 x 10^{-3}	232	172	344
Pst 0.2 x 10^{-4}	6	10	34
Pst 0.2 x 10^{-5}	2	2	0
Pst 0.2 x 10^{-6}	0	0	0

transcriptional response could be seen (Figure 3.8), strongly suggesting that the presence of *PstavrRpm1* in the adjacent leaf region at lower levels than could be recovered would not be biologically significant. In addition, infiltration with *Pst* DC3000 deficient in the type III secretion system did not result in (Figure 3.8 (a), (b)), or resulted in significantly less (Figure 3.8 (c)) PR gene induction. This suggests the PR gene response is primarily induced by a secreted factor.

3.4 Discussion

The localisation of defence responses in barley has almost exclusively been tested using the fungal pathogen powdery mildew (*Blumeria graminis*). However, experimental intractability and the absence of a clear frame of reference to a previously characterised SAR-inducing interaction call into question the utility of this pathosystem for such tests. Here, the suitability of *Pseudomonas syringae* as an 'inducer' of AR responses in barley was investigated. The isolates tested induced symptoms and gene expression indicative of induced defence responses. Furthermore, differential responses were seen for each isolate, suggesting differences in the nature of their interaction with barley. This variation allowed comparison of the induction of selected genes previously associated with the barley-*Pss* (*PR1*, *PR5*, *PR9* (Vallelian-Bindschedler *et al.*, 1998)), *Arabidopsis-Pst*/ *Psm* (*PR1*, *PAL* (Cameron *et al.*, 1999, Dong *et al.*, 1991) and barley-powdery mildew (*PR9* (Gregersen *et al.*, 1997, Thordal-Christensen *et al.*, 1992)) interactions. In *Arabidopsis*, strong locally induced defence is associated with SAR induction (Mishina & Zeier, 2007a). Here, PR gene induction appeared to be strongest after infiltration of Golden Promise with isolate *PstavrRpm1*, at an inoculation density of OD_{600} 0.2 (Figures 3.4 and 3.6). As such, this was selected as a suitable 'inducer' isolate for use in subsequent tests of the localisation of AR in barley.

Without more detailed genetic tests, it is difficult to fully determine the nature of the interactions between the *Pseudomonas* isolates tested and Golden Promise. Macro (and micro)-scopic symptoms, and rapid growth in leaf tissue (Figure 3.2) indicate that PS86 and PS13 are compatible. The differential symptoms and growth of *PstavrRpm1* and the TTSS deficient *hrcC*-strain strongly suggest the resistance to *PstavrRpm1* is effector-mediated, at least in part. Furthermore, the differential symptoms resulting from infiltration with *PstavrRpm1* and *Pst* DC3000 suggest *avrRpm1* may be recognised, however further tests of the *in planta* growth of *Pst* DC3000 would be needed to confirm this. The TTSS of *Pseudomonas* has been shown to contribute to the induction of defence by non-host bacteria, as well as in avirulent interactions with host bacteria (Mishina & Zeier, 2007b), and as such the interaction between *PstavrRpm1* and

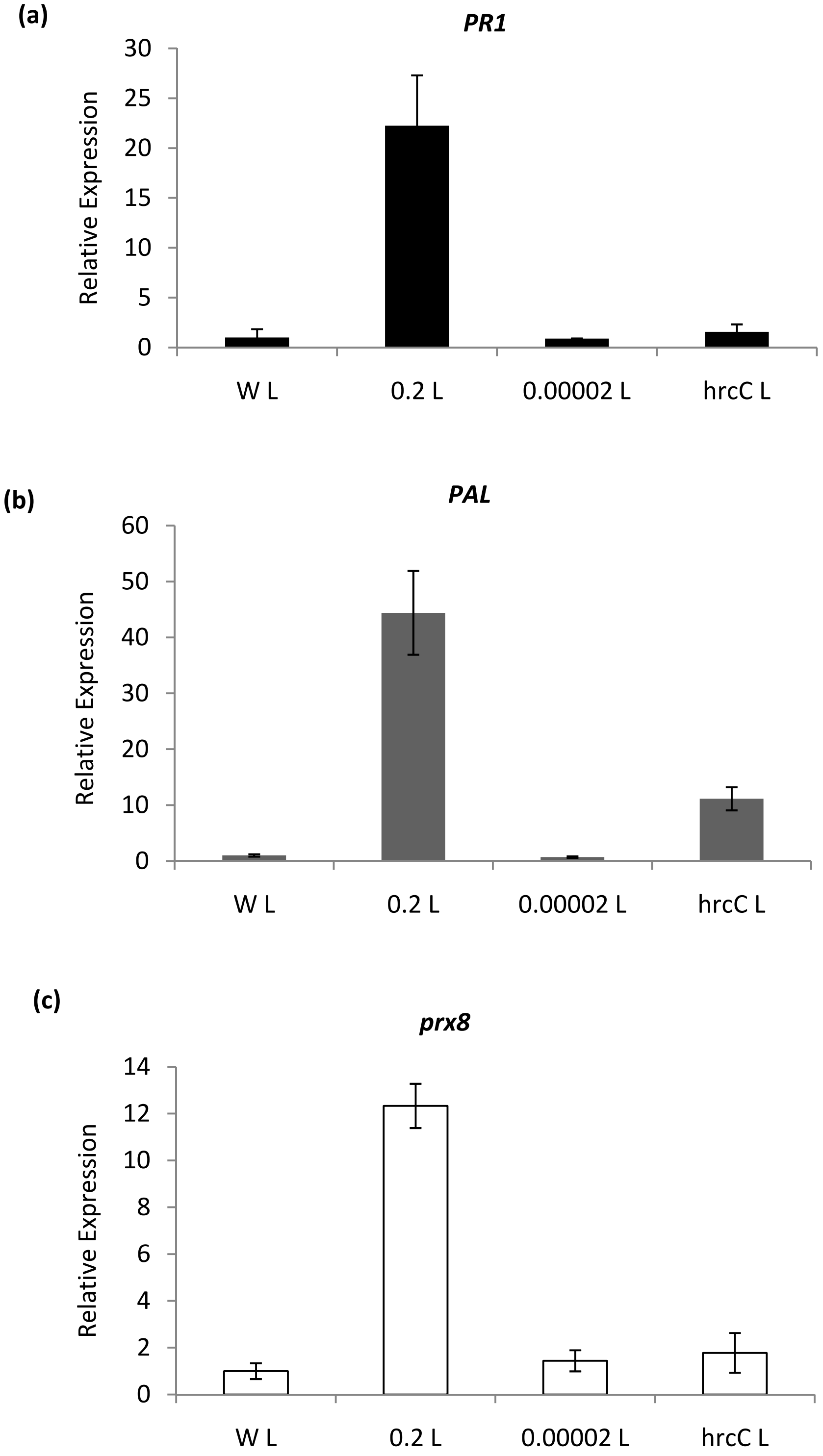


Figure 3.8 Bacterial contamination below level of recovery does not lead to PR gene induction. Leaf tissue (local) was sampled for qRT-PCR 24 hrs post-infiltration with *PstavrRpm1* at OD_{600} 0.2 (10^8 CFU mL^{-1}) (0.2 L)); with the lowest inoculation density that can be recovered (OD_{600} 0.2 x 10^{-4} (0.00002 L)); or with *Pst DC3000 hrcC-* (OD_{600} 0.2 (10^8 CFU mL^{-1}) (hrcC L)). Expression of *PR1* **(a)**, *PAL* **(b)** and *prx8* **(c)** was quantified relative to a water infiltrated control (W L, values set to 1). Bars show mean values (± SD) of two or three biological replicates, each consisting of multiple pooled individuals. Transcript levels were normalised to *α-tubulin 2.*

Golden Promise could fall into either category. Interestingly, *PAL* induction in *Arabidopsis* by host and non-host bacteria is independent of the type three secretion system (TTSS) (*Pst* DC3000 *hrcC-*); being induced by avirulent, non-host and a TTSS deficient non-host isolate (Mishina & Zeier, 2007b). Consistent with this, in this study *PAL* was the only PR gene tested to be significantly induced by both *PstavrRpm1* and *Pst* DC3000 *hrcC-*, although induction was attenuated with *hrcC-* (Figure 3.8). The differential induction of *PR1* and *PR9* and reduced induction of *PAL* by *Pst* DC3000 *hrcC-* does however again suggest that secreted effectors are contributing to the responses induced by *PstavrRpm1* in Golden Promise. However, the interaction between *Arabidopsis* and compatible (host) isolates does not result in the induction of *PAL*, whereas here *PAL* is induced in interactions between Golden Promise and both PS13 and PS86. This suggests that while there are key common elements between *Arabidopsis* and barley in terms of their response to *Pseudomonas*-derived PAMPs and effectors, there may also be some differences.

In *Arabidopsis*, virulent *Pst* DC3000 induced significantly more efficient SAR than an avirulent strain of the same isolate, and a non-adapted isolate (Mishina & Zeier, 2007a). For virulent and avirulent isolates, the efficiency of SAR induction was related to the strength of active local defence response, rather than the extent of local necrosis or tissue collapse (Mishina & Zeier, 2007a). Local defence induction (SA accumulation and PR gene induction) by avirulent and virulent host isolates is stronger overall than that induced by non-adapted strains (Mishina & Zeier, 2007b). Here, local PR gene induction was generally stronger in Golden Promise in response to infiltration with *PstavrRpm1*, than to compatible strains PS13 and PS86. This could be related to the nature of the interaction between Golden Promise and *PstavrRpm1*, or it is also possible that the genes tested were not representative of the extent of the defence response in the infiltrated leaves. In wheat, treatment with the *Pss*-derived elicitor syringolin led to the induction of a set of previously uncharacterised defence genes (Waspi *et al.*, 2001), suggesting that there may be many as-yet-uncharacterised genes involved in this response. A more global analysis of the gene expression associated with this interaction would provide a basis for further optimisation of the local defence response. Further parameters, such as SA accumulation, could also be tested (Mishina & Zeier, 2007a).

In addition to an ‘inducer’ interaction, it is also necessary to ‘challenge’ inoculated seedlings to test induction of AR responses. When SAR is induced in *Arabidopsis*, virulent challenge interactions result in symptoms equivalent to those of an avirulent interaction (Cameron *et al.*, 1994). The rapid growth of *Pss* isolate PS86 in Golden Promise tissue suggest it could be used as a challenger isolate. Given that localised AR induced by powdery mildew is effective against both powdery mildew (Ouchi *et al.*, 1974) and *Magnaporthe oryzae* (Jarosch *et al.*, 2003), these would also be appropriate challengers. The following chapter will explore whether the resistance responses induced locally by *PstavrRpm1* are strictly localised, or translocated within, or between, barley leaves.

Chapter 4: *Pseudomonas*-induced acquired resistance in barley

4.1 Aim

The primary aim of the work described in this chapter was to characterise the extent to which resistance responses, induced by the assay described in Chapter 3, are translocated within, and between, leaves of barley cultivar Golden Promise. The second aim was to investigate the nature of any acquired resistance (AR) identified.

4.2 Introduction

The localisation of acquired resistance in barley is unclear. Induced inaccessibility to a previously virulent *Blumeria graminis* f. sp. *hordei* isolate can be induced by a failed penetration attempt by virulent or avirulent isolates of *Blumeria graminis* f. sp. *hordei* (*Bgh*)*,* or non-host isolates *Blumeria graminis* f. sp. *tritici* (*Bgt*) *or Erysiphe pisi* (Kunoh *et al.*, 1988, Lyngkjaer & Carver, 1999, Ouchi *et al.*, 1974). This form of resistance is effective in the same cell, and 1-2 transversely adjacent cells (Kunoh *et al.*, 1988, Kunoh *et al.*, 1989). During defence against *Bgh*, PR gene transcripts accumulate in both the epidermis and mesophyll, despite the pathogen being limited to the epidermis (Gregersen *et al.*, 1997). However, resistance was not observed in cells 5 mm away (Ouchi et al., 1976). In contrast, distinct 'zones' of AR have been described for tobacco, with a 2- 5 mm zone of near-immunity immediately surrounding the HR lesion (described as Localised Acquired Resistance (LAR)), and the development of SAR (which confers a lower level of protection) within the rest of the inoculated leaf, and in distal leaves (Dorey *et al.*, 1997, Ross, 1961a, b) (Figure 4.1 (a)). In other work, LAR has been described as Local Acquired Resistance, and defined as the response occurring in symptomless tissue surrounding HR lesions, typically within the same leaf (Malamy, 1996, Mur *et al.*, 1996) (Figure 4.1 (b)). The latter definition broadly groups within-leaf responses and fails to allow for the distinct zones of AR present, which can lead to confusion. For example, Mur *et al.* (1996) report that Local Acquired Resistance develops earlier and provides a higher level of protection than SAR (Mur *et al.*, 1996), which contrasts with the results of Ross et al (1961b) who describes SAR developing within and between leaves at a similar rate. As LAR is defined differently between the tests, it is unclear precisely which leaf region is being described. To avoid such problems here, LAR will denominate Localised Acquired Resistance developing in the 2- 5 mm zone surrounding the HR lesion (as reported by Ross (1961a) and Dorey *et al.* 1997). Tissue within the leaf receiving the primary inoculation, but outside of the LAR zone, will be described as the 'adjacent' leaf region (Figure 4.1 (c)).

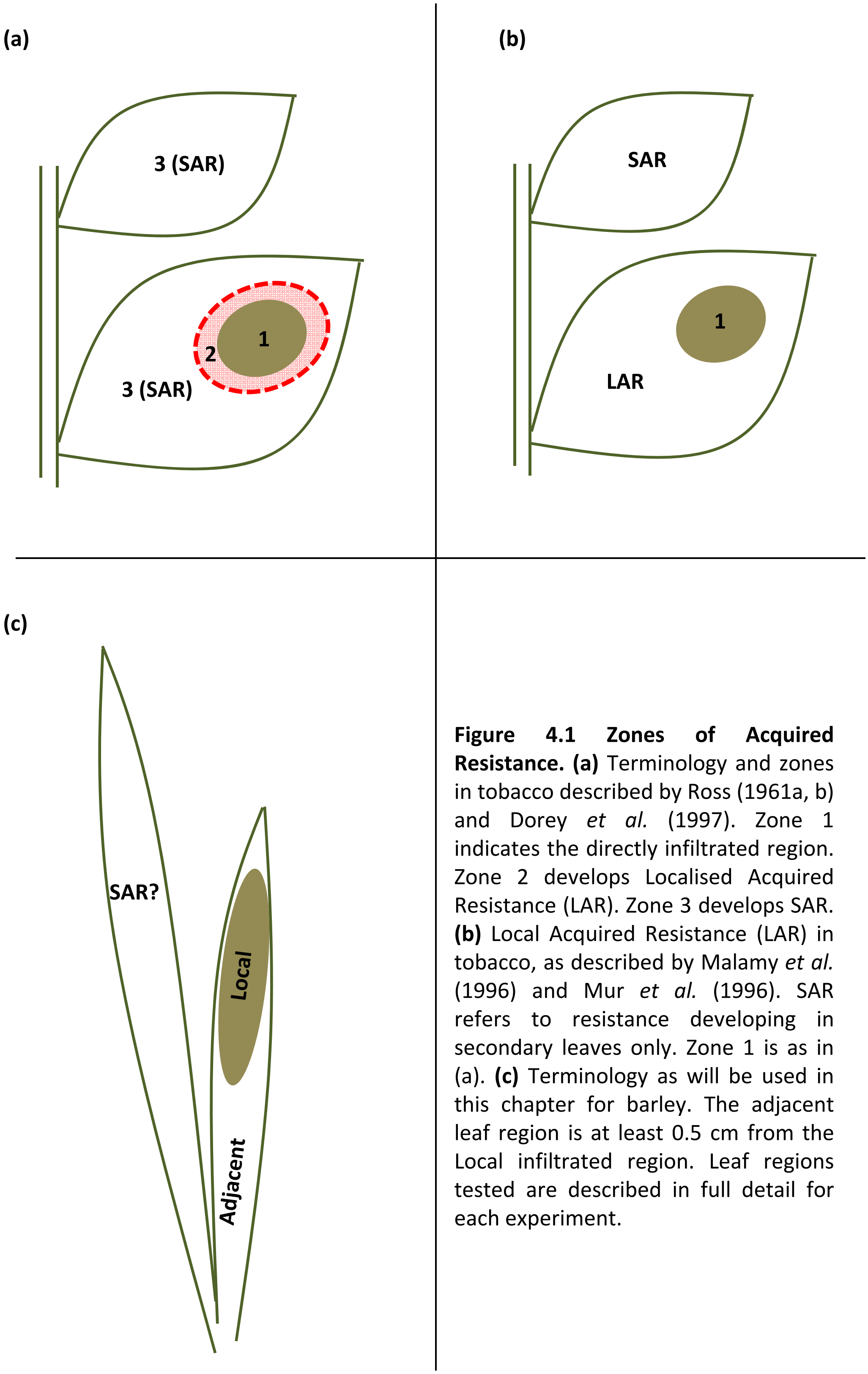


Figure 4.1 Zones of Acquired Resistance. (a) Terminology and zones in tobacco described by Ross (1961a, b) and Dorey *et al.* (1997). Zone 1 indicates the directly infiltrated region. Zone 2 develops Localised Acquired Resistance (LAR). Zone 3 develops SAR. **(b)** Local Acquired Resistance (LAR) in tobacco, as described by Malamy *et al.* (1996) and Mur *et al.* (1996). SAR refers to resistance developing in secondary leaves only. Zone 1 is as in (a). **(c)** Terminology as will be used in this chapter for barley. The adjacent leaf region is at least 0.5 cm from the Local infiltrated region. Leaf regions tested are described in full detail for each experiment.

The relationship between LAR and SAR has not been well characterised, and the LAR signal is currently unknown (Costet *et al.*, 1999). Dorey et al. (1997) and Costet et al. (1999) investigated the spatial and temporal induction of responses in tobacco leaves tissue infiltrated with a *Phytophthora megasperma* glycoprotein known to elicit an HR (Baillieul *et al.*, 1995). The infiltrated leaf region accumulated transcripts of defence genes involved in secondary metabolite biosynthesis, such as *PAL*, which accumulated up to 14 hpi when cells became disrupted due to HR (Dorey et al. 1997). The surrounding LAR zone (zone 2 (Figure 4.1 (a)) also accumulated defence gene transcripts, including those of several PR genes (Dorey *et al.*, 1997). These PR genes did not accumulate in the directly infiltrated area, presumably because the HR curtailed their transcription. High levels of the secondary metabolite scopoletin, and also SA, accumulated in zone 2 but not in the infiltrated leaf region (Dorey *et al.*, 1997). Further work indicated that HR-cell death in the infiltrated leaf region is required for LAR to develop in zone 2 (Costet *et al.*, 1999). This contrasts LAR with SAR, as local HR is not required for SAR to develop (Liu *et al.*, 2010, Mishina & Zeier, 2007a). Costet et al. (1999) propose that a diffusible signal induces LAR, however tests with *nahG* lines indicate this signal is not SA, which is synthesised *de novo* in the LAR zone (Costet et al. 1999). The differential expression of defence genes in different zones of the primary inoculated leaf is not limited to tobacco. Defence gene expression also varied between zone 1 (directly infiltrated), zone 2 (5 mm surrounding lesion) and zone 3 (rest of leaf) in bean (*Phaseolus vulgaris*) leaves infiltrated with *Pseudomonas syringae* pv. *phaseolicola* (*Psp*) (Meier *et al.* 1993). As such, the strict localisation of AR described for barley (Kunoh *et al.*, 1988, Lyngkjaer & Carver, 1999, Ouchi *et al.*, 1976) is at odds with responses reported for dicot species. Furthermore, although induced inaccessibility in barley is transferred to adjacent cells, this does not occur until 25 hours post inoculation (Kunoh *et al.*, 1988). This is inconsistent with the development of LAR and SAR in dicot species, which is usually induced by 24 hpi (Cameron *et al.*, 1994, Kunoh, 2002, Smith *et al.*, 1991). It should however be noted that, in tobacco, SAR increases from 48 hpi up to 10 days post inoculation (dpi) (Ross 1961b), and the efficiency of SAR induction does vary between cultivars and isolates (Ross 1961b, Smith et al. 1991).

In order to characterise the spatial pattern of resistance induced by *PstavrRpm1* in barley, it is logical to first characterise the within-leaf response. The data in this chapter describe *Pseudomonas syringae*-induced AR within infiltrated barley leaves, at sites several centimetres from the initial ‘inducer’ inoculation. Under the conditions tested, this resistance could not be found in secondary leaves.

Several forms of AR have been characterised in plants, and insight into the nature of the AR induced can be gained by considering its transcriptional profile and spectrum of effectiveness (Friedrich *et al.*, 1996, Ryals *et al.*, 1996). SAR is associated with the systemic induction of a distinct set of 'SAR genes' including several families of genes encoding PR proteins (Maleck *et al.*, 2000, Uknes *et al.*, 1992). The 'SAR genes' are also induced by chemical inducers of SAR (Friedrich *et al.*, 1996, Maleck *et al.*, 2000, Uknes *et al.*, 1992, Ward *et al.*, 1991), and represent a subset of those involved in the local defence response (Truman *et al.*, 2007, Ward *et al.*, 1991). In *Arabidopsis*, early transcriptional events in secondary leaves following local infiltration with an avirulent *Pseudomonas syringae* isolate include the accumulation of *Glutathione-S-Transferase (GST)* (1-6 hpi, (Alvarez *et al.*, 1998)); and induction of transcripts of secondary metabolic pathways, jasmonate-responsive genes, and responses associated with insect feeding and local wounding (Truman *et al.*, 2007). In contrast, the onset of Induced Systemic Resistance (ISR) in *Arabidopsis* is not associated with systemic changes in gene expression, instead, colonisation of roots by beneficial microbes results in plants being 'primed' to respond more quickly following pathogen challenge (van Wees *et al.*, 1999, Verhagen *et al.*, 2004). Both SAR and ISR provide broad-spectrum pathogen protection, however it has been reported that in *Arabidopsis* challenged with *Peronospora parasitica*, *Turnip Crinkle Virus*, *Alternaria brassicicola* or *Xanthomonas campestris*, the systemic resistance induced was effective only against pathogens that use the same signalling pathway (ie SA or JA/ ET) to induce basal resistance (Ton *et al.*, 2002).

In barley, AR to previously virulent *Blumeria graminis* isolates can be induced by the chemical activators of SAR, DCINA (2, 6-dichloroisonicotinic acid) and BTH (Besser *et al.*, 2000, Kogel *et al.*, 1994). INA also induces AR to *Magnaporthe oryzae* ((Jarosch *et al.*, 2003). AR to *Blumeria graminis* is associated with whole-cell autofluorescence (indicative of HR) and increased frequency of papilla formation at attempted penetration sites, although the HR may not be causally required for resistance (Kogel *et al.*, 1994). AR to *Magnaporthe oryzae* also appears to be effected via papillae (Jarosch *et al.*, 2003). In terms of transcriptional responses, chemically induced AR in barley is associated with the expression of the Barley Chemically Induced (BCI) genes, and several PR genes (Besser *et al.*, 2000, Kogel *et al.*, 1994). Mechanistically, chemically induced resistance to *Blumeria graminis* appears to be a phenocopy of the race-specific, Mlg-determined resistance previously reported for barley (Kogel *et al.*, 1994). However, several genes are expressed only in the chemically induced response, leading to suggestions that biologically and chemically induced AR are mediated by separate pathways (Besser *et al.*, 2000, Jansen *et al.*, 2005). The situation is similar in wheat (Schaffrath *et al.*, 1997) and rice (Schweizer et al., 1999). Similarities between both the spectrum of pathogen protection and gene expression induced by BTH in wheat and tobacco suggest that chemically induced AR is analagous to that induced in dicots (Friedrich *et al.*, 1996, Gorlach *et al.*, 1996). It remains unclear however, how biologically induced AR in barley, wheat and other monocots is related to biologically induced LAR or SAR in dicots.

As in tobacco, the *Pseudomonas*-induced AR reported in this chapter is effective at a distance from the local lesion. The use of a bacterial 'inducer' pathogen facilitates comparisons with the model *Arabidopsis* SAR pathosystem, and also provides a contrast to the pathosystem previously used in these studies, *Blumeria graminis*. As such, it provides an ideal opportunity to further explore the AR response. The following chapter also includes an analysis of the transcriptome of *Pseudomonas*-induced AR in barley, using the Affymetrix 22K Barley1 GeneChip. The Barley1 GeneChip comprises 22, 000 unique probe sets, corresponding to around 16, 000 genes (Close, 2005). The chip has been used in rigorous analyses of the barley – barley powdery mildew interaction (Caldo *et al.*, 2006, Caldo *et al.*, 2004, Meng *et al.*, 2009). The transcriptional response to interactions with *Fusarium* (Boddu *et al.*, 2006), stem rust (Zhang *et al.*, 2008), *Polymyxa* (McGrann *et al.*, 2009) and aphid feeding (Delp *et al.*, 2009) have also been characterised, as have responses to salinity stress (Walia *et al.*, 2007, Walia *et al.*, 2006). In addition to GeneChip data, several global transcription studies have identified defence related transcripts in barley using custom cDNA arrays (Eichmann *et al.*, 2006, Gjetting *et al.*, 2007, Gjetting *et al.*, 2004, Zierold *et al.*, 2005). The results presented below provide an important insight into biologically induced AR in barley, and its significance in relation to previously described monocot and dicot resistance responses is discussed.

4.3 Results

4.3.1 PR genes are induced in the adjacent leaf region

In order to test whether the PR gene induction identified in *Pseudomonas*-infiltrated areas of the leaf (described in Chapter 3) was strictly localised, the distal half of first leaves of Golden Promise seedlings was infiltrated with *PstavrRpm1* (or a water control, as described in Chapter 3). The adjacent, non-infiltrated leaf section was sampled 24 hrs later for qRT-PCR (for leaf regions see Figure 4.2 (a)). The expression of a selection of the genes shown in Chapter 3 to be induced in response to infiltration with *Pseudomonas* was tested in the adjacent leaf region. As described in Section 3.3.4, these genes were selected on the basis of a biomarker analysis using microarray database and meta-analysis program Genevestigator (Zimmermann *et al.*, 2008), which indicated that *prx8* (AJ276227.1, encoding a peroxidase with similarity to *PR9*) and *PAL* are consistently highly induced in barley in response to pathogen attack (data not shown). As the most commonly

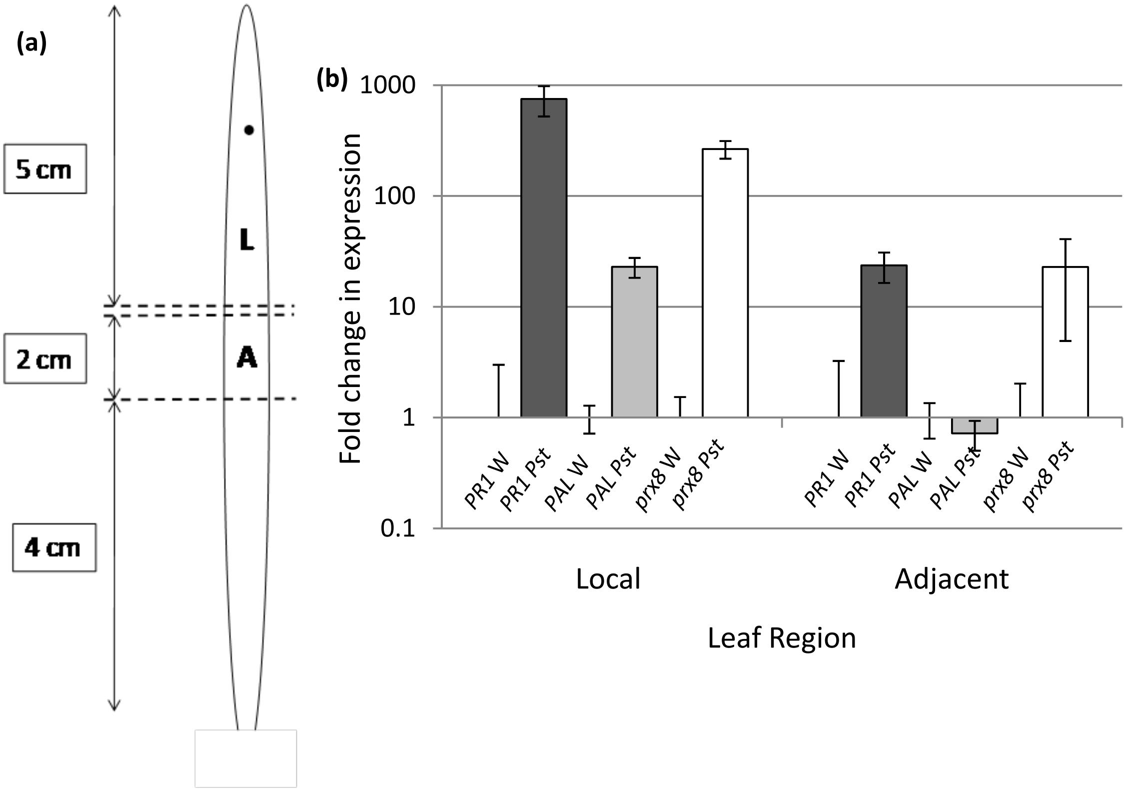


Figure 4.2 PR gene transcripts in the adjacent leaf region. (a) Leaf regions L (local, *PstavrRpm1* infiltrated) and A (adjacent, uninfiltrated) were sampled 24 hrs post *PstavrRpm1* infiltration. Controls were infiltrated with water in the L region. Distances indicated are approximate, the L region represents the distal half of the leaf and as such varied with leaf size. **(b)** qRT-PCR of *PR1*, *PAL*, and *prx8* transcripts. Bars show expression in *Pst*-induced samples (*PR1 Pst*; *PAL Pst*; *prx8 Pst*) relative to water infiltrated controls (*PR1* W; *PAL* W; *prx8* W, values set to 1), values are means ± SD of three biological replicates, each consisting of three pooled individuals. Seedlings were 18 days old at time of *PstavrRpm1* inoculation. Transcript levels were normalised to *α-tubulin 2* and barley *Ubiquitin 1*. Similar data were obtained in two independent experiments.

used marker of SAR in Arabidopsis (Uknes *et al.*, 1992) a barley *PR1* gene was also tested. Results indicated that *PstavrRpm1* infiltration lead to enhanced expression of *PR1* and *Peroxidase 8* in the adjacent leaf region, relative to the water infiltrated control (Figure 4.2 (b)). Induction was less than that observed in the 'local' *PstavrRpm1* infiltrated leaf area (Figure 4.2 (b)).

4.3.2 Resistance to *Pseudomonas syringae* pv. *syringae* is induced in the adjacent leaf region

To determine whether adjacent PR gene induction results in AR, the adjacent leaf region was challenged by infiltration with *Pseudomonas syringae pv. syringae* isolate PS86. PS86 has previously been shown to grow in Golden Promise leaf tissue (10^3 in 24 hpi; Figure 3.2, Chapter 3). The adjacent challenge took place 24 hours post local infiltration with *PstavrRpm1,* and recovery of PS86 24 hours post-PS86 challenge was reduced by 6-7-fold in seedlings induced by *PstavrRpm1* infiltration compared to water infiltrated controls (Figure 4.3).

4.3.3 Adjacent resistance is effective against *Magnaporthe oryzae*

Although not generally considered a field pathogen of barley, the hemibiotrophic fungus *Magnaporthe oryzae* can infect the species (Sweigard *et al.*, 1998, Jarosch *et al.*, 1999, Jarosch *et al.*, 2003). The adjacent leaf region was challenged with *Magnaporthe oryzae* isolate *Guy11* 24 hours post local 'inducer' infiltration with *PstavrRpm1*. Diseased leaf area was significantly reduced in the adjacent section of *Pst*-induced leaves, in comparison to water infiltrated controls (Figure 4.4). This suggests that the resistance induced in the adjacent leaf region is also effective against *Magnaporthe oryzae*.

4.3.4 Local and adjacent PR gene induction may be affected by seedling age

Results from several independent experiments revealed that local and adjacent PR gene induction varied with leaf age (Figure 4.5 (a)-(c)). Seedling age seemed to correlate with the strength of local PR gene induction observed: 18 day old seedlings showed 750 fold *PR1* induction; 20 day old seedlings showed 31 fold induction; and 21 day old seedlings showed 22 fold induction (Figure 4.5 (a)-(c)). Seedlings showing the weakest (22 fold) local induction of PR1 did not show adjacent PR gene induction (Figure 4.5 (c)), which suggests that a threshold local response might be required for adjacent induction, or that the adjacent response develops more slowly when the local response is weaker. To determine whether the absence of a strong adjacent *PR1* response compromised adjacent resistance, 22 day old barley seedlings were challenged with PS86 (Figure

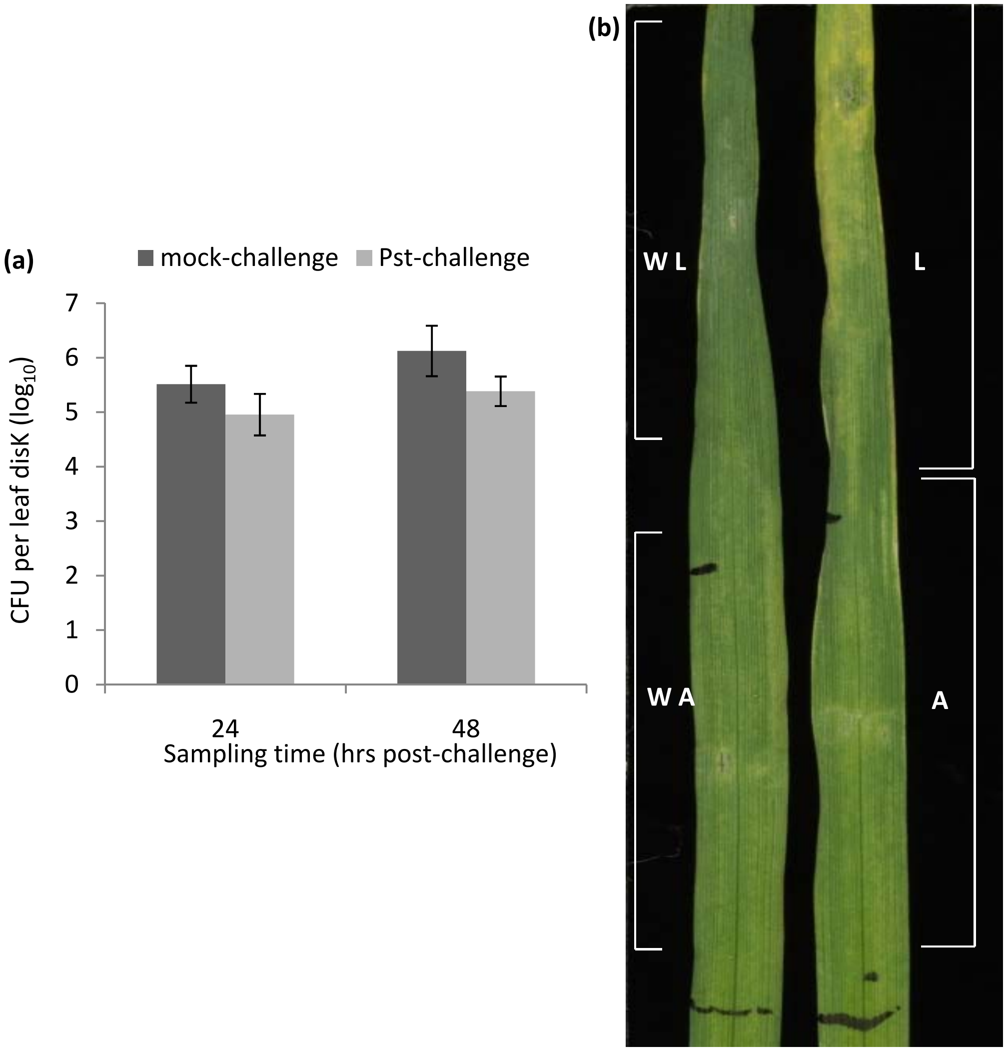


Figure 4.3 Resistance to PS86 in the adjacent leaf region. The adjacent leaf region was challenged with PS86 (OD$_{600}$ 0.02) 24 or 48 hours after local infiltration with water or *PstavrRpm1* (OD$_{600}$ 0.2). **(a)** 24 hrs after PS86 challenge a leaf disk was taken from the adjacent region of 4 leaves per treatment, and CFU assayed. Bars show mean values from one representative experiment ± SD. At the 24 hr time-point there was a significant difference between the two treatments (*t-test* $p=0.05$), at the 48 hr time-point the difference was not statistically significant. For the 24 hour time-point, 9 independent experiments (of 10 performed) showed similar results, with a significant effect of treatment ($p<0.001$). For the 48 hr time-point, the test was performed twice with similar results to those presented above. Leaf regions indicated are as in (b). **(b)** Symptoms on representative leaves 48 hrs post PS86 challenge. L indicates local, *PstavrRpm1*-infiltrated region, W L indicates local, water-infiltrated region, A indicates adjacent, PS86-challenged region.

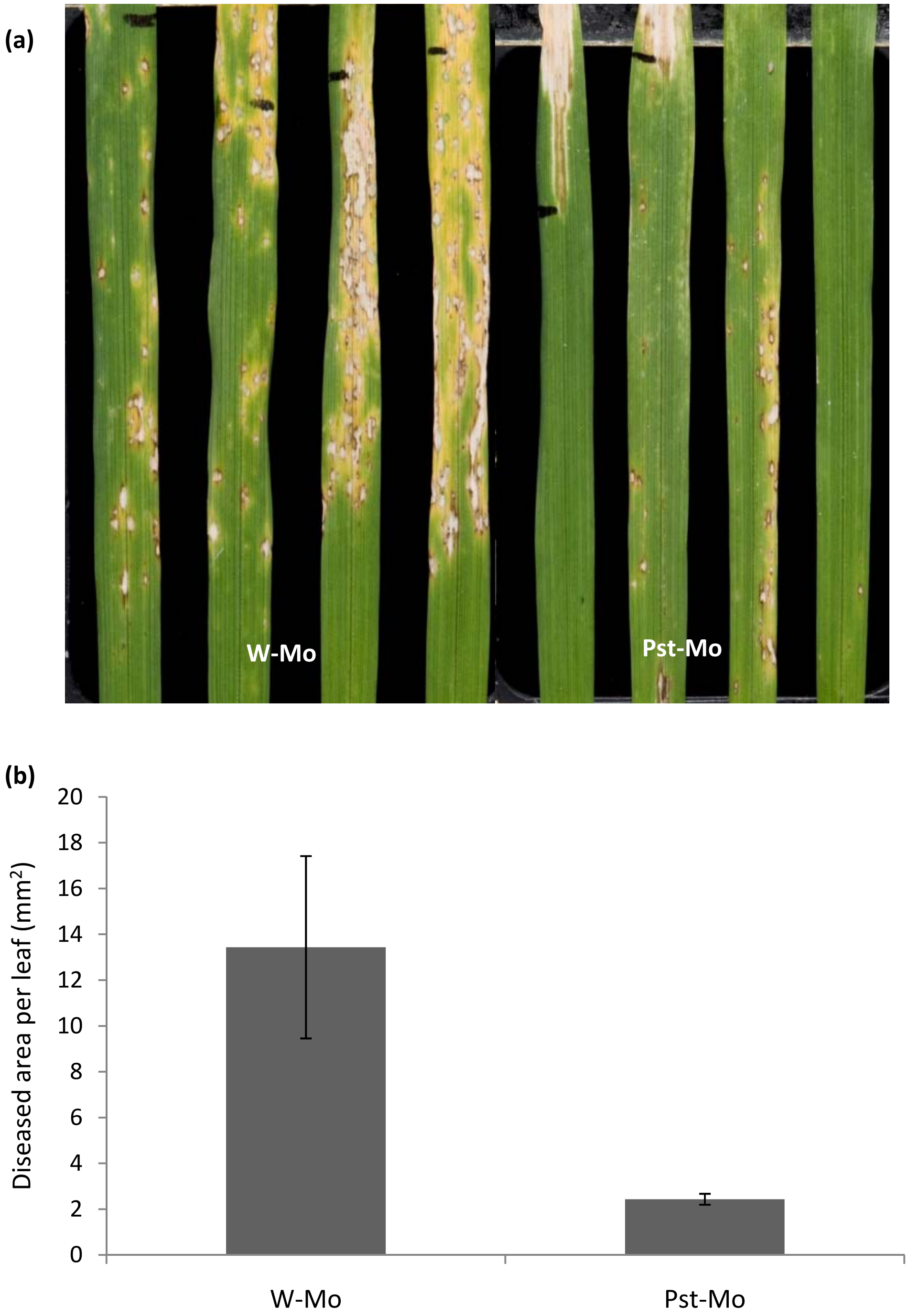


Figure 4.4 Resistance to *Magnaporthe oryzae* in the adjacent leaf region. Leaves were challenged with *Magnaporthe oryzae* isolate *Guy11* 24 hours after water or *PstavrRpm1* 'inducer' infiltration in the local leaf region (see Figure 4.2 (a)). **(a)** Symptoms on leaves 5 days post challenge, 4 representative leaves per treatment. **(b)** Diseased leaf area scored 5 days post challenge. Lesions in proximal 4 cm of leaf were scored. Bars show mean values from three independent experiments ± SE. W-Mo: water controls, Pst-Mo: *PstavrRpm1*-infiltrated leaves. A significant difference was observed between treatments (*t-test, $p<0.001$*).

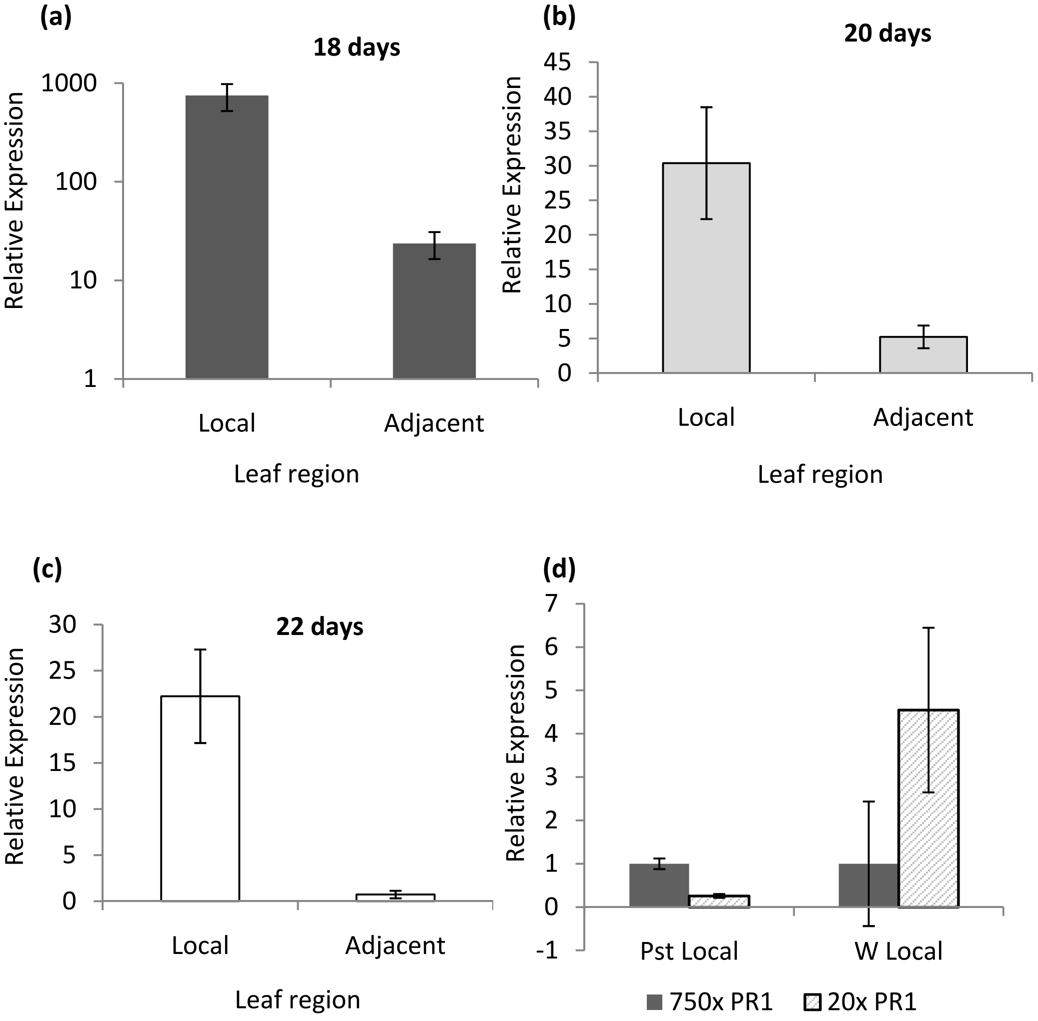


Figure 4.5 The magnitude of *PR1* induction varies with leaf age. All leaf regions as Figure 4.2 (a). **(a)-(c) Local and adjacent induction of *PR1* in 3 independent experiments.** Seedlings received 'inducer' inoculation at (a) 18, (b) 20 and (c) 21 days old. qRT-PCR data, values are means ± SD of 2 or 3 biological replicates, each consisting of 2 or 3 pooled individuals. Expression is calculated relative to the water control for each leaf region, which is set to 1 (data not shown). **(d) Reduced local *PR1* induction is due to both lower transcript level after *Pst* treatment, and higher transcript level in water-treated controls.** Re-analysis of attenuated *PR1* induction. qRT-PCR data from 22 day old seedlings (data shown in (c)) are shown relative to data from 18 day old seedlings (data shown in (a)). For each treatment, transcript level in (c) is shown relative to transcript level in (a). Pst Local indicates *PstavrRpm1* infiltrated leaf; W local indicates water infiltrated leaf.

4.6). A significant difference in growth of the challenger PS86 isolate was still seen, indicating that adjacent resistance was not compromised.

To test this apparent link between seedling age and PR gene induction, seedlings sown 3 days apart were inoculated together, at 17, 20 and 23 days old. Local and adjacent PR gene induction was tested by qRT-PCR (Figure 4.7). Although *PR1* induction was highest in 17 day old seedlings, *PAL* and *Peroxidase 8* were more variable (Figure 4.7). However, PR gene induction was lower at all seedling ages in comparison to previous results, and no adjacent PR gene induction was seen (Figure 4.7). As such, these data do not confirm a link between seedling age and the level of PR gene induction. There may however be a link between the levels of local and adjacent PR gene induction.

Importantly, resistance data from seedlings with and without adjacent PR gene induction indicates that the response of the genes tested can be uncoupled from the AR induced in the adjacent leaf region (Figure 4.6). Together, these data suggest that *PR1* and *prx8* may not be reliable markers for the adjacent resistance response.

4.3.5 The transcriptional profile of *Pseudomonas*-induced AR

Preliminary analysis of secondary leaf responses suggested that the adjacent AR described above was not induced systemically under the conditions tested (Figure 4.8). Therefore, in order to further characterise the nature of the AR, and with the aim of identifying more reliable marker genes for the response, the Affymetrix Barley1 GeneChip was used in a global transcriptomics study profiling the local and adjacent response. Local and adjacent leaf regions were sampled 24 hrs post local infiltration with *PstavrRpm1* (or water (controls)). The proximal third of the leaf (approximately 4 cm) was considered adjacent (Figure 4.9 (a)). A set of seedlings were retained for PS86 challenge in the adjacent region; results were consistent with the induction of adjacent AR (Figure 4.9 (c)). Comparisons were made between local, water infiltrated and local, *Pst* infiltrated, and between adjacent-to-water infiltrated vs adjacent-to-*Pst* infiltrated samples. Genes were considered differentially expressed if they were up or down-regulated by 2 fold or greater, with a false discovery rate adjusted p-value of $p<0.05$.

The local transcriptional response to PstavrRpm is extensive and reflects a shift from housekeeping to defence processes

Locally, infiltration with *PstavrRpm1* resulted in the differential expression of 5109 genes, with 2403 up-regulated and 2706 down-regulated. (Figure 4.10) Functional classification (Figure 4.11

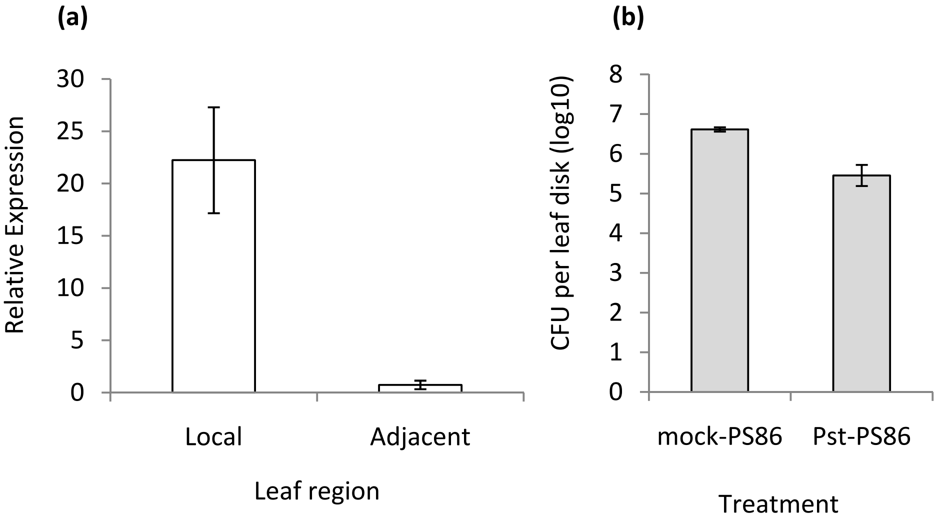
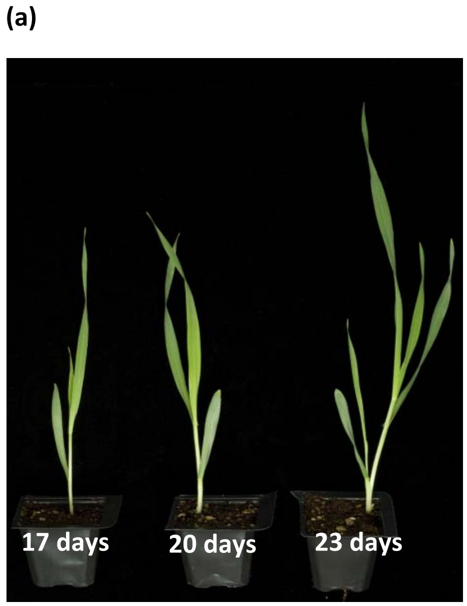


Figure 4.6 Adjacent *PR1* induction is not necessary for adjacent resistance to PS86. (a) qRT-PCR data showing local and adjacent *PR1* expression 24 hours post local *PstavrRpm1* infiltration of 21 day old Golden Promise seedlings (Data also shown in Figure 4.5 (c), see that figure for full details). **(b)** Adjacent resistance to PS86 induced in seedlings grown and inoculated alongside those shown in (a). Bars are as Figure 4.3. Difference between treatments is statistically significant (*t-test p-value<0.001*).



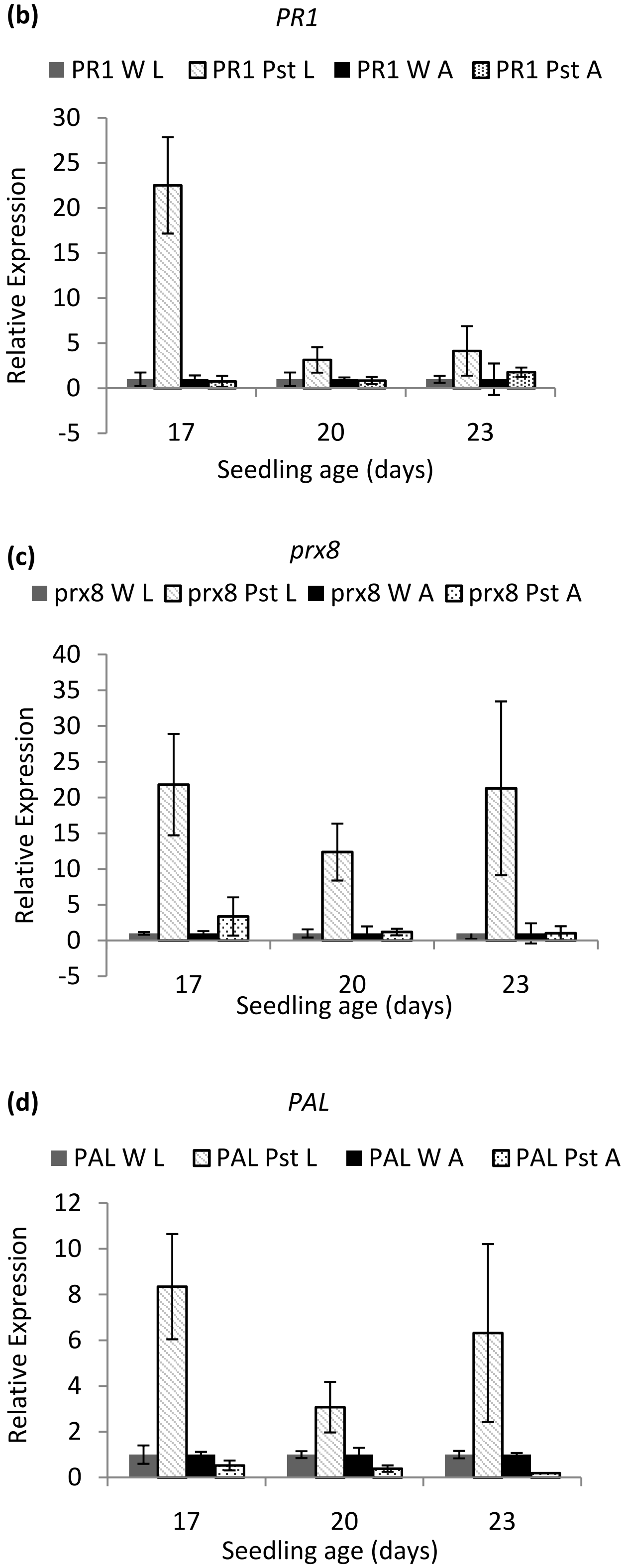


Figure 4.7 No evidence for a link between seedling age and PR gene induction. Local and adjacent leaf regions of 17, 20 and 23 day old seedlings were sampled 24 hrs post local infiltration with *PstavrRpm1*. Leaf regions as Figure 4.2 (a). **(a)** Growth stages of seedlings at point of *PstavrRpm1* infiltration. **(b)-(d)** qRT-PCR data showing local and adjacent expression of *PR1* **(b)**, *prx 8* **(c)** and *PAL* **(d)** quantified relative to a water infiltrated control. W L indicates water infiltrated leaf, local region; W A indicates water infiltrated leaf, adjacent region; Pst L indicates *PstavrRpm1* infiltrated leaf, local region; Pst A indicates *PstavrRpm1* infiltrated leaf, adjacent region. Values of water controls set to 1. Bars show means ± SD of two or three biological replicates, each consisting of multiple pooled individuals. Transcript levels were normalised to *α-tubulin 2* and *cyclophilin*.

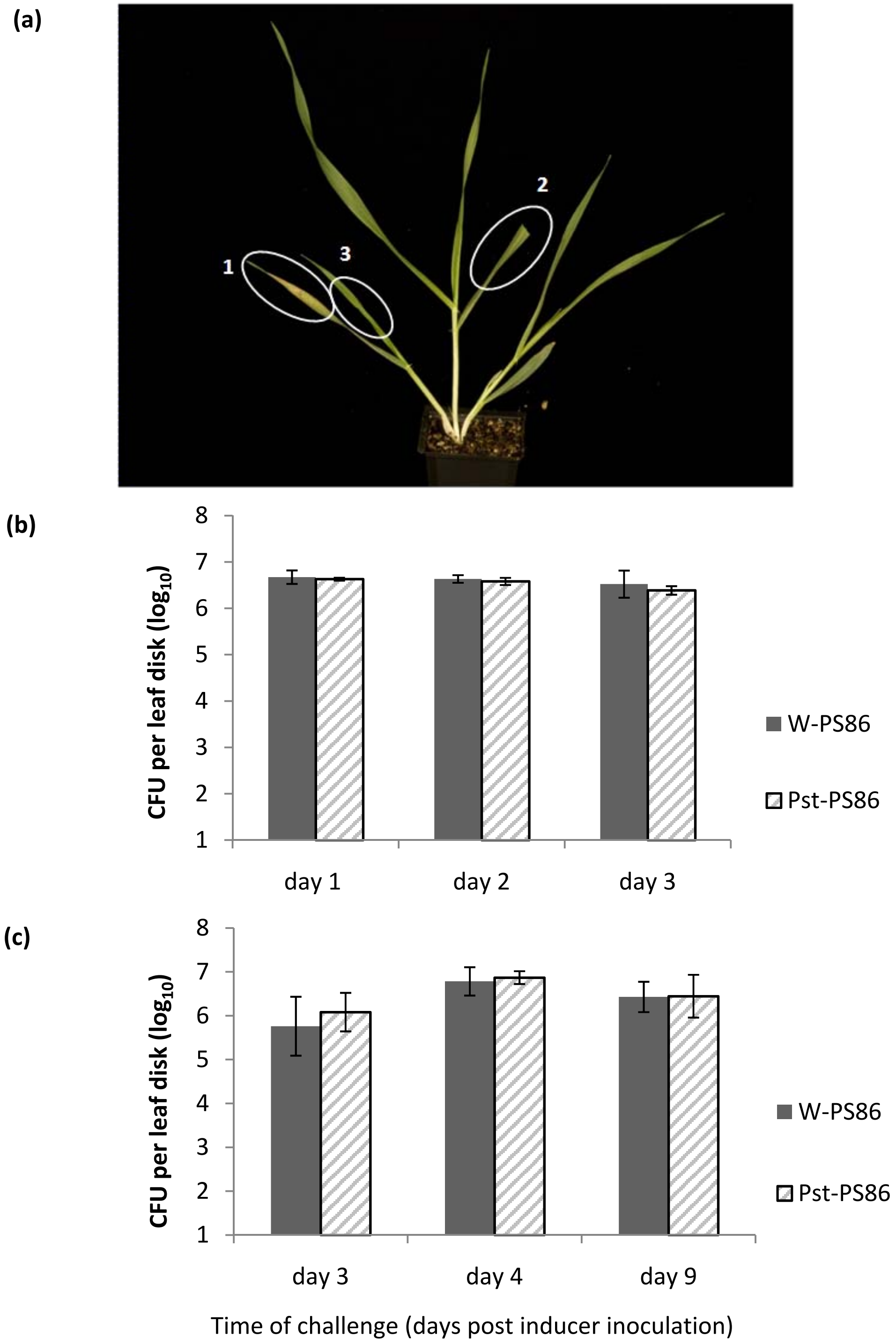
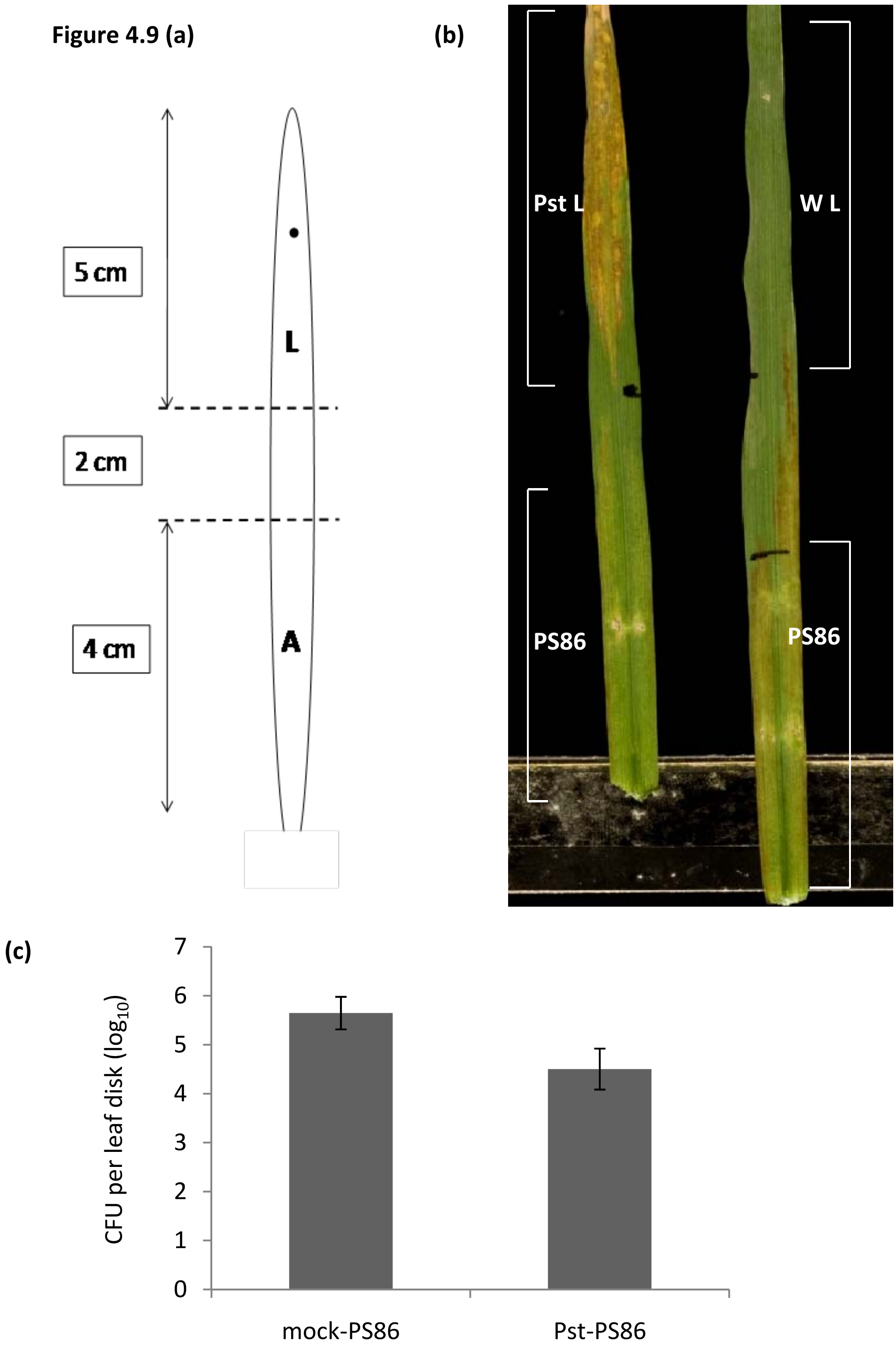


Figure 4.8 Recovery of PS86 challenger isolate suggests no acquired resistance was induced in secondary leaves at the time intervals tested. Golden Promise seedlings (19 days old) were infiltrated in the local region of the first leaf with *PstavrRpm1* (OD_{600} 0.2) ('1' in (a)), or water as a control. One-four days post *PstavrRpm1* infiltration, the second leaf was challenged by infiltration with PS86 (OD_{600} 0.02, central third of leaf) ('2' in (a)). At 9 days post-*PstavrRpm1* infiltration, a younger leaf was tested ('3' in (a)). **(a)** Representative seedling at 24 days old (5 days post *PstavrRpm1* inoculation). **(b)-(c)** Data from two independent experiments. 24 hours post infiltration with PS86 a leaf disc was sampled from each of three replicate seedlings per treatment and CFU assayed. Bars represent mean data from three biological replicates per treatment ± SD .

Figure 4.9 Leaf regions sampled and adjacent resistance induced in microarray study. The local leaf region was infiltrated with *PstavrRpm1* (OD_{600} 0.2) or water (mock). 24 hours later, local and adjacent leaf regions were sampled for microarray study (3 pooled seedlings made up one biological replicate, 3 biological replicates were taken). A set of seedlings were retained for PS86 challenge in the adjacent leaf region 24 hrs post local *PstavrRpm1* infiltration. Twenty-four hours post-PS86 challenge, a single leaf disc was sampled from each of 4 seedlings per treatment, and CFU assayed. **(a) Leaf regions** L (local, *PstavrRpm1* infiltrated) and A (adjacent, uninfiltrated) were sampled 24 hrs post *PstavrRpm1* infiltration. Controls were infiltrated with water in the L region. Distances indicated are approximate, the L region represents the distal half of the leaf and as such varied with leaf size. Figure is repeated from Figure 4.2 (a) for clarity. **b) Representative symptoms** 5 days post *PstavrRpm1* / water inoculation (L) and 4 days post PS86 challenge (A). Pst L indicates local, *PstavrRpm1* infiltrated; WL indicates local, water-infiltrated; PS86 indicates adjacent, PS86-challenged. **(c) Resistance induced in the adjacent leaf region**. Bars indicate mean CFU recovered from 4 biological replicates, ± SD. Difference in recovery of PS86 between the adjacent region of mock and *PstavrRpm1*-induced seedlings is statistically significant (*t-test p-value<0.05*).

Figure 4.9


(a)
5 cm
L
2 cm
4 cm
A
(b)
Pst L
W L
PS86
PS86
(c)
CFU per leaf disk ($\log_{10}$)
7
6
5
4
3
2
1
0
mock-PS86
Pst-PS86

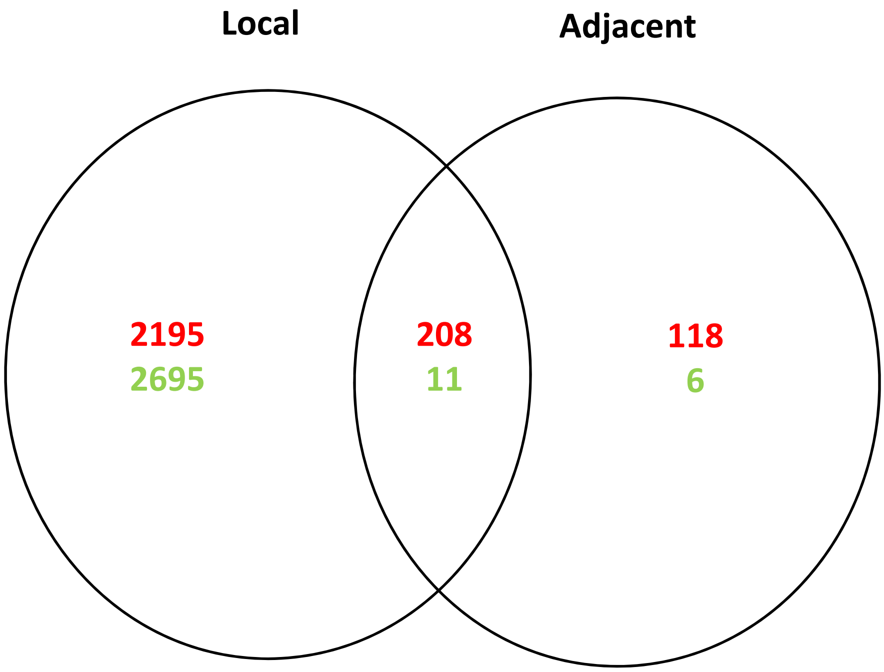


Figure 4.10 Venn diagram showing number of differentially expressed genes in local, adjacent, and both leaf regions 24 hours after local infiltration with *PstavrRpm1*. Overlapping region represents genes differentially expressed in both treatments (direction of change is as in adjacent region). Numbers in red (top) were up-regulated, green (bottom) were down-regulated.

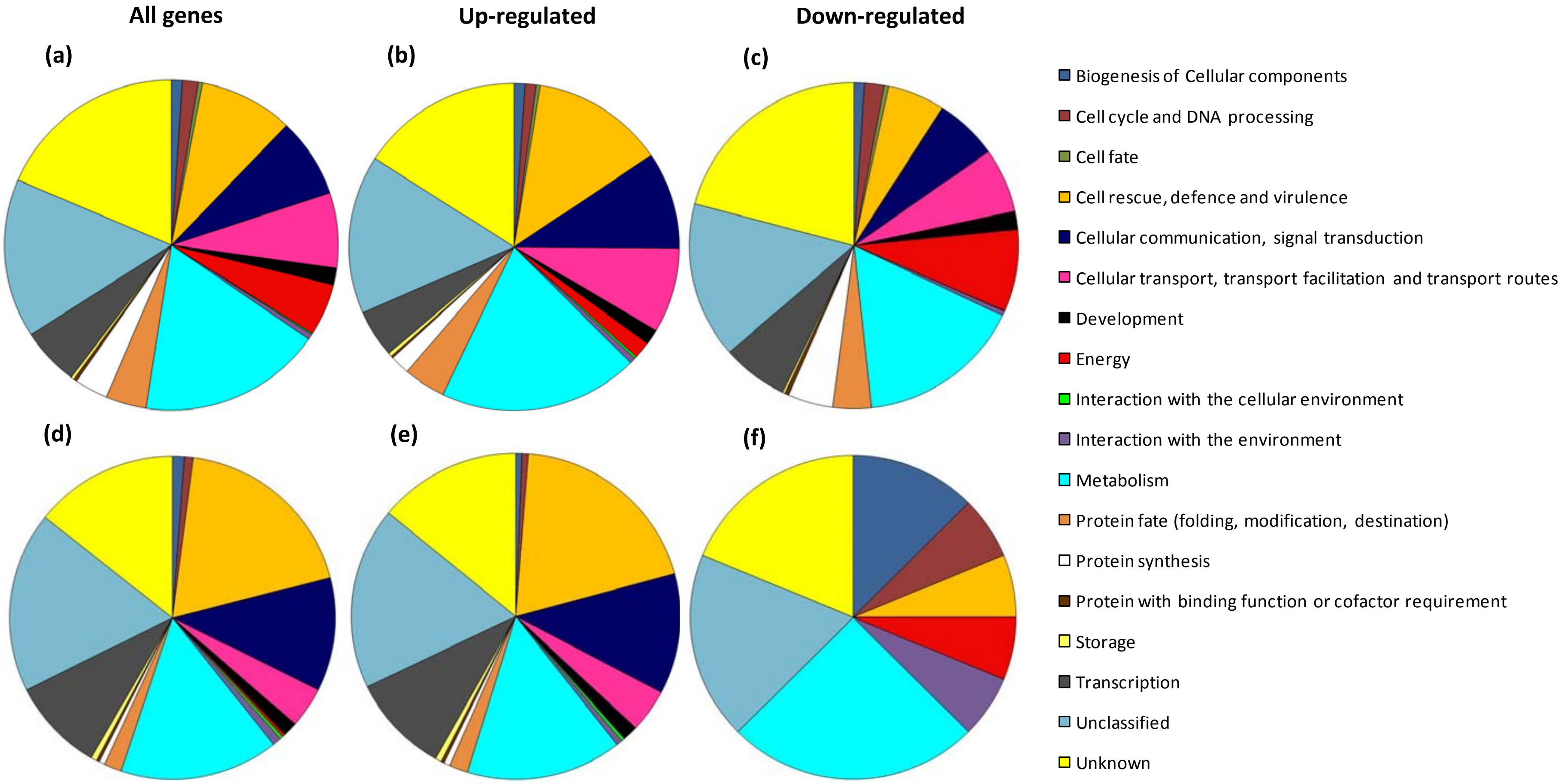


Figure 4.11. Pie charts showing functional categories of differentially expressed genes after local infiltration with *PstavrRpm1* (a-c), and in the adjacent leaf region (d-f). Pie charts show all differentially expressed genes (a), (d), up-regulated genes (b), (e) or down-regulated genes (c), (f). Genes were assigned MIPS functional categories (http://mips.gsf.de/) according to their annotation.

(a)-(c)) revealed that (aside from genes of unknown function) most differentially expressed genes were involved in metabolism (18 %), with similar proportions up and down-regulated. Genes associated with defence, signal transduction, cellular transport, energy and transcription were also differentially expressed (full list Appendix 1). Comparison of up, and down-regulated genes in each functional category suggests that defence related transcripts are predominantly up-regulated at this timepoint, whilst transcripts associated with energy production are predominantly down-regulated (Figure 4.11 (b)-(c)). This indicates a shift from housekeeping functions to defence metabolism (Figure 4.11). At the gene level, local defence-related responses of barley to *PstavrRpm1* included the differential expression of many PR genes, including *PR1*, *PR4*, a *PR5*-precursor, *PR10*, defensin (*PR12*) precursors, peroxidases (*PR9*), oxalate oxidases (*PR15*) and putative β-1-3-glucanases (*PR2*). Transcripts with similarity to genes involved in phenylpropanoid biosynthesis (eg *PAL* and *CHS*) and the oxidative burst (eg *GST*) were also differentially expressed. Several of these genes (such as *PR1*, *PR2*, *PR5*, *GST*, *PAL* and *CHS*) are associated with the *Arabidopsis* response to *Pseudomonas syringae* (Alvarez *et al.*, 1998, Dong *et al.*, 1991, Uknes *et al.*, 1992), and other genes with similarity to the *Arabidopsis* defence signal transduction genes *DIR1*, *EDS5*, and *COI1* were also differentially expressed (Table 4.1, Table 4.2, and full list Appendix 1), which may suggest some common responses to *Pseudomonas syringae* between *Arabidopsis* and barley. Several *DIR1*-like transcripts were also differentially expressed (Contig16375_at, Contig24328_at and Contig25762_at) which may be significant given the role of *Arabidopsis* DIR1 in the production or transmission of the mobile SAR signal (Maldonado *et al.*, 2002). As with local expression of *Arabidopsis DIR1*, these transcripts were all down-regulated.

Common patterns of PR protein induction have been reported in barley to a range of pathogens (Reiss & Bryngelsson, 1996). Furthermore, genes with similarity to known powdery mildew or rust resistance (for example *Mla1*; *Mlo2*, *3*, *7* and *8*; *Yr10*; and *Rpg1*) and defence-related genes (eg syntaxin-like genes, blue-copper binding proteins) are also differentially expressed here (Appendix 1). Of 22 genes identified by Caldo *et al*. (2004) whose expression profiles act as markers of virulent or avirulent responses of barley to powdery mildew, 18 were differentially expressed here in the local response to *Pseudomonas*, indicating that common defence mechanisms are involved in the local response to powdery mildew and *Pseudomonas syringae* (Table 4.3). Strikingly, 17 of these 18 genes showed common regulation with the avirulent *Bgh* interaction (Table 4.3). The most strongly induced gene in the local region is similar to the rice *PIR7B esterase*, transcripts of which are induced in rice by the *Pss* derived elicitor syringolin (Reimmann *et al.*, 1995, Wäspi *et al.*, 1998). It is clear that the local response of barley to *PstavrRpm1* involves extensive transcriptional reprogramming, and that the response (at least in part) involves

Affymetrix Probe Set ID	Annotation	Fold Change (Log2)	FDR Adjusted P Value
Contig10057_s_at	Putative esterase PIR7B	7.52	5.47E-13
Contig19549_at	Putative NADPH HC toxin reductase	6.48	1.29E-13
Contig10057_at	Putative PIR7B Protein	6.41	2.82E-10
Contig1802_at	Phenylalanine ammonia-lyase	6.27	1.91E-10
Contig3017_at	Oxalate oxidase	6.22	1.53E-10
HY03N19u_s_at	Lipoxygenase 2	6.12	1.82E-09
Contig24993_at	Pathogenesis-related protein 1a	6.08	2.78E-13
Contig3501_at	60 kDa jasmonate-induced protein	5.96	7.65E-08
Contig1795_at	Phenylalanine ammonia-lyase	5.67	5.63E-11
Contig1800_at	Phenylalanine ammonia-lyase	5.64	5.63E-11
Contig7887_at	Putative 32.7 kDa jasmonate-induced protein	5.53	4.43E-08
Contig7886_at	Putative 32.7 kDa jasmonate-induced protein	5.43	6.49E-11
Contig12776_at	Glutathione transferase	5.33	6.11E-11
Contig18558_at	Phenylalanine ammonia-lyase	5.23	1.33E-11
Contig23540_at	Chitinase	5.22	2.68E-13
Contig3208_at	Blue copper binding protein	5.21	1.26E-11
Contig2123_s_at	Peroxidase	5.2	6.48E-11
Contig3211_at	Blue copper-binding protein	5.04	2.16E-12
Contig12382_at	Putative xylanase inhibitor	5.01	1.08E-11
Contig15099_s_at	Pathogenesis-related protein 4	5.01	3.01E-11
Contig2789_at	Thaumatin-like protein TLP5	5	2.61E-11
Contig3209_s_at	Blue copper binding protein	4.97	1.11E-10
Contig9764_at	Glutathione-S-transferase Cla47	4.96	9.15E-12
HVSMEa0011L14r2_s_at	Glutathione S-transferase	4.95	2.16E-12
Contig3018_at	Oxalate oxidase 2 precursor (Germin)	4.94	6.47E-11

Table 4.1. Genes up-regulated in the local leaf region. The 25 most strongly induced genes (by fold change) are shown.

Affymetrix Probe Set ID	Annotation	Fold Change (Log$_2$)	FDR Adjusted P Value
Contig11383_at	Pore-forming toxin-like protein Hfr-2	-4.92	1.65E-09
rbah29m06_s_at	Putative beta-glucosidase	-4.52	5.44E-10
Contig11935_at	Putative peroxidase	-4.25	9.24E-10
Contig19029_at	Peroxidase 6	-4.2	3.86E-10
Contig13848_at	Putative subtilisin-like serine protease	-3.98	1.42E-09
Contig13847_s_at	Subtilisin-like proteinase	-3.92	1.04E-09
Contig1867_at	Putative peroxidase	-3.82	2.03E-09
Contig2489_at	Glutathione S-transferase	-3.74	5.16E-08
Contig8515_s_at	Putative L-ascorbate peroxidase	-3.71	4.98E-10
Contig20831_at	Glutathione transferase	-3.61	1.42E-09
Contig2768_s_at	Germin-like protein 1	-3.34	1.63E-08
Contig2988_s_at	Cysteine proteinase	-3.27	1.48E-07
Contig9123_at	Putative stress enhanced protein	-3.24	1.66E-08
HVSMEl0002K15r2_at	Chloroplast sigma factor	-3.22	1.01E-10
Contig972_x_at	Nonspecific lipid-transfer protein 4.2 precursor	-3.19	1.98E-07
Contig4701_at	Putative wound inducive gene	-3.12	1.04E-09
Contig24328_at	DIR1 (Defective in Induced Resistance 1) – like	-3.11	3.02E-08
Contig24930_s_at	Putative beta-glycosidase	-2.94	1.90E-08
HVSMEm0002P02r2_x_at	Peroxidase	-2.94	9.00E-11
Contig11697_at	Putative salt-inducible protein	-2.91	2.32E-08
Contig7356_at	Chalcone synthase	-2.9	2.04E-05
rbasd23b02_s_at	Glb 1 1-3,1-4-beta-D-glucanase precursor	-2.85	8.48E-09
Contig26136_at	Putative alliinase	-2.82	3.42E-08
Contig4520_at	Cold acclimation protein WCOR615	-2.8	4.89E-10
Contig2320_s_at	Drought inducible 22 kD protein	-2.74	3.41E-08

Table 4.2 Genes down-regulated in the local leaf region. The 25 most strongly repressed genes (by fold change) are shown.

Affymetrix Probe Set ID	Annotation	I/C*	C/I*	Fold Change ($\log_2$)	Functional Category
Contig11969_at	None	🟥	🟩	2.09	Unclassified
Contig15413_at	Putative anthranilate N-benzoyltransferase	🟥	🟩	4.68	Metabolism
Contig15515_at	Disease resistance response protein-like	🟥	🟩	3.05	Cell rescue, defence and virulence
Contig15861_at	None	🟥	🟩	2.94	Unclassified
Contig1271_x_at	S-adenosylmethionine synthetase 1	🟥	🟩	1.14	Metabolism
Contig2168_s_at	Serine hydroxymethyltransferase	🟥	🟩	1.83	Metabolism
Contig8605_at	Putative B12D protein	🟥	🟩	3.88	Development
HV_CEb0004O15r2_s_at	Putative glutathione S-transferase	🟥	🟩	4.66	Cell rescue, defence and virulence
Contig24175_at	Putative anion/sugar transporter	🟥	🟩	4.96	Cellular transport, transport facilitation &transport routes
Contig4728_at	Putative plastidic ATP/ADP-transporter	🟥	🟩	4.52	Cellular transport, transport facilitation &transport routes
Contig5108_s_at	Chorismate synthase	🟥	🟩	3.81	Metabolism
HY07P02u_at	Anthranilate synthase alpha 2 subunit	🟥	🟩	4.74	Metabolism
HT09O03u_s_at	None	🟥	🟩	2.13	Unclassified
Contig7815_s_at	Putative N-hydroxycinnamoyl/benzoyl transferase	🟥	🟩	2.28	Metabolism
Contig14426_at	Cinnamoyl CoA reductase	🟥	🟩	1.22	Metabolism
Contig15798_at	None	🟥	🟩	4.14	Unclassified
Contig7705_at	Putative chorismate mutase			2	Metabolism
HI15L07r_s_at	None	🟩	🟥	-1.68	Unclassified

Table 4.3 Comparison of expression profile of genes differentially expressed in response to *Bgh* with local responses to *PstavrRpm1*. *Bgh* induced genes were identified by Caldo *et al.* (2004) as differentially expressed between compatible and incompatible interactions. Columns I/C* and C/I* indicate the direction of expression change in compatible interactions relative to incompatible interactions, and vice versa (Data is published in Caldo *et al*. 2004 Supplementary data Table 1; differential expression occurs from 16 hpi). Red fill indicates up-regulation, green fill indicates down-regulation. 'Fold Change' column indicates fold change in local region of Golden Promise seedlings 24 hours after infiltration with *PstavrRpm1* (this study). This value was calculated relative to the water-infiltrated control. For Contig7705_at, the direction of expression change varies over time in the interaction with *Bgh* and as such it was not included.

elements previously characterised in *Arabidopsis*, barley and rice. Thirty-four percent (1743) of the genes identified as differentially expressed are unknown or unclassified, showing there are many elements of the response yet to be characterised.

The number and profile of transcriptional changes in the adjacent leaf region are similar to those associated with both early and 'maintenance' phase SAR

In order to investigate the nature of the adjacent response described above, analysis focussed on the transcriptional profile of the adjacent leaf region, and its relation to the local response. Of 343 genes differentially expressed in the adjacent leaf region, 326 were up-regulated, and 17 down-regulated (Figure 4.10). The overall functional profile of differentially expressed genes was similar to that of the local response, although a greater proportion of the response was defence related (mainly up-regulation) (Figure 4.11). Metabolism was again important, but a lower proportion of the response was energy-related than in the local response. This profile suggests that at this stage the adjacent leaf region was able to up-regulate defence and prepare for pathogen challenge, without needing to shift resources from housekeeping processes.

Approximately two-thirds (64 %, 219 genes) of the genes differentially expressed in the adjacent region were common to both the local and adjacent response. Of these 219 genes, 208 were up-regulated, and 11 down-regulated. Approximately a third (36 %) of adjacent genes were adjacent-specific, i.e. not differentially expressed in the local region. Of these adjacent-specific genes, 118 were up-regulated, and 6 were down-regulated (Figure 4.10). Adjacent-specific genes at this time-point may be differentially expressed locally earlier or later in the response, and a time course experiment is needed to provide more information about this. However, of the twenty most highly up-regulated transcripts in the adjacent region, thirteen were also differentially expressed in the local response. Three of these were oppositely regulated between the local and adjacent region. Of the remaining ten, eight were more strongly up-regulated in the adjacent response than in the local response. Of the ten most strongly up-regulated transcripts locally, only one is also differentially expressed (up-regulated) in the adjacent leaf region. These results strongly suggest that the adjacent response is distinct from the local response, and not simply a weakened version of locally induced responses.The scale of the adjacent response as well as the overlap between local and adjacent responses appears similar to the situation during early (4 hpi) systemic responses to *avrRpm1* in *Arabidopsis*, where 369 genes were up-regulated and 25 down-regulated, with 149 common to the local and systemic response (*avrRpm1*-specific response, (Truman *et al.*, 2007)). As such, the functional profile of genes common to local, and systemic (*Arabidopsis*) or adjacent (barley) responses was compared between the two species (Figure 4.12,

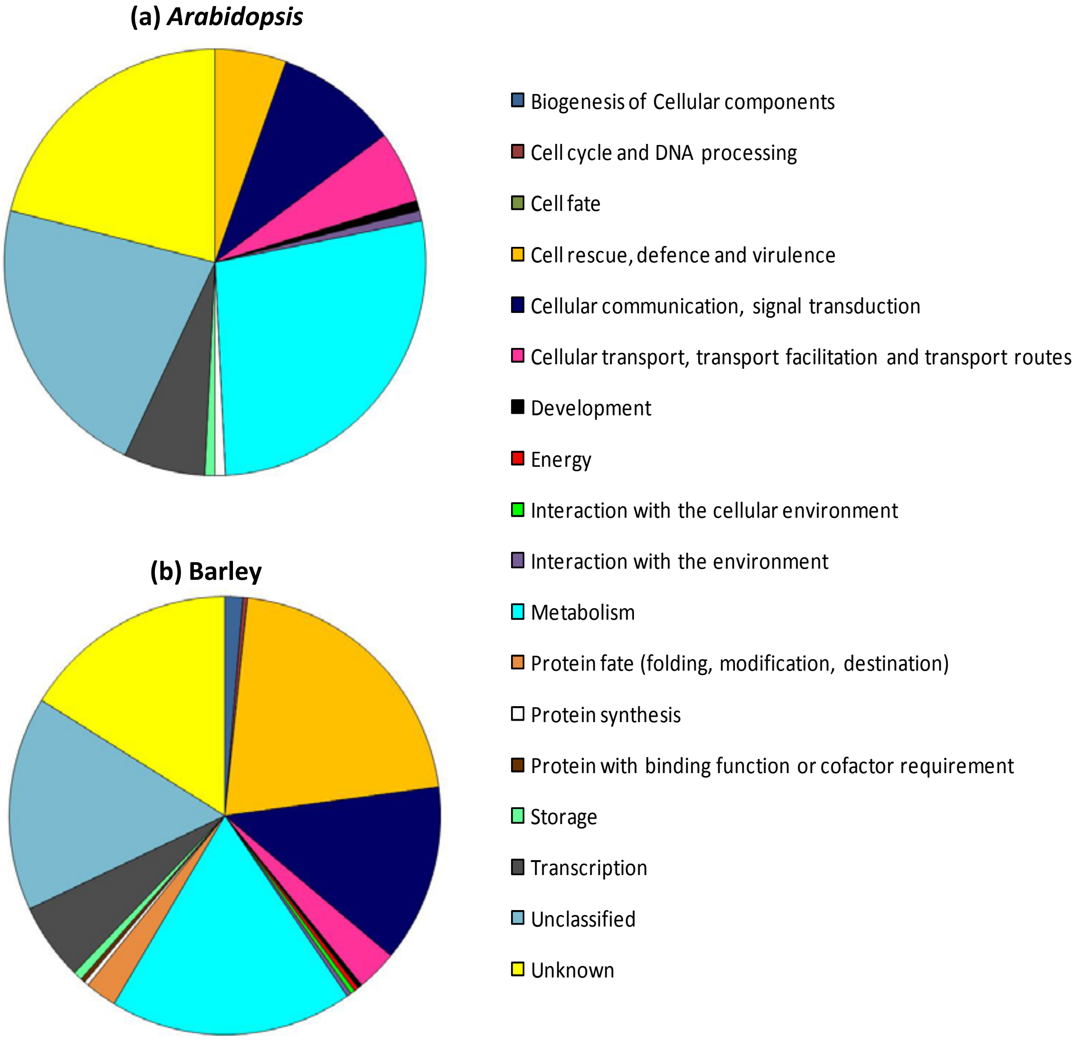


Figure 4.12 Functional categories of genes common to local, and systemic (*Arabidopsis*) or adjacent (barley) response. (a) *Arabidopsis* data taken from Truman et al., 2007 Supplementary Table 3., which shows significantly induced genes common to both innate (basal) defense at 12 hpi (DC3000::hrpA-inducing challenge) and systemic defense (4 hpi, *PstavrRpm1* induced). Genes were assigned MIPS functional categories (http://mips.gsf.de/) based on annotation / Gene Ontology given in Truman *et al.,* 2007. **(b)** Genes common to local and adjacent response 24 hrs after local infiltration with *PstavrRpm1*. Genes assigned functional categories as in Figure 4.10.

Truman *et al.*, (2007) Supplementary data Table 3). Caution must be applied in comparing microarray datasets analysed with different methods, however preliminary comparison suggests both datasets contain a large proportion of transcripts associated with metabolism, transcription and signal transduction. In the *Arabidopsis* dataset, common local and systemic responses include phenylpropanoid and shikimate biosynthesis. The overall systemic response is characterised by jasmonate- biosynthesis and -responsive genes, and also clusters with responses to local wounding and insect feeding (Truman *et al.*, 2007). Here, as in *Arabidopsis*, transcripts associated with phenylpropanoid biosynthesis (PAL and cinnamyl alchohol dehydrogenase) and the shikimate pathway (prephenate dehydratase) were up-regulated, as were transcripts associated with lignin and flavonoid biosynthesis (Figure 4.13). Similarly, genes involved in jasmonate biosynthesis (lipoxygenase, methyljasmonate-inducible lipoxygenase, allene oxide synthase (*AOS*), and 12-oxophytodienoate reductase (*OPR1*)) were up-regulated, as were a putative polygalacturonase and a putative proteinase inhibitor, which could suggest links with local responses to wounding or insect feeding (Bergey *et al.*, 1999, Leon *et al.*, 2001, Ryan, 1990), or to programmed cell death (Solomon *et al.*, 1999). Further similarities between the *Arabidopsis* and barley datasets include the differential expression of heat shock family proteins; bHLH, zinc finger, NAC domain and WRKY transcription factors; cytochrome p450; EF-hand domain containing proteins; leucine rich repeat receptor-like kinases and a nodulin-like protein (Appendix 1).

The full list of defence genes induced in the adjacent region is presented in Table 4.4. As with the local response, these include several PR genes (van Loon *et al.*, 2006), many of which are considered markers of the maintenance phase of SAR (24-48 hpi) in *Arabidopsis* (Maleck *et al.*, 2000, Uknes *et al.*, 1992, Ryals *et al.*, 1996) and / or tobacco (Ward *et al.*, 1991). Inspection of the data by eye suggests that comparison with detailed transcriptional data available for the barley-powdery mildew interaction (Caldo *et al.*, 2004) may be informative. Although 18 of 22 barley genes differentially expressed between virulent or avirulentinteractions with *Bgh* (Caldo *et al.*, 2004) were differentially expressed locally, none were identified from the adjacent leaf region. However, several genes known to be commonly induced in response to avirulent, virulent and non-host powdery mildew isolates (Jansen *et al.*, 2005) were induced here in the adjacent region. This could suggest that the adjacent AR response is similar to basal or non-host defence.

Markers of chemically-induced AR in barley and wheat are differentially expressed

As noted, chemically induced AR in dicots is associated with the induction of ‘SAR genes’ (Friedrich *et al.*, 1996, Uknes *et al.*, 1992, Ward *et al.*, 1991). In wheat and barley, a set of genes associated with chemically-induced AR have also been identified (WCI and BCI genes respectively)

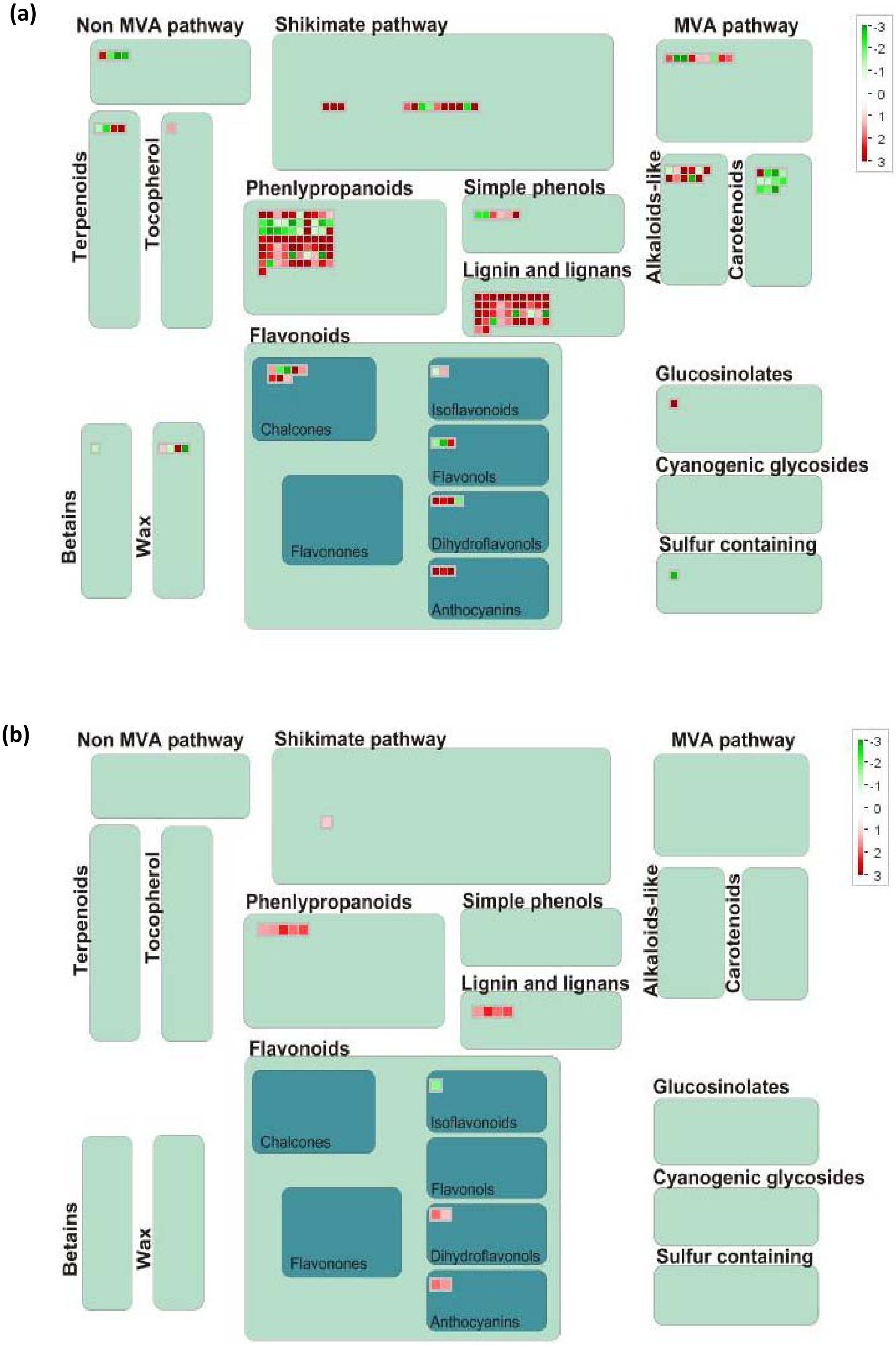


Figure 4.13 Mapman 3.0 analysis of differentially expressed genes involved in secondary metabolism. Differentially expressed genes in the local **(a)** and adjacent **(b)** datasets annotated with EC numbers were mapped to secondary metabolic pathways by Mapman 3.0 (Thimm *et al.*, 2004). Local (199) and adjacent (15) genes were mapped. Individual boxes represent genes, red indicates up-regulation, green indicates down-regulation.

Table 4.4 'Cell rescue, defence and virulence' genes differentially expressed genes in the adjacent leaf region. Genes were assigned functional categories (MIPS functional categories (http://mips.gsf.de/)) based on their annotation. [a] indicates adjacent specific expression, [b] indicates same regulation in local and adjacent, [c] indicates oppositely regulated in local and adjacent leaf regions.

Affymetrix Probe Set ID	Annotation	Regulation	Fold change ($\log_2$)
Contig1570_s_at	Thionin	up[a]	6.10
Contig1580_x_at	Thionin precursor	Up[a]	5.33
Contig8896_s_at	Cysteine proteinase	Up[a]	4.44
Contig1567_x_at	Thionin precursor	Up[a]	3.63
Contig2243_s_at	Wheat aluminum induced protein wali 5	Up[b]	3.55
Contig3017_at	Oxalate oxidase	Up[b]	3.49
Contig2305_at	Methyljasmonate-inducible lipoxygenase 2	Up[a]	3.45
Contig4324_at	Chitinase	Up[b]	3.31
Contig3746_at	Harpin induced gene 1 homolog	Up[b]	2.80
Contig34_s_at	Putative proteinase inhibitor	Up[b]	2.77
Contig19921_at	Immediate-early fungal elicitor protein CMPG1	Up[b]	2.58
rbags15p13_s_at	23 kDa jasmonate-induced protein	Up[b]	2.48
Contig2210_at	Pathogenesis-related protein 1 precursor	Up[b]	2.45
Contig5369_at	Pathogenesis-related protein 1	Up[b]	2.40
Contig3380_s_at	Subtilisin-chymotrypsin inhibitor 2	Up[b]	2.31
Contig2163_at	Pathogen-induced protein WIR1A	Up[b]	2.26
HV14J15u_s_at	Putative beta-1,3-glucanase	Up[b]	2.24
Contig2088_s_at	Bowman-birk type trypsin inhibitor	Up[b]	2.24
Contig8905_at	Xylanase inhibitor protein I	Up[b]	2.24
HVSMEb0010B05r2_x_at	Thionin BTH7 precursor	Up[a]	2.16
Contig15553_at	Putative beta-1,3-glucanase	Up[b]	2.15
EBro03_SQ003_J21_at	Putative peroxidase	Up[b]	2.13
HV_CEb0002J23r2_s_at	Blue copper binding protein	Up[b]	2.10
Contig4324_s_at	Chitinase	Up[b]	2.09
Contig17047_at	Putative stripe rust resistance protein Yr10	Up[a]	2.06
Contig6547_at	Stem rust resistance protein Rpg1	Up[b]	2.05
Contig3315_s_at	Drought-induced hydrophobic protein	Up[b]	1.97
Contig11509_at	Putative peroxidase	Up[b]	1.96
HP01B09w_at	WIR1 protein	Up[b]	1.95
Contig2992_s_at	Chitinase	Up[b]	1.85
Contig10142_at	Dehydration-responsive protein	Up[b]	1.80
Contig634_at	Benzothiadiazole-induced protein (WCI-5)	Up[b]	1.80
Contig9917_at	WIR1 protein	Up[a]	1.74
Contig12574_at	Lipoxygenase	Up[c]	1.71
Contig1582_x_at	Thionin precursor	Up[a]	1.65
Contig2243_at	Wheat aluminum induced protein wali 5	Up[b]	1.58
Contig3744_s_at	Harpin induced gene 1 homolog	Up[b]	1.58
Contig1805_s_at	Phenylalanine ammonia-lyase	Up[b]	1.57
Contig1636_at	Glucan endo-1,3-beta-glucosidase GII precursor	Up[a]	1.46
rbah13p07_s_at	Peroxidase	Up[b]	1.45
Contig13544_at	Putative Avr9/Cf-9 rapidly elicited protein 231	Up[b]	1.42
Contig9632_at	Glutathione S-transferase	Up[b]	1.41
Contig1639_at	Glucan endo-1,3-beta-glucosidase GII precursor	Up[a]	1.40
Contig538_at	Benzothiadiazole-induced protein (WCI-5)	Up[b]	1.36
Contig10193_at	Elicitor-responsive protein	Up[b]	1.35
HVSMEn0015O15f_s_at	Putative respiratory burst oxidase	Up[c]	1.32
HVSMEa0011L14r2_s_at	Glutathione S-transferase	Up[b]	1.29
Contig6230_at	Putative nematode-resistance protein	Up[a]	1.26
Contig939_s_at	Pathogen-induced protein WIR1A	Up[a]	1.21
Contig2990_at	Chitinase	Up[b]	1.21
HVSMEf0020A12r2_s_at	Lipoxygenase	Up[b]	1.19
Contig813_at	Pathogen-induced protein WIR1A	Up[a]	1.18
Contig14679_at	Xylanase inhibitor	Up[b]	1.18
HVSMEb0006O01r2_at	Mlo3	Up[b]	1.17
Contig1852_at	Peroxidase 7	Up[b]	1.16
HVSMEf0019G16r2_at	Putative copper homeostasis factor	Up[a]	1.16
Contig7415_at	Putative glutathione transferase	Up[b]	1.14
Contig2306_s_at	Methyljasmonate-inducible lipoxygenase 2	Up[a]	1.10
HVSMEb0017H11f_at	Putative PrMC3	Up[a]	1.10
Contig2112_at	Peroxidase	Up[b]	1.09
Contig12649_at	Cell death associated protein	Up[b]	1.07
Contig2213_s_at	Pathogenesis-related protein bpr1-1 precursor	Up[b]	1.05
HX14B03r_at	TMV response-related gene product	Up[b]	1.02
Contig10004_at	Putative thaumatin-like protein	Up[b]	1.01
Contig3901_s_at	Cysteine proteinase precursor	Down[a]	-1.22

(Besser *et al.*, 2000, Gorlach *et al.*, 1996). These genes are not induced by powdery mildew, leading to suggestions that chemical and biologically induced AR in wheat and barley act via different signalling pathways, unlike the dicot situation (Besser *et al.*, 2000, Jansen *et al.*, 2005, Schaffrath *et al.*, 1997). Here, all 9 of the BCI genes, as well as several homologues of the WCI genes, are differentially expressed, either locally (*BCI-5* to *8*; *WCI-1*, *2* and *4*), in the adjacent leaf region (*BCI-1*), or in both (*BCI-2,3* and *9*; *WCI-5*) (Table 4.5). Focussing on the BCI genes, *BCI-3*, *5, 6, 7*, and *8* were down-regulated locally, wheras all genes differentially expressed in the adjacent leaf region were up-regulated. Local down-regulation contrasts with chemically induced AR, where all but *BCI-8* were up-regulated (although *BCI-3* was also down-regulated in response to powdery mildew (Besser *et al.*, 2000)). Here, two genes differentially expressed in both the local and adjacent leaf regions (*BCI-3* and *BCI-9*) are down-regulated locally, and up-regulated in the adjacent region. The up-regulation of 5 of the 9 described BCI genes in the adjacent leaf region strongly suggests a common signalling pathway is involved in *Pseudomonas*-induced and chemically-induced AR in barley, in contrast to previous reports for powdery mildew. However, this approach has also shown that these genes make up only a small proportion of those differentially expressed, and their relative contributions to AR have yet to be determined. Examining the expression profiles of these genes over a detailed time course would allow further unravelling of their roles and of the link between local and adjacent expression.

4.3.6 Validation of microarray data

One aim of the microarray study described above was to identify genes more reliably associated with the adjacent resistance response than the previously used marker genes, *PR1*, *prx8* and *PAL*. The microarray study was carried out on seedlings that had shown strong adjacent resistance (Figure 4.9) to maximise the likelihood of identifying the genes involved. It was therefore important to validate the array results by comparing the expression of a selection of genes in independent experiments (Figure 4.14). Five genes identified from the array study were tested using qRT-PCR. The genes tested covered range of expression profiles: local and adjacent; local specific; adjacent specific; and both up and down-regulated. A strong correlation was found between qRT-PCR (means from 3 independent experiments) and array data (r^2=0.91). Adding 2 genes identified before the array experiment as variable (*PR1* and *prx8*) to the analysis reduced the correlation to r^2=0.76, as expected. As such, the array experiment was successful in identifying more reliable marker genes. Although the *PR1* and *prx8* genes tested previously in this chapter were not identified by the array experiment as differentially expressed in the adjacent leaf region,

B/WCI	Affymetrix Probe Set ID	Annotation	Functional Category	Fold Change ($\log_2$)	
				Local	Adjacent
BCI-1	Contig2305_at	Methyljasmonate-inducible lipoxygenase 2	Cell rescue, defence and virulence		3.45
	Contig2306_s_at	Methyljasmonate-inducible lipoxygenase 2	Cell rescue, defence and virulence		1.10
BCI-2	Contig1580_x_at	Thionin BTH7 precursor	Cell rescue, defence and virulence		5.33
	Contig1582_x_at	Thionin BTH7 precursor	Cell rescue, defence and virulence		1.65
	Contig1567_x_at	Thionin BTH7 precursor	Cell rescue, defence and virulence		3.63
	Contig1568_x_at	Thionin BTH7 precursor	Cell rescue, defence and virulence	3.51	
BCI-3	Contig2433_s_at	Putative acid phosphatase	Cellular communication/signal transduction	-1.75	2.01
BCI-4	AJ250283_at	Putative calcium binding EF-hand protein	Cellular communication/signal transduction		2.71
BCI-5	Contig9436_at	Putative plastid-specific ribosomal protein 2	Protein synthesis	-3.1	
BCI-6	Contig2289_s_at	Putative diphosphonucleotide phosphatase	Metabolism	-1.46	
BCI-7	Contig1010_at	Subtilisin-chymotrypsin inhibitor	Cell rescue, defence and virulence	1.28	
BCI-8	Contig9168_s_at	Plastid omega-3 fatty acid desaturase	Metabolism	-3.58	
	Contig9169_at	Plastid omega-3 fatty acid desaturase	Metabolism	-3.57	
BCI-9	Contig3332_at	Apyrase-like protein	Metabolism	-1.69	1.16
WCI1 (AK249973.1)	HVSMEm0015P16r2_at	Jasmonate-induced protein	Cell rescue, defence and virulence	-2.32	
WCI2 (AK248346.1)	Contig1735_s_at				
	Contig1736_at*	Lipoxygenase	Cell rescue, defence and virulence	1.72	
WCI-4 (AM941126.1)	Contig2988_s_at	Cysteine proteinase	Cell rescue, defence and virulence	-3.27	
WCI-5 (EU131175)	Contig538_at	Benzothiadiazole-induced protein (WCI-5)	Cell rescue, defence and virulence	1.69	1.36

Table 4.5 Expression of Barley Chemically Induced (BCI) and Wheat Chemically Induced (WCI) genes in the local and adjacent leaf regions 24 hrs post local infiltration with *PstavrRpm1*. Gene accession numbers (Besser et al., 2000, Gorlach et al., 1996, Pasquer et al., 2005) were used to identify the representative nucleotide sequence. The most similar Affymetrix exemplar sequence was then identified by performing BLASTn against Barley Exemplar sequences (NetAffx^{TM}(www.affymetrix.com/analysis)). * indicates the most similar probe set was not represented in the dataset, but another similar probe set was present (probe ID indicated). For WCI genes, BLASTn of wheat nucleotide sequence was performed against barley to identify the closest homologue (given in brackets).

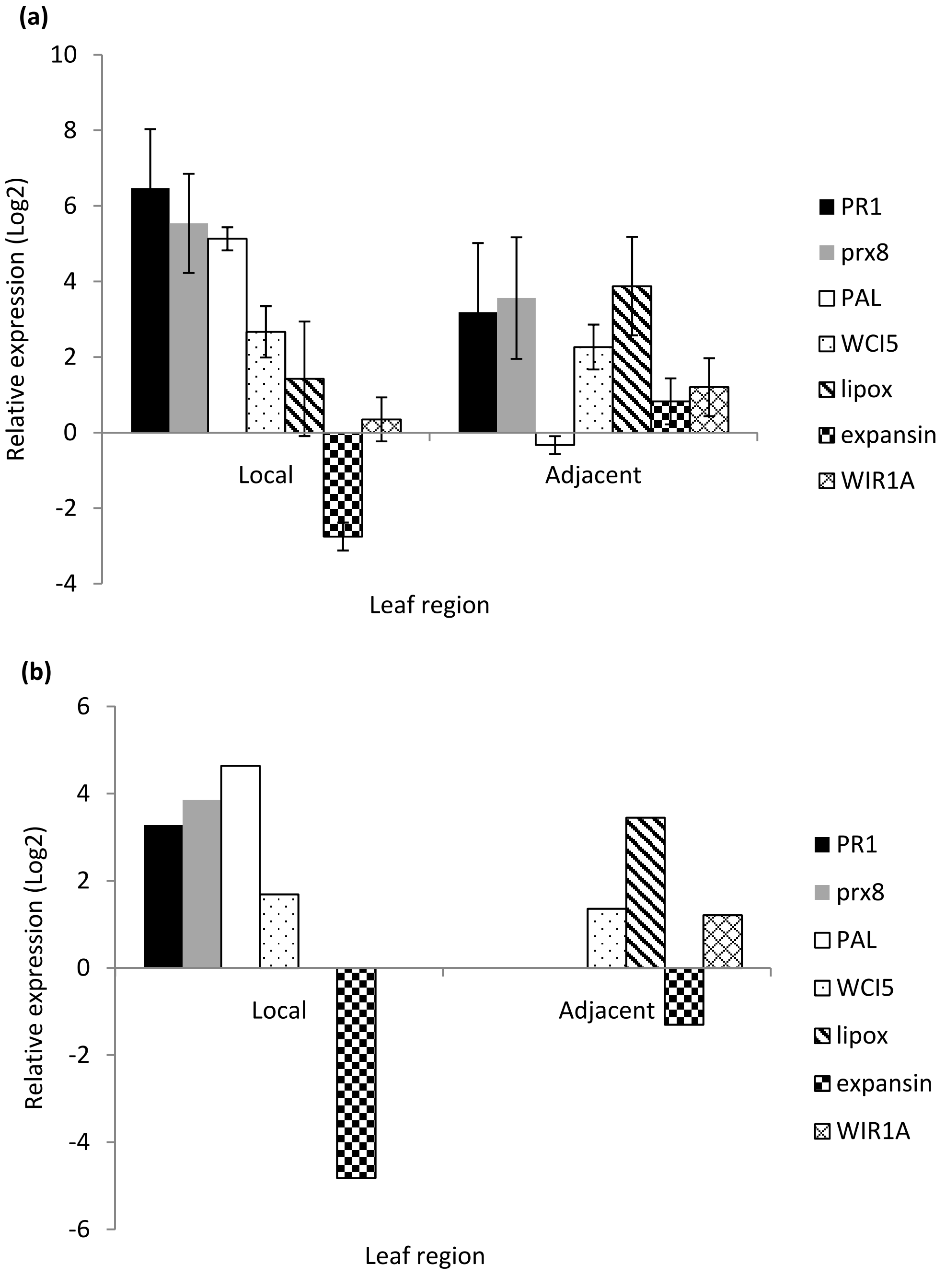


Figure 4.14 Validation of selected differentially expressed genes using qRT-PCR. (a) Expression of seven genes was investigated in local, *PstavrRpm1* infiltrated and adjacent leaf regions 24 hours post *PstavrRpm1* infiltration. For each gene, relative expression was calculated relative to the water infiltrated control. Bars show mean values from 3 independent experiments (each of 3 biological replicates) ± SE. Genes shown are / have closest homology to: PR1 (Contig2212_s_at); prx8 (Contig2119_at); PAL (*Phenylalanine-ammonia-lyase*, Contig1803_at); WCI-5 (*Wheat Chemically Induced-5*, Contig538_at); lipox (Methyl-jasmonate inducible lipoxygenase 2, Contig2305_at); expansin (Contig3674_at); and WIR1A (*Wheat Induced Resistance 1A*, Contig939_s_at).**(b)** Equivalent values from microarray, for comparison. Where bars are missing genes were not identified as differentially expressed.

several *PR1* and peroxidase transcripts were induced. It is important that future tests using these genes target the appropriate gene family members.

4.3.7 Responses in secondary leaves

As noted, preliminary analysis of second leaf responses suggested AR was not induced in secondary leaves under the conditions tested. Challenging secondary leaves of Golden Promise with PS86 at time-points up to 9 days post *PstavrRpm1* infiltration of the first leaf failed to show any AR (Figure 4.8). To examine secondary leaf responses in more detail, samples from secondary, non-infiltrated leaves were taken at time-points up to 6 days following *PstavrRpm1* infiltration of the first leaf. qRT-PCR was performed on selected genes. Genes associated with adjacent AR may be induced in the secondary leaf 24 hours post infiltration of the first leaf (Figure 4.15). *WCI-5* in particular is reliably associated with adjacent AR (Figure 4.14), and appears to be induced 1 and 2 dpi in secondary leaves. There may also be enhanced expression 6 dpi (Figure 4.15). However, the data presented is variable, more genes need to be tested and the experiment needs to be repeated before firm conclusions can be drawn. The future approach to examining resistance responses induced in secondary leaves is discussed below.

4.4 Discussion

4.4.1 Adjacent acquired resistance in barley

The results presented show that *PstavrRpm1* induces broad spectrum AR in first leaves of Golden Promise seedlings, at a distance from the local lesion. This contrasts with the AR induced by powdery mildew in the species, which appears to be strictly localised (Kunoh, 2002, Ouchi et al., 1976), and shows that biologically induced AR can be translocated in barley, albeit within-leaf at this stage. It is notable that local responses to *PstavrRpm1* and avirulent *Bgh* appear to be similar (Table 4.3), yet the spatial profile of the response differs. This apparent failure of powdery mildew to induce a translocated AR raises several questions. The translocation of AR induced by powdery mildew appears to have been tested only by challenge with virulent isolates of the same pathogen. As such, it is possible that AR induced by powdery mildew is translocated, and is effective at a distance against other challenger pathogens. In that case, the 'failure' of the AR against a powdery mildew challenger could be related to the pathogen's highly coevolved relationship with barley (ie effector-mediated suppression could overcome the translocated AR), or the AR could be ineffective against the pathogen, for example, if powdery mildew induced resistance is mediated by a different pathway. The latter seems unlikely however, especially given

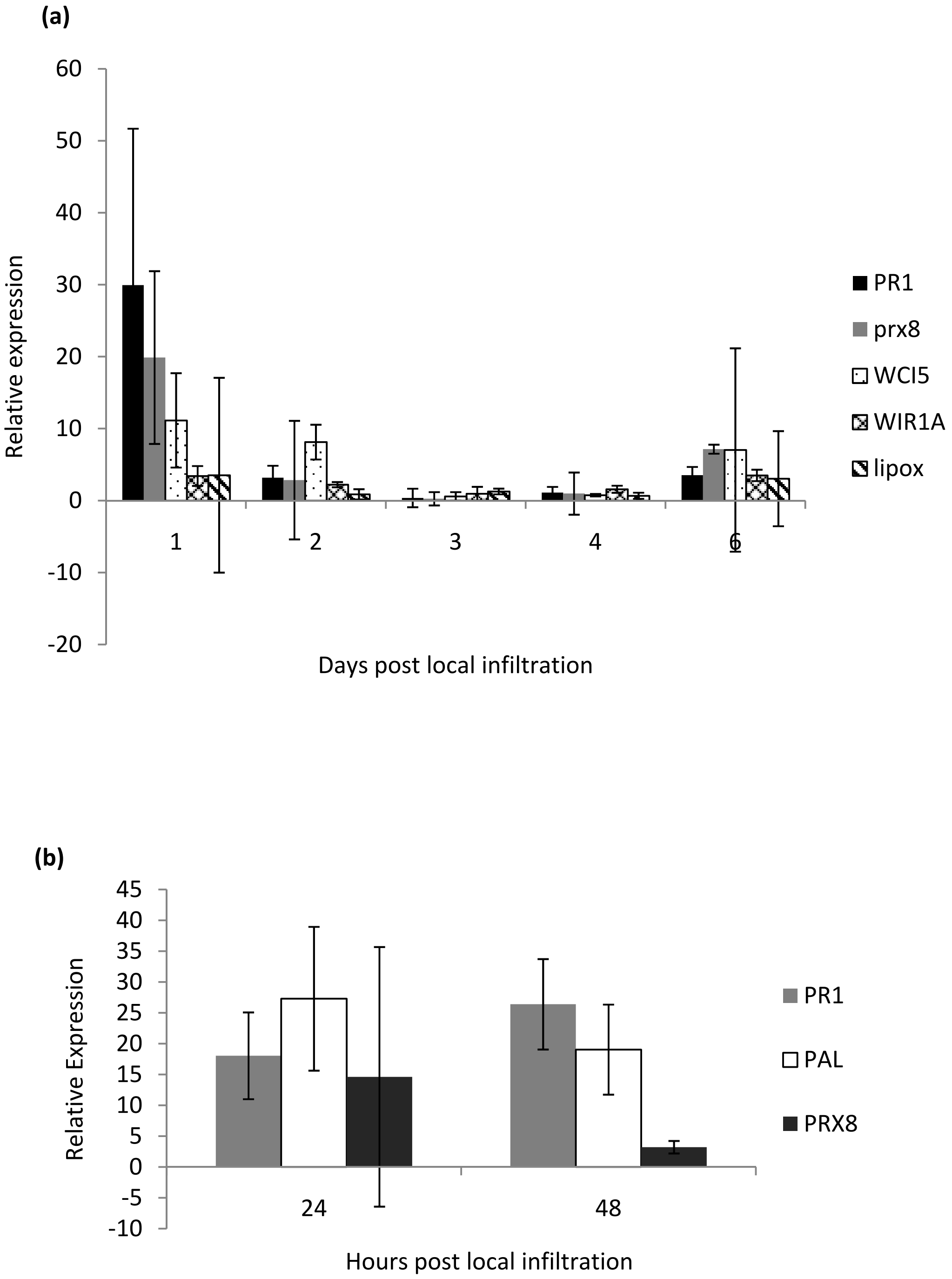


Figure 4.15 Relative expression of genes associated with adjacent AR response in secondary leaf 1 – 6 days post local infiltration of first leaf (a). qRT-PCR data. Bars show mean relative expression (calculated relative to water control for each gene, water control set to 1) of three biological replicates ± SD. Transcript levels were normalised to *α-tubulin 2 and UBC*. **(b) Local PR gene responses were consistent with those seen in previous experiments.**

that chemically-induced AR has been described as a 'phenocopy' of Mlg-mediated powdery mildew resistance (Kogel *et al.*, 1994). The effectiveness of biologically-induced AR against powdery mildew could easily be tested by determining whether *Pseudomonas*-induced adjacent AR is effective against powdery mildew. An alternative (or additional) hypothesis is that powdery mildew may fail to induce a translocated AR response.

As previously described for chemically-induced and localised powdery mildew-induced AR (Jarosch *et al.*, 2003), the *Pseudomonas*-induced AR was effective against *Magnaporthe oryzae*. Alongside transcription data showing differential expression of BCI and WCI genes in the adjacent leaf region, these results suggest that chemically-induced and biologically-induced AR in barley could be mediated by a common signalling pathway. To test this further, it may be informative to compare the mechanisms of resistance; as previously noted, both chemically and mildew-induced AR to *Magnaporthe* appear to be effected via enhanced penetration resistance (Jarosch *et al.*, 2003). Interestingly, Jarosch *et al*., (2003) report that expression of several PR genes is linked to susceptibility to *Magnaporthe*, rather than to AR. The results presented here suggest that these genes (*PR1b*, *PR9*, *PR5*) are up-regulated prior to pathogen challenge in adjacent AR. Profiling the expression of these genes from the induction of adjacent AR to post-*Magnaporthe* challenge may provide insights into a switch from defence to general stress responses.

4.4.2 Transcriptional profiling

The transcriptional profile of adjacent AR was studied, and comparisons made to profiles obtained for *Arabidopsis* SAR (Maleck *et al.*, 2000, Scheideler *et al.*, 2002, Truman *et al.*, 2007), chemically induced AR in barley and wheat (Besser et al., 2000, Gorlach et al., 1996), and barley powdery mildew resistance (Caldo et al., 2004, Jansen et al., 2005). In the local interaction between *Arabidopsis* and *PstavrRpt2* (Scheideler *et al.*, 2002), the number of differentially expressed genes increased from 10 minutes post infection (415 up-regulated, 248 down-regulated) to 7 hpi (950 up-regulated, 927 down-regulated). By the time of HR associated cell collapse (24 hpi) the number of differentially expressed genes had decreased (105 up-regulated, 927 down-regulated) (Scheideler *et al.*, 2002). Here, in the barley interaction, macroscopic necrosis was not seen until 24 hours later (48 hpi), and although a detailed time course study is required to investigate the relative kinetics of the two interactions, this may suggest that in this study the 24 hr time-point is closer to the peak in transcriptional activity. Compared to *Arabidopsis-PstavrRpt2*, approximately twice as many genes were differentially regulated in the barley-*PstavrRpm1* interaction. This could be explained by the relative genome coverage of the arrays used – Scheidler *et al*. (2002) use a custom array with around 5200 unique cDNA clones (around 20% of the *Arabidopsis* genome (Bevan *et al.*, 2001)) whilst the Barley1 GeneChip barley is thought to contain around 14,000 unique genes (approximately 30% of the barley genome (Close, 2005)). Functionally, the *Arabidopsis* interaction is characterised by a shift from housekeeping to defence metabolism, a similar shift is also seen here with down-regulation of photosynthetic processes and up-regulation of secondary metabolism and defence-related transcripts (Figure 4.11).

The scale, functional profile and predicted functions / identities of genes differentially expressed in the adjacent leaf region are similar to the early stage of SAR establishment in *Arabidopsis* (Truman *et al.*, 2007) (Figure 4.12). Markers of the 'maintenance' phase of *Arabidopsis* SAR (48-72 hpi), *PR1*, *PR2*, *PR5* (Uknes *et al.*, 1992) and other members of the *PR1* regulon (Maleck *et al.*, 2000) were also induced. Similarly, markers of SAR in tobacco include *PR1*, β-1-3-glucanases (*PR2* family), class II and III Chitinases (*PR3* family), a hevein-like protein (*PR4*) family, and a thaumatin-like protein (*PR5* family) (Friedrich *et al.*, 1996, Ward *et al.*, 1991); almost all of which were differentially expressed here in the adjacent leaf region. The similarity between these expression profiles strongly suggests that the adjacent AR described here and the dicot SAR response could be analagous. However, even within dicot species, there is some variation in the identity and relative expression of SAR marker genes ((Kessmann *et al.*, 1994, Ryals *et al.*, 1996)), and the global approach taken here is therefore valuable in providing a full profile of the genes involved in the barley AR response. Further, preliminary analysis suggests the adjacent AR response may involve genes associated with basal defence against powdery mildew. This again would support the involvement of an analogous pathway to that induced in *Arabidopsis* (as the SAR response induced by *PstavrRpm1* in that species is similar to basal resistance to *Pseudomonas* (Truman *et al.*, 2007)). Further analysis using an hierarchical clustering approach could be used to provide a more detailed picture of similarity with transcriptional responses to other treatments.

Chemically-induced AR in barley and wheat is associated with the expression of the BCI/ WCI genes (Besser *et al.*, 2000). Here, all BCI genes (and WCI gene homologues) were differentially expressed either locally, and/ or in the adjacent leaf region. Global expression changes in wheat after BTH treatment were examined by Pasquer *et al*. (2005). As expected, *WCI-1, 2, 4*, and *5* were induced, however only 17 genes were differentially expressed, in comparison to the 343 genes differentially expressed here in *Pseudomonas*-induced adjacent AR. This indicates that the establishment of biologically-induced AR involves more extensive transcriptional reprogramming than the chemically-induced response, and also highlights that only a small number of the genes differentially expressed in biologically-induced AR may function in effecting the resistance.

Hormone based signalling pathways play a key role in triggering inducible defence responses in plants, and both SA and JA are known to accumulate locally and systemically during SAR development (Truman *et al.*, 2007, Uknes *et al.*, 1992, Ward *et al.*, 1991). In *Arabidopsis* and tobacco, SA accumulation in systemic tissue is required for the nuclear translocation of key SAR regulator NPR1, and as such the subsequent development of SAR (Kinkema *et al.*, 2000). JA is also important, with some JA synthesis mutants defective in SAR, and JA-dependent gene expression correlated with the onset of SAR in *Arabidopsis* (Truman *et al.*, 2007, Vlot *et al.*, 2008a). Here, the differential expression of key JA synthesis genes in the local and adjacent leaf region (lipoxygenase, methyljasmonate-inducible lipoxygenase, allene oxide synthase (*AOS*), and 12-oxophytodienoate reductase (*OPR1*)) suggest that the JA pathway is also important in the barley AR response. The induction of PAL and shikimate biosynthesis suggests SA could also be involved, although key SA synthesis enzyme isochorismate synthase (Wildermuth *et al.*, 2001) does not appear to be differentially expressed. Chemically-induced AR in wheat also leads to jasmonate-dependent gene expression (Gorlach *et al.*, 1996, Pasquer *et al.*, 2005). Whilst these results do suggest common plant hormone-based signalling pathways between dicots and the cereals, much work remains to be done to understand these responses in the cereals. Application of SA induces only weak WCI gene expression in wheat (Gorlach *et al.*, 1996), unlike in *Arabidopsis* where SA and its chemical analogues induce similar responses (Uknes *et al.*, 1992). In terms of pathogen interactions, SA accumulates in barley after insect feeding (Chaman *et al.*, 2003) and *Pss* infiltration, but not after powdery mildew inoculation (Vallelian-Bindschedler *et al.*, 1998). Genetic studies are needed to fully dissect these pathways and responses in the cereals, particularly if we are to fully understand complex hormone dependent responses such as SAR.

4.4.3 From adjacent AR to SAR

Global transcriptional profiling of the local and adjacent response of barley to *PstavrRpm1* has helped to identify genes that are more reliably associated with the adjacent resistance response than marker genes used in earlier work in this chapter. This transcriptional profile provides a resource that can be developed in several future studies. Investigating the expression profiles of a range of these genes over a time-course is a priority, not only to provide more information about the development of the adjacent (and systemic) AR response, but also to improve understanding of the local, barley-*PstavRpm1* interaction.Virulent, avirulent, and non-host interactions with *Pseudomonas* involve similar gene sets, but differ quantitatively in expression profile over time (Tao *et al.*, 2003). As such, comparing the expression of key genes over time (to develop the work described in Chapter 3) would allow further optimisation of the local interaction with the aim of creating 'ideal' conditions for identifying adjacent or systemic AR.

Under the conditions tested here, the AR response did not appear to be translocated to secondary leaves. However, the tests conducted are far from exhaustive. Although there is evidence to suggest the SAR response develops in leaves of both young and old leaves of *Arabidopsis*, and is translocated to both younger and older leaves (Kiefer & Slusarenko, 2003, Zeier, 2005), this may not be the case in barley. In order to comprehensively test for the response a range of combinations of 'induced' and challenged leaves must be tested (eg *PstavrRpm1* infiltration of second leaf, challenge of first leaf; infiltration of first leaf, challenge of newly unfolded leaf 48 hours later, etc). These tests can be informed both by work in *Arabidopsis* ((Kiefer & Slusarenko, 2003, Zeier, 2005)), and information about patterns of assimilate-transport in cereals, such as that provided by tests with viruses (Haupt *et al.*, 2001, Lucy *et al.*, 1996). qRT-PCR may prove a sensitive tool for identifying transcriptional changes associated with AR in secondary leaves, to inform pathogen challenge experiments.

The identification here of the adjacent AR response in barley suggests comprehensive testing of secondary leaves could prove fruitful in the search for SAR. However, it should be noted that there is no direct evidence from model systems that within-leaf resistance leads to the development of SAR, or that the signals involved are the same. Evidence from tobacco indicates that the LAR signal(s) diffuse(s) from the lesion into the 5 mm surrounding zone, which develops near immunity and accumulates high levels of secondary metabolites (Dorey *et al.*, 1997). The pattern of AR to TMV in tobacco suggests that outside of this zone, but within-leaf, the response is translocated via the veinal system, which could be compatible with the transport of a phloem-mobile signal (Ross, 1961a). In a spatio-temporal scheme of LAR and SAR signalling events proposed by Dorey et al. (1997), the LAR zone 2 (the 5 mm surrounding the lesion) produces the SAR signal, as HR and subsequent cell death limits the role of directly attacked cells. Zone 3 (equivalent to the adjacent region of the barley leaf described here) is expected to develop a 'SAR' response (within-leaf) (Dorey *et al.*, 1997). The most direct route to dissecting the relationship between LAR and SAR would begin with testing the LAR response in mutant lines specifically deficient in SAR (with wild-type local resistance). However, such lines are not currently available in tobacco, and LAR has not been well-studied in *Arabidopsis*. Despite this, our understanding of SAR signalling in dicots has improved in recent years (Vlot *et al.*, 2008a). Alongside further testing of secondary leaf responses, the identification and over-expression of cereal homologues of SAR-specific signalling components from model systems may be a promising avenue to explore in investigating the translocation of the AR response. This will be addressed in the following chapter.

Chapter 5: Investigating conservation in cereals of the SAR-specific *Arabidopsis* gene *Defective in Induced Resistance 1* (*DIR1*)

5.1 Aim

The data presented in this chapter describes several approaches to investigate the capacity of cereals to mount biologically induced SAR. The first approach involves the identification and testing of homologues of the SAR-specific *DIR1* gene. Variation in AR between Golden Promise and barley landraces is also considered. The *Pseudomonas*-based assay described in Chapters 3 and 4 is used throughout.

5.2 Introduction

The conservation of molecular components of the SAR response between *Arabidopsis* and the cereals was outlined in Section 1.6. The identification of the rice homologue of key *Arabidopsis* SAR regulator NPR1 strongly suggests conservation of an NPR1-mediated signalling pathway in the monocots (Chern *et al.*, 2005, Yuan *et al.*, 2007). In *Arabidopsis*, NPR1 regulates the expression of PR genes in acquired resistance, including SAR (Cao *et al.*, 1994, Delaney *et al.*, 1995, Glazebrook *et al.*, 1996). *Os*NPR1 appears to function in the same way as the *Arabidopsis* protein; nuclear localisation is required for function, the protein regulates the expression of SA responsive PR genes as well as antagonistically mediating JA-regulated genes and responses; and over-expression leads to enhanced disease resistance (Chern *et al.*, 2005, Yuan *et al.*, 2007). Heterologous expression of *AtNPR1* in rice leads to similar disease resistance and antagonistic regulation of JA-related responses. There are however some differences in regulation between *Arabidopsis* and rice- *NPR1* appears to activate defence more readily in rice than in *Arabidopsis*, and also appears to be involved in rice in the regulation of SA in response to environmental changes (Chern *et al.*, 2001, Quilis *et al.*, 2008). In wheat, expression of *AtNPR1* leads to enhanced resistance to Fusarium head blight, without the regulatory differences seen in rice (which are likely to be related to the unusually high basal SA levels found in that species) (Makandar *et al.*, 2006). Together this evidence indicates that an NPR1 mediated signalling pathway is conserved in the cereals. However, in *Arabidopsis*, NPR1 does not function specifically in SAR. NPR1 is required for local basal resistance to *Pseudomonas*, and is also a key regulator of ISR (Cao *et al.*, 1994, Pieterse *et al.*, 1998). *OsNPR1* is likely to be similarly involved in local resistance in rice, as expression under its native promoter in the *Arabidopsis npr1-1* mutant restores basal resistance against *Pst* DC3000 (Yuan *et al.*, 2007). Because of its role in local disease resistance and other signalling pathways, the conservation of *NPR1* in the cereals does not necessarily suggest that a full, functional SAR induction pathway is also conserved. Furthermore, resistance resulting from over-expression of *NPR1* represents the systemic expression of local resistance, rather than a true, systemically transmitted, SAR response. The identification of functional cereal homologues of SAR-specific genes would strongly suggest the conservation of a SAR signalling pathway in the cereals.

There is further evidence to suggest that downstream of NPR1, a SAR pathway is conserved in the cereals. SA analogues BTH and INA induce AR in both *Arabidopsis* and cereal species. It has been argued that chemically-induced AR in cereals is mediated by a separate pathway to biologically induced AR, unlike in *Arabidopsis* (Besser et al., 2000, Jansen et al., 2005, Schaffrath et al., 1997, Schweizer et al., 1999). However, data presented in the previous chapter (Section 4.3.5 and 4.4) suggests this is not the case for *Pseudomonas*-induced AR in barley. Importantly, Chaturvedi *et al*. (2008) report that application of petiole exudate from SAR-induced wild-type *Arabidopsis* seedlings to wheat ears induced resistance to Fusarium head blight (*Fusarium graminearum*). Petiole exudate from mock-induced wild-type, or the *sfd1* mutant (deficient in production of a glycerolipid involved in SAR signalling (Nandi *et al.*, 2004)) failed to induce resistance (Chaturvedi *et al.*, 2008). Together, this evidence suggests that downstream of the perception of a (conserved) SAR signal, or SA, rice and other cereal species can mount a SAR response. However, there is no evidence of conservation of molecular components specifically involved in the production, or transmission, of a systemic SAR signal(s) from an ‘induced’ leaf. Several genes have now been described that function specifically in this part of the SAR pathway in *Arabidopsis* (Maldonado *et al.*, 2002, Nandi *et al.*, 2004, Chaturvedi *et al.*, 2008).

Arabidopsis Defective in Induced Resistance 1 (*DIR1*) was the first SAR specific gene to be identified (Maldonado *et al.*, 2002). The *dir1-1* mutant responds as wild-type to local interactions with virulent and avirulent bacterial isolates, however SAR is abolished. Petiole exudate from ‘induced’ *dir1-1* seedlings fails to induce SAR in naïve seedlings, yet the application of exudate from induced wild-type seedlings to *dir1-1* plants leads to the establishment of SAR. This indicates that the SAR defect is limited to the production or transmission of the SAR signal from the induced leaf. In contrast to the situation for *npr1* mutants (Cao *et al.*, 1994, Delaney *et al.*, 1995), the application of INA rescues the *dir1-1* defect, indicating that DIR1 functions upstream of NPR1 in the systemic response (Maldonado *et al.*, 2002). *DIR1* encodes a non-specific Lipid Transfer Protein (nsLTP) (Lascombe *et al.*, 2008, Maldonado *et al.*, 2002), and data from other mutants with SAR-specific defects indicates that it may interact with a glycerolipid derived factor to produce/ transmit a SAR signal (Chaturvedi *et al.*, 2008, Vlot *et al.*, 2008a). Overexpression of *DIR1* does not lead to constitutive SAR in *Arabidopsis* (Maldonado *et al.*, 2002) – again indicating that another factor, produced during the biological induction of SAR, is needed for its function. DIR1 appears to be conserved between species, as a putative *DIR1* orthologue has been detected in the phloem exudate of tomato (Mitton *et al.*, 2009). This apparent conservation, in addition to its specific role in SAR, make *DIR1* an excellent candidate for investigation in the cereals. Identification of functional *DIR1* homologues would strongly suggest that cereal species have the capacity to mount a SAR response.

Non-specific LTPs exist in complex multigene families in *Arabidopsis*, rice and other cereals (Arondel *et al.*, 2000, Boutrot *et al.*, 2005, Boutrot *et al.*, 2008, Vignols *et al.*, 1997), and appear to be ubiquitous in, and restricted to, higher plants (Yeats & Rose, 2008). Proteins in this family share an identical motif of 8 cysteine residues, forming 4 intrachain disulfide bridges, and structural studies indicate the presence of a flexible hydrophobic cavity which interacts non-specifically with lipid molecules (Carvalho & Gomes, 2007, Lee *et al.*, 1998, Samuel *et al.*, 2002, Shin *et al.*, 1995). nsLTPs are typically extracellular, with an amino terminal signal peptide (excised to form the mature peptide) targeting the mature peptide to the cell secretory pathway (Bernhard *et al.*, 1991, Carvalho & Gomes, 2007). Two major subfamilies have been described, designated LTP_1 and LTP_2. Proteins are classified by their molecular weight; LTP_1 family proteins have a molecular weight of around 10kDa, and are encoded by 90-95 amino acids, whereas LTP_2s are usually around 7kDa, encoded by 70 amino acids (Carvalho & Gomes, 2007). LTP_2s also contain a mismatch in the disulfide linkage of cysteine residues when compared to LTP_1s (Douliez *et al.*, 2001). Despite these differences, secondary and tertiary structures appear to be analogous between the two subfamilies (Hoh *et al.*, 2005). Amino acid sequence identity between LTP_1 and LTP_2s is not highly conserved (Douliez *et al.*, 2000), and proteins group by subfamily rather than species (Boutrot *et al.*, 2008). However, identity can be as high as 79% within the *Arabidopsis* LTP_1 subfamily (Arondel *et al.*, 2000). This similarity between gene family members could complicate the accurate identification of homologues. However, structural analysis of DIR1 indicates that the protein is an atypical LTP_2, with a characteristic proline rich domain (Lascombe *et al.*, 2008). Furthermore, a genome-wide analysis of LTP-like genes by Boutrot et al (2008) indicates that there may be up to nine LTP subfamilies in *Arabidopsis* and rice, with DIR1 and its tandem duplicated repeat (At5g48490) part of the small type IV subfamily which has homologues in rice and wheat (Boutrot *et al.*, 2008). The atypical sequence of DIR1 may increase the accuracy of homologue identification.

Functionally, ns-LTPs transfer lipids between membranes *in vitro* (Douliez *et al.*, 2001, Kader, 1997)). Their *in vivo* physiological role has not been fully determined (Carvalho & Gomes, 2007, Yeats & Rose, 2008). The expression pattern and localisation of LTP_1s suggest their involvement in a wide range of biological processes, including cutin synthesis (Pyee *et al.*, 1994), lipid metabolism (Tsuboi *et al.*, 1992), vegetative and reproductive growth and development (Park *et al.*, 2000, Soufleri *et al.*, 1996, Sterk *et al.*, 1991), plant signalling (Blein *et al.*, 2002, Buhot *et al.*, 2001, Buhot *et al.*, 2004), and direct antimicrobial activity against phytopathogens (Cammue *et al.*, 1995, Kristensen *et al.*, 2000, Molina *et al.*, 1993, Regente *et al.*, 2005, Segura *et al.*, 1993). This antimicrobial activity- possibly due to direct effects on membrane permeability (Regente *et al.*, 2005) - has lead to the LTP family being designated PR14 (Pathogenesis-Related 14) (van Loon *et al.*, 2006). In terms of disease resistance signalling, LTP_1s compete with oomycete elicitins for high-affinity receptor binding sites (Blein *et al.*, 2002, Buhot *et al.*, 2001), and tobacco LTP_1 induces resistance in tobacco when applied with its ligand, JA (Buhot *et al.*, 2004). Transcriptionally, some LTP genes are responsive to disease and environmental stress and there are examples from both subfamilies of LTPs regulated by plant hormones such as ABA, SA, ethylene and MeJA (García-Garrido *et al.*, 1998, García-Olmedo *et al.*, 1995, Hughes *et al.*, 1992, Jang *et al.*, 2004, Jung *et al.*, 2003, Plant *et al.*, 1991, Vignols *et al.*, 1997). Given the putative involvement of nsLTPs in such a wide range of biological processes, it is important to note that genes identified as similar to *Arabidopsis DIR1* may not share its function. This also reinforces the need for accurate homologue identification.

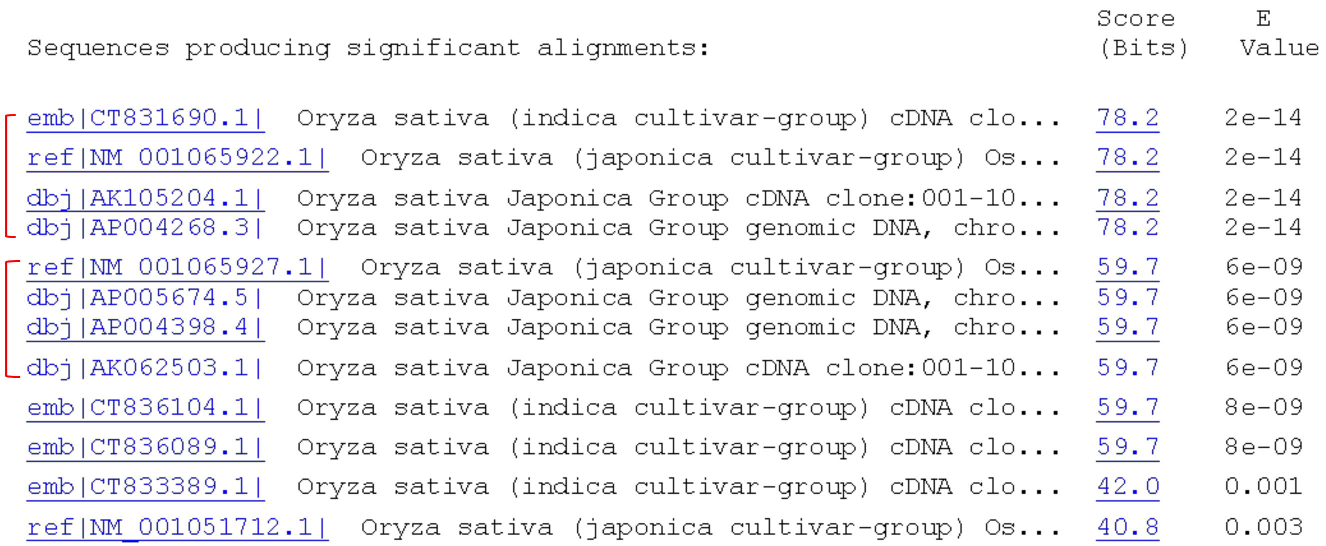
A further aspect to this work concerns the possibility that the capacity of barley to induce SAR could vary between ancient landraces and cultivars which have undergone selective breeding for high yield. It has been hypothesised that the emergence of agriculture and selection of crops for yield and quality traits could have led to the inadvertent loss of strong defence alleles (Iriti & Faoro, 2006). Several studies have indicated that chemical induction of SAR and the constitutive expression of SAR are both associated with fitness costs in the absence of pathogen pressure (Cipollini, 2002, Heidel *et al.*, 2004, Heil *et al.*, 2000, van Hulten *et al.*, 2006). In BTH-treated wheat, fitness costs were greater when nutrient availability was reduced, which may suggest that costs arise from the diversion of resources from growth or reproduction to defence (Heil *et al.*, 2000, Heil, 2002). When under pathogen pressure, *Arabidopsis* seedlings treated with BTH have higher fitness than controls (Van Hulten *et al.*, 2006). In contrast to seedlings treated with BTH, seedlings 'primed' by treatment with a low concentration of BABA (β-amino butyric acid) do not directly activate defence-related genes (Zimmerli *et al.*, 2000). In the absence of pathogens, this priming has little effect on fitness; however under disease conditions primed seedlings have significantly higher fitness than non-induced or BTH-treated seedlings (Van Hulten *et al.*, 2006). It is tempting to speculate that fitness costs associated with the induction of SAR could have led to the loss of SAR specific alleles from cereal cultivars. Furthermore, the apparent differences in costs between SAR and priming could have led to the preservation of components involved in ISR, which appears to be conserved in rice (De Vleesschauwer *et al.*, 2008). However, the extent to which fundamental data on fitness costs of induced resistance can be applied to agriculture is not clear (Brown, 2002). In terms of published data, tests of AR localisation in barley appear to have exclusively used cultivars ((Hwang & Heitefuss, 1982, Kunoh et al., 1988, Lyngkjaer & Carver, 1999, Martinelli, 1990, Ouchi et al., 1976)). As such, the first step in investigating this hypothesis is to establish whether differences in AR between cultivars and ancient landraces can be identified.

Together, the approaches outlined above could provide insight into whether a functional SAR pathway is conserved in cereal species. The data presented below describe first work and results to date from each approach, and potential avenues for future work are also discussed.

5.3 Results

5.3.1 Identification of cereal homologues of *Arabidopsis* DIR1

DIR1 homologues were first investigated in rice, due to the availability of the full rice genome sequence (Goff *et al.*, 2002). Candidate homologues were identified using the tBLASTn specification of the BLAST algorithm (which finds weak protein similarites encoded in nucleotide sequence) (Altschul, 1990) against the NCBI database. This program queries the deduced amino acid sequence of DIR1 against a translated subject sequence. Rice candidates were selected after BLAST searching against the *Oryza sativa* non redundant database. Top matches to the *Arabidopsis* DIR1 (*At*DIR1*)* sequence from the rice database (NCBI) are shown in Figure 5.1. The top two gene hits (NM_001065922 (GI:115471576, *RICE A*) and NM_001065927 (GI:115471586, *RICE B*) returned percentage amino acid identity scores of 51 % and 40 % respectively. From this point percentage identity of hits decreased gradually, and E values (indicative of hit statistical significance) increased above zero.



```
                                                                    Score     E
Sequences producing significant alignments:                        (Bits)   Value

emb|CT831690.1|  Oryza sativa (indica cultivar-group) cDNA clo...  78.2     2e-14
ref|NM 001065922.1|  Oryza sativa (japonica cultivar-group) Os...  78.2     2e-14
dbj|AK105204.1|  Oryza sativa Japonica Group cDNA clone:001-10...  78.2     2e-14
dbj|AP004268.3|  Oryza sativa Japonica Group genomic DNA, chro...  78.2     2e-14
ref|NM 001065927.1|  Oryza sativa (japonica cultivar-group) Os...  59.7     6e-09
dbj|AP005674.5|  Oryza sativa Japonica Group genomic DNA, chro...  59.7     6e-09
dbj|AP004398.4|  Oryza sativa Japonica Group genomic DNA, chro...  59.7     6e-09
dbj|AK062503.1|  Oryza sativa Japonica Group cDNA clone:001-10...  59.7     6e-09
emb|CT836104.1|  Oryza sativa (indica cultivar-group) cDNA clo...  59.7     8e-09
emb|CT836089.1|  Oryza sativa (indica cultivar-group) cDNA clo...  59.7     8e-09
emb|CT833389.1|  Oryza sativa (indica cultivar-group) cDNA clo...  42.0     0.001
ref|NM_001051712.1|  Oryza sativa (japonica cultivar-group) Os...  40.8     0.003
```

Figure 5.1 Results of tBLASTn with *At*DIR1 amino acid sequence against *Oryza sativa* database. Sequences grouped by red bar are representatives of the same locus (eg. PAC / BAC clones, genomic DNA, cDNA). CT836104 and CT836089 from the indica cultivar group share exact amino acid sequence with RICE A, and although they have been allocated to a separate Unigene, are not considered a separate homologue here.

As noted, the level of sequence similarity between LTP gene family members could complicate the accurate identification of functional homologues. The most similar *DIR1* homologue in rice (RICE A) exhibits 51 % identity to DIR1, a level that could be explained by conserved motifs within the family (Arondel *et al.*, 2000). However, BLAST searches in *Arabidopsis* indicate that only one other *Arabidopsis* gene is more than 40 % identical to DIR1 (78 %, At5g48490.1), indicating DIR1 is relatively distinct from other members of the LTP family. This is consistent with the characterisation of *At*DIR1 as an atypical LTP$_2$ (Lascombe *et al.*, 2008), or type IV subfamily LTP (Boutrot *et al.*, 2008). Furthermore, reciprocal BLAST searches against the *Arabidopsis* database (NCBI) show *DIR1* as the most significant hit for both candidate homologues. The relative chromosomal locations of *RICE A* and *B*, and At*DIR1* and *At5g48490.1* are shown in Figure 5.2. Global alignment (Edgar, 2004) between DIR1, RICE A and RICE B is shown in Figure 5.3 (a). Both rice candidates contain a proline-rich region aligned with the characteristic DIR1 PxxPxxP motif, although the motif is not fully conserved (Figure 5.3 (b)). This is in line with the findings of Lascombe et al. (2008), who found this exact motif is unique to DIR1 amongst DIR1-like sequences from a range of plant species (Lascombe *et al.*, 2008). Alignment of the next most similar rice sequence indicates the motif is less well conserved in this sequence (Figure 5.3 (b)).

A range of characteristics were compared between *At*DIR1 and the candidate rice homologues (Table 5.1). Like DIR1, both rice candidates are predicted to contain protease inhibitor/ seed storage/ LTP family domains and an N terminal signal peptide (Pfam (Finn *et al.*, 2008), SignalP 3.0 (Bendtsen *et al.*, 2004)). Molecular weight and isoelectric point predictions (Compute pI (Gasteiger *et al.*, 2005)) are also comparable to those for DIR1 (Maldonado *et al.*, 2002). TIGR annotates both candidates as PVR3-like due to a BLASTp showing high similarity with an *Ananus comusus* sequence (60.5 %) with predicted homology to a root-specific *Phaseolus vulgaris* nsLTP-like protein (PVR3). However, NCBI's more stringent ProtEST tool, which compares UniGene sequences to structurally characterised protein sequences and thus avoids derived annotations (Cuff *et al.*, 2000), specified *DIR1* as the most closely related homologue (at 43.27 % (global) for RICE A). The relationship between *At*DIR1, At5g48490, RICE A and RICE B is also supported by analysis with the GreenPhyl Orthologs Search Tool (GOST), which predicts phylogenomic relationships between rice and *Arabidopsis* (Conte *et al.*, 2008) (Figure 5.4 (a)).

Identification of barley homologues of AtDIR1

The RICE A amino acid sequence was used to take a similar approach to the identification of barley homologues. ESTs representative of two UniGene loci were identified, Hv.11078, and

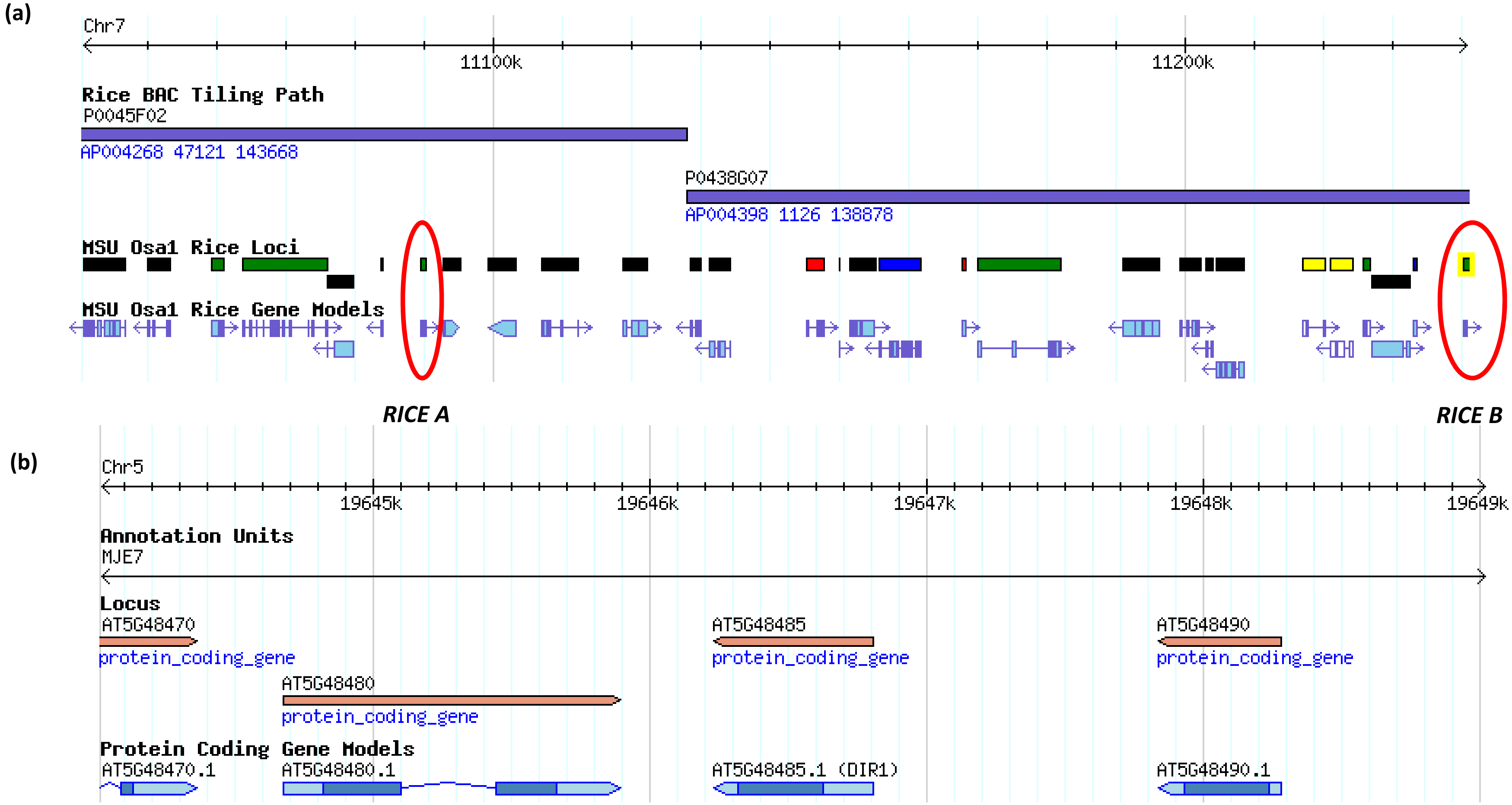
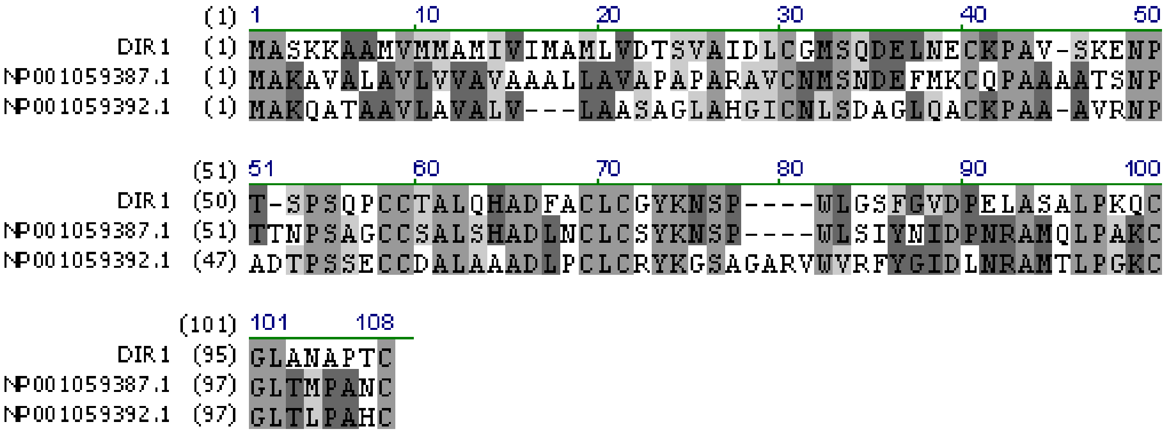


Figure 5.2. Chromosomal locations of **(a)** *RICE A* and *RICE B*, and **(b)** *At DIR1* and *At5g48490.1*. Results viewed in TIGR Genome Browser (http://rice.plantbiology.msu.edu/cgi-bin/gbrowse/rice/), and TAIR Arabidopsis Genome Browser (http://gbrowse.arabidopsis.org/cgi-bin/gbrowse/).

(a)



```
                 (1) 1        10        20        30        40        50
         DIR1    (1) MASKKAAMVMMAMIVIMAMLVDTSVAIDLCGMSQDELNECKPAV-SKENP
NP001059387.1    (1) MAKAVALAVLVVAVAAALLAVAPAPARAVCNMSNDEFMKCQPAAAATSNP
NP001059392.1    (1) MAKQATAAVLAVALV---LAASAGLAHGICNLSDAGLQACKPAA-AVRNP

                (51) 51       60        70        80        90       100
         DIR1   (50) T-SPSQPCCTALQHADFACLCGYKNSP----WLGSFGVDPELASALPKQC
NP001059387.1   (51) TTNPSAGCCSALSHADLNCLCSYKNSP----WLSIYNIDPNRAMQLPAKC
NP001059392.1   (47) ADTPSSECCDALAAADLPCLCRYKGSAGARVWVRFYGIDLNRAMTLPGKC

               (101) 101    108
         DIR1   (95) GLANAPTC
NP001059387.1   (97) GLTMPANC
NP001059392.1   (97) GLTLPAHC
```

(b)

DIR1	N**P**T-S**P**SQ**P**CCT	DIR1	N**P**TS**P**SQ**P**CCT
RICE A	N**P**TTN**P**SAGCCS	'RICE C'	PG-AR**PP**AACCA
RICE B	N**P**ADT**P**SSECCD		

Figure 5.3 (a) Global alignment of RICE A (middle, NP001059387.1) and RICE B (bottom, NP00105932.1) candidate homologues with DIR1 amino acid sequence (top, DIR1). Aligned by MUSCLE (Edgar, 2002) and displayed in GeneDoc (http://www.psc.edu/biomed/genedoc). Colours represent: identical amino acids- medium grey; conservative substitutions- dark grey; block of similar amino acids- light grey. **(b)** Proline rich domains of DIR1 and candidate homologues. Adapted from Lascombe *et al*. 2008. Amino acid positions 49-59. Proline residues highlighted in bold. 'RICE C' indicates NP_001045177.1 (reference protein sequence of NM_001051712.1)

	RICE A	RICE B	DIR1
Gene Identifier	GI:115471576	GI:115471586	
Unigene	Os.11212	Os.24103	
BLAST E value	2.00E-14	6.00E-09	
BLAST % Identity (local alignment)	55%	42%	
BLAST % Similarity	66%	54%	
NEEDLE (global alignment) Identity	43.30%	37.40%	
NEEDLE (global alignment) Similarity	56.70%	49.50%	
NCBI annotation	Plant lipid transfer/seed storage -alpha amylase inhibitor domain containing protein contains InterPro domain(s): IPR003612	Plant lipid transfer/seed storage -alpha amylase inhibitor domain containing protein contains InterPro domain(s): IPR003612	Plant lipid transfer/seed storage -alpha amylase inhibitor domain containing protein contains InterPro domain(s): IPR003612
NCBI ProtEST predicted homology	NP_568699.1 (DIR1)	NP_568699.1 (DIR1)	
TIGR Locus Identifier	LOC_Os07g18750	LOC_Os07g18990	
TIGR annotation	PVR3-like protein, putative, expressed	PVR3-like protein, putative, expressed	
Pfam domain prediction	Tryp_alpha_amyl (30-104)	Tryp_alpha_amyl (27-104)	Tryp_alpha_amyl (32-102)
E value	6.30E-09	2.40E-08	3.5e-07
SignalP (3.0)	Signal peptide, cleavage 28-29 Probability: 1.0	Signal peptide, cleavage 23-24 Probability: 1.0	Signal peptide, cleavage 26-27 Probability: 0.991
ExPasy Isoelectric point prediction	6.67	8.2	4.5
Expasy Molecular weight prediction	8.73 kDa	8.23 kDa	8.0 kDa
Supported by FL-cDNA	AK105204	AK062503	

Table 5.1 ***In silico*** **characterisation of RICE A and RICE B**. BLAST details indicate homology to *At*DIR1, based on tBLASTn with *At*DIR1 amino acid sequence. Details of all prediction programs and databases given in **Table 2.6 (Materials and Methods)**. 'AAI' indicates Alpha Amylase Inhibitor domain. 'Tryp_alpha_amyl' indicates a Protease inhibitor/seed storage/LTP family domain.

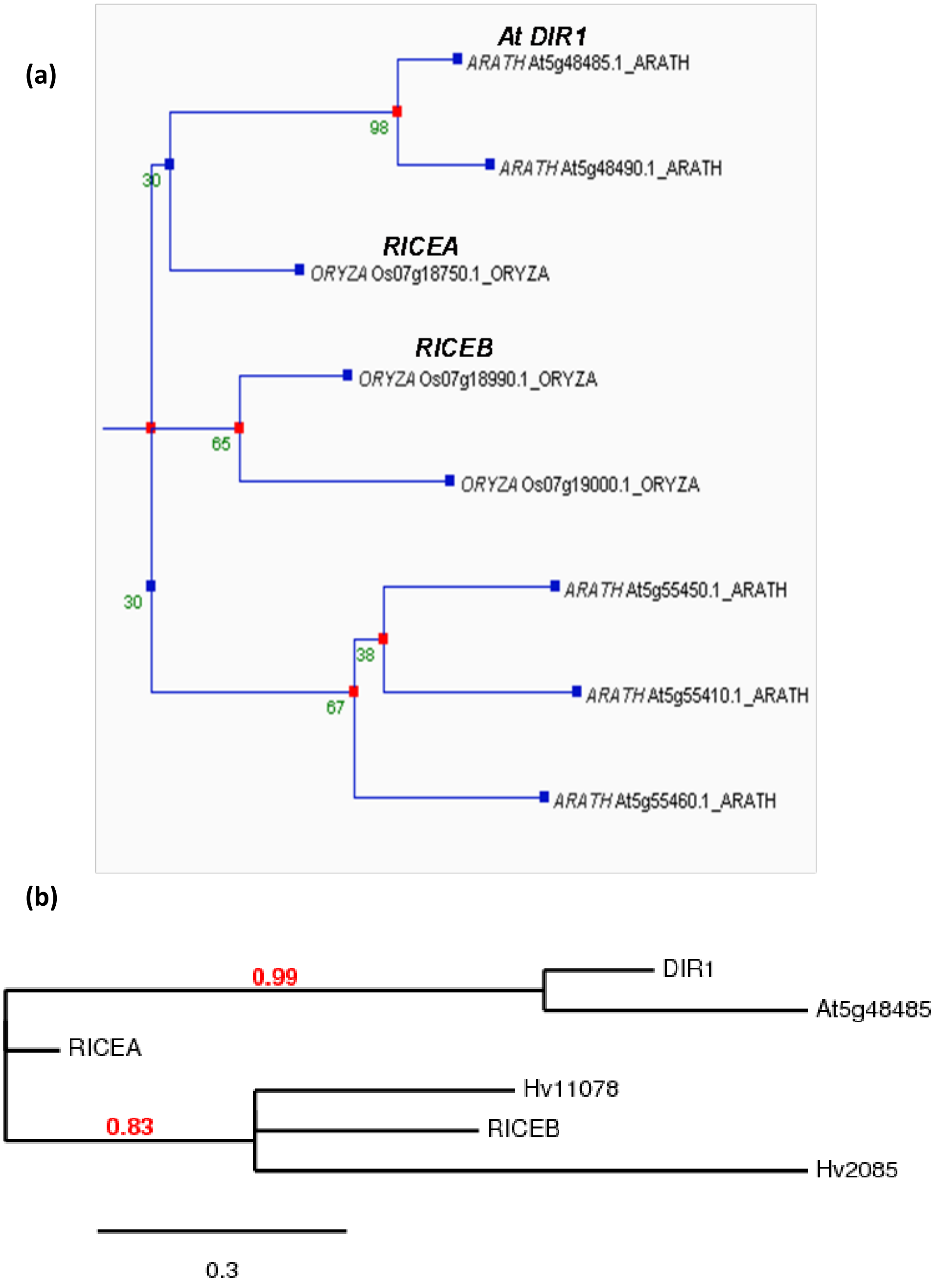


Figure 5.4 Phylogenetic relationships between *Arabidopsis*, rice and barley homologues of DIR1. (a) Phylogenomic analysis of members of the LTP type 3 subfamily 1, predicted using the GreenPhyl database's 'GreenPhyl Orthologs Search Tool' (GOST) (http://greenphyl.cirad.fr/cgi-bin/greenphyl.cgi) (Conte *et al*. 2008). *ARATH* prefix indicates *Arabidopsis*, *ORYZA* indicates rice sequence. Number in green (at nodes) indicates bootstrap support for the node (%). (b) Predicted phylogenetic relationships between the sequences indicated. Deduced amino acid sequences were used. Values in red indicate bootstrap support for the node. Analysis performed using 'One click' tool available at http://www.phylogeny.fr/version2_cgi/index.cgi

Hv.2085. For each locus, Sixpack (EMBOSS (Rice, 2000)) provided 6 frame translations of the reference mRNA sequence, and the correct translation frame was identified by comparing each to the alignment provided by BLAST. tBLASTn searches of the NCBI barley database found Hv.11078 was the only significant match for *At*DIR1 and the top hit for both RICE A and RICE B. Reciprocal tBLASTn searches using the predicted Hv.11078 amino acid sequence found that DIR1 was the top *Arabidopsis* hit, and RICE B was the top rice hit, followed by RICE A. This could indicate that Hv.11078 is paralogous to DIR1 rather than orthologous, possibly due to gene duplications in the cereals. For Hv.2085, DIR1 and RICE A were identified as similar in reciprocal tBLASTn searches against *Arabidopsis* and rice respectively, however several other sequences in each species were more similar (data not shown). This suggests this sequence is less likely to be functionally related to DIR1. Phylogenetic analysis of the barley candidate homologues alongside RICE A and B and *At*DIR1 further supports that Hv.11078 is more closely related to RICE B than RICE A, and that Hv.2085 is less closely related (Figure 5.4 (b)). Data was compiled describing Hv.11078, as for the rice homologues (Table 5.2). Domain prediction by the Phobius prediction algorithm (Kall *et al.*, 2007) suggests Hv.11078 lacks an N-terminal signal peptide, and in its place predicts a transmembrane domain. However, differentiation between signal peptide and transmembrane domains is known to be problematic (Käll *et al.*, 2004) and SignalP (Bendtsen *et al.*, 2004) does predict an N-terminal signal peptide. It must be noted that limited sequence availability for barley is likely to mean other homologues remain unidentified. A tBLASTn search of the recently available 8x coverage *Brachypodium distachyon* genome sequence (http://www.brachypodium.org) indicated there are also two significantly similar DIR1 homologues in that species (with 36 % and 22 % identity to DIR1).

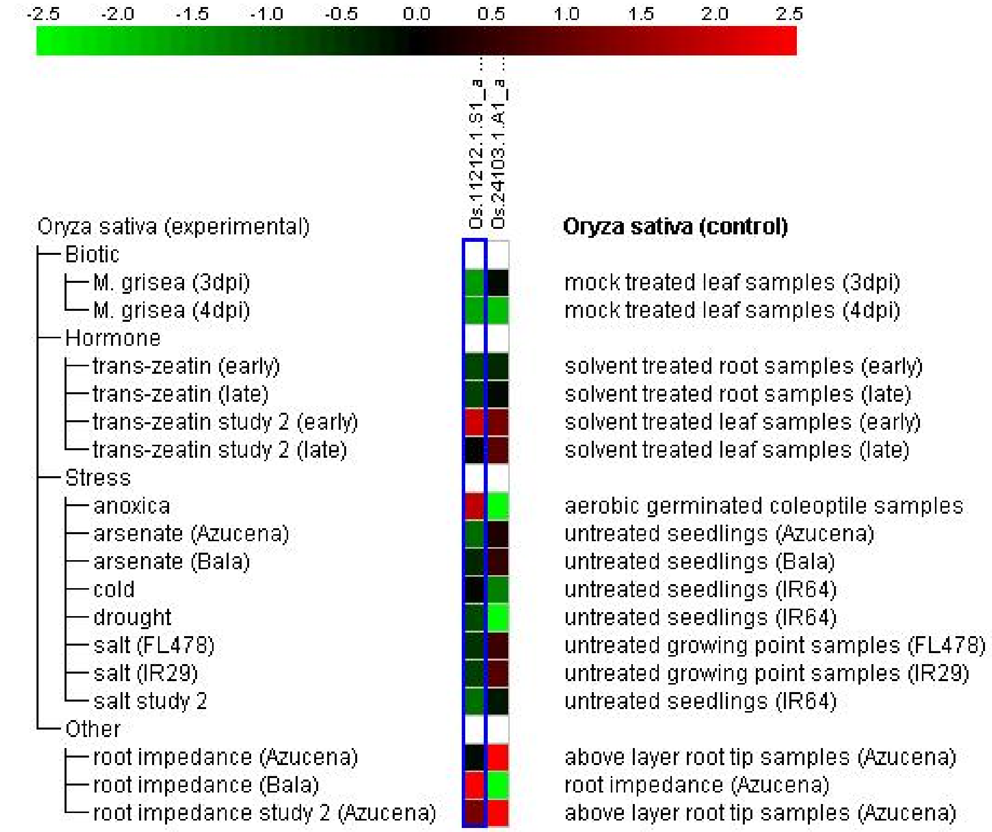
Transcriptional profile of candidate homologues

The expression of *Arabidopsis DIR1* does not change dramatically during the induction of SAR. Transcript levels are low in naïve plants, and drop slightly in both local (induced) and systemic leaves by 6 hours post local inoculation; later increasing slightly in systemic leaves only at 12 hours post local inoculation before reducing again by 24 hpi (Maldonado *et al.*, 2002). Genevestigator meta-analysis of Rice Affymetrix Genome Array probe sets representing *RICE A* and *B* suggests that both rice homologues are generally down-regulated in response to biotic and abiotic stress (Figure 5.5 (a)). Similarly, Hv.11078 appears to be significantly down-regulated in response to local infiltration with *PstavrRpm1* (study described in Chapter 4, Section 4.3.5) (Figure 5.5 (b)). Although several other ns-LTP-like genes are also down-regulated (full list Appendix 1),

	Hv. 11078	
BLAST % Identity (local alignment)	58% (to RICEB)	46% (to DIR1)
BLAST % Similarity	74% (to RICEB)	61% (to DIR1)
BLAST E value	2E-22 (to RICEB)	5E-11 (to DIR1)
NEEDLE (global alignment) Identity	48.3% (to RICEB)	33.9% (to DIR1)
NEEDLE (global alignment) Similarity	61.9% (to RICEB)	47.5% (to DIR1)
NCBI ProtEST predicted homology	weakly similar to NP_001059387.1 (RICE A)	
Pfam domain prediction	Tryp_alpha_amyl (54-114)	
E value	3E-06	
Phobius Signal Peptide / TM domain predicton	Transmembrane domain (12-32)	
SignalP (3.0)	Signal peptide, cleavage 37-38 Prob 0.98	

Table 5.2 ***In silico* characterisation of Hv.11078**. BLAST scores are based on tBLASTn of *Oryza sativa* or *Arabidopsis thaliana* non-redundant database with the Hv.11078 predicted amino acid sequence. Details of all databases in **Table 2.6, Materials and Methods**. Domain prediction was performed using predicted amino acid sequence.

(a)



(b)

Affymetrix Probe Set ID	Annotation	Log$_2$ Fold change	Functional Category
Contig24328_at	*DIR1*-like	-3.11	Cell rescue, defence and virulence
Contig16375_at	*DIR1*-like	-2.03	Cell rescue, defence and virulence
Contig25762_at	*DIR1*-like	-2.1	Cell rescue, defence and virulence

Figure 5.5 Transcriptional responses of cereal *DIR1* homologues. (a) Transcriptional profile of probe sets representing *RICE A* (left) and *RICE B* (right) on the Affymetrix GeneChip Rice Genome Array. Analysis performed using the Genevestigator microarray database and expression meta-analysis tool (see Table 2.6). Each box corresponds to a GeneChip based experiment, the colour / depth of colour indicates the direction / magnitude of transcriptional response. **(b)** Transcriptional response of barley *DIR1* homologues showing significant changes in expression in response to local infiltration with *PstavrRpm1* (study described in Section 4.3.5). None of these probes sets were significantly differentially expressed in the adjacent leaf region.

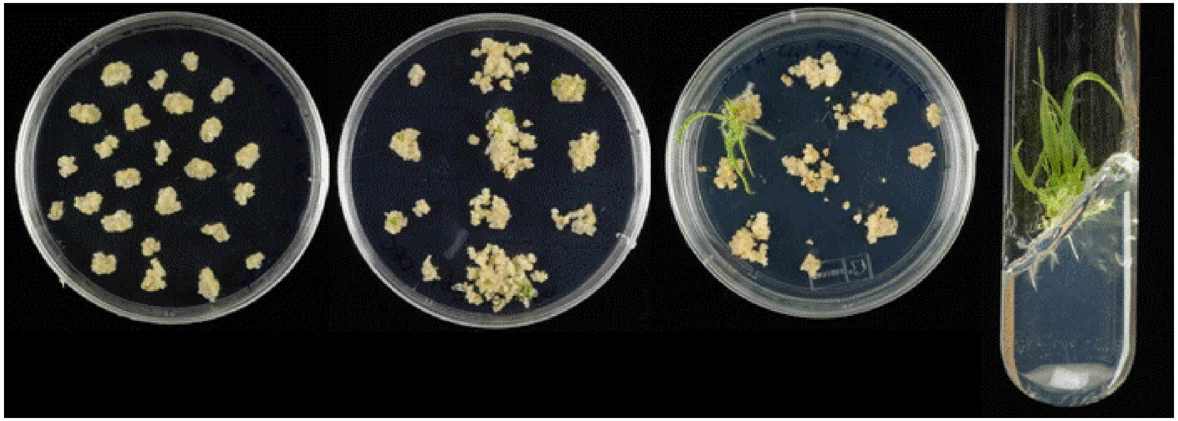
the common pattern of down-regulation of these genes in response to biotic stress generally supports the selection of these genes as candidate homologues.

5.3.2 Heterologous expression of *DIR1*, *RICE A* or *RICE B* in barley may affect local resistance

In order to investigate whether *Arabidopsis DIR1, RICE A*, or *RICE B* can affect AR in barley, *Agrobacterium*-mediated transformation was used to produce Golden Promise lines heterologously expressing each gene. Rice homologues were selected for functional analysis at this stage (over barley homologues) due to the availability of the full rice genome sequence. The limited sequence availability for barley could mean more appropriate homologues have been overlooked. Full-length cDNA clones (*RICE A* and *B*) or the coding sequence (*DIR1*) of each gene were cloned into a Gateway compatible expression vector (pBRACT 214), under the control of the maize ubiquitin promoter. Three transformation experiments were performed, with transformation efficiency of up to 33 % (Figure 5.6 and Section 2.2.8.2, Materials and Methods). The copy number of the transgene was determined in each T_0 line by qPCR of the hygromycin selectable marker (performed by Pete Isaac, iDNA Genetics) (Figure 5.7 (a)). The presence of the transgene in T_0 lines was further confirmed by PCR of the respective coding sequence from genomic DNA of single copy lines (Figure 5.7 (b)). Segregation in the T_1 was tested by assaying leaf bleaching on hygromycin-containing media (Wang & Waterhouse, 1997) (Figure 5.7 (c), performed by Ruth Maccormack). Based on this assay, zygosity was confirmed in 'homozygous' and 'null' T_1 lines by qPCR of the hygromycin selectable marker (performed by Pete Isaac, iDNA Genetics) (Figure 5.7 (d)). From these analyses, at least 5 independent, single-copy, homozygous lines (plus null segregants) of each construct were identified for further tests (Figure 5.7 (e)). Expression of each transgene (and absence of expression in the null segregant) was confirmed in these T_1 and T_2 lines by qRT-PCR of the respective coding sequence (Figure 5.7 (f)).

In Golden Promise, infiltration of the upper third of the first seedling leaf with *PstavrRpm1* resulted in the induction of AR to a compatible *Pseudomonas* isolate (PS86) infiltrated into the adjacent leaf region 24 hours later (Section 4.3.2). To test whether the expression of *DIR1* or its rice homologues affected the adjacent AR response in Golden Promise, the same test was applied to *Ubi:DIR1*, *Ubi:RICE A* and *Ubi:RICE B* Golden Promise lines. In the homozygous lines tested, adjacent resistance did not appear to be induced (Figure 5.8). Furthermore, adjacent resistance was not induced in null-segregants of *Ubi:RICE A* or *Ubi:DIR1*. The response of these null segregants must be tested alongside Golden Promise to determine if these apparent differences

(a)



(b)

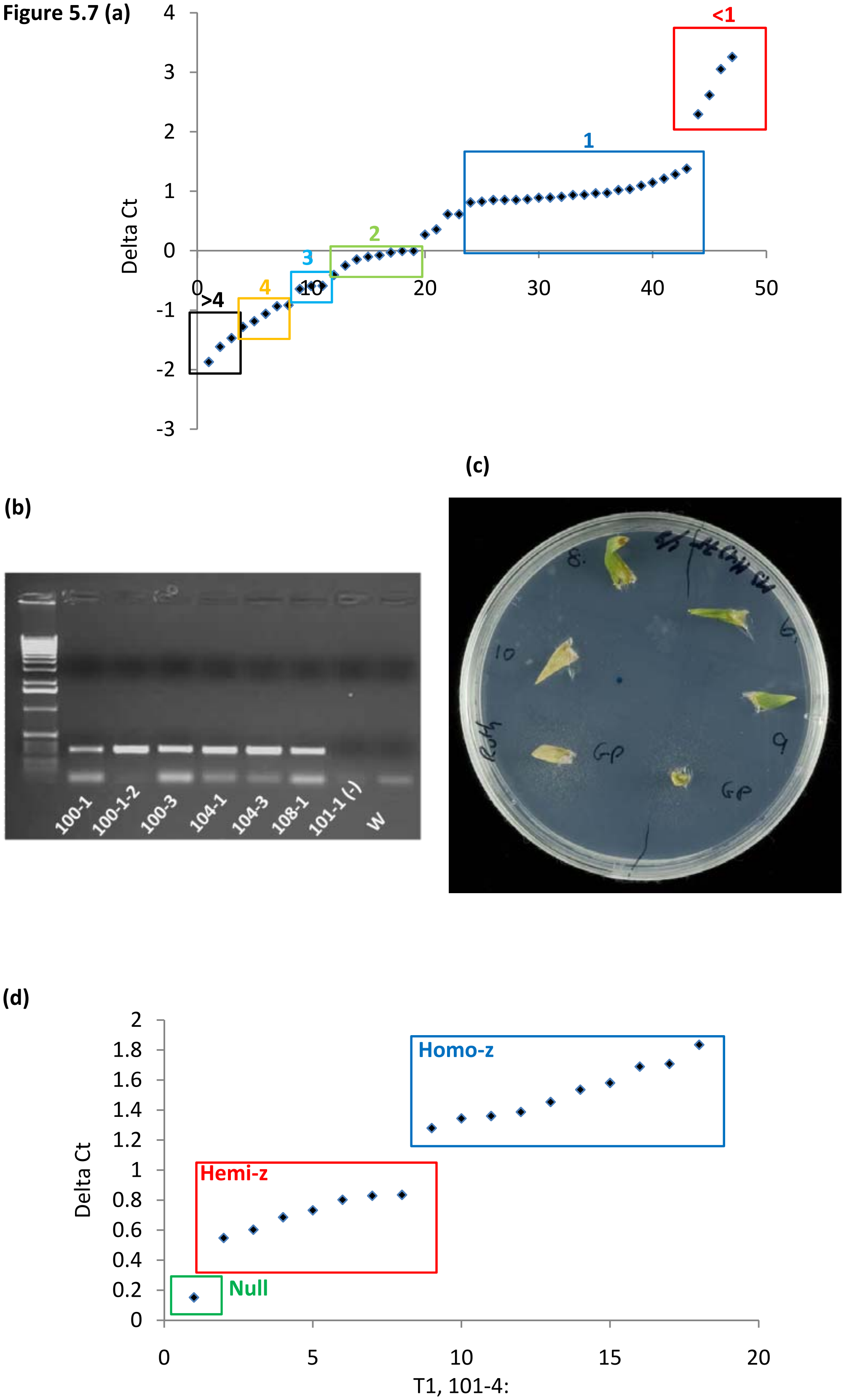
Experiment	Construct	Line	Number of embryos	Independent hygromycin-resistant plants	Transformation efficiency
1	pBract 214 *At DIR1*	100	48	16	33.3
	pBract 214 *RICE A*	101	43	12	27.9
	pBract 214 *RICE B*	102	52	10	19.2
	p204	103	38	5	13.2
2	pBract 214 *At DIR1*	104	42	3	7.1
	pBract 214 *RICE A*	105	51	3	5.9
	pBract 214 *RICE B*	106	49	4	8.2
	p204	107	25	2	8.0
3	pBract 214 *At DIR1*	108	49	5	10.2
	pBract 214 *RICE A*	109	47	4	8.5
	pBract 214 *RICE B*	110	45	4	8.9
	p204	111	35	3	8.6

Figure 5.6 *Agrobacterium*-mediated transformation of Golden Promise. **(a)** Immature Golden Promise embryos were excised, inoculated with *Agrobacterium* and placed on callus induction media. Over a period of 10-12 weeks on hygromycin containing regeneration media, calli developed, and green shoots were transferred to individual tubes, and then soil. Images show a selection of transformation stages. (b) **Efficiency of *Agrobacterium*-mediated transformation of Golden Promise**. Transformation efficiency is the percentage of treated embryos producing green, hygromycin resistant plants. p204 is a control vector, expressing an intron of the β-glucuronidase gene.

Figure 5.7 Production of transgenic Golden Promise lines heterologously expressing *DIR1*, *RICE A* or *RICE B*. (a) Copy number was estimated in each T_0 line by qPCR of the hygromycin selectable marker, relative to an internal positive control (IPC). Lines were ranked by the difference in signal to the IPC (Delta Ct), and classified for copy number. **(b)** PCR of the coding sequence of each transgene was performed on genomic DNA to confirm its presence in T_0 lines. *DIR1* example is shown. '-' indicates non-transformed control, 'W' indicates water control. **(c)** Hygromycin-based leaf bleaching assay. Leaves expressing the selectable marker remain green. **(d)** qPCR based estimation of zygosity. qPCR was performed as in (b), except Delta Ct was ranked within each T_1 line. **(e)** Homozygous / null, single copy lines available. For the T_0, the first three digits of the line identifier refer to experiment number. All lines, including those with the same experiment number are independent. T_1 zygosity was confirmed by presence / absence of transcript in T_1 and T_2. **(f)** Expression level of transgenes in homozygous T_1 lines. Expression is shown relative to one line, indicated on vertical axis. Bars show values from a single plant. RNA levels were normalised to *alpha-tubulin 2*.

Figure 5.7 (e) to (f) are shown overleaf

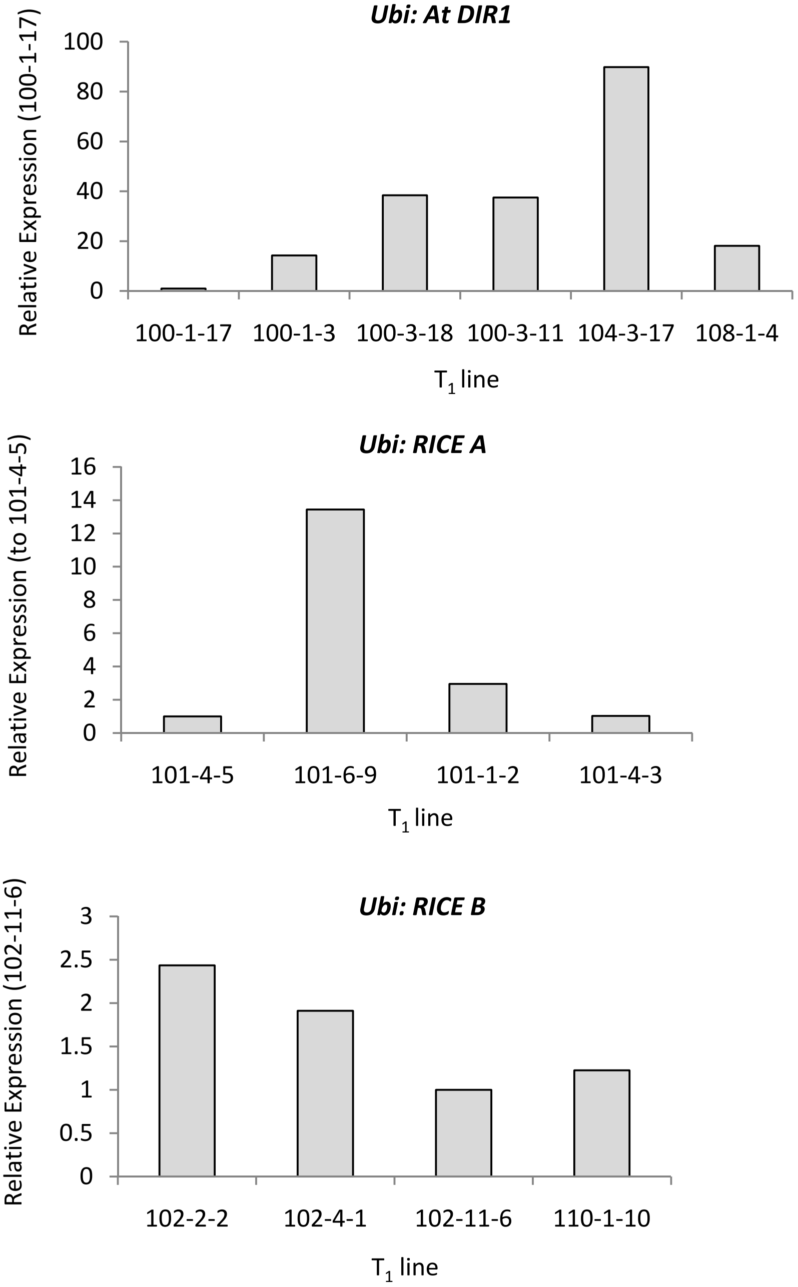
Figure 5.7


(a)
Delta Ct
4
3
2
1
0
-1
-2
-3
0
10
20
30
40
50
<1
1
2
3
4
>4
(b)
100-1
100-1-2
100-3
104-1
104-3
108-1
101-1 (-)
W
(c)
8
6
10
9
GP
GP
(d)
Delta Ct
2
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
5
10
15
20
T1, 101-4:
Homo-z
Hemi-z
Null

(e)

		T_1 zygosity		
	Exp no-T_0-	Homozygous	Null	Copy no. in T_0
pBract 214 *At DIR1*	100-1-	17, 14, 3, 16	5, 10	1 to 2 (probably 2)
	100-3-	18, 11	16, 19	1
	104-3-	17	18, 3	1
	108-1-	4	9	1
pBract 214 *RICE A*	101-1-	12, 2	6	1
	101-4-	5, 3, 8	10	1
	101-6-	9	8, 13	1
pBract 214 *RICE B*	102-2-	2	1	1
	102-4-	1	14	4
	102-11-	6	17, 10	1
	110-1-	10, 9	3, 5	1

(f)



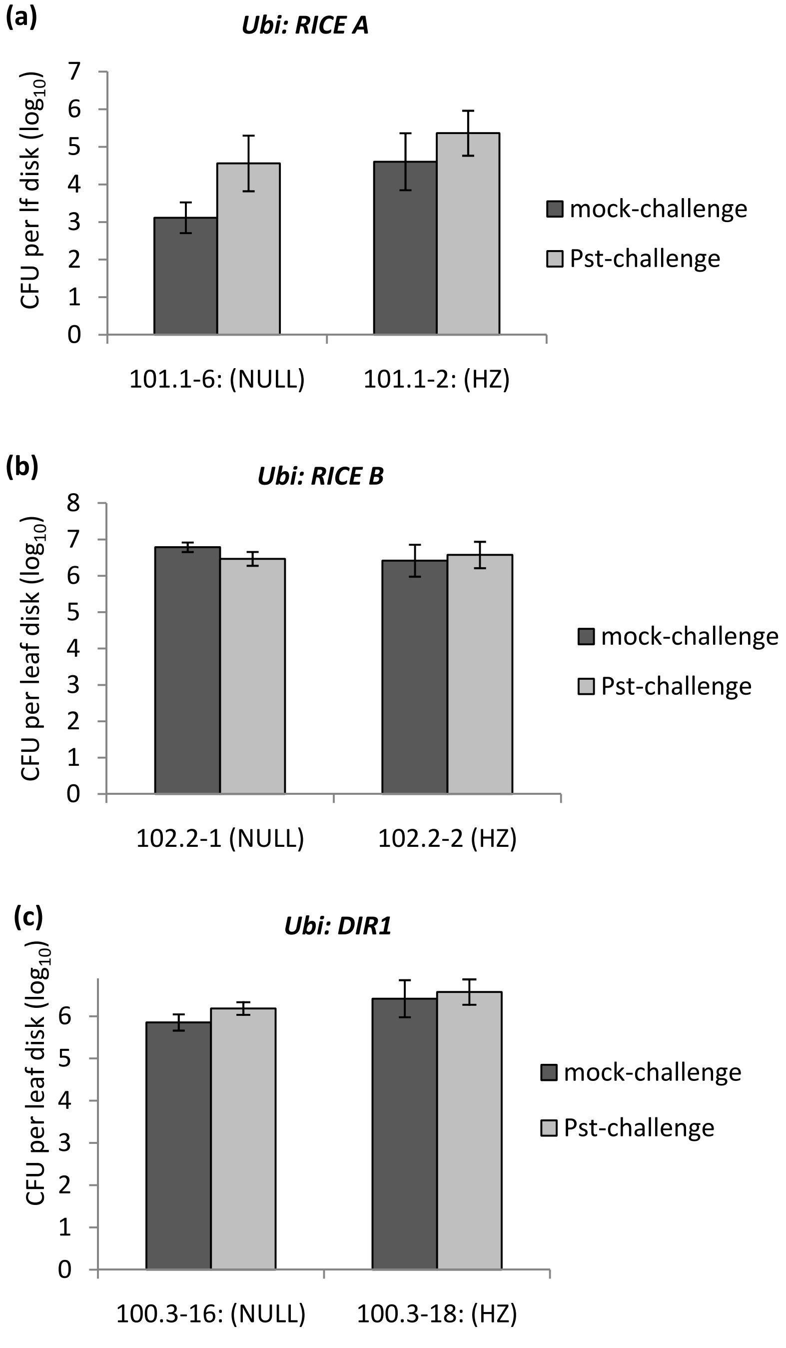


Figure 5.8 Adjacent Resistance to PS86 is not induced in Golden Promise lines expressing *RICE A* (a), *RICE B* (b) or *DIR1* (c). The adjacent leaf region was challenged with PS86 24 hours after local infiltration with water (mock-challenge) or *PstavrRpm1* (Pst-challenge). 24 hrs later a leaf disk was taken from the adjacent region of 4 leaves per treatment, and CFU assayed. Bars show mean values ± SD. 'NULL' indicates line is a null-segregant, 'HZ' indicates line is homozygous. In (a), the difference between mock-challenge results for 101.1-6: and 101.1-2: is not statistically significant (*p=0.1*, t-test).

from wild-type are due to experimental, or line-specific, factors. More lines must also be tested (including tests with other challengers) before firm conclusions can be drawn regarding the effect of these transgenes on adjacent resistance.

qRT-PCR data indicates that there are no clear differences in adjacent defence gene induction between Golden Promise and transgenic lines (Figure 5.9 (a)). Transcriptional responses in the local, *PstavrRpm1*-infiltrated leaf region are more distinct, with clear differential defence gene induction between lines (Figure 5.9 (b) and (c)). Symptoms resulting from local infiltration with *PstavrRpm1* also seem to vary between lines; within each of the lines tested higher local defence gene induction is seen in the line with reduced necrosis (Figure 5.9 (d)). Again, more data is needed to confirm this. For the *Ubi:DIR1* lines tested, more extensive necrosis was seen in the line with highest transgene expression in the T_1 (Figure 5.7). This trend was not seen with the *Ubi:RICE A* lines, in which the difference in transgene expression level is only 2 fold (Figure 5.7). Together, these results currently suggest that when expressed heterologously in barley, *DIR1* and its rice homologues may affect local responses. There is no evidence to suggest an effect on adjacent responses, however data is equivocal at this stage.

5.3.3 Rice homologues of *DIR1* may complement the *Arabidopsis dir1-1* mutant

In order to determine whether *RICE A* and *RICE B* are functional homologues of *AtDIR1,* complementation of the *Arabidopsis dir1-1* mutant with these genes was attempted. Full-length cDNA clones (*RICE A* and *B*) or the coding sequence (*DIR1*) of each gene was cloned into a Gateway compatible expression vector (pMDC32), under the control of a double 35S promoter (Curtis & Grossniklaus, 2003). The *Arabidopsis dir1-1* mutant (Maldonado *et al.*, 2002) was then transformed by *Agrobacterium*-mediated transformation. Ws lines were also transformed, to allow a comparison of the effect of the transgenes in the *Arabidopsis* wild-type if necessary. An 'empty' vector control was also transformed into both backgrounds. T_1 seedlings were screened for hygromycin resistance (standard nomenclature in *Arabidopsis* transformation denotes the parent plant T_0, wheras in barley T_0 refers to the seedling regenerated from transformed callus). The presence of the transgene was confirmed by PCR in hygromycin resistant lines (performed by Ruth Maccormack, data not shown). T_2 lines segregating approximately 3:1 for hygromcyin resistance (suggestive of a single copy line) were tested for the presence of the transgene in the DNA (selected lines, Figure 5.10 (a)), and expression of the transgene was also confirmed by qRT-PCR (Figure 5.10 (b)). Segregation of hygromycin resistance was then tested in number of T_3 lines

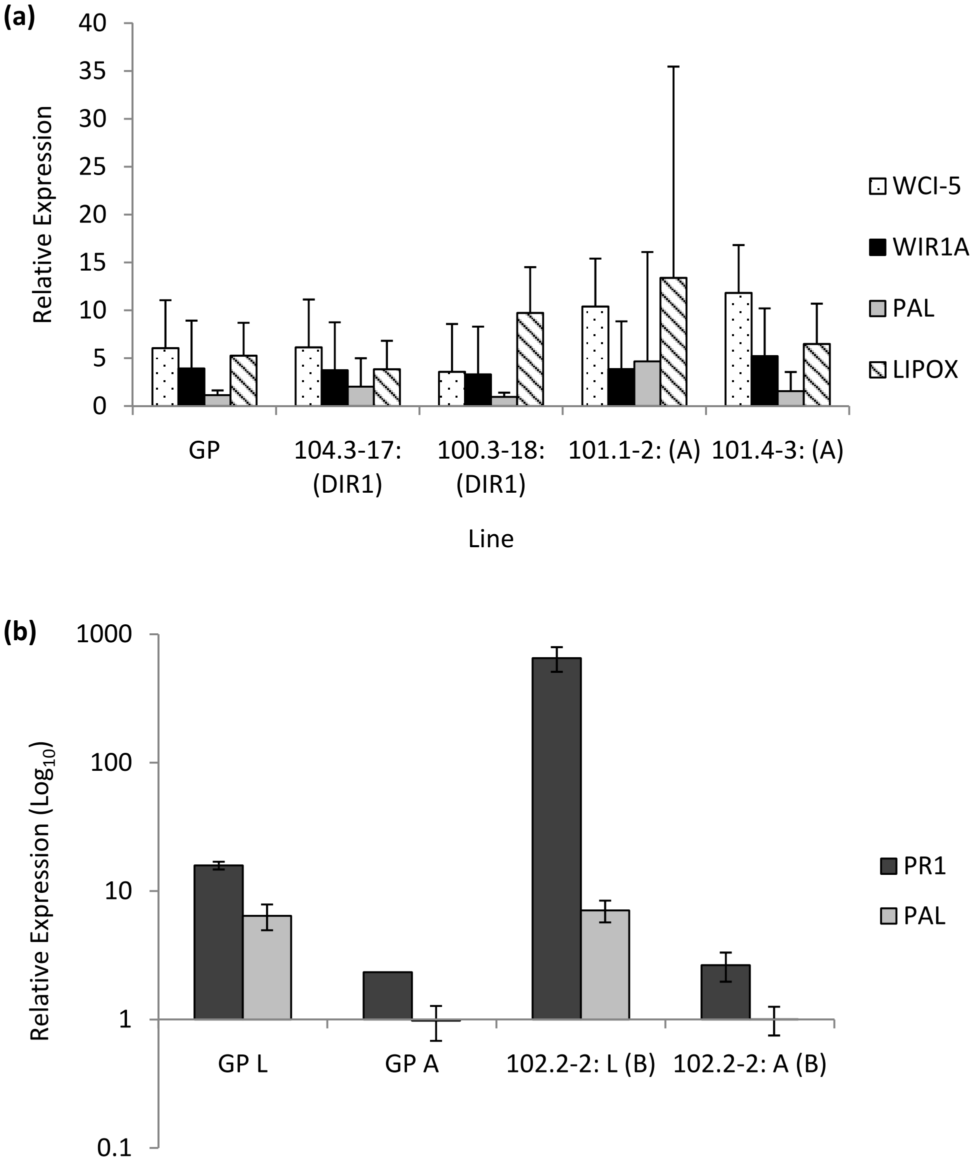
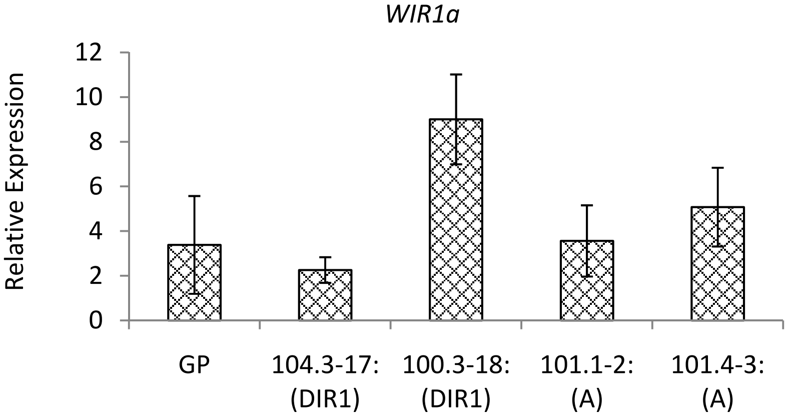
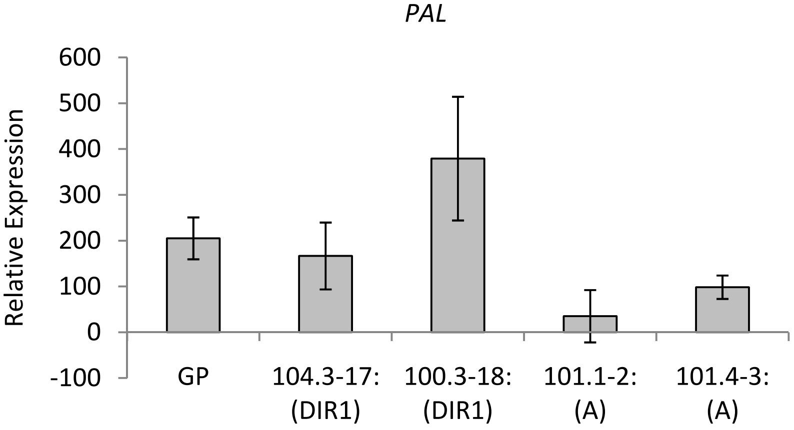


Figure 5.9 Local and adjacent defence gene induction in Golden Promise and transgenic lines 24 hrs post local infiltration with *PstavrRpm1*. qRT-PCR data, based on two-three replicates, each comprising leaf samples from three pooled seedlings. Expression of each gene calculated relative to a water infiltrated control (for each line). Transcript levels normalised to *UBC*. Bars show mean values, + (or ±) SD. **(a)** Adjacent defence gene induction in Golden Promise (GP) and *Ubi:DIR1* and *Ubi:RICE A* lines. Seedlings were 19 days old at time of local infiltration. **(b)** Local and adjacent PR gene induction in one *Ubi:RICE B* line vs Golden Promise (GP). 'L' indicates local, *PstavrRpm1* infiltrated tissue. 'A' indicates adjacent leaf region. '(B)' indicates *Ubi:RICE B*. Seedlings 15 days old at time of inoculation. Experiment performed by Graham McGrann and Ruth Maccormack. **(c) (overleaf)** Variation in local defence gene induction between Golden Promise (GP) and *Ubi:DIR1* and *Ubi:RICE A* lines 24 hpi with *PstavrRpm1* at OD_{600} 0.2. **(d) (overleaf)** Symptoms on leaves of Golden Promise and *Ubi:RICE A* lines 72 hours post infiltration with *PstavrRpm1*. Symptoms on *Ubi:RICE B* lines (not shown) were similar. All water infiltrated controls appear as Golden Promise.

Figure 5.9 (c)


WIR1a
Relative Expression
12
10
8
6
4
2
0
GP
104.3-17: (DIR1)
100.3-18: (DIR1)
101.1-2: (A)
101.4-3: (A)


PAL
Relative Expression
600
500
400
300
200
100
0
-100
GP
104.3-17: (DIR1)
100.3-18: (DIR1)
101.1-2: (A)
101.4-3: (A)

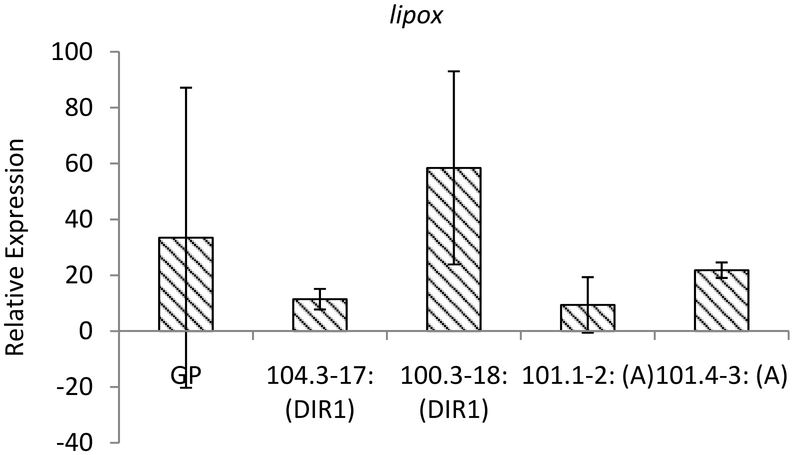

lipox
Relative Expression
100
80
60
40
20
0
-20
-40
GP
104.3-17: (DIR1)
100.3-18: (DIR1)
101.1-2: (A)
101.4-3: (A)

Figure 5.9 (d)


GP / W
GP / Pst
Ubi:DIR1 (104.3-17:) / Pst
Ubi:DIR1 (100.3-18:) / Pst
Ubi:RICE A (101.1-2:) / Pst
Ubi:RICE A (101.4-3:) / Pst

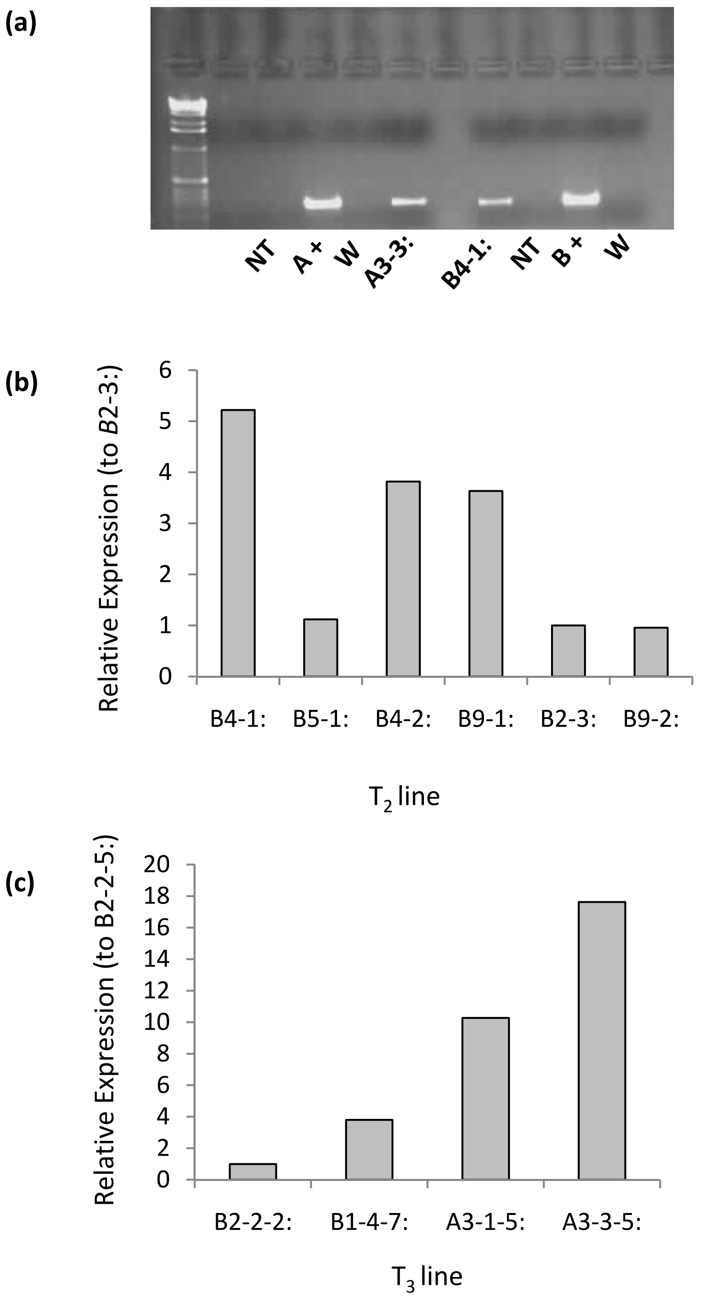


Figure 5.10 Production of *Arabidopsis dir1-1 35S:DIR1, 35S:RICE A and 35S:RICE B* complementation lines. Nomenclature gives number of parent plant (T_0)-T_1-T_2 etc, ':' indicates individuals from subsequent generation were tested. **(a) Presence of *RICE A/ RICE B* in genomic DNA was verified by PCR in selected T_2 lines**. Example is shown. 'NT' indicates non-transformed control, '+' indicates positive control (plasmid), 'W' indicates no sample control. Band indicates presence of *RICE A* transgene in *dir1-1 RICE A*3-3:, and *RICE B* transgene in *dir1-1 RICE B*4-1: . **(b)-(c) Expression of *DIR1*, *RICE A* and *RICE B* was verified by qRT-PCR in selected T_2 (b) and T_3 (c) lines.** Examples are shown. Expression is shown relative to line with lowest expression. Expression levels normalised to *UBQ5*.

(data not shown). Expression was also subsequently confirmed in selected non-segregating T_3 lines (presumed to be homozygous) (Figure 5.10 (c)).

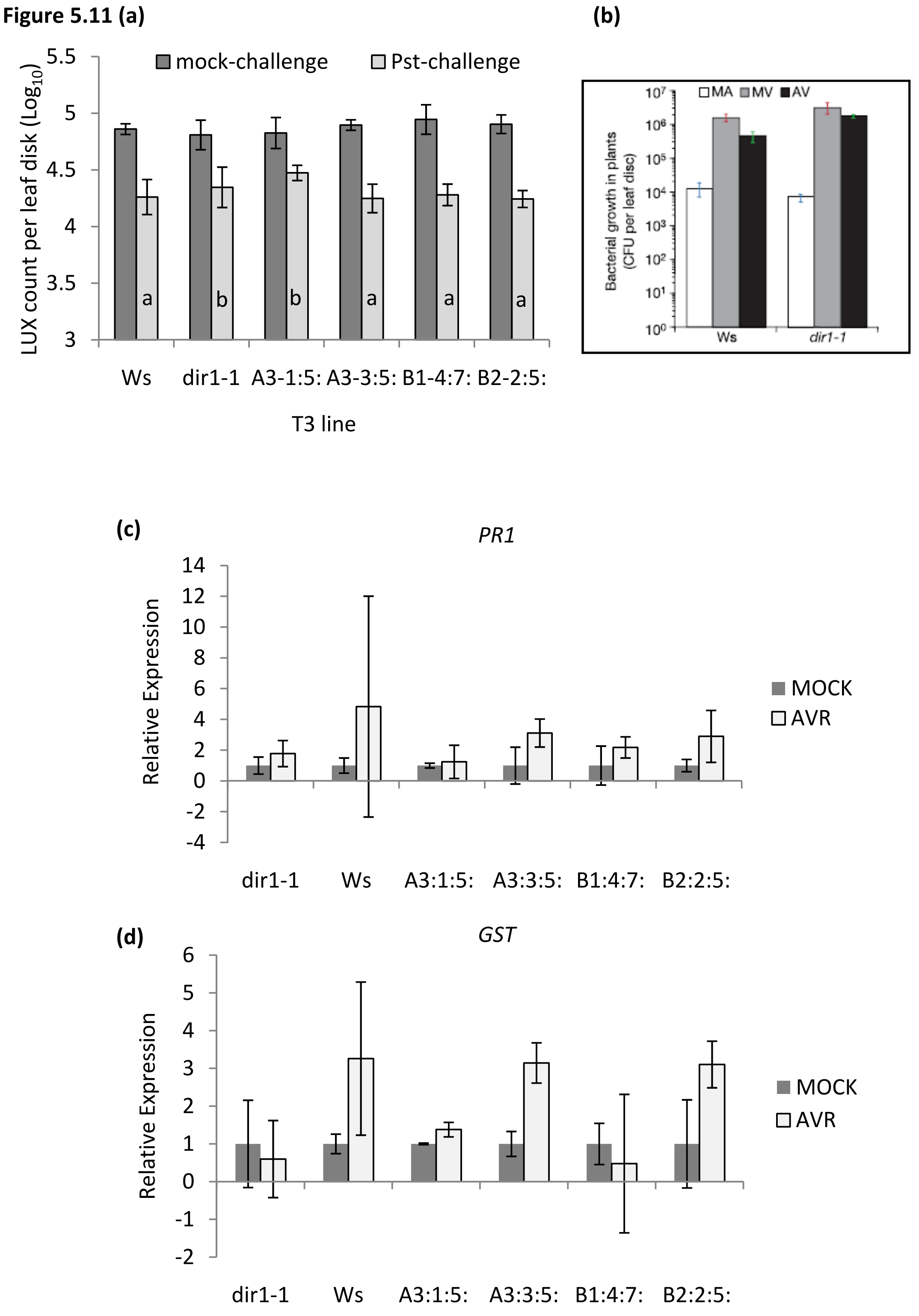
At this stage, the SAR phenotype of selected *dir1-1 35S:RICE A* and *35S:RICE B* lines was tested (Figure 5.11 (a)). A single leaf of each seedling was inoculated with *PstavrRpm1* (OD_{600} 0.002). 48 hours later, 3 leaves per seedling were challenged with luciferase tagged *Pst* DC3000 (OD_{600} 0.02) (Fan *et al.*, 2008). After a further 24-48 hours, the growth of *Pst* DC3000 was estimated by measuring Luciferase emissions. The reduction in challenger bacterial growth resulting from the *dir1-1* mutation (Maldonado *et al.*, 2002) is relatively small (Figure 5.11 (b)), and this reduction was not consistently reproduced here. All lines tested show a reduction in challenger growth consistent with the induction of SAR (Figure 5.11 (a)). However, statistical analysis (generalised linear regression; fitting experiment number, plant number within experiment, and line; t-value from predicted means) does suggest a trend towards complementation. Challenger growth (in secondary leaves) after a local mock, water infiltration did not vary between Ws, *dir1-1* and the *35S:RICE A* or *35s:RICE B* lines tested. However, challenger growth was significantly different ($p<0.05$) between Ws and both *dir1-1* and *35s:RICE A3-1-5:*, but not between Ws and the three other transgenic lines tested. While this does suggest that (in all except *35s:RICE A3-1-5:)) RICE A* and *B* can complement the SAR defect, further tests are clearly needed to reproduce the *dir1-1* defect described in Maldonado et al. (2002). It has been reported that expression of several PR genes is abolished in secondary leaves of 'induced' *dir1-1* seedlings (Maldonado *et al.*, 2002). Here, induction of *GST* was abolished in secondary leaves of *dir1-1*, consistent with published data (Figure 5.11). However, the transcript level in secondary leaves of Ws was variable, for *GST* and particularly for *PR1*. In this test, three of the four *35S:RICE A* or *B* lines tested express *GST* in secondary leaves of 'induced' seedlings (Figure 5.11 (d)). Again, this hints at complementation, but needs to be tested further. Additional independent lines would also need to be tested to confirm this result.

5.3.4 Barley landraces may show natural variation in the adjacent AR response

As noted, published data suggests that AR has been examined in a limited range of barley cultivars. As such, local and adjacent AR responses were tested in a selection of barley landraces (Table 5.3), to determine if the response varies between these accessions. Firstly, symptoms resulting from local infiltration with *PstavrRpm1* were compared between accessions, as differences in the local response might affect the development of AR. At 72 hpi, relatively similar symptoms were recorded (Figure 5.12 (a)), however differences between some accessions

Figure 5.11 Induction of SAR in Ws (WT), *dir1-1*, and *dir1-1 RICE A* or *RICE B* lines. (a) A single leaf of each seedling was inoculated with *PstavrRpm1* (OD_{600} 0.002). 48 hours later, 3 leaves per seedling were challenged with luciferase tagged *Pst DC3000* (OD_{600} 0.002) (Fan *et al.*, 2008). 24-48 hours later, growth of *Pst DC3000* was estimated by measuring photon count (LUX). Bars indicate mean LUX count per leaf disk (equivalent to bacterial growth) in challenged leaves of mock induced (mock-challenge) or *Pst*-induced (Pst-challenge) *Arabidopsis* seedlings, ±SE (pooled data from three independent experiments). **a** and **b** indicate significant differences between Ws and differently labelled bars (generalised linear model fitting experiment number, plant number within experiment, and line; t-test p value *<0.05*). The same model found no significant difference in challenger growth between mock-induced lines. **(b)** The published SAR phenotype of the *Arabidopsis dir1-1* mutant line, reproduced from Maldonado *et al*. (2002). MA indicates mock inducer, avirulent challenger; MV indicates mock inducer, virulent challenger; AV indicates avirulent inducer, virulent challenger. **(c)-(d)** qRT-PCR data showing transcript level of *PR1* **(c)** and *Glutathione-S-Transferase* (*GST*) **(d)** in secondary (systemic) leaves 24 hours post local inoculation with *PstavrRpm1* ('Avr'). Transcript levels are shown relative to level in equivalent secondary leaves of 'Mock' (water) inoculated seedlings of each line. Bars show mean values of 2-3 biological replicates, each made up of pooled leaves from 3 seedlings (3 leaves per seedling) ± SD. RNA levels were normalised to *Actin*.

Figure 5.11


(a)
LUX count per leaf disk (Log_{10})
mock-challenge
Pst-challenge
5.5
5
4.5
4
3.5
3
a
b
b
a
a
a
Ws
dir1-1
A3-1:5:
A3-3:5:
B1-4:7:
B2-2:5:
T3 line
(b)
MA
MV
AV
Bacterial growth in plants (CFU per leaf disc)
10^7
10^6
10^5
10^4
10^3
10^2
10^1
10^0
Ws
dir1-1
(c)
PR1
Relative Expression
14
12
10
8
6
4
2
0
-2
-4
MOCK
AVR
dir1-1
Ws
A3:1:5:
A3:3:5:
B1:4:7:
B2:2:5:
(d)
GST
Relative Expression
6
5
4
3
2
1
0
-1
-2
MOCK
AVR
dir1-1
Ws
A3:1:5:
A3:3:5:
B1:4:7:
B2:2:5:

Country of origin	Accession	Name	Donor	Donor Number	Type
China	4457	China	Gatersleben	Hor 2351/62	S
Pakistan	3469	Gilgit 7	E Howell		S
Saudi Arabia	3402	Arabische 4716	Hoofddorp		S
Sweden	3464	Gotlands			S
Turkey	4447	Anatolien	Gatersleben	Hor 1178/66	S

Table 5.3 Details of barley landraces. Landraces provided by Mike Ambrose, JIC. ‘S’ indicates spring type.

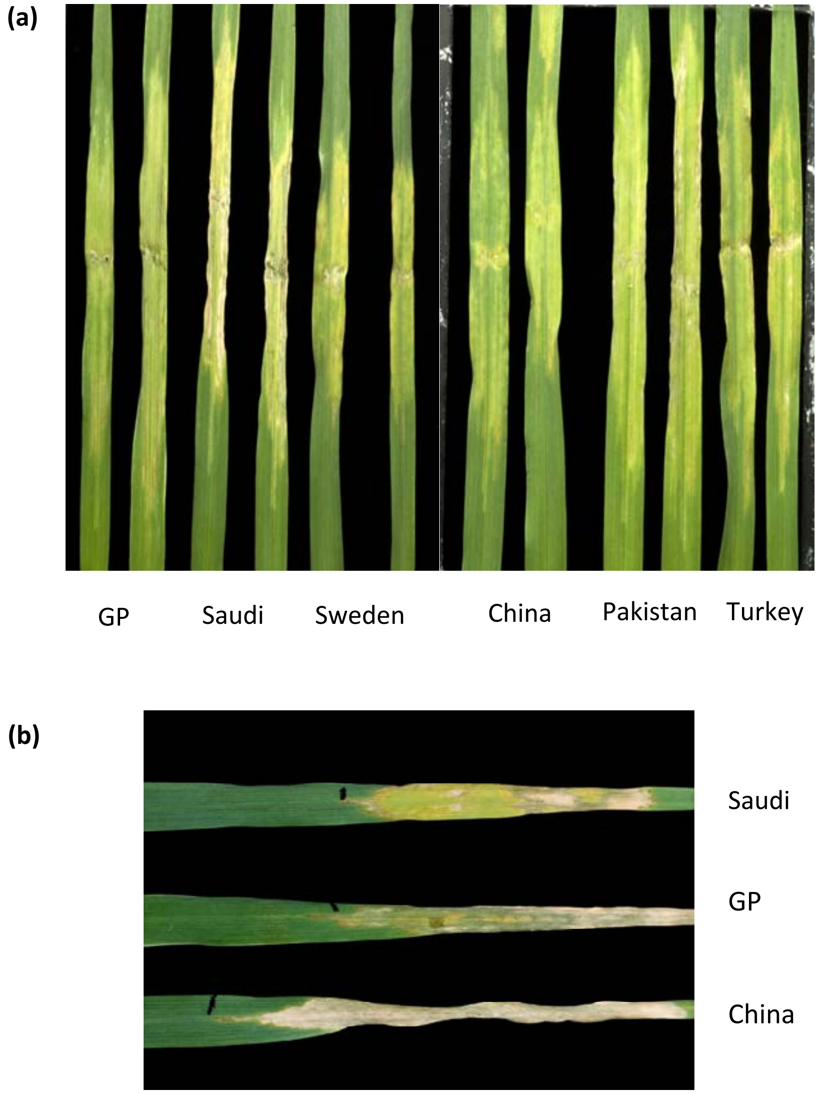


Figure 5.12 Symptoms resulting from *PstavrRpm1* infiltration of barley landraces. (a) The central third of first leaves of 17 day old seedlings were infiltrated with *PstavrRpm1* (OD_{600} 0.2) and symptoms recorded 72 hours later. Two seedlings of each line are shown. Water controls showed no symptoms. **(b)** The local leaf region of 18 day old seedlings was infiltrated with *PstavrRpm1* (OD_{600} 0.2) and symptoms recorded 96 hours later. Water controls showed no symptoms.

became more apparent 92 hpi (Figure 5.12 (b)). Apart from *PR1*, local defence gene induction 24 hours post infiltration with *PstavrRpm1* showed minimal variation between accessions (Figure 5.13 (a)). There were greater differences in adjacent defence gene induction between the accessions tested. The magnitude of adjacent PR gene induction did not follow the same pattern as local induction (Figure 5.13 (b)). It was noted that control, water-infiltrated samples differed in the level of transcript accumulation (Figure 5.13 (c)). Here, in the adjacent leaf region, this did appear to have a significant effect on results. For example, landrace ‘China’ shows stronger adjacent gene induction than Golden Promise, however this may be due to lower transcript levels in the water-infiltrated control, rather than higher transcript levels after local infiltration with *PstavrRpm1* (Figure 5.13). During the inoculation procedure, differences in ease of infiltration of landraces and Golden Promise were noticed, with several of the landraces more resistant to infiltration. As such, these tests must be repeated with non-inoculated controls in order to determine if this effect is due to a differential effect of water infiltration on defence gene induction, or differences in basal transcript level between landraces.

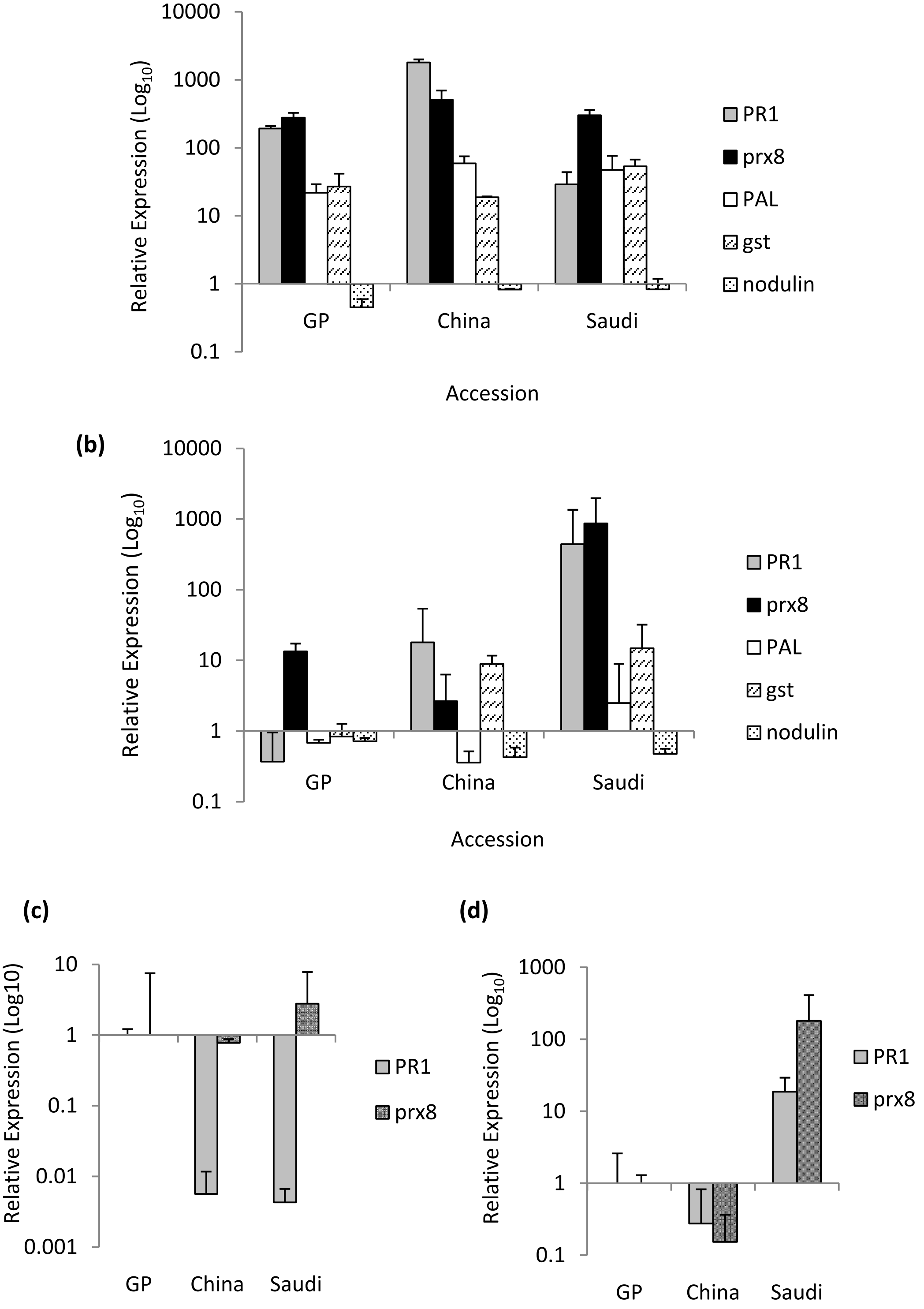
Tests of AR in the adjacent leaf region suggest that variation in AR induced by Golden Promise and the landraces tested is not extensive (Figure 5.14). However, ‘Turkey’ is the only landrace to show statistically significant induction of adjacent AR, with a similar reduction in bacterial growth to that seen in Golden Promise (Figure 5.14 (c)). Local symptoms (72 hpi) developing in ‘Turkey’ were not distinctively different from other lines (eg ‘Pakistan’ shows similar symptoms). In terms of secondary leaf responses, a single test of landrace ‘Pakistan’ indicated that AR did not develop in secondary leaves (Figure 5.14 (e)).

5.4 Discussion

The *in silico* analysis presented above suggests that *DIR1* homologues are present in the rice genome. This is supported by subsequent genome-wide analysis of LTPs in rice and *Arabidopsis* (Boutrot *et al.*, 2008) which identifies both *DIR1* (and *At5g48485*) and *RICE A* and *B* as Type IV subfamily ns-LTPs, and both pairs of genes as tandem duplicated repeats. *RICE A* has also been identified by Vergne *et al.* (2007) as a rice homologue of *Arabidopsis DIR1* in a study examining the expression of putative homologues of *Arabidopsis* defence-related genes during the interaction between rice and *Magnaporthe oryzae* (Vergne *et al.*, 2007). LTPs are ubiquitous in higher plants, and the subfamilies identified by Boutrot et al. 2008 appear to have been present prior to the monocot/ dicot divergence (Boutrot *et al.*, 2008). However, functional homologues of *Arabidopsis DIR1* have not been identified in any species. As such, determining the function of

Figure 5.13 Local and adjacent defence gene induction in Golden Promise and barley landraces. 24 hours post local infiltration with *PstavrRpm1* (OD$_{600}$ 0.2). qRT-PCR data, based on two-three replicates, each comprising leaf samples from three pooled seedlings. Seedlings were incoulated at 17 days old. Expression levels normalised to *alpha-tubulin 2* and *UBC*. Bars show mean values, + SD. **(a)** Local defence gene induction. Expression of each gene calculated relative to a water infiltrated control (for each line) **(b)** Adjacent defence gene induction. Expression of each gene calculated relative to a water infiltrated control (for each line) **(c)** Transcript levels in the adjacent region of water-infiltrated control samples, relative to Golden Promise **(d)** Transcript levels in the adjacent region of *Pst*-infiltrated samples, relative to Golden Promise.

Figure 5.13 (a)



10000
1000
100
10
1
0.1
Relative Expression (Log$_{10}$)
GP
China
Saudi
Accession
▨ PR1
■ prx8
☐ PAL
▨ gst
▨ nodulin
(b)
10000
1000
100
10
1
0.1
Relative Expression (Log$_{10}$)
GP
China
Saudi
Accession
▨ PR1
■ prx8
☐ PAL
▨ gst
▨ nodulin
(c)
10
1
0.1
0.01
0.001
Relative Expression (Log10)
GP
China
Saudi
▨ PR1
▨ prx8
(d)
1000
100
10
1
0.1
Relative Expression (Log$_{10}$)
GP
China
Saudi
▨ PR1
▨ prx8

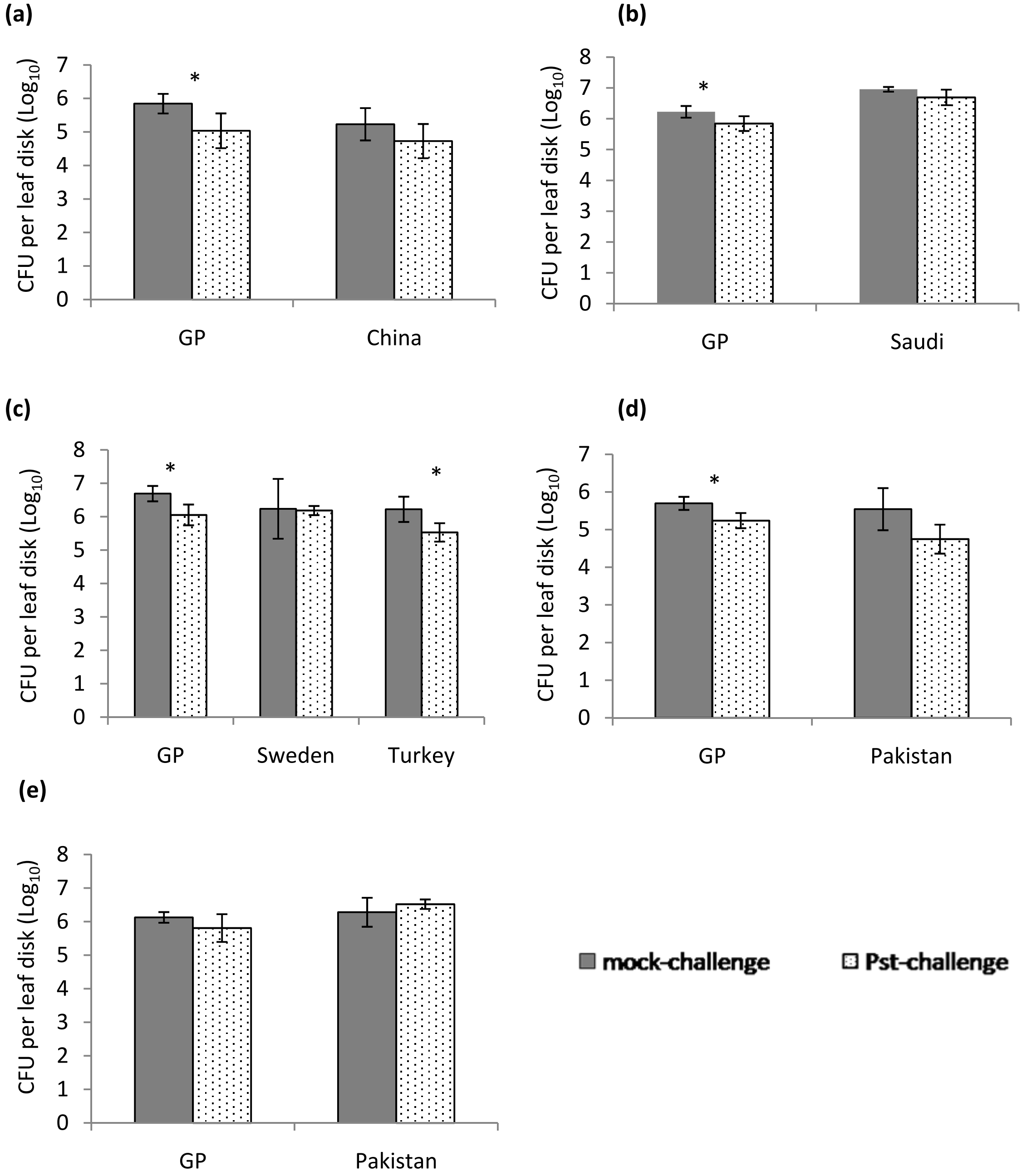


Figure 5.14 Adjacent resistance to PS86 in Golden Promise and barley landraces. The adjacent leaf region of Golden Promise and 'China' **(a)**, 'Saudi' **(b)**, 'Sweden' and 'Turkey' **(c)**, and 'Pakistan' **(d)** was challenged with PS86 24 hours post local infiltration with *PstavrRpm1* (OD_{600} 0.2) (Pst-challenge) or a water (control, mock-challenge). 24 hours later a leaf disc was sampled from the challenged region and CFU assayed. Bars indicate mean value of 3-4 replicates (one seedling per replicate) (±SD). Seedlings were 16-19 days old at time of *PstavrRpm1* inoculation. GP indicates Golden Promise. **(e)** Resistance to PS86 in a secondary leaf 6 days post local *PstavrRpm1* infiltration. Bars are as (a)-(d).

RICE A and B is important, and could provide insight into whether rice and other cereal species share a conserved SAR signalling pathway with *Arabidopsis*.

Data collected to date suggests that heterologous expression of *DIR1*, *RICE A* or *RICE B* in Golden Promise does not have an effect on adjacent acquired resistance, or adjacent PR gene induction, induced by local infiltration with *PstavrRpm1*. It is not known whether, in *Arabidopsis*, DIR1 functions in translocating AR within, as well as between, leaves. As such, it would now be interesting to test if heterologous expression of *DIR1*, *RICE A* or *RICE B* affects (or even confers) AR responses in secondary, non-inoculated leaves of these transgenic lines. In contrast to the situation for adjacent resistance to PS86, qRT-PCR data does suggest that induction of genes associated with defence may vary in local, *PstavrRpm1*-infiltrated tissue of the transgenic lines described. A reduction in necrosis appeared to be associated with increased level of gene induction. As noted, further tests are necessary to confirm this. Interestingly, enhanced induction of PR genes in infected tissue of transgenic wheat expressing an LTP has previously been reported (Roy-Barman *et al.*, 2006). In that case, expression of *Ace*-AMP1 (*Allium cepa*-AntiMicrobial Protein 1), encoding an LTP_1 from onion (*Allium cepa*) known to have strong direct antimicrobial effects on a wide range of plant pathogenic fungi and bacteria (Cammue *et al.*, 1995), led to enhanced resistance to wheat powdery mildew (*Blumeria graminis* f. sp. *tritici*) and Karnal bunt (caused by *Neovossia indica*) (Roy-Barman *et al.*, 2006). Furthermore, ears of transgenic wheat lines infected with *N. indica* showed enhanced expression of *PAL*, *PR2* and *PR3,* compared to null segregants. SA levels were also enhanced by 2-3 fold in the same tissue (Roy-Barman *et al.*, 2006). *Ace*AMP1 is unable to transfer phospholipids, due to an atypical structure whereby aromatic residues obstruct the characteristic LTP hydrophobic cavity. However, the protein is still able to interact with membrane lipids (Tassin *et al.*, 1998). The mechanism by which PR genes and SA are enhanced in *Ace*AMP1 transgenic wheat is unclear, and data is limited. Nevertheless, if expression of *DIR1* or its rice homologues can be shown to affect local resistance in barley (without having direct effects) this case will provide an interesting comparison.

In order to determine whether RICE A or B can function in the induction of SAR in the well-characterised *Arabidopsis* system, these genes were expressed in *Arabidopsis dir1-1* under the control of the 35S promoter, and seedlings tested for SAR. Although results do suggest that several of the *dir1-1 RICE A* / *B* lines have been complemented, firm conclusions cannot be drawn due to the minimal reduction in SAR seen in the *dir1-1* mutant line tested. This discrepancy with the effect reported by Maldonado *et al.* (2002) could be due to slight differences in experimental procedure - seedlings were challenged in secondary leaves with a ten-fold higher bacterial inoculum (10^6 CFU mL^{-1}) in order to produce consistent LUX counts. The SAR defect in *dir1-1* does appear to be more distinct when seedlings are challenged with the oomycete *Peronospora parasitica* (Maldonado et al. (2002)), and this may provide an alternative avenue for investigating complementation in these lines. If complementation can be demonstrated, this would strongly suggest that, when all other factors are in place, *RICE A* and / or *B* are able to function in SAR. DIR1 is thought to interact with other essential factors needed for the induction of SAR- shown by the fact that overexpression of *DIR1* in *Arabidopsis* does not lead to the constitutive induction of SAR (Maldonado *et al.* (2002)). As such, if RICE A and B are able to function in SAR in *Arabidopsis*, whilst failing to affect the translocation of AR in barley, this would suggest other necessary factors are missing from the SAR induction process/ pathway in barley. At this stage however, further data is needed before such conclusions could be drawn. The relatively small (but significant) reduction in SAR seen in *dir1-1*, and the difficulty seen here in reproducing this effect, highlights that any effect on adjacent and/ or systemic AR conferred by heterologous expression may be small. For such effects to be identified, wild-type responses in Golden Promise must be well characterised, and transgenic lines must be tested with a range of pathosystems.

In the landraces tested, increased adjacent defence gene induction 24 hours after local infiltration with *PstavrRpm1* was not associated with enhanced adjacent AR to PS86 (Figure 5.13 (b), Figure 5.14). As noted above, enhanced adjacent PR gene induction may be related to differential responses to infiltration, and as such increased adjacent gene induction may not reflect overall levels of PR gene transcripts. However, only one of five landraces tested showed significant adjacent AR, compared to a water-infiltrated control from the same accession. As noted above, accession-specific differences in the response of Golden Promise to *PstavrRpm1* (and/ or PS86) could affect results. It is known in *Arabidopsis* that differential local responses affect the induction of SAR (Mishina & Zeier, 2007a). Here, symptoms resulting from *PstavrRpm1* do appear to vary between landraces (Figure 5.12), and this differential response could be leading to the variation seen in adjacent resistance (Figure 5.14). However, the induction of adjacent AR could not be linked to the local symptoms induced, i.e. ‘China’ and ‘Saudi’ show different symptoms, yet neither shows adjacent AR. Whilst it is also possible that variation in genetic components specifically affecting AR could be contributing to the differences in adjacent AR seen, this may be difficult to elucidate in this system. Key questions to be addressed are whether further tests can link local variation in response to *PstavrRpm1* to adjacent AR, and whether the variation extends to secondary leaves.

Chapter 6: General discussion

The results presented in the previous chapters provide important insights into AR in cereals. Despite mounting evidence for the conservation in cereals of molecular components of SAR, and for the existence of local AR responses, there is limited evidence for biologically induced SAR in any cereal species (Kogel & Langen, 2005). Localisation of induced resistance in cereals has best been characterised in the barley – powdery mildew pathosystem, in which induced inaccessibility is strictly localised (Kunoh et al., 1988, Lyngkjaer & Carver, 1999, Ouchi et al., 1976). As attention focuses on durable sources of pathogen resistance in crops (Gust *et al.*, 2010), we still know very little about defence signalling pathways in cereal species (Kogel & Langen, 2005, Piffanelli *et al.*, 1999). SAR provides broad-spectrum, long-lasting resistance in dicot species, and as such, identifying, and improving our understanding of, the response in cereals could lead to improved strategies for disease control in cereal crops.

6.1 *Pseudomonas syringae* as an inducer of acquired resistance in barley

The development of a robust bioassay for biologically-induced AR in barley, described in Chapter 3, provides a model system for future investigations. The use of *Pseudomonas syringae* as an inducer of AR provides a clear frame of reference to the well-characterised *Arabidopsis-Pseudomonas syringae* SAR induction system (Cameron *et al.*, 1994), facilitating translation from the *Arabidoposis* model to barley. Use of *Pseudomonas syringae* also allows comparison with results from rice, where *Pseudomonas syringae* isolates have previously been reported to induce SAR (Jin *et al.*, 1997, Smith & Metraux, 1991). In other tests, this response could not be repeated (Reimmann *et al.*, 1995), however it is possible that once a robust bioassay has been established, information from rice could be informative in studies of barley. For example, Jin et al. (1997) report that application of the bacterial harpin elicitor can induce SAR in rice (as it can in *Arabidopsis* (Dong *et al.*, 1999)), and this could be tested in the barley system.

The interaction between inducer-isolate *PstavrRpm1* and barley appears to be that of a non-adapted pathogen, mediated by effector-recognition (Chapter 3). In *Arabidopsis*, non-host *Pseudomonas syringae* pathovars *glycinea* and *phaseolicola* have been shown to induce SAR, albeit less efficiently than adapted pathovars (Mishina & Zeier, 2007a). The tractability of *Pseudomonas syringae* in terms of genetic manipulation means it is now possible to return to the inducing interaction and investigate which elements are necessary for the induction of the adjacent response. For example, results described in Chapter 3 indicate that infiltration of Golden

Promise with the *Pst* DC3000 *hrcC*- mutant, which is deficient in the type- three secretion system (TTSS), does not result in macroscopically visible cell death or strong induction of defence genes. Testing adjacent responses after local infiltration with this isolate would provide information on whether the adjacent response is PAMP-triggered, giving further insight into possible signalling pathways involved. Adjacent responses to virulent isolates could also be tested. It has been reported that the efficiency and timing of SAR induction varies with the inducing interaction (Mishina & Zeier, 2007a, Smith et al., 1991), and as such it may be possible to further optimise adjacent defence induction by changing parameters of the local response. This could also affect the development of responses in secondary leaves, and as such could aid in the identification of a systemic response.

6.2 Acquired resistance in barley is translocated to the adjacent leaf region

The induction of adjacent resistance by *Pseudomonas syringae* indicates that AR in barley is not strictly localised (Chapter 4), contrary to the situation in the barley – powdery mildew interaction. This suggests that there may be important differences between the resistance pathways involved in mildew-induced, and *Pseudomonas*-induced resistance in barley. As noted, it has been reported that the interaction between *Pseudomonas syringae* pv. *syringae* and barley results in SA accumulation, wheras inoculation of barley with barley powdery mildew (*Blumeria graminis* f. sp. *hordei* (*Bgh*)) or wheat powdery mildew (*Blumeria graminis* f. sp. *tritici* (*Bgt*)) does not (Vallelian-Bindschedler *et al.*, 1998). As SAR signal generation appears to be a general feature of SA-mediated defence (Vlot *et al.*, 2008a), this may be important. However, in *Arabidopsis* and tobacco, accumulation of SA itself is not required in the primary inoculated leaf for SAR to develop, as *nahG* lines (that express salicylate hydrolase and therefore fail to accumulate SA) still develop SAR when secondary leaves have been grafted from wild-type plants (Vernooij *et al.*, 1994). Our understanding of the role of plant hormones such as SA in cereal defence signalling pathways is currently limited. In tests of Induced Systemic Resistance (ISR) in rice, De Vleesschauwer et al. (2008) used *nahG* rice lines to determine that, as in *Arabidopsis*, ISR develops independently of SA signalling. An *OsEIN2*-suppressed line, and JA-deficient *hebiba* line were also used to show that the response in rice is JA/ET dependent (De Vleesschauwer *et al.*, 2008). Equivalent lines are not currently available in barley, but production of barley *nahG* lines could contribute greatly to our understanding of the importance of SA in defence signalling in this species. A stabilised DELLA mutant line is available for barley, and as findings in *Arabidopsis* suggest such a line might be affected in the balance of SA/ JA signalling (Navarro *et al.*, 2008), testing this line for effects on adjacent resistance might be informative. Investigation of the interaction between powdery mildew and *Arabidopsis*, and whether this interaction leads to the induction of SAR, could also provide more answers.

Under the conditions tested to date, the adjacent AR described did not develop into systemic resistance. Without comprehensive tests of a greater range of leaves, pathogens and incubation periods, it cannot be concluded that resistance is not translocated to secondary leaves in barley. SAR in dicots appears to be a fairly ubiquitous response to a local pathogen interaction, and the difficulty associated with identifying a systemic response in barley does indicate that the development of the response differs in some respects to the dicot situation. However, the characterisation of the adjacent response provides an excellent basis for further study of secondary leaf responses.

6.3 Adjacent AR in barley shows similarity to *Arabidopsis* SAR

The results described in Chapter 4 indicate that the adjacent AR response in barley shares strong similarities with the *Arabidopsis* SAR response. Both forms of resistance are broad-spectrum, and both are associated with the induction of a subset of the PR-genes associated with local defence. The adjacent response in barley involves the up-regulation of 5 of the 9 described Barley Chemically Induced (BCI) genes, associated with chemically-induced AR in the species. This strongly suggests there is at least some overlap between the signalling involved in biologically and chemically-induced AR in barley. Furthermore, the differential regulation of BCI genes between the local and adjacent leaf region (Chapter 4) could provide an explanation as to why the majority of these genes have not previously been associated with pathogen-induced defence. The similarity between the transcriptional profiles of SAR in *Arabidopsis* and adjacent AR in barley does suggest that a similar mechanism might mediate resistance in both cases. However, several up-regulated transcripts showed homology to genes not traditionally associated with the dicot response. For example, a *Wheat Induced Resistance 1* homologue, and genes with homology to xylanase inhibitors and oxalate oxidases were all up-regulated in the adjacent region. Oxalate oxidases are associated with the production in barley of hydrogen peroxide during the resistance response to barley powdery mildew (Zhang *et al.*, 1995), suggesting they might play a direct role in the adjacent resistance seen here. Even in dicots, slightly different gene profiles are associated with SAR in different species, likely reflecting the particular challenges and spectrum of pathogens faced by each species (Kessmann *et al.*, 1994). As such, the identification of genes involved in biologically-induced AR in barley could help to determine the particular characteristics of the response in this species.

6.4 Mechanisms of acquired resistance in barley

The characterisation of adjacent AR in barley provides a starting point for investigating the molecular basis of the response. The relationship between local AR and *mlo*-mediated resistance in barley has been investigated with chemically-induced AR, and local induced resistance to *Bgt* (Jarosch *et al.*, 2003). The recessive *mlo* allele confers broad-spectrum penetration resistance to powdery mildew in barley, however *mlo* lines are also hypersensitive to *Magnaporthe oryzae*. Chemically, and *Bgt*-induced local AR provides protection in both *Mlo* and *mlo* lines, indicating that the barley AR pathway is separate to that involved in *mlo*-mediated resistance (Jarosch *et al.*, 2003).

In both *mlo* and *Mlo* barley, chemically and biologically-induced AR to *Magnaporthe oryzae* was associated with enhanced formation of effective papillae (Jarosch *et al.*, 2003). As with AR to *Magnaporthe*, AR to *Bgh* induced by DCINA in barley was associated with a higher frequency of effective papillae formation in short epidermal cells (Kogel *et al.*, 1994). HR was also reported in both cases, but whether this response has a causal role in AR remains unclear. During AR to *Magnaporthe oryzae*, mesophyll cell HR was associated with susceptibility. DCINA-induced AR to *Bgh* was associated with HR occuring prior to the formation of fungal haustoria, but the HR may not have been causally required for resistance (Kogel *et al.*, 1994). Interestingly, barley seedlings treated with DCINA show transient down-regulation of Barley *BAX inhibitor 1*- a suppressor of cell death. This down-regulation correlates with the onset of resistance, suggesting host cell death is involved in AR (Huckelhoven *et al.*, 2003, Kogel & Langen, 2005). It would be interesting to determine the mechanisms behind the adjacent AR described above. In particular, a comparison of the resistance mechanisms involved in adjacent AR to the bacterium PS86 and the fungus *Magnaporthe oryzae* would provide some insight into how broad-spectrum resistance provides protection against diverse challengers. Monitoring and comparing the transcriptional profile post-challenge with each of these challengers would also be informative. Interestingly, Jarosch *et al.* (2003) found that *PR1b, PR5, PR9, BCI1* and *BCI3* were up-regulated in response to inoculation of barley with *Magnaporthe oryzae*, but seemed to be associated with susceptibility. PR genes are not generally considered good markers of induced resistance in cereals (Kogel & Langen, 2005), but in the adjacent AR response described here, these genes are up-regulated prior to challenge in the adjacent leaf region showing enhanced resistance. Profiling the expression of these genes pre-to-post challenge could provide more information about their role in AR, and could contribute to the elucidation of their function. It is possible that these genes may play different roles, depending on the nature of the challenger.

A further aspect of the adjacent AR described above that remains to be tested is its efficacy against necrotrophic challengers. Although SAR in dicots is associated with resistance to biotrophic challengers (Ton *et al.*, 2002), expression of the *Arabidopsis NPR1* gene in wheat leads to enhanced resistance to Fusarium head blight, caused by the necrotrophic fungus *Fusarium graminearum* (Makandar *et al.*, 2006). Furthermore, petiole exudate from SAR-induced *Arabidopsis* leaves induced resistance to the same disease when applied to wheat spikelets (Chaturvedi *et al.*, 2008). However, BTH application failed to induce resistance to FHB in wheat (Yu & Muehlbauer, 2001). It would be interesting to test if the adjacent AR described here is effective against necrotrophic challengers. This would provide further insight into whether the response is similar to dicot SAR.

The bioinformatic analysis presented in Chapter 5 indicates that homologues of *Arabidopsis DIR1* are present in rice. Although tests of *dir1-1* mutant lines expressing *RICE A* or *RICE B* have not provided unequivocal results so far, there is some indication that complementation may be possible. If confirmed, this would strongly suggest that, where all other components are in place, rice has a functional pathway for the biological induction of SAR. In contrast, heterologous expression of *Arabidopsis DIR1*, *RICE A* or *RICE B* in barley does not appear to affect the translocation of AR (although further tests are needed to confirm this). However, these transgenic lines may be affected in local responses. Over-expression of *DIR1* in *Arabidopsis* does not affect local basal defence responses (Maldonado *et al.*, 2002), and as such, if this result is confirmed, this would suggest that there are differences between these species in the molecular basis of AR. Relatively little is currently known about the *in vivo* function of LTPs (Blein *et al.*, 2002). LTPs share structural similarity with oomycete elicitins, and a wheat LTP competes for the same plasma membrane receptor (Buhot *et al.*, 2001). Binding to this receptor triggers downstream defence signalling (Ponchet *et al.*, 1999). Furthermore, sensitivity to elicitins seems to be affected by the endogenous level of LTP in different plant species (Blein *et al.*, 2002). It is possible that differences between receptors, lipid profiles or binding affinity to the LTP in question could mean that the same LTPs act differently in different species. Interestingly, heterologous expression in wheat of an onion LTP, *Ace*AMP1, affected both pathogen resistance and PR gene levels (Roy-Barman *et al.*, 2006). The structure of *Ace*AMP1 means it is unable to transfer lipids (Tassin *et al.*, 1998), which suggests its effect in wheat is not related to lipid-binding. *Ace*AMP1 does have antimicrobial activity, which could explain its effect on pathogen resistance. However, this doesn't explain the associated changes in PR gene expression. Further tests of the differential local responses seen here in barley lines expressing *Arabidopsis DIR1*, *RICE A* and *RICE B* could provide important insights into the functions of lipid transfer proteins in plant defence, both in cereals, and in *Arabidopsis*.

6.6 Overall conclusion

The research presented in this thesis demonstrates that *Pseudomonas syringae* can be used as an inducer of acquired resistance in barley. Infiltration of first leaves of barley cultivar Golden Promise with isolates of *Pss*, *Psj* and *Pst* resulted in the local induction of active defence responses; these were maximal 24 hours after infiltration with *PstavrRpm1*. Induced defence responses to *PstavrRpm1* included up-regulation of PR gene transcripts and hypersensitive cell death. This local response appeared to be mediated by secreted effectors, as the *Pst* DC3000 *hrcC*- mutant (deficient in type III secretion) elicits a much weakened response.

In addition to local defence, infiltration with *PstavrRpm1* induces broad-spectrum AR in barley, at a distance from the local lesion. This 'adjacent' AR was effective against compatible *Pss* isolate PS86, and *Magnaporthe oryzae*. Transcriptional profiling of the adjacent response revealed a similar functional profile to that associated with *Arabidopsis* SAR, and up-regulation of transcripts with similarity to the Arabidopsis SAR marker genes. Furthermore, the adjacent response included the up-regulation of transcripts associated with chemically-induced acquired resistance in the cereals, basal defence, and also included defence-related transcripts that have not been associated with acquired resistance in dicots. These similarities and differences provide insight into possible mechanisms of acquired resistance in cereal and dicot species, and also provide a basis for further elucidation of the signalling pathways involved.

In order to investigate the conservation in cereals of an *Arabidopsis* gene known to function specifically in SAR, bioinformatics were used to identify candidate homologues in the cereals. Homologues of the SAR-specific *Arabidopsis DIR1* gene were identified in rice, and complementation tests using the *Arabidopsis dir1-1* mutant appear to suggest these may be able to function in SAR in *Arabidopsis*. However, results from heterologous expression suggest *Arabidopsis DIR1* and its rice homologues may affect local defence responses in barley, with transgenic lines showing reduced symptoms and enhanced defence gene induction after infiltration with *PstavrRpm1* As such, it appears that while rice homologues of *Arabidopsis DIR1* may be able to function in the induction of SAR, the mechanisms involved in SAR induction may differ between dicots and cereal species. It has been hypothesised that yield-focussed selective breeding could lead to the loss of strong defence alleles, which could account for differences in the regulation and mechanisms of AR between dicots and cereal cultivars. However, results of tests with barley landraces indicated there was little variation in the magnitude of adjacent AR induction between accessions. This fails to support the above hypothesis, and, together with the local effects in barley of heterologous *DIR1* expression, these results indicate that the differences between dicots and cereals in the induction of AR may be more fundamental. The results presented here further our understanding of AR in cereals, and provide an excellent basis for future dissection of the mechanisms involved.

Appendix

Appendix 1 is attached as a CD (inside front cover).

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Appendix 1 Table 1: Full list of genes significantly down-regulated in the local leaf region.

Affymetrix Probe Set ID	Annotation	Fold Change (Log2)	FDR Adjusted P Value	Functional Classification
Contig3674_at	Expansin	-4.82	7.75E-12	Biogenesis of cellular components
HS05F12u_s_at	Expansin	-4.63	5.48E-11	Biogenesis of cellular components
Contig2672_at	Xyloglucan xyloglucosyl transferase	-3.18	4.98E-11	Biogenesis of cellular components
Contig13674_at	Beta-D-xylosidase	-3.11	1.15E-07	Biogenesis of cellular components
Contig13673_at	Pumilio-family RNA binding repeat containing protein	-2.72	1.41E-06	Biogenesis of cellular components
Contig11667_at	Probable protein ABIL4	-2.02	1.38E-06	Biogenesis of cellular components
Contig12094_at	Expansin-like protein 1	-1.75	1.37E-07	Biogenesis of cellular components
Contig20224_at	Microtubule associated protein family protein	-1.64	3.80E-08	Biogenesis of cellular components
Contig4253_at	Putative ankyrin	-1.53	3.41E-06	Biogenesis of cellular components
Contig8475_at	Putative annexin	-1.46	3.44E-08	Biogenesis of cellular components
Contig17152_at	Exo70 exocyst complex subunit domain containing protein	-1.43	2.64E-05	Biogenesis of cellular components
Contig1394_at	Actin	-1.42	2.04E-05	Biogenesis of cellular components
Contig15410_at	Putative alpha subunit of F-actin capping protein	-1.4	1.43E-06	Biogenesis of cellular components
Contig1512_at	Tubulin beta-5 chain	-1.39	5.66E-08	Biogenesis of cellular components
Contig7068_at	Cellulose synthase-like H1	-1.38	7.62E-07	Biogenesis of cellular components
Contig7289_at	Ankyrin-like protein	-1.35	6.26E-08	Biogenesis of cellular components
Contig4811_s_at	Ankyrin-like protein	-1.32	5.31E-08	Biogenesis of cellular components
Contig14865_at	Microtubule-associated protein MAP65-1a	-1.31	2.86E-08	Biogenesis of cellular components
HV_CEa0014H05r2_at	Putative UDP-N-acetylmuramoylananyl-D-glutamate ligase	-1.21	2.55E-05	Biogenesis of cellular components
Contig4949_at	Putative callose synthase 1	-1.19	3.38E-06	Biogenesis of cellular components
Contig7166_s_at	CesA3 protein	-1.16	2.87E-06	Biogenesis of cellular components
Contig411_at	Tubulin alpha-3 chain	-1.15	5.56E-07	Biogenesis of cellular components
Contig1394_s_at	Actin	-1.12	1.11E-06	Biogenesis of cellular components
Contig20783_at	CESA4 - cellulose synthase	-1.12	3.98E-07	Biogenesis of cellular components
Contig17329_at	Putative cytoskeletal protein	-1.1	4.10E-07	Biogenesis of cellular components
Contig323_at	Probable protein ABIL3	-1.1	8.10E-06	Biogenesis of cellular components
Contig5010_s_at	Actin-depolymerizing factor 1	-1.08	5.62E-05	Biogenesis of cellular components
Contig18024_at	Profilin	-1.03	0	Biogenesis of cellular components

Contig5874_s_at	DNA damage inducible	-4.5	4.67E-09	Cell cycle and DNA processing
Contig10045_at	DNA helicase-like	-3.15	6.30E-10	Cell cycle and DNA processing
Contig139_x_at	Histone H4	-2.78	3.78E-09	Cell cycle and DNA processing
Contig24544_at	Cyclin-like	-2.69	6.31E-10	Cell cycle and DNA processing
Contig18984_s_at	Putative CAO protein	-2.59	4.79E-08	Cell cycle and DNA processing
Contig9948_at	Cell division inhibitor-like	-2.37	9.61E-10	Cell cycle and DNA processing
Contig26393_at	cyclin-dependent protein kinase	-2.35	4.63E-08	Cell cycle and DNA processing
Contig10869_s_at	DegP2 protease	-2.25	4.35E-08	Cell cycle and DNA processing
Contig11294_at	DNA helicase	-2.23	4.12E-10	Cell cycle and DNA processing
Contig20728_at	Putative helicase	-2.12	2.19E-07	Cell cycle and DNA processing
Contig7583_at	Protein linker histone H1 and H5 family protein	-2.05	8.30E-09	Cell cycle and DNA processing
Contig13824_at	Putative MAR-binding protein MFP1	-1.96	1.63E-07	Cell cycle and DNA processing
Contig695_s_at	Histone H4	-1.9	1.10E-07	Cell cycle and DNA processing
Contig140_at	Histone H4	-1.88	1.17E-08	Cell cycle and DNA processing
Contig7244_at	SET domain-containing protein	-1.87	1.05E-05	Cell cycle and DNA processing
Contig9381_at	PREG-like protein	-1.82	7.29E-10	Cell cycle and DNA processing
Contig12533_at	Cell division protease ftsH homolog 9	-1.76	2.38E-07	Cell cycle and DNA processing
Contig12872_at	Flap endonuclease	-1.75	1.65E-06	Cell cycle and DNA processing
Contig10393_at	Putative single-strand binding protein	-1.74	1.57E-07	Cell cycle and DNA processing
Contig11731_at	Cell division protein FtsH-like protein	-1.71	4.59E-08	Cell cycle and DNA processing
Contig7850_at	Nuf2 family protein	-1.66	7.25E-08	Cell cycle and DNA processing
Contig10421_at	Putative DNA polymerase I	-1.65	2.06E-07	Cell cycle and DNA processing
Contig316_s_at	Histone H4	-1.53	6.44E-08	Cell cycle and DNA processing
Contig11061_at	Translin family protein	-1.44	3.06E-06	Cell cycle and DNA processing
Contig17831_at	Kinesin-related protein	-1.42	1.28E-08	Cell cycle and DNA processing
Contig2253_s_at	Histone H1-like protein	-1.4	5.86E-07	Cell cycle and DNA processing
Contig12279_at	Cell division protein ftsZ	-1.37	1.71E-07	Cell cycle and DNA processing
Contig13470_at	PolI-like DNA polymerase	-1.35	4.04E-05	Cell cycle and DNA processing
Contig12225_at	Cell division protease ftsH homolog 7	-1.34	2.29E-08	Cell cycle and DNA processing
Contig10416_at	Cell cycle control protein	-1.32	2.87E-06	Cell cycle and DNA processing
Contig5800_at	Cryptochrome 1b	-1.32	3.11E-07	Cell cycle and DNA processing
Contig13352_at	Putative glucose inhibited division protein A	-1.31	5.89E-07	Cell cycle and DNA processing
Contig6507_at	Replication factor C 38 kDa subunit	-1.31	2.65E-07	Cell cycle and DNA processing

Contig9753_at	Meiotic recombination protein DMC1	-1.31	8.59E-05	Cell cycle and DNA processing
Contig8265_at	Putative cleavage stimulation factor subunit 1	-1.29	6.67E-06	Cell cycle and DNA processing
Contig145_at	Histone H2A.2	-1.27	7.47E-05	Cell cycle and DNA processing
Contig25010_at	Putative DNA mismatch repair protein	-1.25	9.00E-06	Cell cycle and DNA processing
rbaal12h24_at	Putative copia-type polyprotein	-1.2	1.93E-05	Cell cycle and DNA processing
Contig1161_at	Histone H2B.2	-1.14	2.66E-05	Cell cycle and DNA processing
Contig145_x_at	Histone H2A.2	-1.14	2.53E-05	Cell cycle and DNA processing
Contig2185_at	Cell division protease ftsH homolog 2	-1.12	0	Cell cycle and DNA processing
Contig12853_at	Putative nuclear matrix constituent protein 1	-1.11	1.18E-07	Cell cycle and DNA processing
Contig427_s_at	Histone H2A-like protein	-1.11	5.16E-07	Cell cycle and DNA processing
Contig2260_at	Histone H1-like protein HON101	-1.1	2.68E-05	Cell cycle and DNA processing
HY03H15u_s_at	Putative CENP-E like kinetochore protein	-1.1	1.40E-06	Cell cycle and DNA processing
Contig1157_at	Histone H2B	-1.09	0	Cell cycle and DNA processing
Contig11077_at	Putative MFP1 attachment factor 1	-1.04	1.92E-05	Cell cycle and DNA processing
Contig15447_at	Type III restriction enzyme, res subunit family protein,	-1.03	7.23E-06	Cell cycle and DNA processing
Contig4316_at	Pescadillo-like protein	-1.03	0	Cell cycle and DNA processing
Contig6506_s_at	Replication factor C 38 kDa subunit	-1.02	1.97E-06	Cell cycle and DNA processing
Contig131_at	Histone H4	-1.01	1.67E-06	Cell cycle and DNA processing
Contig14247_at	Putative DNA-(Apurinic or apyrimidinic site) lyase (ARP	-1	4.77E-05	Cell cycle and DNA processing
Contig7509_at	Putative DAG protein	-3.42	3.35E-09	Cell fate
Contig9398_s_at	Senescence-associated protein	-2.73	5.00E-09	Cell fate
Contig13371_at	Putative senescence-associated protein	-2.27	9.54E-07	Cell fate
Contig13370_s_at	Putative senescence-associated protein	-2.2	3.20E-07	Cell fate
Contig844_at	Putative senescence-associated protein	-2.19	3.53E-08	Cell fate
Contig15658_at	Putative Phytosulfokines precursor	-2.06	4.49E-08	Cell fate
EBro04_SQ003_H15_s_at	Putative phytosulfokine peptide	-1.9	4.05E-08	Cell fate
Contig10815_at	Putative senescence-associated protein	-1.77	8.66E-08	Cell fate
Contig9858_at	Putative ppf1 protein	-1.65	3.68E-08	Cell fate
Contig21080_at	Putative senescence-associated protein	-1.41	3.07E-07	Cell fate
HS09N08u_at	Putative EL5	-1.15	8.82E-05	Cell fate
Contig8847_at	Cleft lip and palate transmembrane 1 protein	-1.09	1.04E-06	Cell fate
Contig11383_at	Pore-forming toxin-like protein Hfr-2	-4.92	1.65E-09	Cell rescue, defence and virulence
rbah29m06_s_at	Putative beta-glucosidase	-4.52	5.44E-10	Cell rescue, defence and virulence

Contig11935_at	Putative peroxidase	-4.25	9.24E-10	Cell rescue, defence and virulence
Contig19029_at	Peroxidase 6	-4.2	3.86E-10	Cell rescue, defence and virulence
Contig13848_at	Putative subtilisin-like serine protease	-3.98	1.42E-09	Cell rescue, defence and virulence
Contig13847_s_at	Subtilisin-like proteinase	-3.92	1.04E-09	Cell rescue, defence and virulence
Contig1867_at	Putative peroxidase	-3.82	2.03E-09	Cell rescue, defence and virulence
Contig2489_at	Glutathione S-transferase	-3.74	5.16E-08	Cell rescue, defence and virulence
Contig8515_s_at	Putative L-ascorbate peroxidase	-3.71	4.98E-10	Cell rescue, defence and virulence
Contig20831_at	Glutathione transferase	-3.61	1.42E-09	Cell rescue, defence and virulence
Contig2768_s_at	Germin-like protein 1	-3.34	1.63E-08	Cell rescue, defence and virulence
Contig2988_s_at	Cysteine proteinase	-3.27	1.48E-07	Cell rescue, defence and virulence
Contig9123_at	Putative stress enhanced protein	-3.24	1.66E-08	Cell rescue, defence and virulence
HVSMEl0002K15r2_at	Chloroplast sigma factor	-3.22	1.01E-10	Cell rescue, defence and virulence
Contig972_x_at	Nonspecific lipid-transfer protein 4.2 precursor	-3.19	1.98E-07	Cell rescue, defence and virulence
Contig4701_at	Putative wound inducive gene	-3.12	1.04E-09	Cell rescue, defence and virulence
Contig24328_at	DIR1 (DEFECTIVE IN INDUCED RESISTANCE 1)	-3.11	3.02E-08	Cell rescue, defence and virulence
Contig24930_s_at	Putative beta-glycosidase	-2.94	1.90E-08	Cell rescue, defence and virulence
HVSMEm0002P02r2_x_at	Peroxidase	-2.94	9.00E-11	Cell rescue, defence and virulence
Contig11697_at	Putative salt-inducible protein	-2.91	2.32E-08	Cell rescue, defence and virulence
Contig7356_at	Chalcone synthase	-2.9	2.04E-05	Cell rescue, defence and virulence
rbasd23b02_s_at	Glb 1 1-3,1-4-beta-D-glucanase precursor	-2.85	8.48E-09	Cell rescue, defence and virulence
Contig26136_at	Putative alliinase	-2.82	3.42E-08	Cell rescue, defence and virulence
Contig4520_at	Cold acclimation protein WCOR615	-2.8	4.89E-10	Cell rescue, defence and virulence
Contig2320_s_at	Drought inducible 22 kD protein	-2.74	3.41E-08	Cell rescue, defence and virulence
Contig8961_at	Abscisic acid- and stress-induced protein	-2.74	5.61E-09	Cell rescue, defence and virulence
Contig8606_at	Putative beta-glucosidase	-2.7	3.20E-08	Cell rescue, defence and virulence
Contig4135_at	L-ascorbate peroxidase	-2.69	2.68E-10	Cell rescue, defence and virulence
Contig11092_at	Putative stress enhanced protein	-2.65	5.74E-08	Cell rescue, defence and virulence
Contig698_at	Lipid transfer protein 7a2b	-2.65	3.17E-09	Cell rescue, defence and virulence
Contig9041_s_at	Sigma factor SIG6	-2.64	3.00E-09	Cell rescue, defence and virulence
Contig20090_at	Putative membrane-associated salt-inducible protein	-2.59	3.02E-08	Cell rescue, defence and virulence
HVSMEm0013I03r2_at	Sigma factor protein	-2.57	4.03E-09	Cell rescue, defence and virulence
Contig717_x_at	Nonspecific lipid-transfer protein 4.2 precursor	-2.56	9.67E-07	Cell rescue, defence and virulence
X68656_s_at	Nonspecific Lipid Transfer Protein 3	-2.47	7.26E-08	Cell rescue, defence and virulence

Contig24930_at	Putative beta-glycosidase	-2.44	4.40E-10	Cell rescue, defence and virulence
Contig12309_s_at	Disease resistance protein RPM1 homolog	-2.41	7.08E-09	Cell rescue, defence and virulence
Contig1383_s_at	Metallothionein	-2.41	1.96E-08	Cell rescue, defence and virulence
Contig825_s_at	Putative L-ascorbate peroxidase	-2.4	2.72E-07	Cell rescue, defence and virulence
Contig8367_at	Glutathione peroxidase	-2.38	5.94E-10	Cell rescue, defence and virulence
Contig20718_at	Plastid sigma factor SIG5	-2.36	8.12E-09	Cell rescue, defence and virulence
Contig2488_s_at	Glutathione S-transferase	-2.34	1.39E-07	Cell rescue, defence and virulence
EBro07_SQ002_B04_s_at	Ultraviolet-B-repressible protein	-2.33	9.25E-07	Cell rescue, defence and virulence
HVSMEm0015P16r2_at	Jasmonate-induced protein	-2.32	3.20E-07	Cell rescue, defence and virulence
rbah54a21_s_at	Putative beta-glucosidase	-2.32	7.56E-09	Cell rescue, defence and virulence
Contig3241_at	Peroxidase 6	-2.25	3.72E-08	Cell rescue, defence and virulence
rbasd16a13_s_at	Lipid transfer protein	-2.24	2.56E-07	Cell rescue, defence and virulence
Contig13888_at	PAP fibrillin family protein	-2.23	4.54E-09	Cell rescue, defence and virulence
HV_CEa0004P03r2_at	Seven transmembrane protein Mlo8	-2.23	2.74E-08	Cell rescue, defence and virulence
Contig13949_at	Putative PrMC3	-2.2	1.57E-08	Cell rescue, defence and virulence
Contig17827_at	Seven transmembrane protein Mlo7	-2.18	3.01E-08	Cell rescue, defence and virulence
Contig959_x_at	Non-specific lipid-transfer protein	-2.16	5.43E-07	Cell rescue, defence and virulence
Contig3776_s_at	Lipid transfer protein-like protein	-2.12	0	Cell rescue, defence and virulence
Contig25762_at	DIR1-like	-2.1	3.46E-05	Cell rescue, defence and virulence
Contig4679_s_at	Monodehydroascorbate reductase	-2.08	6.43E-08	Cell rescue, defence and virulence
Contig11428_at	Sigma factor SIG2B	-2.07	2.01E-07	Cell rescue, defence and virulence
Contig12563_s_at	Putative chalcone synthase	-2.07	1.39E-08	Cell rescue, defence and virulence
rbaal5f06_at	Putative beta-glucosidase	-2.07	8.31E-09	Cell rescue, defence and virulence
Contig3216_at	Defensin precursor	-2.05	6.61E-08	Cell rescue, defence and virulence
Contig3243_x_at	Peroxidase 6	-2.05	4.06E-09	Cell rescue, defence and virulence
HF12K17r_at	Putative NADPH HC toxin reductase	-2.04	7.64E-09	Cell rescue, defence and virulence
Contig16375_at	DIR1-like	-2.03	5.38E-06	Cell rescue, defence and virulence
Contig2147_at	Putative subtilisin-like proteinase	-2.02	1.31E-08	Cell rescue, defence and virulence
Contig26389_at	PAP fibrillin family protein	-1.99	3.82E-06	Cell rescue, defence and virulence
Contig14392_at	Putative subtilisin-like proteinase	-1.98	5.52E-08	Cell rescue, defence and virulence
Contig2403_at	Cysteine proteinase 1 precursor	-1.92	3.41E-08	Cell rescue, defence and virulence
HK03H11r_x_at	Lipid transfer protein precursor	-1.92	6.41E-07	Cell rescue, defence and virulence
Contig2864_s_at	Beta-glucosidase homolog F8K4.3	-1.91	3.26E-08	Cell rescue, defence and virulence

Contig12367_at	NBS-LRR disease resistance protein homologue	-1.89	1.21E-08	Cell rescue, defence and virulence
Contig6218_at	Lipid transfer protein-like	-1.88	1.43E-08	Cell rescue, defence and virulence
Contig7015_at	ABC1 family protein kinase-like protein	-1.86	1.77E-07	Cell rescue, defence and virulence
HVSMEk0005A23r2_at	Legumain-like protease	-1.85	1.07E-08	Cell rescue, defence and virulence
Contig23795_at	Lipoxygenase	-1.84	1.64E-05	Cell rescue, defence and virulence
Contig845_s_at	Lipid transfer protein precursor	-1.83	9.19E-07	Cell rescue, defence and virulence
HV_CEb0010L15r2_s_at	Plastid-lipid associated protein PAP/fibrillin family-like	-1.78	4.50E-08	Cell rescue, defence and virulence
Contig2868_at	Peroxisome type ascorbate peroxidase	-1.77	8.06E-09	Cell rescue, defence and virulence
Contig12262_at	NBS-LRR resistance protein	-1.76	4.95E-09	Cell rescue, defence and virulence
Contig2111_s_at	Peroxidase	-1.76	3.42E-07	Cell rescue, defence and virulence
Contig12842_at	Beta-D-glucan exohydrolase-like protein	-1.75	9.23E-07	Cell rescue, defence and virulence
Contig7753_at	Cold acclimation WCOR413-like protein gamma form	-1.72	2.83E-08	Cell rescue, defence and virulence
rbah31f14_s_at	Putative wound inductive gene	-1.71	8.52E-08	Cell rescue, defence and virulence
Contig3120_at	Salt stress root protein RS1	-1.67	2.63E-07	Cell rescue, defence and virulence
Contig14166_at	Enhanced disease susceptibility 5	-1.66	4.36E-07	Cell rescue, defence and virulence
Contig191_at	Putative CutA protein	-1.65	1.51E-07	Cell rescue, defence and virulence
Contig6972_at	Hypersensitive-induced reaction protein 2	-1.64	4.36E-06	Cell rescue, defence and virulence
Contig6664_at	Cadmium-induced protein-like	-1.63	7.77E-08	Cell rescue, defence and virulence
Contig8160_at	Putative mlo2 protein	-1.63	4.61E-09	Cell rescue, defence and virulence
Contig366_at	Wali7 protein	-1.59	1.21E-07	Cell rescue, defence and virulence
Contig3239_at	Peroxidase 6	-1.59	2.16E-06	Cell rescue, defence and virulence
Contig12785_at	Fatty acid hydroperoxide lyase	-1.58	4.36E-07	Cell rescue, defence and virulence
Contig15181_at	Macrophage migration inhibitory factor (MIF) family	-1.58	1.15E-06	Cell rescue, defence and virulence
HZ62K09r_at	Peroxidase	-1.58	2.81E-08	Cell rescue, defence and virulence
Contig110_at	Metallothioneine type2	-1.57	1.51E-07	Cell rescue, defence and virulence
Contig16511_at	Florfenicol resistance protein-like	-1.54	2.96E-07	Cell rescue, defence and virulence
Contig6505_at	Low-temperature induced protein lt101.1	-1.54	0	Cell rescue, defence and virulence
Contig11554_at	Putative stress inducible protein	-1.53	1.33E-06	Cell rescue, defence and virulence
Contig2864_at	Beta-glucosidase homolog F8K4.3	-1.53	1.89E-07	Cell rescue, defence and virulence
Contig2346_at	Putative beta-glucosidase	-1.52	5.64E-06	Cell rescue, defence and virulence
Contig12785_x_at	Fatty acid hydroperoxide lyase	-1.5	2.59E-06	Cell rescue, defence and virulence
Contig6595_at	Probable plastid-lipid-associated protein 3	-1.5	1.18E-07	Cell rescue, defence and virulence
HV_CEa0018D10f_s_at	Wali7 protein	-1.5	1.51E-08	Cell rescue, defence and virulence

Contig16224_at	Glutathione S-transferase GST16-like protein	-1.49	3.15E-07	Cell rescue, defence and virulence
Contig8927_at	Beta-glucosidase	-1.49	1.43E-08	Cell rescue, defence and virulence
Contig12267_at	Peroxidase-like protein	-1.47	1.39E-07	Cell rescue, defence and virulence
Contig9527_at	Putative glutathione reductase	-1.47	2.63E-06	Cell rescue, defence and virulence
Contig3839_at	Macrophage migration inhibitory factor (MIF) family	-1.46	1.53E-06	Cell rescue, defence and virulence
Contig8063_at	Putative CuZn-superoxide dismutase	-1.46	7.04E-07	Cell rescue, defence and virulence
HVSMEn0015O15f_s_at	Putative respiratory burst oxidase	-1.45	0	Cell rescue, defence and virulence
Contig2856_s_at	Cold acclimation protein homolog	-1.44	4.31E-06	Cell rescue, defence and virulence
HS18F13u_s_at	Peroxisome type ascorbate peroxidase	-1.44	3.39E-07	Cell rescue, defence and virulence
HVSMEa0006M12r2_at	Putative alliinase	-1.44	1.17E-06	Cell rescue, defence and virulence
Contig11234_at	Putative disease resistance protein (CC-NBS-LRR class)	-1.41	3.70E-08	Cell rescue, defence and virulence
Contig7629_at	Putative dehydration-responsive protein RD22 precursor	-1.41	3.84E-06	Cell rescue, defence and virulence
HVSMEn0023O21f_s_at	Cysteine protease component of protease-inhibitor complex	-1.41	2.96E-06	Cell rescue, defence and virulence
Contig2556_s_at	Cysteine protease component of protease-inhibitor complex	-1.4	1.08E-05	Cell rescue, defence and virulence
Contig5309_at	Biostress-resistance-related protein	-1.4	9.04E-08	Cell rescue, defence and virulence
HU12K14u_at	ABC1-like	-1.4	1.92E-08	Cell rescue, defence and virulence
Contig8063_s_at	Putative CuZn-superoxide dismutase	-1.34	8.31E-07	Cell rescue, defence and virulence
Contig1374_at	Metallothionein	-1.29	0	Cell rescue, defence and virulence
Contig12574_at	Lipoxygenase	-1.28	9.01E-05	Cell rescue, defence and virulence
Contig3215_s_at	Defensin precursor	-1.28	0	Cell rescue, defence and virulence
Contig3197_at	Superoxide dismutase	-1.26	1.99E-07	Cell rescue, defence and virulence
Contig6213_s_at	Class1 chitinase	-1.26	3.02E-07	Cell rescue, defence and virulence
Contig3573_s_at	Endo-1,3;1,4-beta-D-glucanase precursor	-1.25	1.45E-05	Cell rescue, defence and virulence
HV_CEa0004N03r2_at	Peroxidase	-1.25	1.50E-05	Cell rescue, defence and virulence
Contig6305_at	Coronatine-insensitive protein 1-like	-1.23	2.12E-06	Cell rescue, defence and virulence
Contig3750_at	Elicitor-inducible protein	-1.22	1.25E-05	Cell rescue, defence and virulence
Contig4298_at	Cysteine proteinase inhibitor	-1.22	0	Cell rescue, defence and virulence
Contig2769_s_at	Germin-like protein 1	-1.21	1.87E-05	Cell rescue, defence and virulence
Contig10131_s_at	Putative dehydroascorbate reductase	-1.2	1.74E-06	Cell rescue, defence and virulence
Contig2617_at	Interferon responsive family protein / GILT family protein	-1.2	3.28E-07	Cell rescue, defence and virulence
Contig3810_s_at	WSI76 protein	-1.18	5.58E-06	Cell rescue, defence and virulence
rbags25i16_x_at	Thioredoxin peroxidase	-1.18	2.23E-06	Cell rescue, defence and virulence
Contig2281_at	Putative metacaspase	-1.17	1.33E-06	Cell rescue, defence and virulence

Contig8357_at	Pathogenesis-related genes transcriptional activator PTI6	-1.16	3.46E-06	Cell rescue, defence and virulence
Contig21706_at	Glutathione S-transferase	-1.15	4.66E-07	Cell rescue, defence and virulence
Contig6735_at	Cystatin Hv-CPI3	-1.15	1.45E-05	Cell rescue, defence and virulence
Contig22790_at	Coronatine-insensitive 1 (COI1)	-1.11	1.25E-05	Cell rescue, defence and virulence
Contig2348_s_at	Beta-glucosidase	-1.11	3.92E-06	Cell rescue, defence and virulence
HV14K05u_s_at	Chitinase	-1.11	1.21E-06	Cell rescue, defence and virulence
Contig9808_at	Low temperature-induced protein	-1.1	7.93E-05	Cell rescue, defence and virulence
Contig2555_at	Cysteine protease component of protease-inhibitor complex	-1.09	3.01E-05	Cell rescue, defence and virulence
Contig777_at	Metallothioneine type1	-1.09	0	Cell rescue, defence and virulence
HV_CEa0002I05r2_at	Putative PrMC3	-1.08	4.21E-06	Cell rescue, defence and virulence
HV10C01u_s_at	Cysteine proteinase inhibitor	-1.07	1.10E-05	Cell rescue, defence and virulence
Contig10131_at	Putative dehydroascorbate reductase	-1.06	5.88E-07	Cell rescue, defence and virulence
Contig15302_at	Peroxidase	-1.06	8.86E-06	Cell rescue, defence and virulence
Contig845_at	Nonspecific lipid-transfer protein Cw18 precursor	-1.05	2.15E-05	Cell rescue, defence and virulence
Contig15480_at	8-oxoguanine DNA glycosylase-like protein	-1.03	3.67E-07	Cell rescue, defence and virulence
Contig5952_at	Response regulator 5	-1.02	1.88E-06	Cell rescue, defence and virulence
rbaal14c13_at	Putative Cf2/Cf5 disease resistance protein	-1.02	2.91E-06	Cell rescue, defence and virulence
Contig3449_s_at	Cold induced protein-like	-1	1.72E-05	Cell rescue, defence and virulence
Contig1762_s_at	Auxin-repressed protein-like protein	-3.91	1.60E-09	Cellular communication, signal transduction
Contig7941_s_at	Putative receptor-like kinase	-3.23	6.93E-09	Cellular communication, signal transduction
Contig8466_s_at	Leucine-rich repeat protein LRP	-3.21	6.97E-09	Cellular communication, signal transduction
Contig4243_at	Peroxiredoxin-2E-2	-3.2	5.11E-08	Cellular communication, signal transduction
Contig18956_at	Putative receptor protein kinase	-3.17	1.43E-08	Cellular communication, signal transduction
Contig5702_at	Extracellular calcium sensing receptor	-3.15	3.14E-08	Cellular communication, signal transduction
Contig12188_s_at	Shaggy-like protein kinase	-3.1	4.95E-11	Cellular communication, signal transduction
Contig16827_at	HPt phosphotransmitter	-3.05	8.71E-11	Cellular communication, signal transduction
Contig11167_at	Serine/threonine protein kinase	-3.02	3.97E-10	Cellular communication, signal transduction
HVSMEg0006F05r2_s_at	Extracellular calcium sensing receptor	-3.02	1.22E-07	Cellular communication, signal transduction
Contig2504_at	Auxin-responsive Aux/IAA gene family member	-2.94	1.29E-09	Cellular communication, signal transduction
Contig7678_at	Auxin-regulated protein	-2.92	2.44E-08	Cellular communication, signal transduction
HV_CEb0007D16r2_at	Putative protein kinase	-2.8	6.11E-11	Cellular communication, signal transduction
Contig5948_at	Calcineurin-like phosphoesterase family protein	-2.78	4.21E-09	Cellular communication, signal transduction
Contig14249_at	Ser/Thr protein phosphatase family protein	-2.7	3.42E-10	Cellular communication, signal transduction

Contig13011_s_at	Receptor-like protein kinase-like	-2.56	2.79E-08	Cellular communication, signal transduction
Contig10850_at	Protein phosphatase-2C	-2.53	3.89E-09	Cellular communication, signal transduction
Contig7988_at	Serine/threonine-protein kinase SNT7	-2.53	2.25E-07	Cellular communication, signal transduction
Contig24168_at	RPT2 protein	-2.51	2.97E-10	Cellular communication, signal transduction
Contig9746_at	Guanine nucleotide-binding protein beta subunit-like protein	-2.5	9.74E-09	Cellular communication, signal transduction
Contig5104_s_at	Peroxiredoxin Q	-2.49	5.92E-09	Cellular communication, signal transduction
Contig7208_at	Putative abscisic acid-induced protein	-2.46	1.51E-09	Cellular communication, signal transduction
Contig17124_at	Putative Rho GDP-dissociation inhibitor	-2.45	7.59E-09	Cellular communication, signal transduction
Contig17921_at	Putative auxin-regulated	-2.45	1.25E-08	Cellular communication, signal transduction
Contig2503_s_at	Auxin-responsive protein	-2.4	2.90E-08	Cellular communication, signal transduction
Contig1765_at	Auxin-repressed protein-like protein	-2.36	3.57E-09	Cellular communication, signal transduction
Contig9673_s_at	Putative protein phosphatase 2C	-2.32	7.22E-09	Cellular communication, signal transduction
Contig4419_at	Auxin-regulated protein	-2.28	2.30E-08	Cellular communication, signal transduction
Contig19395_at	Putative auxin-regulated protein	-2.22	1.31E-07	Cellular communication, signal transduction
Contig15125_at	Auxin-responsive protein	-2.21	2.02E-08	Cellular communication, signal transduction
Contig16201_at	Putative sphingosine kinase	-2.17	5.17E-09	Cellular communication, signal transduction
Contig14698_at	Acid phosphatase	-2.11	1.62E-09	Cellular communication, signal transduction
Contig7768_s_at	Putative signal recognition particle receptor	-2.1	2.22E-09	Cellular communication, signal transduction
Contig26452_at	Putative Adenylate kinase	-2.08	1.67E-08	Cellular communication, signal transduction
Contig13334_at	Putative leucine-rich repeat transmembrane protein kinase 1	-2.07	1.12E-07	Cellular communication, signal transduction
Contig24914_at	Putative nitric-oxide synthase	-2.05	3.54E-09	Cellular communication, signal transduction
Contig5953_at	Response regulator 6	-2.04	9.15E-10	Cellular communication, signal transduction
Contig2503_at	IAA30-auxin-responsive Aux/IAA family member	-2.03	6.13E-09	Cellular communication, signal transduction
rbah19o01_s_at	Two-component response regulator-like PRR95	-1.99	2.39E-08	Cellular communication, signal transduction
Contig5105_at	Peroxiredoxin Q	-1.98	6.11E-08	Cellular communication, signal transduction
Contig8523_s_at	Ser/Thr protein phosphatase family protein	-1.98	1.53E-08	Cellular communication, signal transduction
Contig13990_at	Transducin-like enhancer protein 4	-1.95	6.91E-08	Cellular communication, signal transduction
Contig9674_at	Probable protein phosphatase 2C	-1.95	1.45E-07	Cellular communication, signal transduction
Contig4515_at	Calcium ion binding protein	-1.94	1.04E-09	Cellular communication, signal transduction
Contig11409_at	Protein phosphatase type-2C	-1.91	8.45E-10	Cellular communication, signal transduction
Contig322_at	Auxin-responsive protein IAA3	-1.9	2.36E-08	Cellular communication, signal transduction
Contig13701_at	Putative OsLRK1	-1.89	7.37E-08	Cellular communication, signal transduction
Contig6533_at	Two-component response regulator-like PRR95	-1.89	6.67E-09	Cellular communication, signal transduction

Contig14415_at	Protein kinase -like	-1.8	8.29E-07	Cellular communication, signal transduction
Contig12078_at	Protein kinase domain containing protein	-1.79	5.12E-10	Cellular communication, signal transduction
Contig14822_at	CBL-interacting protein kinase	-1.79	8.65E-09	Cellular communication, signal transduction
Contig6306_at	Phosphatidate cytidylyltransferase	-1.79	5.27E-09	Cellular communication, signal transduction
Contig8936_at	Nucleoside diphosphate kinase 1	-1.78	6.06E-07	Cellular communication, signal transduction
Contig5912_at	Phosphatidylinositol-4-phosphate 5-kinase	-1.78	1.99E-06	Cellular communication, signal transduction
Contig6974_at	Auxin-responsive protein IAA31	-1.77	3.00E-07	Cellular communication, signal transduction
Contig7516_at	Auxin-repressed protein	-1.77	9.72E-07	Cellular communication, signal transduction
Contig12000_at	PB1 domain containing protein	-1.76	2.42E-08	Cellular communication, signal transduction
Contig2433_s_at	Putative acid phosphatase	-1.75	0	Cellular communication, signal transduction
Contig14720_s_at	Phosphatidylinositol-4-phosphate 5-Kinase	-1.74	3.74E-07	Cellular communication, signal transduction
Contig4275_at	Calcineurin-like protein	-1.74	4.28E-08	Cellular communication, signal transduction
Contig5558_at	Putative serine/threonine protein phosphatase	-1.73	3.51E-08	Cellular communication, signal transduction
Contig7147_at	Calcium-binding EF hand family protein	-1.73	1.81E-08	Cellular communication, signal transduction
Contig13012_at	Receptor-like protein kinase	-1.7	8.25E-09	Cellular communication, signal transduction
Contig11052_at	Two-component response regulator-like PRR73	-1.69	2.18E-07	Cellular communication, signal transduction
Contig9376_at	Two-component response regulator-like PRR73	-1.69	4.61E-06	Cellular communication, signal transduction
Contig7501_s_at	Putative calcium-binding protein	-1.66	3.26E-07	Cellular communication, signal transduction
Contig10761_at	Leucine-rich repeat transmembrane protein kinase	-1.65	2.13E-07	Cellular communication, signal transduction
HZ51M12r_s_at	Protein kinase-like	-1.62	7.94E-10	Cellular communication, signal transduction
Contig18344_at	Serine/threonine-protein kinase-like protein	-1.61	1.21E-09	Cellular communication, signal transduction
Contig7768_at	Signal recognition particle receptor	-1.6	8.84E-08	Cellular communication, signal transduction
Contig11205_at	Auxin-regulated protein-like	-1.59	8.13E-07	Cellular communication, signal transduction
Contig7609_s_at	BRI1-KD interacting protein 130	-1.58	1.50E-07	Cellular communication, signal transduction
Contig9618_s_at	Acid phosphatase	-1.58	2.85E-08	Cellular communication, signal transduction
Contig26476_at	Truncated putative purple acid phosphatase	-1.57	0.01	Cellular communication, signal transduction
Contig12768_at	MAP3K protein kinase-like protein	-1.56	2.29E-06	Cellular communication, signal transduction
Contig17607_at	Protein kinase-like	-1.56	2.61E-07	Cellular communication, signal transduction
HVSMEg0006F05r2_x_at	Extracellular calcium sensing receptor	-1.56	1.06E-07	Cellular communication, signal transduction
Contig18615_at	MAP/microtubule affinity-regulating kinase 4	-1.55	3.16E-08	Cellular communication, signal transduction
Contig9300_at	Histidine kinase	-1.55	2.38E-08	Cellular communication, signal transduction
Contig4218_at	Phosphatidylinositol 3-and 4-kinase family-like	-1.52	3.70E-07	Cellular communication, signal transduction
Contig20622_at	BRI1-associated receptor kinase 1	-1.51	1.14E-06	Cellular communication, signal transduction

Contig21325_at	Rac GTPase activating protein 1	-1.51	4.47E-08	Cellular communication, signal transduction
Contig4811_at	Ankyrin protein kinase	-1.51	7.74E-08	Cellular communication, signal transduction
Contig11248_at	Putative auxin-repressed protein	-1.5	2.80E-08	Cellular communication, signal transduction
Contig21059_at	Putative receptor kinase	-1.5	1.93E-08	Cellular communication, signal transduction
Contig26133_at	Protein kinase	-1.5	1.97E-07	Cellular communication, signal transduction
Contig6300_at	Von Willebrand factor type A domain containing protein	-1.5	2.76E-08	Cellular communication, signal transduction
Contig11262_at	Gibberellin receptor GID1L2	-1.49	4.87E-08	Cellular communication, signal transduction
Contig11741_at	Probable protein ABIL1	-1.48	2.40E-07	Cellular communication, signal transduction
Contig13376_at	Putative protein phosphatase 2C	-1.48	3.02E-08	Cellular communication, signal transduction
Contig8019_at	Calcium-binding EF hand family protein	-1.48	2.12E-08	Cellular communication, signal transduction
Contig7265_s_at	Protein kinase CK2 regulatory subunit CK2B3	-1.47	1.38E-06	Cellular communication, signal transduction
Contig15820_at	CBL-interacting protein kinase	-1.45	4.70E-06	Cellular communication, signal transduction
Contig18504_s_at	Serine/threonine-protein kinase SAPK5	-1.44	5.66E-08	Cellular communication, signal transduction
Contig9099_at	Protein phosphatase 2C-like protein	-1.44	2.38E-08	Cellular communication, signal transduction
Contig9829_at	Protein tyrosine phosphatase	-1.4	5.87E-07	Cellular communication, signal transduction
Contig12846_at	Putative receptor-like protein kinase	-1.38	6.79E-07	Cellular communication, signal transduction
Contig14472_at	Putative leucine-rich receptor-like protein kinase	-1.38	1.32E-07	Cellular communication, signal transduction
Contig14957_at	NAD kinase	-1.38	8.99E-07	Cellular communication, signal transduction
Contig17603_at	Putative mitogen-activated protein kinase	-1.38	6.84E-08	Cellular communication, signal transduction
Contig10299_at	GA 2-oxidase 5 (GA2ox5)	-1.37	9.83E-07	Cellular communication, signal transduction
Contig9342_at	Auxin-responsive protein	-1.37	5.35E-06	Cellular communication, signal transduction
Contig5251_at	Auxin-responsive protein	-1.36	4.31E-06	Cellular communication, signal transduction
Contig8075_at	Antigen receptor-like	-1.36	2.72E-05	Cellular communication, signal transduction
Contig6687_at	Protein phosphatase 2C-related	-1.35	7.91E-07	Cellular communication, signal transduction
Contig20012_at	Putative ABA-responsive protein	-1.32	5.65E-07	Cellular communication, signal transduction
Contig2434_at	Putative acid phosphatase	-1.32	0	Cellular communication, signal transduction
Contig24765_at	Two-component response regulator ARR1	-1.32	7.85E-08	Cellular communication, signal transduction
Contig6755_s_at	Putative phosphoinositide phosphatase	-1.31	8.77E-08	Cellular communication, signal transduction
Contig15223_at	Dual specificity protein phosphatase 12	-1.29	5.18E-05	Cellular communication, signal transduction
HY01F11u_at	Putative zinc ribbon 1	-1.29	1.25E-06	Cellular communication, signal transduction
Contig10952_at	Auxin response factor 9	-1.28	4.02E-07	Cellular communication, signal transduction
Contig1537_at	TaWIN2-like protein	-1.28	9.25E-08	Cellular communication, signal transduction
Contig5523_at	Putative protein phosphatase	-1.28	1.52E-05	Cellular communication, signal transduction

Contig8327_at	Serine/threonine-protein kinase SAPK9	-1.28	6.62E-07	Cellular communication, signal transduction
Contig5913_s_at	Phosphatidylinositol-4-phosphate 5-kinase	-1.26	6.58E-08	Cellular communication, signal transduction
Contig10209_at	Auxin-regulated protein	-1.25	1.20E-07	Cellular communication, signal transduction
Contig10889_at	Wpk4 protein kinase	-1.25	2.86E-05	Cellular communication, signal transduction
Contig9756_at	Putative PTI1-like kinase	-1.25	1.55E-07	Cellular communication, signal transduction
Contig13148_at	Homeobox-leucine zipper protein HOX6	-1.24	6.55E-06	Cellular communication, signal transduction
Contig16082_at	Protein kinase	-1.24	3.61E-07	Cellular communication, signal transduction
Contig19622_at	Histidine-containing phosphotransfer protein-like	-1.24	2.42E-05	Cellular communication, signal transduction
Contig8926_at	Putative protein kinase C inhibitor	-1.24	2.89E-07	Cellular communication, signal transduction
Contig9343_s_at	Auxin-responsive protein	-1.24	1.12E-06	Cellular communication, signal transduction
Contig14513_at	Putative MAP3K alpha 1 protein kinase	-1.23	3.09E-07	Cellular communication, signal transduction
Contig6206_s_at	Receptor-like protein kinase 5	-1.22	1.48E-05	Cellular communication, signal transduction
Contig20608_at	Calcium-dependent protein kinase	-1.21	3.85E-06	Cellular communication, signal transduction
rbags23g17_s_at	Protein kinase domain	-1.21	3.95E-06	Cellular communication, signal transduction
Contig11532_at	Serine/threonine-protein kinase	-1.18	1.82E-07	Cellular communication, signal transduction
Contig10157_at	Ankyrin repeat protein	-1.17	2.38E-05	Cellular communication, signal transduction
Contig15196_at	Putative auxin-regulated protein	-1.17	1.26E-07	Cellular communication, signal transduction
Contig5112_at	Putative casein kinase I	-1.17	8.29E-07	Cellular communication, signal transduction
Contig8444_at	Protein kinase 1	-1.17	1.47E-07	Cellular communication, signal transduction
HV_CEb0015B10r2_at	Receptor-like protein kinase precursor	-1.17	1.96E-05	Cellular communication, signal transduction
Contig12845_at	Auxin response factor 8	-1.16	2.45E-05	Cellular communication, signal transduction
Contig19292_at	G protein alpha subunit	-1.16	1.46E-05	Cellular communication, signal transduction
Contig5644_at	Serine/threonine protein phosphatase PP2A-5	-1.16	2.36E-06	Cellular communication, signal transduction
Contig10759_at	Homeodomain leucine zipper protein	-1.15	2.09E-06	Cellular communication, signal transduction
Contig13357_at	Armadillo/beta-catenin-like repeat family protein	-1.14	5.15E-06	Cellular communication, signal transduction
Contig6347_s_at	Calmodulin-binding protein-like	-1.14	5.97E-07	Cellular communication, signal transduction
Contig9360_at	MutT domain protein-like	-1.14	2.84E-06	Cellular communication, signal transduction
Contig10196_at	Protein kinase domain containing protein	-1.13	5.19E-07	Cellular communication, signal transduction
Contig15997_at	Putative calcium-dependent protein kinase	-1.13	4.74E-07	Cellular communication, signal transduction
Contig6691_at	Calcium-binding EF hand family protein	-1.13	9.04E-07	Cellular communication, signal transduction
HVSMEc0006P11r2_at	Putative receptor-like protein kinase	-1.13	1.53E-07	Cellular communication, signal transduction
Contig11424_at	Probable calcium-binding protein	-1.12	0	Cellular communication, signal transduction
Contig14069_at	RAC-ROP-like G-protein	-1.12	7.10E-06	Cellular communication, signal transduction

Contig3420_at	Casein kinase II, alpha chain	-1.12	9.80E-07	Cellular communication, signal transduction
Contig7534_at	CBL-interacting protein kinase	-1.11	1.49E-06	Cellular communication, signal transduction
HVSMEb0011B17r2_s_at	CREG2-protein-like	-1.11	5.87E-07	Cellular communication, signal transduction
HS06E04u_s_at	Protein kinase CK2 regulatory subunit CK2B3	-1.1	7.58E-06	Cellular communication, signal transduction
Contig11246_at	Putative calmodulin-binding protein	-1.1	0	Cellular communication, signal transduction
Contig14136_at	1-phosphatidylinositol-3-phosphate 5-kinase-like	-1.08	1.49E-06	Cellular communication, signal transduction
Contig11001_at	Ankyrin repeat domain protein 2	-1.07	2.13E-06	Cellular communication, signal transduction
Contig12817_at	Receptor-like protein kinase homolog	-1.07	3.85E-05	Cellular communication, signal transduction
Contig19357_at	Putative LSTK-1-like kinase	-1.06	6.67E-05	Cellular communication, signal transduction
Contig5228_s_at	MAPK4 protein	-1.06	6.59E-07	Cellular communication, signal transduction
Contig7268_s_at	Homeobox-leucine zipper protein ROC2	-1.06	2.10E-07	Cellular communication, signal transduction
Contig8292_at	Calmodulin binding protein	-1.06	1.14E-06	Cellular communication, signal transduction
Contig14172_at	Putative caltractin	-1.05	0	Cellular communication, signal transduction
HVSMEi0002K06f_x_at	Putative acid phosphatase	-1.04	0	Cellular communication, signal transduction
Contig6535_s_at	Serine/threonine-protein phosphatase PP2A	-1.03	1.47E-06	Cellular communication, signal transduction
Contig8078_at	Putative MAP kinase	-1.02	2.52E-07	Cellular communication, signal transduction
HM11D03r_s_at	Calmodulin binding protein	-1.02	1.19E-06	Cellular communication, signal transduction
Contig14766_at	Auxin response factor 7b	-1.01	1.55E-06	Cellular communication, signal transduction
Contig15114_at	Putative protein kinase	-1.01	7.16E-06	Cellular communication, signal transduction
Contig13746_at	Putative receptor protein kinase PERK1	-1	9.23E-07	Cellular communication, signal transduction
Contig26195_at	Calmodulin-binding protein	-1	1.86E-05	Cellular communication, signal transduction
Contig2859_s_at	Putative membrane protein	-4.38	3.47E-11	Cellular transport, transport facilitation and transport routes
Contig385_s_at	Vacuolar proton-inorganic pyrophosphatase	-4.1	2.48E-09	Cellular transport, transport facilitation and transport routes
Contig19438_at	Ferric reductase	-3.68	7.86E-11	Cellular transport, transport facilitation and transport routes
Contig8050_s_at	Major facilitator superfamily antiporter	-3.56	3.70E-10	Cellular transport, transport facilitation and transport routes
Contig19393_at	Probable aquaporin PIP2-7	-3.52	1.81E-08	Cellular transport, transport facilitation and transport routes
Contig12263_at	Phosphate transporter 2-1	-3.44	2.31E-09	Cellular transport, transport facilitation and transport routes
Contig7712_at	Putative nitrate transporter	-3.43	8.68E-09	Cellular transport, transport facilitation and transport routes
rbaal41j07_at	Putative sodium-dicarboxylate cotransporter	-3.3	2.18E-10	Cellular transport, transport facilitation and transport routes
Contig8050_at	Major facilitator superfamily antiporter	-3.19	4.56E-09	Cellular transport, transport facilitation and transport routes
Contig15329_at	Putative auxin transport protein-like	-3.17	4.57E-09	Cellular transport, transport facilitation and transport routes
Contig6917_at	Metal-transporting P-type ATPase-like protein	-3.08	2.47E-10	Cellular transport, transport facilitation and transport routes
Contig2813_at	Peroxisomal membrane protein 11	-2.94	7.36E-09	Cellular transport, transport facilitation and transport routes

Contig13947_at	ABC transporter-like	-2.85	1.81E-08	Cellular transport, transport facilitation and transport routes
Contig9864_at	ATNSI (NUCLEAR SHUTTLE INTERACTING)	-2.85	2.05E-08	Cellular transport, transport facilitation and transport routes
Contig12543_at	Preprotein translocase subunit secY	-2.84	2.54E-09	Cellular transport, transport facilitation and transport routes
Contig442_at	H+-transporting ATP synthase chain 9-like protein	-2.82	4.51E-08	Cellular transport, transport facilitation and transport routes
Contig21002_at	Peptide transporter protein-like	-2.79	4.02E-08	Cellular transport, transport facilitation and transport routes
Contig14412_s_at	Auxilin-like protein	-2.77	5.53E-10	Cellular transport, transport facilitation and transport routes
Contig9724_at	Outward-rectifying potassium channel	-2.67	5.81E-10	Cellular transport, transport facilitation and transport routes
Contig19271_at	Peroxisomal membrane protein	-2.64	2.19E-08	Cellular transport, transport facilitation and transport routes
HVSMEm0024F13f_s_at	Magnesium transporter protein	-2.63	1.18E-08	Cellular transport, transport facilitation and transport routes
Contig15736_at	Putative ABC transporter	-2.56	1.55E-09	Cellular transport, transport facilitation and transport routes
Contig10448_at	Heavy metal-associated domain containing protein	-2.55	3.87E-09	Cellular transport, transport facilitation and transport routes
Contig10915_s_at	Putative anion transporter	-2.53	8.73E-10	Cellular transport, transport facilitation and transport routes
Contig5153_at	Putative chloroplast inner envelope protein	-2.53	3.97E-09	Cellular transport, transport facilitation and transport routes
Contig12390_s_at	Coatomer complex subunit	-2.5	1.03E-08	Cellular transport, transport facilitation and transport routes
Contig14721_at	Probable glutamate receptor	-2.45	2.16E-10	Cellular transport, transport facilitation and transport routes
Contig11770_at	Probable cation transporter HKT6	-2.41	4.64E-08	Cellular transport, transport facilitation and transport routes
Contig12513_at	D-xylose-H+ symporter - like protein	-2.37	2.43E-10	Cellular transport, transport facilitation and transport routes
Contig20253_at	Amino acid transporter-like protein	-2.37	3.35E-09	Cellular transport, transport facilitation and transport routes
Contig3114_at	Triose phosphate/phosphate translocator	-2.37	7.49E-09	Cellular transport, transport facilitation and transport routes
Contig19439_at	Putative peptide transport protein	-2.36	1.35E-09	Cellular transport, transport facilitation and transport routes
rbah48m12_s_at	Putative peroxisomal membrane carrier protein	-2.36	1.29E-07	Cellular transport, transport facilitation and transport routes
HVSMEg0006C07r2_at	Putative membrane protein	-2.32	1.51E-08	Cellular transport, transport facilitation and transport routes
Contig8360_at	Putative sialin	-2.27	2.14E-09	Cellular transport, transport facilitation and transport routes
Contig6252_at	Glutamate/malate translocator	-2.25	4.13E-09	Cellular transport, transport facilitation and transport routes
Contig3479_at	Hexose transporter	-2.24	2.68E-07	Cellular transport, transport facilitation and transport routes
Contig2784_at	2-oxoglutarate/malate translocator	-2.23	1.36E-08	Cellular transport, transport facilitation and transport routes
Contig8347_at	Magnesium transporter	-2.23	1.43E-08	Cellular transport, transport facilitation and transport routes
Contig15736_s_at	Putative ABC transporter	-2.22	3.84E-08	Cellular transport, transport facilitation and transport routes
Contig15639_at	Putative hexose carrier protein	-2.21	5.77E-10	Cellular transport, transport facilitation and transport routes
Contig17624_at	Sodium-dicarboxylate cotransporter-like	-2.21	2.39E-08	Cellular transport, transport facilitation and transport routes
Contig835_s_at	H+-transporting ATP synthase-like protein	-2.15	7.04E-08	Cellular transport, transport facilitation and transport routes
Contig2859_at	Putative 16kDa membrane protein	-2.14	1.44E-06	Cellular transport, transport facilitation and transport routes
Contig8998_at	Integral membrane protein-like	-2.12	3.57E-08	Cellular transport, transport facilitation and transport routes

Contig2859_x_at	Putative membrane protein	-2.12	7.36E-07	Cellular transport, transport facilitation and transport routes
Contig3789_s_at	Amino acid selective channel protein	-2.09	4.76E-09	Cellular transport, transport facilitation and transport routes
Contig10915_at	Putative anion transporter	-2.08	5.80E-08	Cellular transport, transport facilitation and transport routes
Contig12678_at	Carbohydrate transporter/ sugar porter	-2.07	9.85E-09	Cellular transport, transport facilitation and transport routes
Contig12503_s_at	Kinesin heavy chain isolog	-2.06	1.34E-06	Cellular transport, transport facilitation and transport routes
Contig13479_at	Amino acid transporter-like protein	-2.06	8.38E-08	Cellular transport, transport facilitation and transport routes
Contig14413_at	Auxilin-like protein	-2.06	9.95E-08	Cellular transport, transport facilitation and transport routes
Contig21982_at	Putative outward-rectifying potassium channel KCO1	-2.06	1.63E-08	Cellular transport, transport facilitation and transport routes
Contig20839_at	Aluminum-activated malate transporter-like	-2.05	1.51E-09	Cellular transport, transport facilitation and transport routes
Contig18122_at	Nitrate transporter NRT1-2	-2.02	1.32E-07	Cellular transport, transport facilitation and transport routes
Contig4913_at	ABC transporter, ATP-binding protein	-1.99	4.28E-08	Cellular transport, transport facilitation and transport routes
Contig7377_at	Tonoplast membrane integral protein ZmTIP4-2	-1.99	1.67E-06	Cellular transport, transport facilitation and transport routes
Contig16875_at	Vacuolar Na+/H+ antiporter	-1.97	8.22E-09	Cellular transport, transport facilitation and transport routes
Contig4080_s_at	Probable membrane-associated 30 kDa protein	-1.97	6.19E-08	Cellular transport, transport facilitation and transport routes
Contig4927_s_at	Potassium transporter	-1.97	3.89E-09	Cellular transport, transport facilitation and transport routes
Contig721_s_at	Putative ABC transporter	-1.94	4.83E-08	Cellular transport, transport facilitation and transport routes
Contig19305_at	Sulfate transporter protein	-1.93	1.08E-08	Cellular transport, transport facilitation and transport routes
Contig24156_at	Potassium transporter	-1.93	1.91E-08	Cellular transport, transport facilitation and transport routes
Contig4212_s_at	Cation/proton exchanger 1a	-1.93	4.39E-07	Cellular transport, transport facilitation and transport routes
baak19i22_s_at	Putative ABC transporter, ATP-binding protein	-1.89	2.73E-08	Cellular transport, transport facilitation and transport routes
Contig2893_at	37 KD INNER ENVELOPE MEMBRANE PROTEIN	-1.89	1.34E-08	Cellular transport, transport facilitation and transport routes
Contig4211_at	Ca2+/H+-exchanging protein	-1.89	1.14E-08	Cellular transport, transport facilitation and transport routes
Contig7074_s_at	Sulphate transporter protein	-1.89	2.71E-08	Cellular transport, transport facilitation and transport routes
rbaal9k07_at	Putative myosin heavy chain	-1.89	4.16E-08	Cellular transport, transport facilitation and transport routes
Contig13648_at	Putative ABC transporter	-1.8	5.49E-09	Cellular transport, transport facilitation and transport routes
Contig3338_s_at	Membrane related protein	-1.8	1.38E-08	Cellular transport, transport facilitation and transport routes
Contig6708_at	Ureide permease 2	-1.8	6.63E-08	Cellular transport, transport facilitation and transport routes
Contig15411_at	Chloride channel-like (CLC) protein	-1.79	1.57E-07	Cellular transport, transport facilitation and transport routes
Contig10872_at	Myosin heavy chain-like	-1.75	5.28E-07	Cellular transport, transport facilitation and transport routes
Contig16614_at	Sec14 like protein	-1.75	3.16E-07	Cellular transport, transport facilitation and transport routes
Contig20863_at	Putative proton myo-inositol transporter	-1.75	7.45E-08	Cellular transport, transport facilitation and transport routes
Contig7530_s_at	Lipocalin	-1.71	8.33E-08	Cellular transport, transport facilitation and transport routes
HVSMEn0024H20r2_s_at	Amino acid permease	-1.7	7.68E-09	Cellular transport, transport facilitation and transport routes

Contig5618_at	27k vesicle-associated membrane protein-associated protein	-1.68	2.64E-06	Cellular transport, transport facilitation and transport routes
Contig2960_at	Cation transport protein chaC	-1.67	8.29E-05	Cellular transport, transport facilitation and transport routes
Contig3787_at	Amino acid selective channel protein	-1.64	3.79E-07	Cellular transport, transport facilitation and transport routes
Contig11153_at	Putative Tic20 protein	-1.59	3.74E-06	Cellular transport, transport facilitation and transport routes
HVSMEn0009D08r2_at	Putative calmodulin-regulated ion channel protein	-1.59	2.99E-07	Cellular transport, transport facilitation and transport routes
rbaal38a10_at	HvPIP1;3 protein	-1.59	2.02E-07	Cellular transport, transport facilitation and transport routes
Contig25215_at	Chloride channel-like (CLC) protein	-1.58	4.41E-08	Cellular transport, transport facilitation and transport routes
rbaal30a15_s_at	Putative chloroplast outer envelope 86-like protein	-1.58	7.89E-08	Cellular transport, transport facilitation and transport routes
Contig10624_at	HPP family protein	-1.57	1.23E-07	Cellular transport, transport facilitation and transport routes
Contig16151_at	CLC-d chloride channel; anion channel protein	-1.57	1.21E-06	Cellular transport, transport facilitation and transport routes
Contig26333_at	Putative calmodulin-regulated ion channel protein	-1.56	1.47E-07	Cellular transport, transport facilitation and transport routes
Contig6677_s_at	HCF106 protein precursor	-1.52	5.46E-06	Cellular transport, transport facilitation and transport routes
Contig1230_at	Aquaporin PIP1-3/PIP1-4	-1.51	2.31E-07	Cellular transport, transport facilitation and transport routes
Contig11350_at	ABC transporter family protein	-1.5	8.07E-09	Cellular transport, transport facilitation and transport routes
Contig13494_at	Chloride channel	-1.5	5.41E-08	Cellular transport, transport facilitation and transport routes
Contig22088_at	Peroxisomal membrane protein 2	-1.5	6.13E-07	Cellular transport, transport facilitation and transport routes
Contig23705_at	Putative peptide transporter protein	-1.49	1.75E-07	Cellular transport, transport facilitation and transport routes
HVSMEm0014K07r2_at	Cationic amino acid transporter	-1.48	2.31E-07	Cellular transport, transport facilitation and transport routes
Contig17085_at	Sodium/proton antiporter	-1.46	2.49E-07	Cellular transport, transport facilitation and transport routes
Contig1239_s_at	Plasma membrane intrinsic protein BPW2	-1.45	3.31E-07	Cellular transport, transport facilitation and transport routes
Contig16592_at	Dynein light chain	-1.45	9.32E-08	Cellular transport, transport facilitation and transport routes
Contig15496_at	Two pore calcium channel protein 1	-1.44	3.42E-08	Cellular transport, transport facilitation and transport routes
Contig7293_at	Sugar transport protein 5	-1.43	8.25E-07	Cellular transport, transport facilitation and transport routes
Contig14224_at	putative sugar transporter	-1.42	8.00E-07	Cellular transport, transport facilitation and transport routes
Contig3660_at	Putative ABC transporter	-1.41	5.84E-08	Cellular transport, transport facilitation and transport routes
Contig5061_at	Mitochondrial carrier protein family	-1.41	1.46E-07	Cellular transport, transport facilitation and transport routes
Contig6173_at	P-type ATPase	-1.41	4.12E-08	Cellular transport, transport facilitation and transport routes
Contig11562_at	Translocase 7K chain TOM7	-1.4	3.16E-06	Cellular transport, transport facilitation and transport routes
Contig1219_s_at	Aquaporin	-1.4	5.19E-08	Cellular transport, transport facilitation and transport routes
Contig14078_at	Protein translocase subunit secA	-1.4	7.70E-08	Cellular transport, transport facilitation and transport routes
Contig6135_s_at	Putative hexose transporter	-1.39	2.63E-08	Cellular transport, transport facilitation and transport routes
Contig19175_at	P-glycoprotein homologue	-1.39	1.17E-05	Cellular transport, transport facilitation and transport routes
Contig3838_s_at	Putative MATE efflux family protein	-1.38	2.50E-06	Cellular transport, transport facilitation and transport routes

Contig2895_at	Putative 37kDa chloroplast polypeptide	-1.35	9.00E-06	Cellular transport, transport facilitation and transport routes
Contig8128_at	Auxin transporter-like protein	-1.35	4.83E-08	Cellular transport, transport facilitation and transport routes
HS06C20u_s_at	Reticulon	-1.35	1.21E-06	Cellular transport, transport facilitation and transport routes
Contig17741_at	Membrane protein-like	-1.35	1.92E-05	Cellular transport, transport facilitation and transport routes
Contig10080_at	OsTATC-like protein	-1.34	3.04E-08	Cellular transport, transport facilitation and transport routes
Contig13030_s_at	Putative ABC transporter protein	-1.33	3.03E-05	Cellular transport, transport facilitation and transport routes
Contig20488_at	ATPase BadF/BadG/BcrA/BcrD type	-1.32	5.53E-08	Cellular transport, transport facilitation and transport routes
Contig7456_s_at	Myosin-like protein	-1.32	4.63E-07	Cellular transport, transport facilitation and transport routes
HY05O16u_s_at	Putative sugar transporter	-1.32	1.90E-07	Cellular transport, transport facilitation and transport routes
Contig13476_at	Putative ABC transporter	-1.3	3.73E-07	Cellular transport, transport facilitation and transport routes
Contig15964_at	Putative ZIP-like zinc transporter	-1.3	9.76E-07	Cellular transport, transport facilitation and transport routes
Contig1222_s_at	Plasma membrane integral protein ZmPIP2-1	-1.29	1.47E-06	Cellular transport, transport facilitation and transport routes
Contig8145_at	Peroxisomal Membrane Protein PMP22	-1.29	4.19E-08	Cellular transport, transport facilitation and transport routes
Contig17164_at	Transporter, major facilitator family protein	-1.28	1.28E-05	Cellular transport, transport facilitation and transport routes
Contig7838_at	Putative solute carrier family 17 (Anion/sugar transporter)	-1.28	8.00E-07	Cellular transport, transport facilitation and transport routes
Contig2139_at	Membrane related protein CP5	-1.27	4.83E-08	Cellular transport, transport facilitation and transport routes
HVSMEa0004I10f2_s_at	Putative hexose transporter	-1.27	6.26E-08	Cellular transport, transport facilitation and transport routes
Contig15813_at	Tryptophan/tyrosine permease family protein	-1.26	5.50E-08	Cellular transport, transport facilitation and transport routes
Contig7377_s_at	Probable aquaporin	-1.26	1.75E-07	Cellular transport, transport facilitation and transport routes
HV_CEb0001H12r2_at	Transmembrane amino acid transporter protein	-1.26	1.63E-08	Cellular transport, transport facilitation and transport routes
Contig26036_at	Putative ABC transporter	-1.25	1.16E-06	Cellular transport, transport facilitation and transport routes
Contig24221_at	ABC transporter family protein	-1.24	1.62E-05	Cellular transport, transport facilitation and transport routes
Contig25159_at	Mitochondrial substrate carrier family protein	-1.24	7.32E-07	Cellular transport, transport facilitation and transport routes
Contig6952_at	Putative syntaxin-related protein	-1.24	1.28E-05	Cellular transport, transport facilitation and transport routes
Contig8563_at	Transthyretin family protein	-1.24	1.69E-06	Cellular transport, transport facilitation and transport routes
Contig1225_s_at	Aquaporin	-1.23	2.26E-07	Cellular transport, transport facilitation and transport routes
Contig14213_at	phosphatidylinositol-phosphatidylcholine transfer protein	-1.23	6.77E-06	Cellular transport, transport facilitation and transport routes
Contig14791_at	Hexose carrier protein HEX6	-1.23	1.63E-07	Cellular transport, transport facilitation and transport routes
rbah43d09_s_at	Sucrose transporter 2 (sut2 gene)	-1.22	1.17E-06	Cellular transport, transport facilitation and transport routes
Contig6913_x_at	Putative mitochondrial carrier protein	-1.21	4.66E-05	Cellular transport, transport facilitation and transport routes
HVSMEm0001B03r2_at	Integral membrane protein	-1.21	2.67E-06	Cellular transport, transport facilitation and transport routes
Contig26252_at	Zinc transporter ZIP	-1.2	9.16E-05	Cellular transport, transport facilitation and transport routes
Contig13524_at	Amino acid transporter	-1.19	1.63E-06	Cellular transport, transport facilitation and transport routes

Contig6704_at	Putative ABC transporter	-1.19	9.42E-06	Cellular transport, transport facilitation and transport routes
Contig16371_at	Polyamine ABC transporter	-1.18	3.31E-06	Cellular transport, transport facilitation and transport routes
Contig26429_at	Putative peptide transporter	-1.18	9.89E-07	Cellular transport, transport facilitation and transport routes
Contig1237_s_at	Aquaporin	-1.17	2.78E-07	Cellular transport, transport facilitation and transport routes
Contig6132_at	Putative sugar transporter	-1.17	2.63E-07	Cellular transport, transport facilitation and transport routes
HV_CEb0009N15r2_at	Potassium-dependent sodium-calcium exchanger - like protein	-1.14	6.24E-07	Cellular transport, transport facilitation and transport routes
HVSMEf0019H18r2_at	Probable aquaporin TIP1.2	-1.14	1.97E-06	Cellular transport, transport facilitation and transport routes
Contig20387_at	Putative sulfate transporter	-1.13	7.51E-06	Cellular transport, transport facilitation and transport routes
Contig7076_s_at	Putative potassium/H+ antiporter	-1.13	1.89E-06	Cellular transport, transport facilitation and transport routes
Contig14874_at	ATPase-like	-1.12	1.27E-06	Cellular transport, transport facilitation and transport routes
Contig8393_at	Myosin heavy chain	-1.12	4.90E-07	Cellular transport, transport facilitation and transport routes
Contig4161_at	Sodium-dependent bile acid symporter	-1.1	1.22E-05	Cellular transport, transport facilitation and transport routes
Contig7750_at	Integral membrane family protein-like	-1.1	3.33E-06	Cellular transport, transport facilitation and transport routes
Contig8797_at	Chloroplast import-associated channel protein homolog	-1.1	5.46E-06	Cellular transport, transport facilitation and transport routes
HVSMEn0015N02r2_at	Putative peptide transporter	-1.1	9.11E-08	Cellular transport, transport facilitation and transport routes
Contig12951_at	ATP binding protein	-1.08	5.51E-06	Cellular transport, transport facilitation and transport routes
Contig388_at	Plasma membrane H+ ATPase	-1.08	7.32E-07	Cellular transport, transport facilitation and transport routes
Contig6980_at	Putative chloroplast outer envelope 86-like protein	-1.07	3.44E-05	Cellular transport, transport facilitation and transport routes
HV_CEa0013O20r2_s_at	Putative membrane transporter	-1.07	5.07E-06	Cellular transport, transport facilitation and transport routes
Contig1315_s_at	Delta tonoplast intrinsic protein TIP2	-1.06	5.19E-05	Cellular transport, transport facilitation and transport routes
Contig6135_at	Putative hexose transporter	-1.06	0	Cellular transport, transport facilitation and transport routes
X74365_at	H(+)-transporting ATP synthase	-1.06	0.01	Cellular transport, transport facilitation and transport routes
Contig25912_at	Biopterin transport-related protein BT1	-1.05	1.11E-05	Cellular transport, transport facilitation and transport routes
Contig6918_s_at	Metal-transporting P-type ATPase-like protein	-1.05	2.67E-06	Cellular transport, transport facilitation and transport routes
Contig7645_at	Chloroplast inner envelope protein	-1.04	1.44E-05	Cellular transport, transport facilitation and transport routes
Contig11063_at	Sucrose transporter 2	-1.03	9.50E-06	Cellular transport, transport facilitation and transport routes
Contig16183_s_at	Putative vacuolar sorting receptor protein	-1.02	0	Cellular transport, transport facilitation and transport routes
Contig26311_at	Putative proton-dependent oligopeptide transport	-1.02	2.35E-05	Cellular transport, transport facilitation and transport routes
HU14D24u_s_at	Putative ABC transporter	-1	6.24E-07	Cellular transport, transport facilitation and transport routes
Contig20097_at	Putative alpha/beta hydrolase	-3.68	2.54E-11	Development
Contig1071_s_at	Glycine rich protein	-3.45	1.05E-09	Development
Contig10144_s_at	Hydrolase, alpha/beta fold family protein	-3.2	1.55E-09	Development
Contig4700_at	Hydroxyproline-rich glycoprotein-like	-3.14	6.27E-08	Development

Contig25218_at	Metal-dependent hydrolase-like protein	-3.03	6.48E-11	Development
Contig10144_at	Hydrolase, alpha/beta fold family protein	-2.79	1.40E-08	Development
Contig5929_at	Anaerobically inducible early gene 2	-2.75	3.47E-07	Development
EBro05_SQ003_D01_s_at	NAM7 protein	-2.69	4.06E-09	Development
Contig4206_at	Fiddlehead-like protein	-2.66	4.18E-10	Development
Contig4622_s_at	Proline rich protein homolog WCOR518	-2.42	4.55E-07	Development
Contig7196_s_at	Hydrolase, alpha/beta fold family protein	-2.32	2.61E-11	Development
Contig11160_at	Nudix hydrolase 8	-2.24	2.41E-08	Development
Contig2416_at	Early embryogenesis protein	-2.22	5.20E-08	Development
Contig7196_at	Hydrolase, alpha/beta fold family protein	-2.07	6.82E-10	Development
HS16G15u_s_at	Metal-dependent hydrolase-like protein	-2.04	2.49E-09	Development
Contig11161_s_at	Nudix hydrolase	-2.03	3.22E-08	Development
Contig7363_at	Putative SHOOT1 protein	-1.97	3.27E-05	Development
Contig4626_s_at	Spermidine synthase 1	-1.93	1.07E-08	Development
Contig2952_at	Xyloglucan endo-1,4-beta-D-glucanase	-1.89	5.62E-09	Development
Contig2133_x_at	MTN3-like protein	-1.59	1.63E-07	Development
HF17J23r_at	Proline-rich protein family-like	-1.59	6.51E-07	Development
Contig10010_at	Glycine-rich protein	-1.57	6.18E-07	Development
Contig9579_at	Phytochrome C	-1.56	7.81E-08	Development
Contig2135_s_at	Putative MtN3-like protein	-1.55	3.09E-05	Development
Contig5508_at	Hydrolase, alpha/beta fold family protein	-1.51	3.49E-07	Development
Contig12841_at	Putative fruit protein	-1.47	3.80E-09	Development
Contig2133_s_at	MTN3-like protein	-1.42	1.51E-08	Development
Contig12468_at	Fertilization-independent endosperm protein	-1.39	2.26E-07	Development
Contig12623_at	Putative MtN3	-1.39	4.42E-07	Development
Contig5628_at	Hydrolase, alpha/beta fold family protein	-1.35	4.69E-08	Development
Contig14798_at	Hydrolase, alpha/beta fold family	-1.32	1.32E-06	Development
Contig7370_at	Seed maturation protein PM23	-1.3	2.09E-07	Development
Contig2057_at	Early nodulin protein	-1.29	1.42E-06	Development
Contig5352_at	Rapid ALkalinization Factor family protein	-1.28	9.15E-07	Development
Contig12847_at	Phytochrome B	-1.27	4.96E-07	Development
Contig4624_at	Spermidine synthase 1	-1.27	2.05E-05	Development
Contig15448_at	Putative flower development regulator LEUNI protein	-1.25	6.78E-05	Development

Contig5362_at	Putative Cell elongation protein	-1.21	8.35E-06	Development
Contig12597_at	Nodulin-like protein	-1.2	8.75E-08	Development
Contig6939_at	Fasciclin-like protein	-1.2	7.52E-06	Development
Contig7526_at	GRF-interacting factor 2	-1.18	3.55E-06	Development
Contig4806_at	Putative Pollen specific protein C13 precursor	-1.12	2.50E-07	Development
Contig13959_at	Early flowering 3	-1.06	1.78E-06	Development
Contig8473_at	Putative growth-on protein GRO10	-1.06	0	Development
Contig22226_at	Putative somatic embryogenesis related protein	-1.06	1.54E-05	Development
Contig2670_x_at	Xyloglucan endotransglycosylase-like protein (XEA)	-1.04	0	Development
Contig5247_at	Gigantea-like protein	-1.04	3.20E-07	Development
Contig3401_at	MtN3-like protein	-1.02	3.25E-06	Development
Contig4741_s_at	KNOX family class 2 homeodomain protein	-1.01	1.77E-06	Development
Contig828_s_at	Chlorophyll a/b-binding protein WCAB precursor	-5.07	1.13E-10	Energy
Contig997_x_at	Ribulose-bisphosphate carboxylase	-4.96	1.22E-09	Energy
Contig842_x_at	Ribulose bisphosphate carboxylase small chain PW9	-4.93	9.82E-10	Energy
Contig6_x_at	Chlorophyll a/b-binding protein WCAB precursor	-4.65	1.04E-09	Energy
Contig981_s_at	Chlorophyll a/b binding protein	-4.59	1.69E-10	Energy
Contig497_s_at	Ribulose bisphosphate carboxylase small chain PW9	-4.54	7.25E-10	Energy
HV_CEb0017F03r2_s_at	Light-harvesting complex I	-4.42	7.95E-10	Energy
Contig432_x_at	Chlorophyll a-b binding protein	-4.35	1.26E-08	Energy
Contig308_x_at	RIbulose-1,5-bisphosphate	-4.32	4.10E-08	Energy
Contig1529_at	Photosystem I antenna protein	-4.14	1.04E-10	Energy
baak2o06_x_at	Ribulose-1 5-bisphosphate carboxylase	-4.07	2.80E-08	Energy
Contig1208_s_at	Chlorophyll a-b binding protein 1B-21	-4.05	3.02E-09	Energy
Contig2300_s_at	Chlorophyll a-b-binding protein precursor	-4.03	3.56E-09	Energy
HG01F14u_s_at	Fructose-bisphosphate aldolase	-4.03	2.07E-08	Energy
HVSMEh0080L10r2_x_at	Chlorophyll a/b binding protein precursor	-4	2.35E-12	Energy
Contig5026_at	Photosystem II 5 KD protein	-3.99	4.18E-09	Energy
Contig594_x_at	Ribulose bisphosphate carboxylase small chain PW9	-3.99	4.96E-09	Energy
Contig617_x_at	Chlorophyll a-b binding protein	-3.99	2.90E-08	Energy
Contig628_x_at	Chlorophyll a/b-binding protein WCAB precursor	-3.94	4.90E-12	Energy
Contig620_at	Photosystem I reaction center subunit V	-3.93	1.63E-09	Energy
Contig6002_s_at	Oxygen-evolving complex 25.6 kD protein	-3.9	4.28E-08	Energy

Contig194_s_at	Chlorophyll a-b binding protein 1	-3.89	7.83E-09	Energy
Contig1888_at	Chlorophyll a-b-binding protein	-3.83	4.29E-10	Energy
Contig838_s_at	Ribulose-1,5-bisphosphate carboxylase	-3.82	4.55E-09	Energy
Contig841_x_at	Chlorophyll a-b binding protein	-3.82	1.80E-09	Energy
Contig7237_at	Photosystem II reaction center psb28 protein	-3.77	1.08E-10	Energy
Contig636_at	Type III LHCII CAB precursor protein	-3.73	3.40E-10	Energy
Contig926_x_at	Chlorophyll a-b binding protein	-3.71	9.19E-11	Energy
HO10O22S_at	Ribulose bisphosphate carboxylase small chain PW9	-3.71	2.48E-09	Energy
Contig5782_at	Photosystem II protein family	-3.65	4.03E-08	Energy
Contig10628_at	Phosphoribulokinase/uridine kinase-like	-3.63	8.83E-10	Energy
Contig1523_at	Chlorophyll a/b-binding protein CP24 precursor	-3.57	4.95E-09	Energy
Contig1814_at	Light-harvesting chlorophyll a/b binding protein	-3.55	4.44E-08	Energy
Contig2083_s_at	Photosystem I reaction centre subunit III, chloroplast precursor	-3.54	1.67E-08	Energy
Contig3463_at	Fructose-6-phosphate-2-kinase/fructose-2,6-bisphosphatase	-3.54	1.42E-09	Energy
HM14O03r_at	Photosystem 1 subunit 5	-3.51	1.93E-08	Energy
baak21d06_s_at	Ferredoxin-NADP(H) oxidoreductase	-3.49	7.15E-09	Energy
Contig3463_s_at	Fructose-6-phosphate-2-kinase/fructose-2,6-bisphosphatase	-3.46	6.34E-10	Energy
Contig4685_at	Thioredoxin-like	-3.46	1.51E-09	Energy
Contig2142_s_at	Plastocyanin precursor	-3.45	2.35E-10	Energy
Contig2412_at	Oxygen-evolving enhancer protein	-3.44	2.18E-09	Energy
Contig5028_s_at	Photosystem II 5 KD protein	-3.43	2.20E-08	Energy
Contig1916_s_at	Putative photosystem II subunit (22KDa) precursor	-3.4	8.82E-10	Energy
Contig965_at	Ribulose bisphosphate carboxylase small chain	-3.4	3.75E-11	Energy
Contig837_x_at	Chlorophyll a-b binding protein	-3.39	2.77E-07	Energy
baak32n13_at	Chlorophyll a-b binding protein 3C	-3.38	9.76E-10	Energy
Contig15111_at	Putative Oxygen-evolving enhancer protein 3-2	-3.36	4.53E-09	Energy
Contig2277_s_at	Ferredoxin--NADP reductase	-3.35	1.06E-09	Energy
Contig189_s_at	Chlorophyll a-b binding protein	-3.34	9.30E-10	Energy
baak1b18_x_at	Chlorophyll a-b binding protein 3C	-3.33	1.10E-09	Energy
Contig1017_at	Ribulose bisphosphate carboxylase/oxygenase activase	-3.32	1.92E-09	Energy
Contig8236_at	Thylakoid lumen 18.3 kDa protein	-3.32	6.05E-09	Energy
HVSMEa0009E14r2_at	Putative ribulose-1,5-bisphosphate carboxylase	-3.32	9.78E-09	Energy
Contig3221_at	Photosystem I reaction centre subunit N	-3.31	1.44E-08	Energy

Contig820_at	Chlorophyll a/b-binding protein CP29 precursor	-3.29	7.58E-08	Energy
Contig1604_at	Oxygen-evolving enhancer protein 2	-3.27	7.86E-10	Energy
Contig8541_at	NADH dehydrogenase I subunit N	-3.24	2.14E-09	Energy
Contig1192_s_at	Fructose-bisphosphate aldolase	-3.23	1.14E-08	Energy
rbaal10k01_at	Ribulose bisphosphate carboxylase/oxygenase activase	-3.23	4.67E-11	Energy
rbaal21l24_s_at	Phosphoribulokinase	-3.23	1.04E-07	Energy
Contig2766_s_at	Protochlorophyllide reductase B	-3.18	1.63E-07	Energy
Contig859_s_at	Ribulose-1,5-bisphosphate carboxylase	-3.18	6.97E-09	Energy
Contig4015_at	Photosystem I reaction center subunit II	-3.16	5.73E-10	Energy
Contig945_s_at	PsbQ domain protein family	-3.16	2.21E-08	Energy
rbasd17i02_s_at	Fructose 1,6-bisphosphate aldolase	-3.11	1.40E-09	Energy
Contig4772_s_at	Light-induced protein 1-like	-3.09	4.25E-08	Energy
HM09E06r_at	Ribulose bisphosphate carboxylase small chain PW9	-3.06	1.79E-09	Energy
baak1b18_at	Chlorophyll a-b binding protein 3C	-3.03	4.13E-09	Energy
HVSMEn0020J05f_x_at	Chlorophyll a/b-binding protein	-3.03	6.22E-09	Energy
HA10A05u_s_at	Chlorophyll a/b-binding protein	-2.99	9.58E-09	Energy
Contig14611_at	Thylakoid lumenal 21.5 kDa protein	-2.95	3.81E-09	Energy
rbah15o14_s_at	Fructose-1,6-bisphosphatase	-2.95	3.55E-09	Energy
Contig5048_s_at	Thylakoid membrane phosphoprotein 14 kda	-2.94	1.32E-07	Energy
Contig11023_at	Ferredoxin family protein	-2.91	4.51E-10	Energy
Contig16530_at	Ribose 5-phosphate isomerase	-2.88	6.67E-11	Energy
Contig5998_s_at	Putative chlorophyll synthase	-2.87	9.18E-10	Energy
rbah22f22_s_at	Light harvesting chlorophyll a /b binding protein of PSII	-2.87	1.28E-07	Energy
Contig1317_s_at	Ferredoxin B	-2.83	1.59E-07	Energy
Contig10237_s_at	One helix protein	-2.79	2.16E-10	Energy
HVSMEn0017L11f_at	Light harvesting chlorophyll a /b binding protein of PSII	-2.79	2.40E-08	Energy
Contig10900_at	Ribulose bisphosphate carboxylase/oxygenase activase	-2.76	2.58E-08	Energy
Contig3908_at	Photosystem II core complex proteins psbY	-2.76	6.25E-11	Energy
HVSMEh0080N02r2_at	Photosystem I reaction centre subunit N	-2.75	3.74E-09	Energy
Contig1012_s_at	Chlorophyll a-b binding protein	-2.74	4.92E-08	Energy
Contig1198_at	Fructose-bisphosphate aldolase	-2.74	2.36E-08	Energy
rbah35p18_s_at	Cytochrome c biogenesis protein family	-2.74	5.52E-07	Energy
Contig15347_at	Defective chloroplasts and leaves protein	-2.72	5.66E-08	Energy

Contig807_s_at	RuBisCO large subunit-binding protein subunit beta	-2.72	9.74E-08	Energy
Contig5803_s_at	Photosystem II stability/assembly factor HCF136	-2.71	6.65E-09	Energy
Contig832_s_at	Oxygen-evolving enhancer protein 1	-2.7	4.40E-08	Energy
EBem10_SQ001_N01_x_at	Photosystem II 22 kDa protein	-2.69	3.68E-08	Energy
Contig1815_at	PSI type III chlorophyll a/b-binding protein	-2.66	6.41E-09	Energy
Contig934_x_at	Ribulose bisphosphate carboxylase small chain	-2.66	4.16E-09	Energy
Contig1198_x_at	Fructose-bisphosphate aldolase	-2.65	6.43E-08	Energy
Contig2080_at	ATP synthase gamma chain	-2.64	6.93E-10	Energy
Contig418_at	Chlorophyll a/b-binding protein WCAB precursor	-2.64	6.10E-06	Energy
Contig4022_at	Putative thioredoxin F	-2.62	2.58E-08	Energy
Contig19934_at	Thylakoid lumenal 20 kDa protein-like	-2.59	1.14E-09	Energy
Contig2278_at	Ferredoxin--NADP reductase	-2.59	2.54E-09	Energy
Contig2964_at	Fructose-1,6-bisphosphatase	-2.59	4.85E-08	Energy
Contig1307_at	Ferredoxin-2	-2.59	7.47E-07	Energy
Contig2920_at	Ferredoxin-dependent glutamate synthase	-2.57	6.52E-10	Energy
Contig6603_at	Putative rubredoxin	-2.54	2.28E-07	Energy
Contig4747_at	PGR5 protein	-2.5	3.22E-08	Energy
Contig7919_at	Protoporphyrinogen IX oxidase	-2.49	1.88E-08	Energy
Contig950_s_at	Photosystem I reaction center subunit IV	-2.48	5.97E-07	Energy
Contig7239_s_at	Photosystem II protein W-like protein	-2.47	3.72E-08	Energy
Contig9582_at	Thylakoid lumen 15.0 kDa protein	-2.46	5.47E-09	Energy
Contig4437_at	ATP synthase delta chain	-2.43	6.67E-08	Energy
HVSMEm0020L23r2_x_at	Ribulose bisphosphate carboxylase small chains	-2.43	4.55E-07	Energy
Contig2022_at	Photosystem I reaction center subunit psaK	-2.43	3.19E-06	Energy
Contig7522_s_at	Putative oxygen evolving complex protein	-2.41	2.89E-09	Energy
baak26h09_x_at	Chlorophyll a/b-binding protein 1A precursor	-2.39	1.78E-08	Energy
Contig23773_at	Putative glutaredoxin	-2.39	5.24E-07	Energy
Contig4438_s_at	ATP synthase delta chain	-2.37	9.00E-09	Energy
Contig11024_at	Ferredoxin	-2.35	4.29E-09	Energy
Contig11083_at	Ribulose-1,5-bisphosphate carboxylase	-2.35	5.62E-10	Energy
Contig2141_s_at	Plastocyanin precursor	-2.31	2.14E-08	Energy
Contig7882_at	Biogenesis protein (CCDA)	-2.31	2.51E-07	Energy
baak3d17_at	Oxygen-evolving enhancer protein 2	-2.3	9.32E-10	Energy

HG01O06u_s_at	Oxygen-evolving enhancer protein 3-1	-2.29	8.49E-07	Energy
rbaal31m19_s_at	Putative thioredoxin	-2.28	8.61E-09	Energy
Contig4429_at	Fructose-1,6-bisphosphatase	-2.27	4.32E-08	Energy
Contig615_at	Lycopene beta-cyclase	-2.27	6.97E-09	Energy
Contig9613_at	Thylakoid lumenal 17.4 kDa protein	-2.27	1.43E-08	Energy
Contig7863_at	Light-harvesting chlorophyll a/b binding protein	-2.25	2.53E-09	Energy
Contig12833_at	Cytochrome c6	-2.22	2.00E-07	Energy
Contig16116_at	Light-harvesting chlorophyll a/b binding protein	-2.22	1.03E-08	Energy
Contig2379_s_at	Ferredoxin-thioredoxin reductase	-2.22	2.20E-08	Energy
Contig3171_at	Thioredoxin M-type	-2.21	2.49E-08	Energy
Contig1013_s_at	Ribulose-bisphosphate carboxylase activase	-2.2	3.44E-08	Energy
Contig7486_at	Thylakoid lumenal 16.5 kDa protein	-2.2	3.34E-07	Energy
Contig2247_s_at	10.2 kDa photosystem I polypeptide	-2.18	1.29E-07	Energy
Contig9479_s_at	Putative 2Fe-2S iron-sulfur cluster protein	-2.17	1.46E-08	Energy
Contig10237_at	One helix protein	-2.16	1.14E-09	Energy
Contig14916_at	Ferredoxin-thioredoxin reductase	-2.15	1.70E-09	Energy
Contig13608_at	Thioredoxin-like	-2.13	2.40E-09	Energy
Contig953_at	PsbQ domain protein family	-2.1	9.49E-09	Energy
HVSMEi0005B04r2_x_at	Photosystem I reaction centre subunit N	-2.08	2.38E-09	Energy
Contig2247_at	Photosystem I reaction center subunit VI	-2.07	3.41E-08	Energy
Contig1019_at	Ribulose 1,5-bisphosphate carboxylase activase	-2.06	6.52E-06	Energy
Contig23442_at	Glutaredoxin	-2.05	1.67E-06	Energy
Contig433_x_at	Chlorophyll a-b binding protein	-1.99	1.56E-06	Energy
rbags36a18_s_at	RuBisCO subunit binding-protein alpha subunit	-1.99	1.24E-06	Energy
Contig2411_at	Oxygen-evolving enhancer protein 3-1	-1.95	1.56E-07	Energy
Contig807_at	RuBisCO large subunit-binding protein subunit beta	-1.94	8.78E-07	Energy
Contig16987_at	Carotenoid isomerase	-1.92	5.94E-10	Energy
Contig7522_at	Putative oxygen evolving complex protein	-1.9	2.41E-08	Energy
Contig7913_at	Violaxanthin de-epoxidase	-1.9	8.31E-06	Energy
Contig2762_at	NADPH dehydrogenase	-1.89	6.61E-08	Energy
HVSMEm0015O15f_s_at	Photosystem II core complex proteins psbY	-1.87	4.41E-08	Energy
Contig5620_s_at	Putative oxidoreductase	-1.84	1.14E-07	Energy
HV14N20u_x_at	Chlorophyll a-b binding protein 1B-21	-1.84	4.97E-08	Energy

Contig7238_at	Photosystem II reaction center psb28 protein	-1.84	2.55E-08	Energy
Contig8070_at	Oxygen-evolving complex-23 related protein	-1.82	3.42E-05	Energy
X89023_x_at	LHC II type I protein	-1.81	6.89E-08	Energy
Contig347_s_at	Chlorophyll a-b binding protein 3C	-1.79	0	Energy
Contig4782_s_at	Putative iron-sulfur cluster-binding protein	-1.79	2.65E-08	Energy
HVSMEm0001P16r2_s_at	Cytochrome c biogenesis protein precursor	-1.77	1.44E-07	Energy
Contig2177_at	Photosystem I reaction center subunit XI	-1.75	1.36E-07	Energy
Contig4782_at	Putative iron-sulfur cluster-binding protein	-1.75	2.85E-07	Energy
Contig8185_at	Ferredoxin-nitrite reductase	-1.72	8.89E-08	Energy
Contig3808_at	Putative nifU-like protein	-1.71	8.14E-07	Energy
bah36j17_s_at	Ribulose-1,5-bisphosphate carboxylase	-1.69	4.52E-08	Energy
Contig8978_at	Chlorophyll synthase	-1.69	4.27E-08	Energy
S78730_at	Light-harvesting complex I	-1.69	6.60E-08	Energy
Contig74_x_at	Chlorophyll a/b-binding protein 1A precursor	-1.68	1.43E-09	Energy
Contig5890_at	Alternative oxidase	-1.67	1.58E-07	Energy
HVSMEc0015H24f_at	NADH dehydrogenase subunit K	-1.67	3.94E-07	Energy
Contig3517_at	Photosystem II 7kD protein	-1.66	8.39E-08	Energy
HZ40F21r_at	Ribulose-1,5-bisphosphate carboxylase	-1.66	1.00E-06	Energy
Contig1314_s_at	Ferredoxin, chloroplast precursor	-1.65	1.35E-06	Energy
HV14N20u_at	Chlorophyll a-b binding protein 1B-21	-1.64	5.23E-09	Energy
X12735_at	Chlorophyll A-B binding protein 2	-1.64	1.65E-06	Energy
HVSMEm0003E10r2_x_at	Ribulose bisphosphate carboxylase	-1.63	5.96E-07	Energy
Contig425_at	Chlorophyll a/b-binding protein WCAB precursor	-1.62	0	Energy
HVSMEa0022N20f_at	Photosystem I subunit IX-like	-1.62	7.36E-08	Energy
Contig7835_at	Ribose-5-phosphate isomerase	-1.61	1.48E-09	Energy
Contig16904_at	Putative ribulokinase	-1.6	3.97E-07	Energy
ChlorContig3_at	NADH-plastoquinone oxidoreductase 49 kDa subunit	-1.59	4.13E-05	Energy
HV_CEa0005J05r2_s_at	Light harvesting chlorophyll a /b binding protein of PSII	-1.59	1.39E-06	Energy
Contig3354_s_at	Putative calvin cycle protein CP12	-1.58	3.39E-06	Energy
HVSMEl0025G13f_s_at	Light harvesting chlorophyll a /b binding protein of PSII	-1.58	2.24E-05	Energy
Contig10599_at	PfkB type carbohydrate kinase protein family-like	-1.57	5.04E-08	Energy
Contig11175_s_at	Oxygen-evolving complex related protein	-1.57	5.18E-07	Energy
Contig17766_at	2Fe-2S iron-sulfur cluster binding domain containing protein	-1.52	5.65E-05	Energy

Contig168_at	Chlorophyll a/b-binding protein CP29 precursor	-1.48	4.62E-06	Energy
Contig3354_at	Putative calvin cycle protein CP12	-1.48	3.61E-06	Energy
Contig13331_s_at	Violaxanthin de-epoxidase family protein	-1.47	2.75E-06	Energy
Contig12146_at	Thioredoxin-like	-1.46	2.34E-07	Energy
Contig1519_s_at	LHCI-680 photosystem I antenna protein	-1.46	1.10E-06	Energy
HV_CEa0013J19f_at	Photosystem I P700 chlorophyll a apoprotein A1	-1.46	0.03	Energy
Contig5236_at	Putative thioredoxin	-1.43	3.72E-06	Energy
rbaak37h22_at	Thylakoid lumenal 29.8 kDa protein	-1.41	6.00E-07	Energy
Contig5804_at	Photosystem II stability/assembly factor HCF136	-1.4	1.47E-07	Energy
Contig7648_at	Thylakoid lumenal protein-like	-1.34	3.14E-07	Energy
Contig18499_at	THA4	-1.34	2.04E-05	Energy
Contig1419_s_at	Photosystem II 10 kDa polypeptide	-1.33	1.44E-05	Energy
Contig2399_at	Ferredoxin-thioredoxin reductase catalytic chain	-1.32	4.23E-06	Energy
HVSMEm0019O10f_s_at	Photosystem I reaction center subunit XI, chloroplast precursor	-1.3	2.11E-06	Energy
HVSMEc0011A03f_at	Photosystem I assembly protein ycf4	-1.29	2.24E-05	Energy
HVSMEn0003D06r2_at	Putative defective chloroplasts and leaves (DCL) protein	-1.24	2.55E-06	Energy
Contig14290_at	Putative lycopene epsilon-cyclase	-1.23	0	Energy
Contig6688_s_at	6-phosphogluconate dehydrogenase	-1.23	1.01E-06	Energy
Contig14323_at	Putative NADPH:quinone oxidoreductase	-1.22	2.56E-05	Energy
Contig5619_at	Putative thioredoxin reductase	-1.2	5.28E-05	Energy
Contig2181_s_at	FtsH-like protein Pftf	-1.19	5.20E-07	Energy
Contig10700_at	Monothiol glutaredoxin	-1.18	9.05E-06	Energy
Contig10646_at	NADH dehydrogenase	-1.17	1.03E-05	Energy
rbaak37h22_s_at	Thylakoid lumenal 29.8 kDa protein	-1.16	5.72E-05	Energy
Contig6791_at	Fructose-bisphosphate aldolase	-1.15	1.53E-06	Energy
Contig14631_at	Thioredoxin M-like	-1.12	1.30E-06	Energy
HVSMEb0009E07r2_s_at	Chloroplast FtsH protease	-1.12	2.90E-07	Energy
HVSMEb0007O01f_at	Photosystem II 44 kDa reaction center protein	-1.11	1.93E-06	Energy
Contig21764_at	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase	-1.08	1.31E-05	Energy
baak12i08_s_at	Quinone reductase 2	-1.08	0	Energy
Contig21378_at	Putative phytochromobilin synthase	-1.04	5.43E-06	Energy
Contig2761_at	RuBisCO subunit binding-protein alpha subunit	-1.04	2.73E-05	Energy
Contig12438_at	NADH dehydrogenase-like protein	-1.01	9.78E-06	Energy

Contig589_x_at	Ribulose-bisphosphate carboxylase small chain precursor	-1.01	0	Energy
Contig17002_at	Heme oxygenase 2	-2.18	2.10E-08	Interaction with the cellular environment
Contig8698_s_at	Nonphototrophic hypocotyl 1b	-3.19	4.84E-10	Interaction with the environment
Contig9132_at	Deoxyribodipyrimidine photolyase family protein-like	-2.83	1.22E-09	Interaction with the environment
Contig12507_at	Nodulin-like protein	-2.62	1.12E-08	Interaction with the environment
Contig16901_at	Putative nodulin-26	-2.53	4.67E-11	Interaction with the environment
Contig21008_at	Nodulin-like protein	-2.16	2.39E-08	Interaction with the environment
Contig4281_s_at	Cold regulated protein	-2.12	5.05E-08	Interaction with the environment
Contig16708_at	Nodulin-like protein	-2.04	3.03E-10	Interaction with the environment
Contig4281_at	Cold regulated protein	-1.44	1.46E-06	Interaction with the environment
Contig10919_s_at	Nodulin-like protein	-1.42	1.12E-06	Interaction with the environment
Contig14660_at	Putative early nodule-specific-like protein ENOD8	-1.4	3.42E-07	Interaction with the environment
Contig11100_at	Putative nodulin-like protein	-1.16	1.19E-07	Interaction with the environment
Contig4818_at	Putative UOS1	-1.07	3.45E-05	Interaction with the environment
rbaal13j08_at	Nodulin-like protein	-1.06	0	Interaction with the environment
Contig15786_at	Putative cytochrome P450	-4.86	8.00E-12	Metabolism
Contig2985_s_at	Mg-chelatase subunit XANTHA-F	-4.67	1.26E-09	Metabolism
HVSMEm0003G16r2_at	Putative cytochrome P450	-4.45	2.03E-10	Metabolism
Contig21141_at	Flavin containing monooxygenase 3-like	-4.36	1.54E-11	Metabolism
baak1k18_s_at	Glyceraldehyde-3-phosphate dehydrogenase B	-3.96	1.59E-08	Metabolism
HVSMEb0010E16r2_s_at	Fatty acid condensing enzyme CUT1	-3.88	1.16E-08	Metabolism
Contig17991_at	Cytochrome b561	-3.79	4.53E-10	Metabolism
HVSMEn0021L12r2_at	Aspartic proteinase nepenthesin-1 precursor	-3.7	5.45E-12	Metabolism
Contig12508_s_at	Putative cytochrome P450	-3.68	5.48E-11	Metabolism
Contig17756_at	Carbonic anhydrase precursor	-3.66	3.84E-10	Metabolism
Contig4988_at	9-cis-epoxycarotenoid dioxygenase	-3.62	2.46E-09	Metabolism
Contig9660_at	Rhodanese-like domain-containing protein-like	-3.62	1.79E-09	Metabolism
Contig5260_s_at	Putative thiamine biosythesis protein ThiC	-3.6	2.55E-09	Metabolism
Contig9168_s_at	Plastid omega-3 fatty acid desaturase	-3.58	2.59E-09	Metabolism
Contig8678_at	Aspartate kinase-homoserine dehydrogenase	-3.57	8.67E-09	Metabolism
Contig9169_at	Plastid omega-3 fatty acid desaturase	-3.57	3.51E-08	Metabolism
Contig13305_at	Phytoene synthase	-3.54	1.24E-09	Metabolism
Contig4941_at	Farnesyl pyrophosphate synthetase	-3.54	1.73E-08	Metabolism

Contig6963_at	Putative 3-beta hydroxysteroid dehydrogenase/isomerase protein	-3.53	2.65E-10	Metabolism
Contig888_at	Glyceraldehyde-3-phosphate dehydrogenase A	-3.48	2.12E-10	Metabolism
Contig2994_at	Glycine cleavage system H protein	-3.47	2.39E-08	Metabolism
Contig4941_s_at	Farnesyl pyrophosphare synthase	-3.33	7.47E-08	Metabolism
Contig11295_at	Cytochrome P450	-3.31	5.94E-10	Metabolism
Contig5059_s_at	RNase S-like protein	-3.29	3.62E-07	Metabolism
Contig3183_at	Geranylgeranyl hydrogenase	-3.26	5.68E-09	Metabolism
Contig48_at	Phosphoglycerate kinase	-3.26	1.26E-08	Metabolism
Contig2949_s_at	Sedoheptulose-1,7-bisphosphatase	-3.22	6.30E-10	Metabolism
Contig455_s_at	Thiamine biosynthetic enzyme	-3.21	1.22E-09	Metabolism
Contig451_at	Dihydrolipoyl dehydrogenase	-3.2	3.40E-09	Metabolism
baak46p14_s_at	Magnesium-protoporphyrin IX monomethyl ester cyclase	-3.18	4.63E-09	Metabolism
Contig5341_at	Mg-chelatase subunit (Xantha-h)	-3.18	2.62E-09	Metabolism
Contig6799_at	Cinnamoyl CoA reductase	-3.18	6.99E-09	Metabolism
Contig3657_s_at	Cytochrome b6f complex subunit	-3.17	7.68E-08	Metabolism
Contig12019_at	Trehalose-6-phosphate synthase	-3.16	2.60E-10	Metabolism
Contig1953_s_at	Aminotransferase 1	-3.12	1.40E-08	Metabolism
Contig4531_at	Short-chain dehydrogenase/reductase	-3.11	8.82E-10	Metabolism
Contig1824_s_at	Serine hydroxymethyltransferase	-3.08	4.67E-09	Metabolism
Contig7305_at	O-methyltransferase family protein	-3.08	2.40E-07	Metabolism
Contig446_at	Glyceraldehyde-3-phosphate dehydrogenase B	-3.06	2.80E-09	Metabolism
Contig5260_at	Putative thiamine biosythesis protein ThiC	-3.04	8.92E-10	Metabolism
Contig909_s_at	Aminomethyltransferase-like precursor protein	-3.04	3.92E-10	Metabolism
Contig25441_at	Cytochrome P450-like	-3.03	5.65E-09	Metabolism
Contig2262_at	Magnesium-protoporphyrin IX monomethyl ester	-3.02	2.53E-09	Metabolism
rbah53j14_s_at	Glyceraldehyde 3-phosphate dehydrogenase A	-3.02	4.87E-08	Metabolism
Contig24885_at	Putative 3(2),5-bisphosphate nucleotidase	-3	4.95E-09	Metabolism
Contig8678_s_at	Aspartate kinase-homoserine dehydrogenase	-3	5.87E-10	Metabolism
Contig9127_at	Phosphoglycerate mutase family	-2.99	6.58E-09	Metabolism
baak38i16_s_at	Phosphoglycerate kinase	-2.98	4.49E-08	Metabolism
Contig2263_s_at	Magnesium-protoporphyrin IX monomethyl ester cyclase	-2.98	7.86E-09	Metabolism
Contig14534_at	Putative cytochrome P450	-2.97	5.94E-10	Metabolism
Contig7298_at	Rhodanese-like domain protein	-2.97	4.76E-08	Metabolism

Contig4910_at	O-methyltransferase	-2.96	9.71E-05	Metabolism
Contig17236_at	5' nucleotidase family protein	-2.95	6.32E-10	Metabolism
Contig8679_at	Aspartate kinase-homoserine dehydrogenase	-2.95	5.61E-08	Metabolism
S0001000007H12F1_at	Ribose-phosphate pyrophosphokinase 1	-2.94	6.41E-08	Metabolism
Contig1774_at	Putative glycolate oxidase	-2.93	4.34E-09	Metabolism
Contig4187_at	Alpha-galactosidase	-2.93	3.34E-09	Metabolism
Contig6818_at	Omega-6 fatty acid desaturase	-2.91	3.02E-09	Metabolism
Contig6174_at	Probable 6-phosphogluconolactonase	-2.9	1.20E-07	Metabolism
Contig12132_s_at	Putative ubiquinone oxidoreductase subunit 1	-2.89	7.99E-08	Metabolism
Contig13704_at	Flavin containing monooxygenase 3-like	-2.88	2.11E-10	Metabolism
Contig7143_s_at	NAD-dependent epimerase/dehydratase	-2.88	4.56E-09	Metabolism
HV_CEb0003J19r2_at	Cytochrome P450	-2.88	2.01E-09	Metabolism
rbaal1m15_s_at	Glycine dehydrogenase	-2.88	1.75E-10	Metabolism
Contig24054_at	Putative O-methyltransferase	-2.87	2.39E-08	Metabolism
Contig10699_at	Mg-chelatase subunit XANTHA-G precursor	-2.86	4.40E-10	Metabolism
HV_CEa0015D14r2_at	Strictosidine synthase-related	-2.86	1.58E-09	Metabolism
Contig3183_s_at	Geranylgeranyl hydrogenase	-2.83	3.76E-09	Metabolism
Contig2191_at	Phosphoethanolamine methyltransferase	-2.81	3.57E-09	Metabolism
Contig592_at	Aminomethyltransferase	-2.81	2.07E-10	Metabolism
Contig1952_at	Aminotransferase 1	-2.8	2.58E-09	Metabolism
Contig14823_s_at	Glucosyltransferase	-2.77	8.29E-08	Metabolism
Contig10130_at	Putative aldo/keto reductase	-2.76	1.35E-08	Metabolism
Contig14385_at	Putative iron/ascorbate-dependent oxidoreductase	-2.76	1.50E-09	Metabolism
Contig7327_at	Cinnamoyl-CoA reductase - like protein	-2.76	1.61E-08	Metabolism
Contig6661_s_at	Putative cinnamyl-alcohol dehydrogenase	-2.75	9.69E-07	Metabolism
Contig10497_s_at	Galactose dehydrogenase	-2.73	1.14E-09	Metabolism
Contig13174_at	HAD-superfamily hydrolase	-2.71	3.86E-09	Metabolism
Contig14804_s_at	Cytochrome P450	-2.71	3.92E-09	Metabolism
rbaal33b21_s_at	Putative malate dehydrogenase	-2.71	2.00E-08	Metabolism
Contig12340_at	Thiol methyltransferase	-2.69	1.48E-07	Metabolism
Contig5371_s_at	Amine oxidase	-2.69	4.63E-08	Metabolism
HV_CEa0001E19r2_at	Putative decarboxylase	-2.69	7.77E-09	Metabolism
Contig12596_at	Putative NADPH-dependent reductase	-2.68	3.09E-08	Metabolism

Contig4756_at	Glyceraldehyde-3-phosphate dehydrogenase	-2.68	2.63E-08	Metabolism
Contig19853_at	Methionine aminopeptidase	-2.66	3.18E-09	Metabolism
Contig5370_at	Amine oxidase	-2.66	2.22E-08	Metabolism
Contig5658_at	Quinone oxidoreductase-like protein	-2.64	4.12E-08	Metabolism
rbasd2c09_s_at	Flavin containing monooxygenase 3-like	-2.63	1.69E-10	Metabolism
Contig24228_at	Glucose-6-phosphate 1-dehydrogenase	-2.62	7.52E-10	Metabolism
Contig13997_at	Cinnamyl alcohol dehydrogenase	-2.61	1.10E-09	Metabolism
Contig3181_at	Zeaxanthin epoxidase	-2.61	3.30E-08	Metabolism
Contig10497_at	L-galactose dehydrogenase	-2.59	2.70E-09	Metabolism
Contig10062_at	Putative cytochrome b-561	-2.57	1.04E-08	Metabolism
Contig12521_at	Putative cytochrome P450	-2.57	2.44E-08	Metabolism
AB011266_at	Nicotianamine synthase	-2.55	1.42E-09	Metabolism
Contig5712_at	Shikimate kinase family protein	-2.55	5.40E-08	Metabolism
Contig13707_at	Putative 3(2),5-bisphosphate nucleotidase	-2.54	1.21E-08	Metabolism
Contig1672_s_at	Alanine aminotransferase	-2.53	1.26E-09	Metabolism
Contig4341_s_at	Alcohol dehydrogenase	-2.53	1.17E-07	Metabolism
rbaal1n16_s_at	Glyceraldehyde-3-phosphate dehydrogenase	-2.52	1.48E-09	Metabolism
Contig16307_at	Cytochrome P450 family protein	-2.51	1.71E-08	Metabolism
Contig11021_at	Putative linalool synthase	-2.48	1.74E-07	Metabolism
Contig13600_at	Nuclear ribonuclease Z	-2.46	3.56E-08	Metabolism
Contig2515_at	Putative hydroxypyruvate reductase	-2.46	1.11E-08	Metabolism
Contig4192_at	Sorbitol dehydrogenase	-2.46	1.66E-08	Metabolism
rbaal1h20_s_at	Putative aldo/keto reductase	-2.46	8.69E-09	Metabolism
Contig15547_at	Peptide deformylase-like protein	-2.45	1.89E-07	Metabolism
Contig2189_s_at	Phosphoethanolamine methyltransferase	-2.44	1.33E-08	Metabolism
Contig20654_at	Ribonuclease II-like protein	-2.43	1.26E-08	Metabolism
Contig3212_s_at	Flavin containing polyamine oxidase precursor	-2.43	1.56E-06	Metabolism
Contig10632_s_at	Laccase LAC5-4	-2.41	1.33E-08	Metabolism
Contig5409_at	Putative sterol-C5(6)-desaturase	-2.41	2.13E-09	Metabolism
Contig8727_s_at	Formamidase	-2.41	2.26E-08	Metabolism
Contig16209_at	Starch binding domain containing protein	-2.4	3.58E-09	Metabolism
Contig5780_at	Oxidase	-2.4	5.31E-09	Metabolism
Contig10268_at	Cytochrome P450 monooxygenase	-2.39	1.73E-08	Metabolism

Contig7304_s_at	Flavonoid 7-O-methyltransferase-like	-2.39	2.84E-08	Metabolism
HV12A17u_s_at	Putative esterase D	-2.39	2.89E-08	Metabolism
Contig320_at	Non-specific monooxygenase	-2.38	1.00E-07	Metabolism
Contig5344_at	Putative sulfolipid synthase	-2.38	8.48E-09	Metabolism
Contig1672_at	Alanine aminotransferase	-2.37	3.20E-08	Metabolism
Contig5866_at	Putative CTP synthase	-2.37	2.98E-08	Metabolism
HVSMEa0004F18f2_s_at	Glutamine synthetase 2	-2.37	6.95E-09	Metabolism
Contig17460_at	Xylulose kinase	-2.36	6.39E-08	Metabolism
Contig9878_at	Rhodanese family protein-like	-2.36	5.36E-08	Metabolism
Contig7273_s_at	Putative replication protein A2	-2.35	3.08E-08	Metabolism
Contig11259_at	Phytoene synthase 2	-2.34	9.53E-07	Metabolism
Contig15291_at	Putative glucosyltransferase	-2.34	9.19E-09	Metabolism
Contig1771_s_at	Probable (S)-2-hydroxy-acid oxidase	-2.34	5.12E-08	Metabolism
Contig7624_at	Aldo-keto reductase/ oxidoreductase	-2.34	2.59E-09	Metabolism
Contig8979_at	Putative cinnamoyl-CoA reductase	-2.34	3.42E-08	Metabolism
Contig4724_at	Gamma hydroxybutyrate dehydrogenase	-2.33	6.18E-09	Metabolism
Contig15432_at	Saccharopine dehydrogenase	-2.32	1.90E-09	Metabolism
Contig7987_at	Putative glyoxalase I	-2.32	6.81E-09	Metabolism
Contig10632_at	Laccase LAC5-4	-2.31	6.56E-08	Metabolism
Contig16326_at	Coenzyme F420 hydrogenase family protein	-2.31	1.57E-09	Metabolism
Contig11957_at	Cytochrome P450	-2.3	1.97E-08	Metabolism
Contig14384_at	Lipase-like	-2.3	9.13E-10	Metabolism
Contig22113_at	Lecithin:cholesterol acyltransferase	-2.3	2.15E-09	Metabolism
Contig12464_at	Pyruvate dehydrogenase E1 component beta subunit	-2.29	5.49E-09	Metabolism
Contig1828_at	Serine hydroxymethyltransferase	-2.29	2.73E-08	Metabolism
Contig18583_at	Beta-ketoacyl-ACP synthase I	-2.29	1.29E-07	Metabolism
Contig11631_at	Tryptophan decarboxylase	-2.27	4.44E-08	Metabolism
Contig19388_at	Coproporphyrinogen III oxidase	-2.27	1.26E-07	Metabolism
Contig1646_at	Glutamine synthetase	-2.26	1.26E-09	Metabolism
Contig21949_s_at	Phytoene synthase 2	-2.26	6.21E-07	Metabolism
Contig2928_s_at	Malate dehydrogenase	-2.24	9.52E-09	Metabolism
Contig8619_at	Putative serine acetyltransferase	-2.24	5.65E-10	Metabolism
Contig588_at	4-nitrophenylphosphatase	-2.23	2.84E-08	Metabolism

Contig21250_at	Phosphoglycerate dehydrogenase	-2.22	6.63E-09	Metabolism
Contig2993_at	Putative glycine decarboxylase subunit	-2.22	6.82E-08	Metabolism
Contig5478_at	Putative Proline synthetase associated protein	-2.22	1.93E-08	Metabolism
Contig7624_s_at	Aldo/keto reductase family protein	-2.21	4.54E-09	Metabolism
Contig12701_at	Putative copper amine oxidase	-2.19	5.40E-08	Metabolism
Contig3761_at	Starch branching enzyme IIa	-2.19	3.82E-09	Metabolism
HVSMEm0020M20r2_s_at	Putative aldo/keto reductase family protein	-2.19	1.58E-07	Metabolism
rbah53j14_at	Glyceraldehyde 3-phosphate dehydrogenase A	-2.19	5.36E-09	Metabolism
Contig16475_at	Sucrose-phosphate synthase	-2.18	1.13E-09	Metabolism
Contig9547_at	Putative ethanolamine kinase 1	-2.17	2.16E-10	Metabolism
Contig5852_at	Oxidoreductase-like	-2.16	1.91E-09	Metabolism
Contig16785_at	Acyl-activating enzyme 14	-2.15	5.09E-08	Metabolism
Contig1380_s_at	Putative glutamate decarboxylase	-2.14	9.30E-09	Metabolism
Contig1646_s_at	Glutamine synthetase	-2.14	9.78E-11	Metabolism
Contig6662_at	Putative cinnamyl alcohol dehydrogenase	-2.14	1.20E-05	Metabolism
Contig13408_at	Putative esterase	-2.12	2.28E-08	Metabolism
Contig11056_at	Cyclase/dehydrase	-2.11	1.56E-08	Metabolism
Contig8066_s_at	Cytosolic IMP-GMP specific 5'-nucleotidase	-2.11	5.48E-08	Metabolism
HVSMEb0005F19r2_at	Lipase-like protein	-2.11	9.77E-05	Metabolism
Contig2019_s_at	Inorganic pyrophosphatase	-2.1	8.71E-10	Metabolism
Contig7625_at	Aldo/keto reductase family protein	-2.1	1.12E-07	Metabolism
Contig10075_at	Putative oxidoreductase	-2.09	1.65E-07	Metabolism
Contig14804_at	Cytochrome P450	-2.09	8.32E-09	Metabolism
Contig391_at	Malate dehydrogenase	-2.08	2.19E-08	Metabolism
Contig1808_at	Starch synthase I	-2.07	3.18E-09	Metabolism
HVSMEf0006A19r2_at	Putative esterase	-2.07	2.55E-07	Metabolism
Contig21515_s_at	Cytochrome P450	-2.06	2.45E-08	Metabolism
Contig5527_at	AMP-binding protein	-2.06	1.51E-08	Metabolism
Contig2825_at	Trehalose-6-phosphate phosphatase	-2.05	1.07E-08	Metabolism
EBem04_SQ004_M07_s_at	Hydroxyacylglutathione hydrolase	-2.05	1.06E-07	Metabolism
EBro03_SQ004_E10_at	1-aminocyclopropane-1-carboxylate oxidase	-2.05	2.05E-08	Metabolism
Contig13312_at	1-aminocyclopropane-1-carboxylate oxidase	-2.04	3.70E-07	Metabolism
Contig14300_at	Putative geranylgeranyl diphosphate synthase	-2.03	1.81E-08	Metabolism

Contig19273_at	Uracil phosphoribosyltransferase-like protein	-2.03	7.51E-10	Metabolism
rbags14a15_s_at	Delta-aminolevulinic acid dehydratase	-2.02	4.11E-08	Metabolism
Contig11693_at	Putative pectinacetylesterase	-2.01	2.31E-09	Metabolism
Contig6862_s_at	Methionine aminopeptidase	-2	1.47E-06	Metabolism
Contig5728_at	Pyruvate dehydrogenase kinase 1	-1.99	1.99E-08	Metabolism
EBpi01_SQ001_I04_s_at	Gamma hydroxybutyrate dehydrogenase	-1.99	2.59E-09	Metabolism
bags7h06_at	Invertase inhibitor homolog	-1.98	2.43E-07	Metabolism
Contig19896_at	Phosphoenolpyruvate carboxylase	-1.98	1.41E-08	Metabolism
Contig2640_s_at	1-aminocyclopropane-1-carboxylate oxidase	-1.98	1.28E-09	Metabolism
Contig9444_at	Putative aldo/keto reductase	-1.98	1.23E-07	Metabolism
Contig1483_at	Glycine dehydrogenase	-1.97	3.53E-09	Metabolism
Contig20568_at	Putative serine decarboxylase	-1.96	2.87E-09	Metabolism
Contig5479_s_at	Proline synthetase associated protein	-1.95	2.24E-08	Metabolism
Contig9155_s_at	GCN5-related N-acetyltransferase	-1.95	4.05E-08	Metabolism
Contig897_s_at	Carbonic anhydrase	-1.94	5.58E-09	Metabolism
Contig2188_s_at	Phosphoethanolamine methyltransferase	-1.93	0	Metabolism
Contig9281_at	Putative acyltransferase	-1.92	6.87E-09	Metabolism
rbaal20i06_s_at	Hydroxyacid dehydrogenase/reductase	-1.92	1.11E-08	Metabolism
rbasd24g02_s_at	1-aminocyclopropane-1-carboxylate oxidase	-1.92	5.71E-08	Metabolism
Contig3596_at	Arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II	-1.91	2.82E-08	Metabolism
Contig6208_at	Sterol desaturase family protein	-1.91	1.88E-06	Metabolism
Contig20626_at	Alcohol dehydrogenase-like protein	-1.9	4.42E-07	Metabolism
HW06K22u_s_at	Diphosphate-fructose-6-phosphate 1-phosphotransferase	-1.9	7.80E-07	Metabolism
Contig16550_at	Riboflavin biosynthesis protein ribD	-1.89	2.63E-08	Metabolism
Contig22412_at	UDP-glucoronosyl and UDP-glucosyl transferase family protein	-1.89	4.65E-09	Metabolism
Contig24721_at	Cytochrome P450 family protein	-1.89	1.04E-06	Metabolism
Contig7928_s_at	Homoserine dehydrogenase-like	-1.88	7.41E-09	Metabolism
Contig13038_at	Indole-3-glycerol phosphate lyase	-1.86	4.27E-07	Metabolism
Contig7908_at	Methyltransferase-like	-1.86	1.16E-07	Metabolism
HI08K02r_at	Alpha-1,3/4-fucosidase precursor	-1.85	6.10E-06	Metabolism
HVSMEn0025G16r2_at	Glucosyltransferase-13	-1.85	1.56E-07	Metabolism
Contig5401_s_at	Coproporphyrinogen oxidase	-1.84	1.16E-06	Metabolism
HK05G21r_s_at	Putative hydrolase	-1.84	1.33E-07	Metabolism

HVSMEg0007G16r2_s_at	Malate dehydrogenase	-1.84	4.03E-09	Metabolism
HVSMEi0003A10r2_s_at	Monoterpene synthase	-1.84	2.53E-07	Metabolism
Contig10944_at	Cysteine synthase	-1.83	6.06E-09	Metabolism
Contig16478_at	UbiE/COQ5 methyltransferase-like (As(III) methyltransferase)	-1.83	2.27E-08	Metabolism
Contig7831_at	Farnesyl pyrophosphate synthase	-1.83	1.08E-08	Metabolism
rbags20j15_s_at	DNA/panthothenate metabolism flavoprotein family protein	-1.83	1.16E-08	Metabolism
Contig5058_x_at	RNase S-like protein	-1.82	6.40E-06	Metabolism
Contig5588_at	Transferase family	-1.81	3.57E-07	Metabolism
Contig9958_s_at	Radical SAM domain-containing protein-like	-1.81	1.78E-07	Metabolism
Contig4518_s_at	FAD-dependent oxidoreductase family protein	-1.8	1.82E-08	Metabolism
Contig8964_at	Putative steroid sulfotransferase	-1.8	3.26E-07	Metabolism
Contig7423_at	Phosphopantothenate--cysteine ligase	-1.8	2.02E-06	Metabolism
Contig1302_at	Cysteine synthase	-1.78	4.14E-08	Metabolism
Contig8716_at	Nitrate reductase	-1.78	4.28E-08	Metabolism
Contig5714_s_at	Shikimate kinase family protein	-1.77	1.96E-09	Metabolism
Contig5133_s_at	Phosphoglycerate mutase-like protein	-1.76	1.21E-08	Metabolism
HX08J20r_at	Betaine aldehyde dehydrogenase-like	-1.76	6.04E-09	Metabolism
Contig10771_s_at	Haloacid dehalogenase-like hydrolase family protein	-1.75	5.89E-07	Metabolism
Contig11933_at	Putative serine acetyltransferase	-1.75	4.67E-09	Metabolism
Contig12208_at	Granule-bound starch synthase 1b	-1.75	5.13E-07	Metabolism
Contig15062_at	Thiol methyltransferase 1	-1.75	1.64E-08	Metabolism
Contig10284_at	Putative alpha-galactosidase	-1.74	3.23E-07	Metabolism
Contig12712_at	Arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II	-1.74	7.53E-09	Metabolism
Contig14033_at	Cytochrome P450	-1.74	7.70E-10	Metabolism
Contig21227_at	Putative beta-mannosidase	-1.74	6.13E-09	Metabolism
Contig5572_at	Phosphoenolpyruvate carboxylase	-1.73	4.27E-08	Metabolism
Contig7565_at	Formiminotransferase-cyclodeaminase	-1.73	6.44E-08	Metabolism
HV_CEb0010H17r2_at	Aspartic proteinase nepenthesin-2 precursor	-1.73	8.62E-07	Metabolism
HX08J20r_s_at	Betaine aldehyde dehydrogenase-like	-1.73	1.64E-08	Metabolism
Contig3332_at	Apyrase-like protein	-1.69	7.85E-06	Metabolism
Contig3375_at	Putative trehalose-6-phosphate synthase/phosphatase	-1.69	2.63E-08	Metabolism
HVSMEa0017O08r2_at	NAD synthetase	-1.69	8.53E-08	Metabolism
Contig10620_at	Arginine N-methyltransferase	-1.68	1.45E-07	Metabolism

Contig5133_at	Phosphoglycerate mutase-like protein	-1.64	1.04E-08	Metabolism
Contig8885_s_at	Putative GMP synthetase	-1.64	5.30E-07	Metabolism
Contig9187_at	Putative aldo/keto reductase family protein	-1.64	7.35E-06	Metabolism
Contig13808_at	Putative ribonuclease E	-1.63	9.86E-08	Metabolism
Contig14542_at	Putative alpha-amylase	-1.62	3.05E-07	Metabolism
Contig18338_at	Galactoside 2-L-fucosyltransferase	-1.62	2.49E-08	Metabolism
Contig3927_s_at	Putative S-formylglutathione hydrolase	-1.62	4.36E-07	Metabolism
Contig6428_s_at	Putative amidotransferase	-1.62	7.77E-09	Metabolism
Contig13107_at	Putative D-threonine dehydrogenase	-1.61	8.34E-08	Metabolism
Contig3891_s_at	Flavonol synthase-like protein	-1.61	4.13E-05	Metabolism
Contig10054_s_at	Putative aldose reductase	-1.6	1.44E-06	Metabolism
Contig14339_at	Cytosolic aldehyde dehydrogenase	-1.6	5.76E-09	Metabolism
Contig17116_at	CTP synthase	-1.6	0.01	Metabolism
HVSMEb0006N17f_at	Probable phytol kinase	-1.6	4.57E-09	Metabolism
Contig10722_at	Putative starch synthase III	-1.59	1.68E-08	Metabolism
Contig16368_at	Plastidic alpha 1,4-glucan phosphorylase 3	-1.58	7.56E-06	Metabolism
Contig4470_s_at	Extracellular invertase	-1.58	1.72E-08	Metabolism
Contig9212_s_at	Triacylglycerol Lipase	-1.58	1.48E-06	Metabolism
Contig12418_at	Putative UDP-glucose:salicylic acid glucosyltransferase	-1.57	6.21E-08	Metabolism
Contig10283_at	Putative alpha-galactosidase	-1.56	1.02E-06	Metabolism
Contig17143_at	Aspartic proteinase nepenthesin II-like	-1.56	1.92E-07	Metabolism
Contig6413_at	Putative hydrolase	-1.56	3.20E-06	Metabolism
Contig5530_s_at	AMP-binding protein	-1.55	5.27E-07	Metabolism
Contig9958_at	Radical SAM domain-containing protein	-1.55	3.23E-06	Metabolism
HS16E24u_s_at	Trehalose-phosphatase B	-1.55	3.89E-07	Metabolism
Contig9131_s_at	Putative 1-aminocyclopropane-1-carboxylate synthase	-1.54	3.42E-09	Metabolism
Contig13094_s_at	Metallo-beta-lactamase protein-like	-1.53	5.13E-06	Metabolism
Contig15730_at	Putative muconate cycloisomerase-like protein	-1.52	4.84E-06	Metabolism
Contig6684_at	Acetolactate synthase	-1.52	1.50E-07	Metabolism
Contig6846_s_at	Pyridoxal biosynthesis protein PDX2	-1.52	4.29E-07	Metabolism
Contig1644_at	Cytochrome b6-f complex iron-sulfur subunit	-1.51	5.49E-08	Metabolism
Contig23957_at	Putative glycerol-3-phosphate dehydrogenase	-1.51	2.44E-06	Metabolism
Contig9055_at	Putative 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme	-1.51	1.78E-08	Metabolism

HVSMEb0014C02r2_at	Thiazole biosynthetic enzyme 1-2	-1.51	6.49E-09	Metabolism
Contig22570_at	Putative cytochrome p450	-1.5	6.73E-08	Metabolism
Contig3810_at	Galactinol synthase	-1.5	4.50E-05	Metabolism
Contig7901_at	Putative lecithin diacylglycerol cholesterol acyltransferase	-1.5	8.58E-08	Metabolism
HVSMEg0007G16r2_at	Malate dehydrogenase	-1.5	1.36E-08	Metabolism
Contig9154_at	N-acetyltransferase	-1.49	6.27E-09	Metabolism
Contig8673_s_at	Putative epoxide hydrolase	-1.48	2.23E-06	Metabolism
Contig9584_at	Phosphoribosylformylglycinamidine cyclo-ligase	-1.48	2.51E-06	Metabolism
Contig12113_at	Diphosphonucleotide phosphatase 1	-1.47	9.95E-07	Metabolism
Contig17227_at	Putative naphthoate synthase menB	-1.47	2.45E-07	Metabolism
Contig20263_at	Putative adenosine kinase	-1.47	4.02E-06	Metabolism
Contig6840_at	Transaldolase-like protein	-1.47	4.17E-06	Metabolism
HY06D12u_s_at	Aldose 1-epimerase-like	-1.47	2.31E-08	Metabolism
Contig24534_at	S-adenosyl-L-methionine	-1.46	2.32E-06	Metabolism
HVSMEk0022L04r2_s_at	Putative trehalose-6-phosphate synthase	-1.46	6.60E-09	Metabolism
Contig2289_s_at	Putative diphosphonucleotide phosphatase	-1.46	4.71E-06	Metabolism
Contig6517_at	Alpha-glucan phosphorylase, H isozyme	-1.45	0	Metabolism
Contig16954_at	Endoribonuclease E-like protein	-1.44	8.89E-08	Metabolism
Contig12760_s_at	Sulfolipid biosynthesis protein SQD1	-1.43	2.90E-07	Metabolism
Contig20267_at	Cytochrome p450	-1.43	1.94E-07	Metabolism
Contig25582_at	Putative urease accessory protein G	-1.43	4.63E-07	Metabolism
Contig5718_s_at	Methylthioribose kinase	-1.43	2.35E-07	Metabolism
Contig9561_at	5'-AMP-activated protein kinase beta-1 subunit-related	-1.43	8.09E-07	Metabolism
Contig14171_at	Menaquinone biosynthesis methyltransferase	-1.42	1.98E-06	Metabolism
Contig5956_at	Porphobilinogen deaminase	-1.42	3.38E-05	Metabolism
Contig2724_s_at	Sucrose-phosphatase	-1.41	1.19E-05	Metabolism
Contig11591_at	Putative deoxyguanosine kinase	-1.4	1.89E-06	Metabolism
Contig4938_s_at	Lactoylglutathione lyase	-1.4	1.16E-05	Metabolism
Contig5267_at	ADP-glucose pyrophosphorylase large subunit	-1.4	2.52E-06	Metabolism
Contig9278_s_at	Putative pectinacetylesterase	-1.4	1.31E-06	Metabolism
HK03P19r_s_at	Amidase-like protein	-1.4	5.41E-09	Metabolism
Contig12090_at	Adenylosuccinate-AMP lyase	-1.39	1.08E-06	Metabolism
Contig16062_at	Phosphoglucan, water dikinase	-1.39	7.23E-08	Metabolism

Contig17399_at	S-adenosyl-L-methionine:L-methionine S-methyltransferase	-1.39	5.57E-08	Metabolism
Contig18745_at	Phospholipid/glycerol acyltransferase-like protein	-1.39	8.31E-08	Metabolism
rbaal1d15_s_at	Acetolactate synthase	-1.39	5.53E-08	Metabolism
Contig16937_at	Hydrolase	-1.38	1.15E-07	Metabolism
Contig583_at	Thiosulfate sulfurtransferase	-1.37	1.07E-07	Metabolism
Contig8031_at	Aminolevulinate dehydratase	-1.37	2.16E-06	Metabolism
Contig13297_at	Betaine aldehyde dehydrogenase-like	-1.36	2.94E-06	Metabolism
Contig4635_at	Pyruvate dehydrogenase E1 alpha subunit	-1.36	4.79E-08	Metabolism
Contig7273_at	Putative replication protein A2	-1.36	5.56E-07	Metabolism
Contig7392_at	Putative inositol-1-monophosphatase	-1.36	6.83E-08	Metabolism
Contig13982_at	Putative glucosyltransferase	-1.36	5.61E-05	Metabolism
Contig11145_at	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	-1.36	2.40E-06	Metabolism
Contig10590_at	Alpha-N-acetylglucosaminidase	-1.35	2.73E-07	Metabolism
Contig12759_at	Sulfolipid biosynthesis protein	-1.35	4.43E-09	Metabolism
Contig7013_at	1,4-dihydroxy-2-naphthoate octaprenyltransferase	-1.35	1.75E-05	Metabolism
HT01D22w_at	Sucrose synthase	-1.35	1.21E-07	Metabolism
Contig13138_at	Starch synthase isoform IV	-1.33	1.81E-07	Metabolism
Contig1357_at	Putative D-isomer specific 2-hydroxyacid dehydrogenase	-1.33	4.38E-07	Metabolism
Contig10453_at	Putative linalool synthase	-1.32	2.06E-07	Metabolism
Contig15310_at	S-adenosylmethionine:2-demethylmenaquinone methyltransferase-like	-1.32	2.38E-08	Metabolism
Contig5268_s_at	ADP-glucose pyrophosphorylase large subunit	-1.32	1.66E-07	Metabolism
HY10B09u_s_at	Putative quinone oxidoreductase	-1.32	9.63E-07	Metabolism
rbags17k13_s_at	Putative cinnamoyl-CoA reductase	-1.31	1.18E-06	Metabolism
Contig10839_at	Putative cis-prenyltransferase	-1.28	3.75E-06	Metabolism
Contig17360_at	Methionine aminopeptidase	-1.28	1.85E-07	Metabolism
Contig4542_at	3'(2'),5'-bisphosphate nucleotidase	-1.28	1.35E-06	Metabolism
Contig5719_at	Methylthioribose kinase	-1.28	2.28E-07	Metabolism
Contig7478_at	Putative S-like ribonuclease RNS2	-1.28	2.67E-06	Metabolism
Contig13407_s_at	Putative esterase	-1.27	1.60E-08	Metabolism
Contig3024_at	Putative lipase	-1.27	1.92E-06	Metabolism
Contig6086_at	3-beta hydroxysteroid dehydrogenase/isomerase family protein	-1.27	1.12E-06	Metabolism
Contig7473_at	Fructokinase	-1.27	2.16E-07	Metabolism
Contig331_x_at	Putative geranylgeranyl diphosphate synthase	-1.26	2.82E-06	Metabolism

Contig3591_s_at	Inositol-3-phosphate synthase	-1.26	4.08E-07	Metabolism
Contig6111_at	Triosephosphate isomerase	-1.26	9.11E-05	Metabolism
Contig16821_at	Putative lipase homolog	-1.25	6.09E-06	Metabolism
Contig3376_at	Putative trehalose-6-phosphate synthase	-1.25	7.06E-07	Metabolism
HVSMEb0014C02r2_s_at	Thiazole biosynthetic enzyme 1-2, chloroplast precursor	-1.25	6.82E-07	Metabolism
Contig4930_at	Beta-galactosidase	-1.24	1.11E-05	Metabolism
Contig7832_at	Glycosyl transferase family 8 protein-like	-1.24	3.35E-07	Metabolism
Contig9308_s_at	Putative cytochrome P450	-1.24	0	Metabolism
Contig1673_s_at	Alanine aminotransferase	-1.23	4.64E-07	Metabolism
Contig5189_at	Tropinone reductase	-1.23	4.16E-06	Metabolism
HVSMEf0016E23r2_s_at	Transferase family protein	-1.23	5.88E-06	Metabolism
Contig3806_s_at	Putative stearoyl-acyl-carrier protein desaturase	-1.22	3.12E-06	Metabolism
Contig4955_s_at	HAD-superfamily hydrolase	-1.22	1.26E-06	Metabolism
Contig2362_s_at	Putative nitrilase-associated protein	-1.21	7.32E-06	Metabolism
HVSMEb0011P07r2_at	AMI1 (AMIDASE 1)	-1.21	1.39E-06	Metabolism
Contig11298_at	Thiamin pyrophosphokinase	-1.2	1.82E-06	Metabolism
Contig16471_at	Oxoacyl-synthase I	-1.2	2.13E-06	Metabolism
Contig3592_at	Inositol-3-phosphate synthase	-1.2	1.71E-06	Metabolism
Contig14452_at	Urease accessory protein UreF	-1.19	6.64E-07	Metabolism
Contig14570_at	Putative aldehyde decarbonylase enzyme CER1	-1.19	0	Metabolism
Contig16101_at	Putative tRNA pseudouridine synthase	-1.19	8.60E-06	Metabolism
Contig9574_at	HD domain containing protein	-1.19	3.04E-07	Metabolism
Contig21326_at	Short-chain dehydrogenase	-1.18	1.44E-07	Metabolism
Contig24207_at	Putative branched-chain amino acid aminotransferase	-1.18	3.69E-07	Metabolism
Contig5989_s_at	Acetyl-CoA carboxylase	-1.18	5.99E-07	Metabolism
Contig8671_at	Putative epoxide hydrolase	-1.18	4.29E-06	Metabolism
Contig14292_at	Isoflavone reductase homolog	-1.18	0.02	Metabolism
Contig7417_at	Hydroxymethylglutaryl-coa lyase	-1.17	5.03E-06	Metabolism
HS02M04r_s_at	O-diphenol-O-methyl transferase	-1.17	1.85E-06	Metabolism
Contig9977_at	Phytoene dehydrogenase-like protein	-1.17	1.33E-05	Metabolism
Contig12244_at	Beta-galactosidase	-1.16	6.88E-08	Metabolism
Contig24856_at	Syringomycin biosynthesis enzyme-like	-1.16	3.71E-05	Metabolism
Contig8162_at	Quinone reductase 2	-1.16	6.50E-05	Metabolism

Contig14990_at	Isoamylase	-1.15	1.12E-05	Metabolism
Contig15290_s_at	Putative glucosyltransferase	-1.15	1.90E-05	Metabolism
Contig4374_s_at	Putative cinnamoyl-CoA reductase	-1.15	5.29E-06	Metabolism
Contig5587_at	Transferase family	-1.15	1.04E-06	Metabolism
Contig15078_at	Alpha-glucosidase like protein	-1.15	3.57E-05	Metabolism
Contig13602_at	Amine oxidase	-1.14	1.96E-06	Metabolism
Contig8267_at	Threonine synthase	-1.14	1.30E-06	Metabolism
Contig9106_s_at	Acyl-CoA oxidase homolog	-1.14	6.27E-08	Metabolism
Contig9532_at	Putative ACT domain-containing protein	-1.14	6.87E-08	Metabolism
rbaal38e16_at	Carbonic anhydrase	-1.14	0	Metabolism
Contig10489_at	Putative prolyl 4-hydroxylase, alpha subunit	-1.13	9.76E-06	Metabolism
Contig11640_at	GCN5-related N-acetyltransferase (GNAT) family-like protein	-1.13	1.60E-05	Metabolism
Contig3975_at	ACT domain-containing protein	-1.13	1.75E-06	Metabolism
Contig7010_at	Arginine methyltransferase	-1.13	3.04E-05	Metabolism
Contig10935_at	Esterase/lipase/thioesterase-like protein	-1.12	2.45E-06	Metabolism
Contig16738_at	Putative 4-coumarate-CoA ligase	-1.12	1.85E-07	Metabolism
Contig6654_at	Putative 4-alpha-glucanotransferase	-1.12	2.83E-05	Metabolism
Contig6329_at	Uroporphyrinogen decarboxylase	-1.11	1.15E-06	Metabolism
Contig13049_at	Tropinone reductase 2	-1.1	6.13E-05	Metabolism
Contig13832_at	Rhodanese-like family protein	-1.1	1.17E-06	Metabolism
Contig5639_at	Probable imidazoleglycerol-phosphate dehydratase	-1.1	1.12E-06	Metabolism
Contig8183_at	Cysteine synthase	-1.1	5.64E-06	Metabolism
HVSMEm0012J09r2_at	Aminotransferase	-1.1	6.77E-05	Metabolism
Contig10053_at	Putative aldose reductase	-1.1	0	Metabolism
Contig20235_s_at	Lipase-like protein	-1.1	0.01	Metabolism
Contig14100_at	Putative thiol-disulphide oxidoreductase	-1.09	1.37E-05	Metabolism
Contig6362_s_at	Putative short chain alcohol dehydrogenase	-1.09	2.03E-05	Metabolism
Contig17401_at	Hexokinase	-1.07	1.99E-06	Metabolism
Contig9278_at	Putative pectinacetylesterase	-1.07	4.01E-05	Metabolism
Contig24680_at	Putative fatty acid elongase 3-ketoacyl-CoA synthase 1	-1.06	2.75E-06	Metabolism
Contig3237_at	Methylenetetrahydrofolate reductase	-1.06	6.84E-05	Metabolism
Contig11117_at	DNA methyltransferase DMT106	-1.05	1.30E-06	Metabolism
Contig12778_at	5-formyltetrahydrofolate cyclo-ligase	-1.05	4.52E-06	Metabolism

Contig15004_at	6-phosphogluconolactonase	-1.05	3.46E-05	Metabolism
Contig2165_at	Serine hydroxymethyltransferase	-1.05	5.74E-07	Metabolism
Contig7042_at	Alkaline/neutral invertase	-1.05	1.15E-06	Metabolism
Contig9211_at	Triacylglycerol Lipase	-1.05	1.00E-06	Metabolism
HVSMEi0012H03r2_at	Dioxygenase homolog	-1.05	0	Metabolism
Contig10495_s_at	L-galactose dehydrogenase	-1.04	1.05E-06	Metabolism
Contig12502_at	Putative diphosphate-fructose-6-phosphate 1-phosphotransferase	-1.04	4.36E-05	Metabolism
Contig16447_at	Putative aminoalcoholphosphotransferase	-1.04	5.63E-06	Metabolism
Contig5196_at	Putative CTP synthase	-1.04	4.56E-06	Metabolism
Contig10771_at	Haloacid dehalogenase-like hydrolase family protein	-1.03	1.42E-05	Metabolism
Contig1650_at	Phosphoglucomutase	-1.03	5.53E-06	Metabolism
Contig7088_at	Alpha-amylase type A, EC 3.2.1.1	-1.03	7.06E-06	Metabolism
HVSMEa0003M04r2_at	Cytochrome P450-like	-1.02	0	Metabolism
Contig10498_at	L-galactose dehydrogenase	-1.02	2.20E-05	Metabolism
Contig2189_at	Phosphoethanolamine methyltransferase	-1.02	3.70E-06	Metabolism
Contig2267_s_at	ADP-glucose pyrophosphorylase small subunit	-1.02	6.94E-06	Metabolism
Contig4954_s_at	HAD-superfamily hydrolase	-1.02	0	Metabolism
Contig5486_at	Prolyl 4-hydroxylase	-1.02	1.08E-05	Metabolism
Contig7383_at	Quinone oxidoreductase homolog	-1.02	3.20E-07	Metabolism
HS18E12u_s_at	Putative inosine monophosphate dehydrogenase	-1.02	1.20E-05	Metabolism
Contig15163_at	Allyl alcohol dehydrogenase-like protein	-1.02	2.42E-05	Metabolism
Contig23929_at	Putative short-chain dehydrogenase/reductase	-1.02	3.81E-05	Metabolism
Contig8747_at	Inosine-5'-monophosphate dehydrogenase	-1.01	2.88E-05	Metabolism
Contig5190_at	Short chain alcohol dehydrogenase-like	-1.01	2.08E-05	Metabolism
Contig4372_s_at	Putative cinnamoyl-CoA reductase	-1	3.54E-05	Metabolism
Contig2779_at	Asparaginyl endopeptidase	-4.25	8.35E-09	Protein fate (folding, modification, destination)
Contig12407_at	Kelch repeat-containing F-box-like	-4.09	1.57E-09	Protein fate (folding, modification, destination)
Contig10888_at	ATP-dependent protease La (LON) domain-containing protein	-3.38	9.76E-11	Protein fate (folding, modification, destination)
Contig15931_at	GTP-binding protein-like	-3.1	6.64E-09	Protein fate (folding, modification, destination)
HVSMEb0015P10r2_at	Peptidyl-olyl cis-trans isomerase	-3.07	1.95E-09	Protein fate (folding, modification, destination)
Contig12408_at	ATP-dependent protease	-3.03	5.10E-10	Protein fate (folding, modification, destination)
Contig14490_at	GTP-binding protein	-2.99	7.17E-09	Protein fate (folding, modification, destination)
Contig18354_at	Putative MRP protein (ATP/GTP-binding protein)	-2.97	4.20E-09	Protein fate (folding, modification, destination)

Contig6416_s_at	Putative GTP-binding protein	-2.94	4.57E-09	Protein fate (folding, modification, destination)
Contig12022_at	Signal recognition particle protein	-2.89	1.04E-09	Protein fate (folding, modification, destination)
HVSMEg0001H24r2_s_at	Tetratricopeptide repeat(TPR)-containing protein-like	-2.87	1.19E-07	Protein fate (folding, modification, destination)
Contig5365_s_at	Tetratricopeptide repeat (TPR)-containing protein	-2.83	4.82E-08	Protein fate (folding, modification, destination)
Contig14024_at	FKBP-type peptidyl-prolyl cis-trans isomerase	-2.82	7.37E-08	Protein fate (folding, modification, destination)
Contig6518_at	Putative Peptidyl-prolyl cis-trans isomerase	-2.8	5.95E-09	Protein fate (folding, modification, destination)
Contig4207_s_at	Putative DNAJ domain	-2.78	2.60E-06	Protein fate (folding, modification, destination)
Contig14258_at	Peptidyl-olyl cis-trans isomerase	-2.73	7.44E-10	Protein fate (folding, modification, destination)
Contig13689_at	Peptidyl-prolyl cis-trans isomerase	-2.64	7.79E-08	Protein fate (folding, modification, destination)
Contig9313_at	Chaperonin	-2.63	2.04E-09	Protein fate (folding, modification, destination)
Contig8370_at	CAAX amino terminal protease family protein	-2.6	2.69E-09	Protein fate (folding, modification, destination)
Contig5768_at	ATP-dependent Clp protease proteolytic subunit	-2.57	6.33E-07	Protein fate (folding, modification, destination)
Contig7069_at	Trigger factor-like protein	-2.57	1.38E-08	Protein fate (folding, modification, destination)
Contig6692_s_at	ATP-dependent Clp protease proteolytic subunit	-2.49	5.89E-09	Protein fate (folding, modification, destination)
Contig8086_at	DNAJ domain containing protein	-2.45	1.50E-09	Protein fate (folding, modification, destination)
Contig10790_at	Chaperonin 21 precursor	-2.42	1.07E-07	Protein fate (folding, modification, destination)
Contig12679_at	Putative X-prolyl aminopeptidase	-2.39	2.00E-08	Protein fate (folding, modification, destination)
Contig7254_s_at	DNAJ protein homolog	-2.38	1.64E-07	Protein fate (folding, modification, destination)
Contig4207_at	DNAJ heat shock N-terminal domain-containing protein	-2.37	1.09E-08	Protein fate (folding, modification, destination)
HVSMEl0002L06r2_at	Putative 20 kDa chaperonin	-2.31	4.98E-10	Protein fate (folding, modification, destination)
Contig12695_at	FKBP-type peptidyl-prolyl cis-trans isomerase	-2.28	5.61E-09	Protein fate (folding, modification, destination)
Contig14849_at	Peptidyl-prolyl cis-trans isomerase	-2.26	3.43E-09	Protein fate (folding, modification, destination)
Contig11928_at	FKBP-type peptidyl-prolyl cis-trans isomerase	-2.25	9.69E-10	Protein fate (folding, modification, destination)
Contig4497_at	ATP-dependent Clp protease proteolytic subunit (ClpR2)	-2.25	1.27E-07	Protein fate (folding, modification, destination)
Contig12257_at	ATP-dependent Clp protease ATP-binding subunit	-2.22	7.69E-09	Protein fate (folding, modification, destination)
Contig10271_at	Putative GTP-binding protein typA	-2.18	8.23E-08	Protein fate (folding, modification, destination)
rbah44m04_s_at	HSP100/ClpB	-2.13	9.34E-08	Protein fate (folding, modification, destination)
Contig2780_s_at	Asparaginyl endopeptidase	-2.12	2.70E-08	Protein fate (folding, modification, destination)
Contig1430_at	Ubiquitin-conjugating enzyme	-2.11	1.41E-08	Protein fate (folding, modification, destination)
HU02C06u_at	GTP-binding protein typA	-2.11	1.04E-05	Protein fate (folding, modification, destination)
Contig20885_at	5-AMP-activated protein kinase	-2.1	4.43E-09	Protein fate (folding, modification, destination)
Contig9199_at	Putative tetratricopeptide repeat(TPR)-containing protein	-2.09	5.12E-09	Protein fate (folding, modification, destination)
Contig9809_at	Bundle sheath defective protein	-2.06	2.51E-08	Protein fate (folding, modification, destination)

Contig8846_at	Chaperone protein DNAJ-related-like	-2.02	7.29E-08	Protein fate (folding, modification, destination)
Contig5121_s_at	ATP-dependent Clp protease proteolytic subunit 1	-2.01	4.40E-08	Protein fate (folding, modification, destination)
EBro04_SQ002_I16_s_at	Ubiquitin-conjugating enzyme OsUBC5a	-1.97	1.25E-08	Protein fate (folding, modification, destination)
Contig9976_at	ATP-dependent Clp protease proteolytic subunit (ClpR4)	-1.93	3.12E-09	Protein fate (folding, modification, destination)
Contig7279_at	Tetratricopeptide repeat(TPR)-containing protein-like	-1.89	1.43E-06	Protein fate (folding, modification, destination)
Contig6073_at	Farnesylated protein 3	-1.86	5.72E-08	Protein fate (folding, modification, destination)
HB31N03r_s_at	Putative ubiquitin-specific protease 3	-1.84	7.98E-08	Protein fate (folding, modification, destination)
Contig16354_at	TPR Domain containing protein	-1.83	3.58E-09	Protein fate (folding, modification, destination)
Contig14198_at	Putative DNAJ homolog subfamily protein	-1.82	2.80E-08	Protein fate (folding, modification, destination)
Contig8955_at	Farnesylated protein 2	-1.82	4.35E-07	Protein fate (folding, modification, destination)
Contig3906_s_at	Ubiquitin-conjugating enzyme E2-23 kDa	-1.8	1.21E-09	Protein fate (folding, modification, destination)
Contig2772_s_at	DNAK-type molecular chaperone	-1.76	7.07E-09	Protein fate (folding, modification, destination)
Contig5120_at	ATP-dependent Clp protease proteolytic subunit 3	-1.75	5.52E-07	Protein fate (folding, modification, destination)
Contig1262_at	Ubiquitin-specific protease 3	-1.74	4.69E-08	Protein fate (folding, modification, destination)
HV_CEb0016H24f_s_at	Putative peptidyl-prolycis-trans isomerase protein	-1.7	5.03E-07	Protein fate (folding, modification, destination)
Contig6571_at	FKBP-type peptidyl-prolyl cis-trans isomerase	-1.62	1.64E-08	Protein fate (folding, modification, destination)
HVSMEb0006O18r2_s_at	DNAJ protein homolog-like	-1.61	3.80E-08	Protein fate (folding, modification, destination)
Contig5149_at	ATP-dependent Clp protease proteolytic subunit	-1.6	8.40E-07	Protein fate (folding, modification, destination)
Contig14719_s_at	E2, ubiquitin-conjugating enzyme	-1.59	2.11E-06	Protein fate (folding, modification, destination)
Contig7575_at	Putative GTP-binding protein	-1.59	7.29E-07	Protein fate (folding, modification, destination)
Contig15056_at	Putative Prolyl Oligopeptidase homologue	-1.59	0	Protein fate (folding, modification, destination)
Contig10930_s_at	Peptidyl-prolyl cis-trans isomerase	-1.55	1.99E-07	Protein fate (folding, modification, destination)
Contig13147_at	Tetratricopeptide repeat domain 5-like protein	-1.55	1.41E-08	Protein fate (folding, modification, destination)
HV05A09u_s_at	Signal recognition particle 54 kDa subunit (Srp 54-3)	-1.55	4.33E-06	Protein fate (folding, modification, destination)
Contig12579_at	Putative CAAX amino terminal protease family protein	-1.52	1.73E-07	Protein fate (folding, modification, destination)
Contig8604_at	ATP-dependent Clp protease proteolytic subunit	-1.51	7.04E-07	Protein fate (folding, modification, destination)
Contig4825_at	Chaperone protein DNAJ-like	-1.48	3.84E-09	Protein fate (folding, modification, destination)
Contig13895_at	Putative subtilase	-1.47	1.06E-06	Protein fate (folding, modification, destination)
Contig18901_at	Tetratricopeptide repeat protein-like	-1.47	7.65E-09	Protein fate (folding, modification, destination)
Contig16181_at	Putative peptidyl-prolycis-trans isomerase protein	-1.46	8.17E-07	Protein fate (folding, modification, destination)
Contig4099_at	Signal recognition particle 54 kDa protein	-1.41	2.62E-07	Protein fate (folding, modification, destination)
Contig3840_at	Putative chaperonin 21	-1.4	7.64E-07	Protein fate (folding, modification, destination)
Contig3907_at	Ubiquitin-conjugating enzyme E2-23 kDa	-1.39	7.40E-08	Protein fate (folding, modification, destination)

Contig8440_at	F-box family protein-like	-1.39	6.22E-08	Protein fate (folding, modification, destination)
Contig8033_at	Putative CaLB (calcium-dependent lipid binding) protein	-1.37	2.38E-06	Protein fate (folding, modification, destination)
Contig19209_at	Peptidyl-prolyl cis-trans isomerase	-1.36	5.96E-06	Protein fate (folding, modification, destination)
Contig9488_at	GTP binding protein-like	-1.35	2.52E-06	Protein fate (folding, modification, destination)
Contig8623_s_at	Peptidase M48	-1.34	2.13E-07	Protein fate (folding, modification, destination)
Contig17120_at	Chaperone protein DNAJ	-1.33	3.77E-08	Protein fate (folding, modification, destination)
Contig9937_at	F-box protein-like	-1.31	3.43E-08	Protein fate (folding, modification, destination)
Contig8530_at	Signal peptide peptidase-like 3	-1.29	2.64E-07	Protein fate (folding, modification, destination)
Contig13883_at	DNAJ protein-like	-1.28	1.65E-07	Protein fate (folding, modification, destination)
Contig10649_at	Kelch repeat-containing F-box protein-like	-1.27	5.59E-06	Protein fate (folding, modification, destination)
HVSMEb0006O18r2_at	DnAJ protein homolog-like	-1.25	0	Protein fate (folding, modification, destination)
Contig10698_at	F-box protein FKF1/ADO3	-1.24	2.21E-05	Protein fate (folding, modification, destination)
HU05A05u_s_at	F-box domain and LRR containing protein	-1.22	1.48E-05	Protein fate (folding, modification, destination)
Contig8788_at	ATP-dependent Clp protease ATP-binding subunit clpA	-1.21	8.76E-06	Protein fate (folding, modification, destination)
Contig9747_at	Peptidyl-prolyl cis-trans isomerase	-1.19	7.08E-07	Protein fate (folding, modification, destination)
Contig86_at	Thiol protease aleurain	-1.18	6.08E-07	Protein fate (folding, modification, destination)
Contig11386_s_at	F-box domain containing protein	-1.17	2.96E-06	Protein fate (folding, modification, destination)
Contig12152_at	F-box protein family	-1.16	3.92E-06	Protein fate (folding, modification, destination)
Contig9998_at	Kelch repeat-containing F-box family protein	-1.15	1.14E-06	Protein fate (folding, modification, destination)
Contig21862_at	GTP-binding protein	-1.11	7.41E-07	Protein fate (folding, modification, destination)
Contig12351_at	Putative Kelch motif containing protein	-1.1	5.76E-07	Protein fate (folding, modification, destination)
Contig7921_s_at	Putative tetratricopeptide repeat (TPR)-containing protein	-1.09	4.09E-07	Protein fate (folding, modification, destination)
Contig3330_at	ATP-dependent clp protease	-1.09	0	Protein fate (folding, modification, destination)
Contig6788_at	Copper chaperone	-1.07	0	Protein fate (folding, modification, destination)
Contig13551_at	Membrane-anchored ubiquitin-fold protein 2 (NTGP5)	-1.05	1.37E-05	Protein fate (folding, modification, destination)
Contig1437_s_at	Ubiquitin-conjugating enzyme	-1.03	4.02E-06	Protein fate (folding, modification, destination)
Contig18871_at	PNGase (peptide N-glycanase)	-1.01	2.15E-06	Protein fate (folding, modification, destination)
Contig8713_at	Putative O-sialoglycoprotein endopeptidase	-1.01	2.52E-05	Protein fate (folding, modification, destination)
Contig3148_at	Glutamyl-tRNA reductase	-3.94	2.24E-10	Protein synthesis
Contig4439_at	Putative ribosomal protein S5	-3.91	2.31E-08	Protein synthesis
Contig5492_at	50S ribosomal protein L9	-3.86	2.09E-08	Protein synthesis
Contig5240_at	Putative 50S ribosomal protein L3	-3.78	5.76E-09	Protein synthesis
Contig6936_at	Putative ribosomal protein L13	-3.65	1.32E-09	Protein synthesis

HVSMEm0004N19r2_s_at	Ribosomal protein	-3.64	2.11E-10	Protein synthesis
Contig5659_at	Plastid-specific ribosomal protein 6	-3.6	4.35E-10	Protein synthesis
Contig466_at	Ribosomal protein L1	-3.57	5.49E-09	Protein synthesis
Contig4490_s_at	30S ribosomal protein S17, chloroplast precursor	-3.53	4.61E-10	Protein synthesis
rbags18k24_s_at	Ribosomal protein L17-like protein	-3.44	1.65E-07	Protein synthesis
Contig3659_at	Elongation factor Ts	-3.4	7.27E-09	Protein synthesis
HVSMEg0001I10f_s_at	Ribosomal protein L28-like	-3.35	2.24E-07	Protein synthesis
HA28J12r_s_at	Ribosomal protein L3 precursor	-3.32	4.34E-08	Protein synthesis
Contig5102_s_at	50S ribosomal protein L34	-3.3	5.72E-10	Protein synthesis
Contig3659_s_at	Elongation factor Ts	-3.29	1.07E-07	Protein synthesis
Contig2941_at	50S ribosomal protein l19	-3.25	1.43E-09	Protein synthesis
Contig10356_at	Ribosomal protein L17-like protein	-3.24	8.91E-09	Protein synthesis
Contig5526_s_at	Ribosomal protein precursor	-3.24	8.03E-10	Protein synthesis
Contig12793_at	50S ribosomal protein L12	-3.21	1.35E-08	Protein synthesis
Contig4873_s_at	Putative ribosomal protein	-3.21	3.80E-09	Protein synthesis
Contig9109_at	Putative ribosomal S1 protein	-3.18	1.07E-09	Protein synthesis
Contig9436_at	Putative plastid-specific ribosomal protein 2	-3.1	5.29E-08	Protein synthesis
Contig9437_at	50S ribosomal protein L29	-3.07	4.92E-08	Protein synthesis
Contig8437_at	50S ribosomal protein L27	-3.06	2.89E-10	Protein synthesis
Contig4380_s_at	Putative ribosomal protein L28	-3.04	9.85E-11	Protein synthesis
Contig8956_at	Putative plastid ribosomal protein S6	-3.01	1.11E-08	Protein synthesis
Contig9108_at	Putative ribosomal S1 protein	-2.98	2.17E-09	Protein synthesis
Contig3443_at	Elongation factor G	-2.94	9.72E-08	Protein synthesis
Contig5585_s_at	50S ribosomal protein L18	-2.93	8.31E-10	Protein synthesis
Contig5680_s_at	50S ribosomal protein L15	-2.93	1.27E-08	Protein synthesis
Contig8125_at	50S ribosomal protein L12-1	-2.93	4.61E-08	Protein synthesis
rbags18k24_x_at	Ribosomal protein L17-like protein	-2.79	9.03E-07	Protein synthesis
Contig4380_at	Putative ribosomal protein L28	-2.77	1.09E-09	Protein synthesis
Contig8436_s_at	50S ribosomal protein L27	-2.75	1.92E-08	Protein synthesis
HVSMEk0007B01r2_s_at	40S ribosomal protein S12	-2.74	2.81E-10	Protein synthesis
HV_CEa0008K08r2_s_at	Plastid ribosomal protein S10 precursor	-2.73	7.82E-09	Protein synthesis
Contig9274_at	50S ribosomal protein L35	-2.69	1.28E-08	Protein synthesis
Contig13073_at	Heat shock protein - like	-2.68	2.51E-09	Protein synthesis

Contig10834_at	Ribosomal large subunit pseudouridine synthase-like	-2.67	4.28E-08	Protein synthesis
Contig5004_at	Ribosome recycling factor	-2.66	2.35E-10	Protein synthesis
Contig6148_at	50S ribosomal protein L24	-2.66	6.94E-09	Protein synthesis
Contig9928_at	Heat shock factor protein hsf8-like	-2.66	1.27E-07	Protein synthesis
Contig3263_at	Elongation factor Tu	-2.61	5.49E-09	Protein synthesis
Contig5775_at	50S ribosomal protein L5	-2.54	2.32E-09	Protein synthesis
Contig7428_at	Translation initiation factor IF-2	-2.52	1.81E-08	Protein synthesis
Contig5776_s_at	50S ribosomal protein L5	-2.5	1.09E-08	Protein synthesis
Contig10093_s_at	9S ribosomal protein	-2.45	1.74E-08	Protein synthesis
HV08J24u_s_at	Putative methionyl-tRNA synthetase	-2.45	2.02E-09	Protein synthesis
Contig3853_s_at	50S ribosomal protein L31	-2.39	4.87E-08	Protein synthesis
HV05C10u_s_at	Plastid-specific 30S ribosomal protein 3	-2.39	4.12E-10	Protein synthesis
Contig14179_at	Putative methionyl-tRNA synthetase	-2.37	5.41E-09	Protein synthesis
Contig6675_at	Plastid-specific 30S ribosomal protein 3	-2.37	8.86E-09	Protein synthesis
Contig9274_s_at	50S ribosomal protein L35	-2.34	2.29E-09	Protein synthesis
Contig1943_s_at	Ribosomal protein L10	-2.33	2.23E-08	Protein synthesis
Contig20322_at	Protease Do-like 5	-2.31	1.47E-08	Protein synthesis
Contig4590_at	Ribosome-like protein	-2.28	3.25E-07	Protein synthesis
Contig9806_at	Chloroplast 30S ribosomal protein S10	-2.28	5.94E-10	Protein synthesis
Contig12718_at	Alanyl-tRNA synthetase	-2.27	5.66E-09	Protein synthesis
Contig18897_at	Peptidase of D1 protein	-2.25	6.66E-09	Protein synthesis
Contig3960_at	50S ribosomal protein L21	-2.24	1.15E-08	Protein synthesis
Contig17190_at	Putative heat shock protein	-2.23	7.26E-08	Protein synthesis
Contig428_at	30S ribosomal protein S1	-2.23	1.05E-07	Protein synthesis
Contig15445_at	Putative heat shock protein	-2.17	1.14E-09	Protein synthesis
Contig8638_at	Isoleucyl-tRNA synthetase	-2.16	2.53E-09	Protein synthesis
ChlorContig17_s_at	50S ribosomal protein L2	-2.1	5.88E-08	Protein synthesis
Contig16053_at	Glu-tRNA(Gln) amidotransferase subunit C	-2.07	1.96E-08	Protein synthesis
Contig5573_at	50S ribosomal protein L6	-2.05	1.18E-07	Protein synthesis
Contig9938_at	50S ribosomal protein L4	-2.04	1.53E-07	Protein synthesis
Contig8084_at	Putative plastid ribosomal protein L11	-1.93	6.10E-07	Protein synthesis
MitoContig7_at	Ribosomal protein L2	-1.93	8.61E-07	Protein synthesis
Contig11739_at	Ribosomal protein S8	-1.92	2.63E-05	Protein synthesis

Contig14141_s_at	Glutamyl-tRNA(Gln) amidotransferase, B subunit	-1.88	6.53E-09	Protein synthesis
Contig6501_s_at	Glycyl tRNA synthetase	-1.85	2.29E-07	Protein synthesis
Contig8405_at	Phenylalanyl-tRNA synthetase class IIc family protein	-1.85	2.38E-08	Protein synthesis
HV09A09u_s_at	Eukaryotic translation initiation factor 5A	-1.83	2.20E-07	Protein synthesis
Contig2580_5_s_at	Translation initiation factor 5A	-1.79	1.76E-05	Protein synthesis
Contig9936_at	Elongation factor TS	-1.79	5.98E-07	Protein synthesis
Contig16906_at	Aspartyl aminopeptidase	-1.77	2.11E-08	Protein synthesis
Contig20187_s_at	Serine carboxypeptidase	-1.77	8.56E-09	Protein synthesis
Contig11882_at	Ribosomal protein S3	-1.75	9.01E-05	Protein synthesis
Contig14141_at	Glutamyl-tRNA(Gln) amidotransferase	-1.72	3.80E-07	Protein synthesis
Contig12345_at	Putative asparaginyl-tRNA synthetase	-1.67	6.45E-08	Protein synthesis
Contig13597_at	Peptide chain release factor 1	-1.65	7.34E-06	Protein synthesis
Contig848_at	Eukaryotic initiation factor subunit	-1.61	5.01E-09	Protein synthesis
Contig16917_at	Putative leucyl-tRNA synthetase	-1.6	5.55E-07	Protein synthesis
Contig5708_at	Ribosomal protein S31	-1.58	4.59E-08	Protein synthesis
Contig10834_s_at	Ribosomal large subunit pseudouridine synthase-like	-1.57	7.01E-06	Protein synthesis
Contig17155_at	Elongation factor P	-1.51	5.65E-07	Protein synthesis
Contig22285_at	Putative threonyl-tRNA synthetase	-1.48	1.32E-07	Protein synthesis
Contig5680_at	Plastid ribosomal protein CL15	-1.46	7.17E-08	Protein synthesis
Contig10183_at	tRNA-dihydrouridine synthase A	-1.45	5.51E-07	Protein synthesis
Contig1947_at	Ribosomal protein L10	-1.45	8.58E-07	Protein synthesis
Contig11738_at	Ribosomal protein L16	-1.44	2.47E-05	Protein synthesis
Contig13379_at	Putative tryptophanyl-tRNA synthetase	-1.36	2.05E-08	Protein synthesis
Contig4981_s_at	Putative ribosomal protein	-1.31	2.09E-06	Protein synthesis
HVSMEn0023M22r2_at	Serine carboxypeptidase I precursor	-1.31	9.28E-06	Protein synthesis
Contig2580_3_s_at	Translation initiation factor 5A	-1.3	3.48E-07	Protein synthesis
Contig26034_at	Seryl-tRNA synthetase family protein	-1.28	4.91E-07	Protein synthesis
Contig4983_s_at	Ribosomal protein	-1.28	3.06E-06	Protein synthesis
Contig5141_at	Putative heat shock protein	-1.27	9.83E-07	Protein synthesis
Contig4982_at	Ribosomal protein	-1.26	0	Protein synthesis
HA01L11u_s_at	Putative 60S ribosomal protein L30	-1.26	2.46E-05	Protein synthesis
Contig7597_at	Glu-tRNA(Gln) amidotransferase subunit A	-1.25	8.19E-06	Protein synthesis
Contig17131_at	Peptide chain release factor 2 family protein	-1.24	6.49E-07	Protein synthesis

Contig4647_s_at	Putative ribosome biogenesis regulatory protein	-1.24	1.01E-05	Protein synthesis
Contig20645_at	Putative aspartyl-tRNA synthetase	-1.23	1.14E-06	Protein synthesis
Contig11306_at	101 kDa heat shock protein	-1.22	2.69E-08	Protein synthesis
HZ58F11r_at	Protein synthesis inhibitor II (Ribosome-inactivating protein II)	-1.21	1.87E-05	Protein synthesis
Contig827_x_at	Putative elongation factor 2	-1.2	1.15E-05	Protein synthesis
rbaal35o24_at	Putative heat shock protein	-1.2	6.13E-08	Protein synthesis
Contig10814_at	Putative tyrosyl-tRNA synthetase	-1.18	2.04E-05	Protein synthesis
HB05P23r_at	Peptidyl-tRNA hydrolase-like	-1.17	9.99E-06	Protein synthesis
Contig17549_at	50S ribosomal protein L18 family	-1.15	5.01E-07	Protein synthesis
HV08I08u_at	Glycyl-tRNA synthetase 2	-1.13	1.84E-06	Protein synthesis
Contig4555_at	Serine carboxypeptidase II-3	-1.1	1.27E-05	Protein synthesis
Contig7566_at	Putative prolyl-tRNA synthetase	-1.1	1.52E-07	Protein synthesis
Contig25153_at	Putative translation releasing factor2	-1.09	7.08E-06	Protein synthesis
HY09G23u_s_at	Elongation factor 1-beta	-1.07	2.54E-05	Protein synthesis
EBem09_SQ003_P12_s_at	Translation initiation factor 5A	-1.06	1.03E-06	Protein synthesis
Contig11235_at	Putative ribosomal protein I	-1.02	1.44E-05	Protein synthesis
Contig17974_at	Metal ion binding protein	-4.48	4.70E-11	Protein with binding function or cofactor requirement
Contig11681_at	Putative FK506-binding protein	-2.2	2.67E-07	Protein with binding function or cofactor requirement
Contig8060_at	Putative relA/spoT homologous protein RSH2	-1.83	7.95E-10	Protein with binding function or cofactor requirement
Contig3745_at	Copper binding - like protein	-1.74	1.48E-07	Protein with binding function or cofactor requirement
HV_CEa0008C11r2_at	SOUL heme-binding protein-like	-1.7	5.70E-07	Protein with binding function or cofactor requirement
Contig5030_at	Ferrochelatase II	-1.57	6.55E-07	Protein with binding function or cofactor requirement
Contig15129_at	SOUL heme-binding protein-like	-1.5	9.72E-09	Protein with binding function or cofactor requirement
Contig10313_at	Putative crp1 (cysteine rich) protein	-1.45	1.17E-08	Protein with binding function or cofactor requirement
Contig23628_at	Putative heme binding protein	-1.3	2.02E-07	Protein with binding function or cofactor requirement
Contig10360_at	Putative heme binding protein 2	-1.24	5.39E-06	Protein with binding function or cofactor requirement
Contig20771_at	Biotin holocarboxylase synthetase	-1.2	4.24E-05	Protein with binding function or cofactor requirement
Contig3533_at	Seed storage protein	-4.83	5.36E-10	Storage
Contig18313_at	Starch associated protein R1	-1.72	1.16E-07	Storage
Contig2715_s_at	Ferritin	-1.43	1.57E-05	Storage
Contig4459_at	Seed imbibition protein	-1.3	2.29E-06	Storage
Contig11464_at	Alkaline alpha-galactosidase seed imbibition protein	-1.03	3.71E-05	Storage
Contig15039_at	Patatin-like protein	-1.02	1.64E-05	Storage

Contig8578_s_at	Basic helix-loop-helix (bHLH) family protein	-4.59	2.72E-09	Transcription
Contig18051_at	Myb-related protein-like	-4.25	1.39E-10	Transcription
Contig8578_at	Basic helix-loop-helix (bHLH) family protein	-4.16	1.93E-10	Transcription
EBem09_SQ004_B23_s_at	CCCH-type zinc finger protein-like	-3.71	4.34E-10	Transcription
Contig7360_at	CONSTANS-like protein (CO3)	-3.63	1.72E-08	Transcription
Contig12973_at	Chloroplast RNA-binding protein	-3.59	8.83E-08	Transcription
Contig5988_at	Putative ribonucleoprotein	-3.49	3.55E-09	Transcription
Contig11109_at	Putative nascent polypeptide associated complex alpha chain	-3.41	2.00E-10	Transcription
Contig12233_at	GATA zinc finger protein	-3.4	4.30E-12	Transcription
Contig8775_at	Putative mRNA binding protein	-3.27	2.87E-09	Transcription
Contig16848_at	Putative bHLH transcription factor	-3.19	6.95E-09	Transcription
Contig4797_at	Forkhead-associated domain-containing protein	-3.14	1.37E-09	Transcription
Contig15617_at	CBF1-like protein BCBF1	-3.11	6.11E-11	Transcription
Contig13717_at	Dof zinc finger protein	-3.1	2.61E-11	Transcription
Contig4432_at	Putative 29 kDa ribonucleoprotein A	-3.03	2.91E-08	Transcription
Contig7241_at	ATP-dependent RNA helicase	-2.91	1.08E-07	Transcription
Contig6600_at	Pentatricopeptide (PPR) repeat-containing protein	-2.84	1.14E-09	Transcription
Contig7834_at	RNA-binding protein	-2.82	2.07E-09	Transcription
Contig1760_s_at	RNA binding protein	-2.81	1.45E-08	Transcription
Contig13672_at	RNA recognition motif (RRM)-containing protein-like	-2.78	1.48E-06	Transcription
Contig3552_s_at	O-methyltransferase	-2.77	2.68E-06	Transcription
Contig8362_at	MTERF family protein	-2.76	1.49E-10	Transcription
Contig12158_at	Putative ZF-HD homeobox protein	-2.75	1.03E-08	Transcription
rbasd3a10_s_at	Cp31AHv	-2.72	2.88E-08	Transcription
Contig10976_at	Pentatricopeptide (PPR) repeat-containing protein-like protein	-2.7	1.03E-07	Transcription
Contig19707_at	SWIB/MDM2 domain protein	-2.7	4.67E-09	Transcription
Contig15271_at	PPR-repeat protein	-2.69	1.04E-09	Transcription
Contig22244_at	AP2 domain transcription factor	-2.68	2.71E-09	Transcription
Contig25725_at	Putative nucleoid DNA-binding protein cnd41	-2.67	1.16E-08	Transcription
Contig8597_at	Chloroplast RNA-binding protein cp33	-2.64	1.94E-09	Transcription
Contig14342_at	Putative nucleoid DNA-binding protein cnd41	-2.62	6.85E-09	Transcription
Contig17195_at	Pentatricopeptide repeat protein	-2.59	1.21E-09	Transcription
Contig7360_s_at	CONSTANS-like protein (CO3)	-2.56	3.40E-09	Transcription

Contig5393_at	LIM transcription factor homolog	-2.53	1.17E-08	Transcription
Contig13417_at	RRM-containing protein	-2.5	8.75E-10	Transcription
Contig12587_at	DEAD/DEAH box RNA helicase protein	-2.48	3.74E-10	Transcription
Contig5881_s_at	Putative transcription regulator	-2.41	3.70E-08	Transcription
HVSMEb0004M17r2_at	Putative Myb-related protein Zm38	-2.41	3.07E-07	Transcription
Contig3835_s_at	Zinc finger protein	-2.4	6.18E-09	Transcription
Contig4948_s_at	Myb family transcription factor	-2.36	1.91E-09	Transcription
Contig17914_at	FT-like protein	-2.35	4.12E-07	Transcription
Contig13989_at	Dof zinc finger protein	-2.33	1.23E-09	Transcription
Contig9000_at	Putative chloroplast nucleoid DNA-binding protein cnd41	-2.32	1.70E-09	Transcription
Contig6640_at	CRM family member	-2.29	9.72E-09	Transcription
Contig10555_at	MYB transcription factor	-2.26	3.90E-09	Transcription
Contig13242_at	Pentatricopeptide	-2.17	1.84E-09	Transcription
Contig3548_at	O-methyltransferase	-2.17	3.86E-06	Transcription
Contig15937_at	Zinc finger (C3HC4-type RING finger) family protein	-2.1	4.19E-09	Transcription
Contig7429_s_at	Putative bZIP DNA-binding protein	-2.09	1.03E-09	Transcription
Contig11081_at	HAP3-like transcriptional-activator	-2.08	8.41E-10	Transcription
Contig5815_at	Putative snRNP splicing factor-related	-2.05	1.20E-08	Transcription
Contig11363_at	WRKY DNA binding domain containing protein	-2.04	7.91E-09	Transcription
Contig10233_s_at	Putative DNA-binding protein p24	-2.01	2.35E-07	Transcription
Contig15391_at	Transcription factor RAU1	-1.96	1.38E-07	Transcription
Contig15309_at	AP2/EREBP transcription factor BABY BOOM2	-1.94	8.32E-09	Transcription
Contig471_s_at	Glycine-rich RNA binding protein	-1.94	4.56E-06	Transcription
Contig8147_at	Auxin response transcription factor(ARF6)	-1.93	2.34E-06	Transcription
Contig8750_s_at	GATA zinc finger protein	-1.9	5.83E-09	Transcription
Contig8132_s_at	Myb family transcription factor	-1.89	1.27E-08	Transcription
Contig4580_at	Pspzf zinc finger protein-like	-1.88	3.01E-08	Transcription
Contig7471_at	Putative Myb factor protein	-1.85	1.16E-08	Transcription
Contig9445_at	DEAD-box ATP-dependent RNA helicase	-1.83	5.93E-07	Transcription
Contig10303_s_at	Sterol-regulatory element protease containing protein	-1.79	5.89E-07	Transcription
Contig11226_s_at	Glycine-rich RNA-binding protein-like	-1.78	1.11E-08	Transcription
Contig26600_at	Pentatricopeptide (PPR) repeat-containing protein	-1.78	1.07E-08	Transcription
Contig8369_at	Transcription factor AP2D23-like	-1.78	4.92E-08	Transcription

Contig12033_at	Zinc finger transcription factor WRKY1	-1.76	2.22E-09	Transcription
Contig5688_at	CCCH-type zinc finger protein-like	-1.76	6.61E-08	Transcription
Contig10986_at	Putative transcription factor	-1.74	3.59E-06	Transcription
Contig3353_s_at	Putative NAC transcription factor	-1.72	8.15E-06	Transcription
Contig3873_at	LHY protein	-1.72	6.78E-08	Transcription
Contig6075_at	Zinc finger (C3HC4-type RING finger) family protein	-1.72	0.01	Transcription
Contig10078_at	Putative Transcription initiation factor IIE	-1.71	1.43E-08	Transcription
Contig1966_at	Putative DNA-binding protein	-1.69	7.48E-07	Transcription
Contig25611_at	Putative pentatricopeptide (PPR) repeat-containing protein	-1.68	5.08E-06	Transcription
Contig4911_at	O-methyltransferase	-1.68	0	Transcription
Contig15023_at	Pentatricopeptide repeat protein	-1.67	1.07E-08	Transcription
Contig6526_at	Putative EREBP-like protein	-1.67	2.73E-08	Transcription
Contig16357_at	Zinc finger (C3HC4-type RING finger) family protein	-1.66	2.59E-08	Transcription
HVSMEa0019D10r2_at	CONSTANS-like protein CO5	-1.66	1.99E-08	Transcription
Contig2830_at	Zinc finger (C3HC4-type RING finger) family protein	-1.65	3.29E-08	Transcription
Contig3835_at	Zinc finger protein ZFP-like	-1.65	7.32E-06	Transcription
Contig4780_at	Probable zinc finger protein	-1.63	4.76E-07	Transcription
Contig6484_at	Putative NAC domain protein NAC1	-1.63	3.35E-07	Transcription
Contig8533_at	CCAAT-box transcription factor	-1.61	3.20E-07	Transcription
Contig10280_at	PHD zinc finger protein	-1.6	5.29E-08	Transcription
Contig4517_at	MADS box protein VRT-2	-1.6	3.21E-09	Transcription
HVSMEh0088I08r2_s_at	Glycine-rich RNA-binding protein 2	-1.6	2.07E-06	Transcription
Contig18280_at	Putative transcription factor OsGLK2	-1.59	4.92E-09	Transcription
Contig23344_at	Putative DNA binding domain containing protein	-1.57	7.60E-07	Transcription
Contig26555_at	Mitochondrial transcription termination factor-like protein	-1.57	6.04E-07	Transcription
Contig2821_at	Bas1 protein	-1.57	3.86E-07	Transcription
Contig8575_s_at	Putative pentatricopeptide (PPR) repeat-containing protein	-1.57	2.22E-07	Transcription
Contig8667_at	RNA binding protein	-1.57	1.64E-08	Transcription
Contig8872_at	CONSTANS-like protein CO6	-1.56	3.83E-08	Transcription
Contig15334_at	BZIP transcription factor	-1.55	4.90E-08	Transcription
Contig16255_s_at	Telomere binding protein TBP1	-1.55	1.94E-08	Transcription
HVSMEg0003O11r2_at	Putative transcription factor	-1.55	5.82E-08	Transcription
Contig13884_at	Putative RNA-binding protein	-1.54	2.42E-06	Transcription

Contig7395_at	RNA-binding protein-like protein	-1.53	2.21E-08	Transcription
Contig23791_at	Transcription factor-like	-1.51	4.65E-06	Transcription
Contig5840_at	Protein SUPPRESSOR OF GENE SILENCING 3 homolog	-1.51	3.41E-07	Transcription
Contig9659_at	Putative tubby related protein	-1.5	3.15E-09	Transcription
Contig19398_at	Helix-loop-helix DNA-binding domain containing protein	-1.47	6.41E-07	Transcription
rbaak22p05_s_at	Transcriptional coactivator - like protein	-1.46	2.83E-06	Transcription
HVSMEc0005D12r2_s_at	Putative bHLH transcription factor	-1.45	7.62E-07	Transcription
Contig11226_at	Glycine-rich RNA-binding protein-like	-1.44	1.55E-05	Transcription
Contig12995_at	Putative zinc finger protein	-1.43	5.23E-07	Transcription
Contig22282_at	Pentatricopeptide	-1.42	8.20E-06	Transcription
Contig22529_at	DNA-directed RNA polymerase alpha chain	-1.41	3.70E-05	Transcription
Contig7243_at	Probable WRKY transcription factor 20	-1.4	5.55E-08	Transcription
HA11C13u_s_at	Putative transcription factor BTF3	-1.39	4.32E-07	Transcription
Contig20074_at	RNA recognition motif (RRM)-containing protein	-1.37	7.89E-07	Transcription
Contig22334_at	S1 RNA-binding domain-containing protein	-1.37	3.13E-08	Transcription
Contig17566_at	Putative single-strand DNA binding protein	-1.36	1.24E-06	Transcription
Contig3041_at	Glycine-rich RNA-binding protein 2	-1.36	2.64E-06	Transcription
Contig5214_at	Zinc finger CCCH domain-containing protein	-1.36	1.11E-07	Transcription
rbaal15j13_s_at	Susiba2	-1.36	2.29E-07	Transcription
Contig12796_at	Maf family protein	-1.35	4.09E-07	Transcription
Contig15705_at	MYB transcription factor	-1.35	5.73E-08	Transcription
Contig8916_at	RNA Polymerase II subunit 14.5 kD-like protein	-1.35	1.75E-06	Transcription
Contig13988_at	Nodule inception protein-like	-1.34	1.16E-06	Transcription
Contig15402_at	DNA-directed RNA polymerase	-1.34	1.20E-06	Transcription
Contig19858_at	ZF-HD homeobox protein	-1.33	8.49E-07	Transcription
Contig21278_at	Pentatricopeptide (PPR) repeat-containing protein	-1.33	2.32E-06	Transcription
Contig7245_s_at	SET domain containing protein	-1.33	1.97E-05	Transcription
Contig15335_s_at	BZIP transcription factor ABI5 (ABI5)	-1.32	1.37E-07	Transcription
Contig8132_at	Myb family transcription factor	-1.32	1.09E-06	Transcription
Contig5165_at	Putative RNA polymerase I, II and III 16.5 kDa subunit	-1.31	1.33E-06	Transcription
Contig4662_at	RNA polymerase II subunit	-1.31	2.93E-05	Transcription
Contig12953_at	RNA Polymerase II subunit	-1.3	2.58E-07	Transcription
HR01I06u_at	Zinc finger protein-like	-1.3	1.51E-06	Transcription

Z48624_x_at	Glycine-rich RNA binding protein	-1.3	1.59E-05	Transcription
Contig11227_at	Glycine-rich RNA-binding protein-like	-1.29	5.19E-05	Transcription
Contig20361_at	Putative bHLH transcription factor	-1.29	2.97E-06	Transcription
HVSMEg0001I20f_x_at	Putative CCR4-NOT transcription complex subunit	-1.29	1.56E-07	Transcription
rbags14j23_s_at	SET domain containing protein	-1.29	5.27E-07	Transcription
Contig7585_at	RNA polymerase Rpb5	-1.27	1.12E-06	Transcription
Contig15369_at	Putative bZIP protein HY5	-1.25	0	Transcription
Contig3135_at	Nuclear transcription factor SLN1	-1.25	2.32E-06	Transcription
Contig14677_at	Zinc finger POZ domain protein	-1.24	5.02E-08	Transcription
Contig2314_at	Lil3 protein	-1.24	3.66E-07	Transcription
Contig14119_at	MYB family transcription factor	-1.21	2.60E-06	Transcription
Contig3875_s_at	Putative LHY protein	-1.21	1.14E-06	Transcription
rbaal14f06_s_at	MADS-box protein 5	-1.21	5.24E-05	Transcription
Contig11996_at	Putative nucleoid DNA-binding protein cnd41	-1.2	0	Transcription
HZ51F23r_at	Zinc finger, C3HC4 type domain containing protein	-1.18	1.71E-05	Transcription
Contig12449_at	Putative homeodomain protein	-1.17	2.81E-07	Transcription
Contig9684_at	Putative PRLI-interacting factor G	-1.17	3.95E-07	Transcription
Contig4462_at	OCS-element binding factor 1 (OCSBF-1)	-1.16	1.21E-06	Transcription
Contig14905_s_at	PRLI-interacting factor L	-1.14	2.03E-07	Transcription
Contig7925_at	Myb family transcription factor	-1.14	4.98E-07	Transcription
Contig14220_at	Putative Myb-like DNA-binding protein	-1.13	6.39E-08	Transcription
Contig9191_at	Zinc finger A20 and AN1 domain-containing stress-associated protein	-1.13	2.73E-07	Transcription
Contig16560_at	Zinc finger (CCCH-type) protein-like	-1.12	8.34E-06	Transcription
Contig4579_s_at	Argonaute-like protein	-1.12	2.75E-05	Transcription
Contig10348_at	Putative transcription factor	-1.11	1.24E-05	Transcription
Contig17530_at	Putative transcription factor X1	-1.1	6.90E-07	Transcription
Contig17701_at	Leaf development protein Argonaute	-1.1	4.12E-06	Transcription
Contig13620_at	Finger protein pcp1-like	-1.09	2.74E-06	Transcription
Contig4263_at	Putative RNA binding protein	-1.09	7.03E-07	Transcription
Contig8575_at	Putative pentatricopeptide (PPR) repeat-containing protein	-1.09	6.18E-07	Transcription
Contig13204_at	RING zinc finger protein	-1.08	7.99E-07	Transcription
Contig5213_at	Putative RNA-binding protein	-1.08	2.16E-06	Transcription
Contig8860_at	DEAD-box ATP-dependent RNA helicase	-1.08	1.65E-05	Transcription

Contig16618_at	Putative zinc-finger protein	-1.07	2.15E-06	Transcription
Contig11869_at	DNA-directed RNA polymerase	-1.05	5.00E-07	Transcription
Contig17582_at	Putative transcription factor	-1.05	1.80E-06	Transcription
Contig24321_at	N-acetyltransferase and Transcription factor-like protein	-1.05	0	Transcription
Contig6946_at	Putative MCB2 protein	-1.05	0	Transcription
Contig20055_at	DNA-binding protein	-1.04	2.47E-05	Transcription
Contig64_at	RNA binding protein	-1.03	2.55E-05	Transcription
Contig7464_at	Chloroplast nucleoid DNA-binding protein-like	-1.03	1.29E-05	Transcription
Contig8817_at	Putative zinc finger protein	-1.03	4.32E-06	Transcription
rbags1n23_s_at	Transcriptional regulators of NagC/XylR (ROK)-like	-1.03	5.09E-06	Transcription
rbaal33f21_s_at	Putative ethylene-responsive transcriptional coactivator	-1	5.55E-07	Transcription
EBro07_SQ003_G24_s_at	None	-5.34	8.64E-11	Unclassified
HK05P14r_s_at	None	-4.69	8.71E-08	Unclassified
Contig2082_x_at	None	-4.63	4.70E-08	Unclassified
Contig7914_at	None	-4.08	5.13E-09	Unclassified
Contig26439_at	None	-4.05	2.88E-09	Unclassified
Contig11540_s_at	None	-3.98	1.72E-09	Unclassified
Contig17058_s_at	None	-3.79	7.12E-09	Unclassified
EBro07_SQ002_G23_s_at	None	-3.74	1.71E-09	Unclassified
Contig2894_s_at	None	-3.7	5.83E-09	Unclassified
Contig25076_at	None	-3.6	3.01E-11	Unclassified
HA10M12u_s_at	None	-3.6	5.66E-09	Unclassified
Contig21540_at	None	-3.56	3.98E-09	Unclassified
Contig8390_s_at	None	-3.55	5.49E-09	Unclassified
HVSMEl0010I15r2_s_at	None	-3.55	2.57E-07	Unclassified
Contig9923_at	None	-3.53	1.74E-07	Unclassified
EBpi07_SQ002_O11_s_at	None	-3.48	1.89E-08	Unclassified
HVSMEf0013I09r2_at	None	-3.47	2.29E-11	Unclassified
rbasd23b03_s_at	None	-3.41	1.00E-08	Unclassified
Contig24154_at	None	-3.36	5.13E-11	Unclassified
HV_CEa0001D22f_at	None	-3.3	4.12E-10	Unclassified
Contig13088_at	None	-3.29	5.48E-11	Unclassified
Contig15252_at	None	-3.29	1.36E-09	Unclassified

Contig20426_at	None	-3.28	3.52E-10	Unclassified
HO10P07S_at	None	-3.28	4.83E-08	Unclassified
Contig9922_s_at	None	-3.26	4.86E-07	Unclassified
Contig9570_s_at	None	-3.22	7.80E-08	Unclassified
Contig9042_s_at	None	-3.21	2.40E-09	Unclassified
HK03F11r_at	None	-3.21	2.93E-10	Unclassified
rbaal1l19_s_at	None	-3.13	1.53E-11	Unclassified
Contig18255_at	None	-3.11	1.21E-09	Unclassified
Contig19768_at	None	-3.11	1.90E-08	Unclassified
Contig12648_at	None	-3.08	8.37E-08	Unclassified
Contig8466_at	None	-3.07	2.39E-08	Unclassified
Contig11540_at	None	-3.02	7.19E-09	Unclassified
rbaal11m15_at	None	-3.02	4.16E-09	Unclassified
Contig17657_at	None	-3	1.27E-08	Unclassified
Contig10125_s_at	None	-2.98	2.31E-08	Unclassified
Contig10204_s_at	None	-2.96	1.04E-09	Unclassified
Contig13719_at	None	-2.95	1.66E-10	Unclassified
Contig21971_at	None	-2.95	6.18E-09	Unclassified
HZ45N21r_at	None	-2.93	5.62E-10	Unclassified
HVSMEa0005E13r2_s_at	None	-2.9	1.13E-08	Unclassified
Contig19893_at	None	-2.89	4.01E-10	Unclassified
EBes01_SQ002_E05_at	None	-2.88	3.53E-10	Unclassified
HVSMEb0014B13r2_at	None	-2.87	2.57E-08	Unclassified
HV_CEa0010K11f_x_at	None	-2.86	6.37E-07	Unclassified
Contig5949_s_at	None	-2.83	1.14E-08	Unclassified
basd23g06_s_at	None	-2.8	3.63E-07	Unclassified
Contig14203_s_at	None	-2.79	8.98E-08	Unclassified
Contig21096_at	None	-2.76	3.39E-07	Unclassified
Contig3834_at	None	-2.76	6.21E-08	Unclassified
EBpi05_SQ002_I18_s_at	None	-2.76	2.48E-09	Unclassified
EBpi05_SQ003_H04_at	None	-2.72	2.22E-09	Unclassified
HV_CEa0016F11f_at	None	-2.72	1.51E-09	Unclassified
Contig11524_s_at	None	-2.71	1.60E-07	Unclassified

HS06C04u_s_at	None	-2.71	2.38E-08	Unclassified
Contig16172_at	None	-2.7	3.81E-10	Unclassified
Contig18687_at	None	-2.66	1.06E-08	Unclassified
rbaal1b14_s_at	None	-2.65	5.38E-09	Unclassified
HO04H12S_s_at	None	-2.64	2.90E-08	Unclassified
rbaal33e01_s_at	None	-2.63	4.92E-09	Unclassified
HVSMEb0001J09r2_s_at	None	-2.62	6.23E-10	Unclassified
Contig15031_at	None	-2.61	7.37E-10	Unclassified
Contig9774_s_at	None	-2.61	5.37E-08	Unclassified
Contig955_s_at	None	-2.6	1.16E-08	Unclassified
rbaal38f16_at	None	-2.6	3.65E-08	Unclassified
Contig20887_s_at	None	-2.59	1.86E-09	Unclassified
Contig2193_s_at	None	-2.59	9.48E-07	Unclassified
Contig7052_s_at	None	-2.57	4.67E-09	Unclassified
Contig9042_x_at	None	-2.57	1.71E-10	Unclassified
Contig11413_at	None	-2.56	4.20E-11	Unclassified
Contig4034_at	None	-2.5	6.36E-10	Unclassified
Contig22734_at	None	-2.49	8.25E-09	Unclassified
HV_CEb0022B03r2_s_at	None	-2.49	8.08E-09	Unclassified
HVSMEm0007K09r2_at	None	-2.48	8.56E-09	Unclassified
Contig17166_at	None	-2.44	1.43E-09	Unclassified
Contig20602_at	None	-2.44	1.86E-09	Unclassified
Contig15941_at	None	-2.41	4.01E-11	Unclassified
Contig22781_at	None	-2.4	9.26E-08	Unclassified
Contig9239_s_at	None	-2.4	7.54E-08	Unclassified
Contig15140_at	None	-2.39	1.78E-09	Unclassified
Contig8052_at	None	-2.39	2.05E-06	Unclassified
Contig20346_at	None	-2.38	1.58E-07	Unclassified
HM01J06w_s_at	None	-2.37	2.45E-09	Unclassified
rbah25c12_s_at	None	-2.37	3.44E-09	Unclassified
HVSMEl0012A13f_at	None	-2.36	1.03E-05	Unclassified
S0000700012G10F2_at	None	-2.36	1.72E-07	Unclassified
HVSMEc0006M13r2_s_at	None	-2.34	8.09E-09	Unclassified

Contig15590_at	None	-2.32	4.01E-07	Unclassified
Contig13801_s_at	None	-2.31	5.07E-09	Unclassified
Contig10600_s_at	None	-2.3	7.01E-08	Unclassified
HVSMEc0003A01f_at	None	-2.29	2.18E-06	Unclassified
Contig18081_at	None	-2.28	6.18E-08	Unclassified
Contig8833_at	None	-2.28	4.75E-08	Unclassified
Contig4855_s_at	None	-2.27	3.70E-08	Unclassified
rbaal1f12_s_at	None	-2.27	2.71E-09	Unclassified
Contig9688_s_at	None	-2.24	4.88E-09	Unclassified
HVSMEb0005B20r2_s_at	None	-2.23	2.68E-07	Unclassified
Contig12100_at	None	-2.22	1.93E-07	Unclassified
Contig25262_at	None	-2.21	4.40E-10	Unclassified
Contig13801_at	None	-2.2	1.23E-07	Unclassified
Contig9713_s_at	None	-2.2	4.19E-09	Unclassified
baak20o05_s_at	None	-2.19	7.13E-08	Unclassified
Contig24772_at	None	-2.19	2.43E-07	Unclassified
Contig6817_at	None	-2.19	1.96E-07	Unclassified
Contig7004_at	None	-2.18	1.50E-08	Unclassified
EBma03_SQ003_D20_at	None	-2.18	1.74E-07	Unclassified
HVSMEa0012K02r2_at	None	-2.18	2.77E-09	Unclassified
Contig25828_at	None	-2.17	1.14E-08	Unclassified
HV_CEa0010M13r2_s_at	None	-2.17	7.57E-08	Unclassified
Contig13447_s_at	None	-2.15	8.23E-09	Unclassified
HV08O06r_s_at	None	-2.14	3.13E-09	Unclassified
Contig21858_at	None	-2.13	1.00E-06	Unclassified
HY08M06u_x_at	None	-2.13	2.23E-08	Unclassified
Contig22530_at	None	-2.12	3.89E-10	Unclassified
Contig7694_at	None	-2.12	7.95E-10	Unclassified
Contig11413_s_at	None	-2.1	7.93E-10	Unclassified
Contig12460_at	None	-2.1	7.48E-07	Unclassified
EBro03_SQ008_F20_at	None	-2.1	2.12E-07	Unclassified
Contig15707_at	None	-2.09	9.81E-07	Unclassified
Contig4016_s_at	None	-2.08	4.78E-07	Unclassified

EBma01_SQ005_J20_at	None	-2.08	6.02E-08	Unclassified
Contig9758_s_at	None	-2.07	4.13E-07	Unclassified
EBro05_SQ003_E05_at	None	-2.07	2.52E-08	Unclassified
Contig22849_at	None	-2.06	7.53E-09	Unclassified
rbaal24c05_s_at	None	-2.06	5.14E-08	Unclassified
Contig15499_at	None	-2.05	2.29E-07	Unclassified
Contig24835_at	None	-2.03	1.26E-08	Unclassified
Contig24309_at	None	-2.03	6.42E-05	Unclassified
Contig8389_s_at	None	-2.01	5.74E-09	Unclassified
HP01K13T_at	None	-2	3.24E-10	Unclassified
Contig17966_s_at	None	-1.99	3.83E-08	Unclassified
Contig3553_at	None	-1.99	7.89E-07	Unclassified
Contig13323_at	None	-1.98	1.04E-08	Unclassified
Contig25428_at	None	-1.98	1.83E-07	Unclassified
Contig8526_at	None	-1.98	3.19E-08	Unclassified
Contig10140_s_at	None	-1.97	5.08E-07	Unclassified
Contig19204_at	None	-1.97	4.71E-08	Unclassified
Contig25428_x_at	None	-1.96	4.85E-08	Unclassified
HVSMEh0086M12r2_s_at	None	-1.96	1.47E-09	Unclassified
Contig9743_at	None	-1.95	9.41E-09	Unclassified
HZ45O16r_at	None	-1.94	4.67E-09	Unclassified
HA11I24u_s_at	None	-1.94	3.82E-06	Unclassified
Contig26142_at	None	-1.93	1.77E-08	Unclassified
EBem10_SQ004_C11_at	None	-1.93	1.63E-06	Unclassified
Contig11287_s_at	None	-1.92	2.44E-08	Unclassified
Contig19333_at	None	-1.92	1.04E-08	Unclassified
Contig8668_at	None	-1.91	7.27E-08	Unclassified
Contig17287_at	None	-1.9	2.50E-09	Unclassified
HVSMEn0024D12r2_at	None	-1.9	3.88E-08	Unclassified
Contig14088_x_at	None	-1.89	1.22E-06	Unclassified
Contig13024_at	None	-1.87	2.32E-09	Unclassified
Contig1968_s_at	None	-1.87	8.55E-07	Unclassified
HV09F14u_at	None	-1.87	6.95E-09	Unclassified

rbaal13n12_s_at	None	-1.87	9.19E-09	Unclassified
Contig1768_at	None	-1.86	8.73E-08	Unclassified
Contig24666_at	None	-1.86	1.68E-08	Unclassified
Contig24126_at	None	-1.85	6.33E-08	Unclassified
Contig9847_s_at	None	-1.85	3.11E-08	Unclassified
HVSMEf0017C20f2_s_at	None	-1.84	5.99E-09	Unclassified
Contig14088_s_at	None	-1.83	4.73E-06	Unclassified
Contig6026_at	None	-1.83	4.96E-08	Unclassified
Contig9073_s_at	None	-1.83	2.44E-08	Unclassified
HS06B24u_at	None	-1.83	4.27E-06	Unclassified
Contig10522_at	None	-1.82	4.31E-08	Unclassified
Contig20674_at	None	-1.82	6.27E-08	Unclassified
HV_CEa0002D23r2_at	None	-1.82	3.02E-08	Unclassified
HVSMEc0008I05r2_s_at	None	-1.82	2.88E-07	Unclassified
Contig11525_at	None	-1.81	1.73E-05	Unclassified
Contig19890_at	None	-1.81	8.17E-06	Unclassified
rbags22g19_at	None	-1.81	5.83E-08	Unclassified
Contig17275_at	None	-1.8	6.21E-08	Unclassified
HI12K05r_s_at	None	-1.8	2.76E-06	Unclassified
HVSMEi0007O15r2_at	None	-1.8	2.49E-08	Unclassified
HVSMEn0006E24f2_s_at	None	-1.8	1.13E-08	Unclassified
Contig16125_at	None	-1.8	1.50E-05	Unclassified
Contig25876_at	None	-1.79	2.52E-06	Unclassified
Contig9740_s_at	None	-1.79	4.57E-09	Unclassified
HVSMEm0004N07r2_s_at	None	-1.79	9.46E-07	Unclassified
EBem10_SQ002_L14_s_at	None	-1.79	9.77E-05	Unclassified
HV_CEb0011H17r2_at	None	-1.78	1.00E-06	Unclassified
HVSMEh0083J23r2_s_at	None	-1.78	1.87E-08	Unclassified
Contig11288_x_at	None	-1.77	2.64E-07	Unclassified
Contig17966_at	None	-1.77	3.27E-08	Unclassified
HVSMEm0023L23r2_s_at	None	-1.75	7.78E-09	Unclassified
rbaal22m22_s_at	None	-1.74	1.03E-07	Unclassified
Contig13718_at	None	-1.73	7.97E-09	Unclassified

Contig3986_s_at	None	-1.73	6.88E-08	Unclassified
Contig1894_at	None	-1.73	2.53E-06	Unclassified
Contig14789_at	None	-1.72	1.81E-08	Unclassified
Contig21281_at	None	-1.71	6.71E-07	Unclassified
Contig22600_at	None	-1.71	1.81E-05	Unclassified
EBem09_SQ007_D05_s_at	None	-1.71	5.69E-09	Unclassified
HT01D24w_s_at	None	-1.71	1.17E-07	Unclassified
Contig23137_at	None	-1.7	7.08E-06	Unclassified
EBem04_SQ004_P12_at	None	-1.7	2.90E-07	Unclassified
Contig16632_at	None	-1.69	3.35E-08	Unclassified
Contig10485_at	None	-1.68	1.20E-08	Unclassified
Contig12505_at	None	-1.68	3.84E-08	Unclassified
Contig16645_at	None	-1.68	1.40E-06	Unclassified
HI15L07r_s_at	None	-1.68	7.06E-09	Unclassified
Contig15524_at	None	-1.67	1.31E-07	Unclassified
Contig11122_s_at	None	-1.66	1.81E-08	Unclassified
EBma03_SQ003_J21_s_at	None	-1.66	8.30E-08	Unclassified
HVSMEf0015I21r2_s_at	None	-1.66	6.35E-09	Unclassified
Contig4544_s_at	None	-1.65	3.29E-08	Unclassified
Contig4809_at	None	-1.65	1.04E-07	Unclassified
Contig13634_at	None	-1.64	9.97E-09	Unclassified
Contig8526_s_at	None	-1.62	3.17E-09	Unclassified
HVSMEb0006I12r2_s_at	None	-1.62	9.15E-08	Unclassified
rbags14a22_at	None	-1.62	2.03E-06	Unclassified
Contig14437_at	None	-1.62	5.53E-06	Unclassified
Contig11397_s_at	None	-1.6	8.48E-07	Unclassified
Contig18766_at	None	-1.6	7.53E-08	Unclassified
Contig24936_at	None	-1.6	1.94E-05	Unclassified
HA14G19r_at	None	-1.6	6.87E-08	Unclassified
HK04P22r_s_at	None	-1.6	3.85E-06	Unclassified
HV_CEa0014N02r2_at	None	-1.6	1.27E-06	Unclassified
Contig10957_at	None	-1.59	1.11E-05	Unclassified
Contig16351_at	None	-1.57	7.26E-08	Unclassified

Contig9775_at	None	-1.57	3.05E-07	Unclassified
HVSMEb0003H09r2_at	None	-1.57	8.11E-08	Unclassified
rbags19e09_s_at	None	-1.57	4.13E-07	Unclassified
Contig15338_at	None	-1.56	1.59E-07	Unclassified
HM10P11r_s_at	None	-1.56	7.37E-09	Unclassified
Contig8467_at	None	-1.55	1.23E-05	Unclassified
HV06P16u_s_at	None	-1.55	2.02E-07	Unclassified
Contig14485_at	None	-1.54	1.11E-08	Unclassified
Contig558_s_at	None	-1.54	4.07E-05	Unclassified
HV05D02u_x_at	None	-1.54	1.81E-08	Unclassified
Contig16930_at	None	-1.53	1.41E-06	Unclassified
Contig3063_x_at	None	-1.53	1.14E-06	Unclassified
Contig3414_s_at	None	-1.53	3.12E-08	Unclassified
rbags24a14_x_at	None	-1.53	2.62E-08	Unclassified
HO08C10S_at	None	-1.52	1.36E-07	Unclassified
HY08M06u_at	None	-1.52	2.98E-07	Unclassified
Contig25763_at	None	-1.51	5.08E-09	Unclassified
Contig16957_at	None	-1.5	1.67E-07	Unclassified
Contig11917_at	None	-1.49	6.04E-07	Unclassified
Contig20641_at	None	-1.49	9.61E-07	Unclassified
Contig9715_at	None	-1.49	5.21E-06	Unclassified
S0000800042H10F1_s_at	None	-1.49	3.08E-08	Unclassified
Contig19976_at	None	-1.48	7.71E-07	Unclassified
rbags13e14_s_at	None	-1.48	5.71E-08	Unclassified
Contig18859_at	None	-1.48	3.35E-06	Unclassified
Contig2704_s_at	None	-1.48	9.90E-05	Unclassified
Contig16728_at	None	-1.47	1.62E-07	Unclassified
Contig20723_at	None	-1.47	7.07E-08	Unclassified
EBma03_SQ002_M07_at	None	-1.47	7.64E-08	Unclassified
HV_CEa0009K11r2_at	None	-1.47	8.29E-07	Unclassified
Contig14006_at	None	-1.46	2.61E-06	Unclassified
HR01N22u_s_at	None	-1.46	2.99E-06	Unclassified
rbaal0d01_at	None	-1.46	4.12E-08	Unclassified

Contig8467_x_at	None	-1.46	1.12E-05	Unclassified
EBpi01_SQ002_N15_at	None	-1.45	9.30E-06	Unclassified
Contig10126_at	None	-1.44	0	Unclassified
Contig4512_s_at	None	-1.44	7.12E-06	Unclassified
HV_CEa0005A05r2_s_at	None	-1.44	2.12E-08	Unclassified
HVSMEc0001C18f2_s_at	None	-1.44	1.47E-07	Unclassified
HW02E22u_at	None	-1.44	1.47E-06	Unclassified
Contig10749_at	None	-1.43	3.20E-06	Unclassified
Contig19458_at	None	-1.43	1.56E-07	Unclassified
HVSMEm0012B17r2_at	None	-1.43	4.32E-06	Unclassified
HW04H17u_s_at	None	-1.43	8.61E-08	Unclassified
HVSMEm0004L13r2_s_at	None	-1.43	1.40E-05	Unclassified
Contig26634_at	None	-1.42	2.29E-07	Unclassified
HI02C22u_at	None	-1.41	8.92E-07	Unclassified
HVSMEa0001H15r2_at	None	-1.41	1.83E-08	Unclassified
HVSMEa0011H12r2_x_at	None	-1.41	4.16E-08	Unclassified
HVSMEf0017C20f2_at	None	-1.41	3.11E-07	Unclassified
rbags8d18_s_at	None	-1.41	4.71E-08	Unclassified
Contig15168_at	None	-1.4	1.19E-07	Unclassified
HVSMEm0006M10r2_at	None	-1.4	7.79E-06	Unclassified
Contig19526_at	None	-1.39	9.06E-07	Unclassified
Contig10283_x_at	None	-1.37	1.23E-06	Unclassified
Contig14406_at	None	-1.37	3.15E-06	Unclassified
HV09O14u_s_at	None	-1.37	7.90E-07	Unclassified
Contig16695_at	None	-1.35	1.96E-06	Unclassified
baak4c06_at	None	-1.35	0	Unclassified
Contig21611_at	None	-1.34	2.93E-07	Unclassified
Contig17475_at	None	-1.33	1.64E-06	Unclassified
Contig20024_at	None	-1.33	1.06E-05	Unclassified
Contig26001_at	None	-1.33	5.03E-07	Unclassified
Contig16766_at	None	-1.32	2.75E-07	Unclassified
Contig17527_at	None	-1.32	2.51E-07	Unclassified
Contig18129_at	None	-1.32	3.42E-07	Unclassified

Contig19631_at	None	-1.32	1.13E-07	Unclassified
EBem08_SQ004_M17_at	None	-1.32	2.50E-08	Unclassified
HK04L13r_s_at	None	-1.32	1.10E-06	Unclassified
HT09D09u_at	None	-1.31	6.35E-08	Unclassified
HA15K23r_s_at	None	-1.3	1.18E-06	Unclassified
HVSMEf0013K24r2_s_at	None	-1.3	1.31E-07	Unclassified
HVSMEi0022O01f2_s_at	None	-1.3	1.35E-07	Unclassified
HVSMEk0002N06r2_at	None	-1.3	1.22E-06	Unclassified
Contig14264_at	None	-1.29	1.72E-07	Unclassified
HM13E09r_x_at	None	-1.29	2.80E-07	Unclassified
HW02D01u_at	None	-1.29	4.47E-08	Unclassified
Contig26491_at	None	-1.28	2.63E-07	Unclassified
HVSMEh0086A12r2_s_at	None	-1.28	5.74E-07	Unclassified
rbaal1j08_s_at	None	-1.28	6.09E-07	Unclassified
HVSMEh0085O09r2_s_at	None	-1.28	0	Unclassified
HW02G06T_s_at	None	-1.28	3.07E-05	Unclassified
Contig18348_at	None	-1.27	3.75E-07	Unclassified
Contig19116_at	None	-1.27	4.38E-06	Unclassified
HVSMEf0023A03f_s_at	None	-1.27	5.42E-07	Unclassified
rbaal18i13_s_at	None	-1.27	1.26E-07	Unclassified
Contig7123_at	None	-1.26	4.85E-08	Unclassified
EBpi01_SQ003_L11_at	None	-1.26	3.59E-06	Unclassified
HM02H10u_at	None	-1.26	1.35E-07	Unclassified
Contig14511_at	None	-1.25	4.93E-07	Unclassified
Contig20951_at	None	-1.25	2.42E-07	Unclassified
Contig4808_s_at	None	-1.25	3.78E-07	Unclassified
basd21o15_at	None	-1.24	1.25E-06	Unclassified
Contig15298_at	None	-1.24	6.05E-05	Unclassified
Contig25964_at	None	-1.24	2.66E-06	Unclassified
Contig26580_at	None	-1.24	1.47E-07	Unclassified
HVSMEh0082I16r2_s_at	None	-1.23	2.52E-05	Unclassified
Contig23530_s_at	None	-1.22	0	Unclassified
Contig8452_at	None	-1.22	1.46E-06	Unclassified

HI04K10u_at	None	-1.22	2.45E-06	Unclassified
HK06O22r_s_at	None	-1.22	3.66E-06	Unclassified
Contig10890_s_at	None	-1.21	7.41E-07	Unclassified
Contig19665_at	None	-1.21	2.15E-07	Unclassified
Contig6039_at	None	-1.21	1.77E-07	Unclassified
HVSMEc0003N05r2_at	None	-1.21	1.70E-05	Unclassified
Contig7251_at	None	-1.2	1.32E-06	Unclassified
HVSMEn0006A08f2_s_at	None	-1.2	3.56E-07	Unclassified
Contig17972_at	None	-1.19	2.90E-07	Unclassified
EBem05_SQ004_G20_at	None	-1.19	1.98E-05	Unclassified
EBpi01_SQ003_I06_at	None	-1.19	1.09E-05	Unclassified
HO06E11S_at	None	-1.19	4.18E-06	Unclassified
rbaal4b13_at	None	-1.19	6.03E-07	Unclassified
HVSMEb0014M03r2_at	None	-1.18	7.32E-07	Unclassified
HVSMEb0002K02r2_s_at	None	-1.18	0	Unclassified
Contig10500_at	None	-1.17	1.22E-06	Unclassified
Contig11080_at	None	-1.17	2.38E-06	Unclassified
Contig13896_at	None	-1.17	2.89E-06	Unclassified
Contig15278_at	None	-1.17	0	Unclassified
Contig6940_at	None	-1.17	5.69E-07	Unclassified
Contig23738_at	None	-1.16	3.14E-06	Unclassified
EBma03_SQ003_L14_s_at	None	-1.16	0	Unclassified
HW09P09u_s_at	None	-1.16	4.76E-06	Unclassified
HF01J12w_s_at	None	-1.15	3.42E-07	Unclassified
rbags21p23_at	None	-1.15	1.23E-07	Unclassified
rbags29h17_s_at	None	-1.15	7.37E-06	Unclassified
Contig19596_at	None	-1.15	0.01	Unclassified
Contig22762_at	None	-1.14	1.61E-05	Unclassified
Contig7209_at	None	-1.14	2.27E-06	Unclassified
Contig7746_s_at	None	-1.14	4.28E-07	Unclassified
Contig9498_at	None	-1.14	2.91E-07	Unclassified
rbaal38l09_s_at	None	-1.14	3.24E-06	Unclassified
Contig11558_at	None	-1.13	1.86E-05	Unclassified

Contig5424_at	None	-1.13	7.37E-07	Unclassified
HV_CEa0006I05r2_s_at	None	-1.13	1.14E-05	Unclassified
HW04D13u_at	None	-1.13	1.95E-06	Unclassified
HZ40B21r_s_at	None	-1.13	1.55E-07	Unclassified
Contig18508_at	None	-1.13	0	Unclassified
Contig13202_at	None	-1.12	8.55E-06	Unclassified
Contig23673_at	None	-1.12	1.40E-06	Unclassified
Contig2643_at	None	-1.12	4.63E-06	Unclassified
Contig8669_s_at	None	-1.12	3.57E-06	Unclassified
Contig8930_s_at	None	-1.12	7.56E-06	Unclassified
Contig19851_at	None	-1.12	6.84E-05	Unclassified
Contig5513_at	None	-1.12	0	Unclassified
EBpi01_SQ005_G20_x_at	None	-1.12	0	Unclassified
HVSMEl0002P14r2_s_at	None	-1.11	0	Unclassified
HW04O09u_at	None	-1.11	2.79E-05	Unclassified
Contig23732_at	None	-1.11	4.60E-06	Unclassified
Contig15508_at	None	-1.1	1.28E-06	Unclassified
Contig18066_at	None	-1.1	4.95E-05	Unclassified
HK05M22r_at	None	-1.1	1.47E-05	Unclassified
rbags17a19_s_at	None	-1.1	1.04E-06	Unclassified
HVSMEk0006H23r2_at	None	-1.1	3.84E-05	Unclassified
Contig15137_at	None	-1.09	4.01E-06	Unclassified
Contig15620_at	None	-1.09	1.37E-05	Unclassified
Contig18751_at	None	-1.09	7.71E-05	Unclassified
HV03D18u_at	None	-1.09	6.80E-08	Unclassified
Contig25699_at	None	-1.09	0.01	Unclassified
Contig18611_at	None	-1.08	7.51E-06	Unclassified
Contig18726_at	None	-1.08	5.58E-07	Unclassified
Contig2395_at	None	-1.08	3.39E-06	Unclassified
Contig24381_at	None	-1.08	1.66E-06	Unclassified
Contig25809_s_at	None	-1.08	7.61E-07	Unclassified
EBem04_SQ003_J01_at	None	-1.08	2.02E-06	Unclassified
EBma01_SQ005_P22_s_at	None	-1.08	1.68E-06	Unclassified

EBro07_SQ003_K04_s_at	None	-1.08	1.90E-07	Unclassified
HVSMEf0016A18r2_at	None	-1.08	1.18E-06	Unclassified
HW07N21u_at	None	-1.08	6.48E-07	Unclassified
Contig19949_at	None	-1.08	1.69E-05	Unclassified
Contig9830_s_at	None	-1.07	1.11E-07	Unclassified
HVSMEb0007H07r2_at	None	-1.07	1.04E-06	Unclassified
HW04C21u_at	None	-1.07	3.28E-06	Unclassified
baak4o13_s_at	None	-1.07	2.17E-05	Unclassified
Contig18699_at	None	-1.07	0	Unclassified
Contig2710_s_at	None	-1.06	0.02	Unclassified
Contig9975_at	None	-1.06	7.31E-05	Unclassified
Contig15285_at	None	-1.05	7.61E-05	Unclassified
Contig24342_at	None	-1.05	6.22E-05	Unclassified
EBem10_SQ004_P21_x_at	None	-1.05	0	Unclassified
HB30J05r_at	None	-1.05	1.31E-05	Unclassified
rbaal40g12_at	None	-1.05	4.66E-06	Unclassified
Contig7717_s_at	None	-1.04	6.24E-06	Unclassified
Contig7966_at	None	-1.04	7.34E-05	Unclassified
Contig11899_at	None	-1.03	4.59E-05	Unclassified
Contig1434_s_at	None	-1.03	1.07E-07	Unclassified
Contig18674_at	None	-1.03	1.30E-06	Unclassified
Contig21895_at	None	-1.03	4.50E-07	Unclassified
Contig24770_at	None	-1.03	3.08E-06	Unclassified
Contig10600_at	None	-1.02	9.81E-06	Unclassified
Contig8806_s_at	None	-1.02	4.87E-06	Unclassified
HV_CEb0010C12r2_at	None	-1.02	0	Unclassified
rbags36i03_s_at	None	-1.02	9.02E-06	Unclassified
baal34n21_x_at	None	-1.01	3.46E-07	Unclassified
Contig3065_x_at	None	-1.01	5.89E-06	Unclassified
EBem05_SQ004_K20_at	None	-1.01	2.93E-06	Unclassified
HVSMEg0015J02r2_s_at	None	-1.01	1.92E-05	Unclassified
S0000700025G01F1_s_at	None	-1.01	3.32E-06	Unclassified
HS16M03u_x_at	None	-1	1.81E-05	Unclassified

S0000200068D04F1_s_at	None	-1	2.29E-05	Unclassified
Contig2812_at	Late embryogenesis abundant protein	-4.52	5.69E-08	Unknown
HVSMEg0017A08r2_at	Putative protein	-4.47	1.36E-10	Unknown
Contig8830_at	Unknown protein	-4.18	2.80E-09	Unknown
Contig10822_at	Hypothetical protein	-4.11	1.16E-08	Unknown
Contig24253_at	Hypothetical protein	-3.83	5.27E-09	Unknown
Contig5364_at	Putative protein	-3.82	2.40E-09	Unknown
Contig2632_s_at	Hypothetical protein	-3.74	2.03E-08	Unknown
Contig3396_s_at	Hypothetical protein	-3.67	1.99E-09	Unknown
Contig13885_at	Putative uncharacterized protein	-3.6	2.28E-08	Unknown
Contig7285_at	Putative protein	-3.6	1.35E-10	Unknown
Contig1758_s_at	Hypothetical protein	-3.58	3.86E-10	Unknown
Contig22222_at	Hypothetical protein	-3.5	5.94E-10	Unknown
Contig24709_at	Hypothetical protein	-3.44	1.89E-09	Unknown
Contig5734_at	Hypothetical protein	-3.44	7.72E-09	Unknown
Contig4215_at	Unknown protein	-3.38	1.06E-10	Unknown
Contig21011_at	Uncharacterized protein	-3.37	2.24E-10	Unknown
Contig14168_s_at	Putative uncharacterized protein	-3.36	1.17E-08	Unknown
Contig9763_s_at	Hypothetical protein	-3.35	2.11E-07	Unknown
Contig5198_s_at	Hypothetical protein	-3.33	8.64E-10	Unknown
Contig6455_at	Unknown protein	-3.32	3.42E-10	Unknown
Contig14066_at	Putative uncharacterized protein	-3.3	3.98E-09	Unknown
Contig7748_at	Putative uncharacterized protein	-3.3	1.63E-09	Unknown
Contig10546_at	Putative protein	-3.29	9.43E-08	Unknown
Contig9489_at	Hypothetical protein	-3.26	9.04E-10	Unknown
Contig7995_at	Unknown protein	-3.19	1.56E-09	Unknown
Contig10874_at	Putative uncharacterized protein	-3.17	4.32E-08	Unknown
Contig9952_at	Hypothetical protein	-3.16	3.92E-08	Unknown
Contig26021_at	Expressed protein	-3.15	1.19E-10	Unknown
Contig12809_at	Putative leaf protein	-3.14	7.72E-09	Unknown
Contig14639_at	hypothetical protein	-3.14	3.14E-08	Unknown
Contig8096_at	Putative uncharacterized protein	-3.13	6.64E-10	Unknown
Contig24791_at	Unknown protein	-3.08	1.72E-07	Unknown

Contig12928_at	Hypothetical protein	-3.06	1.24E-10	Unknown
Contig10009_at	Expressed protein	-3.05	6.59E-08	Unknown
Contig6024_at	Putative uncharacterized protein	-3.05	2.04E-09	Unknown
Contig8658_at	Putative uncharacterized protein	-3	5.66E-09	Unknown
HU05L05u_s_at	Hypothetical protein	-2.99	2.54E-09	Unknown
HV_CEa0012B15f_s_at	Hypothetical protein	-2.98	4.88E-08	Unknown
Contig13313_at	Hypothetical protein	-2.97	1.16E-09	Unknown
Contig14102_at	Expressed protein	-2.93	1.56E-07	Unknown
Contig9951_s_at	Hypothetical protein	-2.93	1.05E-07	Unknown
Contig14228_at	Putative protein	-2.91	2.82E-08	Unknown
Contig20580_at	33 kDa secretory protein	-2.91	2.10E-09	Unknown
Contig11013_at	Putative protein	-2.9	3.31E-08	Unknown
Contig24302_at	Hypothetical protein	-2.9	1.32E-08	Unknown
Contig7600_at	Expressed protein	-2.9	1.69E-08	Unknown
HVSMEm0023L02r2_s_at	Hypothetical protein	-2.88	5.66E-09	Unknown
Contig10310_at	Expressed protein	-2.87	3.80E-08	Unknown
Contig12301_at	Hypothetical protein	-2.87	2.72E-08	Unknown
Contig5198_at	Hypothetical protein	-2.87	1.32E-08	Unknown
Contig6504_s_at	Hypothetical protein	-2.86	9.98E-08	Unknown
Contig13690_at	Putative protein	-2.85	9.30E-09	Unknown
HVSMEa0005L24r2_s_at	Expressed protein	-2.85	1.09E-08	Unknown
Contig6474_s_at	Putative uncharacterized protein	-2.84	9.03E-09	Unknown
HO13D02S_at	Hypothetical protein	-2.83	8.44E-09	Unknown
Contig17574_at	Uncharacterized protein	-2.82	1.07E-08	Unknown
Contig18178_at	Hypothetical protein	-2.82	3.01E-09	Unknown
Contig9412_s_at	Unknown protein	-2.82	1.04E-07	Unknown
Contig18643_at	Unknown protein	-2.8	5.15E-08	Unknown
Contig5410_at	Hypothetical protein	-2.79	2.23E-08	Unknown
Contig11763_s_at	Putative protein	-2.78	5.36E-09	Unknown
Contig10939_at	Expressed protein	-2.77	9.40E-09	Unknown
Contig13457_s_at	Expressed protein	-2.77	5.33E-09	Unknown
Contig15715_at	Hypothetical protein	-2.76	7.18E-09	Unknown
Contig14587_s_at	Expressed protein	-2.75	2.68E-10	Unknown

Contig16154_at	Unknown protein	-2.73	2.03E-10	Unknown
HV_CEa0014I08r2_s_at	Hypothetical protein	-2.73	7.53E-10	Unknown
Contig4255_s_at	Unknown protein	-2.72	4.79E-08	Unknown
HVSMEa0014K13r2_s_at	Putative protein	-2.72	2.65E-10	Unknown
Contig4043_at	Unknown protein	-2.7	4.90E-09	Unknown
Contig11633_at	Putative uncharacterized protein	-2.69	9.93E-10	Unknown
Contig14285_at	Putative protein	-2.69	3.17E-08	Unknown
Contig18212_at	Hypothetical protein	-2.69	4.07E-09	Unknown
Contig11203_at	Hypothetical protein	-2.68	5.29E-10	Unknown
Contig12879_at	Hypothetical protein	-2.67	8.87E-10	Unknown
Contig14005_at	Expressed protein	-2.66	4.16E-09	Unknown
Contig9412_at	Hypothetical protein	-2.66	1.58E-08	Unknown
Contig18478_at	Unknown protein	-2.65	2.38E-08	Unknown
Contig7499_at	Hypothetical protein	-2.65	7.20E-07	Unknown
Contig15646_at	Hypothetical protein	-2.64	3.41E-08	Unknown
Contig4545_s_at	Expressed protein	-2.63	1.47E-09	Unknown
Contig8404_at	Hypothetical protein	-2.63	1.61E-08	Unknown
Contig8701_at	Unknown protein	-2.63	2.89E-07	Unknown
Contig23482_at	Hypothetical protein	-2.62	5.31E-09	Unknown
Contig10306_s_at	Putative protein	-2.61	3.53E-08	Unknown
Contig10931_at	Putative uncharacterized protein	-2.61	3.42E-09	Unknown
Contig12096_at	Hypothetical protein	-2.61	1.89E-08	Unknown
Contig14708_at	Expressed protein	-2.61	9.52E-09	Unknown
Contig15503_at	Putative protein	-2.61	1.56E-10	Unknown
Contig11408_at	Hypothetical protein	-2.6	3.79E-10	Unknown
Contig3081_at	Putative uncharacterized protein	-2.59	8.59E-10	Unknown
Contig12640_at	Hypothetical protein	-2.57	6.80E-09	Unknown
Contig16000_at	Putative protein	-2.56	1.20E-08	Unknown
Contig12617_at	Putative uncharacterized protein	-2.55	1.11E-08	Unknown
rbaal30k13_s_at	Unknown protein	-2.54	3.67E-10	Unknown
HV_CEb0001E04r2_s_at	Expressed protein	-2.53	4.23E-09	Unknown
Contig12545_at	Expressed protein	-2.52	1.34E-07	Unknown
Contig9868_at	Hypothetical protein	-2.52	1.22E-09	Unknown

Contig25063_at	Hypothetical protein	-2.51	1.07E-08	Unknown
Contig18152_at	Hypothetical protein	-2.5	1.03E-08	Unknown
Contig9596_at	Unknown protein	-2.5	3.13E-09	Unknown
Contig17968_at	Expressed protein	-2.49	3.65E-10	Unknown
Contig8260_s_at	Hypothetical protein	-2.49	1.99E-08	Unknown
Contig4610_s_at	Putative uncharacterized protein	-2.48	7.45E-08	Unknown
HT04E01r_at	Hypothetical protein	-2.48	4.99E-10	Unknown
Contig13271_at	Expressed protein	-2.47	5.79E-10	Unknown
Contig16773_at	Hypothetical protein	-2.47	2.46E-08	Unknown
Contig16595_at	Putative uncharacterized protein	-2.46	1.06E-08	Unknown
Contig8508_at	Unknown protein	-2.46	2.70E-09	Unknown
Contig9438_s_at	Putative uncharacterized protein	-2.45	9.86E-08	Unknown
Contig13172_at	Hypothetical protein	-2.44	1.91E-09	Unknown
Contig24476_at	Hypothetical protein	-2.44	7.06E-08	Unknown
Contig7122_s_at	Unknown protein	-2.44	7.74E-10	Unknown
Contig13785_at	Expressed protein	-2.43	1.57E-08	Unknown
Contig15509_at	Expressed protein	-2.42	1.91E-09	Unknown
Contig17849_at	Hypothetical protein	-2.42	1.80E-08	Unknown
Contig3905_at	Hypothetical protein	-2.42	1.54E-08	Unknown
Contig5950_s_at	Unknown protein	-2.42	2.57E-09	Unknown
Contig10942_at	Hypothetical protein	-2.41	4.51E-08	Unknown
Contig11406_at	Hypothetical protein	-2.41	4.11E-10	Unknown
Contig23045_at	Expressed protein	-2.41	2.94E-07	Unknown
Contig852_at	Hypothetical protein	-2.41	8.37E-07	Unknown
Contig3271_s_at	Hypothetical protein	-2.4	1.68E-08	Unknown
Contig9442_at	Hypothetical protein	-2.4	2.01E-09	Unknown
Contig18384_at	Hypothetical protein	-2.39	2.29E-08	Unknown
Contig4707_x_at	Expressed protein	-2.39	1.16E-08	Unknown
Contig10162_s_at	Hypothetical protein	-2.38	2.72E-07	Unknown
Contig12344_at	Remorin-like protein	-2.38	5.62E-09	Unknown
Contig13131_at	Expressed protein	-2.38	3.66E-09	Unknown
Contig13409_at	Putative uncharacterized protein	-2.38	1.67E-08	Unknown
Contig15038_at	Hypothetical protein	-2.38	8.73E-10	Unknown

Contig12966_at	Expressed protein	-2.37	9.36E-09	Unknown
Contig7474_at	Hypothetical protein	-2.37	1.36E-08	Unknown
Contig11985_at	Putative protein	-2.36	4.87E-08	Unknown
HVSMEf0001F16r2_s_at	Hypothetical protein	-2.36	7.06E-09	Unknown
Contig5772_at	Unknown protein	-2.35	2.40E-07	Unknown
Contig5582_s_at	Unknown protein	-2.33	4.65E-08	Unknown
Contig7474_s_at	Hypothetical protein	-2.32	2.09E-09	Unknown
Contig24976_at	Hypothetical protein	-2.31	5.92E-09	Unknown
Contig25503_at	NHL repeat-containing protein-like	-2.31	5.68E-10	Unknown
Contig4707_at	Expressed protein	-2.31	2.70E-08	Unknown
Contig12710_at	Unknown protein	-2.29	7.45E-08	Unknown
Contig14073_at	Uncharacterized protein	-2.29	1.24E-07	Unknown
rbaal21l22_s_at	Putative protein	-2.29	5.25E-08	Unknown
Contig13146_at	Hypothetical protein	-2.27	4.08E-08	Unknown
Contig14709_at	Expressed protein	-2.27	1.36E-09	Unknown
Contig17314_at	Expressed protein	-2.26	6.97E-09	Unknown
Contig9016_at	Putative protein	-2.26	6.19E-10	Unknown
HVSMEb0017B20r2_at	Remorin-like protein	-2.26	1.67E-08	Unknown
Contig19361_at	Unknown protein	-2.25	1.19E-08	Unknown
Contig7034_at	Uncharacterized protein	-2.25	6.11E-10	Unknown
Contig9115_at	Hypothetical protein	-2.25	1.97E-05	Unknown
Contig7256_at	Expressed protein	-2.24	9.85E-10	Unknown
Contig9264_s_at	Expressed protein	-2.23	8.30E-10	Unknown
Contig14994_at	Unknown protein	-2.22	6.66E-07	Unknown
Contig7180_at	Expressed protein	-2.21	4.80E-10	Unknown
HVSMEa0012N22r2_at	Hypothetical protein	-2.21	1.42E-09	Unknown
Contig16020_at	Putative uncharacterized protein	-2.2	1.39E-08	Unknown
Contig5818_at	D1 CtpA arboxy-terminal protease	-2.2	9.56E-09	Unknown
Contig4861_at	Remorin-like protein	-2.19	2.22E-08	Unknown
Contig4961_s_at	Unknown protein	-2.19	2.54E-08	Unknown
Contig9914_at	Hypothetical protein	-2.19	1.01E-07	Unknown
Contig3716_at	Hypothetical protein	-2.18	4.39E-08	Unknown
Contig4014_at	Expressed protein	-2.18	3.37E-09	Unknown

Contig10169_at	Hypothetical protein	-2.17	2.00E-09	Unknown
Contig20821_at	Hypothetical protein	-2.17	1.29E-09	Unknown
Contig4282_at	Expressed protein	-2.17	3.70E-08	Unknown
Contig6142_at	Putative protein	-2.17	4.40E-09	Unknown
Contig8411_at	Hypothetical protein	-2.17	5.21E-08	Unknown
Contig9939_at	Hypothetical protein	-2.17	8.87E-09	Unknown
Contig3270_s_at	Unknown protein	-2.16	1.07E-08	Unknown
Contig14813_at	Expressed protein	-2.15	2.27E-08	Unknown
Contig3057_s_at	Putative uncharacterized protein	-2.15	2.00E-06	Unknown
Contig8598_at	Expressed protein	-2.15	5.46E-09	Unknown
Contig14925_at	Expressed protein	-2.13	5.12E-09	Unknown
Contig16249_at	Hypothetical protein	-2.13	5.51E-08	Unknown
Contig6150_at	Hypothetical protein	-2.13	5.59E-06	Unknown
HV_CEa0006L03r2_at	Hypothetical protein	-2.13	6.31E-09	Unknown
Contig1064_at	Putative protein	-2.12	5.36E-09	Unknown
Contig23996_at	Unknown protein	-2.12	5.85E-07	Unknown
Contig7396_at	Putative protein	-2.12	3.76E-08	Unknown
Contig7996_at	Hypothetical protein	-2.1	3.27E-09	Unknown
Contig8506_at	Unknown protein	-2.1	3.34E-08	Unknown
Contig9125_at	Expressed protein	-2.1	1.69E-06	Unknown
Contig13243_s_at	Expressed protein	-2.09	3.60E-09	Unknown
Contig8992_at	Unknown protein	-2.09	1.60E-08	Unknown
Contig4119_at	Apospory-associated protein C-like	-2.08	4.69E-09	Unknown
Contig12619_at	Putative uncharacterized protein	-2.06	3.02E-08	Unknown
Contig12756_at	Hypothetical protein	-2.06	6.31E-09	Unknown
Contig11328_at	Putative protein	-2.05	2.64E-09	Unknown
Contig12089_at	Unknown protein	-2.05	6.78E-07	Unknown
Contig8586_s_at	Hypothetical protein	-2.05	2.73E-06	Unknown
Contig13953_at	Unknown protein	-2.04	1.94E-09	Unknown
Contig16431_at	Expressed protein	-2.04	1.34E-06	Unknown
Contig7885_at	Hypothetical protein	-2.04	2.57E-09	Unknown
Contig10437_at	Unknown protein	-2.02	8.14E-09	Unknown
Contig17764_at	Hypothetical protein	-2.02	4.57E-09	Unknown

Contig5880_at	Putative protein	-2.02	2.84E-09	Unknown
Contig13702_at	Hypothetical protein	-2.01	4.02E-09	Unknown
Contig23320_at	Hypothetical protein	-2.01	2.40E-08	Unknown
Contig23917_at	Hypothetical protein	-2.01	2.69E-08	Unknown
Contig12581_at	Putative uncharacterized protein	-2	1.88E-08	Unknown
Contig3718_s_at	Putative uncharacterized protein	-2	5.48E-08	Unknown
Contig7748_s_at	Hypothetical protein	-2	2.89E-09	Unknown
Contig14646_s_at	Hypothetical protein	-1.99	1.76E-08	Unknown
Contig21442_at	Hypothetical protein	-1.99	4.45E-08	Unknown
Contig11597_at	Hypothetical protein	-1.98	6.21E-09	Unknown
Contig8498_at	CDK5RAP1-like protein	-1.98	2.39E-08	Unknown
HK01E08r_s_at	Hypothetical protein	-1.98	6.43E-07	Unknown
Contig12592_at	Putative uncharacterized protein	-1.97	3.04E-09	Unknown
Contig9890_at	Putative protein	-1.97	1.04E-09	Unknown
Contig12088_at	Putative protein	-1.96	5.66E-08	Unknown
Contig9220_at	Expressed protein	-1.96	1.43E-09	Unknown
Contig8587_s_at	Hypothetical protein	-1.95	3.42E-07	Unknown
Contig10081_at	Putative protein	-1.94	1.32E-07	Unknown
Contig20695_at	Unknown protein	-1.94	2.90E-08	Unknown
Contig24273_at	Putative nuclear-encoded plastid	-1.94	1.37E-08	Unknown
Contig9242_at	Unknown protein	-1.94	8.32E-09	Unknown
Contig272_s_at	Hypothetical protein	-1.92	9.30E-10	Unknown
Contig14509_at	Hypothetical protein	-1.91	3.23E-09	Unknown
Contig6632_at	Hypothetical protein	-1.91	1.40E-05	Unknown
Contig16807_at	Hypothetical protein	-1.9	2.36E-07	Unknown
HV_CEa0002E21r2_at	Unknown protein	-1.9	3.34E-09	Unknown
Contig4591_at	Putative protein	-1.89	1.27E-08	Unknown
Contig10543_at	Putative uncharacterized protein	-1.88	6.42E-09	Unknown
Contig9507_at	Expressed protein	-1.88	2.02E-08	Unknown
Contig9696_s_at	Expressed protein	-1.88	1.44E-08	Unknown
Contig16958_at	Putative protein	-1.87	2.93E-08	Unknown
Contig12765_at	Hypothetical protein	-1.86	1.48E-07	Unknown
Contig13508_at	Hypothetical protein	-1.86	1.44E-08	Unknown

Contig20669_at	Hypothetical protein	-1.86	6.31E-09	Unknown
Contig6357_at	Hypothetical protein	-1.86	3.84E-07	Unknown
Contig13867_s_at	Unnamed protein product	-1.86	0	Unknown
Contig11799_at	Putative uncharacterized protein	-1.85	8.14E-08	Unknown
Contig16071_at	Hypothetical protein	-1.85	1.61E-06	Unknown
Contig16879_at	Expressed protein	-1.85	1.62E-07	Unknown
Contig16397_at	Putative uncharacterized protein	-1.84	1.91E-07	Unknown
Contig4368_at	Putative protein	-1.84	5.13E-07	Unknown
Contig721_at	Expressed protein	-1.84	3.45E-06	Unknown
Contig5438_s_at	Hypothetical protein	-1.83	1.07E-07	Unknown
Contig7673_at	Hypothetical protein	-1.83	1.97E-07	Unknown
Contig12675_s_at	Hypothetical protein	-1.82	5.16E-08	Unknown
Contig16285_at	Hypothetical protein	-1.82	1.78E-08	Unknown
Contig19984_at	Hypothetical protein	-1.82	8.31E-10	Unknown
Contig12132_at	Expressed protein	-1.81	2.83E-07	Unknown
Contig13194_at	Unknown protein	-1.81	1.06E-07	Unknown
Contig13298_at	Expressed protein	-1.81	1.39E-06	Unknown
Contig13784_at	Hypothetical protein	-1.81	5.97E-07	Unknown
Contig14021_at	Putative protein	-1.8	4.92E-09	Unknown
Contig14841_s_at	Hypothetical protein	-1.8	4.52E-08	Unknown
Contig15750_at	Hypothetical protein	-1.8	1.99E-08	Unknown
Contig2963_at	Unknown protein	-1.8	1.55E-07	Unknown
Contig5570_s_at	Putative protein	-1.8	1.29E-09	Unknown
Contig19653_at	Putative protein	-1.79	1.70E-07	Unknown
Contig4370_at	Hypothetical protein	-1.79	1.69E-09	Unknown
Contig9767_at	Unknown protein	-1.79	1.46E-07	Unknown
Contig16379_s_at	Unknown protein	-1.78	6.05E-09	Unknown
Contig16487_at	Putative protein	-1.78	9.32E-09	Unknown
Contig23105_at	Unknown protein	-1.78	1.23E-07	Unknown
HV_CEa0003L23f_s_at	Hypothetical protein	-1.78	5.23E-06	Unknown
Contig11411_at	Hypothetical protein	-1.77	9.33E-08	Unknown
Contig15225_at	Expressed protein	-1.77	3.85E-09	Unknown
Contig9569_at	Expressed protein	-1.77	1.50E-09	Unknown

Contig9795_at	Putative uncharacterized protein	-1.77	5.29E-06	Unknown
Contig10963_at	Hypothetical protein	-1.76	1.99E-07	Unknown
Contig11737_at	Hypothetical protein	-1.76	2.69E-09	Unknown
Contig8374_at	Unknown protein	-1.76	1.64E-07	Unknown
Contig11479_s_at	Hypothetical protein	-1.75	1.46E-07	Unknown
Contig15384_at	Putative uncharacterized protein	-1.75	2.69E-08	Unknown
Contig2594_s_at	CBS domain containing protein	-1.75	4.35E-08	Unknown
Contig2748_at	Hypothetical protein	-1.75	1.32E-06	Unknown
Contig7573_at	Putative uncharacterized protein	-1.75	7.53E-09	Unknown
Contig16736_at	Hypothetical protein	-1.74	4.95E-09	Unknown
Contig5630_at	Hypothetical protein	-1.74	1.00E-07	Unknown
Contig7407_at	Putative protein	-1.73	3.09E-08	Unknown
Contig10302_at	Putative uncharacterized protein	-1.72	4.44E-08	Unknown
Contig14454_at	Unknown protein	-1.72	7.75E-07	Unknown
Contig17805_at	Expressed protein	-1.72	6.02E-06	Unknown
HVSMEa0019A17r2_at	Expressed protein	-1.72	2.68E-06	Unknown
Contig20316_at	Hypothetical protein	-1.71	1.03E-08	Unknown
Contig8535_s_at	Putative protein	-1.71	5.73E-08	Unknown
Contig8899_at	Expressed protein	-1.71	5.70E-07	Unknown
Contig9036_at	Uncharacterized protein	-1.71	1.31E-09	Unknown
Contig9752_at	Unknown protein	-1.71	1.25E-07	Unknown
Contig4426_at	Unknown protein	-1.7	2.47E-08	Unknown
Contig14891_at	Hypothetical protein	-1.69	6.10E-06	Unknown
Contig2358_s_at	CBS domain containing protein	-1.69	5.70E-07	Unknown
Contig6460_at	Putative SF16 protein	-1.69	3.55E-09	Unknown
HV_CEb0003K13r2_s_at	Hypothetical protein	-1.69	1.20E-06	Unknown
Contig7726_at	Expressed protein	-1.68	1.21E-07	Unknown
Contig911_s_at	Hypothetical protein	-1.68	4.11E-08	Unknown
Contig9862_at	Putative uncharacterized protein	-1.68	7.58E-08	Unknown
HVSMEb0005B15f_s_at	Hypothetical protein	-1.67	1.65E-06	Unknown
Contig15511_at	Putative protein	-1.66	9.59E-07	Unknown
Contig16504_at	Hypothetical protein	-1.66	6.19E-08	Unknown
Contig19730_at	Putative uncharacterized protein	-1.66	8.58E-09	Unknown

HVSMEg0011O17r2_s_at	Hypothetical protein	-1.66	5.85E-09	Unknown
Contig4367_s_at	Putative protein	-1.66	5.31E-06	Unknown
Contig11846_at	Expressed protein	-1.65	3.02E-07	Unknown
Contig7338_at	Putative uncharacterized protein	-1.65	6.53E-06	Unknown
Contig9837_at	Hypothetical protein	-1.65	1.33E-06	Unknown
HS17I17u_s_at	Hypothetical protein	-1.65	4.44E-06	Unknown
Contig10417_at	Putative protein	-1.64	3.64E-08	Unknown
Contig12123_at	Hypothetical protein	-1.64	1.21E-07	Unknown
Contig15934_at	Hypothetical protein	-1.64	1.66E-07	Unknown
Contig5914_at	Putative uncharacterized protein	-1.64	7.32E-07	Unknown
Contig7410_at	Hypothetical protein	-1.64	3.19E-06	Unknown
Contig2592_at	Putative protein	-1.63	9.95E-07	Unknown
Contig10826_at	Expressed protein	-1.62	3.72E-07	Unknown
Contig13800_at	D-protein	-1.62	5.25E-06	Unknown
Contig6868_s_at	Hypothetical protein	-1.62	6.79E-08	Unknown
Contig11767_at	Hypothetical protein	-1.61	1.93E-08	Unknown
Contig16113_at	Putative protein	-1.61	1.66E-07	Unknown
Contig3790_at	Apospory-associated protein C-like	-1.61	8.97E-08	Unknown
Contig3791_at	Apospory-associated protein C-like	-1.59	5.92E-08	Unknown
Contig9106_at	Putative protein	-1.59	3.78E-08	Unknown
Contig13530_at	Putative uncharacterized protein	-1.58	1.36E-06	Unknown
Contig24017_at	D1 protease precursor	-1.58	6.35E-09	Unknown
Contig10306_at	Putative protein	-1.57	3.52E-06	Unknown
Contig13157_s_at	Unknown protein	-1.57	3.07E-07	Unknown
Contig13951_at	Hypothetical protein	-1.57	5.31E-09	Unknown
Contig4061_at	Putative protein	-1.57	7.19E-08	Unknown
Contig8064_at	Putative uncharacterized protein	-1.57	7.31E-07	Unknown
Contig6063_s_at	Hypothetical protein	-1.57	9.51E-05	Unknown
Contig10905_at	Putative uncharacterized protein	-1.56	1.27E-08	Unknown
Contig21092_at	Hypothetical protein	-1.56	6.24E-09	Unknown
Contig6633_at	Hypothetical protein	-1.56	1.00E-06	Unknown
Contig8787_s_at	Hypothetical protein	-1.56	6.47E-07	Unknown
Contig16161_at	Expressed protein	-1.55	3.37E-07	Unknown

Contig2358_at	CBS domain containing protein	-1.55	7.60E-07	Unknown
Contig6632_s_at	Putative protein	-1.55	3.99E-07	Unknown
Contig9533_at	Unknown protein	-1.55	5.61E-07	Unknown
Contig8039_at	Putative protein	-1.54	6.27E-08	Unknown
Contig10232_at	Unknown protein	-1.53	4.43E-07	Unknown
Contig10803_s_at	Putative uncharacterized protein	-1.53	8.68E-08	Unknown
Contig18772_at	Expressed protein	-1.53	8.09E-07	Unknown
Contig7411_at	Unknown protein	-1.53	2.26E-08	Unknown
HM04N04u_at	Putative uncharacterized protein	-1.53	3.11E-08	Unknown
Contig22007_at	Hypothetical protein	-1.52	2.32E-06	Unknown
Contig22680_at	Hypothetical protein	-1.52	7.54E-08	Unknown
Contig6142_s_at	Putative protein	-1.52	1.99E-06	Unknown
Contig7341_s_at	Hypothetical protein	-1.51	1.26E-07	Unknown
Contig9941_at	Putative protein	-1.51	2.28E-07	Unknown
rbaal16g11_s_at	Hypothetical protein	-1.51	5.11E-08	Unknown
Contig228_s_at	Hypothetical protein	-1.51	6.60E-05	Unknown
Contig10241_at	Unknown protein	-1.5	5.42E-08	Unknown
Contig9406_at	Cyanobacteria-specific protein-like	-1.5	2.77E-08	Unknown
Contig12539_s_at	Expressed protein	-1.49	1.51E-08	Unknown
Contig14686_at	Hypothetical protein	-1.49	6.59E-06	Unknown
Contig7851_s_at	Hypothetical protein	-1.49	1.04E-07	Unknown
Contig9465_at	Hypothetical protein	-1.49	1.26E-07	Unknown
Contig9465_s_at	Hypothetical protein	-1.48	9.52E-08	Unknown
Contig10389_at	Unknown protein	-1.47	1.44E-07	Unknown
Contig12065_at	Putative protein	-1.47	3.70E-08	Unknown
Contig16765_at	Hypothetical protein	-1.47	1.89E-06	Unknown
Contig22605_at	Unknown protein	-1.47	4.03E-08	Unknown
Contig8268_at	Putative protein	-1.47	2.55E-07	Unknown
HVSMEa0013I11r2_s_at	Hypothetical protein	-1.47	5.84E-06	Unknown
Contig10506_at	Hypothetical protein	-1.46	1.05E-07	Unknown
Contig14444_s_at	Unknown protein	-1.46	2.20E-06	Unknown
Contig25962_at	Putative protein	-1.46	9.62E-09	Unknown
HD04D15u_at	Putative uncharacterized protein	-1.46	2.93E-06	Unknown

HVSMEm0005N22r2_s_at	Expressed protein	-1.46	6.97E-06	Unknown
Contig10362_at	Putative uncharacterized protein	-1.45	9.23E-08	Unknown
Contig11209_at	Putative VHS2 protein	-1.45	9.43E-08	Unknown
Contig14599_at	Putative protein	-1.45	1.06E-06	Unknown
Contig5513_s_at	Hypothetical protein	-1.45	9.03E-08	Unknown
Contig7446_at	Expressed protein	-1.45	2.33E-06	Unknown
Contig6656_at	Hypothetical protein	-1.44	2.94E-06	Unknown
Contig10044_at	Crs1/yhby domain containing protein	-1.43	1.14E-08	Unknown
Contig12996_at	Putative protein	-1.43	9.05E-07	Unknown
Contig22332_at	Hypothetical protein	-1.43	1.52E-07	Unknown
Contig3791_s_at	Apospory-associated protein C-like	-1.43	9.77E-08	Unknown
Contig5897_at	Hypothetical protein	-1.43	1.10E-07	Unknown
Contig15149_at	Hypothetical protein	-1.42	3.97E-07	Unknown
Contig8932_s_at	Putative protein	-1.42	2.84E-07	Unknown
Contig12494_at	Putative uncharacterized protein	-1.41	2.41E-07	Unknown
Contig13816_at	Hypothetical protein	-1.41	8.67E-09	Unknown
Contig15138_at	Unknown protein	-1.41	2.44E-06	Unknown
Contig19088_at	Hypothetical protein	-1.41	5.27E-06	Unknown
Contig23696_at	WD-repeat protein-like	-1.41	1.36E-08	Unknown
Contig12333_at	Putative protein	-1.4	2.45E-06	Unknown
Contig16920_at	Putative protein	-1.4	2.42E-07	Unknown
Contig18933_s_at	Unknown protein	-1.4	6.07E-07	Unknown
Contig22289_at	Hypothetical protein	-1.4	4.69E-06	Unknown
Contig15072_at	Hypothetical protein	-1.4	6.39E-06	Unknown
Contig13116_at	Hypothetical protein	-1.39	2.35E-07	Unknown
Contig15478_s_at	Hypothetical protein	-1.39	5.88E-06	Unknown
Contig21043_at	Putative uncharacterized protein	-1.39	1.61E-07	Unknown
Contig25351_at	Hypothetical protein	-1.39	5.51E-06	Unknown
Contig4375_at	Putative uncharacterized protein	-1.39	9.69E-07	Unknown
Contig4984_at	Putative large secreted protein	-1.39	1.39E-07	Unknown
Contig9576_at	Unknown protein	-1.39	1.28E-06	Unknown
HVSMEg0010H15r2_s_at	Hypothetical protein	-1.39	4.77E-08	Unknown
Contig10346_at	Putative protein	-1.38	5.52E-05	Unknown

Contig13116_s_at	Hypothetical protein	-1.38	1.27E-07	Unknown
Contig13145_at	Serine-rich protein	-1.38	5.21E-07	Unknown
Contig10006_at	Putative uncharacterized protein	-1.37	2.49E-06	Unknown
Contig16713_at	Putative uncharacterized protein	-1.37	6.96E-08	Unknown
Contig19389_at	Hypothetical protein	-1.37	3.26E-08	Unknown
Contig5710_at	Putative CBS domain containing protein	-1.37	4.42E-05	Unknown
Contig7745_at	Unknown protein	-1.37	6.11E-06	Unknown
Contig8363_at	Putative uncharacterized protein	-1.37	4.31E-06	Unknown
rbah41a21_s_at	Hypothetical protein	-1.37	2.31E-07	Unknown
Contig12585_at	Putative uncharacterized protein	-1.36	1.46E-07	Unknown
Contig6164_s_at	Putative protein	-1.36	5.21E-06	Unknown
Contig6598_at	NC domain-containing protein	-1.36	3.06E-07	Unknown
Contig7012_at	Hypothetical protein	-1.36	6.65E-06	Unknown
HS08N07u_at	Hypothetical protein	-1.35	3.56E-08	Unknown
Contig10303_at	Putative protein	-1.34	3.99E-06	Unknown
Contig20190_at	Putative protein	-1.34	2.36E-06	Unknown
Contig11224_at	Unknown protein	-1.33	6.33E-08	Unknown
Contig13852_at	Expressed protein	-1.33	7.04E-07	Unknown
Contig23998_at	Putative protein	-1.33	7.17E-07	Unknown
Contig8456_at	Putative uncharacterized protein	-1.33	1.52E-06	Unknown
HVSMEh0089C16r2_at	Hypothetical protein	-1.33	1.60E-06	Unknown
Contig12782_at	Uncharacterized protein	-1.32	1.78E-05	Unknown
Contig14460_at	Putative uncharacterized protein	-1.32	7.72E-06	Unknown
Contig5336_s_at	Hypothetical protein	-1.32	2.47E-06	Unknown
Contig6283_at	Putative protein	-1.32	1.20E-05	Unknown
Contig7602_s_at	Hypothetical protein	-1.32	2.30E-07	Unknown
HVSMEc0014G08r2_at	Hypothetical protein	-1.32	1.47E-06	Unknown
Contig11417_at	Hypothetical protein	-1.31	1.57E-07	Unknown
Contig6170_s_at	Unknown protein	-1.31	0	Unknown
Contig9524_at	Expressed protein	-1.31	1.72E-07	Unknown
HV_CEb0015L05r2_at	Putative uncharacterized protein	-1.31	3.76E-06	Unknown
Contig19139_at	Unknown protein	-1.31	0	Unknown
Contig8809_at	Expressed protein	-1.3	4.96E-07	Unknown

Contig18031_at	Hypothetical protein	-1.29	1.77E-08	Unknown
Contig18381_at	Putative uncharacterized protein	-1.29	4.41E-07	Unknown
Contig4063_at	Hypothetical protein	-1.29	8.72E-06	Unknown
Contig7665_at	Hypothetical protein	-1.29	2.31E-07	Unknown
Contig19861_at	Hypothetical protein	-1.29	0	Unknown
Contig15737_at	Unknown protein	-1.28	4.34E-06	Unknown
Contig25007_at	Expressed protein	-1.28	4.64E-06	Unknown
Contig6856_at	Putative protein	-1.28	6.99E-08	Unknown
Contig7285_s_at	Hypothetical protein	-1.28	1.21E-07	Unknown
HT09L15u_s_at	Hypothetical protein	-1.28	1.82E-07	Unknown
Contig12638_at	Hypothetical protein	-1.27	9.25E-06	Unknown
Contig15363_at	Hypothetical protein	-1.27	3.27E-07	Unknown
Contig23874_at	Unknown protein	-1.27	4.11E-05	Unknown
Contig9264_at	Unknown protein	-1.27	3.72E-06	Unknown
Contig14081_at	Putative uncharacterized protein	-1.26	4.71E-08	Unknown
Contig8792_s_at	Hypothetical protein	-1.26	2.69E-07	Unknown
HVSMEa0004J10r2_at	Expressed protein	-1.26	1.74E-05	Unknown
Contig14780_at	Unknown protein	-1.25	2.59E-05	Unknown
Contig24071_at	Expressed protein	-1.25	4.35E-08	Unknown
Contig24540_at	Putative uncharacterized protein	-1.25	8.49E-07	Unknown
Contig7680_at	Putative T-complex protein 11	-1.25	1.81E-07	Unknown
Contig20211_at	Expressed protein	-1.24	8.17E-06	Unknown
Contig7333_at	Hypothetical protein	-1.24	1.18E-06	Unknown
Contig8027_at	Expressed protein	-1.24	4.56E-07	Unknown
Contig11479_at	Hypothetical protein	-1.23	1.92E-05	Unknown
Contig13287_at	Hypothetical protein	-1.23	6.52E-06	Unknown
Contig16243_at	Putative uncharacterized protein	-1.23	7.79E-07	Unknown
Contig17794_at	Expressed protein	-1.23	1.89E-06	Unknown
Contig9396_at	Hypothetical protein	-1.23	4.92E-06	Unknown
Contig6868_at	Hypothetical protein	-1.23	0	Unknown
Contig18640_at	Expressed protein	-1.22	8.55E-07	Unknown
Contig20543_at	Unknown protein	-1.22	4.39E-05	Unknown
Contig8045_at	Putative protein	-1.22	1.73E-07	Unknown

Contig12884_at	Unknown protein	-1.21	1.54E-07	Unknown
Contig17774_at	Putative uncharacterized protein	-1.21	1.91E-06	Unknown
Contig22558_at	Hypothetical protein	-1.21	1.70E-06	Unknown
Contig25813_at	Hypothetical protein	-1.21	1.65E-06	Unknown
Contig5135_s_at	Putative protein	-1.21	1.13E-05	Unknown
Contig10787_at	Putative protein	-1.2	9.13E-08	Unknown
Contig12171_at	Hypothetical protein	-1.2	7.45E-08	Unknown
Contig12180_at	Expressed protein	-1.2	1.36E-07	Unknown
Contig629_s_at	Hypothetical protein	-1.2	4.00E-06	Unknown
Contig16536_at	Hypothetical protein	-1.2	0	Unknown
Contig18021_at	Hypothetical protein	-1.19	2.15E-05	Unknown
Contig2630_at	Hypothetical protein	-1.19	0	Unknown
Contig10994_s_at	Hypothetical protein	-1.18	7.09E-07	Unknown
Contig12056_s_at	Expressed protein	-1.18	4.92E-06	Unknown
Contig17073_at	Putative protein	-1.18	6.09E-06	Unknown
Contig3836_at	Hypothetical protein	-1.18	2.69E-06	Unknown
Contig9136_at	Putative protein	-1.18	6.78E-05	Unknown
Contig14634_at	Hypothetical protein	-1.16	8.92E-06	Unknown
HU01C17w_at	Ternary complex factor MIP1-like	-1.16	2.00E-07	Unknown
Contig7965_at	Hypothetical protein	-1.16	5.16E-08	Unknown
Contig11372_at	Hypothetical protein	-1.15	7.07E-07	Unknown
Contig13735_at	Hypothetical protein	-1.15	1.94E-05	Unknown
Contig15206_at	Hypothetical protein	-1.15	2.88E-07	Unknown
Contig18424_at	Hypothetical protein	-1.15	3.64E-05	Unknown
Contig1881_s_at	Putative uncharacterized protein	-1.15	4.54E-06	Unknown
Contig4826_at	Putative uncharacterized protein	-1.15	6.12E-07	Unknown
Contig8954_at	Expressed protein	-1.15	1.93E-07	Unknown
Contig18074_at	Hypothetical protein	-1.15	2.90E-05	Unknown
Contig14842_at	Hypothetical protein	-1.14	5.03E-06	Unknown
Contig20659_at	Hypothetical protein	-1.14	4.92E-05	Unknown
Contig6169_at	Unknown protein	-1.14	0	Unknown
Contig6283_s_at	Putative protein	-1.14	4.41E-07	Unknown
Contig7955_s_at	Putative protein	-1.14	9.04E-07	Unknown

HVSMEb0005N03r2_at	Putative uncharacterized protein	-1.14	1.72E-06	Unknown
HY03L11u_at	Expressed protein	-1.14	4.66E-07	Unknown
Contig10116_at	Hypothetical protein	-1.13	8.04E-06	Unknown
Contig4345_at	Hypothetical protein	-1.13	2.53E-07	Unknown
Contig863_s_at	Expressed protein	-1.13	1.63E-05	Unknown
Contig8910_at	Unknown protein	-1.13	7.41E-07	Unknown
Contig10446_at	Unknown protein	-1.12	1.15E-06	Unknown
Contig11584_at	Hypothetical protein	-1.12	1.29E-05	Unknown
Contig12153_at	Hypothetical protein	-1.12	2.24E-05	Unknown
Contig18449_at	Hypothetical protein	-1.12	3.91E-07	Unknown
Contig4578_at	Unnamed protein product	-1.12	5.59E-06	Unknown
HY09P21u_s_at	Hypothetical protein	-1.12	6.54E-06	Unknown
Contig8683_at	Putative protein	-1.11	2.79E-05	Unknown
Contig8934_at	Putative protein	-1.11	1.42E-05	Unknown
Contig9920_at	Expressed protein	-1.11	4.94E-07	Unknown
HV_CEb0010O21r2_at	Hypothetical protein	-1.11	5.03E-06	Unknown
Contig12868_at	Expressed protein	-1.1	1.30E-05	Unknown
Contig17088_at	Unknown protein	-1.1	9.55E-07	Unknown
Contig11494_at	Putative uncharacterized protein	-1.09	3.51E-06	Unknown
Contig18324_at	Expressed protein	-1.09	6.38E-06	Unknown
Contig24531_at	Unknown protein	-1.09	6.13E-07	Unknown
Contig6841_at	Putative protein	-1.09	1.73E-05	Unknown
Contig6164_at	Putative protein	-1.08	6.90E-07	Unknown
Contig7508_at	Putative protein	-1.08	6.01E-07	Unknown
Contig12473_at	Expressed protein	-1.07	1.89E-06	Unknown
Contig14014_at	Expressed protein	-1.07	5.20E-06	Unknown
Contig14969_at	Hypothetical protein	-1.07	7.88E-06	Unknown
Contig19802_at	Hypothetical protein	-1.07	1.29E-06	Unknown
Contig4369_at	Putative protein	-1.07	1.54E-06	Unknown
Contig5002_at	Putative uncharacterized protein	-1.07	9.32E-07	Unknown
Contig9230_s_at	Hypothetical protein	-1.07	3.01E-07	Unknown
rbaal15p09_s_at	Hypothetical protein	-1.07	7.65E-05	Unknown
Contig12805_at	Putative protein	-1.06	5.72E-07	Unknown

Contig15122_at	Hypothetical protein	-1.06	6.30E-07	Unknown
Contig17069_at	Hypothetical protein	-1.06	1.20E-06	Unknown
Contig26179_at	Putative protein	-1.06	1.09E-06	Unknown
Contig7556_s_at	Hypothetical protein	-1.06	6.60E-06	Unknown
Contig8567_at	Putative uncharacterized protein	-1.06	8.17E-06	Unknown
Contig11447_at	Expressed protein	-1.05	1.92E-05	Unknown
Contig11867_s_at	Putative PIT1	-1.05	1.69E-05	Unknown
Contig13021_at	Hypothetical protein	-1.05	6.73E-07	Unknown
Contig15357_s_at	Hypothetical protein	-1.05	0	Unknown
Contig16047_at	Hypothetical protein	-1.05	1.45E-06	Unknown
Contig4383_s_at	Expressed protein	-1.05	1.56E-06	Unknown
Contig7792_at	Unknown protein	-1.05	1.59E-05	Unknown
Contig8843_at	Hypothetical protein	-1.05	3.59E-07	Unknown
Contig11560_at	Putative protein	-1.04	6.82E-07	Unknown
Contig13339_at	Unnamed protein product	-1.04	0	Unknown
Contig16410_at	Hypothetical protein	-1.04	7.41E-06	Unknown
Contig20778_at	Brain protein 44-like	-1.04	9.51E-05	Unknown
Contig20825_at	Hypothetical protein	-1.04	5.51E-06	Unknown
Contig5746_at	Putative protein	-1.04	2.75E-06	Unknown
Contig7030_at	Unknown protein	-1.04	2.32E-05	Unknown
Contig11997_at	Hypothetical protein	-1.03	1.40E-06	Unknown
Contig1247_s_at	Expressed protein	-1.03	3.30E-07	Unknown
Contig14987_at	Unknown protein	-1.03	3.08E-06	Unknown
Contig17958_at	Putative protein	-1.03	3.51E-06	Unknown
Contig20700_at	Hypothetical protein	-1.03	4.96E-06	Unknown
Contig5877_at	Putative uncharacterized protein	-1.03	4.47E-05	Unknown
Contig9298_at	Hypothetical protein	-1.03	5.77E-05	Unknown
Contig12981_at	Hypothetical protein	-1.02	5.25E-06	Unknown
Contig19399_at	Putative uncharacterized protein	-1.02	0	Unknown
Contig20791_at	Expressed protein	-1.02	3.71E-06	Unknown
Contig4118_at	Putative apospory-associated protein C	-1.02	3.07E-06	Unknown
Contig5394_at	Putative uncharacterized protein	-1.02	1.55E-05	Unknown
Contig6209_at	Hypothetical protein	-1.02	7.96E-05	Unknown

Contig8024_at	Putative uncharacterized protein	-1.02	6.16E-07	Unknown
Contig11702_at	Expressed protein	-1.02	3.87E-05	Unknown
Contig12668_s_at	Putative uncharacterized protein	-1.01	5.35E-06	Unknown
Contig14754_at	Putative uncharacterized protein	-1.01	1.69E-05	Unknown
Contig12403_at	Hypothetical protein	-1	6.05E-07	Unknown

Appendix 1: Table 2. Full list of genes significantly up-regulated in the local leaf region

Affymetrix Probe Set ID	Annotation	Fold Change (Log2)	FDR Adjusted P Value	Functional Classification
Contig2877_at	Beta-expansin	3.28	1.60E-09	Biogenesis of cellular components
HV10J12u_s_at	Actin depolymerization factor-like protein	3.26	1.75E-10	Biogenesis of cellular components
Contig26515_at	Annexin	3.1	8.38E-11	Biogenesis of cellular components
Contig13144_at	Exocyst subunit EXO70 family protein	2.94	4.60E-11	Biogenesis of cellular components
HVSMEl0013E16r2_s_at	Xyloglucan fucosyltransferase	2.53	1.43E-09	Biogenesis of cellular components
HW08J24V_at	Formin-like protein	2.39	1.67E-08	Biogenesis of cellular components
Contig7773_at	Ankyrin-like protein	2.36	1.41E-10	Biogenesis of cellular components
Contig8067_at	Cellulose synthase-like protein	2.18	6.00E-08	Biogenesis of cellular components
Contig16931_at	Galactoside 2-L-fucosyltransferase	2.1	6.26E-08	Biogenesis of cellular components
HW03A23u_at	Cellulose synthase-like A3	1.76	7.89E-07	Biogenesis of cellular components
Contig9151_at	Actin-like protein	1.59	2.99E-07	Biogenesis of cellular components
Contig17655_at	Putative extensin	1.5	2.24E-07	Biogenesis of cellular components
Contig16241_at	Protein fimbrin 1	1.37	3.38E-08	Biogenesis of cellular components
Contig18356_at	Putative actin interacting protein	1.37	3.59E-07	Biogenesis of cellular components
HB25G16r_at	Putative alpha-expansin OsEXPA16	1.37	0	Biogenesis of cellular components
Contig3643_s_at	Phragmoplastin	1.34	8.01E-06	Biogenesis of cellular components
rbasd15h01_s_at	Cellulose synthase-like protein	1.33	3.32E-06	Biogenesis of cellular components
Contig3349_at	Annexin	1.25	5.75E-07	Biogenesis of cellular components
Contig20968_at	Putative phosphatidylserine synthase	1.23	1.91E-07	Biogenesis of cellular components
Contig1397_at	Actin-1	1.18	2.29E-05	Biogenesis of cellular components
Contig5177_s_at	Putative actin	1.17	6.53E-05	Biogenesis of cellular components
Contig1003_at	Putative elongation factor 2	1.09	1.55E-05	Biogenesis of cellular components
Contig803_x_at	Tubulin alpha chain	1.08	4.47E-07	Biogenesis of cellular components
Contig3992_at	Putative endosomal protein	1.05	7.33E-05	Biogenesis of cellular components
Contig11483_at	Shrunken seed protein	1.02	8.95E-06	Biogenesis of cellular components
Contig803_at	Tubulin alpha-2 chain	1.02	1.38E-05	Biogenesis of cellular components
Contig4113_at	Endonuclease	4.8	1.80E-12	Cell cycle and DNA processing
Contig11623_at	Histone H2B	4.77	1.32E-10	Cell cycle and DNA processing

Contig6214_at	Cell Division Protein AAA ATPase family	4.67	3.00E-13	Cell cycle and DNA processing
Contig4111_at	Nuclease I	2.76	3.33E-09	Cell cycle and DNA processing
Contig94_at	Histone H3	2.52	1.39E-08	Cell cycle and DNA processing
Contig196_s_at	Histone H3	2.5	4.67E-09	Cell cycle and DNA processing
Contig179_s_at	H3 histone	2.36	5.98E-09	Cell cycle and DNA processing
Contig11232_at	B-type cyclin	2.24	8.57E-10	Cell cycle and DNA processing
Contig19871_at	Putative cell cycle dependent kinase C	2.19	1.72E-09	Cell cycle and DNA processing
Contig76_at	Histone H2A	2.07	4.28E-08	Cell cycle and DNA processing
HA12K13u_at	Putative histone H2A	2.05	1.83E-08	Cell cycle and DNA processing
Contig1147_s_at	Histone H2B.2	2.02	2.43E-07	Cell cycle and DNA processing
Contig11076_at	Putative nuclease	1.96	2.01E-09	Cell cycle and DNA processing
HA12K13u_s_at	Putative histone H2A	1.67	5.06E-07	Cell cycle and DNA processing
Contig17628_at	Cyclin-like	1.63	2.63E-06	Cell cycle and DNA processing
rbags21h11_at	Histone H2B.2	1.43	2.14E-07	Cell cycle and DNA processing
Contig17205_at	Putative DNA repair protein rhp16	1.21	2.49E-07	Cell cycle and DNA processing
Contig21355_at	Cell division control protein	1.19	1.44E-07	Cell cycle and DNA processing
Contig8195_at	Ribonucleotide diphosphate reductase	1.19	4.67E-06	Cell cycle and DNA processing
Contig1151_s_at	Histone H2B.2	1.18	9.51E-07	Cell cycle and DNA processing
Contig1179_at	Histone H2B.2	1.15	0	Cell cycle and DNA processing
Contig11418_at	ARTEMIS protein	1.11	3.97E-07	Cell cycle and DNA processing
HU14M07u_s_at	DNA replication licensing factor mcm4	1.1	1.62E-06	Cell cycle and DNA processing
Contig8057_at	DNA-damage inducible protein DDI1-like	1.07	4.04E-06	Cell cycle and DNA processing
HA01J24u_x_at	Histone H2B.2	1.06	8.11E-06	Cell cycle and DNA processing
Contig1156_at	Histone H2B.2	1.05	4.18E-06	Cell cycle and DNA processing
Contig3054_s_at	Senescence-associated protein 5	3.11	2.07E-10	Cell fate
Contig1889_at	Prohibitin	2.28	6.19E-08	Cell fate
HZ45H16r_s_at	Prohibitin	1.85	1.16E-08	Cell fate
Contig10052_at	Putative senescence-associated protein	1.82	3.97E-06	Cell fate
HT11C04u_s_at	Putative senescence-associated protein	1.68	0	Cell fate
Contig8969_at	BRICK1	1.57	5.11E-08	Cell fate
Contig25764_at	Leaf senescence related protein-like	1.2	0	Cell fate
Contig6267_at	Hepatocyte growth factor-regulated-like protein	1.19	2.68E-07	Cell fate
Contig3130_s_at	Putative prohibitin	1.11	0	Cell fate

Contig10057_s_at	Putative esterase PIR7B	7.52	5.47E-13	Cell rescue, defence and virulence
Contig19549_at	Putative NADPH HC toxin reductase	6.48	1.29E-13	Cell rescue, defence and virulence
Contig10057_at	PIR7B Protein	6.41	2.82E-10	Cell rescue, defence and virulence
Contig1802_at	Phenylalanine ammonia-lyase	6.27	1.91E-10	Cell rescue, defence and virulence
Contig3017_at	Oxalate oxidase	6.22	1.53E-10	Cell rescue, defence and virulence
HY03N19u_s_at	Lipoxygenase 2	6.12	1.82E-09	Cell rescue, defence and virulence
Contig24993_at	Pathogenesis-related protein 1a	6.08	2.78E-13	Cell rescue, defence and virulence
Contig3501_at	60 kDa jasmonate-induced protein pir	5.96	7.65E-08	Cell rescue, defence and virulence
Contig1795_at	Phenylalanine ammonia-lyase	5.67	5.63E-11	Cell rescue, defence and virulence
Contig1800_at	Phenylalanine ammonia-lyase	5.64	5.63E-11	Cell rescue, defence and virulence
Contig7887_at	Putative 32.7 kDa jasmonate-induced protein	5.53	4.43E-08	Cell rescue, defence and virulence
Contig7886_at	Putative 32.7 kDa jasmonate-induced protein	5.43	6.49E-11	Cell rescue, defence and virulence
Contig12776_at	Glutathione transferase	5.33	6.11E-11	Cell rescue, defence and virulence
Contig18558_at	Phenylalanine ammonia-lyase	5.23	1.33E-11	Cell rescue, defence and virulence
Contig23540_at	Chitinase	5.22	2.68E-13	Cell rescue, defence and virulence
Contig3208_at	Blue copper binding protein	5.21	1.26E-11	Cell rescue, defence and virulence
Contig2123_s_at	Peroxidase	5.2	6.48E-11	Cell rescue, defence and virulence
Contig3211_at	Blue copper-binding protein	5.04	2.16E-12	Cell rescue, defence and virulence
Contig12382_at	Putative xylanase inhibitor	5.01	1.08E-11	Cell rescue, defence and virulence
Contig15099_s_at	Pathogenesis-related protein 4	5.01	3.01E-11	Cell rescue, defence and virulence
Contig2789_at	Thaumatin-like protein TLP5	5	2.61E-11	Cell rescue, defence and virulence
Contig3209_s_at	Blue copper binding protein	4.97	1.11E-10	Cell rescue, defence and virulence
Contig9764_at	Glutathione-S-transferase Cla47	4.96	9.15E-12	Cell rescue, defence and virulence
HVSMEa0011L14r2_s_at	Glutathione S-transferase	4.95	2.16E-12	Cell rescue, defence and virulence
Contig3018_at	Oxalate oxidase 2 precursor (Germin)	4.94	6.47E-11	Cell rescue, defence and virulence
Contig1805_s_at	Phenylalanine ammonia-lyase	4.88	2.06E-08	Cell rescue, defence and virulence
U43494_at	Chalcone synthase-like protein	4.82	7.78E-13	Cell rescue, defence and virulence
Contig10245_at	Disease resistance response protein	4.81	3.92E-12	Cell rescue, defence and virulence
Contig13968_at	Mlo3	4.75	2.83E-10	Cell rescue, defence and virulence
HV_CEb0004O15r2_s_at	Putative glutathione S-transferase	4.66	3.10E-10	Cell rescue, defence and virulence
Contig7080_at	Putative peroxidase	4.65	4.84E-10	Cell rescue, defence and virulence
Contig1803_at	Phenylalanine ammonia-lyase	4.64	3.26E-10	Cell rescue, defence and virulence
Contig1800_x_at	Phenylalanine ammonia-lyase	4.5	9.92E-11	Cell rescue, defence and virulence

Contig7415_at	Putative glutathione transferase	4.43	2.17E-11	Cell rescue, defence and virulence
Contig5013_at	Blue copper-binding protein homolog	4.41	2.63E-08	Cell rescue, defence and virulence
Contig4633_x_at	Xylanase inhibitor	4.4	5.49E-09	Cell rescue, defence and virulence
Contig6515_at	Peroxidase	4.38	3.18E-12	Cell rescue, defence and virulence
HVSMEb0006O01r2_at	Mlo3	4.36	2.71E-10	Cell rescue, defence and virulence
Contig1800_s_at	Phenylalanine ammonia-lyase	4.28	2.70E-11	Cell rescue, defence and virulence
Contig1799_s_at	Phenylalanine ammonia-lyase	4.27	1.98E-09	Cell rescue, defence and virulence
Contig4406_x_at	Pathogenesis-related protein 10	4.27	6.24E-09	Cell rescue, defence and virulence
Contig13657_at	Putative peroxidase	4.25	8.59E-13	Cell rescue, defence and virulence
Contig14498_at	Chitinase	4.21	1.28E-09	Cell rescue, defence and virulence
Contig6546_at	Safener-induced In2.1-like protein	4.16	6.52E-12	Cell rescue, defence and virulence
EBro08_SQ010_O16_at	Disease resistance response protein-related	4.16	1.64E-10	Cell rescue, defence and virulence
Contig15951_at	Glutathione-S-transferase	4.03	1.37E-10	Cell rescue, defence and virulence
Contig1597_s_at	Putative glutathione-S-transferase	4.03	5.80E-10	Cell rescue, defence and virulence
Contig19921_at	Immediate-early fungal elicitor protein CMPG1	4.02	9.48E-08	Cell rescue, defence and virulence
Contig5369_at	Pathogenesis-related protein 1	4.01	9.36E-10	Cell rescue, defence and virulence
EBro03_SQ003_J21_at	Putative peroxidase	4	6.45E-07	Cell rescue, defence and virulence
HD08F14r_x_at	Pathogenesis-related protein 10	4	2.70E-11	Cell rescue, defence and virulence
Contig4633_at	Xylanase inhibitor	3.99	3.08E-09	Cell rescue, defence and virulence
HI02E21u_s_at	Lipoxygenase 2	3.99	1.43E-10	Cell rescue, defence and virulence
Contig19979_at	Putative NBS-LRR type resistance protein	3.94	3.41E-12	Cell rescue, defence and virulence
Contig5368_at	Pathogenesis-related protein 1	3.92	7.38E-10	Cell rescue, defence and virulence
Contig14679_at	Xylanase inhibitor	3.91	3.28E-10	Cell rescue, defence and virulence
HE01O15u_at	Extracellular dermal glycoprotein	3.86	2.77E-09	Cell rescue, defence and virulence
Contig2119_at	Peroxidase (prx8 gene)	3.85	8.47E-10	Cell rescue, defence and virulence
HVSMEh0081C04r2_s_at	Putative xylanase inhibitor	3.82	3.89E-09	Cell rescue, defence and virulence
Contig3667_s_at	Thaumatin-like protein TLP8	3.79	5.97E-12	Cell rescue, defence and virulence
Contig1518_at	Oxalate oxidase	3.75	3.92E-12	Cell rescue, defence and virulence
Contig4337_at	Peroxidase	3.74	6.30E-10	Cell rescue, defence and virulence
HV_CEb0002J23r2_s_at	Blue copper binding protein	3.72	2.68E-10	Cell rescue, defence and virulence
Contig8958_at	Glutathione-S-transferase Cla47	3.68	5.24E-12	Cell rescue, defence and virulence
Contig4402_s_at	Pathogenesis-related protein 10	3.67	4.58E-10	Cell rescue, defence and virulence
Contig6008_s_at	Glutathione S-transferase GST	3.64	7.14E-12	Cell rescue, defence and virulence

Contig21446_at	Immediate-early fungal elicitor protein CMPG1	3.56	2.24E-10	Cell rescue, defence and virulence
Contig6009_at	Glutathione S-transferase	3.54	9.19E-13	Cell rescue, defence and virulence
Contig2900_at	Jasmonate induced protein	3.52	0	Cell rescue, defence and virulence
Contig1568_x_at	Thionin BTH7 precursor	3.51	0	Cell rescue, defence and virulence
HD07M22r_s_at	Putative protease inhibitor	3.51	4.50E-10	Cell rescue, defence and virulence
Contig10860_at	Germin-like protein	3.47	1.10E-11	Cell rescue, defence and virulence
Contig11789_at	Elicitor-responsive protein 1	3.42	1.92E-10	Cell rescue, defence and virulence
Contig12550_at	Endo-1,3;1,4-beta-D-glucanase precursor	3.39	4.36E-10	Cell rescue, defence and virulence
Contig8905_at	Xylanase inhibitor protein I	3.38	1.58E-09	Cell rescue, defence and virulence
Contig2243_at	Wheat aluminum induced protein wali 5	3.37	3.85E-10	Cell rescue, defence and virulence
Contig6155_at	Jasmonate induced protein	3.36	0	Cell rescue, defence and virulence
Contig6967_at	Glucan endo-1,3-beta-glucosidase	3.36	1.10E-10	Cell rescue, defence and virulence
Contig10004_at	Putative thaumatin-like protein	3.34	2.11E-10	Cell rescue, defence and virulence
Contig12776_s_at	Glutathione transferase	3.33	2.57E-10	Cell rescue, defence and virulence
Contig5023_at	Class III chitinase	3.33	2.58E-10	Cell rescue, defence and virulence
Contig4173_at	Chitinase	3.3	1.04E-10	Cell rescue, defence and virulence
Contig19929_at	Class III peroxidase 70	3.29	3.97E-09	Cell rescue, defence and virulence
HVSMEb0009H14r2_s_at	Wheat aluminum induced protein wali 3	3.29	3.32E-10	Cell rescue, defence and virulence
Contig2087_s_at	Bowman-Birk type trypsin inhibitor	3.28	2.36E-10	Cell rescue, defence and virulence
Contig2212_s_at	Pathogenesis-related protein 1	3.27	2.32E-08	Cell rescue, defence and virulence
Contig4632_s_at	Xylanase inhibitor	3.27	5.57E-09	Cell rescue, defence and virulence
Contig10193_at	Elicitor-responsive protein	3.24	5.38E-11	Cell rescue, defence and virulence
Contig24491_at	Putative beta-glucosidase	3.24	3.02E-11	Cell rescue, defence and virulence
Contig3699_s_at	Non-specific lipid-transfer protein	3.24	7.53E-11	Cell rescue, defence and virulence
EBem10_SQ002_I10_s_at	Thaumatin-like protein TLP8	3.23	8.91E-12	Cell rescue, defence and virulence
Contig3499_at	60 kDa jasmonate-induced protein	3.21	4.18E-09	Cell rescue, defence and virulence
HVSMEm0015M15r2_s_at	PAL	3.2	1.36E-08	Cell rescue, defence and virulence
Contig4324_at	Chitinase	3.19	2.51E-09	Cell rescue, defence and virulence
Contig25420_at	Putative immediate-early fungal elicitor protein CMPG1	3.16	2.96E-09	Cell rescue, defence and virulence
Contig4324_s_at	Chitinase	3.16	3.23E-09	Cell rescue, defence and virulence
Contig4326_s_at	chitinase IV	3.16	2.20E-11	Cell rescue, defence and virulence
Contig2992_s_at	Chitinase	3.14	8.48E-09	Cell rescue, defence and virulence
HT07J20u_x_at	Barwin homolog wheatwin2 precursor	3.14	3.85E-06	Cell rescue, defence and virulence

Contig19197_at	NBS-LRR type disease resistance protein	3.11	5.80E-10	Cell rescue, defence and virulence
HVSMEm0005P05r2_at	Peroxidase	3.11	1.97E-09	Cell rescue, defence and virulence
Contig12649_at	Cell death associated protein	3.1	1.49E-10	Cell rescue, defence and virulence
Contig1737_at	Lipoxygenase	3.08	2.29E-09	Cell rescue, defence and virulence
Contig26335_at	Lipoxygenase-like protein (lox gene)	3.08	1.37E-08	Cell rescue, defence and virulence
Contig18367_at	Putative glutathione S-transferase	3.07	2.31E-07	Cell rescue, defence and virulence
baak13l10_s_at	Putative stripe rust resistance protein Yr10	3.06	9.84E-11	Cell rescue, defence and virulence
Contig1797_x_at	Phenylalanine ammonia-lyase	3.06	3.33E-10	Cell rescue, defence and virulence
HVSMEb0006K18r2_at	NADPH-dependent HC-toxin reductase	3.06	3.18E-11	Cell rescue, defence and virulence
Contig15515_at	Disease resistance response protein-like	3.05	2.01E-09	Cell rescue, defence and virulence
Contig1862_at	Peroxidase	3.05	2.80E-11	Cell rescue, defence and virulence
Contig2790_s_at	Thaumatin-like protein TLP7	3.05	9.56E-10	Cell rescue, defence and virulence
Contig1871_at	Peroxidase	3.02	1.95E-08	Cell rescue, defence and virulence
Contig2736_s_at	Beta-glucosidase	3.01	4.95E-09	Cell rescue, defence and virulence
Contig1679_s_at	23 kDa jasmonate-induced protein	2.98	0	Cell rescue, defence and virulence
Contig3323_at	BAX inhibitor 1	2.96	5.87E-10	Cell rescue, defence and virulence
Contig18459_at	Putative stripe rust resistance protein Yr10	2.95	1.10E-09	Cell rescue, defence and virulence
AF250937_s_at	Germin-like protein	2.92	2.11E-10	Cell rescue, defence and virulence
HF01K09w_at	Putative Avr9/Cf-9 rapidly elicited protein 141	2.91	4.51E-10	Cell rescue, defence and virulence
Contig6333_at	Putative glutathione S-transferase	2.89	1.54E-10	Cell rescue, defence and virulence
Contig19684_at	Putative hypersensitivity-related (Hsr)protein	2.88	6.68E-10	Cell rescue, defence and virulence
Contig11361_at	Putative peroxidase	2.85	6.09E-09	Cell rescue, defence and virulence
Contig13350_at	Beta-1,3-glucanase	2.83	3.18E-09	Cell rescue, defence and virulence
Contig14304_at	Glutathione S-transferase	2.83	1.24E-09	Cell rescue, defence and virulence
Contig2088_s_at	Bowman-Birk type trypsin inhibitor	2.81	2.71E-05	Cell rescue, defence and virulence
Contig13288_at	Lipoxygenase 7	2.8	1.04E-09	Cell rescue, defence and virulence
Contig4405_x_at	Pathogenesis-related protein 10	2.8	7.20E-09	Cell rescue, defence and virulence
Contig7125_s_at	Beta carotene hydroxylase	2.8	2.48E-10	Cell rescue, defence and virulence
Contig2550_x_at	Pathogenesis-related protein 4	2.78	7.52E-10	Cell rescue, defence and virulence
HV04J01r_at	Glutathione peroxidase-like protein	2.78	1.09E-08	Cell rescue, defence and virulence
Contig11146_at	NADPH-dependent HC-toxin reductase	2.76	8.92E-11	Cell rescue, defence and virulence
Contig3814_at	Putative delta-1-pyrroline-5-carboxylate synthetase	2.73	6.30E-10	Cell rescue, defence and virulence
Contig13901_at	Glutathione S-transferase	2.7	8.40E-08	Cell rescue, defence and virulence

Contig2975_s_at	Glutathione S-transferase	2.66	8.03E-10	Cell rescue, defence and virulence
Contig7425_at	Putative stress-induced protein sti1	2.66	1.23E-10	Cell rescue, defence and virulence
Contig4054_s_at	Pathogenesis-related protein 1C precursor	2.65	1.56E-07	Cell rescue, defence and virulence
Contig5705_at	Putative PrMC3	2.65	7.77E-11	Cell rescue, defence and virulence
Contig2946_at	Monodehydroascorbate reductase	2.64	1.03E-08	Cell rescue, defence and virulence
Contig3151_at	Germin A	2.61	3.57E-09	Cell rescue, defence and virulence
Contig17082_at	Bowman-birk type trypsin inhibitor	2.6	4.16E-08	Cell rescue, defence and virulence
Contig22666_at	Non-specific lipid-transfer protein	2.59	9.06E-09	Cell rescue, defence and virulence
Contig4131_at	Probable L-ascorbate peroxidase 7	2.59	1.10E-10	Cell rescue, defence and virulence
Contig1797_at	Phenylalanine ammonia-lyase	2.58	2.15E-09	Cell rescue, defence and virulence
Contig21119_at	Putative HYS1/CPR5	2.58	2.24E-10	Cell rescue, defence and virulence
Contig13952_at	TMV response-related gene product	2.54	8.29E-10	Cell rescue, defence and virulence
Contig7171_s_at	Glutathione-S-transferase	2.54	2.23E-09	Cell rescue, defence and virulence
Contig4326_at	Chitinase IV	2.52	6.93E-08	Cell rescue, defence and virulence
Contig7691_at	Pathogen induced protein 2-4	2.51	1.86E-09	Cell rescue, defence and virulence
Contig2118_at	Peroxidase	2.44	3.00E-08	Cell rescue, defence and virulence
Contig2899_s_at	Jasmonate induced protein	2.43	0	Cell rescue, defence and virulence
Contig23737_at	Putative glutathione S-transferase	2.41	6.05E-09	Cell rescue, defence and virulence
Contig5838_at	Glutathione-S-transferase 2	2.41	3.59E-06	Cell rescue, defence and virulence
Contig6547_at	Stem rust resistance protein Rpg1	2.4	3.06E-09	Cell rescue, defence and virulence
Contig2211_at	Pathogenesis-related protein 1	2.37	5.26E-10	Cell rescue, defence and virulence
Contig2213_s_at	Pathogenesis-related protein bpr1-1 precursor	2.37	2.42E-07	Cell rescue, defence and virulence
Contig4044_at	Putative glutathione S-transferase	2.36	2.15E-09	Cell rescue, defence and virulence
Contig17334_at	Blue copper binding protein-like	2.33	9.68E-10	Cell rescue, defence and virulence
HV14J15u_s_at	Putative beta-1,3-glucanase	2.33	4.83E-06	Cell rescue, defence and virulence
HVSMEn0006O09f2_x_at	Phenylalanine ammonia-lyase	2.32	2.87E-09	Cell rescue, defence and virulence
Contig3155_s_at	Germin A	2.31	1.56E-06	Cell rescue, defence and virulence
Contig3697_at	Copper homeostasis factor	2.31	4.95E-10	Cell rescue, defence and virulence
Contig3744_s_at	Harpin induced gene 1 homolog	2.31	8.01E-07	Cell rescue, defence and virulence
Contig3746_at	Harpin induced gene 1 homolog	2.3	1.35E-07	Cell rescue, defence and virulence
HZ01K16u_s_at	Putative blue copper protein	2.3	1.14E-08	Cell rescue, defence and virulence
Contig10373_at	Probable esterase PIR7A	2.29	1.43E-09	Cell rescue, defence and virulence
Contig18600_at	Probable lipoxygenase 6	2.29	5.49E-09	Cell rescue, defence and virulence

Contig17107_at	Non-specific lipid-transfer protein	2.28	1.40E-08	Cell rescue, defence and virulence
HVSMEf0020A12r2_s_at	Lipoxygenase	2.28	1.37E-08	Cell rescue, defence and virulence
Contig2546_at	Putative vacuolar defense protein	2.25	3.94E-06	Cell rescue, defence and virulence
Contig4056_s_at	Pathogenesis-related protein 1	2.24	6.36E-07	Cell rescue, defence and virulence
Contig9887_at	Putative glutathione S-transferase	2.24	4.92E-09	Cell rescue, defence and virulence
Contig19755_at	Putative PrMC3	2.23	2.95E-08	Cell rescue, defence and virulence
EBem09_SQ006_P13_at	Putative peroxidase	2.23	7.38E-07	Cell rescue, defence and virulence
Contig4970_at	Beta-D-glucan exohydrolase isoenzyme ExoI	2.21	8.07E-09	Cell rescue, defence and virulence
Contig12237_at	Nonspecific lipid-transfer protein precursor (LTP)	2.19	8.83E-10	Cell rescue, defence and virulence
Contig6516_at	Class III peroxidase 130 precursor	2.19	5.90E-06	Cell rescue, defence and virulence
Contig3574_s_at	Chitinase 2	2.18	7.77E-09	Cell rescue, defence and virulence
rbags15p13_s_at	23 kDa jasmonate-induced protein	2.18	0.02	Cell rescue, defence and virulence
Contig3253_at	Hypoxia-responsive family protein	2.17	1.65E-10	Cell rescue, defence and virulence
Contig12046_at	Pathogenesis related protein-1	2.15	1.59E-07	Cell rescue, defence and virulence
rbags12k11_s_at	ASC1-like protein	2.14	8.32E-06	Cell rescue, defence and virulence
Contig6238_s_at	Glutathione transferase F4	2.13	4.79E-07	Cell rescue, defence and virulence
Contig2899_at	Jasmonate induced protein	2.12	0	Cell rescue, defence and virulence
Contig3156_s_at	Oxalate oxidase-like protein or germin-like protein	2.1	0	Cell rescue, defence and virulence
HW09A20u_at	Glutathione transferase F3	2.1	8.78E-08	Cell rescue, defence and virulence
Contig15853_at	Putative Avr9/Cf-9 rapidly elicited protein	2.09	3.70E-10	Cell rescue, defence and virulence
Contig7359_at	Cell death suppressor protein	2.09	6.71E-10	Cell rescue, defence and virulence
HVSMEl0014B21r2_at	Putative cell death associated protein	2.08	2.38E-08	Cell rescue, defence and virulence
Contig1528_s_at	Germin-like protein	2.06	6.84E-07	Cell rescue, defence and virulence
Contig1852_at	Peroxidase 7	2.06	2.41E-05	Cell rescue, defence and virulence
Contig3578_at	Chitinase 2	2.06	1.98E-10	Cell rescue, defence and virulence
Contig1589_s_at	Putative glutathione-S-transferase (bar2 gene)	2.05	1.36E-07	Cell rescue, defence and virulence
Contig1637_at	1,3-beta glucan endohydrolase precursor	2.05	5.80E-06	Cell rescue, defence and virulence
Contig14387_at	Glutathione S-transferase	2.03	1.36E-08	Cell rescue, defence and virulence
Contig3381_s_at	Subtilisin-chymotrypsin inhibitor 2	2.03	8.34E-07	Cell rescue, defence and virulence
Contig8937_at	Glutathione-S-transferase Cla47	2.03	2.20E-07	Cell rescue, defence and virulence
Contig4423_at	Peroxidase	2.02	4.58E-07	Cell rescue, defence and virulence
HV_CEa0006B20r2_at	PIR7A PROTEIN	2.02	8.12E-09	Cell rescue, defence and virulence
HX14B03r_at	Protein TMV response-related gene product	2.02	7.32E-08	Cell rescue, defence and virulence

Contig3254_at	Hypoxia-responsive family protein	2.01	1.80E-10	Cell rescue, defence and virulence
Contig2990_at	Chitinase	1.99	2.29E-07	Cell rescue, defence and virulence
Contig3315_s_at	Drought-induced hydrophobic protein	1.99	6.40E-09	Cell rescue, defence and virulence
Contig50_x_at	Subtilisin-chymotrypsin inhibitor	1.97	9.41E-07	Cell rescue, defence and virulence
HV_CEb0022F16r2_at	Blue copper-binding protein-like	1.97	6.48E-07	Cell rescue, defence and virulence
Contig21026_at	Glutathione s-transferase	1.96	3.15E-09	Cell rescue, defence and virulence
Contig10142_at	Putative dehydration-responsive protein	1.95	8.69E-05	Cell rescue, defence and virulence
Contig9852_at	Putative blue copper protein	1.95	5.68E-10	Cell rescue, defence and virulence
HVSMEa0014H14r2_s_at	Glutathione S-transferase GST 37	1.93	6.53E-08	Cell rescue, defence and virulence
Contig19545_at	Putative PrMC3	1.92	1.41E-08	Cell rescue, defence and virulence
Contig34_s_at	Putative proteinase inhibitor	1.91	0.05	Cell rescue, defence and virulence
Contig25401_s_at	Putative immediate-early fungal elicitor protein CMPG1	1.9	1.40E-07	Cell rescue, defence and virulence
Contig639_at	Pathogenesis-related protein 4	1.88	5.60E-06	Cell rescue, defence and virulence
Contig13772_at	L-ascorbate oxidase precursor	1.87	4.81E-08	Cell rescue, defence and virulence
Contig4751_at	Wheat aluminum induced protein wali 3	1.87	3.32E-05	Cell rescue, defence and virulence
Contig2209_at	PR-1-type pathogenesis-related protein	1.85	5.18E-07	Cell rescue, defence and virulence
Contig3389_at	Stress-related protein	1.83	4.03E-08	Cell rescue, defence and virulence
Contig3502_at	60 kDa jasmonate-induced protein	1.83	1.82E-09	Cell rescue, defence and virulence
Contig4090_s_at	Cysteine proteinase	1.83	7.19E-08	Cell rescue, defence and virulence
Contig5974_s_at	WIR1A PROTEIN	1.83	1.53E-07	Cell rescue, defence and virulence
Contig5016_at	Pto kinase interactor 1	1.78	9.18E-07	Cell rescue, defence and virulence
HO11K23S_s_at	Putative glutathione S-transferase	1.78	4.74E-08	Cell rescue, defence and virulence
Contig2210_at	Pathogenesis-related protein 1 precursor	1.76	1.73E-05	Cell rescue, defence and virulence
Contig2453_at	Glutathione peroxidase-like protein	1.74	1.91E-07	Cell rescue, defence and virulence
Contig17759_at	Blue copper-binding protein-like	1.73	2.60E-05	Cell rescue, defence and virulence
Contig11289_at	Glucan endo-1,3-beta-D-glucosidase	1.72	5.31E-09	Cell rescue, defence and virulence
Contig1736_at	Lipoxygenase	1.72	1.87E-05	Cell rescue, defence and virulence
HVSMEm0003C15r2_s_at	1,3-beta glucan endohydrolase precursor	1.72	1.47E-06	Cell rescue, defence and virulence
HVSMEc0003K22r2_at	OTU-like cysteine protease	1.71	2.23E-07	Cell rescue, defence and virulence
Contig13240_s_at	Glutathione transferase	1.7	4.17E-08	Cell rescue, defence and virulence
Contig15264_at	Glutathione S-transferase	1.69	9.55E-08	Cell rescue, defence and virulence
Contig538_at	Benzothiadiazole-induced protein (clone WCI-5)	1.69	5.95E-05	Cell rescue, defence and virulence
Contig12873_at	Putative Mal d 1-associated protein	1.68	3.86E-08	Cell rescue, defence and virulence

Contig3157_at	Germin-like protein	1.68	3.48E-07	Cell rescue, defence and virulence
HP01B09w_at	WIR1 protein	1.68	5.66E-06	Cell rescue, defence and virulence
Contig10717_at	Bowman-Birk type trypsin inhibitor	1.67	1.51E-06	Cell rescue, defence and virulence
Contig9885_at	Glutathione S-transferase	1.67	1.24E-09	Cell rescue, defence and virulence
Contig13748_s_at	Putative lectin receptor-type protein kinase	1.66	3.63E-09	Cell rescue, defence and virulence
Contig1637_s_at	1,3-beta glucan endohydrolase precursor	1.66	5.13E-06	Cell rescue, defence and virulence
Contig3519_at	Cytosolic glutathione reductase	1.66	6.19E-08	Cell rescue, defence and virulence
Contig13544_at	Putative Avr9/Cf-9 rapidly elicited protein 231	1.64	3.05E-05	Cell rescue, defence and virulence
HV04J01r_s_at	Glutathione peroxidase	1.64	4.95E-09	Cell rescue, defence and virulence
Contig6354_s_at	Respiratory burst oxidase protein D	1.63	1.38E-06	Cell rescue, defence and virulence
Contig7079_at	Putative peroxidase	1.62	6.22E-05	Cell rescue, defence and virulence
Contig3638_at	Leucine-rich repeat protein	1.61	1.98E-05	Cell rescue, defence and virulence
Contig2787_s_at	Basic pathogenesis-related protein PR5 precursor	1.6	0	Cell rescue, defence and virulence
Contig18924_at	FH protein interacting protein FIP1	1.57	4.53E-08	Cell rescue, defence and virulence
Contig2788_x_at	Thaumatin-like protein TLP5	1.56	1.17E-05	Cell rescue, defence and virulence
AF016328_at	Thaumatin-like protein	1.55	1.22E-07	Cell rescue, defence and virulence
Contig21968_at	Glutathione-S-transferase Cla47	1.54	9.61E-09	Cell rescue, defence and virulence
Contig4750_at	Wheat aluminum induced protein wali 3	1.53	7.16E-07	Cell rescue, defence and virulence
Contig19510_at	Putative Avr9/Cf-9 rapidly elicited protein 231	1.51	7.04E-07	Cell rescue, defence and virulence
Contig1686_at	23 kDa jasmonate-induced protein	1.49	0	Cell rescue, defence and virulence
Contig8453_at	Putative stress-related protein	1.49	3.29E-08	Cell rescue, defence and virulence
Contig7634_at	Glutathione S-transferase	1.48	1.13E-06	Cell rescue, defence and virulence
HU11H18u_s_at	BAX inhibitor 1	1.48	1.54E-09	Cell rescue, defence and virulence
Contig13477_at	Blue copper protein precursor	1.45	2.69E-08	Cell rescue, defence and virulence
Contig7933_at	Chitin elicitor-binding proein	1.45	4.27E-06	Cell rescue, defence and virulence
Contig14370_at	Putative endo-beta-1,4-glucanase	1.44	7.48E-06	Cell rescue, defence and virulence
Contig634_at	Benzothiadiazole-induced protein (clone WCI-5)	1.44	1.09E-05	Cell rescue, defence and virulence
EBro08_SQ005_A14_at	Putative proteinase inhibitor	1.42	0	Cell rescue, defence and virulence
Contig7078_s_at	Harpin-induced family protein	1.41	5.66E-09	Cell rescue, defence and virulence
Contig1859_at	Peroxidase 10	1.39	9.80E-08	Cell rescue, defence and virulence
Contig18997_at	Putative Avr9/Cf-9 rapidly elicited protein 264	1.38	1.04E-07	Cell rescue, defence and virulence
rbah13p07_s_at	Peroxidase	1.37	2.15E-07	Cell rescue, defence and virulence
Contig11509_at	Putative peroxidase	1.34	7.40E-05	Cell rescue, defence and virulence

Contig12420_at	Respiratory burst oxidase homologue A	1.34	6.54E-07	Cell rescue, defence and virulence
Contig2243_s_at	Wheat aluminum induced protein wali 5	1.34	0	Cell rescue, defence and virulence
Contig25923_at	Putative disease resistance protein	1.31	1.50E-06	Cell rescue, defence and virulence
Contig4245_s_at	Glutathione peroxidase	1.31	5.15E-06	Cell rescue, defence and virulence
Contig13561_at	Mla1	1.29	1.21E-05	Cell rescue, defence and virulence
Contig2730_s_at	Catalase isozyme 1	1.29	2.40E-06	Cell rescue, defence and virulence
Contig1010_at	Subtilisin-chymotrypsin inhibitor	1.28	0	Cell rescue, defence and virulence
Contig3380_s_at	Subtilisin-chymotrypsin inhibitor 2	1.28	0	Cell rescue, defence and virulence
Contig4225_at	Universal stress protein-like	1.28	2.91E-07	Cell rescue, defence and virulence
Contig88_x_at	Putative proteinase inhibitor	1.27	1.78E-06	Cell rescue, defence and virulence
Contig9476_at	Putative beta-glucan binding protein	1.27	5.92E-06	Cell rescue, defence and virulence
Contig4853_at	Delta1-pyrroline-5-carboxylate synthetase	1.25	1.18E-06	Cell rescue, defence and virulence
Contig3626_s_at	Hypersensitive-induced reaction protein 3	1.24	7.65E-06	Cell rescue, defence and virulence
Contig12177_at	Non-specific lipid-transfer protein-like	1.23	2.13E-06	Cell rescue, defence and virulence
Contig2214_s_at	PR-1-type pathogenesis-related protein	1.23	0	Cell rescue, defence and virulence
Contig5024_at	Putative class III chitinase	1.23	0	Cell rescue, defence and virulence
Contig10408_at	Glutathione S-transferase GST 41	1.22	1.13E-06	Cell rescue, defence and virulence
Contig13517_s_at	Putative Cf2/Cf5 disease resistance protein	1.22	0	Cell rescue, defence and virulence
Contig5219_s_at	Putative beta-1,3-glucanase	1.22	5.72E-07	Cell rescue, defence and virulence
Contig3383_at	Subtilisin-chymotrypsin inhibitor 2	1.21	4.64E-07	Cell rescue, defence and virulence
HW03F09u_at	Putative elicitor inducible protein	1.2	4.03E-06	Cell rescue, defence and virulence
Contig4621_at	Cold acclimation protein WCOR518	1.19	0	Cell rescue, defence and virulence
Contig7036_at	Blue copper-binding protein-like	1.19	1.26E-05	Cell rescue, defence and virulence
Contig12199_at	Putative peroxidase	1.17	4.38E-05	Cell rescue, defence and virulence
Contig12328_at	Putative terbinafine resistance locus protein	1.17	1.50E-06	Cell rescue, defence and virulence
Contig12685_at	Putative blue copper binding protein	1.17	0	Cell rescue, defence and virulence
Contig5942_at	Elicitor-responsive gene 3	1.17	6.66E-07	Cell rescue, defence and virulence
HV_CEa0002E17r2_s_at	Superoxide dismutase	1.15	4.41E-08	Cell rescue, defence and virulence
Contig2524_s_at	Delta-1-pyrroline-5-carboxylate dehydrogenase	1.14	2.41E-07	Cell rescue, defence and virulence
Contig8262_at	Putative beta-1,3-glucanase	1.13	4.35E-06	Cell rescue, defence and virulence
Contig4056_at	Pathogenesis-related protein 1A/1B precursor	1.12	0	Cell rescue, defence and virulence
Contig2112_at	Peroxidase	1.1	1.90E-05	Cell rescue, defence and virulence
Contig2208_at	Pathogenisis-related protein 1.2 precursor	1.1	0	Cell rescue, defence and virulence

Contig24573_at	Putative Cf2/Cf5 disease resistance protein homolog	1.1	6.19E-07	Cell rescue, defence and virulence
Contig4730_at	Hypersensitive-induced reaction protein 4	1.1	3.17E-06	Cell rescue, defence and virulence
Contig26201_at	HV1LRR1	1.09	5.77E-05	Cell rescue, defence and virulence
Contig9632_at	Glutathione S-transferase	1.09	2.79E-06	Cell rescue, defence and virulence
HVSMEa0006I22r2_s_at	Dehydrin 5	1.09	0.01	Cell rescue, defence and virulence
Contig1678_s_at	23 kDa jasmonate-induced protein	1.08	0	Cell rescue, defence and virulence
Contig2163_at	Pathogen-induced protein WIR1A - wheat	1.08	6.88E-05	Cell rescue, defence and virulence
Contig7448_s_at	Glutathione S-transferase	1.08	0	Cell rescue, defence and virulence
Contig15713_at	Metacaspase 1	1.07	4.37E-06	Cell rescue, defence and virulence
HT07M06u_at	Drought-induced hydrophobic protein	1.07	3.05E-05	Cell rescue, defence and virulence
HVSMEb0002A22r2_at	Harpin-induced 1	1.07	1.20E-05	Cell rescue, defence and virulence
rbags1c11_at	Glutathione S-transferase GST 38	1.07	1.49E-05	Cell rescue, defence and virulence
Contig9060_at	Chitinase	1.04	1.35E-05	Cell rescue, defence and virulence
Contig2905_at	Jasmonate induced protein	1.02	0	Cell rescue, defence and virulence
Contig9172_s_at	Germin-like protein 5a (GER5a)	1	1.06E-06	Cell rescue, defence and virulence
HT09I19u_at	Putative glutathione S-transferase	1	4.51E-07	Cell rescue, defence and virulence
Contig18712_at	Receptor protein kinase-like protein	4.99	7.21E-12	Cellular communication, signal transduction
HW08C04u_at	Putative protein kinase Xa21	4.76	1.70E-11	Cellular communication, signal transduction
HV_CEb0014M10r2_at	Phosphatidic acid phosphatase	4.72	3.21E-11	Cellular communication, signal transduction
Contig21914_at	Calmodulin-like protein	4.4	4.35E-12	Cellular communication, signal transduction
Contig20521_at	Wall-associated kinase	4.39	9.19E-13	Cellular communication, signal transduction
rbaal10h14_at	Abscisic acid-induced protein	4.38	1.10E-11	Cellular communication, signal transduction
EBro08_SQ004_I20_at	Putative EF hand family protein	4.32	3.02E-11	Cellular communication, signal transduction
Contig14915_at	Calmodulin-binding protein	4.25	3.46E-13	Cellular communication, signal transduction
Contig9408_at	LysM receptor-like kinase	4.25	7.95E-10	Cellular communication, signal transduction
Contig2829_at	Adenylate kinase A	4.2	7.93E-11	Cellular communication, signal transduction
HV_CEb0016L17r2_at	Receptor-like kinase TAK33-like protein	3.91	1.05E-11	Cellular communication, signal transduction
HVSMEm0005L12r2_x_at	Putative receptor protein kinase-like protein	3.9	3.25E-09	Cellular communication, signal transduction
Contig14034_at	Ser/Thr protein phosphatase family protein	3.79	2.93E-11	Cellular communication, signal transduction
Contig12590_at	Probable calcium-binding protein	3.72	3.56E-11	Cellular communication, signal transduction
Contig14243_at	Serine/threonine-specific receptor protein kinase-like	3.72	2.37E-09	Cellular communication, signal transduction
Contig10718_at	Gibberellin 2-oxidase	3.62	2.02E-12	Cellular communication, signal transduction
Contig3636_at	SERK2 protein	3.53	6.92E-10	Cellular communication, signal transduction

HV_CEb0021G08r2_at	Protein kinase domain containing protein	3.47	4.21E-11	Cellular communication, signal transduction
Contig8402_at	Putative phospholipase D beta 1	3.45	2.97E-10	Cellular communication, signal transduction
Contig13821_at	Putative receptor-like kinase	3.42	9.69E-10	Cellular communication, signal transduction
HVSMEm0005L12r2_at	Putative receptor protein kinase-like protein	3.42	4.50E-09	Cellular communication, signal transduction
Contig3995_s_at	Non-symbiotic hemoglobin	3.39	3.06E-09	Cellular communication, signal transduction
Contig24439_at	Protein serine threonine kinase-like	3.26	2.31E-11	Cellular communication, signal transduction
Contig16710_at	Putative receptor-type protein kinase LRK1	3.14	1.74E-07	Cellular communication, signal transduction
Contig9093_at	Auxin-induced protein AIR12	3.13	5.95E-09	Cellular communication, signal transduction
Contig13114_at	Putative cynase	3.04	3.02E-08	Cellular communication, signal transduction
Contig4899_s_at	EF-hand Ca2+-binding protein CCD1	3	5.45E-10	Cellular communication, signal transduction
Contig1903_at	Calreticulin-like protein	2.96	1.03E-10	Cellular communication, signal transduction
Contig13217_at	Putative S-receptor kinase KIK1	2.95	6.67E-10	Cellular communication, signal transduction
Contig24256_at	Serine/threonine-protein kinase NAK	2.93	2.75E-10	Cellular communication, signal transduction
EBro03_SQ005_G05_at	NPK1-related protein kinase-like protein	2.9	4.61E-10	Cellular communication, signal transduction
Contig19569_at	Putative phospholipase	2.87	1.38E-09	Cellular communication, signal transduction
Contig5428_s_at	Probable diacylglycerol kinase	2.84	4.06E-09	Cellular communication, signal transduction
Contig11168_at	Calcium-dependent protein kinase	2.83	8.64E-11	Cellular communication, signal transduction
Contig15359_at	Putative calmodulin	2.83	2.79E-11	Cellular communication, signal transduction
EBem09_SQ006_L23_at	Abscisic acid-induced protein	2.83	4.29E-08	Cellular communication, signal transduction
Contig8468_at	Putative calmodulin-binding protein	2.79	1.20E-08	Cellular communication, signal transduction
Contig3635_s_at	SERK2 protein	2.78	4.95E-09	Cellular communication, signal transduction
Contig16939_at	Serine/threonine protein kinase PKPA-like protein	2.77	7.95E-09	Cellular communication, signal transduction
Contig17335_at	Calmodulin-like protein	2.74	3.62E-09	Cellular communication, signal transduction
HV_CEb0017B21r2_at	Putative protein kinase	2.72	1.41E-09	Cellular communication, signal transduction
Contig5191_at	Calcium dependent protein kinase	2.7	3.22E-08	Cellular communication, signal transduction
Contig13498_at	Serine/threonine-protein kinase receptor	2.67	6.23E-10	Cellular communication, signal transduction
Contig17030_at	Putative protein kinase	2.66	3.54E-10	Cellular communication, signal transduction
Contig21786_at	Receptor serine/threonine kinase PR5K-like	2.66	2.69E-09	Cellular communication, signal transduction
Contig11653_s_at	EF hand family protein	2.65	1.92E-07	Cellular communication, signal transduction
Contig13252_s_at	Putative receptor protein kinase-like protein	2.63	1.36E-08	Cellular communication, signal transduction
Contig19663_at	Serine/threonine protein-like protein	2.57	7.06E-09	Cellular communication, signal transduction
AF026538_at	ABA-responsive protein	2.53	8.90E-10	Cellular communication, signal transduction
Contig18748_at	Leucine-rich repeat transmembrane protein kinase	2.5	4.90E-08	Cellular communication, signal transduction

Contig15156_at	Putative serine/threonine protein kinase	2.49	8.16E-10	Cellular communication, signal transduction
Contig8201_at	Putative regulatory protein	2.49	2.54E-09	Cellular communication, signal transduction
Contig12629_s_at	Wall-associated kinase 4-like	2.46	9.30E-10	Cellular communication, signal transduction
HB18O06r_at	Putative receptor protein kinase PERK1	2.43	2.38E-08	Cellular communication, signal transduction
HO14I22S_s_at	Putative wall-associated kinase	2.42	1.45E-07	Cellular communication, signal transduction
Contig11518_at	Protein kinase-like	2.4	9.87E-09	Cellular communication, signal transduction
Contig9077_at	Putative receptor kinase	2.4	7.00E-09	Cellular communication, signal transduction
Contig18906_at	Putative receptor-like protein kinase 4	2.31	1.80E-07	Cellular communication, signal transduction
Contig19003_at	Putative salicylic acid-binding protein 2	2.28	4.36E-08	Cellular communication, signal transduction
Contig20753_at	Putative diacylglycerol kinase	2.28	5.70E-08	Cellular communication, signal transduction
Contig26139_at	Putative calmodulin-like protein	2.28	9.41E-09	Cellular communication, signal transduction
Contig8353_s_at	Protein kinase-like protein	2.27	2.10E-09	Cellular communication, signal transduction
Contig6958_s_at	Serine/threonine kinase-like protein	2.26	2.54E-09	Cellular communication, signal transduction
Contig16556_at	Receptor-like protein kinase	2.23	1.96E-08	Cellular communication, signal transduction
Contig16998_at	Calcium-dependent protein kinase	2.21	3.18E-09	Cellular communication, signal transduction
Contig6447_at	Calcium-dependent protein kinase	2.19	2.60E-10	Cellular communication, signal transduction
Contig5427_at	Diacylglycerol kinase	2.17	2.04E-09	Cellular communication, signal transduction
Contig19429_at	Phosphatidylinositol 3,5-kinase-like	2.16	3.64E-08	Cellular communication, signal transduction
Contig10585_at	Acid phosphatase-like	2.14	3.83E-08	Cellular communication, signal transduction
Contig23834_at	NPK1-related protein kinase-like protein	2.14	1.15E-07	Cellular communication, signal transduction
Contig12156_at	Putative stromal cell-derived factor 2	2.11	5.49E-09	Cellular communication, signal transduction
HV_CEb0008E13r2_at	Inositol 1,3,4-trisphosphate 5/6-kinase	2.1	2.27E-07	Cellular communication, signal transduction
Contig8354_at	Putative protein kinase	2.06	2.01E-08	Cellular communication, signal transduction
Contig8990_at	Tyrosine-serine-threonine kinase	2.04	2.80E-08	Cellular communication, signal transduction
Contig12245_at	NBS-LRR-like protein	2.03	9.94E-07	Cellular communication, signal transduction
Contig24230_at	GRAB2 protein	2.01	2.94E-09	Cellular communication, signal transduction
Contig3473_at	Putative signal sequence receptor	2.01	1.82E-10	Cellular communication, signal transduction
Contig7535_at	Serine/threonine-protein kinase	2.01	1.05E-08	Cellular communication, signal transduction
Contig11040_at	Phosphatidic acid phosphatase beta-like	2	2.34E-08	Cellular communication, signal transduction
Contig12102_at	Putative auxin-responsive GH3 protein	1.98	1.65E-09	Cellular communication, signal transduction
Contig22773_at	S-receptor kinase homolog 2 precursor	1.98	3.23E-09	Cellular communication, signal transduction
Contig2500_at	Auxin-responsive protein IAA15	1.95	1.68E-06	Cellular communication, signal transduction
Contig19683_at	Serine/threonine protein-like protein	1.89	4.44E-08	Cellular communication, signal transduction

Contig21140_at	Putative serine/threonine kinase	1.89	1.34E-07	Cellular communication, signal transduction
Contig18622_at	Putative protein kinase	1.88	4.21E-08	Cellular communication, signal transduction
Contig19256_at	NPK1-related protein kinase-like protein	1.88	0	Cellular communication, signal transduction
Contig13905_at	Putative receptor-like protein kinase	1.87	2.24E-08	Cellular communication, signal transduction
Contig16157_at	Calcium-dependent protein kinase	1.87	2.53E-09	Cellular communication, signal transduction
Contig14170_at	Auxin response factor	1.86	7.91E-09	Cellular communication, signal transduction
Contig20782_at	Protein kinase domain containing protein	1.84	1.26E-07	Cellular communication, signal transduction
Contig25378_at	S-locus receptor-like kinase RLK14	1.83	1.38E-07	Cellular communication, signal transduction
Contig11154_at	Calcium-dependent protein kinase	1.82	1.89E-08	Cellular communication, signal transduction
Contig17515_at	Putative serine/threonine kinase	1.82	1.39E-07	Cellular communication, signal transduction
Contig14481_at	Ca2+ binding protein cbp1	1.81	7.96E-08	Cellular communication, signal transduction
Contig5422_at	SERK2 protein	1.78	1.23E-08	Cellular communication, signal transduction
HM08O10r_s_at	Leucine Rich Repeat family protein	1.76	1.96E-07	Cellular communication, signal transduction
rbaal11f18_at	Serine/threonine kinase-like protein	1.74	3.51E-09	Cellular communication, signal transduction
Contig18612_at	Leucine-rich repeat transmembrane protein kinase	1.73	2.06E-07	Cellular communication, signal transduction
Contig7911_at	Protein phosphatase 2C	1.73	3.08E-08	Cellular communication, signal transduction
HT05J08u_at	Putative receptor-like protein kinase	1.73	1.28E-07	Cellular communication, signal transduction
Contig14350_at	Putative receptor-protein kinase	1.72	3.01E-08	Cellular communication, signal transduction
Contig6986_at	Putative protein kinase	1.72	5.93E-07	Cellular communication, signal transduction
Contig13446_at	Putative receptor protein kinase CRINKLY4	1.71	3.61E-07	Cellular communication, signal transduction
Contig9269_s_at	Calreticulin interacted protein	1.71	5.99E-08	Cellular communication, signal transduction
HO13O09S_s_at	Auxin response factor 7a	1.71	5.66E-09	Cellular communication, signal transduction
Contig17096_at	Calcium/calmodulin-dependent protein kinase	1.68	1.92E-08	Cellular communication, signal transduction
Contig2597_at	Phospholipase D beta	1.68	3.78E-07	Cellular communication, signal transduction
Contig9095_at	SnRK1-interacting protein 1,	1.64	1.39E-07	Cellular communication, signal transduction
Contig6958_at	Serine/threonine kinase-like protein	1.63	2.13E-07	Cellular communication, signal transduction
Contig7893_at	Adenylate kinase	1.63	6.19E-06	Cellular communication, signal transduction
Contig15966_at	NLI interacting factor (NIF) family protein-like	1.62	3.69E-07	Cellular communication, signal transduction
Contig12341_at	Putative CRK1 protein	1.6	1.24E-06	Cellular communication, signal transduction
Contig8829_at	Probable calcium-binding protein	1.6	0	Cellular communication, signal transduction
rbags16g09_s_at	Calreticulin (CRH1)	1.59	3.50E-08	Cellular communication, signal transduction
Contig2932_at	Leucine-rich repeat protein	1.58	1.81E-08	Cellular communication, signal transduction
Contig13644_at	Serine/threonine kinase-like protein	1.57	9.03E-08	Cellular communication, signal transduction

Contig26172_at	Putative receptor kinase	1.57	5.48E-08	Cellular communication, signal transduction
Contig7016_s_at	Calcium-binding EF-hand family protein-like	1.57	9.90E-05	Cellular communication, signal transduction
Contig5017_s_at	Serine/threonine protein kinase-like protein	1.56	4.04E-06	Cellular communication, signal transduction
rbags16j18_s_at	Calcium/calmodulin-dependent protein kinase	1.56	3.72E-08	Cellular communication, signal transduction
HVSMEn0019K13r2_at	Armadillo/beta-catenin-like repeat family protein	1.55	3.26E-08	Cellular communication, signal transduction
Contig10323_at	Putative serine/threonine phosphatase	1.52	6.16E-08	Cellular communication, signal transduction
Contig24522_at	Serine/threonine protein kinase	1.5	6.94E-06	Cellular communication, signal transduction
Contig6394_at	Protein kinase family protein	1.5	2.99E-08	Cellular communication, signal transduction
Contig10743_at	Receptor-like kinase	1.49	7.26E-07	Cellular communication, signal transduction
Contig1338_s_at	Calmodulin-like protein	1.49	5.75E-07	Cellular communication, signal transduction
Contig13499_at	Receptor protein kinase-like	1.48	2.88E-08	Cellular communication, signal transduction
Contig5373_s_at	Signal peptidase	1.48	9.95E-07	Cellular communication, signal transduction
Contig5761_s_at	Calmodulin-like protein	1.48	7.71E-08	Cellular communication, signal transduction
Contig9427_at	Putative leucine-rich receptor-like protein kinase	1.48	6.60E-08	Cellular communication, signal transduction
HS16D10u_at	Serine/threonine kinase	1.48	1.96E-07	Cellular communication, signal transduction
Contig17857_at	Phosphatidic acid phosphatase alpha	1.46	3.39E-08	Cellular communication, signal transduction
Contig12732_at	Tyrosine phosphatase	1.45	4.38E-06	Cellular communication, signal transduction
HM11A01r_s_at	Putative CBL-interacting protein kinase	1.45	5.14E-06	Cellular communication, signal transduction
Contig17029_at	Putative protein kinase	1.44	3.07E-07	Cellular communication, signal transduction
Contig6089_at	Serine-threonine kinase receptor-associated protein	1.44	2.73E-08	Cellular communication, signal transduction
EBro08_SQ008_N10_at	Receptor-like protein kinase like	1.44	0	Cellular communication, signal transduction
HVSMEb0008O04r2_at	Putative receptor protein kinase PERK1	1.44	2.26E-08	Cellular communication, signal transduction
HVSMEf0011J01r2_s_at	Putative receptor-like protein kinase	1.44	3.41E-08	Cellular communication, signal transduction
Contig10854_s_at	Putative protein kinase	1.42	1.08E-07	Cellular communication, signal transduction
Contig16619_at	Putative wall-associated kinase 4	1.42	7.22E-05	Cellular communication, signal transduction
Contig6018_at	Protein kinase MEK1	1.42	8.16E-09	Cellular communication, signal transduction
HA11O05u_at	Putative PAP-specific phosphatase	1.42	3.26E-05	Cellular communication, signal transduction
HC112E03_T3_s_at	ABA-responsive protein	1.42	1.19E-08	Cellular communication, signal transduction
Contig18089_at	Serine/threonine protein-like protein	1.41	2.50E-06	Cellular communication, signal transduction
Contig25034_at	Putative EF hand family protein	1.41	3.47E-06	Cellular communication, signal transduction
Contig7433_s_at	Protein kinase HvPKABA1	1.41	4.36E-07	Cellular communication, signal transduction
Contig18080_at	Leucine zipper-containing protein-like	1.4	6.90E-08	Cellular communication, signal transduction
Contig21234_at	CBL-interacting protein kinase	1.4	8.85E-08	Cellular communication, signal transduction

Contig21556_at	Acid phosphatase	1.4	5.44E-08	Cellular communication, signal transduction
Contig13460_s_at	Putative phosphatase	1.39	1.63E-07	Cellular communication, signal transduction
Contig7420_at	Putative receptor-associated protein	1.39	5.69E-08	Cellular communication, signal transduction
HVSMEa0018C24r2_s_at	Leucine-rich repeat transmembrane protein kinase	1.39	3.16E-08	Cellular communication, signal transduction
Contig12672_at	MAPK activating protein-like	1.38	6.95E-06	Cellular communication, signal transduction
Contig26495_at	Probable signal peptidase	1.38	4.67E-09	Cellular communication, signal transduction
Contig15318_at	Protein kinase-like	1.37	1.85E-06	Cellular communication, signal transduction
Contig12253_at	Auxin-binding protein	1.36	1.14E-06	Cellular communication, signal transduction
Contig11164_at	Putative Altered Response to Gravity	1.35	4.39E-07	Cellular communication, signal transduction
Contig4711_s_at	MAP kinase homolog	1.35	9.85E-07	Cellular communication, signal transduction
Contig9265_at	Putative serine/threonine phosphatase type 2c	1.35	0	Cellular communication, signal transduction
Contig12213_at	Signal transducer	1.34	1.03E-06	Cellular communication, signal transduction
Contig24995_at	S-receptor kinase-like	1.34	2.05E-05	Cellular communication, signal transduction
Contig7290_at	Putative receptor protein kinase PERK1	1.34	4.29E-08	Cellular communication, signal transduction
Contig13460_at	Putative phosphatase	1.33	3.83E-05	Cellular communication, signal transduction
Contig7433_at	Serine-threonine protein kinase	1.33	3.12E-05	Cellular communication, signal transduction
Contig9591_at	Putative auxin-induced protein	1.33	0	Cellular communication, signal transduction
Contig18012_at	Calcineurin-like phosphoesterase family-like	1.31	1.81E-07	Cellular communication, signal transduction
Contig3474_s_at	Putative signal sequence receptor, alpha subunit (SSR-alpha)	1.31	8.22E-06	Cellular communication, signal transduction
Contig20721_s_at	Putative acid phosphatase	1.3	4.14E-06	Cellular communication, signal transduction
Contig7794_s_at	Signal tranduction protein	1.3	4.08E-07	Cellular communication, signal transduction
HS16P03u_at	Receptor protein kinase-like protein	1.3	1.94E-08	Cellular communication, signal transduction
Contig12770_at	Putative wall-associated serine/threonine kinase	1.27	1.32E-06	Cellular communication, signal transduction
Contig14606_at	Phosphatidylinositol-4-phosphate 5-kinase	1.27	8.45E-08	Cellular communication, signal transduction
Contig4593_at	Putative calcium-dependent protein kinase	1.27	8.73E-07	Cellular communication, signal transduction
Contig6256_s_at	Putative cbl-interacting protein kinase 1	1.27	0	Cellular communication, signal transduction
Contig6993_at	Mitogen-activated protein kinase 6	1.26	1.07E-06	Cellular communication, signal transduction
Contig10510_at	Calcineurin-like phosphoesterase family-like protein	1.25	2.36E-07	Cellular communication, signal transduction
Contig17408_at	Serine threonine kinase-like	1.25	2.61E-05	Cellular communication, signal transduction
Contig14879_at	Putative protein kinase	1.24	1.83E-06	Cellular communication, signal transduction
Contig15476_at	Serine/threonine kinase-like protein	1.24	7.31E-05	Cellular communication, signal transduction
Contig20457_at	Putative PAP-specific phosphatase	1.24	1.66E-08	Cellular communication, signal transduction
Contig2390_at	Putative ER6 protein	1.24	2.37E-06	Cellular communication, signal transduction

Contig4086_at	Receptor-like protein kinase-like	1.24	8.21E-07	Cellular communication, signal transduction
Contig12241_at	Transducin / WD-40 repeat protein-like	1.23	1.63E-06	Cellular communication, signal transduction
Contig7515_at	Signal recognition particle 14 kDa protein	1.23	1.85E-05	Cellular communication, signal transduction
Contig22513_at	Protein kinase-like	1.21	1.77E-06	Cellular communication, signal transduction
Contig11114_at	EF - hand Calcium binding protein	1.18	4.01E-07	Cellular communication, signal transduction
Contig12897_at	Calmodulin-binding protein	1.18	1.66E-06	Cellular communication, signal transduction
Contig13694_at	Auxin response factor 16	1.18	3.50E-06	Cellular communication, signal transduction
Contig4805_at	Putative phospholipase	1.18	8.80E-07	Cellular communication, signal transduction
Contig6659_s_at	Sphingosine-1-phosphate	1.18	7.36E-08	Cellular communication, signal transduction
Contig6097_at	Putative signal recognition particle 72KD protein	1.17	4.31E-08	Cellular communication, signal transduction
Contig9409_s_at	LysM receptor-like kinase	1.17	1.31E-05	Cellular communication, signal transduction
Contig5561_at	Putative receptor-protein kinase	1.16	3.66E-07	Cellular communication, signal transduction
Contig7419_at	ADP-ribosylation factor	1.16	0	Cellular communication, signal transduction
Contig22302_s_at	MAPK activating protein-like	1.15	2.51E-05	Cellular communication, signal transduction
Contig3393_at	Putative abscisic acid-induced protein	1.15	2.30E-07	Cellular communication, signal transduction
Contig26631_at	Leucine Rich Repeat family protein	1.14	6.23E-06	Cellular communication, signal transduction
Contig11178_at	Serine/threonine protein kinase	1.12	4.26E-06	Cellular communication, signal transduction
Contig6356_at	Putative ethylene-responsive protein	1.12	7.65E-06	Cellular communication, signal transduction
HV_CEb0017M09r2_s_at	Putative receptor-type protein kinase LRK1	1.12	0	Cellular communication, signal transduction
Contig13221_at	Putative PLRR-4 polymorphic leucine-rich repeat protein	1.11	6.80E-06	Cellular communication, signal transduction
Contig1471_at	Signal recognition particle receptor-like protein	1.1	2.99E-07	Cellular communication, signal transduction
Contig16179_s_at	Putative receptor-type protein kinase LRK1	1.1	1.09E-06	Cellular communication, signal transduction
Contig18817_at	Leucine-rich repeat transmembrane protein kinase	1.1	1.43E-05	Cellular communication, signal transduction
Contig17818_at	Protein kinase family protein	1.09	0	Cellular communication, signal transduction
Contig20428_at	Cytokinin-regulated kinase 1	1.09	2.20E-06	Cellular communication, signal transduction
Contig9814_at	Calmodulin binding protein	1.09	3.86E-06	Cellular communication, signal transduction
Contig10794_at	EF - hand Calcium binding protein - like	1.08	3.46E-06	Cellular communication, signal transduction
Contig10975_at	Stromal cell-derived factor 2-like protein	1.08	4.61E-06	Cellular communication, signal transduction
Contig12779_at	Putative leucine-rich repeat protein	1.08	2.57E-07	Cellular communication, signal transduction
Contig14555_s_at	Probable calcium-binding protein	1.08	2.92E-05	Cellular communication, signal transduction
Contig8165_at	Calcium-dependent protein kinase CPK1 adapter protein 2-like	1.08	1.94E-07	Cellular communication, signal transduction
Contig12378_at	Putative calcium-independent phospholipase	1.07	2.67E-05	Cellular communication, signal transduction
Contig16924_at	Auxin-responsive protein	1.07	8.17E-06	Cellular communication, signal transduction

Contig18093_at	Putative LRR receptor-like protein kinase	1.06	1.04E-06	Cellular communication, signal transduction
Contig2881_at	BRI1-KD interacting protein 103	1.06	0	Cellular communication, signal transduction
Contig11162_at	Putative phosphatidylinositol 3-kinase	1.05	1.72E-05	Cellular communication, signal transduction
Contig15871_at	Putative phosphatidylinositol kinase	1.04	9.98E-05	Cellular communication, signal transduction
Contig7505_at	Protein kinase	1.04	5.67E-05	Cellular communication, signal transduction
Contig12751_at	Probable NAD kinase 1	1.03	3.88E-06	Cellular communication, signal transduction
bah24p14_at	RING/C3HC4/PHD zinc finger-like protein	1.02	0	Cellular communication, signal transduction
HVSMEh0086D18r2_s_at	Putative CRK1 protein	1.02	3.25E-05	Cellular communication, signal transduction
rbags16i08_s_at	Putative calreticulin	1.02	7.37E-07	Cellular communication, signal transduction
Contig24211_at	Putative receptor protein kinase ZMPK1	1.01	1.40E-06	Cellular communication, signal transduction
Contig4285_at	Probable microsomal signal peptidase 25 kDa subunit	1.01	1.35E-05	Cellular communication, signal transduction
Contig7022_at	Serine/threonine protein phosphatase	1.01	1.01E-05	Cellular communication, signal transduction
Contig8968_at	Putative leucine zipper protein	1.01	3.98E-05	Cellular communication, signal transduction
HV_CEa0008F11r2_at	Putative cytokinin oxidase	1.01	0	Cellular communication, signal transduction
Contig13680_s_at	Putative histidine kinase	1	0.03	Cellular communication, signal transduction
Contig25386_at	Putative peptide transporter protein	5.48	1.75E-12	Cellular transport, transport facilitation and transport routes
Contig20774_at	Putative multidrug resistance protein	5.18	2.37E-12	Cellular transport, transport facilitation and transport routes
Contig11285_at	Mitochondrial phosphate transporter	5.11	9.91E-12	Cellular transport, transport facilitation and transport routes
Contig21298_at	MDR-like ABC transporter	5.07	1.63E-11	Cellular transport, transport facilitation and transport routes
Contig8004_at	Integral membrane protein-like	5.06	8.22E-12	Cellular transport, transport facilitation and transport routes
Contig24175_at	Putative anion/sugar transporter	4.96	1.19E-11	Cellular transport, transport facilitation and transport routes
HV_CEb0022J21r2_at	Putative peptide transporter	4.81	2.93E-11	Cellular transport, transport facilitation and transport routes
Contig15142_at	Putative AAA-type ATPase	4.79	1.70E-12	Cellular transport, transport facilitation and transport routes
Contig6920_at	Putative potassium transporter	4.79	1.31E-10	Cellular transport, transport facilitation and transport routes
Contig2595_at	Sec61 alpha subunit	4.65	2.03E-12	Cellular transport, transport facilitation and transport routes
Contig4728_at	Putative plastidic ATP/ADP-transporter	4.52	1.33E-10	Cellular transport, transport facilitation and transport routes
Contig12753_at	Putative ABC transporter	4.41	1.47E-11	Cellular transport, transport facilitation and transport routes
Contig16923_at	PDR-like ABC transporter	4.35	1.42E-09	Cellular transport, transport facilitation and transport routes
Contig20553_at	PDR-like ABC transporter	4.33	9.87E-10	Cellular transport, transport facilitation and transport routes
rbaal12n12_s_at	Auxin efflux carrier protein-like	4.29	4.13E-11	Cellular transport, transport facilitation and transport routes
HVSMEl0020J06r2_at	PDR-like ABC transporter	4.16	5.38E-11	Cellular transport, transport facilitation and transport routes
Contig6857_at	Putative peroxisomal membrane protein	3.9	6.88E-11	Cellular transport, transport facilitation and transport routes
Contig21659_s_at	PDR-like ABC transporter	3.84	8.03E-09	Cellular transport, transport facilitation and transport routes

Contig4952_x_at	High affinity nitrate transporter	3.84	1.16E-08	Cellular transport, transport facilitation and transport routes
HV_CEb0012P03f_at	MATE efflux protein-like	3.77	3.84E-10	Cellular transport, transport facilitation and transport routes
Contig10529_at	Sec14 like protein	3.65	9.91E-12	Cellular transport, transport facilitation and transport routes
HT01N03w_at	GDP dissociation inhibitor	3.63	5.75E-12	Cellular transport, transport facilitation and transport routes
Contig5378_at	Phosphoenolpyruvate/phosphate translocator	3.6	7.75E-12	Cellular transport, transport facilitation and transport routes
HS06J22u_s_at	Mitochondrial carrier protein family	3.59	1.04E-09	Cellular transport, transport facilitation and transport routes
Contig5689_at	Mitochondrial uncoupling protein 5	3.55	4.67E-09	Cellular transport, transport facilitation and transport routes
Contig9663_at	Monosaccharide transporter 4	3.54	5.61E-10	Cellular transport, transport facilitation and transport routes
HO12F15S_s_at	MRP-like ABC transporter	3.52	1.11E-10	Cellular transport, transport facilitation and transport routes
HX01L18w_at	Putative AAA-type ATPase	3.47	2.12E-10	Cellular transport, transport facilitation and transport routes
Contig15859_at	SEC6	3.4	1.86E-10	Cellular transport, transport facilitation and transport routes
Contig24167_at	Calcium lipid binding protein-like	3.36	5.38E-11	Cellular transport, transport facilitation and transport routes
Contig4952_s_at	High affinity nitrate transporter	3.36	5.81E-10	Cellular transport, transport facilitation and transport routes
Contig5784_s_at	UDP-galactose transporter	3.32	6.70E-10	Cellular transport, transport facilitation and transport routes
Contig16892_at	Purine transmembrane transporter	3.23	2.89E-08	Cellular transport, transport facilitation and transport routes
Contig21904_at	Putative amino acid transporter protein	3.22	9.08E-09	Cellular transport, transport facilitation and transport routes
Contig13986_at	Putative ABC transporter protein	3.2	2.26E-07	Cellular transport, transport facilitation and transport routes
Contig9662_at	Sugar transport protein	3.07	2.73E-08	Cellular transport, transport facilitation and transport routes
Contig4639_s_at	Heavy-metal-associated domain-containing protein	2.96	3.40E-10	Cellular transport, transport facilitation and transport routes
Contig14714_at	P-type ATPase	2.95	2.23E-09	Cellular transport, transport facilitation and transport routes
Contig9827_at	Sulfate transporter ST1	2.95	3.26E-10	Cellular transport, transport facilitation and transport routes
S0001100150B08F1_s_at	Glucose-6-phosphate precursor homolog	2.94	3.58E-09	Cellular transport, transport facilitation and transport routes
Contig17453_at	Putative multidrug resistance protein	2.92	1.08E-07	Cellular transport, transport facilitation and transport routes
Contig12155_at	Putative mitochondrial carrier protein	2.83	1.10E-10	Cellular transport, transport facilitation and transport routes
Contig18326_at	Putative mitochondrial dicarboxylate carrier protein	2.73	2.28E-09	Cellular transport, transport facilitation and transport routes
HW06D22u_at	Secretory carrier-associated membrane protein	2.73	5.62E-10	Cellular transport, transport facilitation and transport routes
HM08H20r_at	Na+/H+ exchanging protein-like	2.68	9.93E-09	Cellular transport, transport facilitation and transport routes
Contig18758_at	Putative potasium transporter	2.67	5.18E-10	Cellular transport, transport facilitation and transport routes
Contig9110_at	Putative C2 domain-containing protein	2.66	1.70E-09	Cellular transport, transport facilitation and transport routes
Contig6707_at	Putative sugar transporter	2.65	2.70E-08	Cellular transport, transport facilitation and transport routes
Contig4329_at	Putative transmembrane protein	2.64	5.47E-10	Cellular transport, transport facilitation and transport routes
HB27O05r_at	Nucleotide-sugar transporter family protein	2.6	5.55E-09	Cellular transport, transport facilitation and transport routes
EBro08_SQ012_H23_at	Protein transport protein Sec61 subunit gamma	2.59	1.01E-10	Cellular transport, transport facilitation and transport routes

Contig17093_at	Putative ABC transporter	2.56	6.87E-09	Cellular transport, transport facilitation and transport routes
Contig4328_at	Putative endomembrane protein emp70	2.54	1.51E-07	Cellular transport, transport facilitation and transport routes
Contig14715_at	P-type ATPase	2.51	1.15E-10	Cellular transport, transport facilitation and transport routes
HVSMEa0005F07r2_s_at	Putative ABC transporter	2.43	2.28E-08	Cellular transport, transport facilitation and transport routes
Contig14075_at	P-type ATPase	2.39	1.27E-07	Cellular transport, transport facilitation and transport routes
Contig9422_at	MRP-like ABC transporter	2.35	5.44E-09	Cellular transport, transport facilitation and transport routes
Contig4290_at	Phosphate/phosphoenolpyruvate translocator protein-like	2.3	1.50E-09	Cellular transport, transport facilitation and transport routes
Contig14280_at	Cation/H+ exchanger	2.28	6.40E-09	Cellular transport, transport facilitation and transport routes
Contig22370_at	Syntaxin	2.28	4.85E-09	Cellular transport, transport facilitation and transport routes
Contig23889_at	Putative transmembrane protein	2.28	4.33E-08	Cellular transport, transport facilitation and transport routes
Contig12769_at	Putative ABC transporter	2.27	1.08E-08	Cellular transport, transport facilitation and transport routes
Contig5447_at	Endomembrane protein 70	2.24	1.27E-08	Cellular transport, transport facilitation and transport routes
Contig6322_at	Transporter-related-like	2.22	4.57E-09	Cellular transport, transport facilitation and transport routes
Contig14345_s_at	Secretory carrier-associated membrane protein	2.2	7.68E-09	Cellular transport, transport facilitation and transport routes
Contig6761_at	Major facilitator superfamily protein	2.2	8.22E-09	Cellular transport, transport facilitation and transport routes
Contig13096_at	Putative UDP-galactose/UDP-glucose transporter	2.19	3.52E-08	Cellular transport, transport facilitation and transport routes
Contig20066_at	Phosphate/phosphoenolpyruvate translocator protein-like	2.15	4.65E-07	Cellular transport, transport facilitation and transport routes
Contig3378_at	Voltage dependent anion channel (VDAC)	2.15	5.41E-09	Cellular transport, transport facilitation and transport routes
Contig6706_at	Putative sugar transporter	2.14	1.98E-09	Cellular transport, transport facilitation and transport routes
Contig8416_at	Heavy metal-associated domain containing protein	2.14	5.18E-07	Cellular transport, transport facilitation and transport routes
Contig20673_at	Putative phosphate translocator	2.09	3.74E-09	Cellular transport, transport facilitation and transport routes
HVSMEa0017L10r2_at	AAA-type ATPase-like protein	2.09	1.23E-09	Cellular transport, transport facilitation and transport routes
Contig6819_at	Phosphate/phosphoenolpyruvate translocator protein-like	2.06	1.07E-08	Cellular transport, transport facilitation and transport routes
Contig14547_at	Putative amino acid transporter	2.04	9.97E-09	Cellular transport, transport facilitation and transport routes
Contig12026_at	Syntaxin SNAP33	2.01	8.12E-07	Cellular transport, transport facilitation and transport routes
Contig10956_at	High-affinity nickel-transport family protein	1.99	1.95E-07	Cellular transport, transport facilitation and transport routes
Contig4691_at	Transport protein subunit-like	1.97	7.49E-09	Cellular transport, transport facilitation and transport routes
Contig7388_at	Nitrate transporter	1.97	2.18E-08	Cellular transport, transport facilitation and transport routes
Contig3058_at	Heavy metal-associated domain containing protein	1.94	2.61E-08	Cellular transport, transport facilitation and transport routes
Contig13933_at	Putative vacuolar-type H(+)-ATPase	1.91	3.14E-07	Cellular transport, transport facilitation and transport routes
HVSMEb0011I23r2_s_at	Voltage dependent anion channel	1.89	1.06E-07	Cellular transport, transport facilitation and transport routes
Contig112_at	C2 domain-containing protein	1.88	8.23E-07	Cellular transport, transport facilitation and transport routes
Contig5537_at	Monosaccharide transporter 3	1.88	3.93E-09	Cellular transport, transport facilitation and transport routes

HS08H14u_s_at	Putative vacuolar-type H(+)-ATPase	1.88	5.08E-08	Cellular transport, transport facilitation and transport routes
Contig9463_at	C2 domain-containing protein	1.87	7.76E-10	Cellular transport, transport facilitation and transport routes
Contig14361_at	Mitochondrial carrier protein-like protein	1.86	4.41E-08	Cellular transport, transport facilitation and transport routes
Contig11471_at	36kDa-peroxisomal membrane protein	1.85	3.44E-08	Cellular transport, transport facilitation and transport routes
Contig12556_s_at	Probable transport protein	1.85	1.21E-08	Cellular transport, transport facilitation and transport routes
Contig1534_s_at	ATP/ADP carrier protein	1.84	2.66E-07	Cellular transport, transport facilitation and transport routes
Contig15864_at	Potential phospholipid-transporting ATPase 8	1.84	1.17E-07	Cellular transport, transport facilitation and transport routes
HV_CEa0011E24r2_s_at	Putative hexose carrier protein HEX6	1.84	1.83E-08	Cellular transport, transport facilitation and transport routes
HV_CEa0014N20r2_at	Amino acid transporter	1.84	1.02E-07	Cellular transport, transport facilitation and transport routes
HVSMEm0005J13r2_at	Putative syntaxin-related protein	1.84	4.54E-09	Cellular transport, transport facilitation and transport routes
Contig14080_at	Permease-like	1.83	1.86E-08	Cellular transport, transport facilitation and transport routes
EBro08_SQ008_C01_at	Putative membrane transporter	1.81	2.09E-08	Cellular transport, transport facilitation and transport routes
Contig9568_at	Putative MATE efflux family protein	1.8	1.17E-07	Cellular transport, transport facilitation and transport routes
Contig6152_at	ABC transporter	1.78	6.18E-09	Cellular transport, transport facilitation and transport routes
Contig8122_at	Putative ABC transporter protein	1.78	1.02E-07	Cellular transport, transport facilitation and transport routes
Contig17664_at	Coatomer delta subunit	1.75	9.76E-09	Cellular transport, transport facilitation and transport routes
Contig9005_at	Putative integral membrane Yip1 family protein	1.75	1.94E-08	Cellular transport, transport facilitation and transport routes
Contig10887_at	ABC transporter family protein	1.74	1.34E-06	Cellular transport, transport facilitation and transport routes
Contig7994_s_at	HVA22-like protein	1.74	8.57E-09	Cellular transport, transport facilitation and transport route
Contig7593_at	Peroxisomal biogenesis factor 11 protein-like	1.72	4.75E-08	Cellular transport, transport facilitation and transport routes
Contig4880_at	Glucose-6-phosphate/phosphate translocator	1.71	1.69E-06	Cellular transport, transport facilitation and transport routes
Contig9341_at	Putative cation-chloride co-transporter	1.71	4.00E-07	Cellular transport, transport facilitation and transport routes
HM02O03r_s_at	Putative transport protein SEC61 beta-subunit	1.71	4.85E-09	Cellular transport, transport facilitation and transport routes
Contig4291_at	Phosphate/phosphoenolpyruvate translocator protein-like	1.69	2.94E-07	Cellular transport, transport facilitation and transport routes
Contig1536_at	ADP,ATP carrier protein, mitochondrial precursor	1.68	1.65E-07	Cellular transport, transport facilitation and transport routes
Contig5579_at	Acyl carrier protein 2	1.68	3.63E-08	Cellular transport, transport facilitation and transport routes
Contig5784_at	UDP-galactose transporter	1.68	2.66E-08	Cellular transport, transport facilitation and transport routes
Contig17245_at	Membrane protein CH1-like	1.67	3.04E-07	Cellular transport, transport facilitation and transport routes
Contig8227_at	Putative component of vesicle-mediated transport	1.67	6.71E-09	Cellular transport, transport facilitation and transport routes
Contig19054_at	Putative permease	1.66	9.23E-08	Cellular transport, transport facilitation and transport routes
Contig3621_at	Delta-COP	1.64	4.19E-08	Cellular transport, transport facilitation and transport routes
HA08e19r_at	Protein transport protein SEC61 gamma subunit	1.61	2.43E-08	Cellular transport, transport facilitation and transport routes
Contig20853_at	Transport protein-like	1.6	1.42E-08	Cellular transport, transport facilitation and transport routes

EBem08_SQ002_D16_s_at	Protein transport protein subunit	1.59	6.55E-07	Cellular transport, transport facilitation and transport routes
HVSMEb0006I05f_s_at	Cation/H+ exchanger	1.59	3.07E-08	Cellular transport, transport facilitation and transport routes
Contig9541_at	Nonclathrin coat protein zeta2-COP	1.58	4.48E-07	Cellular transport, transport facilitation and transport routes
Contig12169_at	MATE efflux family protein	1.57	1.06E-07	Cellular transport, transport facilitation and transport routes
Contig12510_at	Heavy metal-associated domain containing protein	1.57	7.57E-08	Cellular transport, transport facilitation and transport routes
Contig6154_s_at	ABC transporter	1.57	7.45E-08	Cellular transport, transport facilitation and transport routes
Contig8512_at	Putative organic solute transporter	1.56	6.18E-08	Cellular transport, transport facilitation and transport routes
Contig4534_s_at	Coatomer subunit beta	1.53	1.70E-06	Cellular transport, transport facilitation and transport routes
Contig7111_at	Putative vesicle trafficking protein	1.53	2.45E-08	Cellular transport, transport facilitation and transport routes
Contig18416_s_at	MDR-like ABC transporter	1.52	8.93E-07	Cellular transport, transport facilitation and transport routes
Contig13546_at	Sugar transporter	1.5	5.55E-08	Cellular transport, transport facilitation and transport routes
Contig23488_at	Putative sugar transporter protein	1.49	5.53E-08	Cellular transport, transport facilitation and transport routes
Contig10090_at	Integral membrane protein-like	1.48	2.29E-08	Cellular transport, transport facilitation and transport routes
Contig14345_at	Secretory carrier-associated membrane protein	1.48	3.47E-05	Cellular transport, transport facilitation and transport routes
Contig6461_s_at	Coatomer subunit beta'-2	1.47	3.17E-08	Cellular transport, transport facilitation and transport routes
Contig9875_at	Vesicle transport v-SNARE protein-like	1.46	2.11E-08	Cellular transport, transport facilitation and transport routes
HU14O14u_s_at	Acyl carrier protein II (Ac12)	1.45	1.23E-07	Cellular transport, transport facilitation and transport routes
Contig2785_at	2-oxoglutarate/malate translocator	1.42	9.27E-08	Cellular transport, transport facilitation and transport routes
Contig16464_at	Iron-phytosiderophore transporter	1.41	0	Cellular transport, transport facilitation and transport routes
Contig25293_at	P-type ATPase	1.4	3.20E-06	Cellular transport, transport facilitation and transport routes
Contig4158_at	Putative clathrin-associated protein	1.4	1.28E-05	Cellular transport, transport facilitation and transport routes
Contig11777_at	Zinc transporter	1.38	1.03E-08	Cellular transport, transport facilitation and transport routes
Contig9559_at	Cation/H+ exchanger	1.35	5.15E-05	Cellular transport, transport facilitation and transport routes
HVSMEl0025N17f_at	Putative nitrate transporter NTL1	1.34	2.48E-07	Cellular transport, transport facilitation and transport routes
Contig12526_at	Myosin heavy chain	1.32	2.28E-07	Cellular transport, transport facilitation and transport routes
Contig4535_at	Coatomer subunit beta	1.32	9.75E-07	Cellular transport, transport facilitation and transport routes
Contig9475_at	Calcium-transporting ATPase 8, plasma membrane-type	1.3	4.88E-07	Cellular transport, transport facilitation and transport routes
Contig17518_at	Putative hexose carrier protein HEX6	1.29	3.22E-05	Cellular transport, transport facilitation and transport routes
Contig7765_at	Coatomer protein gamma 2-subunit	1.29	1.26E-07	Cellular transport, transport facilitation and transport routes
EBma03_SQ002_J20_x_at	Glucose-6-phosphate/phosphate translocator	1.29	5.75E-07	Cellular transport, transport facilitation and transport routes
Contig8157_at	Putative epsin	1.28	9.41E-07	Cellular transport, transport facilitation and transport routes
Contig2996_at	Amino acid transporter	1.27	4.03E-06	Cellular transport, transport facilitation and transport routes
HVSMEi0010A19r2_s_at	Delta-COP	1.27	6.26E-08	Cellular transport, transport facilitation and transport routes

Contig15210_at	Putative vacuolar protein sorting-associated protein	1.26	5.41E-07	Cellular transport, transport facilitation and transport routes
Contig8949_at	P-type ATPase	1.25	3.30E-07	Cellular transport, transport facilitation and transport routes
Contig16775_at	Mitochondrial carrier protein	1.24	6.64E-07	Cellular transport, transport facilitation and transport routes
Contig1904_at	Auxilin-like protein	1.24	1.85E-06	Cellular transport, transport facilitation and transport routes
Contig4761_at	Transport protein Sec23A	1.24	9.10E-07	Cellular transport, transport facilitation and transport routes
Contig6340_at	Small basic membrane integral protein ZmSIP1-2	1.24	1.18E-07	Cellular transport, transport facilitation and transport routes
HVSMEn0020E03r2_at	ATP dependent copper transporter	1.24	3.46E-07	Cellular transport, transport facilitation and transport routes
Contig11677_s_at	Integral membrane protein-like	1.23	1.62E-07	Cellular transport, transport facilitation and transport routes
HVSMEg0007D18r2_s_at	Putative vesicle transfer ATPase	1.23	2.40E-07	Cellular transport, transport facilitation and transport routes
Contig10182_at	Putative ABC transporter	1.22	4.96E-07	Cellular transport, transport facilitation and transport routes
Contig12277_at	Putative sec14 like protein	1.22	3.20E-06	Cellular transport, transport facilitation and transport routes
Contig6321_at	27k vesicle-associated protein-like	1.22	2.81E-06	Cellular transport, transport facilitation and transport routes
Contig7853_at	Putative proton pump interactor	1.22	4.71E-07	Cellular transport, transport facilitation and transport routes
Contig17276_at	ABC transporter family protein	1.21	2.70E-06	Cellular transport, transport facilitation and transport routes
Contig19214_at	Aquaporin NIP-type	1.21	6.24E-05	Cellular transport, transport facilitation and transport routes
Contig9098_at	SEC15 (S. cerevisiae)-like protein	1.21	1.12E-05	Cellular transport, transport facilitation and transport routes
Contig5231_at	Clathrin heavy chain	1.19	8.81E-07	Cellular transport, transport facilitation and transport routes
Contig9317_at	Coatomer subunit zeta-1	1.18	4.81E-06	Cellular transport, transport facilitation and transport routes
HVSMEf0015M13r2_s_at	ER lumen retaining receptor	1.18	2.66E-06	Cellular transport, transport facilitation and transport routes
Contig12302_at	Putative AAA-type ATPase	1.17	5.36E-06	Cellular transport, transport facilitation and transport routes
Contig3680_s_at	Protein transport protein Sec61 subunit gamma-1	1.17	4.41E-07	Cellular transport, transport facilitation and transport routes
Contig14536_at	Phosphatidylinositol transporter	1.16	1.66E-07	Cellular transport, transport facilitation and transport routes
Contig16577_at	Putative peroxisomal Ca-dependent solute carrier	1.15	4.04E-05	Cellular transport, transport facilitation and transport routes
Contig2881_s_at	Proton pump interactor	1.15	1.51E-07	Cellular transport, transport facilitation and transport routes
Contig4754_at	Putative clathrin assembly protein	1.15	1.52E-06	Cellular transport, transport facilitation and transport routes
HZ42D16r_at	Protein transport protein subunit	1.15	3.13E-05	Cellular transport, transport facilitation and transport routes
Contig17529_at	Putative oligopeptide transporter	1.14	0	Cellular transport, transport facilitation and transport routes
Contig15_s_at	Putative ATP-binding cassette	1.13	0	Cellular transport, transport facilitation and transport routes
Contig2999_at	Amino acid transporter	1.12	3.50E-07	Cellular transport, transport facilitation and transport routes
HA29G15r_at	Putative peptide transport protein	1.12	3.13E-06	Cellular transport, transport facilitation and transport routes
HD12A16r_at	Putative purine permease	1.1	2.53E-06	Cellular transport, transport facilitation and transport routes
Contig22064_at	Putative syntaxin of plants 41	1.09	2.70E-06	Cellular transport, transport facilitation and transport routes
Contig4458_at	Coated vesicle membrane protein-like	1.09	1.21E-07	Cellular transport, transport facilitation and transport routes

Contig8728_at	P-type ATPase	1.09	7.10E-06	Cellular transport, transport facilitation and transport routes
Contig9062_at	Translocation protein-related-like	1.09	3.63E-06	Cellular transport, transport facilitation and transport routes
EBro08_SQ012_E16_at	Integral membrane protein-like	1.09	1.72E-06	Cellular transport, transport facilitation and transport routes
HVSMEg0005J01r2_x_at	Glucose-6-phosphate/phosphate translocator	1.09	9.10E-07	Cellular transport, transport facilitation and transport routes
Contig10742_at	Putative peroxisome assembly protein 2	1.08	2.57E-05	Cellular transport, transport facilitation and transport routes
Contig14052_at	Putative calmodulin binding transporter protein	1.08	4.03E-05	Cellular transport, transport facilitation and transport routes
Contig22343_at	Potassium channel tetramerisation domain-containing protein	1.08	2.59E-05	Cellular transport, transport facilitation and transport routes
Contig4900_at	Synaptobrevin-like protein	1.08	0	Cellular transport, transport facilitation and transport routes
Contig8666_at	ATPase-like protein	1.08	1.79E-07	Cellular transport, transport facilitation and transport routes
Contig14229_at	Aquaporin NIP1-1	1.06	7.46E-05	Cellular transport, transport facilitation and transport routes
Contig18833_at	Putative mitochondrial inner membrane protein	1.04	3.27E-06	Cellular transport, transport facilitation and transport routes
Contig21173_at	NPSN11 (NOVEL PLANT SNARE 11)	1.04	1.25E-05	Cellular transport, transport facilitation and transport routes
Contig8746_at	LMBR1 integral membrane family protein-like	1.04	1.97E-07	Cellular transport, transport facilitation and transport routes
HW07H20u_s_at	Clathrin coat assembly protein	1.04	1.39E-06	Cellular transport, transport facilitation and transport routes
Contig4193_at	Mitochondrial uncoupling protein 2	1.03	3.44E-05	Cellular transport, transport facilitation and transport routes
Contig7744_at	ER lumen protein retaining receptor	1.03	3.79E-07	Cellular transport, transport facilitation and transport routes
Contig7871_s_at	Phosphatidylinositol transporter	1.02	6.63E-06	Cellular transport, transport facilitation and transport routes
Contig14972_s_at	Putative ABC transporter	1.01	4.24E-05	Cellular transport, transport facilitation and transport routes
HA22E11r_s_at	Putative syntaxin	1.01	5.09E-05	Cellular transport, transport facilitation and transport routes
HV09K22u_s_at	Putative ripening-related protein 2	5.92	2.68E-13	Development
Contig2673_at	Xyloglucan endo-1,4-beta-D-glucanase	4.46	2.16E-12	Development
Contig6773_at	Roothairless 3	4.23	1.39E-09	Development
Contig8605_s_at	B12D protein	4.09	2.72E-11	Development
Contig8605_at	Putative B12D protein	3.88	1.36E-10	Development
Contig16272_at	Putative chemocyanin	3.51	4.12E-10	Development
Contig3981_at	Putative ripening-related protein	3.5	1.06E-11	Development
Contig4213_at	Ripening-related protein	3.34	3.69E-10	Development
EBpi01_SQ005_P17_at	Ripening-related protein	3.28	4.67E-11	Development
Contig11118_at	Putative B12D protein	3.15	2.65E-10	Development
Contig9283_at	Protein proline-rich polypeptide 6	3.07	3.30E-08	Development
Contig21945_at	Alpha/beta hydrolase-like protein	2.86	9.57E-10	Development
Contig631_at	Root cap-specific protein	2.32	1.12E-10	Development
Contig2169_at	Putative alpha/beta hydrolase	2.27	3.64E-08	Development

Contig19330_at	Putative proline-rich protein APG	2.16	4.55E-08	Development
Contig2753_at	Seed maturation protein	2.15	1.95E-09	Development
Contig22209_at	Putative pollen specific protein SF21	2.13	1.28E-07	Development
Contig12876_at	Putative glycine-rich protein	1.72	3.00E-09	Development
Contig14137_at	Putative glycine-rich protein	1.72	1.59E-08	Development
Contig6816_at	Putative MtN3	1.58	6.48E-08	Development
Contig13898_at	Nam-like protein 7	1.49	5.48E-08	Development
Contig3956_at	Developmental protein	1.46	2.39E-08	Development
Contig13781_at	Proline-rich cell wall protein-like	1.45	8.48E-07	Development
rbah15i08_s_at	Dem-like protein	1.43	4.69E-08	Development
Contig21432_at	Putative pattern formation protein GNOM	1.42	1.60E-06	Development
Contig7401_at	Roothairless 1	1.37	4.41E-07	Development
Contig6491_at	Ripening-related protein-like	1.32	1.09E-05	Development
Contig11748_at	Growth regulator protein	1.21	7.13E-06	Development
Contig13658_at	Putative NAM (No apical meristem) protein	1.21	3.37E-06	Development
Contig3968_s_at	LON1 protease	1.17	1.42E-06	Development
Contig7314_at	Seed protein B32E	1.14	1.36E-06	Development
Contig24776_at	Auxin-independent growth promoter	1.12	1.26E-07	Development
Contig20720_at	Putative fruit-ripening protein	1.08	5.66E-05	Development
Contig14026_at	NAM protein	1.06	1.75E-05	Development
Contig3968_at	LON1 protease	1.03	2.32E-06	Development
Contig14234_at	Putative glycine-rich protein	1.02	5.17E-05	Development
Contig5887_at	Alternative oxidase AOX3	5.82	1.91E-12	Energy
Contig7354_at	NADPH dehydrogenase	5.65	1.04E-10	Energy
Contig5888_at	Alternative oxidase	4.84	1.59E-12	Energy
Contig15936_at	Alternative oxidase	4.31	3.56E-11	Energy
HI02L18u_at	NAD(P)H-dependent oxidoreductase	3.98	1.47E-11	Energy
Contig2888_at	NADP-dependent malic enzyme	3.68	3.02E-09	Energy
Contig346_at	Ribulose bisphosphate carboxylase small chain	3.37	3.55E-09	Energy
Contig18742_at	Putative NADH dehydrogenase	3.19	2.48E-10	Energy
Contig8371_at	Putative enoyl-CoA-hydratase	3.1	3.40E-10	Energy
Contig3886_at	Ferredoxin III	2.92	3.29E-09	Energy
Contig18638_at	Probable NADPH:quinone oxidoreductase	2.64	2.72E-09	Energy

Contig5363_at	Pyrophosphate--fructose 6-phosphate 1-phosphotransferase	2.6	8.91E-09	Energy
HVSMEn0010L09r2_at	Electron transport SCO1/SenC family protein	2.58	3.98E-10	Energy
Contig1879_at	Cytochrome c	2.54	5.17E-09	Energy
HVSMEl0010B09r2_at	NAD(P)H-dependent oxidoreductase	2.38	2.55E-10	Energy
Contig2600_s_at	Cytosolic 6-phosphogluconate dehydrogenase	2.21	1.51E-10	Energy
HU03G20u_at	Glutaredoxin-related-like protein	2.21	1.80E-10	Energy
Contig940_s_at	Fructose 1-,6-biphosphate aldolase	1.92	1.99E-07	Energy
Contig2598_s_at	Cytosolic 6-phosphogluconate dehydrogenase	1.88	1.02E-06	Energy
Contig3010_s_at	Pyruvate kinase	1.77	6.75E-07	Energy
Contig2940_at	Cytochrome c oxidase polypeptide	1.76	1.61E-08	Energy
HW02P03u_x_at	Ferredoxin-3	1.69	2.83E-07	Energy
Contig5299_at	Ferredoxin precursor	1.65	3.64E-08	Energy
Contig7090_s_at	RuBisCo subunit binding-protein beta subunit	1.65	2.29E-07	Energy
Contig6430_s_at	Electron transfer flavoprotein subunit beta, mitochondrial	1.62	1.96E-07	Energy
Contig6722_at	Putative NADPH-dependent oxidoreductase	1.52	9.49E-07	Energy
HA18O08r_s_at	Fructose 1-,6-biphosphate aldolase	1.49	1.18E-08	Energy
Contig4075_at	NADP-dependent malic enzyme	1.45	2.41E-05	Energy
Contig10375_at	Putative SCO1 protein	1.38	1.55E-07	Energy
Contig5403_at	Ferredoxin--NADP reductase	1.33	3.16E-06	Energy
Contig2940_s_at	Cytochrome c oxidase polypeptide	1.31	4.03E-08	Energy
Contig417_s_at	Fructose-bisphosphate aldolase, cytoplasmic isozyme	1.3	0	Energy
Contig26351_at	Thioredoxin	1.28	6.58E-07	Energy
Contig976_at	Fructose-bisphosphate aldolase, cytoplasmic isozyme	1.23	2.22E-08	Energy
Contig10376_s_at	Putative SCO1 protein	1.22	1.62E-06	Energy
Contig6490_at	Putative pyrophosphate-dependent phosphofructo-1-kinase	1.21	5.09E-07	Energy
HVSMEf0020J20f2_s_at	NADP-dependent malic enzyme	1.19	6.84E-06	Energy
Contig6989_at	Pyruvate kinase	1.16	3.55E-06	Energy
Contig7226_at	Photosystem II protein W-like protein	1.08	2.92E-06	Energy
Contig4077_s_at	Putative chloroplast membrane-associated 30 kD protein	1.05	2.12E-07	Energy
Contig3203_at	Putative cytochrome c oxidase subunit	1.02	3.92E-05	Energy
Contig7538_at	Copine III-like	3.47	1.39E-10	Interaction with the cellular environment
HVSMEn0018G24r2_at	Copine I-like protein	3.2	1.51E-10	Interaction with the cellular environment
Contig16887_at	Copine I-like	1.52	4.76E-08	Interaction with the cellular environment

Contig11103_at	Putative copine I	1.09	7.13E-05	Interaction with the cellular environment
HVSMEl0005L10f_s_at	Putative copine I	1.05	0	Interaction with the cellular environment
Contig1402_at	Putative early nodulin 8	3.69	5.45E-11	Interaction with the environment
Contig1404_x_at	Early nodulin 8	3.16	4.22E-09	Interaction with the environment
Contig12612_at	Ozone-responsive stress-related protein-like	3.08	1.48E-10	Interaction with the environment
Contig1404_at	Putative early nodulin 8	2.73	3.36E-08	Interaction with the environment
Contig6682_at	Universal stress protein / early nodulin ENOD18-like	2.45	2.34E-08	Interaction with the environment
Contig1403_at	Putative early nodulin 8	2.39	9.81E-11	Interaction with the environment
Contig4508_at	Pi starvation-induced protein	2.03	2.35E-09	Interaction with the environment
Contig11699_at	Putative iron deficiency protein Ids3	2	1.41E-08	Interaction with the environment
HVSMEg0002E24r2_s_at	Putative phi-1 (phosphate induced)	1.99	0	Interaction with the environment
Contig10898_at	Early nodulin	1.8	6.06E-07	Interaction with the environment
AF348460_at	Cryptochrome 2	1.75	3.35E-06	Interaction with the environment
Contig14562_at	Cryptochrome 2	1.59	1.31E-07	Interaction with the environment
Contig9820_at	Rhizobium-induced nodule development associated protein	1.31	1.92E-08	Interaction with the environment
HVSMEb0005E20r2_s_at	Putative Rhizobium-induced nodule development protein	1.05	1.73E-05	Interaction with the environment
Contig13210_at	Tyrosine/dopa decarboxylase	6.69	3.00E-13	Metabolism
Contig3047_s_at	Cytochrome P450	6.52	1.53E-12	Metabolism
HVSMEb0010O13f2_at	Monooxygenase/ oxidoreductase	6.48	1.66E-12	Metabolism
HV_CEb0017C08r2_at	Laccase	6.29	1.54E-11	Metabolism
Contig15816_at	1-aminocyclopropane-1-carboxylate synthase	6.17	1.21E-10	Metabolism
Contig18026_at	AMP binding protein	6.08	3.61E-12	Metabolism
Contig15882_s_at	Fatty acid alpha-oxidase	5.88	1.91E-12	Metabolism
HVSMEb0014F22f_s_at	Putative gamma-lyase	5.82	2.08E-11	Metabolism
Contig5638_at	Agmatine coumaroyltransferase	5.61	6.40E-11	Metabolism
Contig14651_at	L-ascorbate oxidase	5.6	2.16E-12	Metabolism
Contig6406_at	Putative indole-3-glycerol phosphate synthase	5.51	7.16E-11	Metabolism
Contig6407_s_at	Putative indole-3-glycerol phosphate synthase	5.46	3.89E-11	Metabolism
Contig1298_at	Enolase	5.34	6.34E-13	Metabolism
HV12E23u_at	Cysteine synthase	5.34	1.02E-09	Metabolism
Contig23667_at	Tryptophan decarboxylase	5.27	1.32E-11	Metabolism
HR01G01r_at	Putative cytochrome	5.21	8.91E-12	Metabolism
Contig15561_s_at	Cytochrome P450	5.2	2.13E-11	Metabolism

Contig3610_s_at	Putative NAD-malate dehydrogenase	5.2	2.27E-10	Metabolism
Contig15150_at	4-coumarate-CoA ligase-like protein	5.13	8.51E-12	Metabolism
Contig5494_at	Phosphoglycerate dehydrogenase-like protein	5.07	7.25E-11	Metabolism
Contig2631_at	Putative lipase	5	5.26E-08	Metabolism
Contig14870_at	Putative trehalose-6-phosphate phosphatase	4.97	1.75E-12	Metabolism
Contig11768_at	Ribose-phosphate pyrophosphokinase 3	4.93	3.09E-11	Metabolism
Contig9196_s_at	Shikimate kinase 2	4.9	6.28E-11	Metabolism
Contig1522_at	Putative Cytochrome P450	4.88	2.16E-10	Metabolism
Contig15147_at	Oxoglutarate dehydrogenase	4.86	5.45E-12	Metabolism
Contig9197_at	Shikimate kinase	4.83	5.61E-10	Metabolism
Contig8527_at	Cinnamoyl-CoA reductase	4.81	1.20E-10	Metabolism
Contig6733_at	Prephenate dehydratase	4.77	1.10E-10	Metabolism
Contig5542_at	Tryptophan synthase alpha	4.76	1.10E-11	Metabolism
Contig11064_at	Phosphoribosylanthranilate isomerase	4.75	2.56E-12	Metabolism
HY07P02u_at	Anthranilate synthase alpha 2 subunit	4.74	9.60E-12	Metabolism
Contig15413_at	Putative anthranilate N-benzoyltransferase	4.68	1.31E-11	Metabolism
Contig5876_at	UDP-glucose: flavonoid 7-O-glucosyltransferase	4.68	7.75E-12	Metabolism
Contig26053_at	Putative S-adenosyl-L-methionine:JA carboxyl methyltransferase	4.64	9.53E-11	Metabolism
Contig13248_at	Indole-3-acetate beta-glucosyltransferase	4.54	2.57E-08	Metabolism
HS07I12u_s_at	Monooxygenase 2	4.54	1.68E-11	Metabolism
HVSMEg0003A16r2_s_at	Putative NAD-malate dehydrogenase	4.54	1.50E-11	Metabolism
HB01C06r_at	Leucoanthocyanidin dioxygenase-like protein	4.52	9.15E-12	Metabolism
Contig18990_at	Putative cytochrome P450	4.41	2.78E-13	Metabolism
HZ50B24r_s_at	Cinnamic acid 4-hydroxylase	4.36	3.21E-10	Metabolism
HY08N20u_at	Putative lipase	4.33	2.71E-10	Metabolism
Contig6732_at	Chorismate mutase/prephenate dehydratase	4.31	1.39E-10	Metabolism
Contig10985_at	Putative cytochrome P450	4.3	5.41E-09	Metabolism
Contig12316_at	L-allo-threonine aldolase	4.3	2.37E-12	Metabolism
Contig15032_at	Replication protein A2	4.23	1.51E-11	Metabolism
Contig1373_at	Glutamate decarboxylase	4.22	1.39E-10	Metabolism
rbags11h24_s_at	Alanine:glyoxylate aminotransferase-like protein	4.18	1.82E-12	Metabolism
Contig22130_at	Putative beta-ketoacyl synthase	4.17	1.20E-10	Metabolism
Contig9219_at	Serine carboxypeptidase family protein	4.14	6.57E-12	Metabolism

Contig5337_at	Putative 2-nitropropane dioxygenase	4.11	2.03E-12	Metabolism
Contig10756_at	Monooxygenase 2	4.08	1.28E-10	Metabolism
Contig8200_at	Anthranilate synthase component II	4.06	1.63E-11	Metabolism
HS05N06r_s_at	4-coumarate-CoA ligase-like protein	4.05	2.38E-11	Metabolism
Contig17478_at	Tryptophan synthase beta chain	4.03	1.53E-10	Metabolism
Contig4273_at	Iron/ascorbate-dependent oxidoreductase	3.99	1.03E-08	Metabolism
Contig3442_at	Cinnamate 4-hydroxylase	3.98	2.36E-10	Metabolism
Contig5574_at	Cytochrome P450 reductase	3.96	3.75E-09	Metabolism
Contig25479_at	Leucoanthocyanidin dioxygenase-like protein	3.94	1.64E-08	Metabolism
Contig10756_x_at	Monooxygenase 2	3.92	1.34E-11	Metabolism
HVSMEm0002M04r2_s_at	Cytochrome P450 reductase	3.92	4.12E-10	Metabolism
Contig9320_at	Putative oxidase-like	3.91	2.21E-09	Metabolism
HY07L14u_at	Putative flavonol glucosyltransferase	3.87	1.14E-09	Metabolism
Contig10937_at	Putative AMP-binding protein	3.86	5.02E-10	Metabolism
Contig6725_at	Omega-3 fatty acid desaturase	3.85	1.93E-09	Metabolism
Contig4986_at	Allene oxide cyclase	3.83	6.16E-09	Metabolism
Contig3045_at	Cytochrome P450	3.82	1.54E-11	Metabolism
Contig5108_s_at	Chorismate synthase	3.81	1.39E-10	Metabolism
HV_CEb0005N09r2_at	Epoxide hydrolase-like protein	3.8	8.70E-10	Metabolism
Contig4084_at	Putative transaldolase	3.78	8.64E-11	Metabolism
Contig4928_at	Glutamate dehydrogenase	3.78	1.91E-09	Metabolism
Contig20828_at	Putative cytochrome P-450 like protein	3.74	7.04E-10	Metabolism
Contig3097_at	Allene oxide synthase	3.74	1.82E-06	Metabolism
Contig3904_at	Tryptophan synthase beta-subunit	3.72	1.16E-10	Metabolism
EBro03_SQ004_A01_s_at	Prephenate dehydratase	3.7	8.73E-10	Metabolism
Contig5994_s_at	Arginine decarboxylase	3.69	4.99E-05	Metabolism
Contig16761_at	Sterol C-22 desaturase-like	3.67	5.68E-10	Metabolism
Contig2021_at	Soluble inorganic pyrophosphatase	3.66	1.91E-10	Metabolism
Contig24329_at	Geranyl diphosphate synthase	3.59	5.93E-12	Metabolism
HV11O04r_s_at	Glutamine-dependent asparagine synthetase 1	3.58	1.04E-09	Metabolism
Contig14397_at	FAD-linked oxidoreductase family	3.57	1.98E-11	Metabolism
Contig9679_at	Acyl-CoA thioester hydrolase-	3.52	2.70E-11	Metabolism
Contig5727_at	Putative epoxide hydrolase	3.49	2.32E-10	Metabolism

HVSMEl0007C14r2_at	Tryptophan decarboxylase	3.49	1.72E-09	Metabolism
Contig25864_at	Putative beta-1,3-galactosyltransferase	3.48	8.64E-11	Metabolism
Contig5146_at	12-oxo-phytodienoic acid reductase	3.48	1.09E-09	Metabolism
Contig16758_at	L-ascorbate oxidase	3.43	7.17E-12	Metabolism
Contig4011_at	Probable inositol oxygenase	3.42	3.47E-11	Metabolism
Contig18214_at	Putative galactosyltransferase	3.41	6.25E-11	Metabolism
Contig2918_s_at	UDP-glucuronic acid decarboxylase	3.41	8.20E-11	Metabolism
Contig15560_at	Cytochrome P450	3.4	4.89E-09	Metabolism
Contig3691_at	Aleurone ribonuclease	3.4	5.92E-09	Metabolism
Contig5879_at	Putative phosphoserine aminotransferase	3.4	7.55E-11	Metabolism
Contig101_at	Fructokinase-1	3.39	5.45E-11	Metabolism
Contig9663_s_at	Transferase family protein	3.39	1.17E-07	Metabolism
Contig17361_at	Flavonoid 7-O-methyltransferase	3.36	1.23E-10	Metabolism
Contig20683_at	Putative alcohol dehydrogenase homolog	3.36	3.81E-10	Metabolism
HV_CEb0020D05r2_s_at	Allene oxide cyclase	3.35	7.10E-08	Metabolism
Contig15844_at	4-coumarate--CoA ligase	3.34	5.88E-09	Metabolism
Contig20510_at	2-oxoglutarate-dependent dioxygenase	3.32	2.50E-11	Metabolism
Contig17025_at	Putative enolase	3.3	2.68E-10	Metabolism
Contig3610_at	Malate dehydrogenase	3.3	2.28E-09	Metabolism
Contig5217_at	Quinone-oxidoreductase QR2	3.3	2.89E-08	Metabolism
Contig1424_at	Methionine synthase 2 enzyme (ms2 gene)	3.29	4.12E-10	Metabolism
Contig17916_at	Lignostilbene-alpha,beta-dioxygenase	3.29	9.61E-11	Metabolism
Contig2916_at	UDP-D-glucuronate decarboxylase	3.23	1.04E-09	Metabolism
Contig3713_s_at	Phospho-2-dehydro-3-deoxyheptonate aldolase 2	3.22	5.83E-09	Metabolism
Contig6058_at	Putative aspartate aminotransferase	3.22	8.00E-11	Metabolism
Contig6435_at	Phosphoenolpyruvate carboxykinase	3.16	4.51E-10	Metabolism
Contig4260_at	Cinnamyl alcohol dehydrogenase	3.14	1.21E-09	Metabolism
Contig16649_at	Pantothenate kinase 1-like	3.13	2.09E-09	Metabolism
Contig7253_at	Putative esterase	3.13	7.52E-10	Metabolism
Contig6194_s_at	12-oxophytodienoic acid reductase	3.12	2.44E-07	Metabolism
Contig10030_at	Pputative lipase homolog	3.11	4.01E-10	Metabolism
Contig11212_at	Flavanone 3-hydroxylase	3.09	1.31E-09	Metabolism
Contig11818_at	Putative cytochrome P450	3.09	2.04E-11	Metabolism

Contig6991_s_at	Arginine decarboxylase	3.07	1.41E-09	Metabolism
Contig11038_at	3-dehydroquinate synthase	3.03	3.71E-09	Metabolism
Contig17722_at	Polyphenol oxidase	3.03	2.14E-11	Metabolism
Contig24300_at	Putative cytokinin dehydrogenase	3.03	2.28E-09	Metabolism
Contig4677_at	4-coumarate--CoA ligase 4CL1	3.03	7.16E-11	Metabolism
Contig8505_s_at	Apyrase 2	3.02	4.20E-11	Metabolism
Contig15771_at	Putative thiamine pyrophosphokinase	3.01	1.63E-08	Metabolism
Contig5885_at	Putative acyl transferase 3	3.01	2.24E-10	Metabolism
Contig11709_at	Glucosyltransferase	3	1.04E-10	Metabolism
Contig25368_at	Putative flavonol glucosyltransferase	3	2.89E-10	Metabolism
Contig5994_at	Arginine decarboxylase	3	3.32E-07	Metabolism
Contig24041_at	Putative glucosyltransferase	2.99	7.29E-08	Metabolism
Contig11701_at	10-deacetylbaccatin III 10-O-acetyltransferase	2.97	2.54E-09	Metabolism
Contig5663_at	Putative fatty acid elongase	2.95	6.70E-09	Metabolism
Contig6770_s_at	N-hydroxycinnamoyl/benzoyl transferase	2.95	2.11E-10	Metabolism
Contig11904_at	Allene oxide synthase	2.94	4.56E-09	Metabolism
Contig6992_at	Arginine decarboxylase	2.94	8.56E-08	Metabolism
Contig15100_at	Amidase family protein	2.93	5.18E-10	Metabolism
Contig16898_at	Quinone-oxidoreductase QR1	2.91	2.31E-10	Metabolism
Contig5648_s_at	Aldose 1-epimerase	2.91	3.46E-09	Metabolism
Contig3205_at	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	2.91	1.28E-11	Metabolism
Contig20411_at	Cinnamyl-alcohol dehydrogenase	2.86	2.40E-09	Metabolism
Contig4346_at	Cinnamyl alcohol dehydrogenase	2.84	7.07E-10	Metabolism
HV_CEb0004J20f_s_at	Putative cytochrome P450	2.84	1.97E-09	Metabolism
Contig7686_at	Glycosyltransferase	2.83	9.85E-09	Metabolism
Contig7739_at	Alanine:glyoxylate aminotransferase-like protein	2.83	8.64E-11	Metabolism
Contig13809_at	Putative nicotinate phosphoribosyltransferase	2.81	6.09E-09	Metabolism
Contig10115_at	Indole-3-glycerol phosphate synthase	2.8	2.55E-07	Metabolism
Contig19364_at	Geranyl diphosphate synthase	2.8	8.44E-09	Metabolism
Contig10710_at	3-methyl-2-oxobutanoate hydroxy-methyl-transferase-like	2.76	8.31E-10	Metabolism
Contig3815_at	ATP-citrate synthase	2.76	5.62E-10	Metabolism
Contig4271_at	Cytochrome P450	2.76	5.10E-11	Metabolism
Contig6569_s_at	Putative acetyl-CoA synthetase	2.75	3.21E-09	Metabolism

Contig25252_at	Putative glycogenin 1	2.73	7.99E-11	Metabolism
Contig6770_at	Hydroxyanthranilate hydroxycinnamoyltransferase	2.73	6.40E-09	Metabolism
Contig12286_s_at	FAD-linked oxidoreductase family	2.72	2.47E-07	Metabolism
Contig14830_at	Putative glucosyltransferase	2.7	2.72E-09	Metabolism
Contig6113_at	Argininosuccinate lyase	2.7	1.43E-09	Metabolism
Contig16253_s_at	Putative oxalyl-CoA decarboxylase	2.69	1.93E-10	Metabolism
Contig7023_at	Acetylornithine aminotransferase	2.69	2.60E-08	Metabolism
Contig3308_at	Glucose-6-phosphate dehydrogenase	2.68	8.56E-09	Metabolism
Contig1634_at	Alpha-1,4-glucan-protein synthase	2.67	9.10E-07	Metabolism
rbah37c06_s_at	Alanine aminotransferase 2	2.67	4.11E-09	Metabolism
Contig12054_at	Putative geranylgeranyl diphosphate synthase	2.66	1.72E-09	Metabolism
HVSMEh0081I20r2_s_at	Cinnamyl alcohol dehydrogenase	2.66	4.67E-09	Metabolism
Contig5833_s_at	3-hydroxy-3-methylglutaryl-coenzyme A reductase	2.62	2.31E-08	Metabolism
Contig11149_at	Metallo-beta-lactamase-like	2.61	8.56E-09	Metabolism
Contig3232_at	Citrate synthase	2.61	3.42E-09	Metabolism
Contig6686_s_at	Putative carboxypeptidase	2.61	5.94E-10	Metabolism
Contig3141_s_at	Putative acyl-CoA oxidase	2.6	1.54E-07	Metabolism
Contig10788_at	Alcohol dehydrogenase-like protein	2.59	6.03E-09	Metabolism
Contig15946_at	Putative serine palmitoyltransferase	2.59	7.13E-09	Metabolism
Contig11517_at	Guanylate kinase	2.58	1.58E-09	Metabolism
Contig12296_at	Hexokinase	2.58	1.08E-07	Metabolism
Contig6830_at	Phosphoserine phosphatase	2.58	1.98E-09	Metabolism
Contig19290_at	Putative glucosyl transferase	2.55	6.84E-06	Metabolism
Contig18028_at	Cinnamoyl CoA reductase	2.54	4.17E-10	Metabolism
Contig4676_at	4-coumarate--CoA ligase 4CL2	2.54	4.34E-09	Metabolism
EBpi07_SQ002_J15_at	Cinnamyl alcohol dehydrogenase 1a	2.54	2.17E-08	Metabolism
Contig12724_at	Flavanone 3-hydroxylase	2.53	2.62E-09	Metabolism
HVSMEa0019P15r2_at	Formate dehydrogenase	2.52	2.70E-09	Metabolism
Contig19947_s_at	AMP-binding protein	2.51	5.11E-08	Metabolism
Contig1942_at	Putative mono-or diacylglycerol acyltransferase	2.5	8.17E-10	Metabolism
Contig2639_at	1-aminocyclopropane-1-carboxylate oxidase	2.49	2.33E-08	Metabolism
Contig22697_at	1-deoxy-D-xylulose 5-phosphate synthase 2	2.48	9.04E-07	Metabolism
Contig5532_at	Pyruvate decarboxylase	2.48	1.58E-09	Metabolism

Contig6685_at	Putative carboxypeptidase	2.46	4.80E-10	Metabolism
Contig6539_s_at	Cell wall invertase	2.44	3.65E-07	Metabolism
Contig6569_at	Putative acetyl-CoA synthetase	2.44	3.08E-08	Metabolism
Contig5883_s_at	Putative phosphoribosylanthranilate transferase	2.43	6.03E-09	Metabolism
Contig17006_at	Putative benzoyl coenzyme A	2.42	1.91E-09	Metabolism
Contig17284_at	Putative cytochrome P450	2.42	5.72E-09	Metabolism
Contig18334_at	Glutamine:fructose-6-phosphate amidotransferase	2.42	1.34E-10	Metabolism
Contig10670_at	Putative anthocyanin 5-O-glucosyltransferase	2.4	5.19E-08	Metabolism
Contig10877_at	Carbonyl reductase 1	2.4	2.24E-10	Metabolism
Contig6382_s_at	Cytosolic aldehyde dehydrogenase	2.4	3.07E-08	Metabolism
HD05F08r_at	Putative anthocyanin 5-O-glucosyltransferase	2.4	2.54E-09	Metabolism
Contig11390_at	Putative threonine dehydratase/deaminase	2.39	2.66E-09	Metabolism
Contig13413_at	Lipase-like protein	2.39	1.65E-07	Metabolism
Contig1926_at	Putative epimerase/dehydratase	2.39	4.20E-10	Metabolism
Contig19680_at	Allyl alcohol dehydrogenase	2.38	7.04E-10	Metabolism
Contig2924_s_at	Aldehyde dehydrogenase	2.38	3.84E-10	Metabolism
Contig21324_at	Putative trehalose-6-phosphate phosphatase	2.37	2.21E-09	Metabolism
Contig20974_at	P450 monooxygenase (CYP72A39)	2.36	7.74E-05	Metabolism
Contig8489_s_at	Monooxygenase 2	2.36	2.56E-08	Metabolism
HT11O15u_s_at	Putative mono-or diacylglycerol acyltransferase	2.36	2.49E-08	Metabolism
EBro08_SQ005_M24_at	Ornithine decarboxylase	2.35	3.68E-08	Metabolism
HVSMEa0003H08r2_at	Putative alanine acetyl transferase	2.35	3.98E-09	Metabolism
Contig14077_at	Putative glycosyltransferase	2.34	2.62E-09	Metabolism
Contig17954_at	Lipase-like	2.34	1.05E-09	Metabolism
Contig18878_at	Phosphoglycerate mutase	2.34	1.62E-09	Metabolism
Contig9135_at	Hydroxymethylglutaryl coenzyme A synthase	2.34	6.92E-08	Metabolism
Contig3811_at	Galactinol synthase 3	2.32	7.84E-09	Metabolism
Contig9556_at	12-oxophytodienoate reductase 3	2.31	1.48E-08	Metabolism
rbasd11p06_s_at	Lipase-like	2.3	5.62E-08	Metabolism
Contig7815_s_at	Putative N-hydroxycinnamoyl/benzoyl transferase	2.28	1.36E-07	Metabolism
EBro02_SQ001_G03_s_at	Putative UDP-glucose glucosyltransferase1	2.28	1.81E-08	Metabolism
Contig26313_at	Putative cytochrome P450	2.26	1.67E-08	Metabolism
Contig11792_at	Putative flavin-containing monooxygenase YUCCA3	2.25	1.38E-06	Metabolism

HV_CEb0003K04f_s_at	Citrate synthase	2.25	1.73E-08	Metabolism
Contig20405_at	Tropinone reductase	2.24	6.95E-09	Metabolism
Contig15050_at	Apoplastic invertase	2.22	2.61E-08	Metabolism
Contig21273_at	Putative amidase	2.22	2.14E-08	Metabolism
Contig3141_at	Probable acyl-CoA oxidase	2.21	9.72E-09	Metabolism
Contig9352_at	Glycosyltransferase	2.21	2.71E-09	Metabolism
HR01O04u_at	UDP-glucoronosyl and UDP-glucosyl transferase	2.21	2.33E-10	Metabolism
Contig14314_at	Putative inorganic pyrophosphatase	2.2	6.45E-05	Metabolism
Contig10466_at	Glycosyltransferase	2.18	1.75E-08	Metabolism
Contig12075_at	Flavonol 3-sulfotransferase	2.18	1.88E-08	Metabolism
Contig1037_at	Cytochrome b6	2.16	1.72E-08	Metabolism
Contig4833_at	N-acetyl-gamma-glutamyl-phosphate reductase	2.16	2.68E-10	Metabolism
Contig7032_at	Alpha-L-arabinofuranosidase/beta-D-xylosidase	2.15	1.24E-09	Metabolism
Contig4696_at	UMP/CMP kinase a	2.12	7.80E-08	Metabolism
Contig19246_at	Putative glucosyl transferase	2.1	6.03E-09	Metabolism
Contig2622_at	Laccase LAC2-1	2.1	3.54E-10	Metabolism
Contig5554_at	Putative hydrolase	2.09	3.28E-09	Metabolism
Contig3953_s_at	Alpha-amylase type B isozyme precursor	2.08	2.43E-10	Metabolism
HK05P12r_x_at	Tryptophan synthase beta-subunit	2.08	7.55E-10	Metabolism
Contig5833_at	3-hydroxy-3-methylglutaryl-CoA reductase	2.06	1.51E-06	Metabolism
Contig18891_at	Crocetin dialdehyde-like	2.05	1.01E-06	Metabolism
Contig9029_at	Cytochrome P450	2.05	1.41E-07	Metabolism
Contig11619_at	Putative ceramide glucosyltransferase	2.04	2.10E-07	Metabolism
Contig6315_s_at	Putative fatty acid hydroxylase	2.04	7.21E-08	Metabolism
basd0c03_s_at	3-phosphoshikimate 1-carboxyvinyltransferase; EPSP-synthase	2.01	3.80E-09	Metabolism
Contig865_3_s_at	Glyceraldehyde 3-phosphate dehydrogenase (GAPDH)	2.01	4.64E-07	Metabolism
Contig7705_at	Putative chorismate mutase	2	4.35E-08	Metabolism
Contig18762_at	Putative ethylene-forming enzyme	1.99	1.66E-08	Metabolism
Contig3441_at	Cytochrome P450	1.99	1.67E-07	Metabolism
Contig4674_at	4-coumarate--CoA ligase 4CL2	1.99	3.38E-08	Metabolism
Contig5922_at	Putative thiolase	1.99	4.45E-08	Metabolism
Contig6771_at	Long-chain acyl-CoA synthetase	1.99	6.35E-09	Metabolism
HW06A08u_s_at	UDP-glucose dehydrogenase	1.98	1.79E-08	Metabolism

Contig13776_at	Nitrate reductase	1.97	1.98E-08	Metabolism
Contig5650_at	Putative inosine-uridine nucleoside N-ribohydrolase	1.97	1.62E-08	Metabolism
Contig19947_at	AMP-binding protein	1.96	8.22E-08	Metabolism
Contig14199_at	Lysine decarboxylase-like protein	1.95	9.72E-08	Metabolism
Contig20070_at	Isopentenyl pyrophosphate:dimethyllallyl pyrophosphate isomerase	1.95	4.01E-08	Metabolism
Contig3710_at	Sucrase-like protein	1.94	4.67E-09	Metabolism
Contig24520_at	Putative cytochrome P450	1.91	3.23E-09	Metabolism
Contig11045_at	Ribonuclease	1.9	9.86E-08	Metabolism
Contig18811_at	Beta3-glucuronyltransferase	1.89	1.14E-07	Metabolism
Contig6542_at	3-dehydroquinate dehydratase	1.89	2.23E-07	Metabolism
HS16J06u_at	Putative UDP-glycosyltransferase 85A8	1.89	1.27E-06	Metabolism
Contig11766_at	Putative metallophosphatase	1.88	1.94E-08	Metabolism
HW01P03u_s_at	Cytochrome P450	1.88	7.55E-08	Metabolism
Contig18594_at	Putative cinnamoyl-CoA reductase	1.87	3.87E-08	Metabolism
Contig6771_s_at	Long-chain acyl-CoA synthetase	1.87	1.05E-09	Metabolism
HA03F12u_s_at	UMP/CMP kinase a	1.87	9.86E-09	Metabolism
Contig1037_s_at	Cytochrome b6	1.86	4.40E-08	Metabolism
Contig4963_at	2-oxoglutarate dehydrogenase	1.86	8.22E-09	Metabolism
HO11E24S_s_at	4-coumarate coenzyme A ligase	1.85	8.33E-07	Metabolism
Contig2168_s_at	Serine hydroxymethyltransferase	1.83	4.13E-06	Metabolism
Contig4121_at	Argininosuccinate synthase, chloroplast precursor	1.83	9.32E-10	Metabolism
Contig484_s_at	Cytochrome P450 like	1.83	0.04	Metabolism
Contig7492_s_at	Rhamnose biosynthetic enzyme 1	1.83	3.00E-09	Metabolism
Contig9397_at	Putative UDP-glucose glucosyltransferase1	1.83	4.24E-08	Metabolism
Contig1385_at	Putative glutamate carboxylase	1.82	1.00E-06	Metabolism
Contig3564_s_at	Iron/ascorbate-dependent oxidoreductase	1.82	7.06E-09	Metabolism
Contig1791_x_at	Adenosylhomocysteinase	1.81	2.83E-07	Metabolism
Contig3608_at	Malate dehydrogenase	1.81	6.90E-08	Metabolism
Contig4793_s_at	Putative deoxycytidine deaminase	1.8	6.66E-09	Metabolism
Contig5012_s_at	Riboflavin biosynthesis protein ribA	1.8	8.92E-09	Metabolism
Contig865_5_s_at	Glyceraldehyde-3-phosphate dehydrogenase	1.8	0	Metabolism
Contig3160_at	Cytochrome P450	1.79	3.97E-09	Metabolism
HM05N11r_at	Cinnamyl alcohol dehydrogenase	1.79	0	Metabolism

HZ48K22r_s_at	Glyceraldehyde 3-phosphate dehydrogenase	1.78	1.12E-07	Metabolism
Contig484_x_at	Cytochrome P450 like	1.77	0.05	Metabolism
Contig654_s_at	Alcohol dehydrogenase	1.77	8.74E-07	Metabolism
Contig5496_at	Putative pyridine nucleotide-disulphide oxidoreductase	1.76	6.34E-05	Metabolism
Contig12437_at	Oxysterol-binding protein	1.75	4.29E-09	Metabolism
Contig16409_at	Phytochelatin synthetase-like protein	1.75	2.17E-08	Metabolism
Contig19854_s_at	Cinnamyl alcohol dehydrogenase	1.75	1.52E-05	Metabolism
Contig7480_at	2-oxoglutarate-dependent dioxygenase	1.75	5.46E-08	Metabolism
Contig15214_at	Lipase-like protein	1.74	4.83E-09	Metabolism
Contig2148_at	Putative UDP-glucose dehydrogenase	1.74	2.86E-09	Metabolism
Contig5553_at	Putative hydrolase	1.74	2.10E-07	Metabolism
Contig619_at	Caffeoyl-CoA O-methyltransferase	1.73	8.30E-06	Metabolism
Contig17768_at	L-aspartate oxidase	1.72	1.28E-07	Metabolism
Contig4017_s_at	Taxadienol acetyl transferase-like	1.72	4.43E-08	Metabolism
Contig10275_s_at	UDP-D-xylose epimerase 2	1.7	1.64E-08	Metabolism
Contig5919_at	Putative glycosyltransferase family	1.7	1.12E-06	Metabolism
Contig11708_at	ABA 8'-hydroxylase 1	1.69	2.86E-06	Metabolism
Contig9175_at	Alanine aminotransferase	1.69	7.67E-08	Metabolism
HV_CEb0017D17f_at	Putative esterase	1.69	1.37E-08	Metabolism
Contig10276_at	UDP-D-xylose epimerase 2	1.68	1.95E-08	Metabolism
Contig11039_at	Multiple inositol polyphosphate phosphatase PhyIIa2	1.68	6.57E-09	Metabolism
Contig11321_at	Pectin-glucuronyltransferase	1.68	4.12E-08	Metabolism
Contig4880_x_at	Glucose-6-phosphate/phosphate translocator	1.68	4.60E-06	Metabolism
Contig14657_at	Hexokinase	1.66	2.25E-06	Metabolism
Contig8703_at	Putative isocitrate lyase	1.66	1.84E-05	Metabolism
Contig12465_at	Homocysteine S-methyltransferase 1	1.63	5.36E-06	Metabolism
Contig4122_s_at	Argininosuccinate synthase	1.62	2.29E-08	Metabolism
Contig5528_at	AMP-binding protein	1.62	2.37E-08	Metabolism
Contig6976_s_at	2-dehydro-3-deoxyphosphooctonate aldolase	1.62	1.21E-06	Metabolism
HV02B02u_at	Putative chalcone synthase	1.62	3.92E-05	Metabolism
Contig10185_at	Peptidase-like protein	1.59	5.25E-08	Metabolism
Contig6942_at	MpV17 transgene-like protein	1.59	2.78E-06	Metabolism
Contig1459_at	Formate dehydrogenase	1.58	3.88E-08	Metabolism

Contig16415_at	L-allo-threonine aldolase	1.58	9.30E-06	Metabolism
HD05F01r_at	Omega-6 fatty acid desaturase	1.58	2.77E-06	Metabolism
Contig8464_at	Putative inosine-uridine nucleoside N-ribohydrolase	1.57	1.33E-08	Metabolism
HI05D22u_at	Cytochrome P450 family protein	1.57	2.88E-08	Metabolism
HVSMEf0002J09r2_at	Putative anthranilate N-benzoyltransferase	1.56	3.13E-08	Metabolism
Contig17609_at	Putative dioxygenase	1.55	5.48E-08	Metabolism
Contig3299_s_at	Pyruvate dehydrogenase E1 beta subunit isoform 2	1.55	1.14E-07	Metabolism
Contig6642_at	Beta-ketoacyl-ACP synthetase I	1.55	2.12E-07	Metabolism
Contig7292_s_at	Cinnamyl alcohol dehydrogenase	1.55	0	Metabolism
Contig8364_at	4-nitrophenylphosphatase-like protein	1.55	2.43E-08	Metabolism
Contig13799_at	Putative alcohol dehydrogenase	1.53	5.66E-08	Metabolism
Contig12799_at	Putative glycosyltransferase protein	1.52	1.45E-06	Metabolism
Contig14663_s_at	Putative cytochrome P450	1.52	7.78E-06	Metabolism
Contig2143_s_at	UDP-glucose dehydrogenase	1.5	1.90E-05	Metabolism
Contig2799_at	Aspartate transaminase	1.5	3.71E-08	Metabolism
Contig7493_at	Rhamnose biosynthetic enzyme 1	1.5	3.43E-05	Metabolism
Contig14827_s_at	UDP-glucoronosyl and UDP-glucosyl transferase family protein	1.49	3.01E-06	Metabolism
Contig7631_at	2-oxoacid dehydrogenase	1.49	1.80E-06	Metabolism
HB13E07r_at	Putative 2-oxoglutarate-dependent oxygenase	1.49	2.18E-06	Metabolism
Contig21905_at	Oxysterol-binding protein-like	1.48	1.64E-06	Metabolism
Contig5724_at	4-hydroxyphenylpyruvate dioxygenase	1.48	2.49E-08	Metabolism
HVSMEf0012H17r2_at	Putative hydroxycinnamoyl transferase	1.48	2.07E-06	Metabolism
Contig16112_at	Puridine kinase/uracil phosphoribosyltransferase	1.47	2.75E-06	Metabolism
Contig6381_at	Cytosolic aldehyde dehydrogenase	1.47	2.93E-07	Metabolism
Contig14368_at	Alpha4-fucosyltransferase	1.46	5.82E-07	Metabolism
Contig1977_s_at	Pyruvate dehydrogenase E1 beta subunit isoform 2	1.46	2.72E-06	Metabolism
Contig5920_s_at	Pectin-glucuronyltransferase	1.46	1.64E-07	Metabolism
Contig4153_at	Hexokinase	1.44	6.19E-06	Metabolism
Contig4350_s_at	Citrate synthase	1.44	3.97E-08	Metabolism
Contig6769_at	Hydroxyanthranilate hydroxycinnamoyltransferase 3	1.44	9.74E-06	Metabolism
Contig9351_s_at	Glycosyltransferase	1.43	2.93E-07	Metabolism
Contig12007_s_at	Monooxygenase 2 (MO2)	1.42	9.36E-07	Metabolism
Contig6274_at	Putative diphosphate-fructose-6-phosphate 1-phosphotransferase	1.42	1.92E-05	Metabolism

Contig14742_at	Putative glucosyltransferase	1.41	4.58E-08	Metabolism
Contig4464_at	Putative oxysterol-binding protein	1.41	7.48E-09	Metabolism
HS05I21u_s_at	Laccase LAC2-1	1.41	1.07E-08	Metabolism
Contig14742_x_at	UDP-glucoronosyl and UDP-glucosyl transferase family protein	1.4	1.12E-07	Metabolism
Contig21780_at	Phosphatidylserine decarboxylase	1.4	1.28E-06	Metabolism
Contig2642_at	1-aminocyclopropane-1-carboxylate oxidase	1.4	1.23E-06	Metabolism
Contig5497_s_at	Putative pyridine nucleotide-disulphide oxidoreductase	1.4	9.14E-07	Metabolism
Contig5770_at	Putative pyruvate dehydrogenase E1 alpha subunit	1.39	0	Metabolism
Contig7736_at	Lactoylglutathione lyase family protein	1.39	0	Metabolism
HK05P12r_s_at	Tryptophan synthase beta-subunit	1.39	4.42E-07	Metabolism
Contig4653_at	NADPH-cytochrome P450 reductase	1.38	4.16E-07	Metabolism
HVSMEl0010P10f_x_at	Arginase	1.37	8.60E-07	Metabolism
Contig16381_at	Putative isoflavone reductase	1.36	4.05E-07	Metabolism
Contig2333_s_at	Putative inorganic pyrophosphatase	1.36	4.22E-06	Metabolism
Contig2495_s_at	Vacuolar invertase	1.36	1.30E-05	Metabolism
EBro08_SQ004_B22_at	Cytochrome P450	1.36	4.05E-07	Metabolism
Contig10435_at	Beta3-glucuronyltransferase	1.35	4.68E-05	Metabolism
Contig6622_at	Putative gamma-lyase	1.35	4.41E-05	Metabolism
HVSMEf0021N07r2_at	Molybdenum cofactor biosynthesis protein Cnx1	1.35	1.10E-07	Metabolism
Contig1294_at	Enolase	1.34	1.22E-05	Metabolism
Contig1747_at	Aspartate aminotransferase	1.34	4.32E-07	Metabolism
Contig19854_at	Cinnamyl alcohol dehydrogenase	1.34	2.09E-05	Metabolism
Contig2528_x_at	Caffeic acid O-methyltransferase	1.34	6.79E-07	Metabolism
Contig4563_at	Dihydrolipoyl dehydrogenase	1.34	1.65E-06	Metabolism
Contig6617_at	NAD-dependent isocitrate dehydrogenase	1.34	1.08E-07	Metabolism
rbags10l09_at	Dolichyl-di-phosphooligosaccharide-protein glycotransferase	1.34	1.14E-07	Metabolism
Contig14826_at	Putative glucosyltransferase	1.33	9.07E-06	Metabolism
Contig3439_s_at	Cytochrome P450	1.33	2.48E-05	Metabolism
HVSMEa0007I03r2_at	Iron/ascorbate-dependent oxidoreductase	1.33	2.43E-06	Metabolism
Contig19044_at	Putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase	1.32	7.86E-07	Metabolism
Contig9086_at	Serine palmitoyltransferase	1.32	7.74E-08	Metabolism
Contig5484_at	Hydrolase-like	1.31	2.02E-07	Metabolism
Contig5547_at	Pantothenate kinase-like	1.31	6.06E-07	Metabolism

Contig6320_at	Putative cytochrome b-561	1.31	7.87E-07	Metabolism
HVSMEn0022F18r2_s_at	hyuC-like protein	1.31	4.33E-07	Metabolism
Contig10066_at	UDP-D-glucose epimerase 2	1.29	4.04E-06	Metabolism
Contig20663_at	Putative lipase homolog	1.29	2.99E-07	Metabolism
Contig4350_at	Citrate synthase	1.29	1.52E-06	Metabolism
Contig7709_at	Cytochrome b5 reductase isoform II	1.29	1.20E-07	Metabolism
Contig1269_at	S-adenosylmethionine synthetase 1	1.28	3.27E-06	Metabolism
Contig3972_at	Cytochrome b5 reductase	1.28	1.09E-06	Metabolism
HS09E20r_s_at	Putative cytochrome	1.28	2.59E-07	Metabolism
Contig10483_at	Sterol desaturase-like	1.27	5.20E-08	Metabolism
Contig10721_at	Anthocyanin biosynthetic gene regulator PAC1	1.27	2.23E-06	Metabolism
Contig5834_at	Probable hydroxymethylglutaryl-CoA reductase	1.27	1.73E-08	Metabolism
Contig68_at	Proline oxidase	1.26	1.08E-05	Metabolism
Contig8532_at	Putative lipase-like protein	1.26	1.02E-05	Metabolism
Contig7331_at	Urate oxidase	1.25	2.49E-06	Metabolism
Contig3563_at	Putative iron/ascorbate-dependent oxidoreductase	1.24	2.18E-07	Metabolism
Contig9990_at	Putative pectin methylesterase	1.24	6.74E-06	Metabolism
Contig18304_at	Succinate dehydrogenase subunit 3	1.23	1.34E-05	Metabolism
Contig5255_at	Alanine-glyoxylate aminotransferase 2	1.23	1.13E-06	Metabolism
Contig14426_at	Cinnamoyl CoA reductase	1.22	2.45E-06	Metabolism
Contig1899_at	Putative pectinacetylesterase	1.22	3.06E-07	Metabolism
Contig2915_at	UDP-D-glucuronate decarboxylase	1.22	2.54E-05	Metabolism
Contig3568_at	Iron/ascorbate-dependent oxidoreductase	1.22	1.11E-06	Metabolism
Contig7707_at	Diphosphomevalonate decarboxylase	1.22	8.09E-07	Metabolism
Contig5939_at	Allyl alcohol dehydrogenase	1.21	6.40E-07	Metabolism
Contig8976_at	Hydroxyacid oxidase 1	1.21	1.27E-07	Metabolism
Contig13725_at	3-beta-glucuronosyltransferase	1.2	7.04E-05	Metabolism
Contig4543_at	3'(2'),5'-bisphosphate nucleotidase	1.2	2.22E-05	Metabolism
Y09233_at	Chalcone synthase 2	1.2	0	Metabolism
Contig12143_at	Glycosyltransferase	1.19	6.98E-05	Metabolism
Contig26545_at	Laccase LAC2-1	1.19	5.66E-05	Metabolism
Contig7194_at	Putative cytochrome P450	1.18	1.79E-06	Metabolism
Contig7857_s_at	Putative branched chain alpha-keto acid dehydrogenase E2 subunit	1.18	9.59E-07	Metabolism

Contig14295_at	Putative anthocyanin 5-aromatic acyltransferase	1.15	2.42E-06	Metabolism
Contig3625_at	Acyl-[acyl-carrier-protein] desaturase	1.15	1.01E-05	Metabolism
Contig917_s_at	Phosphoglycerate kinase	1.15	9.64E-05	Metabolism
Contig11916_at	Glycerol-3-phosphate dehydrogenase-like protein	1.14	1.11E-05	Metabolism
Contig1271_x_at	S-adenosylmethionine synthetase 1	1.14	9.20E-06	Metabolism
Contig16284_at	Acetyl-CoA carboxylase	1.14	4.15E-06	Metabolism
Contig2329_x_at	Putative 12-oxophytodienoic acid reductase	1.14	7.06E-05	Metabolism
Contig2384_at	Putative cinnamoyl-CoA reductase	1.14	5.99E-07	Metabolism
HB22L02r_at	Cytochrome P450-like protein	1.14	1.12E-05	Metabolism
Contig10000_s_at	Putative arabinogalactan protein	1.13	0	Metabolism
Contig4268_s_at	Succinyl-CoA synthetase	1.13	8.87E-06	Metabolism
Contig4348_at	Rhamnose biosynthetic enzyme 1	1.13	2.64E-07	Metabolism
Contig6182_at	Putative oxidoreductase	1.13	4.55E-06	Metabolism
Contig15794_at	Erg28 like protein	1.12	0	Metabolism
Contig17934_at	3-oxo-5-alpha-steroid 4-dehydrogenase	1.12	2.92E-05	Metabolism
Contig1964_at	Putative branched-chain alpha-keto acid decarboxylase	1.12	7.03E-06	Metabolism
Contig2750_s_at	Acetyl-CoA C-acyltransferase	1.12	8.94E-06	Metabolism
Contig3709_s_at	Sucrase-like protein	1.12	1.42E-06	Metabolism
Contig7484_at	B-keto acyl reductase	1.12	4.41E-06	Metabolism
Contig7708_at	ATP-citrate synthase	1.12	4.15E-07	Metabolism
Contig3351_s_at	Aconitate hydratase	1.11	3.83E-06	Metabolism
Contig3720_s_at	Putative glyceraldehyde-3-phosphate dehydrogenase	1.11	8.12E-07	Metabolism
Contig4020_at	Taxadienol acetyl transferase-like	1.11	1.36E-06	Metabolism
Contig6000_at	Beta-phosphoglucomutase-like protein	1.11	3.59E-07	Metabolism
Contig15880_at	Phosphomethylpyrimidine kinase	1.1	2.26E-06	Metabolism
Contig8520_at	Anthranilate phosphoribosyltransferase	1.1	7.44E-05	Metabolism
Contig24607_at	Putative oxidase	1.09	0	Metabolism
HT12P23u_at	Succinate dehydrogenase iron-sulfur protein	1.09	6.24E-06	Metabolism
Contig4689_at	Glycosyltransferase	1.08	2.33E-07	Metabolism
HA11O05u_s_at	Putative 3'(2'),5'-bisphosphate nucleotidase	1.08	1.19E-05	Metabolism
Contig21017_at	Pyrroline-5-carboxylate reductase	1.07	1.32E-06	Metabolism
Contig2284_at	Cytochrome b5	1.07	0	Metabolism
Contig5654_at	Arginase	1.07	2.42E-06	Metabolism

Contig712_at	Malate dehydrogenase	1.07	8.23E-05	Metabolism
Contig14742_s_at	UDP-glucoronosyl and UDP-glucosyl transferase	1.06	3.58E-05	Metabolism
Contig25340_at	Cytochrome P450	1.06	7.83E-06	Metabolism
Contig4530_at	Succinate dehydrogenase iron-protein subunit	1.06	1.23E-05	Metabolism
Contig5040_at	ATP citrate lyase	1.06	8.38E-07	Metabolism
Contig6108_at	Neutral invertase	1.06	4.86E-07	Metabolism
Contig10910_at	3-beta-hydroxysteroid dehydrogenase-like	1.05	1.24E-05	Metabolism
Contig1794_s_at	Adenosylhomocysteinase	1.05	0	Metabolism
Contig6945_at	Pyridoxal kinase	1.05	3.70E-07	Metabolism
Contig16321_at	Esterase/lipase/thioesterase-like protein	1.03	0	Metabolism
Contig3523_at	Peroxisomal fatty acid beta-oxidation multifunctional protein	1.03	2.00E-05	Metabolism
Contig8345_at	Putative phosphoribosylanthranilate transferase	1.03	1.29E-05	Metabolism
EBem10_SQ004_F01_s_at	Putative glutamate decarboxylase	1.03	4.16E-08	Metabolism
EBro02_SQ007_J08_at	Ascorbate oxidase	1.03	0	Metabolism
HB28K03r_x_at	Aspartate aminotransferase	1.03	6.69E-07	Metabolism
Contig14377_at	Glycerophosphoryl diester phosphodiesterase-like	1.02	9.10E-05	Metabolism
Contig16253_at	Putative oxalyl-CoA decarboxylase	1.02	0	Metabolism
Contig3631_at	Methionine aminopeptidase	1.02	2.57E-07	Metabolism
Contig3631_s_at	Methionine aminopeptidase	1.02	2.33E-06	Metabolism
Contig613_s_at	Malate dehydrogenase 1	1.02	1.58E-05	Metabolism
Contig16309_at	Putative dihydroorotase	1.01	1.22E-05	Metabolism
rbags10b05_at	UDP-glucose/GDP-mannose dehydrogenase family	1.01	5.15E-05	Metabolism
Contig22536_at	Putative oxidase	1	3.06E-06	Metabolism
Contig6782_at	Putative arabinogalactan-like protein	1	4.97E-05	Metabolism
Contig8307_s_at	Putative subtilase	5.2	3.11E-10	Protein fate (folding, modification, destination)
Contig4942_at	ATP-dependent Clp protease	4.07	1.86E-11	Protein fate (folding, modification, destination)
Contig15533_at	Putative subtilisin-like serine proteinase	3.89	1.73E-08	Protein fate (folding, modification, destination)
Contig8280_at	Mitochondrial chaperonin-60	3.71	5.95E-10	Protein fate (folding, modification, destination)
Contig15493_at	Putative calmodulin-binding heat-shock protein	3.6	3.36E-11	Protein fate (folding, modification, destination)
Contig22733_at	Putative subtilisin-like serine proteinase	3.58	3.04E-07	Protein fate (folding, modification, destination)
Contig4199_at	Putative endoplasmic reticulum oxidoreductin	3.48	6.52E-12	Protein fate (folding, modification, destination)
Contig6534_at	Kelch repeat-containing F-box-like	3.23	6.84E-11	Protein fate (folding, modification, destination)
HV_CEb0010I11r2_at	GTP-binding protein SAR2	3.23	6.85E-10	Protein fate (folding, modification, destination)

Contig6380_at	Nucellin-like aspartic protease	3.21	7.29E-10	Protein fate (folding, modification, destination)
Contig8308_at	Putative subtilisin-like serine proteinase	3.2	1.51E-08	Protein fate (folding, modification, destination)
Contig20912_at	Putative dymeclin	3	1.56E-09	Protein fate (folding, modification, destination)
HT12E22u_s_at	Putative copper chaperone	2.93	7.93E-11	Protein fate (folding, modification, destination)
Contig11953_at	Putative arm repeat-containing protein	2.63	1.50E-09	Protein fate (folding, modification, destination)
Contig13091_s_at	Aspartic-type endopeptidase/ pepsin A	2.57	1.56E-10	Protein fate (folding, modification, destination)
Contig1560_at	Calnexin homolog precursor	2.54	4.68E-09	Protein fate (folding, modification, destination)
Contig91_at	Endoplasmin homolog precursor	2.5	9.52E-09	Protein fate (folding, modification, destination)
Contig8041_at	Putative DNAJ-like protein	2.45	1.12E-08	Protein fate (folding, modification, destination)
Contig20144_s_at	GTP-binding protein Rab6	2.41	3.18E-08	Protein fate (folding, modification, destination)
Contig3166_at	Ras-related GTP-binding protein	2.41	1.20E-07	Protein fate (folding, modification, destination)
Contig15752_s_at	Putative arm repeat containing protein	2.34	1.88E-08	Protein fate (folding, modification, destination)
Contig20989_at	Putative palmitoyl-protein thioesterase	2.29	6.31E-10	Protein fate (folding, modification, destination)
HV_CEb0009I14r2_s_at	Kelch repeat-containing F-box-like	2.29	3.79E-10	Protein fate (folding, modification, destination)
Contig11141_at	DNAJ protein	2.28	9.26E-08	Protein fate (folding, modification, destination)
HVSMEa0002K13r2_at	Arm repeat protein	2.28	5.30E-09	Protein fate (folding, modification, destination)
Contig2717_s_at	Peptidylprolyl isomerase	2.1	3.57E-09	Protein fate (folding, modification, destination)
Contig12230_s_at	Putative Septum-promoting GTP-binding protein 1	2.07	5.41E-09	Protein fate (folding, modification, destination)
Contig7933_s_at	Putative DNAJ protein	2.07	1.36E-08	Protein fate (folding, modification, destination)
Contig725_s_at	Disulfide isomerase	2.05	5.33E-07	Protein fate (folding, modification, destination)
Contig3165_at	GTP-binding protein	2.04	1.50E-09	Protein fate (folding, modification, destination)
Contig8948_at	Putative ABI3-interacting protein 2, AIP2	1.98	8.83E-09	Protein fate (folding, modification, destination)
Contig4654_at	10 kDa chaperonin	1.97	1.05E-07	Protein fate (folding, modification, destination)
Contig1204_s_at	Cytosolic heat shock protein 90	1.96	1.72E-08	Protein fate (folding, modification, destination)
Contig9905_at	Putative copper chaperone COX17-1	1.93	1.29E-08	Protein fate (folding, modification, destination)
Contig2229_at	Ubiquitin-conjugating enzyme E2	1.92	7.82E-09	Protein fate (folding, modification, destination)
Contig11318_at	GTP-binding nuclear protein Ran-2	1.9	2.26E-10	Protein fate (folding, modification, destination)
Contig3487_at	20S proteasome alpha subunit	1.88	1.22E-09	Protein fate (folding, modification, destination)
Contig632_s_at	DNAJ protein homolog 2	1.88	3.66E-07	Protein fate (folding, modification, destination)
Contig8438_at	F-box family protein-like	1.88	7.68E-09	Protein fate (folding, modification, destination)
Contig5340_at	Proteasome activator subunit 4-like	1.84	3.80E-09	Protein fate (folding, modification, destination)
rbags20m01_at	Lon protease homolog	1.84	1.04E-06	Protein fate (folding, modification, destination)
Contig9255_at	Putative MAWD binding protein	1.82	3.66E-09	Protein fate (folding, modification, destination)

Contig70_x_at	Disulfide-isomerase	1.77	1.44E-08	Protein fate (folding, modification, destination)
Contig3269_at	Proteasome subunit beta type	1.76	6.04E-08	Protein fate (folding, modification, destination)
EBma03_SQ001_K06_x_at	DNAJ protein homolog 2	1.75	7.56E-07	Protein fate (folding, modification, destination)
Contig13308_at	Putative rab7 protein	1.74	4.25E-07	Protein fate (folding, modification, destination)
Contig6385_at	Kelch repeat-containing F-box family protein	1.73	6.62E-07	Protein fate (folding, modification, destination)
Contig416_x_at	Endoplasmin homolog	1.69	2.09E-07	Protein fate (folding, modification, destination)
Contig2442_at	Protein disulfide isomerase	1.66	5.06E-06	Protein fate (folding, modification, destination)
HVSMEi0009N09r2_at	Putative aspartyl protease	1.65	6.11E-08	Protein fate (folding, modification, destination)
Contig15757_at	Putative AAA-type ATPase	1.6	2.92E-05	Protein fate (folding, modification, destination)
Contig2231_s_at	Ubiquitin-conjugating enzyme E2-17 kDa	1.55	1.47E-07	Protein fate (folding, modification, destination)
Contig71_s_at	Endoplasmin homolog	1.52	1.30E-05	Protein fate (folding, modification, destination)
Contig17965_at	Cytochrome c oxidase copper chaperone	1.5	1.07E-08	Protein fate (folding, modification, destination)
Contig18808_s_at	Putative prenylated rab acceptor protein	1.48	4.09E-09	Protein fate (folding, modification, destination)
Contig3328_at	Ubiquitin-activating enzyme E1	1.48	4.53E-08	Protein fate (folding, modification, destination)
Contig5440_at	GPI-anchored protein	1.48	4.85E-08	Protein fate (folding, modification, destination)
Contig3267_at	Proteasome subunit beta	1.45	7.65E-08	Protein fate (folding, modification, destination)
Contig3850_at	Proteasome subunit alpha type 2	1.43	1.39E-06	Protein fate (folding, modification, destination)
Contig6657_at	26S proteasome regulatory particle non-ATPase subunit3	1.4	1.20E-07	Protein fate (folding, modification, destination)
Contig8906_at	Putative chaperone GrpE type 2	1.4	3.65E-07	Protein fate (folding, modification, destination)
Contig5439_s_at	GPI-anchored protein	1.39	4.76E-07	Protein fate (folding, modification, destination)
Contig18387_at	Glycosylation enzyme-like protein	1.37	2.13E-07	Protein fate (folding, modification, destination)
Contig3178_s_at	Proteasome subunit alpha type-3	1.36	3.94E-07	Protein fate (folding, modification, destination)
Contig3169_at	GTP-binding protein	1.35	3.89E-08	Protein fate (folding, modification, destination)
Contig5503_s_at	Putative F-box protein Fbl2	1.35	6.02E-08	Protein fate (folding, modification, destination)
Contig3527_at	26S proteasome RPT6a subunit	1.33	1.46E-08	Protein fate (folding, modification, destination)
Contig9244_at	Putative LYST-interacting protein LIP5	1.33	7.40E-08	Protein fate (folding, modification, destination)
Contig15229_at	Ca2+-dependent lipid-binding protein	1.3	2.04E-07	Protein fate (folding, modification, destination)
Contig4561_at	26S proteasome regulatory particle triple-A ATPase subunit3	1.29	4.46E-08	Protein fate (folding, modification, destination)
Contig2717_at	Peptidylprolyl isomerase	1.27	0	Protein fate (folding, modification, destination)
Contig3485_at	Mitochondrial processing peptidase alpha-chain	1.27	2.87E-06	Protein fate (folding, modification, destination)
Contig4890_at	Proteasome subunit beta type 1	1.27	8.34E-08	Protein fate (folding, modification, destination)
Contig7280_at	DNAJ heat shock family protein	1.27	4.66E-07	Protein fate (folding, modification, destination)
Contig3884_at	PDI-like protein	1.26	4.62E-06	Protein fate (folding, modification, destination)

HVSMEa0003B04r2_s_at	Ubiquitin-activating enzyme E1	1.26	5.23E-07	Protein fate (folding, modification, destination)
Contig3004_at	Proteasome subunit alpha type 5	1.25	2.28E-07	Protein fate (folding, modification, destination)
Contig3408_at	Proteasome subunit beta	1.24	1.32E-07	Protein fate (folding, modification, destination)
Contig3528_at	26S proteasome regulatory subunit 8	1.22	5.14E-07	Protein fate (folding, modification, destination)
Contig7848_at	Proteasome subunit alpha type-4	1.21	3.00E-07	Protein fate (folding, modification, destination)
Contig9161_at	Rac-like GTP-binding protein	1.21	4.31E-06	Protein fate (folding, modification, destination)
Contig8629_at	Ubiquitin family protein	1.2	5.37E-08	Protein fate (folding, modification, destination)
HVSMEk0005D04r2_s_at	Putative 26S proteasome regulatory particle subunit3	1.19	1.23E-07	Protein fate (folding, modification, destination)
Contig4294_s_at	Proteasome subunit beta type 3	1.17	1.97E-05	Protein fate (folding, modification, destination)
HU09N08u_at	DNAJ-like protein	1.17	7.92E-07	Protein fate (folding, modification, destination)
Contig3021_at	26S protease regulatory subunit 4 homolog	1.16	6.92E-05	Protein fate (folding, modification, destination)
Contig3170_at	Ras-related GTP-binding protein	1.16	1.84E-06	Protein fate (folding, modification, destination)
EBes01_SQ004_N07_at	SKP1-like protein 1B	1.16	1.29E-05	Protein fate (folding, modification, destination)
rbags16i17_s_at	Proteasome subunit alpha type 1	1.15	4.33E-07	Protein fate (folding, modification, destination)
Contig3418_at	26S proteasome non-ATPase regulatory subunit	1.13	1.45E-06	Protein fate (folding, modification, destination)
Contig1480_s_at	Putative GTP-binding protein	1.12	9.13E-08	Protein fate (folding, modification, destination)
HS05E04u_s_at	20S proteasome alpha subunit	1.11	1.03E-06	Protein fate (folding, modification, destination)
Contig1046_s_at	Polyubiquitin	1.09	2.69E-06	Protein fate (folding, modification, destination)
Contig11759_at	Putative ras-related GTP-binding protein	1.09	6.07E-06	Protein fate (folding, modification, destination)
Contig3469_at	Proteasome maturation factor-like	1.04	8.79E-05	Protein fate (folding, modification, destination)
Contig8230_at	Putative Der1-like protein	1.04	2.34E-06	Protein fate (folding, modification, destination)
Contig5507_at	26S proteasome non-ATPase regulatory subunit 6	1.03	1.15E-05	Protein fate (folding, modification, destination)
Contig15752_at	Arm repeat protein	1.02	2.26E-06	Protein fate (folding, modification, destination)
Contig4865_at	GTP-binding protein	1.01	7.96E-06	Protein fate (folding, modification, destination)
Contig3286_s_at	Small heat shock protein HSP17.8	4.85	1.51E-11	Protein synthesis
EBro02_SQ002_C17_at	Glutamyl-tRNA reductase 3	4.48	3.23E-11	Protein synthesis
Contig3147_at	Glutamyl-tRNA reductase	4.35	6.31E-10	Protein synthesis
EBro02_SQ002_C17_s_at	Glutamyl-tRNA reductase	4.03	9.91E-12	Protein synthesis
Contig998_s_at	Heat shock protein 70	3.53	6.49E-10	Protein synthesis
Contig3287_x_at	Small heat shock protein HSP17.8	3.22	7.31E-11	Protein synthesis
L32165_s_at	HSP70 precursor	3.12	1.79E-07	Protein synthesis
Contig6096_at	Heat shock protein 70	3.03	2.10E-09	Protein synthesis
EBem05_SQ003_L06_at	Small heat shock protein	2.97	4.57E-09	Protein synthesis

Contig873_s_at	Heat shock protein 70	2.96	1.18E-10	Protein synthesis
Contig12708_at	70kD heat shock protein	2.83	6.10E-09	Protein synthesis
Contig11696_at	Putative peptide chain release factor subunit 1 (ERF1)	2.78	1.46E-10	Protein synthesis
Contig2004_s_at	Heat shock protein 18	2.77	3.50E-09	Protein synthesis
Contig3289_at	Small heat shock protein HSP17.8	2.71	3.49E-10	Protein synthesis
Contig1206_s_at	Heat shock protein 80	2.55	1.36E-10	Protein synthesis
Contig1207_at	Heat shock protein 80	2.38	2.83E-10	Protein synthesis
Contig5096_at	HSP like protein	2.25	1.65E-10	Protein synthesis
HV_CEa0008J10r2_s_at	Alanyl-tRNA synthetase	2.04	6.08E-10	Protein synthesis
Contig7751_at	Alanyl-tRNA synthetase	1.89	3.50E-09	Protein synthesis
Contig6559_at	Small heat shock protein Hsp23.6	1.84	2.46E-09	Protein synthesis
Contig5933_at	Eukaryotic translation initiation factor 4E	1.8	1.16E-07	Protein synthesis
Contig20303_at	Putative serine proteinase	1.77	7.02E-10	Protein synthesis
Contig2820_at	Putative heat shock protein	1.73	2.40E-09	Protein synthesis
HV_CEa0008J10r2_at	Alanyl-tRNA synthetase	1.72	6.49E-09	Protein synthesis
EBro08_SQ011_I03_at	Heat shock protein 18	1.69	8.15E-07	Protein synthesis
Contig15314_at	Putative peptide chain release factor subunit 1 (ERF1)	1.65	1.69E-08	Protein synthesis
Contig26289_at	Putative 26S proteosome regulatory subunit	1.59	9.50E-09	Protein synthesis
Contig2819_at	Putative heat shock protein	1.52	3.77E-08	Protein synthesis
HVSMEl0011L15f2_s_at	Cytosolic heat shock 70 protein	1.52	6.42E-08	Protein synthesis
Contig7490_at	Putative heat shock protein	1.48	3.55E-09	Protein synthesis
Contig21775_at	Heat shock protein 101	1.47	4.45E-06	Protein synthesis
Contig19986_at	Lysyl-tRNA synthetase	1.3	7.10E-08	Protein synthesis
Contig2884_at	Translation initiation factor eIF5	1.29	5.75E-08	Protein synthesis
HV05A02u_s_at	Peptide chain release factor 2	1.28	4.66E-07	Protein synthesis
Contig8995_at	Ribosomal protein S6 kinase homolog	1.25	8.47E-06	Protein synthesis
Contig2222_at	Translational initiation factor	1.23	3.37E-05	Protein synthesis
Contig4646_at	Ribosome biogenesis regulatory protein	1.23	8.36E-06	Protein synthesis
Contig1657_at	26S protease regulatory subunit 7	1.21	1.53E-06	Protein synthesis
Contig11261_at	Peptidyl-tRNA hydrolase 2	1.19	9.59E-07	Protein synthesis
Contig25239_at	Putative LMW heat shock protein	1.19	0	Protein synthesis
Contig1489_at	60S ribosomal protein L10	1.15	1.28E-06	Protein synthesis
Contig6557_s_at	Small heat shock protein	1.13	1.82E-07	Protein synthesis

Contig6555_s_at	Small heat shock protein Hsp23.6 precursor	1.07	0	Protein synthesis
Contig2225_s_at	Eukaryotic initiation factor 4A (eIF-4A)	1.05	1.12E-06	Protein synthesis
Contig1205_s_at	Heat shock protein	1.02	0	Protein synthesis
Contig3284_x_at	Small heat shock protein HSP17.8	1.01	1.49E-05	Protein synthesis
Contig6253_at	Ferrochelatase-2	2.3	4.76E-09	Protein with binding function or cofactor requirement
Contig1615_s_at	Luminal-binding protein	2.07	4.67E-09	Protein with binding function or cofactor requirement
Contig5805_at	SOUL heme-binding protein-like	1.96	1.04E-09	Protein with binding function or cofactor requirement
Contig15230_at	Initiator-binding protein	1.78	9.12E-07	Protein with binding function or cofactor requirement
Contig12425_at	Iron-sulfur cluster assembly protein IscA	1.12	1.87E-05	Protein with binding function or cofactor requirement
Contig10263_at	Globulin-like protein	5.02	8.47E-10	Storage
Contig4194_at	Patatin-like protein	4.64	9.60E-12	Storage
Contig6910_at	Patatin-like protein 1	3.69	6.30E-10	Storage
Contig2714_at	Ferritin 1	3.22	1.36E-05	Storage
Contig15718_at	Patatin-like phospholipase family protein	3	3.92E-10	Storage
Contig4194_s_at	Patatin-like phospholipase family protein	2.93	4.31E-10	Storage
HV12A05u_s_at	Ferritin	2.92	3.63E-05	Storage
Contig2716_s_at	Ferritin	2.54	0	Storage
Contig4195_at	Patatin-like protein	1.87	1.84E-09	Storage
Contig25131_at	ZIM motif family protein	4.8	3.56E-11	Transcription
Contig20450_at	WRKY transcription factor 4	4.45	3.46E-13	Transcription
Contig3362_at	NAC domain-containing protein 68	4.28	1.36E-10	Transcription
HVSMEa0015G15r2_s_at	Putative NAC transcription factor	4.14	1.22E-10	Transcription
Contig23823_at	C2H2 zinc finger protein	3.98	7.21E-12	Transcription
Contig21793_at	C2H2-type zinc finger protein ZFP36	3.88	2.05E-11	Transcription
Contig26350_at	FT-like protein 4	3.55	4.67E-09	Transcription
Contig5841_at	Myb4 transcription factor	3.47	5.80E-12	Transcription
HV06O23u_at	mRNA cleavage factor subunit - like protein	3.4	1.75E-10	Transcription
HW08K02u_at	Zinc finger transcription factor	3.31	2.20E-11	Transcription
Contig15867_at	Putative NAC domain containing protein	3.3	2.27E-11	Transcription
Contig18961_at	Heat stress transcription factor Spl7	3.29	2.16E-12	Transcription
Contig10270_at	Zinc finger family protein	3.21	2.39E-10	Transcription
Contig11225_at	Zim motif family protein	3.16	1.10E-09	Transcription
Contig18088_at	Zinc finger protein 1	3.06	1.72E-08	Transcription

Contig23110_at	DNA-binding protein	3.05	7.75E-09	Transcription
HVSMEa0001M23r2_at	Putative WRKY14	2.75	1.23E-10	Transcription
Contig15241_at	OsNAC6-like protein	2.72	2.82E-10	Transcription
Contig24933_at	Putative zinc finger protein	2.67	4.94E-10	Transcription
Contig20981_at	C2H2 zinc finger protein	2.61	3.75E-09	Transcription
Contig658_at	Putative RNA helicase	2.51	8.45E-08	Transcription
Contig10168_at	WRKY transcription factor 7	2.44	6.74E-11	Transcription
Contig13355_at	Basic helix-loop-helix (BHLH) family protein-like	2.43	9.41E-09	Transcription
Contig3867_at	Transcription factor EREBP1	2.43	4.03E-10	Transcription
Contig5842_s_at	Myb-related protein Myb4	2.36	1.21E-09	Transcription
Contig9431_at	BZIP transcription factor	2.35	3.42E-11	Transcription
Contig10167_at	WRKY transcription factor 7	2.33	1.23E-06	Transcription
Contig9702_at	Putative plastid (P)ppGpp synthase	2.32	8.34E-08	Transcription
EBro02_SQ004_H10_at	WRKY transcription factor 76	2.3	8.45E-10	Transcription
Contig7517_at	Putative WRKY DNA binding protein	2.23	7.95E-09	Transcription
Contig9800_at	Zinc finger and C2 domain protein-like	2.12	1.12E-06	Transcription
Contig26206_at	Pentatricopeptide (PPR) repeat-containing protein-like	2.09	6.44E-08	Transcription
Contig4815_at	ZIM motif family protein	2.09	1.97E-09	Transcription
Contig7483_at	Putative AP2 domain containing protein RAP2.8	2.07	2.88E-08	Transcription
Contig6727_at	Dehydration-responsive AP2 domain transcriptional activator	2.05	6.92E-10	Transcription
Contig6076_s_at	Zinc finger (C3HC4-type RING finger) family protein	2.04	4.65E-09	Transcription
Contig11918_at	Putative RING zinc finger protein	1.94	1.16E-06	Transcription
Contig26105_at	WRKY transcription factor	1.93	3.59E-09	Transcription
Contig14114_at	C2H2 zinc finger protein	1.89	4.17E-06	Transcription
Contig21062_at	RRM-containing protein	1.89	4.05E-08	Transcription
Contig7132_s_at	Putative TF-like protein	1.79	1.50E-08	Transcription
Contig24931_at	Auxin response transcription factor(ARF6)	1.78	7.93E-07	Transcription
Contig23697_at	DNA-binding protein ABF1	1.76	3.80E-07	Transcription
Contig9430_at	Putative SCARECROW gene regulator	1.75	1.58E-07	Transcription
Contig4386_at	WRKY transcription factor	1.74	3.83E-08	Transcription
EBem09_SQ007_G10_at	Pentatricopeptide (PPR) repeat-containing protein-like	1.73	1.93E-09	Transcription
Contig3412_at	Putative poly(A) binding protein II	1.67	4.60E-07	Transcription
S0001000055P18F1_s_at	WRKY transcription factor 45	1.66	1.11E-07	Transcription

Contig12964_at	CCAAT-binding transcription factor subunit A	1.64	2.58E-08	Transcription
Contig18796_at	Putative ethylene-responsive transcriptional coactivator	1.62	7.12E-09	Transcription
Contig3496_at	Transformer serine/arginine-rich ribonucleoprotein	1.62	2.40E-06	Transcription
Contig10172_at	NAC domain-containing protein	1.6	4.02E-06	Transcription
Contig14348_at	MADS-box transcription factor 26	1.57	2.99E-07	Transcription
Contig21110_at	WRKY family transcription factor	1.53	0	Transcription
Contig6454_at	Zinc-finger protein Lsd1	1.53	5.92E-08	Transcription
Contig18148_at	Heat shock transcription factor HSF29	1.51	4.03E-08	Transcription
Contig5180_at	Transcription factor	1.5	1.44E-07	Transcription
HP01H17w_at	Putative AP2 domain transcriptional regulator	1.5	1.17E-07	Transcription
HW07B21u_at	Zinc finger, C3HC4 type family protein	1.48	2.01E-08	Transcription
Contig10652_at	RING-H2 finger protein	1.46	1.25E-08	Transcription
Contig658_s_at	Putative DEAD box RNA helicase	1.45	1.71E-06	Transcription
Contig21005_at	C2H2 zinc finger protein	1.43	1.83E-08	Transcription
Contig7881_at	Zinc finger transcription factor	1.43	6.86E-07	Transcription
Contig9799_s_at	Zinc finger and C2 domain protein-like	1.43	2.61E-08	Transcription
Contig20846_at	LIM domain containing protein-like	1.42	3.40E-07	Transcription
Contig10402_at	Zinc finger (C3HC4-type RING finger)-like protein	1.41	8.28E-06	Transcription
Contig21100_at	Zinc finger POZ domain protein-like	1.4	3.74E-07	Transcription
Contig9429_s_at	Putative SCARECROW gene regulator	1.4	4.91E-06	Transcription
Contig16040_at	WRKY transcription factor	1.39	2.24E-07	Transcription
Contig12005_at	WRKY transcription factor	1.36	0	Transcription
Contig18870_at	Heat shock transcription factor	1.33	1.08E-05	Transcription
Contig5241_at	Putative NAC2	1.32	2.09E-06	Transcription
Contig12594_at	Scarecrow-like protein	1.29	1.57E-06	Transcription
Contig9631_at	Putative homeodomain protein	1.29	5.82E-07	Transcription
HX02B17u_at	Transcription factor OsRS2	1.29	1.74E-07	Transcription
Contig10471_at	WRKY transcription factor	1.28	3.58E-08	Transcription
Contig13765_at	Zinc finger protein-like	1.28	1.88E-06	Transcription
Contig14544_at	Pirin-like protein	1.28	1.93E-06	Transcription
Contig14541_at	Putative transcriptional activator	1.27	5.10E-07	Transcription
Contig12861_at	Putative transcription factor	1.25	1.86E-05	Transcription
Contig18462_at	Putative WRKY5 protein	1.25	1.36E-05	Transcription

Contig1446_s_at	RNA-binding protein-like	1.24	8.22E-06	Transcription
Contig11704_at	Putative tubby protein	1.23	2.11E-07	Transcription
Contig8702_at	Putative bZIP family transcription factor	1.23	1.10E-05	Transcription
Contig10102_at	BHLH protein family-like	1.21	2.29E-07	Transcription
Contig9770_at	Zinc finger protein F35	1.19	2.52E-06	Transcription
Contig13187_at	Putative DNA primase large subunit	1.18	2.08E-06	Transcription
Contig3036_at	RNA binding protein Rp120	1.18	2.29E-07	Transcription
Contig4813_at	ZIM motif family protein	1.18	2.61E-05	Transcription
Contig11096_at	Putative zinc finger protein	1.17	1.64E-06	Transcription
Contig23200_at	Putative transcription factor	1.17	4.44E-05	Transcription
Contig4416_at	Putative CCR4-NOT transcription complex subunit	1.15	4.78E-06	Transcription
Contig7589_at	Zinc finger, C3HC4 type family protein	1.15	9.86E-07	Transcription
Contig10401_s_at	Zinc finger (C3HC4-type RING finger)-like protein	1.14	2.68E-06	Transcription
Contig9692_at	RNA-binding protein-like	1.14	1.90E-06	Transcription
HZ01D23u_s_at	Putative NAC2	1.13	9.12E-07	Transcription
Contig15869_at	WRKY transcription factor	1.11	3.67E-06	Transcription
Contig15950_at	Putative zinc finger protein	1.11	4.07E-05	Transcription
Contig25870_at	Zinc finger (C3HC4-type RING finger) family protein	1.11	1.77E-06	Transcription
Contig15911_at	RBP2 protein	1.1	1.50E-06	Transcription
Contig8981_at	Putative MYC transcription factor	1.08	7.63E-06	Transcription
Contig15957_at	WRKY transcription factor 45	1.07	2.53E-05	Transcription
Contig8931_at	Putative zinc finger protein	1.07	3.93E-06	Transcription
Contig17684_at	GATA-1 zinc finger protein	1.06	9.51E-07	Transcription
Contig7157_at	Zinc finger protein-like	1.06	1.48E-06	Transcription
Contig7384_s_at	Putative zinc finger protein	1.06	0	Transcription
Contig19168_at	Putative zinc finger protein	1.04	1.45E-05	Transcription
Contig3894_at	Tubby-like protein	1.04	1.56E-06	Transcription
HI11M05r_s_at	Zinc finger protein	1.03	4.18E-06	Transcription
Contig3031_s_at	Putative RNA binding protein	1.02	2.69E-05	Transcription
Contig4812_at	ZIM motif family protein	1.02	9.24E-05	Transcription
Contig4695_at	Putative RNA recognition motif (RRM)-containing protein	1.01	9.08E-05	Transcription
Contig7127_at	Putative TF-like protein	1.01	2.82E-05	Transcription
Contig10179_s_at	None	7.1	1.29E-13	Unclassified

EBem10_SQ001_I05_at	None	5.94	2.30E-12	Unclassified
HS14L06r_at	None	5.66	3.00E-13	Unclassified
Contig19902_at	None	5.46	2.88E-12	Unclassified
Contig13015_at	None	5.19	1.74E-12	Unclassified
EBem10_SQ004_D16_at	None	4.85	1.05E-11	Unclassified
Contig26482_at	None	4.8	3.00E-13	Unclassified
HV_CEa0009O07r2_s_at	None	4.65	9.15E-12	Unclassified
HV12F07u_at	None	4.62	2.95E-12	Unclassified
HB20B10r_at	None	4.56	6.95E-09	Unclassified
HY06G13u_at	None	4.55	2.15E-11	Unclassified
Contig10441_at	None	4.51	2.35E-10	Unclassified
Contig12336_at	None	4.5	3.86E-10	Unclassified
Contig18399_at	None	4.49	2.65E-10	Unclassified
Contig15108_at	None	4.45	2.68E-10	Unclassified
Contig25977_at	None	4.38	8.05E-11	Unclassified
Contig26496_at	None	4.32	5.75E-11	Unclassified
Contig6741_at	None	4.32	2.18E-10	Unclassified
EBpi01_SQ002_L02_at	None	4.31	1.39E-10	Unclassified
Contig16935_at	None	4.29	5.45E-12	Unclassified
Contig8178_at	None	4.27	1.80E-12	Unclassified
Contig14743_at	None	4.17	1.47E-10	Unclassified
Contig15798_at	None	4.14	7.03E-11	Unclassified
HU11H03u_s_at	None	4.12	4.05E-11	Unclassified
EBpi01_SQ002_L02_x_at	None	4.1	1.75E-10	Unclassified
EBro02_SQ004_C14_at	None	4.09	2.61E-11	Unclassified
Contig17960_at	None	4	1.11E-10	Unclassified
HV_CEb0004D24r2_at	None	3.98	4.30E-11	Unclassified
Contig5303_at	None	3.88	1.89E-08	Unclassified
HO10M16S_at	None	3.87	1.04E-10	Unclassified
EBro02_SQ006_L04_x_at	None	3.85	8.29E-10	Unclassified
baak1o23_s_at	None	3.77	3.47E-11	Unclassified
EBro03_SQ002_D18_at	None	3.72	1.85E-10	Unclassified
HY07D14u_s_at	None	3.7	1.04E-11	Unclassified

Contig15759_at	None	3.68	1.63E-11	Unclassified
HV_CEa0009C05r2_s_at	None	3.66	5.24E-12	Unclassified
Contig23462_at	None	3.62	2.95E-08	Unclassified
Contig17528_at	None	3.58	1.84E-11	Unclassified
Contig7378_at	None	3.58	9.11E-11	Unclassified
HVSMEf0011A19f_s_at	None	3.56	7.30E-11	Unclassified
EBro02_SQ006_L04_at	None	3.53	8.31E-10	Unclassified
Contig17087_at	None	3.45	1.37E-09	Unclassified
EBro08_SQ011_N18_at	None	3.42	7.31E-11	Unclassified
EBpi01_SQ001_G04_at	None	3.38	2.59E-11	Unclassified
HVSMEi0003D06r2_at	None	3.38	5.75E-12	Unclassified
Contig12584_s_at	None	3.37	5.63E-11	Unclassified
Contig13218_at	None	3.36	2.66E-11	Unclassified
Contig19593_at	None	3.27	5.53E-09	Unclassified
Contig9874_s_at	None	3.24	2.11E-07	Unclassified
HVSMEi0019L06r2_at	None	3.24	1.52E-10	Unclassified
Contig13189_at	None	3.22	1.61E-10	Unclassified
Contig10626_at	None	3.21	1.82E-09	Unclassified
EBpi01_SQ002_N08_at	None	3.18	2.57E-09	Unclassified
EBma05_SQ003_C16_s_at	None	3.13	2.79E-11	Unclassified
HVSMEf0016E08r2_at	None	3.12	5.87E-07	Unclassified
Contig16886_at	None	3.11	2.67E-08	Unclassified
HS08J14u_x_at	None	3.1	2.57E-10	Unclassified
Contig12700_at	None	3.09	1.50E-11	Unclassified
Contig7923_s_at	None	3.08	3.17E-08	Unclassified
HY08G17u_s_at	None	3.06	5.24E-11	Unclassified
Contig16529_at	None	3.01	5.68E-10	Unclassified
Contig12523_s_at	None	3	6.99E-11	Unclassified
HV10O20u_x_at	None	3	2.03E-10	Unclassified
Contig11611_at	None	2.99	6.78E-08	Unclassified
HVSMEl0025L16f_at	None	2.98	4.11E-10	Unclassified
HV_CEb0006A14f_s_at	None	2.96	2.36E-09	Unclassified
Contig15861_at	None	2.94	1.37E-07	Unclassified

Contig21316_at	None	2.91	1.68E-10	Unclassified
EBro02_SQ006_C05_at	None	2.9	2.23E-08	Unclassified
HX03D12u_at	None	2.9	2.18E-11	Unclassified
HS09O21u_at	None	2.89	1.20E-10	Unclassified
HK04A15r_at	None	2.85	1.85E-11	Unclassified
Contig24294_at	None	2.84	2.24E-10	Unclassified
HT05D14u_s_at	None	2.83	8.64E-10	Unclassified
HU05H13u_s_at	None	2.83	1.22E-09	Unclassified
Contig4391_s_at	None	2.82	1.89E-08	Unclassified
Contig17528_s_at	None	2.81	2.03E-10	Unclassified
Contig5302_at	None	2.81	1.13E-08	Unclassified
EBro08_SQ012_C01_at	None	2.79	2.58E-09	Unclassified
baak23m11_s_at	None	2.77	1.30E-09	Unclassified
HV_CEb0001N11r2_at	None	2.74	2.57E-10	Unclassified
Contig7498_at	None	2.72	4.15E-09	Unclassified
HV_CEb0009D09r2_at	None	2.7	2.10E-07	Unclassified
Contig18290_at	None	2.67	2.40E-09	Unclassified
EBro08_SQ008_K12_at	None	2.6	8.38E-08	Unclassified
Contig21256_at	None	2.59	4.32E-10	Unclassified
Contig9863_at	None	2.57	2.16E-06	Unclassified
HW02N10u_at	None	2.57	3.14E-09	Unclassified
HB20H10r_at	None	2.56	1.78E-10	Unclassified
HVSMEf0003G07r2_at	None	2.55	1.69E-10	Unclassified
Contig17635_at	None	2.54	4.29E-10	Unclassified
HF06A04r_at	None	2.54	1.08E-10	Unclassified
Contig26269_at	None	2.52	1.32E-09	Unclassified
Contig26368_at	None	2.52	8.88E-09	Unclassified
HR01A09u_at	None	2.52	6.35E-10	Unclassified
Contig17521_at	None	2.51	9.64E-10	Unclassified
HVSMEn0016K19r2_at	None	2.51	9.59E-10	Unclassified
Contig25691_at	None	2.5	7.70E-10	Unclassified
HY02G07u_at	None	2.5	2.89E-10	Unclassified
Contig10409_s_at	None	2.48	8.50E-10	Unclassified

Contig18382_at	None	2.47	7.10E-10	Unclassified
Contig4309_at	None	2.46	2.82E-10	Unclassified
Contig6309_at	None	2.46	7.95E-10	Unclassified
HV_CEb0001D02r2_at	None	2.46	3.84E-09	Unclassified
EBem08_SQ004_K18_at	None	2.45	1.68E-08	Unclassified
Contig24217_at	None	2.44	6.93E-10	Unclassified
HI09N21r_s_at	None	2.44	2.53E-09	Unclassified
HVSMEh0094M14f_s_at	None	2.43	2.48E-09	Unclassified
HVSMEn0020J21r2_s_at	None	2.43	2.57E-08	Unclassified
HY02O18u_s_at	None	2.43	2.18E-08	Unclassified
rbaal1k11_s_at	None	2.43	5.21E-09	Unclassified
HVSMEi0013J13r2_at	None	2.42	1.35E-07	Unclassified
Contig477_at	None	2.41	1.60E-08	Unclassified
HI05P01u_at	None	2.41	2.69E-09	Unclassified
HY01N09u_at	None	2.41	7.69E-09	Unclassified
Contig11664_at	None	2.38	2.05E-10	Unclassified
EBro04_SQ003_G13_at	None	2.33	1.26E-09	Unclassified
Contig12044_at	None	2.32	1.63E-07	Unclassified
Contig12794_at	None	2.32	2.74E-08	Unclassified
Contig22642_at	None	2.32	1.15E-10	Unclassified
HVSMEk0017E01r2_s_at	None	2.32	4.14E-10	Unclassified
Contig6014_at	None	2.31	1.45E-08	Unclassified
Contig25706_at	None	2.3	3.06E-09	Unclassified
HVSMEf0023D17f_s_at	None	2.3	4.40E-08	Unclassified
HVSMEm0019L10r2_at	None	2.3	9.85E-09	Unclassified
HY01N09u_x_at	None	2.28	5.86E-08	Unclassified
Contig23928_at	None	2.26	1.04E-10	Unclassified
HVSMEk0006L18r2_at	None	2.25	3.70E-10	Unclassified
Contig14685_at	None	2.24	3.25E-10	Unclassified
HK04D15u_at	None	2.24	6.43E-08	Unclassified
HVSMEk0011E15r2_at	None	2.24	6.23E-10	Unclassified
Contig26386_at	None	2.22	1.05E-08	Unclassified
HB29G06r_at	None	2.22	4.93E-09	Unclassified

Contig15721_at	None	2.21	3.27E-08	Unclassified
Contig14263_at	None	2.2	5.62E-10	Unclassified
HVSMEf0022D18r2_s_at	None	2.2	2.59E-09	Unclassified
Contig15849_at	None	2.18	2.44E-09	Unclassified
HVSMEn0020J21r2_at	None	2.18	5.84E-08	Unclassified
baak4a13_at	None	2.16	6.52E-07	Unclassified
Contig16526_at	None	2.15	9.84E-07	Unclassified
HV_CEb0004G20r2_s_at	None	2.15	2.45E-08	Unclassified
Contig23016_at	None	2.14	4.56E-08	Unclassified
Contig23149_at	None	2.14	7.41E-09	Unclassified
HVSMEg0008C16r2_s_at	None	2.14	1.97E-09	Unclassified
HT09O03u_s_at	None	2.13	1.06E-06	Unclassified
Contig15795_at	None	2.12	2.51E-05	Unclassified
Contig7343_s_at	None	2.1	2.20E-09	Unclassified
Contig11969_at	None	2.09	2.11E-05	Unclassified
HB16L13r_x_at	None	2.09	1.68E-10	Unclassified
HB26N23r_at	None	2.08	2.35E-07	Unclassified
rbaal3d15_s_at	None	2.08	5.49E-09	Unclassified
Contig10411_at	None	2.07	1.20E-09	Unclassified
Contig14296_at	None	2.07	4.51E-10	Unclassified
HU13L18u_s_at	None	2.07	2.21E-09	Unclassified
Contig24413_at	None	2.06	8.96E-07	Unclassified
Contig23681_at	None	2.01	2.47E-07	Unclassified
Contig4307_s_at	None	2.01	7.44E-10	Unclassified
Contig12469_at	None	2	1.89E-06	Unclassified
HW07P08u_s_at	None	2	2.53E-07	Unclassified
Contig7315_at	None	1.99	8.42E-05	Unclassified
23381122_R_1101-1898_at	None	1.96	2.64E-08	Unclassified
HS09G19u_s_at	None	1.93	5.67E-07	Unclassified
HVSMEb0005E07r2_at	None	1.93	1.96E-08	Unclassified
Contig10022_at	None	1.9	5.16E-08	Unclassified
EBro02_SQ006_C03_at	None	1.9	5.19E-09	Unclassified
Contig16640_at	None	1.89	2.27E-09	Unclassified

HD04N07u_at	None	1.89	2.53E-08	Unclassified
HW01K06u_s_at	None	1.88	3.00E-07	Unclassified
EBpi01_SQ005_A03_at	None	1.87	2.46E-07	Unclassified
EBpi03_SQ001_I14_at	None	1.86	1.48E-06	Unclassified
Contig20755_at	None	1.85	1.48E-09	Unclassified
EBro01_SQ005_L10_at	None	1.85	5.73E-06	Unclassified
HVSMEm0019L10r2_s_at	None	1.83	5.95E-09	Unclassified
HVSMEn0012L05r2_at	None	1.83	1.08E-07	Unclassified
HW06G18u_at	None	1.83	1.96E-06	Unclassified
HZ40E11r_at	None	1.83	1.06E-07	Unclassified
HZ65O04r_at	None	1.83	6.39E-08	Unclassified
EBed01_SQ002_L05_s_at	None	1.82	1.54E-08	Unclassified
HV12D18u_at	None	1.82	7.24E-10	Unclassified
HZ37P18r_at	None	1.82	4.63E-08	Unclassified
HD13A24r_at	None	1.81	8.67E-09	Unclassified
Contig16680_at	None	1.8	4.44E-07	Unclassified
HVSMEi0006I22r2_at	None	1.79	9.41E-08	Unclassified
HVSMEf0001H14r2_at	None	1.78	8.21E-07	Unclassified
HO15C14S_s_at	None	1.77	1.69E-06	Unclassified
rbags13d01_s_at	None	1.77	1.48E-07	Unclassified
Contig15374_at	None	1.76	1.72E-05	Unclassified
HVSMEf0005H03r2_s_at	None	1.76	1.29E-08	Unclassified
HVSMEa0005O15r2_s_at	None	1.74	1.61E-08	Unclassified
Contig6811_s_at	None	1.73	8.71E-10	Unclassified
HS18K19u_s_at	None	1.73	1.01E-06	Unclassified
HVSMEb0005E07r2_s_at	None	1.73	1.67E-07	Unclassified
HT08H12u_s_at	None	1.72	3.62E-09	Unclassified
Contig12633_at	None	1.71	2.48E-08	Unclassified
EBro01_SQ002_M14_at	None	1.7	1.20E-08	Unclassified
HV_CEa0004G02r2_at	None	1.69	1.29E-07	Unclassified
Contig19265_at	None	1.68	8.03E-07	Unclassified
EBpi01_SQ001_B04_s_at	None	1.68	3.35E-09	Unclassified
HVSMEa0008M19r2_at	None	1.68	8.03E-07	Unclassified

Contig20754_at	None	1.67	1.38E-08	Unclassified
HVSMEi0009J18r2_at	None	1.66	2.25E-06	Unclassified
Contig7668_at	None	1.65	1.42E-07	Unclassified
Contig8729_at	None	1.65	8.36E-08	Unclassified
Contig14008_at	None	1.64	9.85E-05	Unclassified
HVSMEb0009A03r2_s_at	None	1.64	5.10E-08	Unclassified
HW02O09u_s_at	None	1.64	5.32E-08	Unclassified
Contig11037_at	None	1.62	2.26E-08	Unclassified
rbaal11e19_x_at	None	1.61	2.34E-08	Unclassified
Contig23097_at	None	1.6	1.57E-05	Unclassified
Contig11548_at	None	1.59	3.62E-08	Unclassified
rbags11k20_s_at	None	1.59	2.88E-07	Unclassified
Contig21386_at	None	1.57	2.39E-08	Unclassified
HVSMEk0012K02r2_at	None	1.56	2.23E-05	Unclassified
Contig6701_s_at	None	1.55	0	Unclassified
Contig21083_at	None	1.54	1.94E-07	Unclassified
Contig22191_at	None	1.54	1.19E-09	Unclassified
HU03F22u_at	None	1.54	1.60E-08	Unclassified
Contig1412_at	None	1.53	1.65E-09	Unclassified
Contig21524_at	None	1.53	1.54E-06	Unclassified
Contig16058_at	None	1.52	7.25E-09	Unclassified
Contig17926_at	None	1.52	3.60E-06	Unclassified
Contig16046_at	None	1.51	3.71E-07	Unclassified
EBro01_SQ004_M15_at	None	1.51	1.41E-08	Unclassified
HF08D05r_at	None	1.51	9.85E-07	Unclassified
HVSMEf0011L03r2_s_at	None	1.51	1.28E-07	Unclassified
Contig24068_at	None	1.5	5.42E-07	Unclassified
Contig6310_at	None	1.5	4.86E-07	Unclassified
HT09B07u_s_at	None	1.5	2.74E-06	Unclassified
HW06C04u_s_at	None	1.5	3.20E-07	Unclassified
Contig12084_at	None	1.49	1.04E-06	Unclassified
Contig9765_s_at	None	1.49	4.87E-07	Unclassified
EBem05_SQ002_D05_s_at	None	1.49	1.64E-08	Unclassified

Contig5034_at	None	1.48	2.66E-07	Unclassified
HW03C10u_at	None	1.48	6.98E-07	Unclassified
Contig15956_at	None	1.47	8.29E-09	Unclassified
HT09D12u_at	None	1.47	2.15E-07	Unclassified
Contig22204_at	None	1.46	1.89E-06	Unclassified
EBro03_SQ006_A01_at	None	1.46	2.36E-07	Unclassified
Contig19291_at	None	1.45	7.49E-06	Unclassified
HF04I11r_s_at	None	1.45	3.56E-07	Unclassified
HVSMEl0007O17r2_at	None	1.44	0	Unclassified
HW06J04u_s_at	None	1.44	4.44E-05	Unclassified
Contig4445_at	None	1.43	2.02E-07	Unclassified
HO09C11S_at	None	1.43	4.29E-06	Unclassified
HVSMEh0088M04f_x_at	None	1.43	1.88E-06	Unclassified
Contig10316_s_at	None	1.42	1.05E-08	Unclassified
Contig23974_at	None	1.42	5.84E-08	Unclassified
Contig8309_at	None	1.42	1.20E-07	Unclassified
EBpi07_SQ001_A11_at	None	1.42	3.29E-07	Unclassified
Contig10545_at	None	1.41	2.33E-07	Unclassified
Contig16748_at	None	1.41	1.54E-07	Unclassified
Contig17487_at	None	1.4	5.10E-06	Unclassified
Contig24662_at	None	1.4	2.37E-06	Unclassified
HVSMEc0001D14f_x_at	None	1.4	0.02	Unclassified
Contig1082_at	None	1.39	3.43E-08	Unclassified
HP01L10T_at	None	1.39	1.71E-07	Unclassified
HY08M12u_x_at	None	1.39	2.95E-07	Unclassified
Contig10333_at	None	1.38	2.87E-07	Unclassified
rbags7l20_s_at	None	1.38	4.85E-06	Unclassified
Contig23882_at	None	1.37	1.23E-07	Unclassified
Contig2470_s_at	None	1.37	0	Unclassified
EBma03_SQ003_O14_at	None	1.37	1.28E-07	Unclassified
HF08O15r_at	None	1.37	3.57E-08	Unclassified
HS16L14r_s_at	None	1.37	1.90E-08	Unclassified
Contig17122_at	None	1.36	1.16E-06	Unclassified

Contig23004_at	None	1.36	5.25E-08	Unclassified
rbaal1e15_at	None	1.36	5.43E-08	Unclassified
rbaal20n01_s_at	None	1.36	7.12E-09	Unclassified
Contig17000_s_at	None	1.35	2.62E-07	Unclassified
Contig19376_at	None	1.35	9.63E-06	Unclassified
Contig8558_s_at	None	1.35	3.79E-07	Unclassified
EBro01_SQ005_J04_at	None	1.35	5.65E-05	Unclassified
EBro02_SQ008_C12_s_at	None	1.35	2.59E-07	Unclassified
rbags16n18_at	None	1.35	3.05E-07	Unclassified
Contig19731_at	None	1.34	1.56E-08	Unclassified
Contig26527_at	None	1.34	5.73E-08	Unclassified
HA05k01r_at	None	1.34	8.10E-09	Unclassified
HD04G07u_s_at	None	1.34	3.03E-06	Unclassified
MitoContig11_at	None	1.34	0.01	Unclassified
HW02P01u_x_at	None	1.32	8.92E-08	Unclassified
HW08N11u_s_at	None	1.32	1.57E-07	Unclassified
Contig20536_at	None	1.31	1.26E-06	Unclassified
Contig23603_at	None	1.31	1.17E-06	Unclassified
Contig4307_at	None	1.31	2.21E-06	Unclassified
Contig9575_at	None	1.31	1.71E-06	Unclassified
HA03H15u_at	None	1.31	9.33E-07	Unclassified
EBpi07_SQ001_E20_at	None	1.29	2.17E-07	Unclassified
HF01F13w_s_at	None	1.29	0	Unclassified
S0001000013A11F1_s_at	None	1.29	8.81E-06	Unclassified
Contig5986_s_at	None	1.28	2.63E-08	Unclassified
HV_CEb0006C16r2_at	None	1.28	5.86E-08	Unclassified
Contig19701_at	None	1.27	6.62E-05	Unclassified
Contig4431_s_at	None	1.27	5.82E-07	Unclassified
HK04L12r_s_at	None	1.27	5.97E-08	Unclassified
HVSMEn0016A01r2_at	None	1.27	0	Unclassified
HW01E18u_at	None	1.27	2.35E-07	Unclassified
rbaal3d15_x_at	None	1.27	5.67E-07	Unclassified
rbaal5d06_s_at	None	1.27	7.82E-07	Unclassified

Contig15839_s_at	None	1.26	6.94E-07	Unclassified
Contig19403_at	None	1.26	2.45E-08	Unclassified
Contig26471_at	None	1.26	2.63E-06	Unclassified
EBro03_SQ008_J07_s_at	None	1.26	2.16E-07	Unclassified
HVSMEa0019B22f2_at	None	1.26	1.15E-07	Unclassified
HW07B05u_at	None	1.26	5.24E-07	Unclassified
Contig6065_s_at	None	1.25	6.24E-05	Unclassified
Contig9116_at	None	1.25	4.65E-05	Unclassified
Contig24160_at	None	1.24	1.63E-06	Unclassified
Contig25181_at	None	1.24	4.62E-07	Unclassified
Contig26263_at	None	1.24	6.70E-06	Unclassified
Contig9030_at	None	1.24	4.90E-08	Unclassified
HM05D10r_s_at	None	1.24	6.21E-08	Unclassified
HT05E09u_s_at	None	1.24	7.89E-07	Unclassified
HVSMEa0005F21r2_at	None	1.24	1.21E-06	Unclassified
Contig12321_at	None	1.23	0	Unclassified
Contig16826_at	None	1.23	8.11E-06	Unclassified
HV_CEb0004G20r2_x_at	None	1.23	1.37E-07	Unclassified
Contig4430_at	None	1.22	6.49E-07	Unclassified
Contig11373_at	None	1.21	7.34E-06	Unclassified
HI14F16r_s_at	None	1.21	5.25E-07	Unclassified
HVSMEa0006G22r2_at	None	1.21	8.30E-07	Unclassified
Contig24823_at	None	1.2	1.83E-06	Unclassified
EBma04_SQ002_L13_s_at	None	1.2	2.91E-07	Unclassified
HV03N17u_s_at	None	1.19	3.43E-07	Unclassified
Contig21196_at	None	1.18	4.21E-06	Unclassified
Contig23750_at	None	1.18	3.39E-07	Unclassified
HVSMEi0013L12r2_s_at	None	1.18	0	Unclassified
HVSMEc0009K16f_s_at	None	1.17	0	Unclassified
Contig2907_s_at	None	1.16	5.21E-06	Unclassified
HU05B08u_s_at	None	1.16	1.12E-05	Unclassified
HV05P16u_at	None	1.16	1.34E-05	Unclassified
Contig15498_at	None	1.15	3.93E-07	Unclassified

EBro03_SQ007_M08_at	None	1.15	7.15E-07	Unclassified
HS08O16u_s_at	None	1.15	0.03	Unclassified
HT07O19u_s_at	None	1.15	9.48E-08	Unclassified
HVSMEf0003M09r2_at	None	1.15	3.54E-06	Unclassified
HVSMEk0006G11r2_s_at	None	1.15	3.79E-07	Unclassified
HU11E18u_at	None	1.14	5.06E-07	Unclassified
HVSMEf0013D09r2_at	None	1.14	3.62E-06	Unclassified
HX14A13r_s_at	None	1.13	3.12E-06	Unclassified
Contig11968_at	None	1.12	1.63E-07	Unclassified
HS08B18u_x_at	None	1.12	6.71E-06	Unclassified
HU11F22u_s_at	None	1.12	7.81E-06	Unclassified
Contig12750_at	None	1.11	0	Unclassified
EBro07_SQ001_A12_at	None	1.11	6.35E-05	Unclassified
HVSMEf0021H03r2_s_at	None	1.11	9.78E-07	Unclassified
HW07E14u_s_at	None	1.11	2.07E-06	Unclassified
EBem06_SQ003_J07_at	None	1.1	2.74E-06	Unclassified
HF16B18r_at	None	1.1	3.59E-07	Unclassified
HVSMEf0009M18r2_at	None	1.1	0	Unclassified
EBro02_SQ007_J14_at	None	1.09	0	Unclassified
EBro03_SQ007_C24_at	None	1.09	6.74E-06	Unclassified
Contig16356_at	None	1.08	1.36E-05	Unclassified
Contig21068_at	None	1.08	2.03E-06	Unclassified
EBma08_SQ003_L03_at	None	1.08	4.07E-07	Unclassified
HO07I11S_at	None	1.08	3.02E-06	Unclassified
Contig21576_at	None	1.07	0	Unclassified
HW04N01u_at	None	1.07	3.40E-07	Unclassified
Contig11710_at	None	1.06	1.61E-05	Unclassified
Contig12406_at	None	1.06	1.10E-05	Unclassified
Contig8626_at	None	1.06	5.96E-07	Unclassified
Contig11067_s_at	None	1.05	2.28E-06	Unclassified
HU05D16u_s_at	None	1.05	3.76E-05	Unclassified
Contig4046_s_at	None	1.04	2.91E-06	Unclassified
HS07N11u_at	None	1.04	1.27E-05	Unclassified

HVSMEi0013P16r2_s_at	None	1.04	2.22E-06	Unclassified
rbaal21e22_x_at	None	1.04	6.78E-07	Unclassified
S0000700018E12F1_s_at	None	1.04	1.03E-05	Unclassified
S0001100124F04F1_at	None	1.03	3.59E-06	Unclassified
Contig13977_at	None	1.02	9.11E-05	Unclassified
Contig19539_at	None	1.02	6.88E-06	Unclassified
HA13O21r_s_at	None	1.02	1.62E-05	Unclassified
Contig18530_s_at	None	1.01	2.20E-06	Unclassified
Contig21391_at	None	1.01	1.97E-05	Unclassified
Contig25133_at	None	1.01	0	Unclassified
EBem04_SQ004_O17_s_at	None	1.01	8.31E-05	Unclassified
HVSMEi0004C18r2_at	None	1	0	Unclassified
Contig22839_at	Embryo-abundant protein EMB	5.08	1.54E-11	Unknown
Contig11416_at	Expressed protein	4.87	8.00E-12	Unknown
Contig12195_at	Expressed protein	4.87	4.71E-11	Unknown
HVSMEk0012J02r2_at	Unknown protein	4.79	2.16E-12	Unknown
Contig15351_s_at	Hypothetical protein	4.75	2.79E-11	Unknown
baak20j05_s_at	Unknown protein	4.63	1.10E-11	Unknown
Contig14054_at	Hypothetical protein	4.62	4.70E-11	Unknown
Contig12445_at	Hypothetical protein	4.52	2.16E-12	Unknown
HO14C15S_at	Expressed protein	4.52	2.57E-12	Unknown
Contig7443_at	Unknown protein	4.5	2.37E-12	Unknown
Contig25476_at	Hypothetical protein	4.43	2.88E-12	Unknown
HVSMEb0011I17r2_s_at	Expressed protein	4.38	4.85E-08	Unknown
Contig17283_s_at	Putative protein	4.29	1.75E-10	Unknown
Contig15773_at	Expressed protein	4.26	4.40E-12	Unknown
HV_CEb0020C01r2_at	Hypothetical protein	4.15	2.97E-10	Unknown
Contig18037_at	Unknown protein	3.96	1.33E-11	Unknown
Contig11805_at	Putative protein	3.92	5.10E-09	Unknown
HVSMEf0019G08r2_s_at	Putative protein	3.9	8.74E-09	Unknown
Contig11998_at	Expressed protein	3.87	3.26E-10	Unknown
Contig7437_at	Expressed protein	3.81	1.09E-11	Unknown
Contig13419_at	Hypothetical protein	3.78	2.16E-12	Unknown

Contig13994_s_at	Unknown protein	3.72	3.10E-10	Unknown
Contig6541_at	Putative nuclear protein	3.64	1.02E-11	Unknown
Contig11800_at	Expressed protein	3.62	1.23E-10	Unknown
Contig20750_at	Hypothetical protein	3.56	9.68E-10	Unknown
Contig4491_s_at	Unknown protein	3.56	5.81E-10	Unknown
Contig20239_at	Hypothetical protein	3.43	6.52E-12	Unknown
Contig5469_at	Hypothetical protein	3.41	2.85E-09	Unknown
Contig7319_at	Putative protein	3.4	4.13E-11	Unknown
Contig20431_at	Hypothetical protein	3.35	1.12E-10	Unknown
Contig358_at	Secretory protein	3.33	1.25E-10	Unknown
Contig15187_at	Unknown protein	3.31	9.60E-12	Unknown
Contig5468_at	Putative uncharacterized protein	3.29	1.33E-09	Unknown
HM04D16u_s_at	Hypothetical protein	3.27	1.34E-11	Unknown
Contig11198_at	Unknown protein	3.25	1.27E-10	Unknown
Contig9369_s_at	Hypothetical protein	3.23	3.47E-11	Unknown
Contig10895_at	Expressed protein	3.22	6.31E-10	Unknown
Contig22479_at	Hypothetical protein	3.17	7.06E-10	Unknown
Contig6082_at	Putative cellular retinaldehyde-binding protein	3.16	1.51E-10	Unknown
Contig4389_at	Expressed protein	3.14	3.17E-09	Unknown
Contig18843_at	Hypothetical protein	3.13	1.26E-10	Unknown
Contig8220_at	Late embryogenesis abundant protein	3.13	9.97E-11	Unknown
HV_CEa0015C01r2_at	BLE2 protein	3.12	1.58E-09	Unknown
Contig5351_at	Hypothetical protein	3.09	1.10E-11	Unknown
Contig11753_at	Putative protein	3.08	1.14E-11	Unknown
Contig16853_at	Expressed protein	3.07	8.03E-10	Unknown
HV_CEa0011J22r2_at	Unknown protein	3.03	5.84E-11	Unknown
Contig13700_at	Unknown protein	3.01	7.49E-09	Unknown
HVSMEa0006N15r2_s_at	Hypothetical protein	3	1.07E-10	Unknown
Contig10152_at	Putative protein	2.99	1.26E-08	Unknown
Contig25015_at	Expressed protein	2.99	1.04E-10	Unknown
Contig14032_at	Expressed protein	2.92	4.44E-11	Unknown
Contig11655_at	Uncharacterized protein	2.89	4.99E-10	Unknown
Contig20575_at	Hypothetical protein	2.88	2.80E-11	Unknown

Contig13562_at	Hypothetical protein	2.84	3.23E-11	Unknown
Contig19553_at	Hypothetical protein	2.83	3.75E-09	Unknown
Contig19809_at	Expressed protein	2.83	1.31E-09	Unknown
Contig6083_at	Putative cellular retinaldehyde-binding protein	2.8	2.35E-09	Unknown
Contig13932_at	Hypothetical protein	2.79	2.50E-10	Unknown
HX04B03u_at	Putative protein	2.77	5.97E-08	Unknown
Contig17964_at	Putative protein	2.76	8.40E-09	Unknown
Contig9368_at	Hypothetical protein	2.76	8.51E-11	Unknown
Contig12800_at	Hypothetical protein	2.75	3.08E-09	Unknown
Contig2481_s_at	Hypothetical protein	2.73	5.23E-10	Unknown
Contig26080_at	Putative protein	2.73	2.18E-07	Unknown
Contig590_at	Hypothetical protein	2.71	9.79E-10	Unknown
Contig8601_s_at	Hypothetical protein	2.71	1.03E-08	Unknown
Contig14332_at	Hypothetical protein	2.7	1.07E-09	Unknown
Contig15613_at	Expressed protein	2.7	2.48E-08	Unknown
Contig1246_at	Putative r40c2 protein	2.69	1.84E-10	Unknown
Contig14777_at	Hypothetical protein	2.69	4.34E-09	Unknown
Contig15650_at	Unknown protein	2.69	1.04E-09	Unknown
Contig15548_at	Unknown protein	2.68	1.12E-08	Unknown
Contig3253_s_at	Hypothetical protein	2.68	1.28E-09	Unknown
Contig5106_at	Hypothetical protein	2.68	1.09E-09	Unknown
HI01L19w_at	Hypothetical protein	2.68	1.21E-07	Unknown
Contig12481_at	Expressed protein	2.67	3.89E-10	Unknown
Contig13420_at	Unknown protein	2.65	3.11E-09	Unknown
Contig25605_at	Putative uncharacterized protein	2.65	2.12E-07	Unknown
Contig10286_at	Expressed protein	2.64	1.64E-11	Unknown
Contig10379_at	Hypothetical protein	2.63	2.40E-07	Unknown
Contig16445_at	Unknown protein	2.63	7.94E-09	Unknown
Contig13615_at	VQ motif family protein	2.61	5.94E-10	Unknown
Contig6363_at	Putative protein	2.6	3.01E-09	Unknown
Contig8085_at	Cupin family protein	2.59	1.01E-08	Unknown
HO04L23S_at	Hypothetical protein	2.59	1.06E-08	Unknown
Contig10439_at	Putative protein	2.58	8.82E-10	Unknown

Contig17841_at	Unknown protein	2.58	3.27E-11	Unknown
Contig1988_at	Expressed protein	2.56	4.53E-09	Unknown
Contig14554_s_at	Expressed protein	2.54	2.78E-10	Unknown
Contig6337_at	Unknown protein	2.52	9.30E-09	Unknown
Contig13866_at	Putative protein	2.49	5.17E-09	Unknown
Contig15443_at	Expressed protein	2.48	3.65E-10	Unknown
Contig22948_at	Hypothetical protein	2.46	1.35E-09	Unknown
Contig8997_at	Expressed protein	2.46	1.19E-08	Unknown
HP01E21w_s_at	Expressed protein	2.45	3.75E-07	Unknown
Contig12952_at	Aromatic-rich family protein-like	2.44	1.11E-08	Unknown
Contig13033_at	Hypothetical protein	2.41	5.94E-10	Unknown
Contig11276_at	Putative protein	2.4	6.28E-08	Unknown
Contig7879_at	Late embryogenesis abundant protein	2.4	4.60E-09	Unknown
Contig4306_s_at	Hypothetical protein	2.38	5.83E-09	Unknown
HVSMEf0019O11r2_at	Putative protein	2.37	2.32E-09	Unknown
Contig11615_s_at	Putative YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	2.33	2.45E-06	Unknown
Contig12061_at	Putative protein	2.33	7.68E-09	Unknown
Contig20206_at	Unknown protein	2.33	2.70E-09	Unknown
Contig4976_at	Hypothetical protein	2.32	3.48E-06	Unknown
Contig11615_at	Putative uncharacterized protein	2.31	2.94E-09	Unknown
Contig13677_at	Expressed protein	2.28	5.74E-09	Unknown
Contig7551_at	Hypothetical protein	2.28	1.04E-10	Unknown
HVSMEg0018C11r2_at	Putative protein	2.24	6.19E-10	Unknown
Contig12800_s_at	Putative protein	2.23	5.26E-10	Unknown
Contig13863_at	Hypothetical protein	2.23	1.56E-08	Unknown
Contig18844_at	Putative uncharacterized protein	2.23	1.18E-08	Unknown
Contig17563_at	Unknown protein	2.22	2.52E-09	Unknown
Contig3341_at	Putative MtN19	2.21	3.01E-08	Unknown
Contig11816_at	Hypothetical protein	2.19	2.01E-09	Unknown
HT09L21r_at	Hypothetical protein	2.19	4.96E-09	Unknown
Contig20159_at	Hypothetical protein	2.18	6.71E-10	Unknown
Contig4994_at	Hypothetical protein	2.18	1.75E-08	Unknown
Contig19086_at	Putative protein	2.16	5.04E-07	Unknown

Contig10970_at	Hypothetical protein	2.13	6.32E-07	Unknown
Contig13632_at	Putative uncharacterized protein	2.12	4.89E-08	Unknown
Contig12081_at	Hypothetical protein	2.11	1.57E-09	Unknown
Contig13421_at	Expressed protein	2.11	4.54E-09	Unknown
Contig6797_at	Unknown protein	2.09	8.52E-08	Unknown
Contig11572_at	Hypothetical protein	2.08	1.22E-07	Unknown
Contig26489_at	Putative protein	2.08	2.26E-08	Unknown
Contig13143_s_at	Unknown protein	2.07	1.08E-07	Unknown
Contig16306_at	Hypothetical protein	2.07	1.68E-08	Unknown
Contig6995_at	Hypothetical protein	2.07	1.55E-09	Unknown
HVSMEm0001B08r2_at	Hypothetical protein	2.06	7.73E-08	Unknown
Contig11133_at	Hypothetical protein	2.01	5.84E-09	Unknown
Contig4994_s_at	Hypothetical protein	2.01	1.44E-08	Unknown
Contig12512_at	Putative protein	1.99	2.31E-07	Unknown
Contig590_s_at	Hypothetical protein	1.98	2.83E-06	Unknown
Contig7633_at	Putative protein	1.98	2.46E-09	Unknown
Contig17793_s_at	Unknown protein	1.97	5.65E-09	Unknown
Contig18763_at	Unknown protein	1.96	5.10E-08	Unknown
Contig3413_s_at	Hypothetical protein	1.96	6.35E-09	Unknown
Contig8822_at	Expressed protein	1.96	1.30E-08	Unknown
Contig15208_at	Unknown protein	1.94	1.38E-08	Unknown
Contig10407_at	Hypothetical protein	1.93	7.44E-05	Unknown
Contig7598_at	Unknown protein	1.93	8.00E-06	Unknown
Contig14020_at	Unknown protein	1.92	3.72E-08	Unknown
Contig15811_at	Unknown protein	1.92	1.85E-06	Unknown
Contig10608_at	Putative protein	1.91	4.23E-07	Unknown
Contig11684_at	Hypothetical protein	1.91	5.76E-09	Unknown
Contig17653_at	Hypothetical protein	1.9	2.57E-07	Unknown
Contig14113_at	Hypothetical protein	1.89	7.94E-09	Unknown
Contig15764_at	Hypothetical protein	1.89	7.31E-05	Unknown
Contig7137_at	Hypothetical protein	1.89	1.00E-07	Unknown
Contig12520_at	Hypothetical protein	1.86	7.71E-10	Unknown
Contig8593_s_at	Hypothetical protein	1.85	9.89E-09	Unknown

Contig9865_at	Hypothetical protein	1.85	9.51E-08	Unknown
Contig7833_at	Hypothetical protein	1.84	4.51E-08	Unknown
Contig8416_s_at	Unknown protein	1.84	2.18E-06	Unknown
Contig9607_at	Putative protein	1.83	1.22E-07	Unknown
HVSMEb0001J13r2_at	Hypothetical protein	1.82	6.62E-09	Unknown
Contig18427_s_at	Expressed protein	1.81	1.32E-08	Unknown
Contig8557_at	33 kDa secretory protein-like	1.8	1.36E-07	Unknown
Contig6076_at	Putative uncharacterized protein	1.79	2.72E-09	Unknown
HVSMEa0003J18r2_s_at	Hypothetical protein	1.78	2.40E-07	Unknown
Contig10257_at	Hypothetical protein	1.77	7.22E-07	Unknown
Contig11778_at	Putative protein	1.77	1.72E-07	Unknown
Contig24110_at	Unknown protein	1.77	1.97E-07	Unknown
Contig8996_s_at	Expressed protein	1.76	8.55E-08	Unknown
Contig13151_at	Putative protein	1.75	7.27E-08	Unknown
Contig2849_at	Hypothetical protein	1.75	1.25E-08	Unknown
Contig13143_at	Unknown protein	1.74	8.44E-07	Unknown
Contig14712_at	Putative protein	1.74	2.23E-05	Unknown
Contig3841_x_at	Putative uncharacterized protein	1.74	3.54E-06	Unknown
Contig8484_at	Hypothetical protein	1.74	4.38E-08	Unknown
Contig12017_at	Hypothetical protein	1.73	1.16E-08	Unknown
Contig13241_at	Expressed protein	1.73	5.08E-07	Unknown
Contig14427_at	Putative uncharacterized protein	1.73	1.75E-07	Unknown
Contig18801_at	Hypothetical protein	1.73	2.86E-05	Unknown
Contig3379_at	Hypothetical protein	1.72	3.98E-09	Unknown
Contig4897_at	Unnamed protein product	1.72	6.32E-07	Unknown
Contig10859_at	Hypothetical protein	1.71	7.45E-08	Unknown
Contig3978_at	Hypothetical protein	1.71	1.55E-07	Unknown
Contig7369_at	Hypothetical protein	1.71	2.49E-07	Unknown
EBes01_SQ004_M24_at	Expressed protein	1.71	2.65E-08	Unknown
Contig24409_at	Expressed protein	1.7	1.64E-07	Unknown
Contig12552_s_at	Putative protein	1.69	2.40E-06	Unknown
Contig15192_s_at	Putative protein	1.69	8.68E-09	Unknown
EBpi01_SQ004_I24_s_at	Hypothetical protein	1.69	4.26E-07	Unknown

ChlorContig9_at	Hypothetical protein	1.68	3.17E-06	Unknown
Contig25556_at	Hypothetical protein	1.68	5.15E-06	Unknown
Contig6567_at	Unknown protein	1.68	1.11E-08	Unknown
HW06F15u_at	Putative uncharacterized protein	1.68	1.86E-08	Unknown
Contig11915_at	CBS domain containing protein	1.66	4.66E-09	Unknown
Contig7447_at	Hypothetical protein	1.66	9.27E-07	Unknown
Contig7487_at	Uncharacterized protein	1.66	3.21E-09	Unknown
HW02N11u_at	Putative protein	1.66	2.54E-06	Unknown
Contig13706_at	Putative protein	1.65	1.08E-07	Unknown
Contig16025_at	Putative protein	1.65	1.22E-06	Unknown
Contig18588_at	Hypothetical protein	1.65	7.59E-09	Unknown
HT07K23u_at	Hypothetical protein	1.65	3.53E-06	Unknown
HVSMEn0006O04f2_at	Hypothetical protein	1.64	1.08E-08	Unknown
Contig9184_at	Unknown protein	1.63	4.30E-07	Unknown
Contig13083_at	Putative protein	1.62	2.71E-08	Unknown
Contig13256_at	Hypothetical protein	1.62	9.29E-07	Unknown
Contig19799_at	Hypothetical protein	1.62	1.99E-07	Unknown
Contig7044_at	Putative uncharacterized protein	1.61	5.83E-08	Unknown
Contig6721_s_at	Expressed protein	1.59	6.13E-08	Unknown
Contig15491_at	Hypothetical protein	1.58	3.08E-09	Unknown
Contig19228_at	Hypothetical protein	1.58	2.98E-06	Unknown
Contig3994_at	Expressed protein	1.58	6.39E-08	Unknown
HT09J11u_at	Hypothetical protein	1.58	2.57E-07	Unknown
Contig10025_s_at	Putative protein	1.56	3.10E-08	Unknown
Contig11653_at	Ative uncharacterized protein	1.56	2.28E-05	Unknown
Contig16005_at	Expressed protein	1.56	4.00E-06	Unknown
Contig3841_at	Unknown protein	1.56	2.98E-06	Unknown
Contig14450_at	Hypothetical protein	1.55	1.95E-08	Unknown
Contig18347_at	Hypothetical protein	1.54	2.25E-06	Unknown
Contig9871_at	Putative uncharacterized protein	1.54	1.89E-06	Unknown
Contig13948_at	Expressed protein	1.52	6.01E-07	Unknown
Contig7836_at	Unknown protein	1.52	3.23E-09	Unknown
Contig24322_at	Embryogenesis transmembrane protein-like	1.51	2.03E-07	Unknown

Contig4804_at	Hypothetical protein	1.51	9.74E-08	Unknown
Contig5845_at	Hypothetical protein	1.51	1.04E-07	Unknown
Contig6495_at	Expressed protein	1.51	2.50E-07	Unknown
Contig11862_at	WD-40 repeat family protein / beige-related	1.5	2.88E-06	Unknown
Contig12289_at	Putative uncharacterized protein	1.5	3.17E-06	Unknown
Contig15608_at	Putative protein	1.5	5.27E-09	Unknown
Contig12043_at	Unknown protein	1.49	2.41E-06	Unknown
Contig12066_at	Hypothetical protein	1.49	1.14E-08	Unknown
Contig7546_s_at	Putative protein	1.49	2.70E-08	Unknown
Contig10137_at	Unknown protein	1.48	4.82E-08	Unknown
Contig12919_s_at	Hypothetical protein	1.48	0	Unknown
Contig13208_at	Putative protein	1.48	7.45E-08	Unknown
Contig8677_at	Putative protein	1.47	9.78E-07	Unknown
HU05L02u_s_at	Expressed protein	1.47	1.00E-08	Unknown
Contig20371_at	Hypothetical protein	1.46	2.88E-08	Unknown
Contig15193_at	Putative protein	1.45	4.88E-08	Unknown
Contig1642_at	Reversibly glycosylated polypeptide	1.45	2.32E-07	Unknown
Contig18108_at	Putative protein	1.45	9.42E-06	Unknown
Contig7160_at	Hypothetical protein	1.45	5.23E-07	Unknown
Contig9675_at	Putative uncharacterized protein	1.45	2.61E-06	Unknown
HT09B09u_s_at	Unknown protein	1.45	1.35E-07	Unknown
Contig15704_at	Hypothetical protein	1.43	3.53E-06	Unknown
Contig21865_at	Hypothetical protein	1.43	4.06E-08	Unknown
Contig2942_at	Putative arginine-rich protein	1.43	3.21E-07	Unknown
Contig5661_at	Putative protein	1.43	2.12E-05	Unknown
HA06i14r_s_at	Reversibly glycosylated polypeptide	1.43	7.58E-08	Unknown
HVSMEa0002F14r2_at	Ataxin 3-like protein	1.43	3.75E-07	Unknown
Contig14713_at	Unnamed protein product	1.41	4.28E-08	Unknown
Contig4575_s_at	Unknown protein	1.41	4.01E-06	Unknown
Contig16341_s_at	Putative human tumor susceptibility gene-like protein	1.4	4.16E-07	Unknown
Contig4760_s_at	Putative late embryogenesis abundant protein	1.4	2.27E-06	Unknown
Contig10257_s_at	Hypothetical protein	1.39	7.01E-07	Unknown
Contig10470_at	Expressed protein	1.39	6.35E-07	Unknown

Contig7112_at	Putative protein	1.39	2.13E-07	Unknown
Contig13026_at	Hypothetical protein	1.38	6.55E-07	Unknown
Contig8862_at	Putative protein	1.38	7.48E-06	Unknown
Contig9286_at	Hypothetical protein	1.38	2.19E-08	Unknown
rbah55a21_s_at	Putative protein	1.38	9.62E-06	Unknown
Contig3852_at	Unknown protein	1.37	8.92E-07	Unknown
Contig9240_s_at	Putative uncharacterized protein	1.37	5.76E-08	Unknown
Contig26355_at	Expressed protein	1.36	6.81E-06	Unknown
HT11C12u_s_at	Hypothetical protein	1.36	6.76E-05	Unknown
Contig21441_at	Expressed protein	1.35	1.24E-05	Unknown
Contig7365_at	Unknown protein	1.35	4.69E-08	Unknown
Contig11062_at	Putative protein	1.34	3.57E-07	Unknown
Contig13913_at	SPX (SYG1/Pho81/XPR1) domain-containing protein-like	1.33	0	Unknown
Contig17099_at	Expressed protein	1.32	4.62E-06	Unknown
Contig5392_at	Putative VHS1 protein	1.32	1.95E-06	Unknown
Contig7332_at	Unknown protein	1.32	4.45E-08	Unknown
HV_CEb0011D15r2_s_at	Putative protein	1.32	8.14E-07	Unknown
Contig10285_at	Putative protein	1.31	3.48E-08	Unknown
Contig19347_at	Unknown protein	1.31	4.17E-07	Unknown
Contig20014_at	Putative uncharacterized protein	1.31	6.83E-07	Unknown
Contig6537_at	Hypothetical protein	1.31	1.63E-07	Unknown
Contig8592_at	Hypothetical protein	1.31	9.59E-07	Unknown
Contig5320_at	Unknown protein	1.3	8.57E-08	Unknown
Contig6651_at	Expressed protein	1.3	1.97E-07	Unknown
Contig6723_at	Expressed protein	1.29	4.49E-08	Unknown
Contig8762_at	Expressed protein	1.29	4.30E-08	Unknown
HP01G01w_s_at	Unknown protein	1.29	1.23E-06	Unknown
Contig11450_at	Hypothetical protein	1.28	2.80E-08	Unknown
Contig24087_at	Hypothetical protein	1.28	8.98E-06	Unknown
EBro04_SQ004_O07a_at	Putative uncharacterized protein	1.28	4.25E-08	Unknown
HVSMEc0005O17f_x_at	Hypothetical protein	1.27	0.04	Unknown
Contig10615_at	Hypothetical protein	1.26	0	Unknown
Contig14805_at	Putative uncharacterized protein	1.26	2.18E-06	Unknown

Contig24429_at	Unknown protein	1.26	6.46E-09	Unknown
Contig3743_at	Hypothetical protein	1.26	7.49E-06	Unknown
Contig14948_at	Expressed protein	1.25	1.23E-05	Unknown
Contig17301_at	VQ motif-containing protein-like	1.25	8.65E-08	Unknown
Contig23747_at	Expressed protein	1.25	3.73E-06	Unknown
Contig11187_at	Mitochondrial glycoprotein-like	1.24	5.59E-06	Unknown
Contig13177_at	Hypothetical protein	1.24	1.18E-06	Unknown
Contig17354_at	Putative protein	1.24	5.48E-08	Unknown
Contig18869_at	Putative protein	1.24	2.43E-06	Unknown
Contig6067_at	Unknown protein	1.23	6.85E-05	Unknown
Contig17683_at	Polyprotein-like	1.22	2.66E-06	Unknown
Contig18496_at	Expressed protein	1.22	1.77E-06	Unknown
Contig19892_at	Putative protein	1.22	5.00E-08	Unknown
Contig20759_at	Putative protein	1.22	6.23E-06	Unknown
Contig5416_s_at	Putative protein	1.22	1.24E-05	Unknown
Contig6066_s_at	Unknown protein	1.22	1.62E-05	Unknown
Contig14571_at	Unknown protein	1.21	1.45E-06	Unknown
Contig5720_at	Putative protein	1.21	2.17E-05	Unknown
Contig7178_s_at	Hypothetical protein	1.21	1.28E-08	Unknown
HW03O22u_s_at	Putative secretory protein	1.21	0	Unknown
Contig14618_at	Hypothetical protein	1.2	6.71E-07	Unknown
Contig16211_at	Putative protein	1.2	6.03E-07	Unknown
Contig7671_at	Expressed protein	1.2	8.36E-06	Unknown
Contig8030_at	Expressed protein	1.2	5.89E-07	Unknown
Contig10747_at	Hypothetical protein	1.19	1.85E-06	Unknown
Contig21197_at	Unknown protein	1.18	3.65E-07	Unknown
Contig5862_at	UDP-glucuronyltransferase	1.18	2.12E-05	Unknown
Contig14048_at	Expressed protein	1.17	8.72E-06	Unknown
Contig15351_at	Hypothetical protein	1.17	1.74E-07	Unknown
Contig16143_at	Hypothetical protein	1.17	2.63E-05	Unknown
Contig17100_at	Expressed protein	1.17	2.37E-08	Unknown
Contig8596_at	Expressed protein	1.17	4.31E-06	Unknown
Contig9079_at	Unknown protein	1.17	1.68E-06	Unknown

Contig10190_at	Hypothetical protein	1.16	1.58E-06	Unknown
Contig10684_at	Unknown protein	1.16	6.61E-07	Unknown
Contig15209_at	Hypothetical protein	1.16	2.05E-06	Unknown
Contig17196_at	Unknown protein	1.16	5.00E-06	Unknown
Contig20556_at	Expressed protein	1.16	2.26E-06	Unknown
Contig7391_at	Putative protein	1.16	1.81E-08	Unknown
Contig11659_at	Putative protein	1.15	0	Unknown
Contig21645_at	Putative protein	1.15	2.35E-05	Unknown
Contig5383_s_at	Hypothetical protein	1.15	9.50E-06	Unknown
Contig10785_at	Expressed protein	1.14	9.13E-06	Unknown
Contig25578_at	Putative uncharacterized protein	1.13	1.77E-05	Unknown
Contig2756_at	Putative uncharacterized protein	1.13	3.62E-07	Unknown
EBro02_SQ003_A18_at	Putative protein	1.13	1.50E-05	Unknown
Contig13914_at	SPX129-like protein	1.12	3.94E-05	Unknown
Contig2291_at	Putative uncharacterized protein	1.12	1.68E-06	Unknown
Contig5415_at	Putative protein	1.12	1.31E-05	Unknown
Contig7935_s_at	Expressed protein	1.12	2.27E-07	Unknown
Contig10492_at	Unknown protein	1.11	6.51E-06	Unknown
Contig10693_at	Hypothetical protein	1.11	2.70E-06	Unknown
Contig14238_at	Hypothetical protein	1.11	5.59E-06	Unknown
Contig15355_at	Hypothetical protein	1.11	9.20E-07	Unknown
HVSMEb0007D15r2_at	VQ motif family protein	1.11	6.02E-05	Unknown
HVSMEc0011H17f_x_at	Hypothetical protein	1.11	0.02	Unknown
Contig1168_at	Putative protein	1.1	0	Unknown
Contig11966_at	Putative protein	1.1	2.86E-06	Unknown
Contig270_at	Unknown protein	1.1	1.01E-06	Unknown
Contig4415_at	Unknown protein	1.1	6.68E-07	Unknown
Contig6754_at	Unknown protein	1.1	2.65E-06	Unknown
Contig10082_at	Putative protein	1.09	2.71E-07	Unknown
Contig21159_at	Expressed protein	1.09	1.04E-07	Unknown
Contig21224_at	Unknown protein	1.09	1.35E-05	Unknown
Contig13987_at	Unknown protein	1.08	8.86E-06	Unknown
Contig14814_at	Hypothetical protein	1.08	4.01E-05	Unknown

Contig16659_at	Hypothetical protein	1.08	3.49E-06	Unknown
Contig20034_at	Unknown protein	1.08	3.26E-06	Unknown
Contig9241_at	Hypothetical protein	1.08	3.69E-06	Unknown
HVSMEg0010P18r2_s_at	Putative uncharacterized protein	1.08	5.30E-06	Unknown
Contig10573_s_at	Putative protein	1.07	2.19E-05	Unknown
Contig14510_at	Putative oxidase-like	1.07	0.04	Unknown
Contig16757_at	Putative protein	1.07	1.25E-06	Unknown
Contig19070_at	Putative protein	1.07	2.85E-05	Unknown
Contig4603_at	Hypothetical protein	1.07	1.09E-06	Unknown
Contig5595_at	Hypothetical protein	1.07	3.52E-06	Unknown
Contig10357_at	Expressed protein	1.06	1.50E-07	Unknown
Contig5816_at	Unknown protein	1.06	3.03E-06	Unknown
HVSMEi0007J05r2_s_at	Unknown protein	1.06	1.36E-05	Unknown
Contig13864_at	Hypothetical protein	1.05	2.81E-05	Unknown
Contig9612_s_at	Unknown protein	1.05	1.56E-06	Unknown
HO06I09S_at	Hypothetical protein	1.05	8.79E-06	Unknown
HVSMEn0007G22f2_at	Unknown protein	1.05	1.05E-06	Unknown
Contig10127_at	Hypothetical protein	1.04	1.20E-05	Unknown
Contig10451_at	Expressed protein	1.04	1.48E-06	Unknown
Contig17649_at	Expressed protein	1.04	1.89E-05	Unknown
Contig6034_at	Hypothetical protein	1.04	4.07E-06	Unknown
Contig8214_at	Expressed protein	1.04	6.16E-05	Unknown
Contig13564_at	Putative protein	1.03	9.43E-05	Unknown
Contig9259_at	Expressed protein	1.03	7.61E-07	Unknown
Contig10616_at	Hypothetical protein	1.02	6.61E-06	Unknown
Contig7695_s_at	Unknown protein	1.02	4.99E-07	Unknown
HVSMEn0011N06r2_at	Hypothetical protein	1.02	1.35E-06	Unknown
Contig16699_at	Unknown protein	1.01	3.65E-06	Unknown
Contig19171_at	Expressed protein	1.01	4.46E-05	Unknown
Contig23454_at	Hypothetical protein	1.01	3.59E-06	Unknown
Contig25401_at	Hypothetical protein	1.01	0	Unknown
Contig6871_s_at	Unknown protein	1.01	5.92E-06	Unknown

Appendix 1: Table 3. Full list of genes significantly differentially expressed in the adjacent leaf region. Up/ down[a] indicates adjacent specific expression, [b] indicates opposite regulation in local and adjacent leaf region, [c] indicates common regulation in local and adjacent leaf region.

Contig ID	Annotation	Fold Change (Log2)	Regulation	FDR Adjusted P Value	Functional classification
Contig7773_at	Ankyrin-like protein	2.40	up[c]	6.51E-09	Biogenesis of cellular components
HW03A23u_at	Cellulose synthase-like A3	1.03	up[c]	0	Biogenesis of cellular components
HS05F12u_s_at	Expansin	-1.23	down[c]	0	Biogenesis of cellular components
Contig3674_at	Expansin	-1.30	down[c]	7.76E-05	Biogenesis of cellular components
Contig41_at	Histone H3 variant H3.3	1.99	up[a]	0	Cell cycle and DNA processing
Contig41_x_at	Histone H3 variant H3.3	1.53	up[a]	0	Cell cycle and DNA processing
Contig1157_at	Histone H2B	-1.06	down[c]	0	Cell cycle and DNA processing
Contig1570_s_at	Thionin	6.10	up[a]	2.83E-06	Cell rescue, defence and virulence
Contig1580_x_at	Thionin precursor	5.33	up[a]	9.00E-08	Cell rescue, defence and virulence
Contig8896_s_at	Cysteine proteinase	4.44	up[a]	0	Cell rescue, defence and virulence
Contig1567_x_at	Thionin precursor	3.63	up[a]	1.52E-07	Cell rescue, defence and virulence
Contig2243_s_at	Wheat aluminum induced protein wali 5	3.55	up[c]	5.89E-07	Cell rescue, defence and virulence
Contig3017_at	Oxalate oxidase	3.49	up[c]	2.00E-06	Cell rescue, defence and virulence
Contig2305_at	Methyljasmonate-inducible lipoxygenase 2	3.45	up[a]	0	Cell rescue, defence and virulence
Contig4324_at	Chitinase	3.31	up[c]	1.03E-07	Cell rescue, defence and virulence
Contig3746_at	Harpin induced gene 1 homolog	2.80	up[c]	8.47E-07	Cell rescue, defence and virulence
Contig34_s_at	Putative proteinase inhibitor	2.77	up[c]	0.04	Cell rescue, defence and virulence
Contig19921_at	Immediate-early fungal elicitor protein CMPG1	2.58	up[c]	0	Cell rescue, defence and virulence
rbags15p13_s_at	23 kDa jasmonate-induced protein	2.48	up[c]	0.04	Cell rescue, defence and virulence
Contig2210_at	Pathogenesis-related protein 1 precursor	2.45	up[c]	2.00E-05	Cell rescue, defence and virulence
Contig5369_at	Pathogenesis-related protein 1	2.40	up[c]	6.43E-06	Cell rescue, defence and virulence
Contig3380_s_at	Subtilisin-chymotrypsin inhibitor 2	2.31	up[c]	0	Cell rescue, defence and virulence
Contig2163_at	Pathogen-induced protein WIR1A	2.26	up[c]	1.69E-06	Cell rescue, defence and virulence
HV14J15u_s_at	Putative beta-1,3-glucanase	2.24	up[c]	0	Cell rescue, defence and virulence
Contig2088_s_at	Bowman-birk type trypsin inhibitor	2.24	up[c]	0	Cell rescue, defence and virulence
Contig8905_at	Xylanase inhibitor protein I	2.24	up[c]	4.05E-06	Cell rescue, defence and virulence
HVSMEb0010B05r2_x_at	Thionin BTH7 precursor	2.16	up[a]	1.50E-05	Cell rescue, defence and virulence
Contig15553_at	Putative beta-1,3-glucanase	2.15	up[a]	6.93E-07	Cell rescue, defence and virulence
EBro03_SQ003_J21_at	Putative peroxidase	2.13	up[c]	0	Cell rescue, defence and virulence

HV_CEb0002J23r2_s_at	Blue copper binding protein	2.10	up[c]	3.27E-06	Cell rescue, defence and virulence
Contig4324_s_at	Chitinase	2.09	up[c]	8.19E-06	Cell rescue, defence and virulence
Contig17047_at	Putative stripe rust resistance protein Yr10	2.06	up[a]	1.69E-06	Cell rescue, defence and virulence
Contig6547_at	Stem rust resistance protein Rpg1	2.05	up[c]	7.30E-07	Cell rescue, defence and virulence
Contig3315_s_at	Drought-induced hydrophobic protein	1.97	up[c]	3.91E-07	Cell rescue, defence and virulence
Contig11509_at	Putative peroxidase	1.96	up[c]	4.86E-05	Cell rescue, defence and virulence
HP01B09w_at	WIR1 protein	1.95	up[c]	3.59E-05	Cell rescue, defence and virulence
Contig2992_s_at	Chitinase	1.85	up[c]	6.00E-05	Cell rescue, defence and virulence
Contig10142_at	Dehydration-responsive protein	1.80	up[c]	0	Cell rescue, defence and virulence
Contig634_at	Benzothiadiazole-induced protein (WCI-5)	1.80	up[c]	3.38E-05	Cell rescue, defence and virulence
Contig9917_at	WIR1 protein	1.74	up[a]	6.52E-06	Cell rescue, defence and virulence
Contig12574_at	Lipoxygenase	1.71	up[b]	0	Cell rescue, defence and virulence
Contig1582_x_at	Thionin precursor	1.65	up[a]	0	Cell rescue, defence and virulence
Contig2243_at	Wheat aluminum induced protein wali 5	1.58	up[c]	2.64E-05	Cell rescue, defence and virulence
Contig3744_s_at	Harpin induced gene 1 homolog	1.58	up[c]	0	Cell rescue, defence and virulence
Contig1805_s_at	Phenylalanine ammonia-lyase	1.57	up[c]	0.01	Cell rescue, defence and virulence
Contig1636_at	Glucan endo-1,3-beta-glucosidase GII precursor	1.46	up[a]	0	Cell rescue, defence and virulence
rbah13p07_s_at	Peroxidase	1.45	up[c]	4.62E-06	Cell rescue, defence and virulence
Contig13544_at	Putative Avr9/Cf-9 rapidly elicited protein 231	1.42	up[c]	0	Cell rescue, defence and virulence
Contig9632_at	Glutathione S-transferase	1.41	up[c]	6.92E-06	Cell rescue, defence and virulence
Contig1639_at	Glucan endo-1,3-beta-glucosidase GII precursor	1.40	up[a]	0	Cell rescue, defence and virulence
Contig538_at	Benzothiadiazole-induced protein (WCI-5)	1.36	up[c]	0.01	Cell rescue, defence and virulence
Contig10193_at	Elicitor-responsive protein	1.35	up[c]	1.06E-05	Cell rescue, defence and virulence
HVSMEn0015O15f_s_at	Putative respiratory burst oxidase	1.32	up[b]	0.01	Cell rescue, defence and virulence
HVSMEa0011L14r2_s_at	Glutathione S-transferase	1.29	up[c]	2.82E-05	Cell rescue, defence and virulence
Contig6230_at	Putative nematode-resistance protein	1.26	up[a]	0	Cell rescue, defence and virulence
Contig939_s_at	Pathogen-induced protein WIR1A	1.21	up[a]	3.38E-05	Cell rescue, defence and virulence
Contig2990_at	Chitinase	1.21	up[c]	0	Cell rescue, defence and virulence
HVSMEf0020A12r2_s_at	Lipoxygenase	1.19	up[c]	0	Cell rescue, defence and virulence
Contig813_at	Pathogen-induced protein WIR1A	1.18	up[a]	0	Cell rescue, defence and virulence
Contig14679_at	Xylanase inhibitor	1.18	up[c]	0	Cell rescue, defence and virulence
HVSMEb0006O01r2_at	Mlo3	1.17	up[c]	0	Cell rescue, defence and virulence
Contig1852_at	Peroxidase 7	1.16	up[c]	0.02	Cell rescue, defence and virulence
HVSMEf0019G16r2_at	Putative copper homeostasis factor	1.16	up[a]	0	Cell rescue, defence and virulence

Contig7415_at	Putative glutathione transferase	1.14	up[c]	0	Cell rescue, defence and virulence
Contig2306_s_at	Methyljasmonate-inducible lipoxygenase 2	1.10	up[a]	0	Cell rescue, defence and virulence
HVSMEb0017H11f_at	Putative PrMC3	1.10	up[a]	0.01	Cell rescue, defence and virulence
Contig2112_at	Peroxidase	1.09	up[c]	0	Cell rescue, defence and virulence
Contig12649_at	Cell death associated protein	1.07	up[c]	0	Cell rescue, defence and virulence
Contig2213_s_at	Pathogenesis-related protein bpr1-1 precursor	1.05	up[c]	0.01	Cell rescue, defence and virulence
HX14B03r_at	TMV response-related gene product	1.02	up[c]	0	Cell rescue, defence and virulence
Contig10004_at	Putative thaumatin-like protein	1.01	up[c]	0	Cell rescue, defence and virulence
Contig3901_s_at	Cysteine proteinase precursor	-1.22	down[a]	0.01	Cell rescue, defence and virulence
Contig2427_at	Putative acid phosphatase	4.85	up[a]	1.23E-07	Cellular communication/signal transduction
EBro08_SQ004_I20_at	EF hand family protein	3.84	up[c]	5.00E-09	Cellular communication/signal transduction
Contig13114_at	Putative cynase	2.73	up[c]	3.96E-06	Cellular communication/signal transduction
AJ250283_at	Putative calcium binding EF-hand protein	2.71	up[a]	1.98E-07	Cellular communication/signal transduction
Contig8635_at	Vacuolar targeting receptor bp-80	2.57	up[a]	3.49E-07	Cellular communication/signal transduction
Contig8829_at	Probable calcium-binding protein	2.13	up[c]	0	Cellular communication/signal transduction
Contig2433_s_at	Putative acid phosphatase	2.01	up[b]	0	Cellular communication/signal transduction
Contig9265_at	Putative serine/threonine phosphatase type 2c	2.00	up[c]	0	Cellular communication/signal transduction
Contig8468_at	Putative calmodulin-binding protein	1.78	up[c]	4.15E-05	Cellular communication/signal transduction
Contig10323_at	Putative serine/threonine phosphatase	1.74	up[c]	7.68E-07	Cellular communication/signal transduction
Contig14350_at	Putative receptor-protein kinase	1.58	up[c]	3.04E-06	Cellular communication/signal transduction
Contig2430_at	Putative acid phosphatase	1.55	up[a]	0	Cellular communication/signal transduction
Contig8551_at	BTH-induced protein phosphatase 2C 2 K2 form	1.55	up[a]	0	Cellular communication/signal transduction
HVSMEi0002K06f_x_at	Putative acid phosphatase	1.54	up[b]	0	Cellular communication/signal transduction
Contig6986_at	Putative protein kinase	1.48	up[c]	8.09E-05	Cellular communication/signal transduction
Contig14243_at	Serine/threonine-specific receptor protein kinase-like	1.45	up[c]	0	Cellular communication/signal transduction
EBro08_SQ008_N10_at	Receptor-like protein kinase like	1.45	up[c]	0	Cellular communication/signal transduction
Contig5761_s_at	Calmodulin-like protein	1.44	up[c]	4.05E-06	Cellular communication/signal transduction
Contig19256_at	NPK1-related protein kinase-like protein	1.44	up[c]	0.01	Cellular communication/signal transduction
bah24p14_at	RING/C3HC4/PHD zinc finger-like protein	1.32	up[c]	0	Cellular communication/signal transduction
Contig24926_at	Putative leucine rich repeat containing protein kinase	1.32	up[a]	0	Cellular communication/signal transduction
Contig13905_at	Putative receptor-like protein kinase	1.29	up[c]	3.66E-05	Cellular communication/signal transduction
Contig23368_at	Putative S-receptor kinase	1.23	up[a]	4.67E-05	Cellular communication/signal transduction
HVSMEf0011J01r2_s_at	Putative receptor-like protein kinase	1.20	up[c]	8.81E-06	Cellular communication/signal transduction
Contig18914_at	Putative receptor serine/threonine kinase	1.14	up[a]	8.65E-05	Cellular communication/signal transduction

Contig11653_s_at	EF hand family protein	1.14	up[c]	0.01	Cellular communication/signal transduction
Contig21234_at	CBL-interacting protein kinase	1.13	up[c]	2.80E-05	Cellular communication/signal transduction
Contig7061_s_at	Putative receptor-like protein kinase	1.12	up[a]	0	Cellular communication/signal transduction
Contig14875_at	Calmodulin-binding protein	1.11	up[a]	6.64E-05	Cellular communication/signal transduction
HW06H18u_s_at	Putative protein kinase	1.10	up[a]	0	Cellular communication/signal transduction
HV_CEb0024B09r2_s_at	Auxin-responsive protein IAA6	1.07	up[a]	0	Cellular communication/signal transduction
HV_CEb0024B09r2_s_at	Auxin-responsive protein IAA6	1.07	up[a]	0.01	Cellular communication/signal transduction
Contig17030_at	Putative protein kinase	1.07	up[c]	0	Cellular communication/signal transduction
Contig12245_at	NBS-LRR-like protein	1.04	up[c]	0.01	Cellular communication/signal transduction
Contig20457_at	Putative PAP-specific phosphatase	1.03	up[c]	4.62E-06	Cellular communication/signal transduction
Contig24882_at	Receptor-like protein kinase	1.03	up[a]	1.32E-05	Cellular communication/signal transduction
HM11A01r_s_at	Putative CBL-interacting protein kinase	1.02	up[c]	0	Cellular communication/signal transduction
Contig11424_at	Probable calcium-binding protein	1.01	up[b]	0.01	Cellular communication/signal transduction
Contig12732_at	Tyrosine phosphatase	1.00	up[c]	0	Cellular communication/signal transduction
Contig6707_at	Putative sugar transporter	2.61	up[c]	1.53E-06	Cellular transport, transport facilitation and transport routes
Contig11332_at	Putative major facilitator superfamily antiporter	2.14	up[a]	7.52E-05	Cellular transport, transport facilitation and transport routes
Contig23909_at	Putative peptide transport protein	1.79	up[a]	0	Cellular transport, transport facilitation and transport routes
Contig8122_at	Putative ABC transporter protein	1.41	up[c]	3.69E-05	Cellular transport, transport facilitation and transport routes
Contig19175_at	Multidrug resistance protein 1	1.33	up[b]	0	Cellular transport, transport facilitation and transport routes
Contig6706_at	Putative sugar transporter	1.29	up[c]	1.22E-05	Cellular transport, transport facilitation and transport routes
Contig25228_at	Transmembrane transport protein-like	1.28	up[a]	0	Cellular transport, transport facilitation and transport routes
Contig9110_at	Putative C2 domain-containing protein	1.12	up[c]	0	Cellular transport, transport facilitation and transport routes
Contig13096_at	Putative UDP-galactose/UDP-glucose transporter	1.05	up[c]	0	Cellular transport, transport facilitation and transport routes
Contig22550_at	Amino acid permease	1.05	up[a]	0	Cellular transport, transport facilitation and transport routes
Contig17453_at	Putative multidrug resistance protein	1.04	up[c]	0.02	Cellular transport, transport facilitation and transport routes
Contig9463_at	Putative C2 domain-containing protein	1.04	up[c]	1.10E-05	Cellular transport, transport facilitation and transport routes
Contig22370_at	Syntaxin	1.01	up[c]	0	Cellular transport, transport facilitation and transport routes
Contig16352_at	Putative zinc transporter protein	1.00	up[a]	0.01	Cellular transport, transport facilitation and transport routes
Contig14732_at	MutT/nudix-like	1.61	up[a]	0.01	Development
rbaal22i06_at	Putative mtN3 protein-like	1.51	up[a]	8.11E-05	Development
Contig18182_at	Flowering promoting factor-like 1	1.32	up[a]	4.83E-05	Development
Contig4092_at	Spermidine synthase	1.10	up[a]	0	Development
Contig11160_at	Nudix hydrolase 8	1.09	up[b]	0	Development
Contig347_s_at	Chlorophyll a/b-binding protein	-1.04	down[c]	0.04	Energy

HVSMEl0005L10f_s_at	Putative copine I	1.58	up[c]	8.85E-05	Interaction with the cellular environment
HVSMEg0002E24r2_s_at	Putative phi-1	2.09	up[c]	0	Interaction with the environment
Contig6582_at	Phi-1	1.00	up[a]	0.01	Interaction with the environment
Contig14067_at	Nodulin-like family protein	-1.20	down[a]	2.62E-05	Interaction with the environment
Contig20235_s_at	Lipase-like protein	4.63	up[b]	3.91E-07	Metabolism
Contig3096_s_at	Allene oxide synthase	3.45	up[a]	8.47E-07	Metabolism
HVSMEb0005F19r2_at	Lipase-like protein	2.98	up[b]	8.68E-05	Metabolism
Contig393_at	Alcohol dehydrogenase	2.73	up[a]	1.68E-09	Metabolism
Contig4273_at	Iron/ascorbate-dependent oxidoreductase	2.72	up[c]	2.00E-05	Metabolism
Contig3097_at	Allene oxide synthase	2.68	up[c]	0	Metabolism
Contig9663_s_at	Transferase family protein	2.43	up[c]	0	Metabolism
Contig4260_at	Cinnamyl alcohol dehydrogenase	2.30	up[c]	1.29E-06	Metabolism
HVSMEh0081I20r2_s_at	Cinnamyl alcohol dehydrogenase	2.09	up[c]	2.36E-06	Metabolism
Contig21604_at	Glutathione synthetase	1.88	up[a]	0.01	Metabolism
HM05N11r_at	Cinnamyl alcohol dehydrogenase	1.85	up[c]	0	Metabolism
Contig2143_s_at	UDP-glucose dehydrogenase	1.75	up[c]	0	Metabolism
Contig26313_at	Putative cytochrome P450	1.72	up[c]	1.04E-05	Metabolism
HVSMEa0019P15r2_at	Formate dehydrogenase	1.69	up[c]	6.23E-06	Metabolism
Contig6407_s_at	Putative indole-3-glycerol phosphate synthase	1.67	up[c]	0	Metabolism
Contig2639_at	1-aminocyclopropane-1-carboxylate oxidase	1.64	up[c]	5.42E-05	Metabolism
Contig3212_s_at	Flavin containing polyamine oxidase precursor	1.63	up[b]	0	Metabolism
Contig12075_at	Flavonol 3-sulfotransferase	1.60	up[c]	1.76E-05	Metabolism
Contig3691_at	Aleurone ribonuclease	1.58	up[c]	0	Metabolism
Contig25479_at	Leucoanthocyanidin dioxygenase-like protein	1.57	up[c]	0	Metabolism
HS07I12u_s_at	Monooxygenase 2	1.54	up[c]	2.43E-05	Metabolism
Contig5638_at	Agmatine coumaroyltransferase	1.47	up[c]	0	Metabolism
Contig7736_at	Lactoylglutathione lyase family protein	1.42	up[c]	0	Metabolism
Contig9171_s_at	Putative polygalacturonase	1.41	up[a]	8.78E-05	Metabolism
Contig6406_at	Putative indole-3-glycerol phosphate synthase	1.40	up[c]	0	Metabolism
Contig14830_at	Putative glucosyltransferase	1.36	up[c]	8.65E-05	Metabolism
HVSMEm0001O15r2_s_at	Putative 1-aminocyclopropane-1-carboxylate oxidase	1.31	up[a]	0	Metabolism
Contig8518_s_at	Lipase-like protein	1.30	up[a]	5.20E-05	Metabolism
Contig5554_at	Putative hydrolase	1.30	up[c]	1.57E-05	Metabolism
Contig11701_at	10-deacetylbaccatin III 10-O-acetyltransferase	1.27	up[c]	0	Metabolism

Contig9468_at	Glycosyl transferase-like protein	1.26	up[a]	0	Metabolism
Contig6611_at	Similar to lipases	1.23	up[a]	0	Metabolism
Contig2642_at	1-aminocyclopropane-1-carboxylate oxidase	1.18	up[c]	0	Metabolism
Contig25368_at	Putative flavonol glucosyltransferase	1.18	up[c]	0	Metabolism
HVSMEm0001J08r2_s_at	Putative glycerophosphodiester phosphodiesterase	1.17	up[a]	0	Metabolism
Contig3332_at	Apyrase-like protein	1.16	up[b]	0	Metabolism
Contig11766_at	Putative metallophosphatase	1.15	up[c]	9.09E-05	Metabolism
Contig5217_at	Quinone-oxidoreductase QR2	1.14	up[c]	0.01	Metabolism
Contig16112_at	Uridine kinase/uracil phosphoribosyltransferase	1.14	up[c]	0	Metabolism
Contig17006_at	Putative benzoyl coenzyme A, benzyl alcohol benzoyl transferase	1.11	up[c]	0	Metabolism
EBro03_SQ004_A01_s_at	Prephenate dehydratase	1.10	up[c]	0	Metabolism
Contig2148_at	Putative UDP-glucose dehydrogenase	1.09	up[c]	1.26E-05	Metabolism
Contig2329_x_at	12-oxophytodienoate reductase (OPR1)	1.07	up[c]	0	Metabolism
Contig5059_s_at	RNase S-like protein	1.05	up[b]	0.05	Metabolism
Contig14826_at	Putative glucosyltransferase	1.04	up[c]	0	Metabolism
HB19M13r_s_at	Metallo-beta-lactamase-like	1.04	up[a]	0	Metabolism
Contig2918_s_at	UDP-glucuronic acid decarboxylase	1.04	up[c]	0	Metabolism
Contig5879_at	Putative phosphoserine aminotransferase	1.04	up[c]	0	Metabolism
Contig3308_at	Glucose-6-phosphate dehydrogenase	1.02	up[c]	0	Metabolism
Contig10756_at	Monooxygenase 2	1.00	up[c]	0	Metabolism
Contig13674_at	Beta-D-xylosidase	-1.06	down[c]	0.02	Metabolism
AB011266_at	Nicotianamine synthase	-1.09	down[c]	0	Metabolism
HVSMEn0021L12r2_at	Aspartic proteinase nepenthesin-1 precursor	-1.27	down[c]	5.25E-06	Metabolism
Contig14292_at	Isoflavone reductase	-1.65	down[c]	0.02	Metabolism
Contig13091_s_at	Aspartic-type endopeptidase/ pepsin A	2.79	up[c]	4.77E-09	Protein fate (folding, modification, destination)
Contig6229_s_at	Ubiquitin-specific protease 5 (UBP5)	2.68	up[a]	1.68E-06	Protein fate (folding, modification, destination)
Contig4942_at	ATP-dependent Clp protease	1.62	up[c]	5.58E-06	Protein fate (folding, modification, destination)
Contig17122_at	Chaperone protein dnaJ	1.21	up[c]	0	Protein fate (folding, modification, destination)
Contig91_at	Endoplasmin homolog precursor	1.20	up[c]	0	Protein fate (folding, modification, destination)
Contig20144_s_at	GTP-binding protein Rab6	1.06	up[c]	0	Protein fate (folding, modification, destination)
Contig25239_at	Putative LMW heat shock protein	1.45	up[c]	0	Protein synthesis
Contig17452_at	Putative methionyl-tRNA synthetase	1.02	up[a]	0	Protein synthesis
Contig17974_at	Metal ion binding protein	1.04	up[c]	0	Protein with binding function
Contig6075_at	Storage protein	3.85	up[b]	0	Storage

Contig15718_at	Patatin-like phospholipase family protein	1.42	up[c]	2.60E-05	Storage
Contig4386_at	WRKY transcription factor	3.55	up[c]	2.82E-09	Transcription
Contig21110_at	WRKY family transcription factor	3.35	up[c]	2.14E-06	Transcription
Contig18088_at	Zinc finger protein 1	3.13	up[c]	7.24E-07	Transcription
Contig12005_at	WRKY5 transcription factor	2.96	up[c]	1.52E-05	Transcription
Contig26350_at	FT-like protein 4	2.88	up[c]	1.71E-06	Transcription
S0001000055P18F1_s_at	WRKY transcription factor 45	2.87	up[c]	3.17E-08	Transcription
Contig7722_at	Ethylene responsive element binding factor3	2.67	up[a]	5.71E-05	Transcription
Contig23697_at	DNA-binding protein ABF1	2.65	up[c]	3.46E-07	Transcription
Contig15957_at	WRKY transcription factor 45	2.62	up[c]	1.52E-07	Transcription
Contig19506_at	Putative zinc finger protein	2.10	up[a]	0	Transcription
Contig7031_at	bHLH protein	2.07	up[a]	2.72E-05	Transcription
Contig6759_at	Putative CCCH-type zinc finger protein	1.93	up[a]	3.72E-05	Transcription
EBro02_SQ004_H10_at	WRKY transcription factor 76	1.85	up[c]	3.91E-07	Transcription
HM11K07r_at	Putative RING-H2 finger protein	1.74	up[a]	5.04E-07	Transcription
Contig20981_at	C2H2 zinc finger protein	1.63	up[c]	1.69E-05	Transcription
Contig10167_at	WRKY transcription factor	1.60	up[c]	0	Transcription
Contig2479_at	DRE-binding protein 1A	1.53	up[a]	0.01	Transcription
Contig7517_at	Putative WRKY DNA binding protein	1.40	up[c]	3.38E-05	Transcription
Contig6636_at	Ethylene responsive element binding factor3	1.34	up[a]	0	Transcription
Contig13355_at	Basic helix-loop-helix (BHLH) family protein-like	1.26	up[c]	0	Transcription
Contig17684_at	GATA-1 zinc finger protein	1.24	up[c]	6.78E-06	Transcription
Contig1783_at	Multiple stress-responsive zinc-finger protein	1.22	up[a]	0	Transcription
Contig3361_at	NAC domain transcription factor	1.22	up[a]	6.64E-05	Transcription
Contig7481_at	DNA-binding protein RAV1-like	1.22	up[a]	2.68E-05	Transcription
Contig11225_at	Zim motif family protein	1.15	up[c]	0	Transcription
Contig10472_at	AP2-related transcription factor	1.12	up[a]	5.27E-05	Transcription
Contig13103_at	bHLH protein	1.10	up[a]	0	Transcription
Contig4815_at	ZIM motif family protein	1.03	up[c]	7.87E-05	Transcription
Contig5841_at	Myb4 transcription factor	1.03	up[c]	2.49E-05	Transcription
Contig14085_at	Putative RING-H2 finger protein	1.01	up[a]	0	Transcription
HB25K10r_at	Putative WRKY2 protein	1.01	up[a]	0	Transcription
Contig12925_at	SCARECROW-like protein	1.01	up[a]	0	Transcription
Contig14008_at	None	4.26	up[c]	3.46E-07	Unclassified

HVSMEb0002K02r2_s_at	None	3.72	up[b]	9.00E-08	Unclassified
Contig9874_s_at	None	3.58	up[c]	3.13E-06	Unclassified
EBro04_SQ003_G13_at	None	3.34	up[c]	2.82E-09	Unclassified
Contig14625_at	None	3.25	up[a]	0	Unclassified
Contig10441_at	None	3.18	up[c]	3.91E-07	Unclassified
Contig5303_at	None	3.11	up[c]	7.11E-06	Unclassified
Contig12321_at	None	3.08	up[c]	5.39E-06	Unclassified
Contig11611_at	None	2.94	up[c]	3.39E-06	Unclassified
Contig24662_at	None	2.89	up[c]	9.00E-08	Unclassified
HW02N10u_at	None	2.79	up[c]	9.00E-08	Unclassified
EBro01_SQ005_J04_at	None	2.76	up[c]	1.68E-06	Unclassified
Contig10096_at	None	2.58	up[a]	2.75E-05	Unclassified
Contig17926_at	None	2.50	up[c]	9.27E-07	Unclassified
HB20B10r_at	None	2.41	up[c]	0	Unclassified
Contig15795_at	None	2.24	up[c]	0	Unclassified
Contig25977_at	None	2.09	up[c]	4.62E-06	Unclassified
Contig2470_s_at	None	1.98	up[c]	0	Unclassified
Contig12724_at	None	1.85	up[c]	2.69E-06	Unclassified
Contig9863_at	None	1.85	up[c]	0	Unclassified
Contig11373_at	None	1.71	up[c]	7.08E-06	Unclassified
HD04G07u_s_at	None	1.71	up[c]	8.81E-06	Unclassified
HV_CEb0004G20r2_s_at	None	1.69	up[c]	1.10E-05	Unclassified
Contig26368_at	None	1.64	up[c]	2.57E-05	Unclassified
Contig7315_at	None	1.64	up[c]	0.01	Unclassified
Contig12044_at	None	1.64	up[c]	0	Unclassified
HVSMEb0005E07r2_s_at	None	1.62	up[c]	1.22E-05	Unclassified
Contig5302_at	None	1.57	up[c]	0	Unclassified
HT07C05r_s_at	None	1.54	up[a]	0	Unclassified
HD04H12r_at	None	1.53	up[a]	2.66E-06	Unclassified
Contig6065_s_at	None	1.52	up[c]	0	Unclassified
EBro02_SQ006_C05_at	None	1.39	up[c]	0	Unclassified
Contig11920_s_at	None	1.38	up[a]	0	Unclassified
Contig24039_at	None	1.38	up[a]	4.24E-05	Unclassified
Contig21297_at	None	1.37	up[a]	0	Unclassified

rbaal1k11_s_at	None	1.31	up[c]	8.69E-05	Unclassified
HW02G06T_s_at	None	1.30	up[b]	0	Unclassified
EBro02_SQ006_L04_at	None	1.29	up[c]	0	Unclassified
Contig1185_at	None	1.27	up[a]	0	Unclassified
EBro02_SQ006_L04_x_at	None	1.21	up[c]	0	Unclassified
Contig9923_at	None	1.19	up[b]	0.03	Unclassified
HVSMEn0007B19f_s_at	None	1.18	up[a]	0	Unclassified
Contig11161_s_at	None	1.16	up[b]	0	Unclassified
Contig23016_at	None	1.14	up[c]	0	Unclassified
HVSMEf0021H03r2_s_at	None	1.13	up[c]	2.68E-05	Unclassified
HR01A09u_at	None	1.13	up[c]	6.64E-05	Unclassified
Contig11919_at	None	1.12	up[a]	0	Unclassified
EBpi01_SQ001_G04_at	None	1.11	up[c]	4.60E-05	Unclassified
Contig1159_s_at	None	1.11	up[a]	0	Unclassified
EBpi01_SQ002_N08_at	None	1.11	up[c]	0	Unclassified
Contig9922_s_at	None	1.08	up[b]	0.04	Unclassified
EBro03_SQ006_M21_at	None	1.08	up[a]	5.42E-05	Unclassified
Contig477_at	None	1.07	up[c]	0	Unclassified
Contig11283_at	None	1.07	up[a]	0	Unclassified
Contig7343_s_at	None	1.07	up[c]	6.71E-05	Unclassified
Contig18290_at	None	1.05	up[c]	0	Unclassified
Contig16826_at	None	1.04	up[c]	0	Unclassified
HVSMEb0005E07r2_at	None	1.02	up[c]	0	Unclassified
Contig7378_at	None	1.02	up[c]	0	Unclassified
Contig11003_at	None	-1.19	down[a]	0.01	Unclassified
HVSMEf0013I09r2_at	None	-1.55	down[c]	2.36E-06	Unclassified
rbaal21f05_s_at	None	-2.00	down[a]	0	Unclassified
Contig11615_s_at	Putative YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	3.60	up[c]	1.26E-06	Unknown
Contig15374_at	VQ motif family protein	3.42	up[c]	8.36E-07	Unknown
HVSMEb0011I17r2_s_at	Expressed protein	3.10	up[c]	5.61E-05	Unknown
Contig6170_s_at	Unknown protein	3.01	up[b]	4.62E-06	Unknown
Contig13615_at	VQ motif family protein	2.98	up[c]	8.70E-09	Unknown
Contig6169_at	Unknown protein	2.95	up[b]	1.26E-06	Unknown
Contig4976_at	Expressed protein	2.72	up[c]	2.27E-05	Unknown

HVSMEb0007D15r2_at	VQ motif family protein	2.67	up[c]	3.91E-07	Unknown
Contig12216_at	Hypothetical protein	2.43	up[a]	2.85E-06	Unknown
Contig11805_at	Putative protein	2.38	up[c]	2.80E-05	Unknown
Contig10407_at	Hypothetical protein	2.18	up[c]	0	Unknown
Contig10137_at	Unknown protein	2.17	up[c]	9.00E-08	Unknown
HW03O22u_s_at	Putative secretory protein	2.13	up[c]	0	Unknown
Contig4641_s_at	Hypothetical protein	2.13	up[a]	7.29E-07	Unknown
Contig14712_at	Putative protein	1.95	up[c]	0	Unknown
EBro04_SQ003_B10_s_at	Embryonic abundant protein-like	1.94	up[a]	9.00E-08	Unknown
Contig10192_at	Putative protein	1.94	up[a]	0	Unknown
Contig15764_at	Hypothetical protein	1.94	up[c]	0	Unknown
Contig22839_at	Embryo-abundant protein EMB	1.92	up[c]	7.30E-06	Unknown
Contig11993_at	Expressed protein	1.92	up[a]	0	Unknown
Contig12919_s_at	Hypothetical protein	1.90	up[c]	0	Unknown
Contig3743_at	Hypothetical protein	1.67	up[c]	1.40E-05	Unknown
Contig358_at	Secretory protein	1.65	up[c]	5.06E-06	Unknown
Contig6495_at	Expressed protein	1.65	up[c]	4.05E-06	Unknown
Contig6656_at	Hypothetical protein	1.60	up[b]	3.24E-05	Unknown
Contig6066_s_at	Unknown protein	1.59	up[c]	3.54E-05	Unknown
HVSMEf0019G08r2_s_at	Putative protein	1.51	up[c]	0	Unknown
Contig6013_at	Putative uncharacterized protein	1.44	up[a]	2.14E-06	Unknown
Contig17964_at	Putative protein	1.39	up[c]	0	Unknown
HP01E21w_s_at	Expressed protein	1.36	up[c]	0	Unknown
Contig13852_at	Expressed protein	1.35	up[b]	2.00E-05	Unknown
Contig19915_at	Cotton fiber expressed protein-like protein	1.33	up[a]	0	Unknown
Contig18427_s_at	Expressed protein	1.19	up[c]	3.38E-05	Unknown
Contig13712_at	Unknown protein	1.17	up[a]	0	Unknown
Contig10152_at	Putative protein	1.16	up[c]	0	Unknown
Contig6067_at	Unknown protein	1.14	up[c]	0	Unknown
Contig7598_at	Unknown protein	1.14	up[c]	0.01	Unknown
Contig23747_at	Expressed protein	1.13	up[c]	0	Unknown
Contig4640_s_at	Hypothetical protein	1.10	up[a]	6.82E-05	Unknown
Contig14095_at	Hypothetical protein	1.09	up[a]	0	Unknown
Contig10615_at	Hypothetical protein	1.04	up[c]	0.01	Unknown

Contig18037_at	Unknown protein	1.03	up[c]	0	Unknown
HX01N16w_s_at	Putative WD repeat protein	1.03	up[a]	0	Unknown
Contig14777_at	Hypothetical protein	1.01	up[c]	0	Unknown
rbags23g22_at	Embryogenesis transmembrane protein	1.01	up[a]	0	Unknown
HI02P10u_at	Putative protein	1.00	up[a]	0	Unknown
Contig5345_at	Uncharacterized protein	-1.04	down[a]	0.03	Unknown
Contig9506_at	PQ loop repeat domain containing protein	-1.04	down[a]	0.01	Unknown
Contig11985_at	Putative protein	-1.05	down[c]	0	Unknown